Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2025 – 07:37 PM EDT

PDB ID	:	9O3I / pdb_00009o3i
Title	:	Crystal structure of the wild-type Thermus thermophilus 70S ribosome in complex with ketolide telithromycin, mRNA, aminoacylated A-site Lys-tRNAlys, P-site fMRC-peptidyl-tRNAmet, and deacylated E-site tRNAlys at 2.80A resolution
Authors	:	Syroegin, E.A.; Aleksandrova, E.V.; Kruglov, A.A.; Paranjpe, M.N.; Svetlov, M.S.; Polikanov, Y.S.
Deposited on	:	2025-04-07
Resolution	:	2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

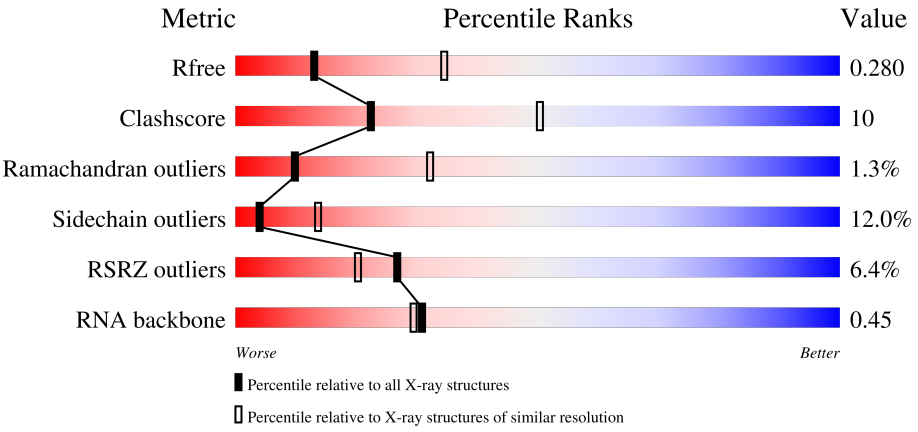
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3657 (2.80-2.80)
Clashscore	180529	4123 (2.80-2.80)
Ramachandran outliers	177936	4071 (2.80-2.80)
Sidechain outliers	177891	4073 (2.80-2.80)
RSRZ outliers	164620	3659 (2.80-2.80)
RNA backbone	3690	1037 (3.00-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1A	2915	4% 59% 32% 8%
1	2A	2915	3% 53% 35% 8%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

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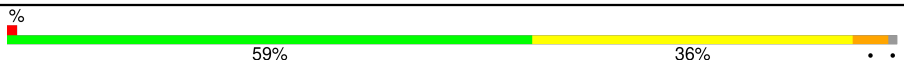
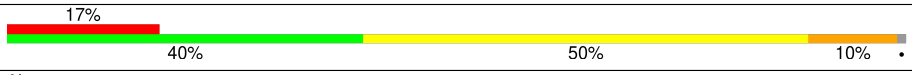
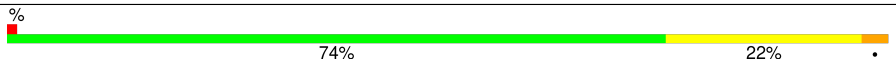
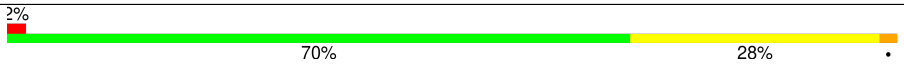
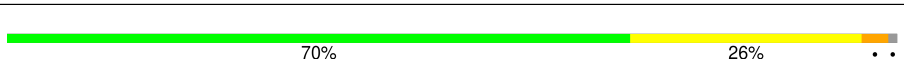
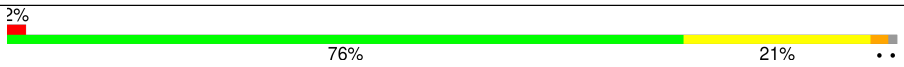
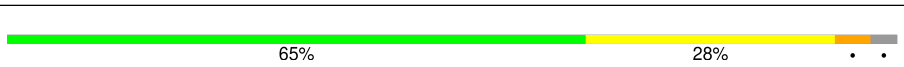
Mol	Chain	Length	Quality of chain
2	1B	121	
2	2B	121	
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
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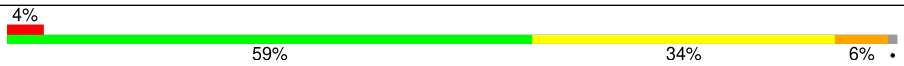
6	1G	182	
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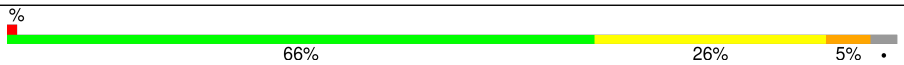
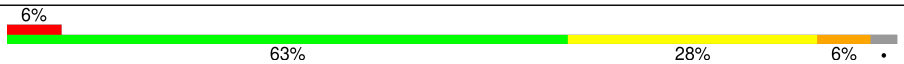
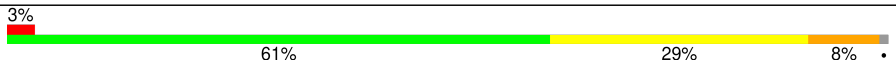
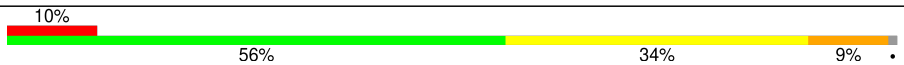
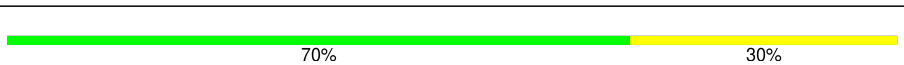
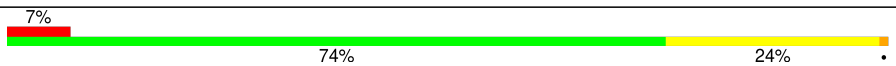
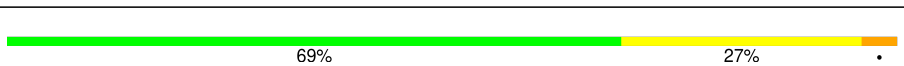
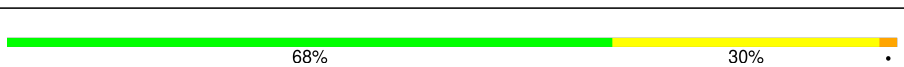
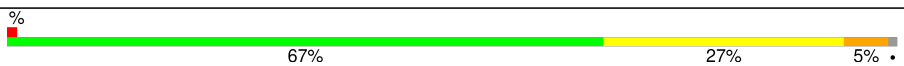
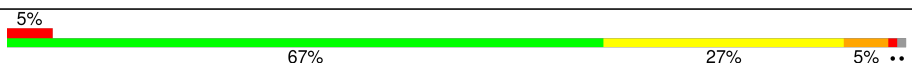
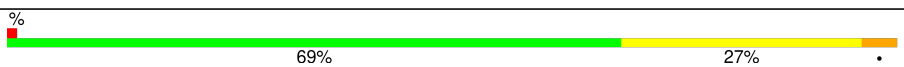
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
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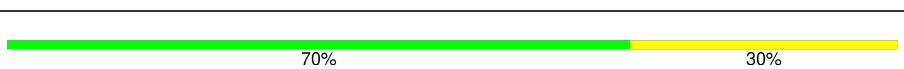
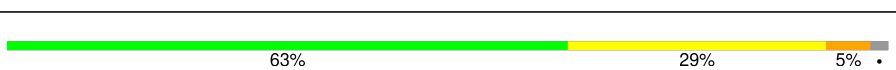
13	2R	118	
14	1S	112	

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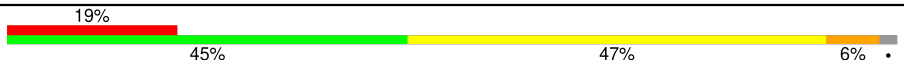
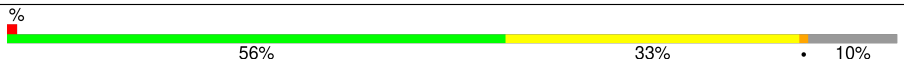
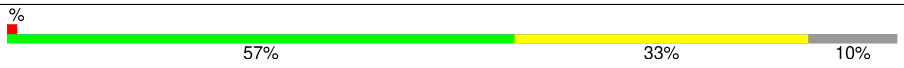
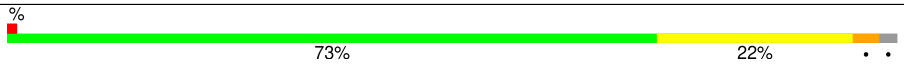
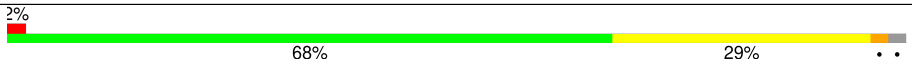
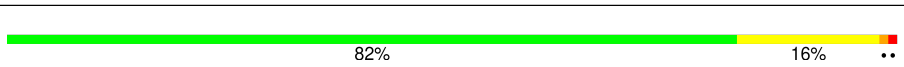
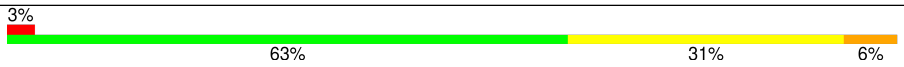
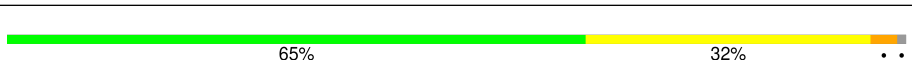
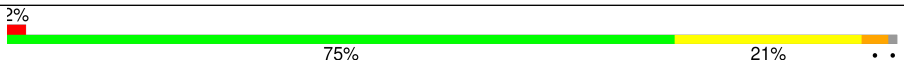
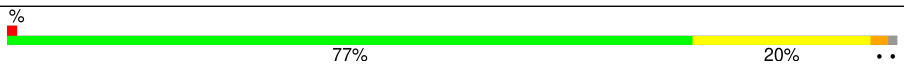
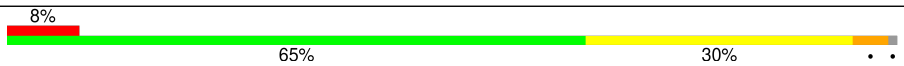
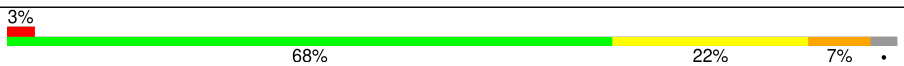
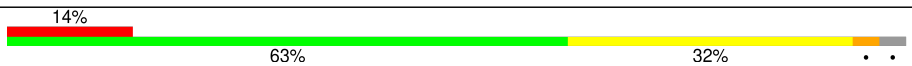
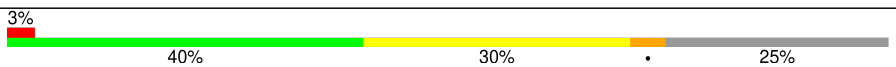
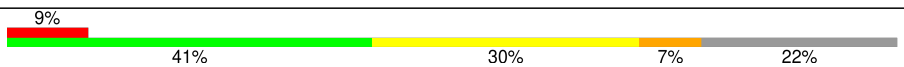
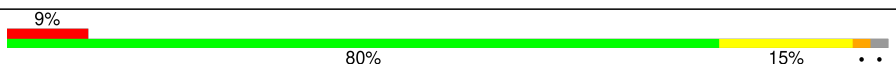
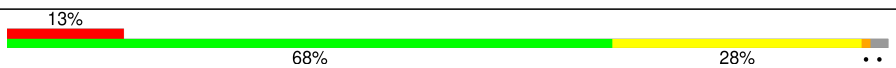
Mol	Chain	Length	Quality of chain
14	2S	112	
15	1T	146	
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
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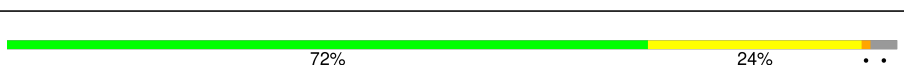
24	12	72	
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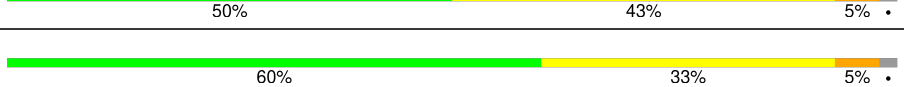
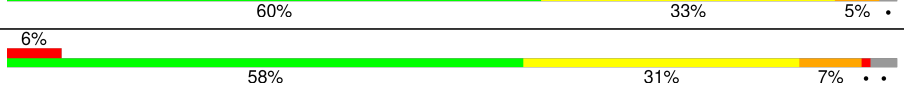
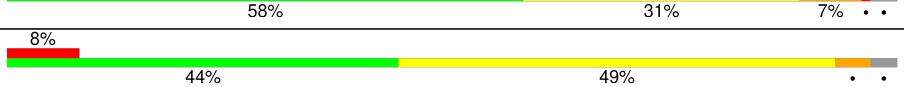
25	23	60	
26	14	71	
26	24	71	

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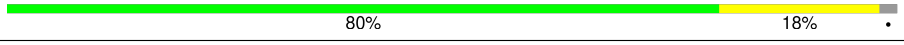
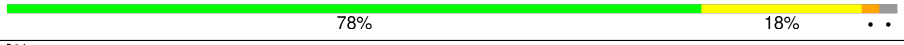
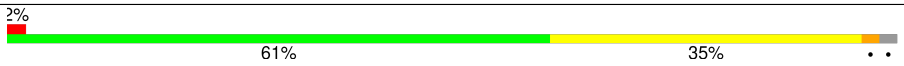
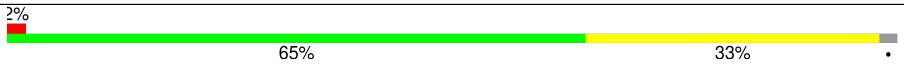
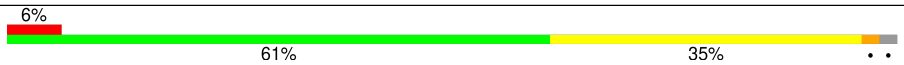
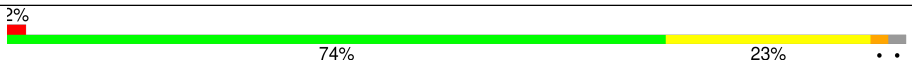
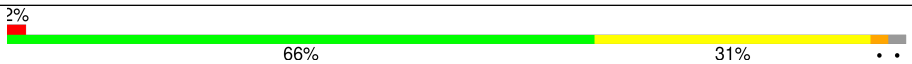
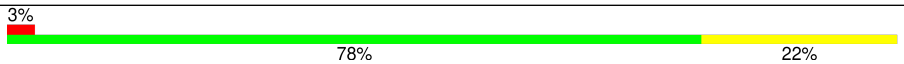
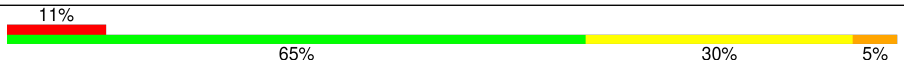
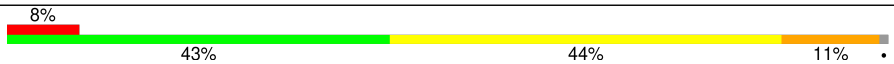
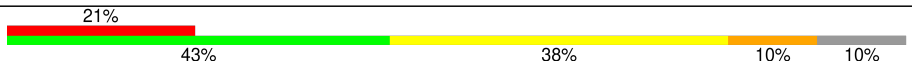
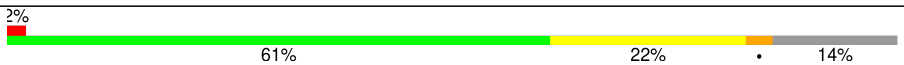
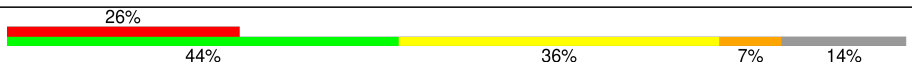
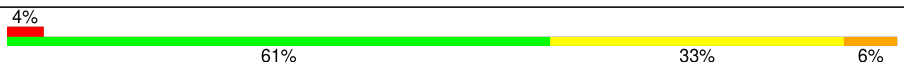
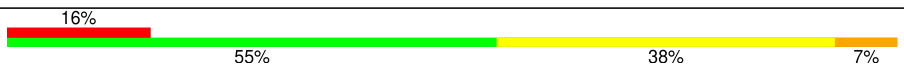
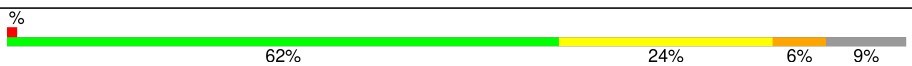
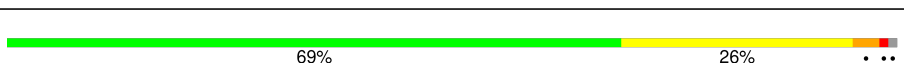
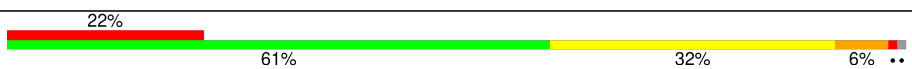
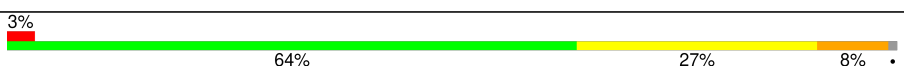
Mol	Chain	Length	Quality of chain
27	15	60	
27	25	60	
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	

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Mol	Chain	Length	Quality of chain
39	2h	138	14% 55% 40%
40	1i	128	11% 69% 27%
40	2i	128	45% 45% 47% 8%
41	1j	105	10% 50% 38% 8%
41	2j	105	26% 42% 42% 8% 9%
42	1k	129	5% 61% 24% 12%
42	2k	129	9% 61% 24% 12%
43	1l	132	6% 61% 27% 5% 8%
43	2l	132	11% 58% 30% 8%
44	1m	126	9% 60% 33%
44	2m	126	29% 44% 41% 11%
45	1n	61	8% 67% 28%
45	2n	61	54% 48% 39% 11%
46	1o	89	2% 66% 28%
46	2o	89	4% 67% 27%
47	1p	88	14% 55% 33% 6% 7%
47	2p	88	5% 57% 32% 5% 7%
48	1q	105	7% 66% 26% 6%
48	2q	105	12% 54% 33% 5% 6%
49	1r	88	2% 56% 22% 23%
49	2r	88	48% 27% 23%
50	1s	93	4% 63% 25% 11%
50	2s	93	26% 37% 43% 10% 11%
51	1t	106	10% 61% 26% 9%
51	2t	106	9% 60% 24% 7% 9%

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Mol	Chain	Length	Quality of chain
52	1u	27	11% 59% 22% 15%
52	2u	27	41% 41% 41% 15%
53	1v	24	12% 38% 12% 46%
53	2v	24	17% 8% 29% 17% 46%
54	1w	76	16% 30% 42% 24%
54	2w	76	18% 24% 50% 22%
55	1x	77	3% 43% 51% 6%
55	2x	77	9% 36% 55% 9%
56	1z	3	100%
56	2z	3	33% 33% 33% 33%
57	1y	76	9% 18% 42% 36%
57	2y	76	21% 18% 46% 33%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	MG	2A	3715	-	-	-	X
62	SF4	2d	303	-	-	X	-

2 Entry composition (i)

There are 63 unique types of molecules in this entry. The entry contains 299377 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2871	Total	C	N	O	P	0	0	0
			61852	27531	11572	19878	2871			
1	2A	2800	Total	C	N	O	P	0	0	0
			60322	26848	11284	19390	2800			

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2577	1146	476	835	120			
2	2B	120	Total	C	N	O	P	0	0	0
			2575	1146	476	833	120			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	1E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	2E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	1F	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	2F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1423	913	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1428	913	258	253	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1097	701	191	204	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1064	681	186	196	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	2O	122	Total 933	C 588	N 171	O 170	S 4	0	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total 1135	C 706	N 230	O 196	S 3	0	0	0
11	2P	149	Total 1135	C 706	N 230	O 196	S 3	0	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	1Q	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0
12	2Q	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	1R	118	Total 968	C 604	N 203	O 160	S 1	0	0	0
13	2R	118	Total 968	C 604	N 203	O 160	S 1	0	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total 873	C 550	N 174	O 149	0	0	0
14	2S	110	Total 870	C 549	N 173	O 148	0	0	0

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	1T	131	Total 1091	C 680	N 225	O 185	S 1	0	0	0
15	2T	131	Total 1083	C 675	N 224	O 183	S 1	0	0	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	1U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	2U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	1W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	2W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	1X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	2X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	154	Total	C	N	O	S	0	0	0
			1240	795	222	220	3			
21	2Z	160	Total	C	N	O	S	0	0	0
			1271	814	228	227	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
22	20	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
23	21	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	12	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	22	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	13	59	Total	C	N	O	0	0	0
			469	298	90	81			
25	23	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
27	25	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	16	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
28	26	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	17	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	27	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	18	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	19	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	29	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	2a	1503	Total	C	N	O	P	0	0	0
			32327	14396	5990	10438	1503			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
33	2b	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1548	973	301	273	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1655	1038	326	284	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			810	514	144	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			983	623	193	167			
40	2i	127	Total	C	N	O	0	0	0
			978	619	190	169			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			709	440	138	131			
41	2j	96	Total	C	N	O	0	0	0
			714	445	138	131			

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			829	516	155	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	1l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
43	2l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	123	Total	C	N	O	S	0	0	0
			958	592	198	166	2			
44	2m	122	Total	C	N	O	S	0	0	0
			950	586	197	165	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	1o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
46	2o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	1p	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
47	2p	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	1q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
48	2q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	1r	68	Total	C	N	O	0	0	0
			555	355	108	92			
49	2r	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
50	2s	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
51	2t	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	1u	23	Total	C	N	O	0	0	0
			199	122	48	29			
52	2u	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 53 is a RNA chain called MET-LYS-mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	13	Total	C	N	O	P	0	0	0
			283	128	59	83	13			
53	2v	13	Total	C	N	O	P	0	0	0
			283	128	59	83	13			

- Molecule 54 is a RNA chain called A-site Aminoacyl-tRNA Lys-tRNAlys.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1599	718	282	524	74	1			
54	2w	74	Total	C	N	O	P	S	0	0	0
			1599	718	282	524	74	1			

- Molecule 55 is a RNA chain called P-site Peptidyl-tRNA fMRC-tRNAcys RNA-part.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	77	Total	C	N	O	P	S	0	0	0
			1646	734	298	536	77	1			
55	2x	77	Total	C	N	O	P	S	0	0	0
			1646	734	298	536	77	1			

- Molecule 56 is a protein called P-site Peptidyl-tRNA fMRC-tRNAcys Peptide-part.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	1z	3	Total	C	N	O	S	0	0	0
			27	15	6	4	2			
56	2z	3	Total	C	N	O	S	0	0	0
			27	15	6	4	2			

- Molecule 57 is a RNA chain called E-site Deacylated tRNAlys.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
57	1y	74	Total	C	N	O	P	S	0	0	0
			1577	705	277	520	74	1			
57	2y	74	Total	C	N	O	P	S	0	0	0
			1577	705	277	520	74	1			

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	1A	1080	Total	Mg	0	0
			1080	1080		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1B	40	Total Mg 40 40	0	0
58	1D	12	Total Mg 12 12	0	0
58	1E	12	Total Mg 12 12	0	0
58	1F	11	Total Mg 11 11	0	0
58	1G	5	Total Mg 5 5	0	0
58	1N	6	Total Mg 6 6	0	0
58	1O	4	Total Mg 4 4	0	0
58	1P	9	Total Mg 9 9	0	0
58	1Q	7	Total Mg 7 7	0	0
58	1R	7	Total Mg 7 7	0	0
58	1S	1	Total Mg 1 1	0	0
58	1T	2	Total Mg 2 2	0	0
58	1U	10	Total Mg 10 10	0	0
58	1V	8	Total Mg 8 8	0	0
58	1W	7	Total Mg 7 7	0	0
58	1X	5	Total Mg 5 5	0	0
58	1Y	2	Total Mg 2 2	0	0
58	1Z	3	Total Mg 3 3	0	0
58	10	11	Total Mg 11 11	0	0
58	11	5	Total Mg 5 5	0	0
58	12	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	13	4	Total Mg 4 4	0	0
58	14	1	Total Mg 1 1	0	0
58	15	8	Total Mg 8 8	0	0
58	16	2	Total Mg 2 2	0	0
58	17	7	Total Mg 7 7	0	0
58	18	6	Total Mg 6 6	0	0
58	19	1	Total Mg 1 1	0	0
58	1a	209	Total Mg 209 209	0	0
58	1b	1	Total Mg 1 1	0	0
58	1d	1	Total Mg 1 1	0	0
58	1e	1	Total Mg 1 1	0	0
58	1f	2	Total Mg 2 2	0	0
58	1l	2	Total Mg 2 2	0	0
58	1m	1	Total Mg 1 1	0	0
58	1n	2	Total Mg 2 2	0	0
58	1p	2	Total Mg 2 2	0	0
58	1t	1	Total Mg 1 1	0	0
58	1v	1	Total Mg 1 1	0	0
58	1w	5	Total Mg 5 5	0	0
58	1x	12	Total Mg 12 12	0	0
58	2A	824	Total Mg 824 824	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	2B	19	Total Mg 19 19	0	0
58	2D	8	Total Mg 8 8	0	0
58	2E	7	Total Mg 7 7	0	0
58	2F	6	Total Mg 6 6	0	0
58	2G	1	Total Mg 1 1	0	0
58	2N	1	Total Mg 1 1	0	0
58	2O	2	Total Mg 2 2	0	0
58	2P	2	Total Mg 2 2	0	0
58	2Q	2	Total Mg 2 2	0	0
58	2R	2	Total Mg 2 2	0	0
58	2T	3	Total Mg 3 3	0	0
58	2U	1	Total Mg 1 1	0	0
58	2V	2	Total Mg 2 2	0	0
58	2W	4	Total Mg 4 4	0	0
58	2X	2	Total Mg 2 2	0	0
58	2Y	1	Total Mg 1 1	0	0
58	2Z	1	Total Mg 1 1	0	0
58	20	2	Total Mg 2 2	0	0
58	21	4	Total Mg 4 4	0	0
58	23	3	Total Mg 3 3	0	0
58	25	3	Total Mg 3 3	0	0

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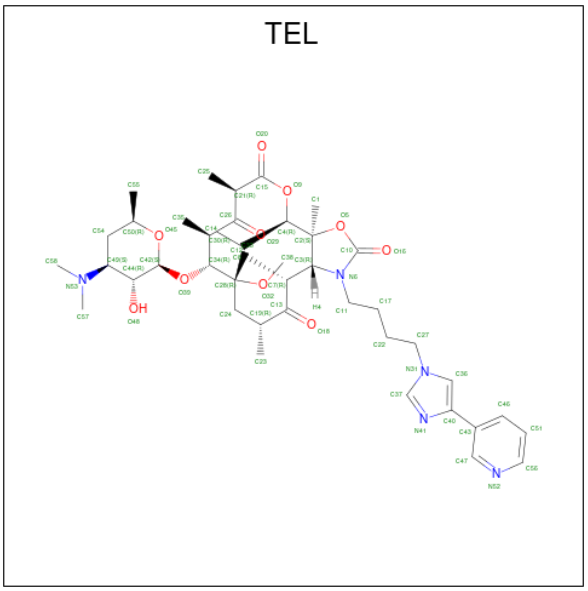
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	27	3	Total Mg 3 3	0	0
58	28	2	Total Mg 2 2	0	0
58	2a	211	Total Mg 211 211	0	0
58	2d	2	Total Mg 2 2	0	0
58	2e	1	Total Mg 1 1	0	0
58	2f	1	Total Mg 1 1	0	0
58	2g	1	Total Mg 1 1	0	0
58	2j	1	Total Mg 1 1	0	0
58	2k	1	Total Mg 1 1	0	0
58	2l	4	Total Mg 4 4	0	0
58	2q	2	Total Mg 2 2	0	0
58	2r	1	Total Mg 1 1	0	0
58	2t	1	Total Mg 1 1	0	0
58	2v	3	Total Mg 3 3	0	0
58	2w	2	Total Mg 2 2	0	0
58	2x	5	Total Mg 5 5	0	0

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	1	Total K 1 1	0	0
59	2A	1	Total K 1 1	0	0

- Molecule 60 is TELITHROMYCIN (CCD ID: TEL) (formula: $C_{43}H_{65}N_5O_{10}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	1	Total C N O 58 43 5 10	0	0
60	2A	1	Total C N O 58 43 5 10	0	0

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1Y	1	Total Zn 1 1	0	0
61	14	1	Total Zn 1 1	0	0
61	15	1	Total Zn 1 1	0	0
61	16	1	Total Zn 1 1	0	0
61	19	1	Total Zn 1 1	0	0
61	1n	1	Total Zn 1 1	0	0
61	2Y	1	Total Zn 1 1	0	0
61	24	1	Total Zn 1 1	0	0
61	25	1	Total Zn 1 1	0	0
61	26	1	Total Zn 1 1	0	0

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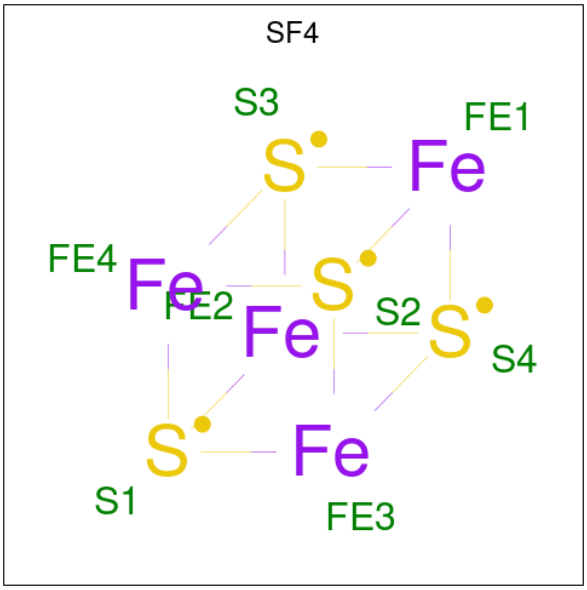
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	29	1	Total Zn 1 1	0	0
61	2n	1	Total Zn 1 1	0	0

- Molecule 62 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1d	1	Total Fe S 8 4 4	0	0
62	2d	1	Total Fe S 8 4 4	0	0

- Molecule 63 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1A	1780	Total O 1780 1780	0	0
63	1B	57	Total O 57 57	0	0
63	1D	24	Total O 24 24	0	0
63	1E	22	Total O 22 22	0	0
63	1F	14	Total O 14 14	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1G	2	Total O 2 2	0	0
63	1H	2	Total O 2 2	0	0
63	1I	1	Total O 1 1	0	0
63	1N	7	Total O 7 7	0	0
63	1O	4	Total O 4 4	0	0
63	1P	19	Total O 19 19	0	0
63	1Q	6	Total O 6 6	0	0
63	1R	13	Total O 13 13	0	0
63	1S	4	Total O 4 4	0	0
63	1T	11	Total O 11 11	0	0
63	1U	10	Total O 10 10	0	0
63	1V	9	Total O 9 9	0	0
63	1W	10	Total O 10 10	0	0
63	1X	4	Total O 4 4	0	0
63	1Y	1	Total O 1 1	0	0
63	1Z	1	Total O 1 1	0	0
63	10	13	Total O 13 13	0	0
63	11	9	Total O 9 9	0	0
63	12	4	Total O 4 4	0	0
63	13	4	Total O 4 4	0	0
63	15	6	Total O 6 6	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	16	2	Total O 2 2	0	0
63	17	5	Total O 5 5	0	0
63	18	9	Total O 9 9	0	0
63	1a	226	Total O 226 226	0	0
63	1b	1	Total O 1 1	0	0
63	1e	2	Total O 2 2	0	0
63	1l	7	Total O 7 7	0	0
63	1m	1	Total O 1 1	0	0
63	1n	1	Total O 1 1	0	0
63	1q	2	Total O 2 2	0	0
63	1v	5	Total O 5 5	0	0
63	1w	5	Total O 5 5	0	0
63	1x	3	Total O 3 3	0	0
63	1y	1	Total O 1 1	0	0
63	2A	850	Total O 850 850	0	0
63	2B	16	Total O 16 16	0	0
63	2D	18	Total O 18 18	0	0
63	2E	10	Total O 10 10	0	0
63	2F	12	Total O 12 12	0	0
63	2N	1	Total O 1 1	0	0
63	2O	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	2P	1	Total O 1 1	0	0
63	2Q	1	Total O 1 1	0	0
63	2R	2	Total O 2 2	0	0
63	2T	4	Total O 4 4	0	0
63	2U	2	Total O 2 2	0	0
63	2W	2	Total O 2 2	0	0
63	2X	2	Total O 2 2	0	0
63	2Z	1	Total O 1 1	0	0
63	20	3	Total O 3 3	0	0
63	21	5	Total O 5 5	0	0
63	25	1	Total O 1 1	0	0
63	27	2	Total O 2 2	0	0
63	28	2	Total O 2 2	0	0
63	29	1	Total O 1 1	0	0
63	2a	148	Total O 148 148	0	0
63	2d	1	Total O 1 1	0	0
63	2e	1	Total O 1 1	0	0
63	2i	1	Total O 1 1	0	0
63	2l	5	Total O 5 5	0	0
63	2p	2	Total O 2 2	0	0
63	2t	2	Total O 2 2	0	0

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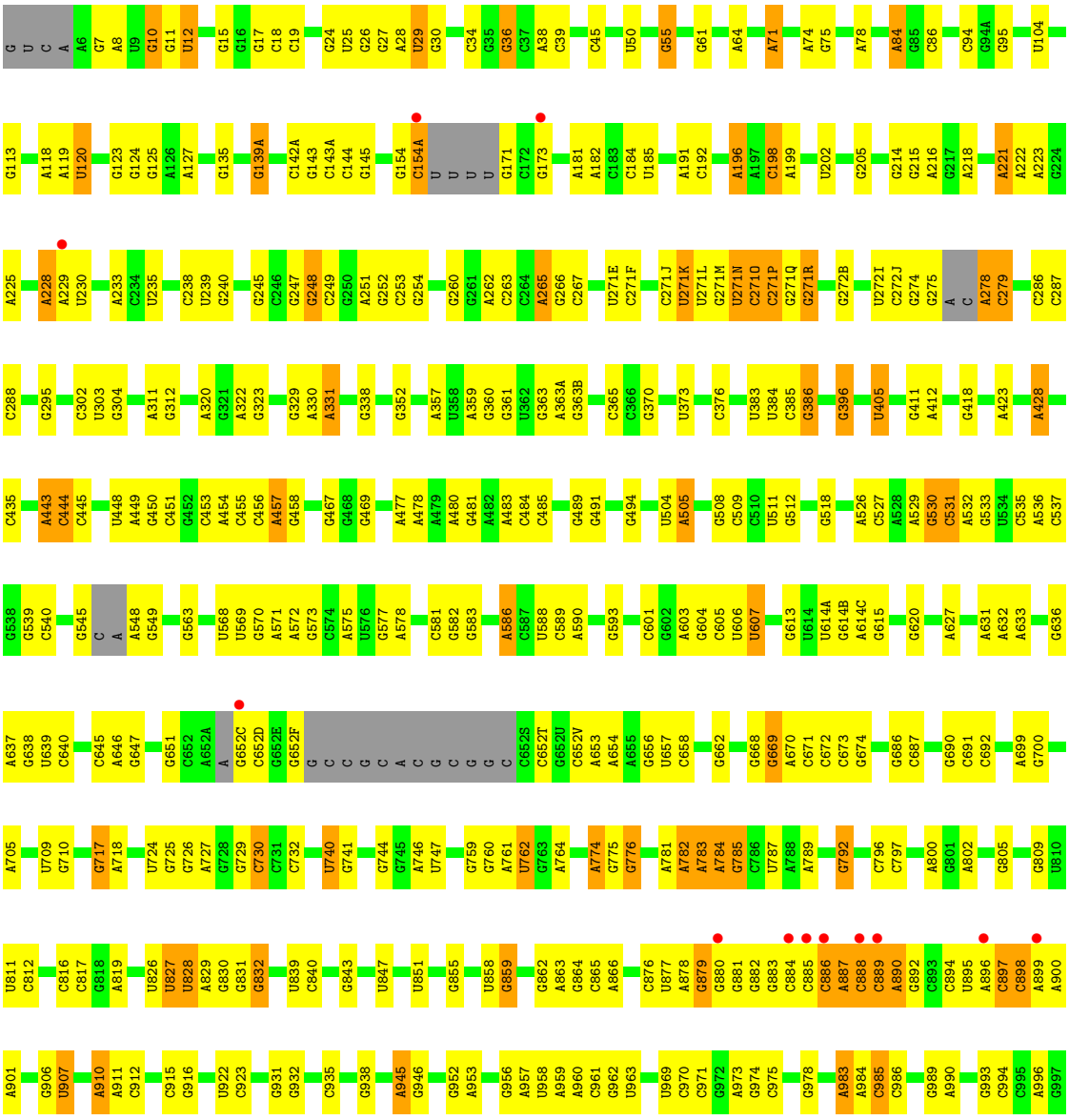
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	2v	1	Total O 1 1	0	0
63	2w	4	Total O 4 4	0	0
63	2x	4	Total O 4 4	0	0

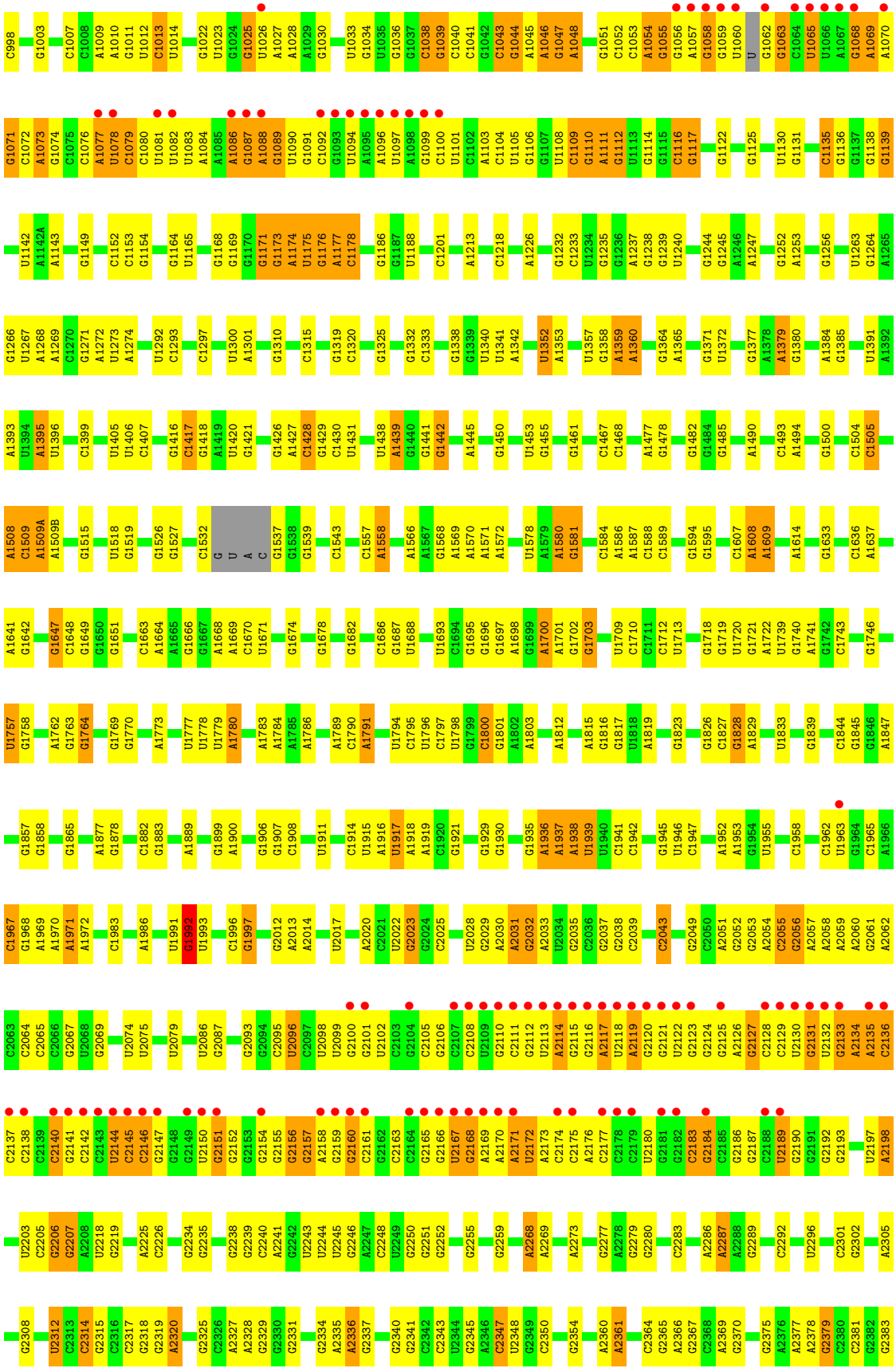
3 Residue-property plots (i)

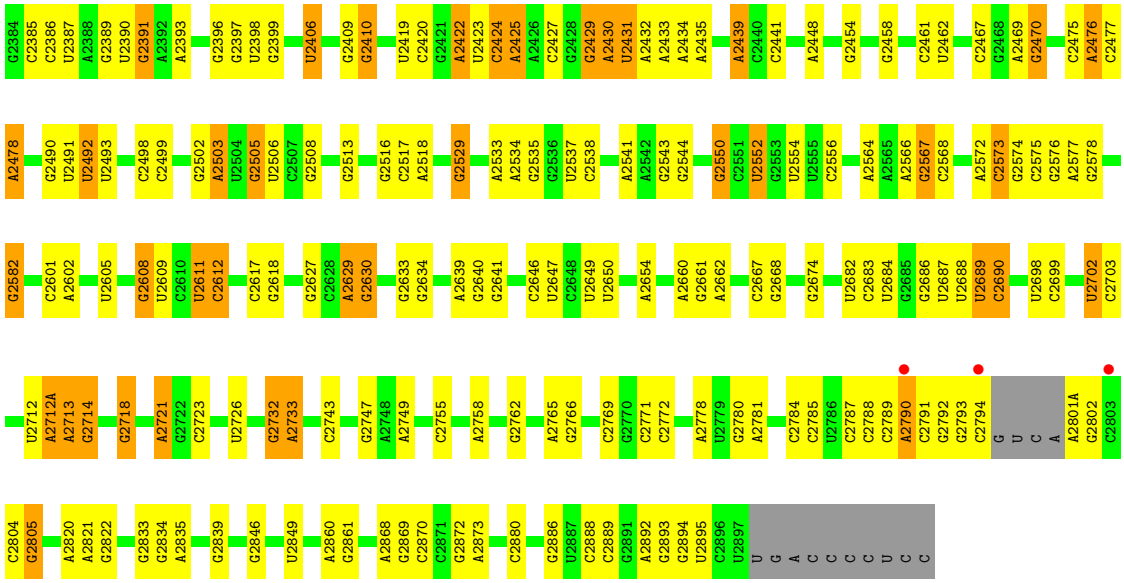
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 23S Ribosomal RNA

Chain 1A:

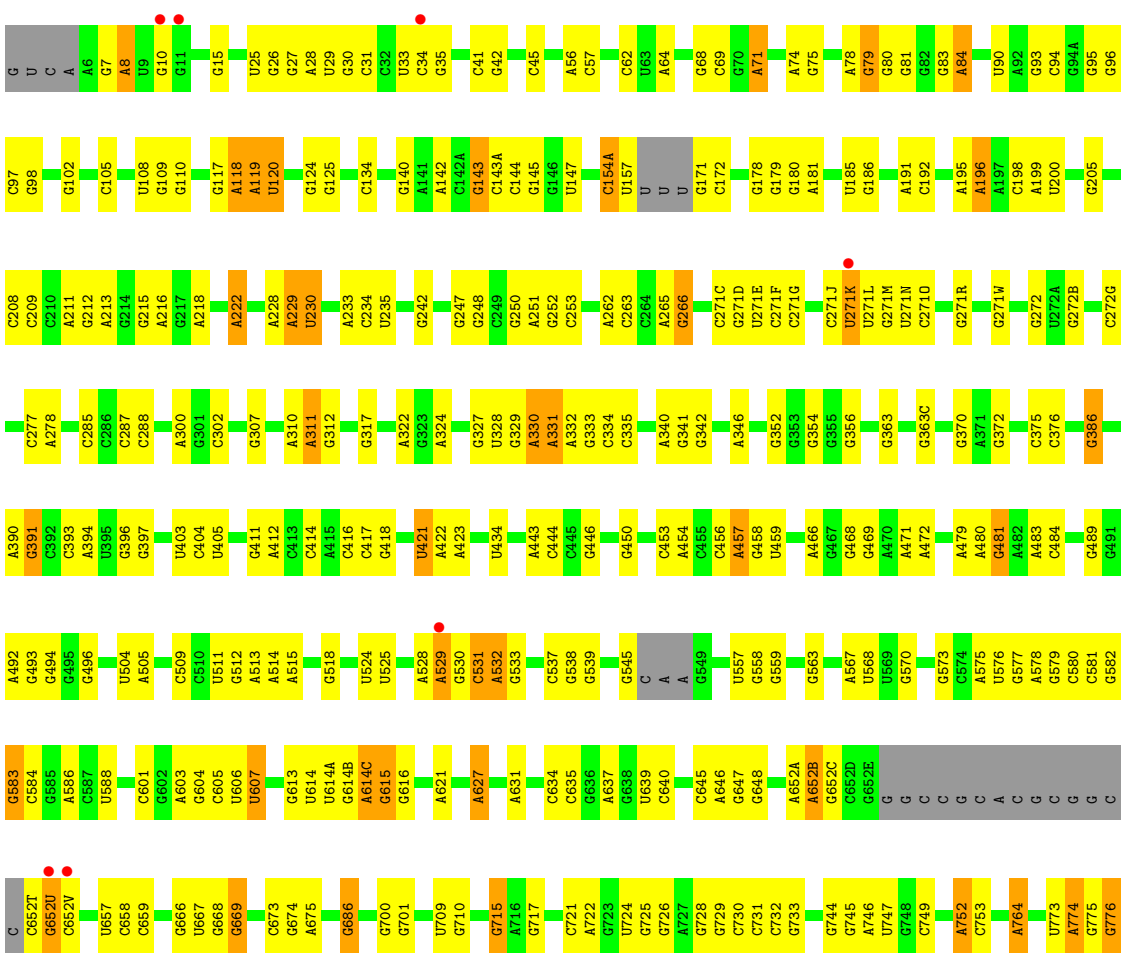


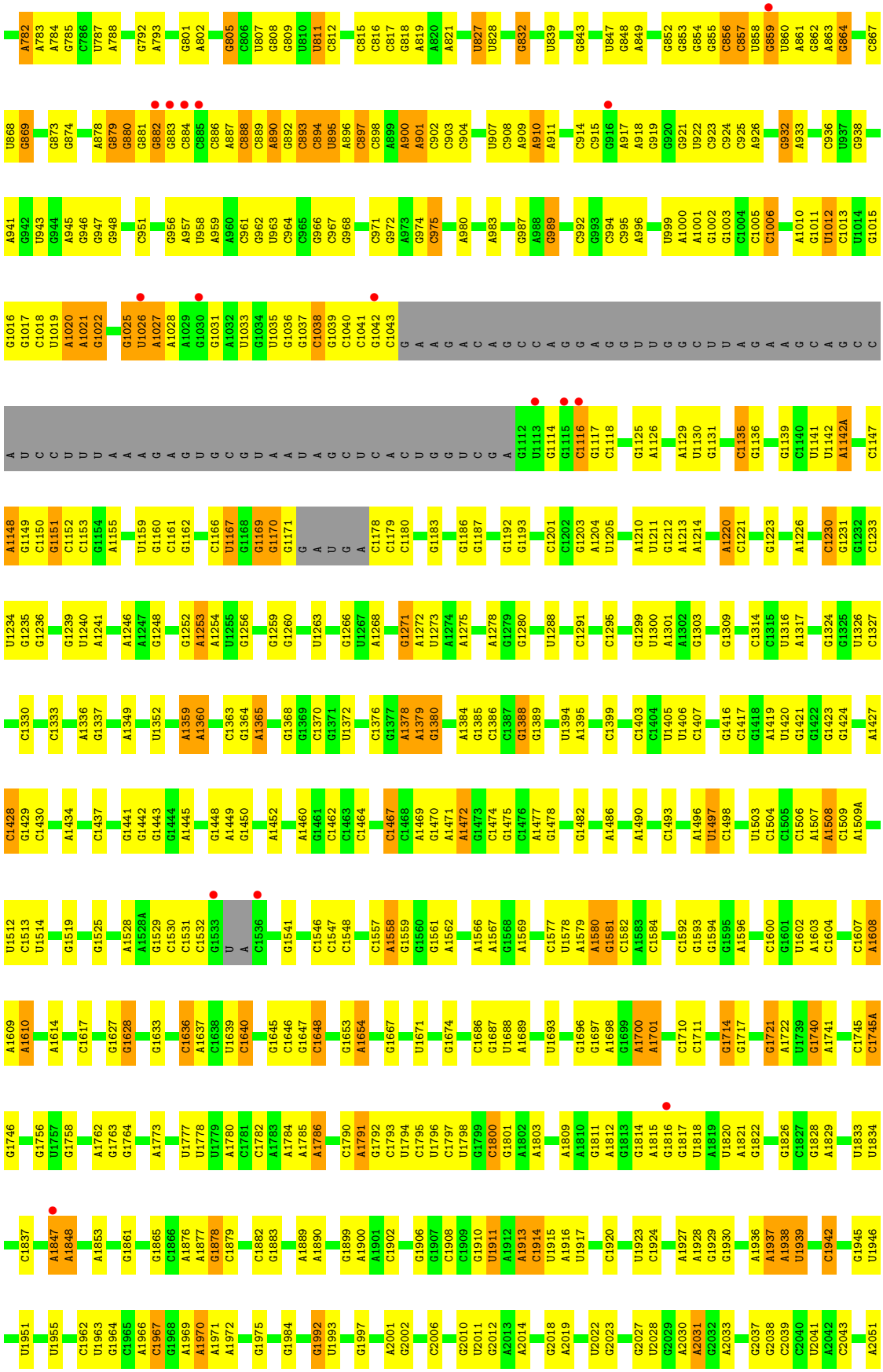


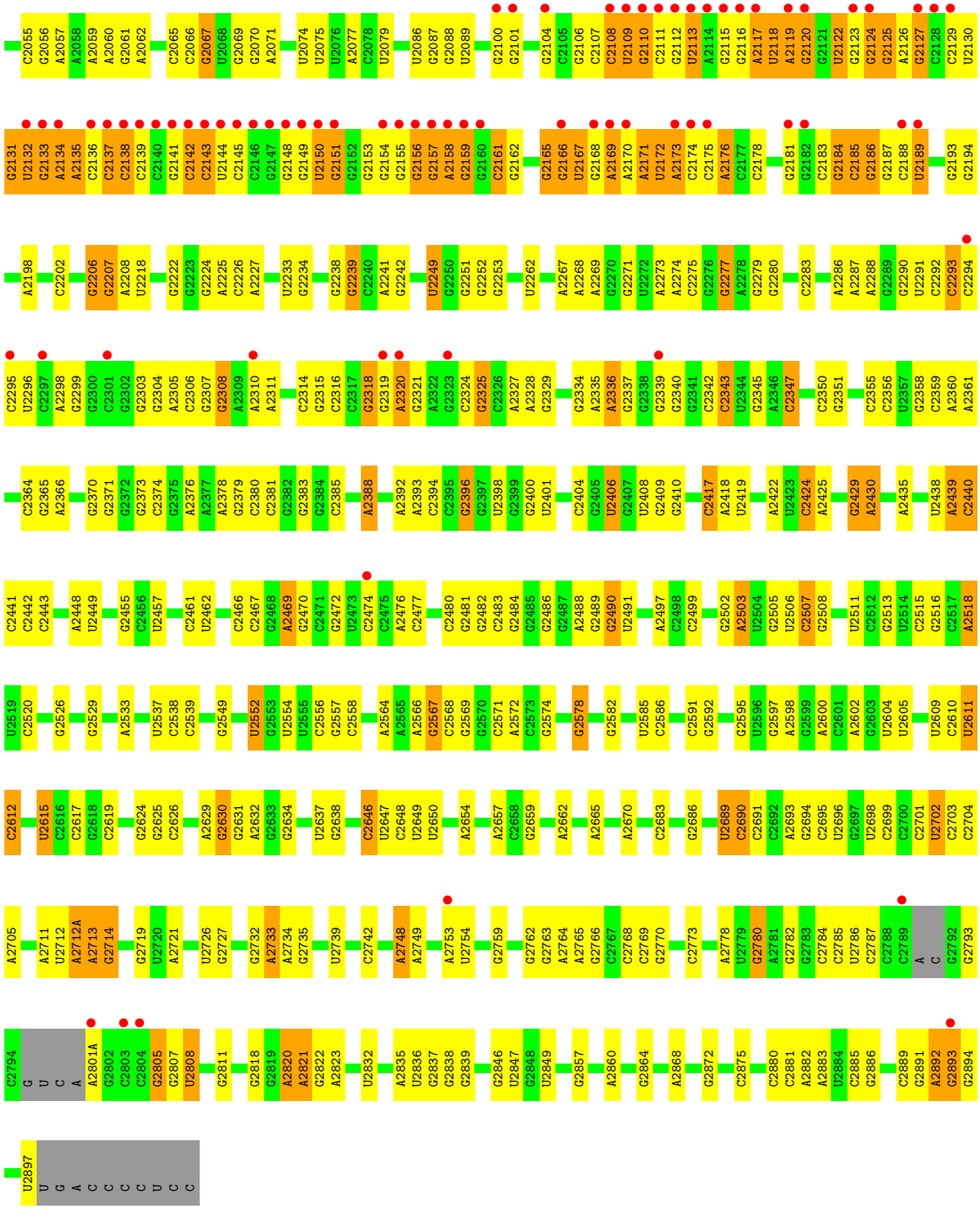


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

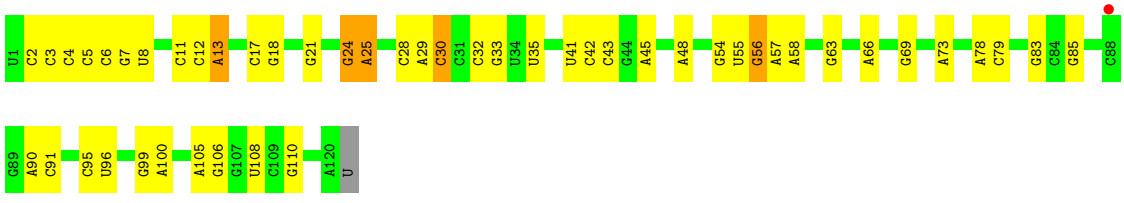






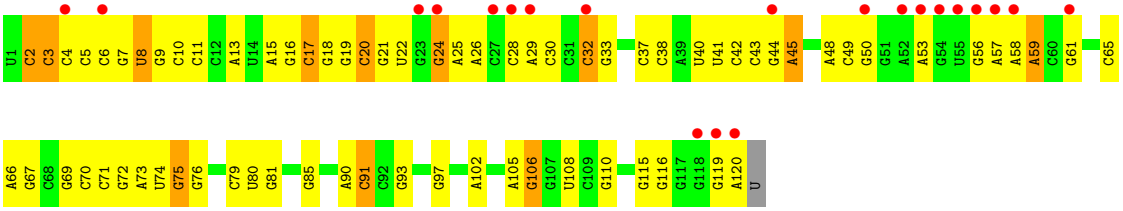
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



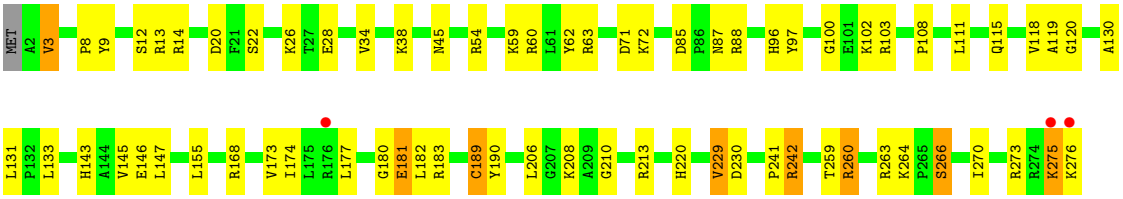
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



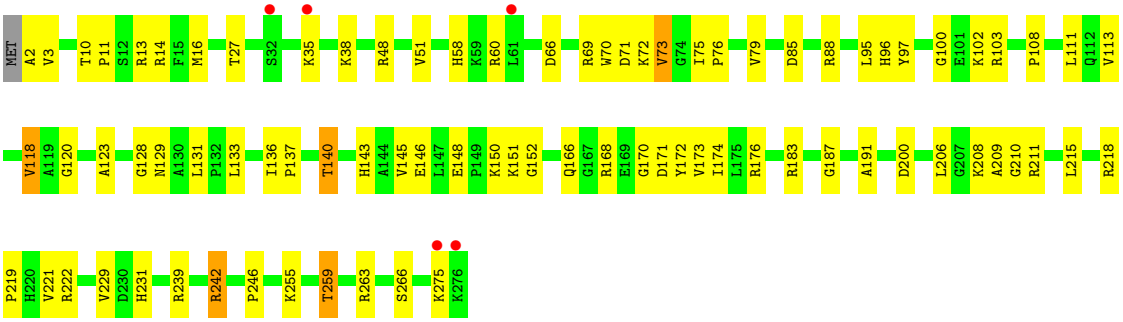
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



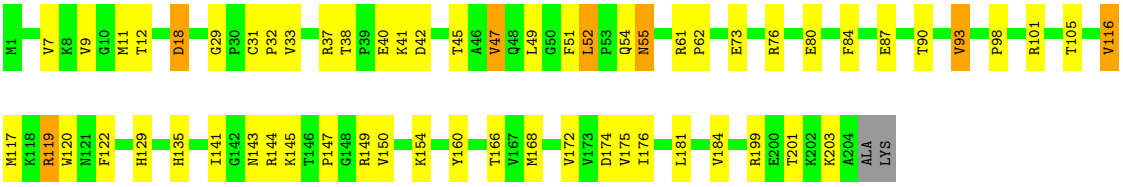
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



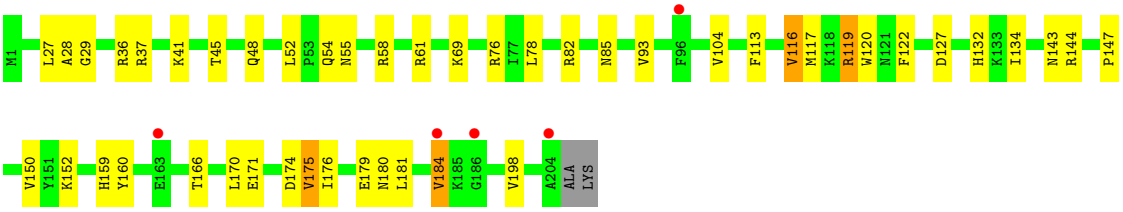
• Molecule 4: 50S ribosomal protein L3

Chain 1E:

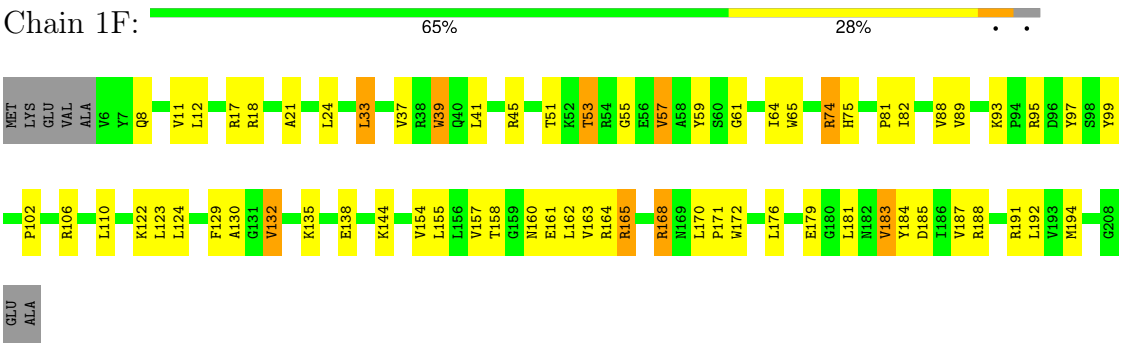


• Molecule 4: 50S ribosomal protein L3

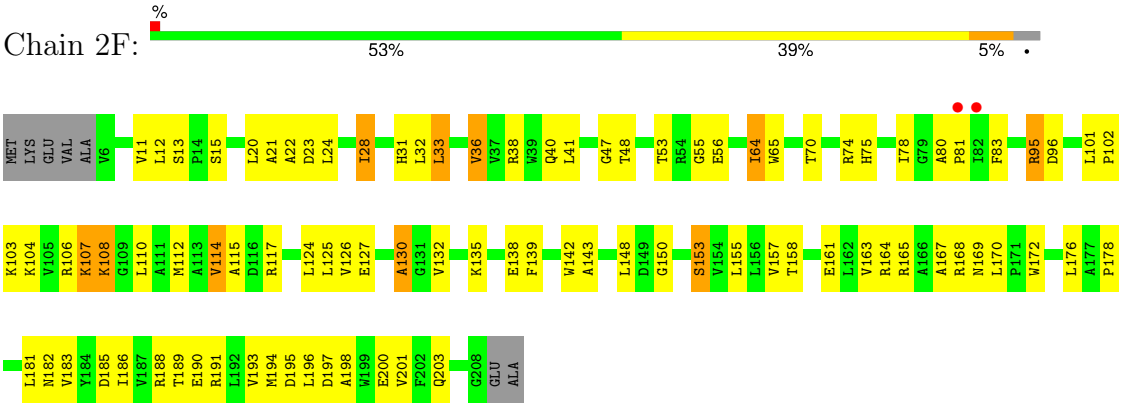
Chain 2E:



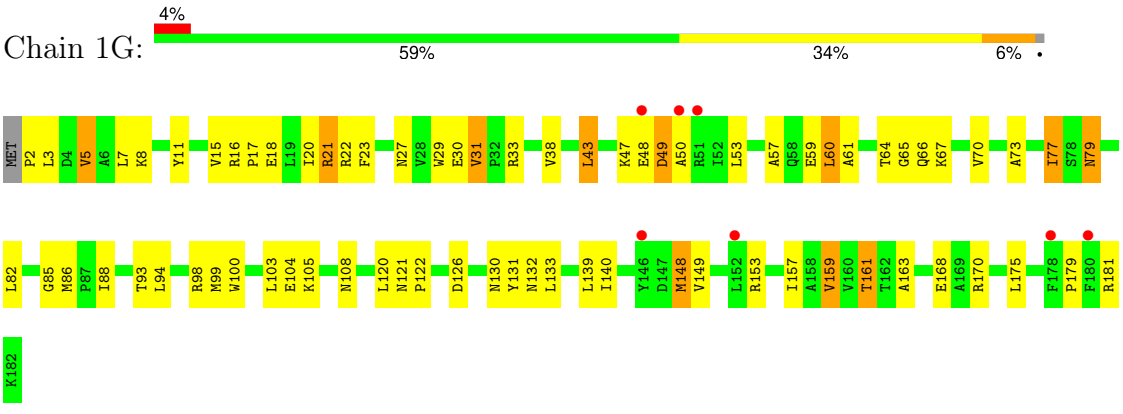
• Molecule 5: 50S ribosomal protein L4



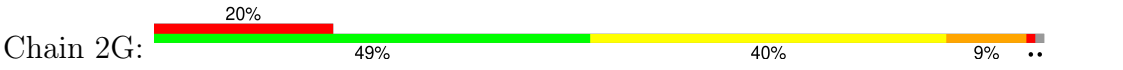
• Molecule 5: 50S ribosomal protein L4

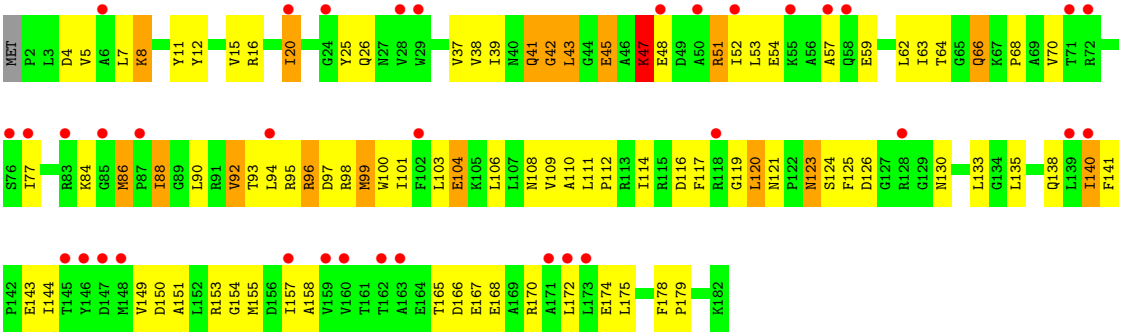


• Molecule 6: 50S ribosomal protein L5



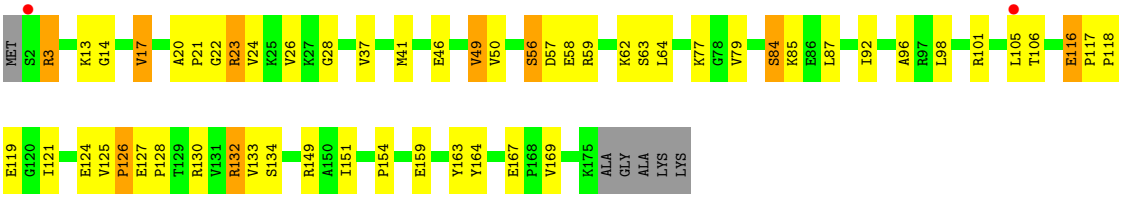
• Molecule 6: 50S ribosomal protein L5





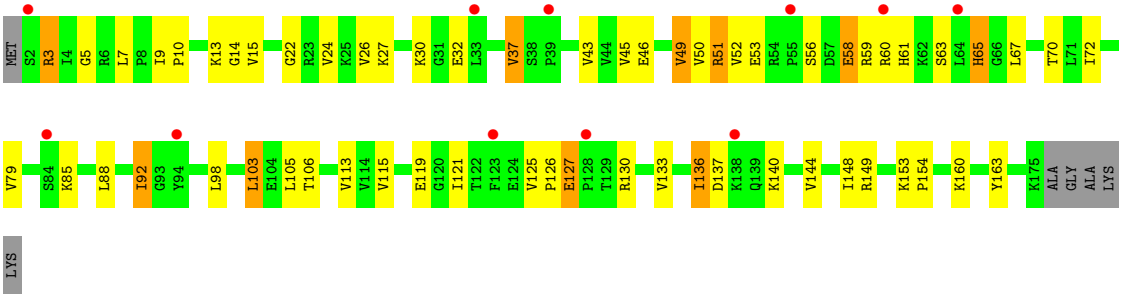
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



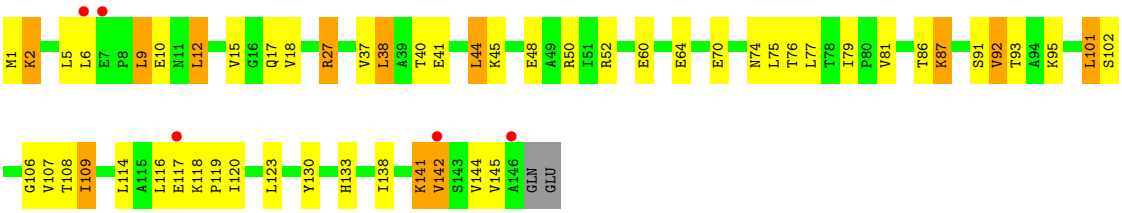
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



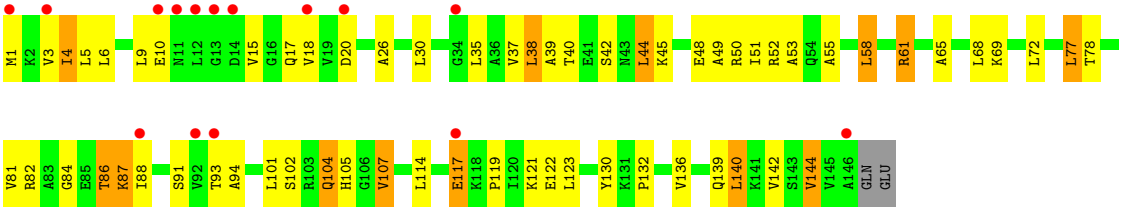
• Molecule 8: 50S ribosomal protein L9

Chain 1I:

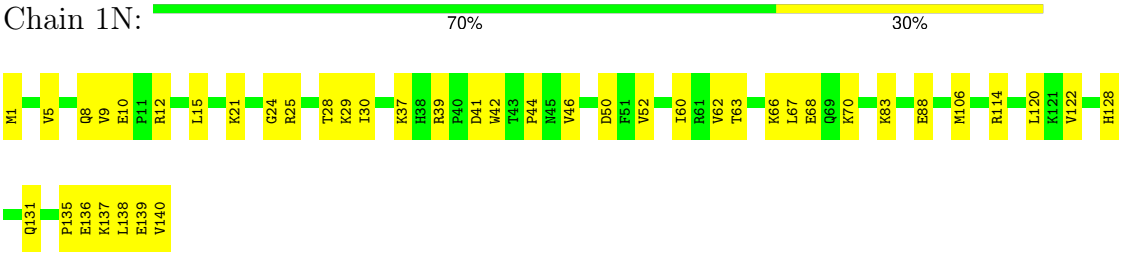


• Molecule 8: 50S ribosomal protein L9

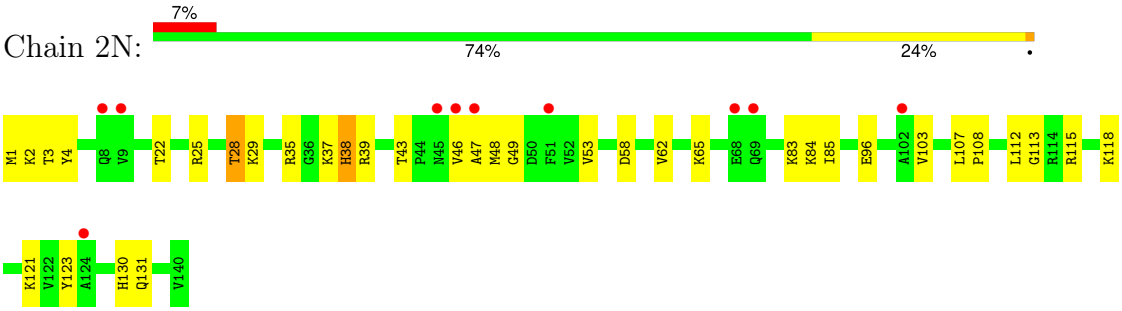
Chain 2I:



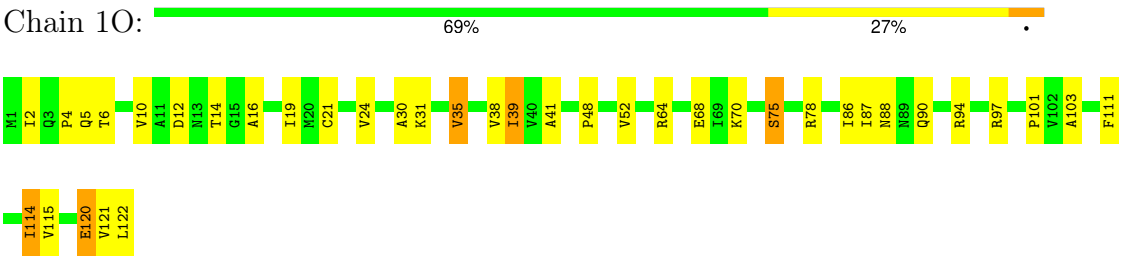
• Molecule 9: 50S ribosomal protein L13



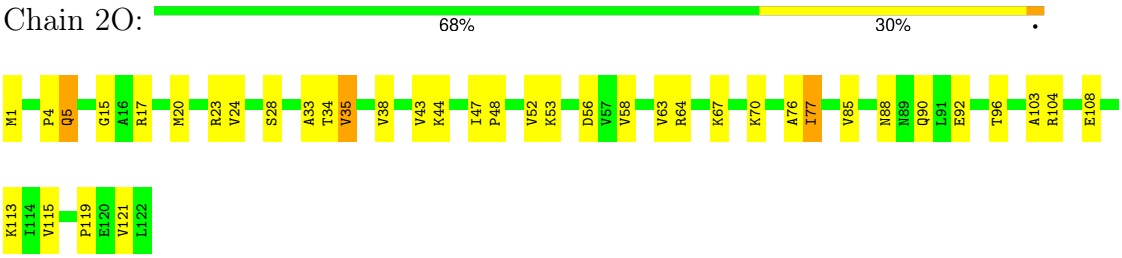
• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14

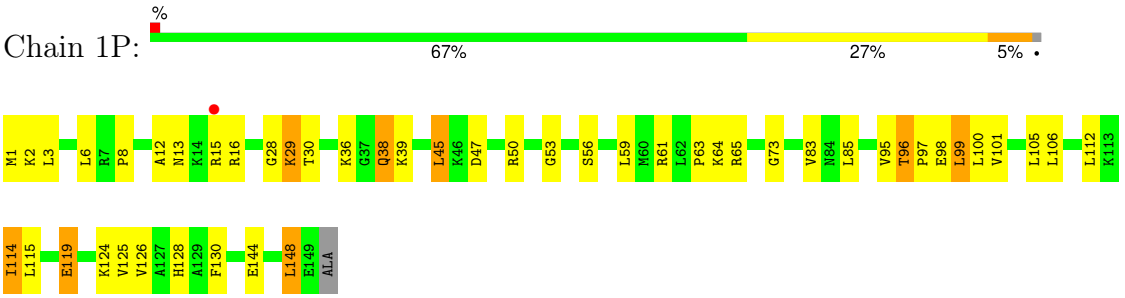


• Molecule 10: 50S ribosomal protein L14



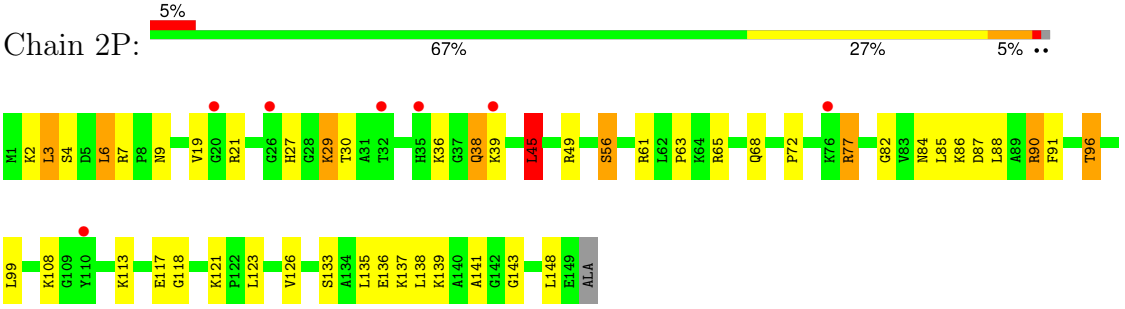
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



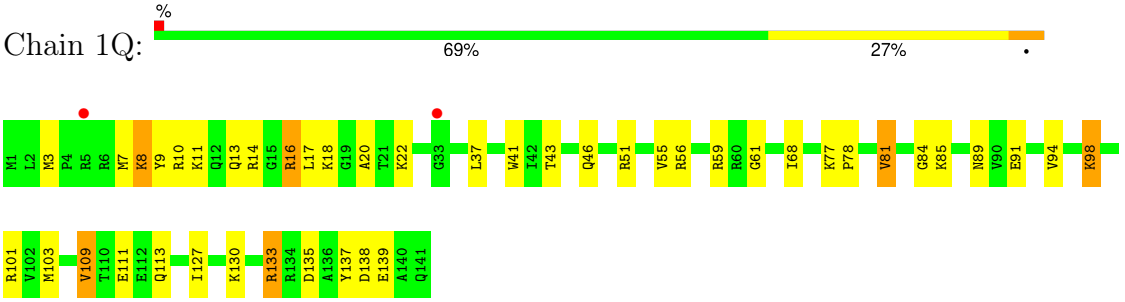
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



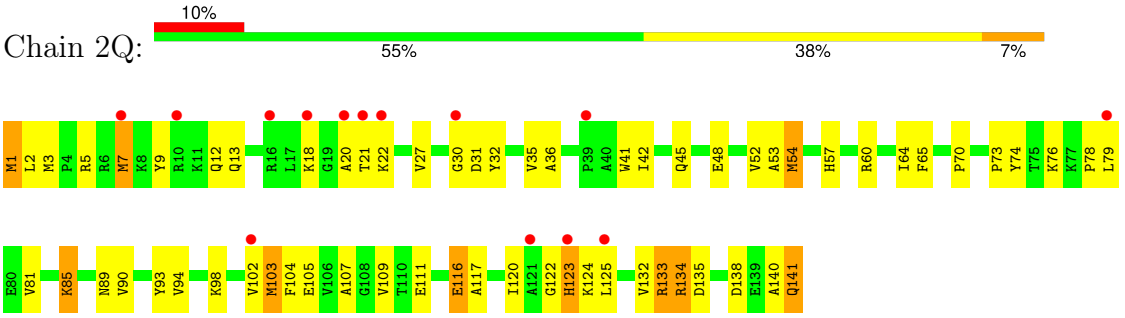
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



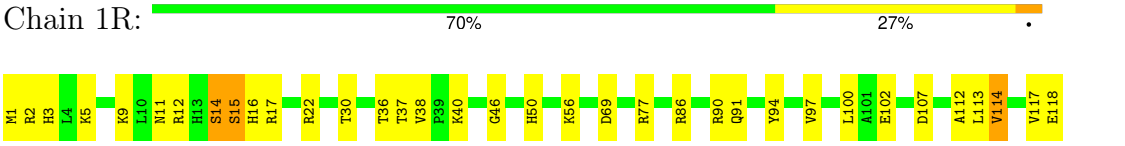
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



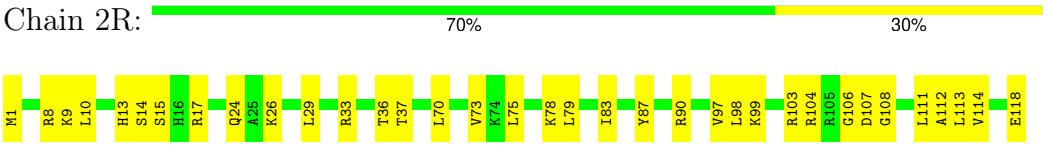
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



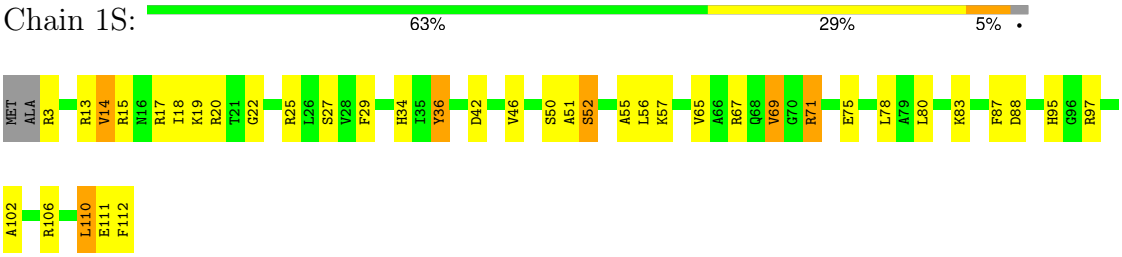
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



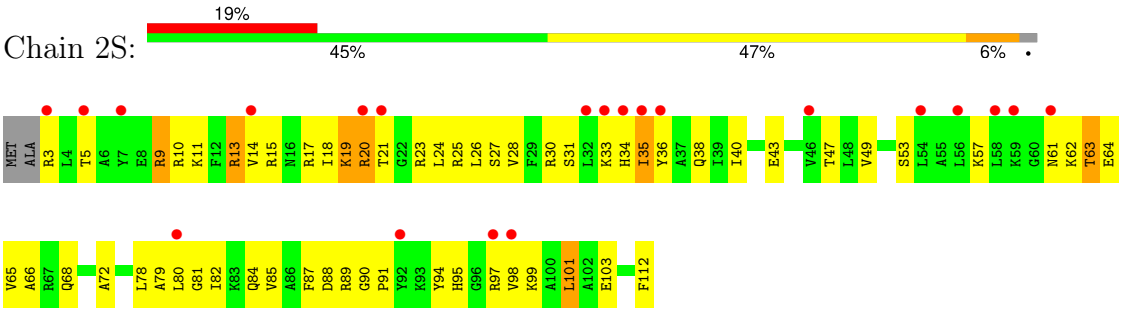
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



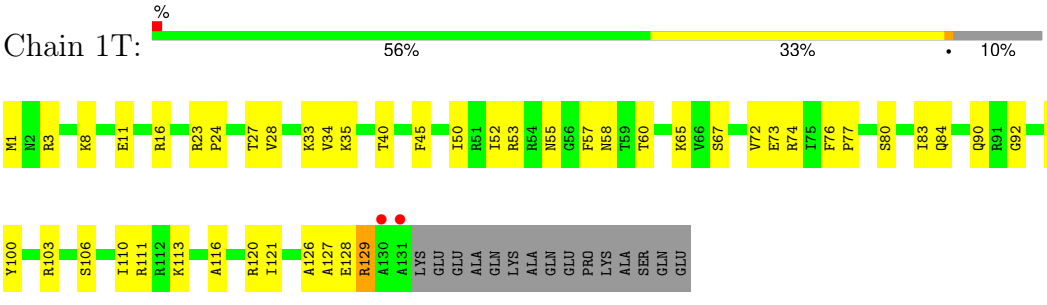
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



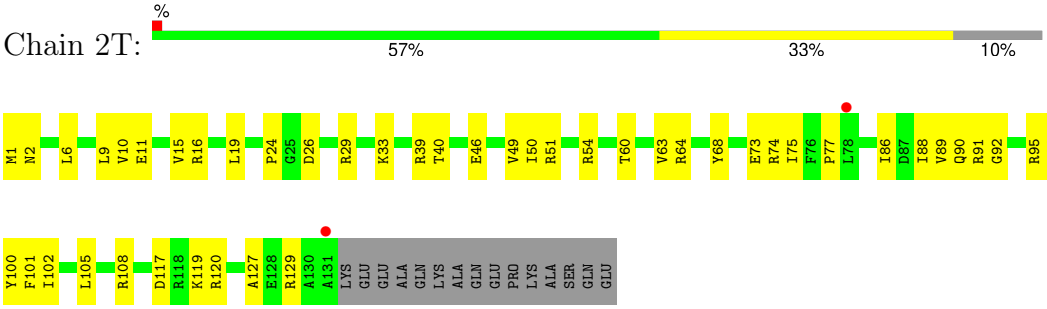
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



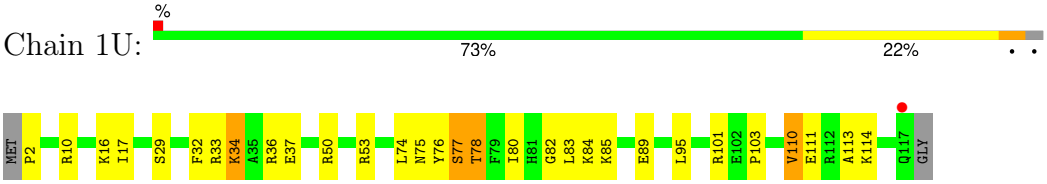
• Molecule 15: 50S ribosomal protein L19

Chain 2T:



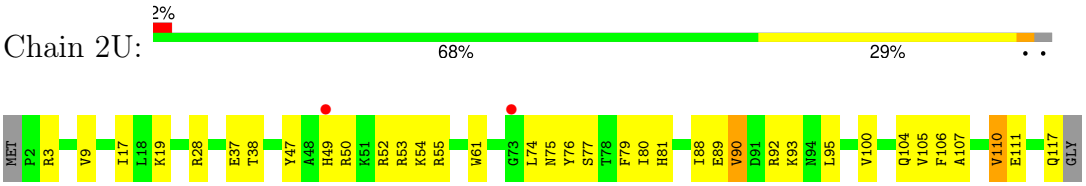
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



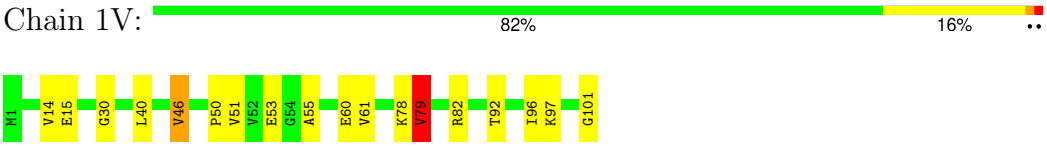
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



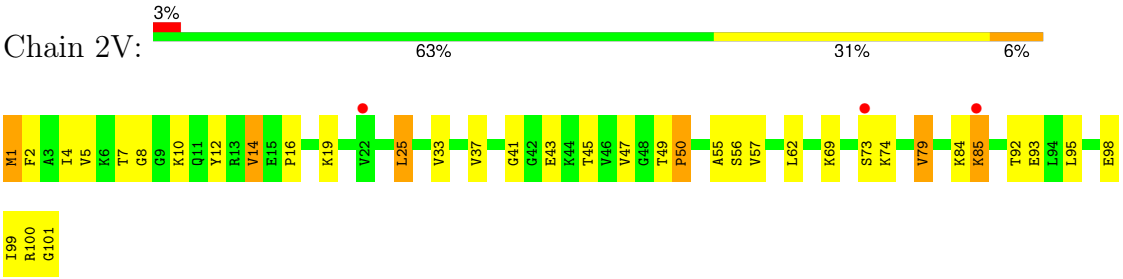
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



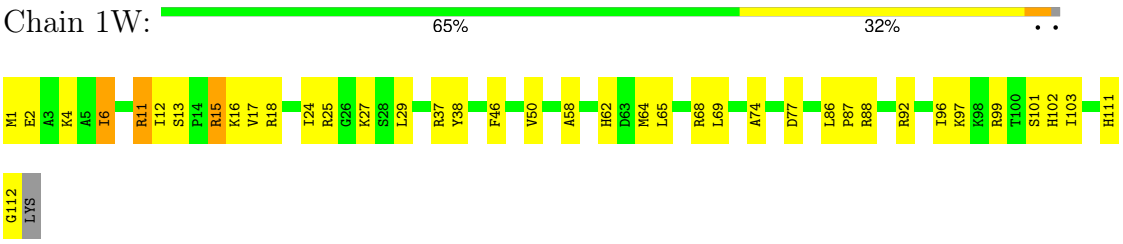
• Molecule 17: 50S ribosomal protein L21

Chain 2V:



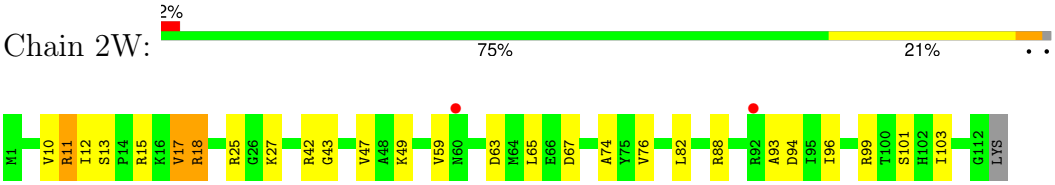
• Molecule 18: 50S ribosomal protein L22

Chain 1W:



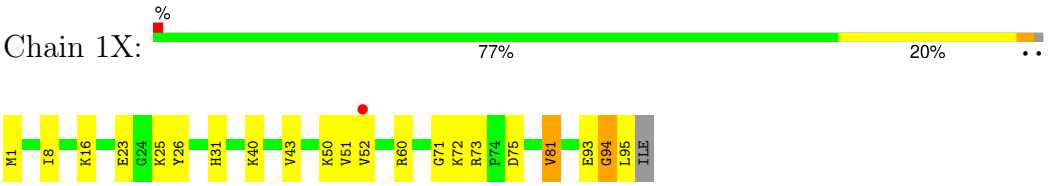
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



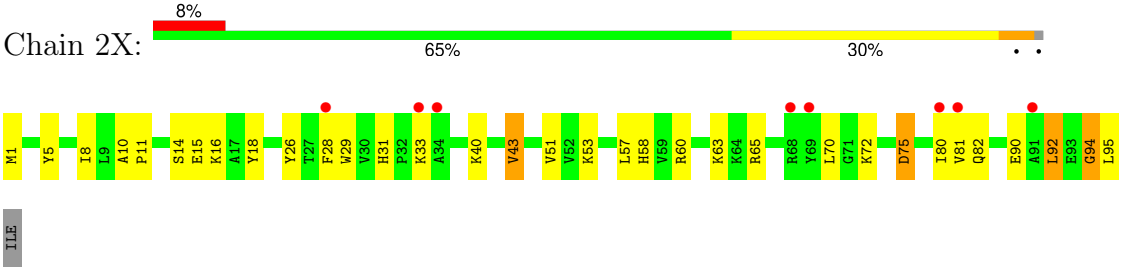
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



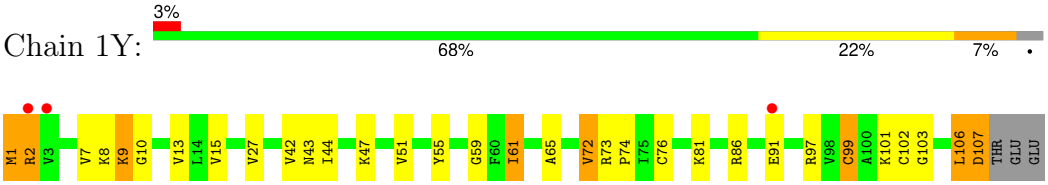
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



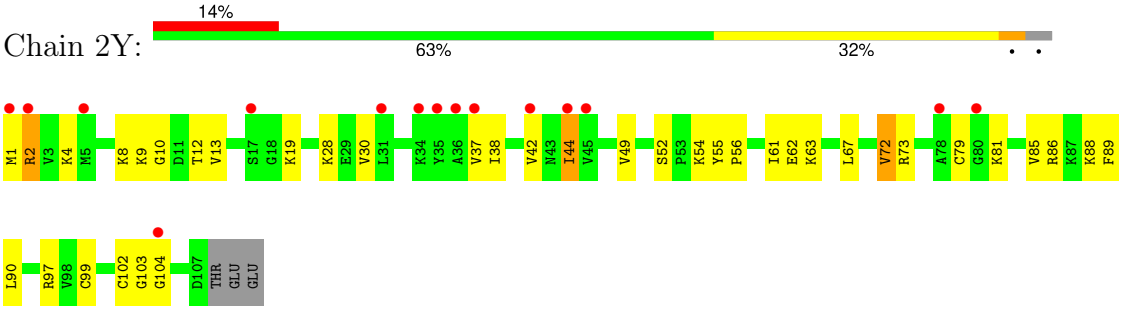
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



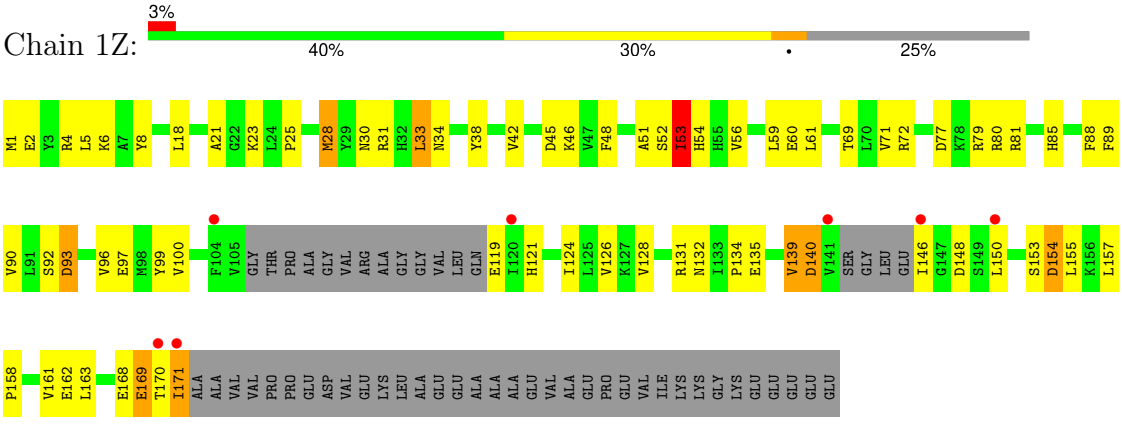
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:

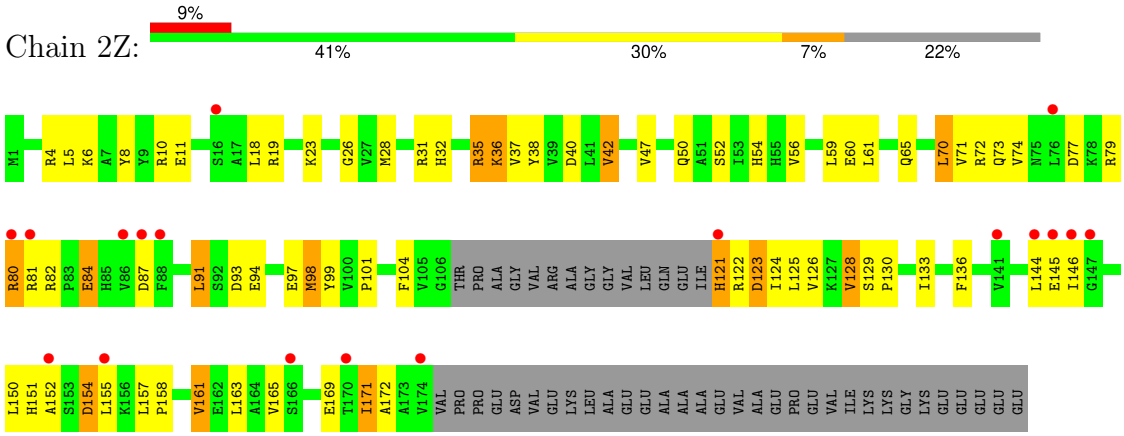


• Molecule 21: 50S ribosomal protein L25

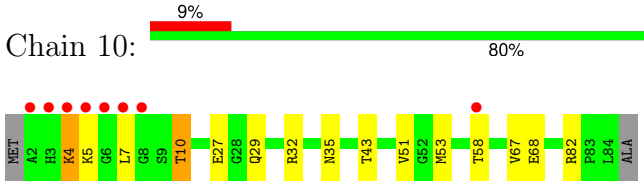
Chain 1Z:



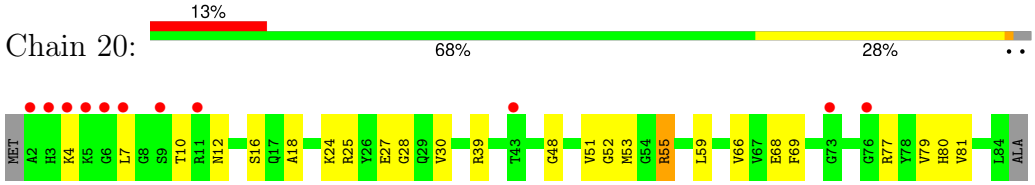
• Molecule 21: 50S ribosomal protein L25



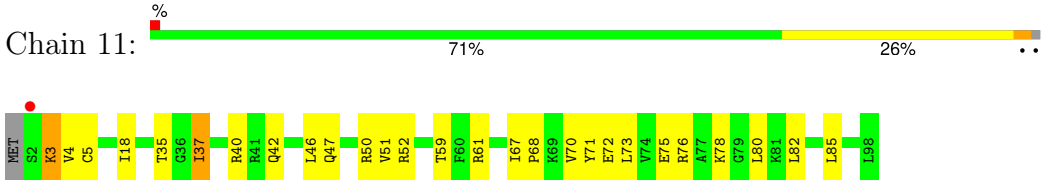
• Molecule 22: 50S ribosomal protein L27



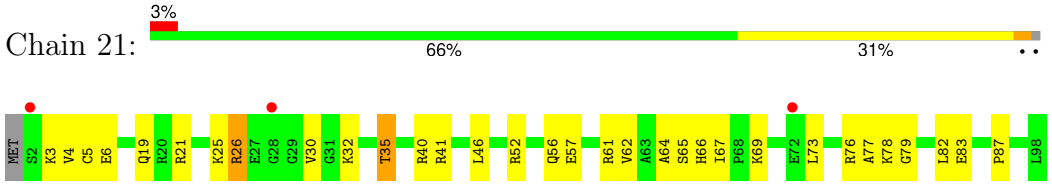
• Molecule 22: 50S ribosomal protein L27



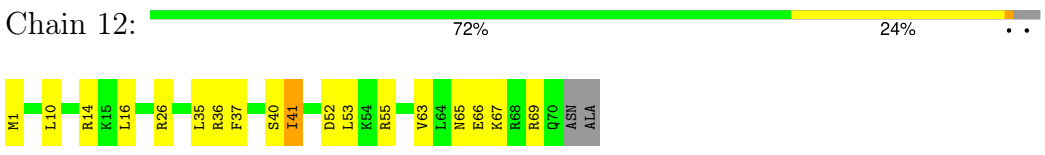
• Molecule 23: 50S ribosomal protein L28



• Molecule 23: 50S ribosomal protein L28

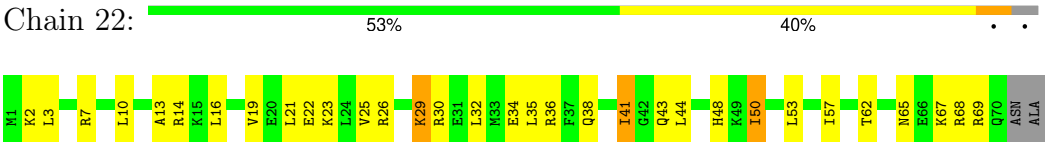


• Molecule 24: 50S ribosomal protein L29



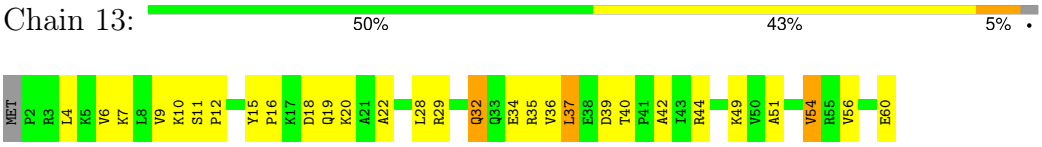
• Molecule 24: 50S ribosomal protein L29

Chain 22:



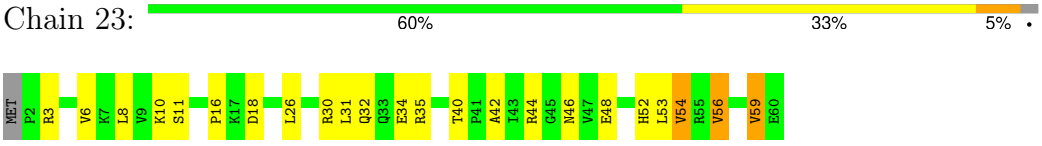
• Molecule 25: 50S ribosomal protein L30

Chain 13:



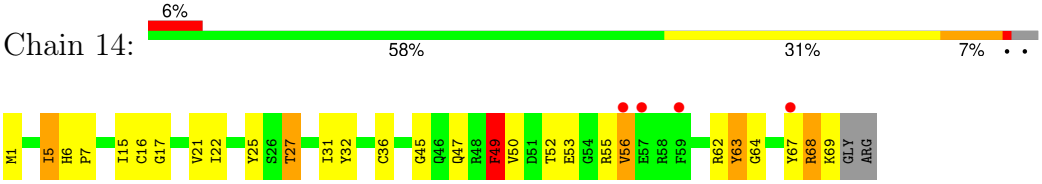
• Molecule 25: 50S ribosomal protein L30

Chain 23:



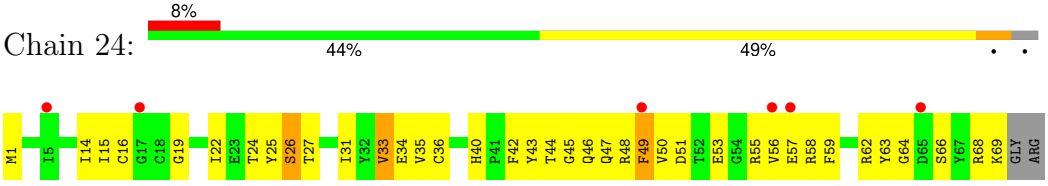
• Molecule 26: 50S ribosomal protein L31

Chain 14:



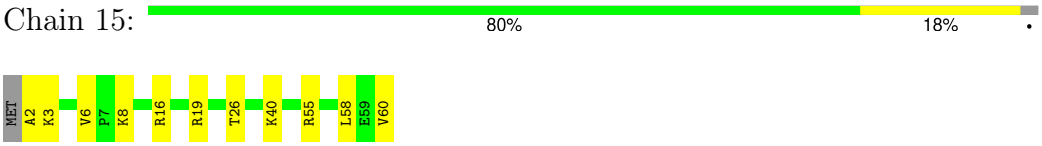
• Molecule 26: 50S ribosomal protein L31

Chain 24:



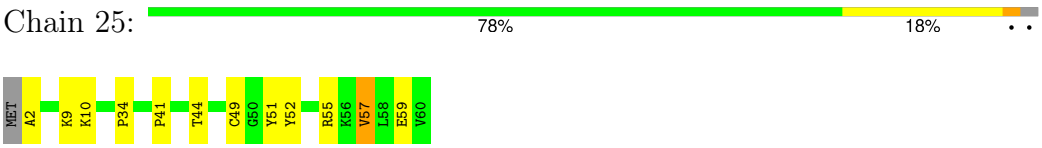
• Molecule 27: 50S ribosomal protein L32

Chain 15:



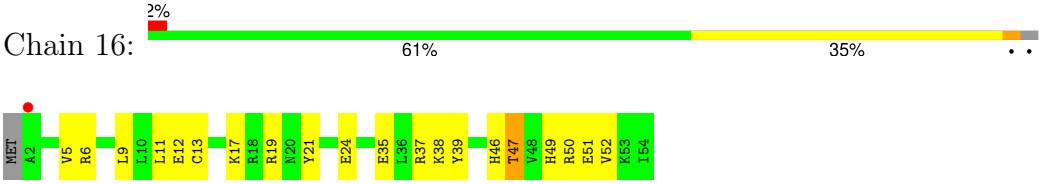
• Molecule 27: 50S ribosomal protein L32

Chain 25:



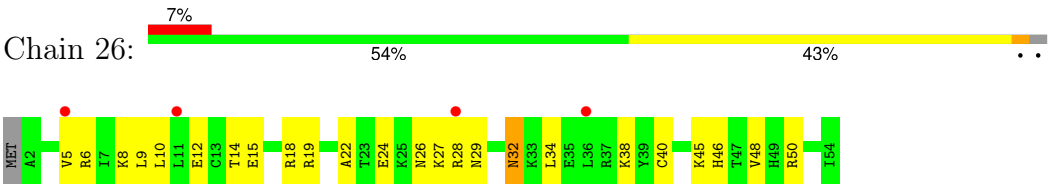
• Molecule 28: 50S ribosomal protein L33

Chain 16:



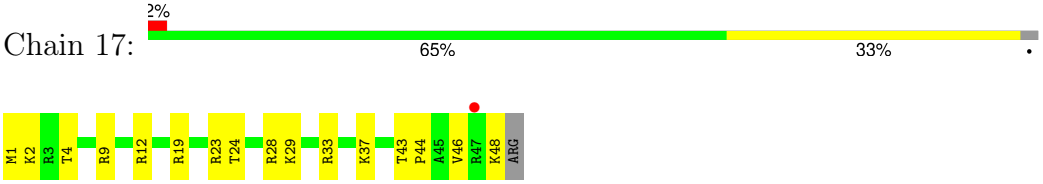
• Molecule 28: 50S ribosomal protein L33

Chain 26:



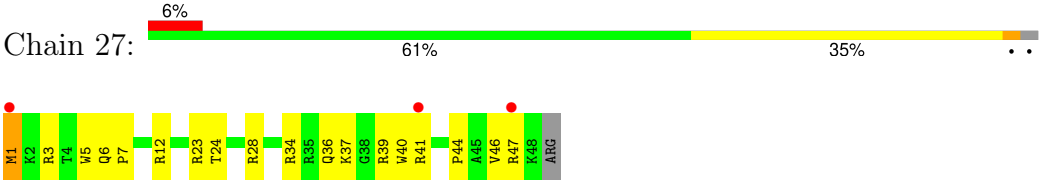
• Molecule 29: 50S ribosomal protein L34

Chain 17:



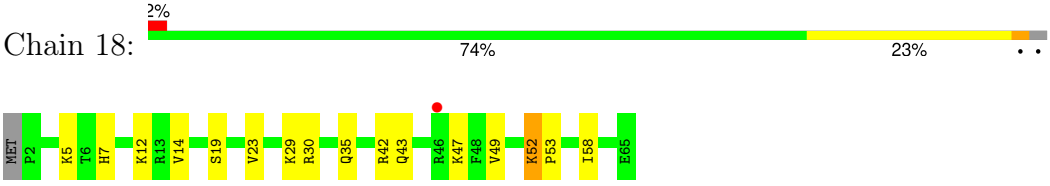
• Molecule 29: 50S ribosomal protein L34

Chain 27:



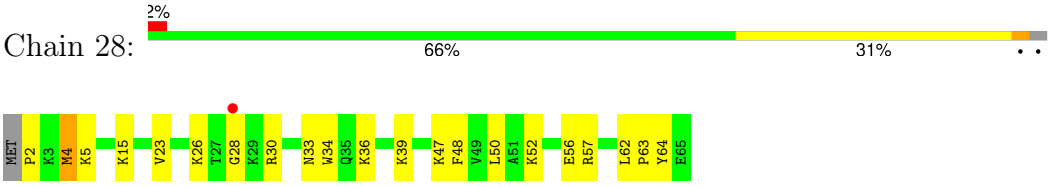
• Molecule 30: 50S ribosomal protein L35

Chain 18:



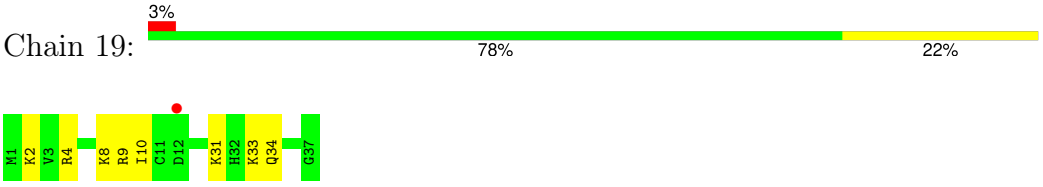
• Molecule 30: 50S ribosomal protein L35

Chain 28:



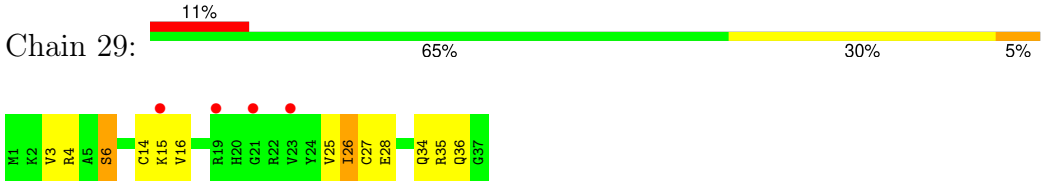
• Molecule 31: 50S ribosomal protein L36

Chain 19:



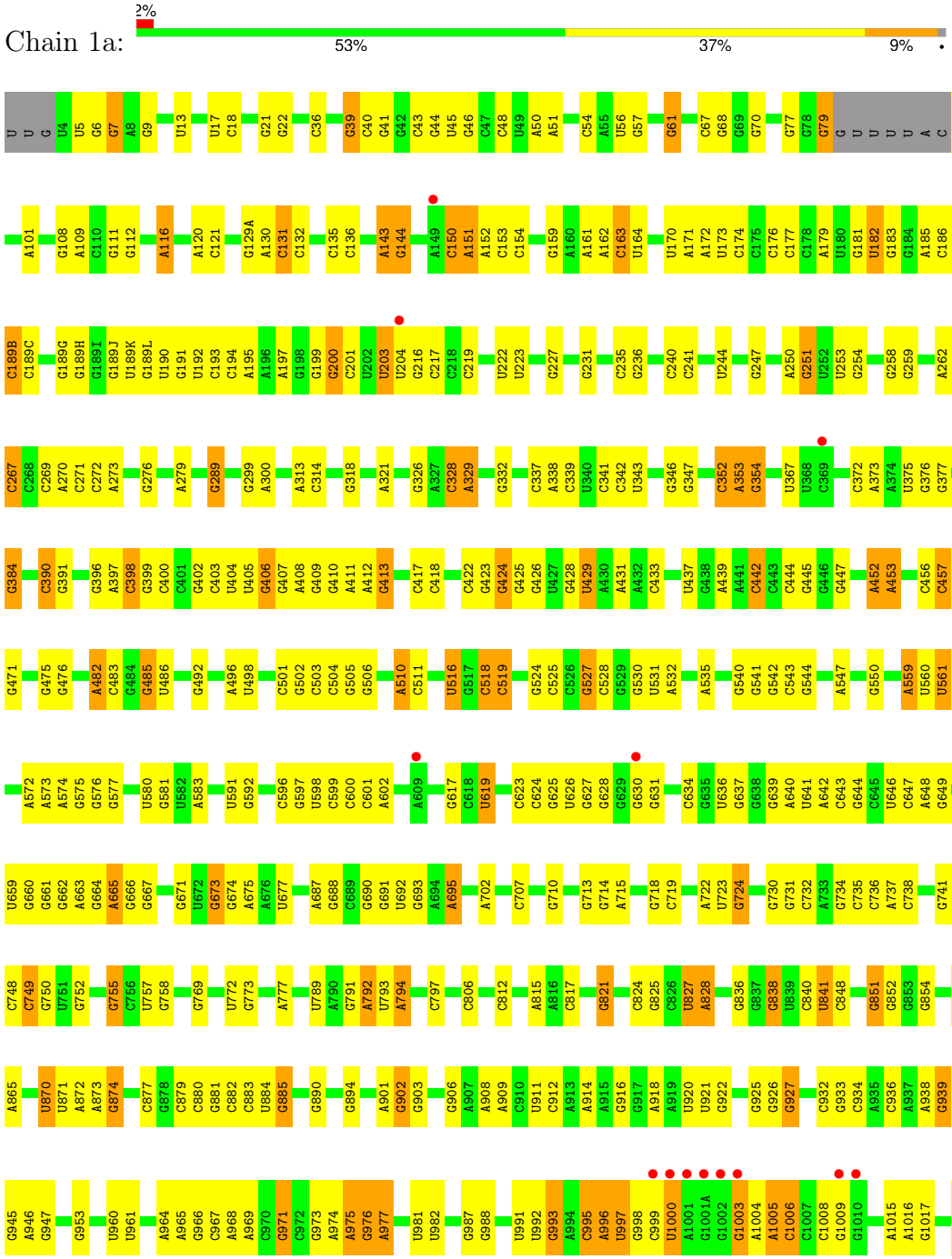
• Molecule 31: 50S ribosomal protein L36

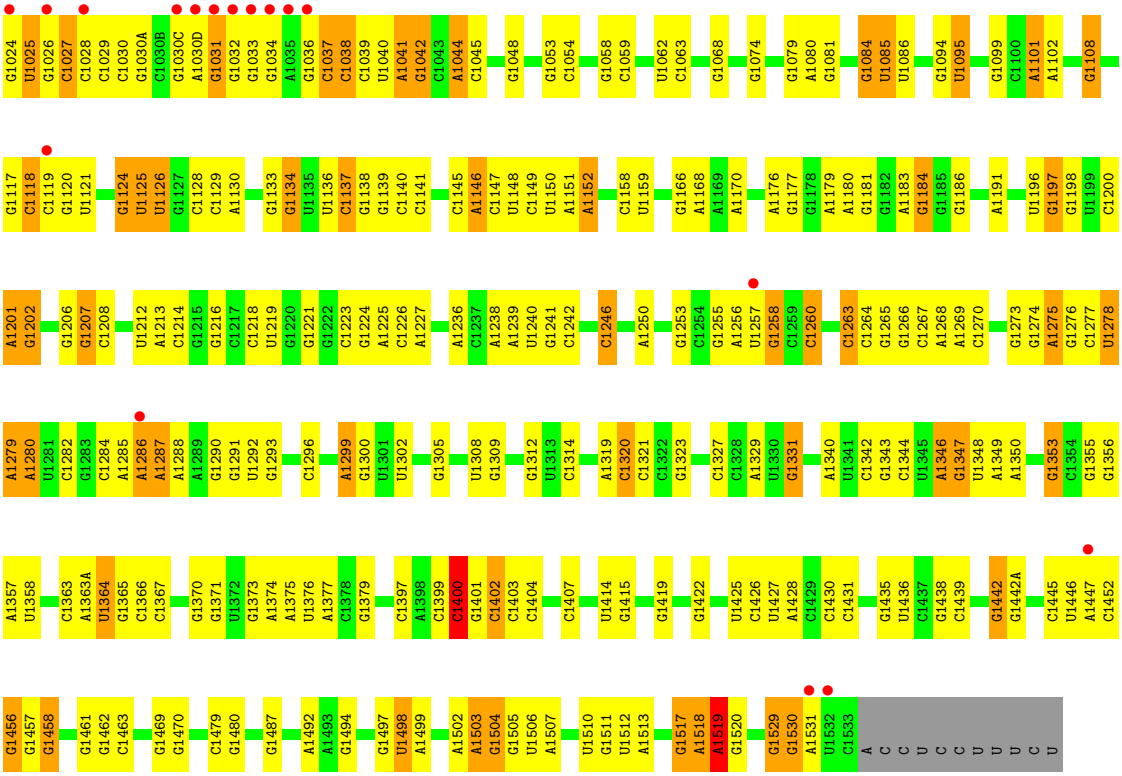
Chain 29:



• Molecule 32: 16S Ribosomal RNA

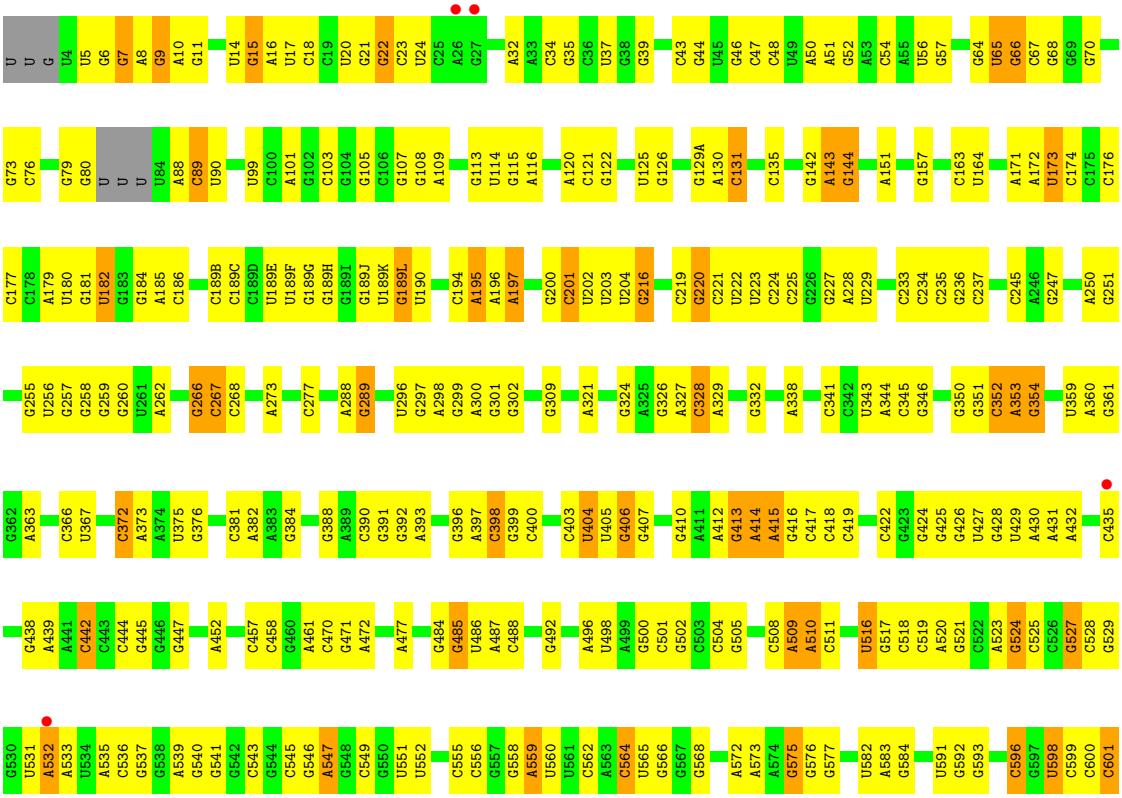
Chain 1a:

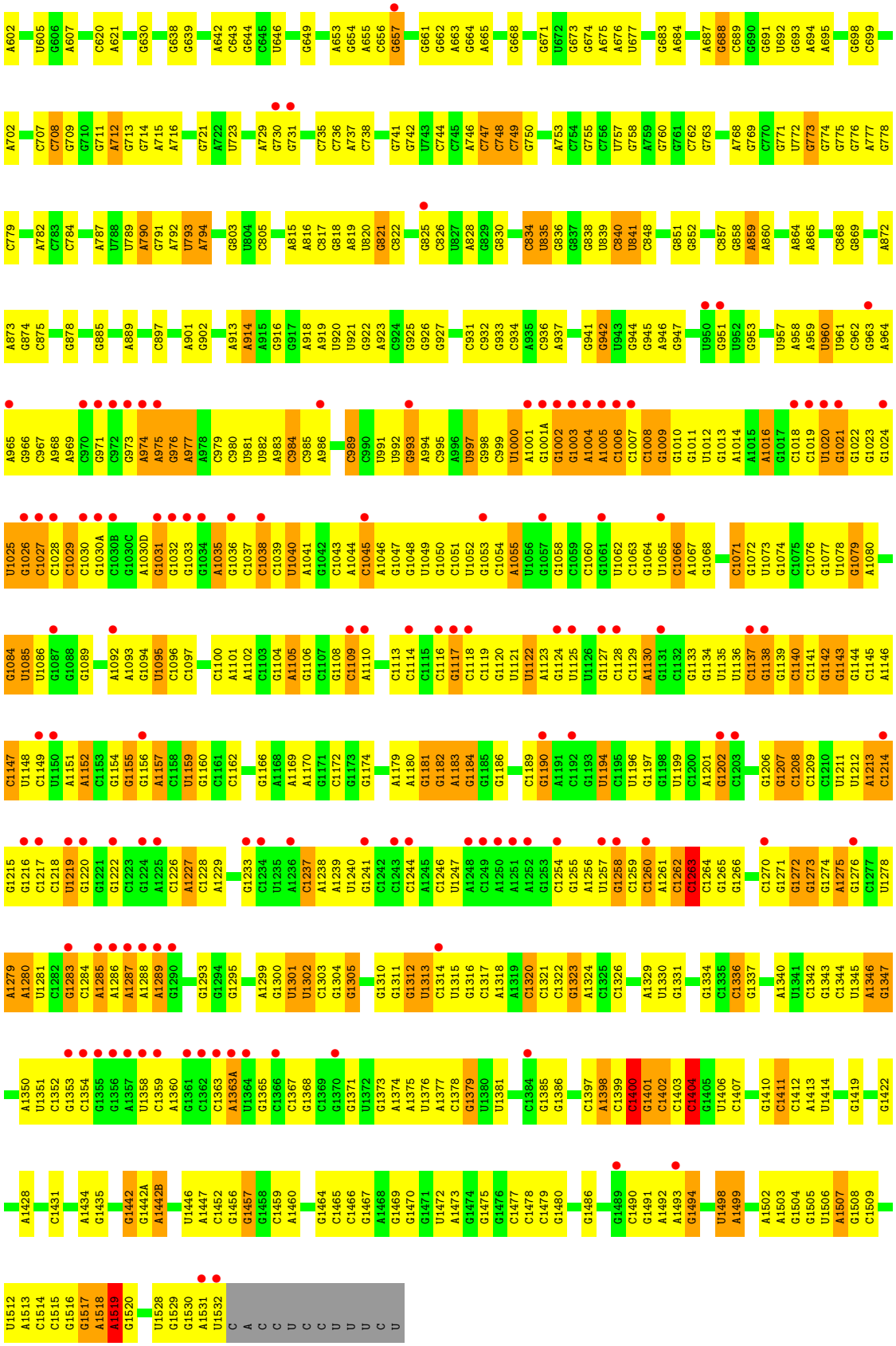




• Molecule 32: 16S Ribosomal RNA

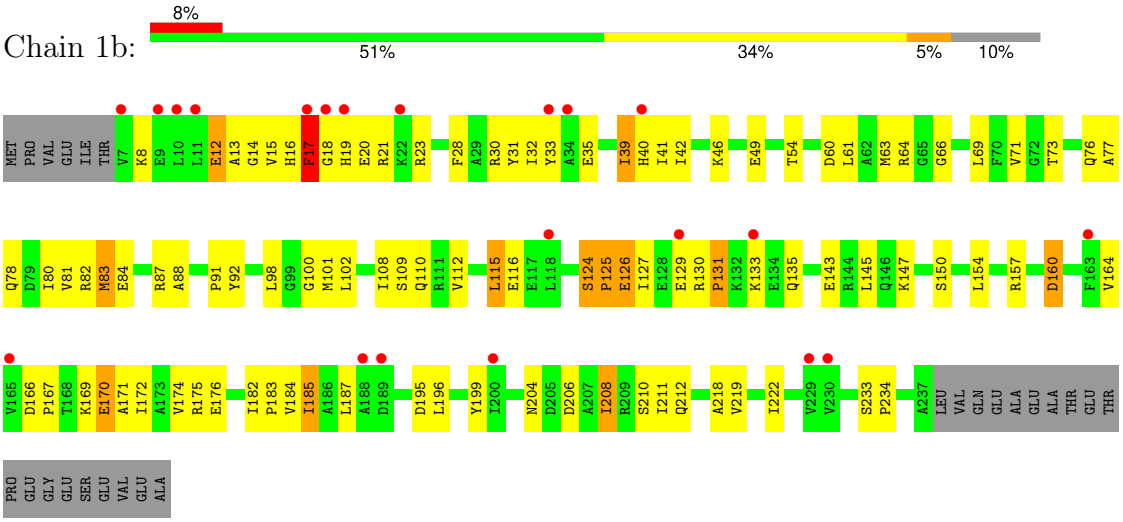
Chain 2a:





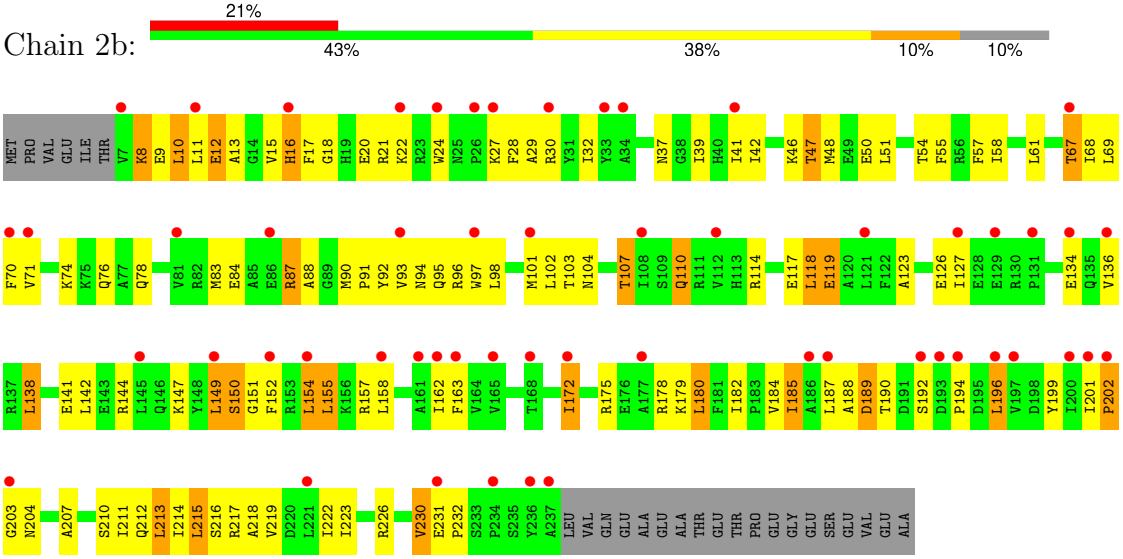
• Molecule 33: 30S ribosomal protein S2

Chain 1b:



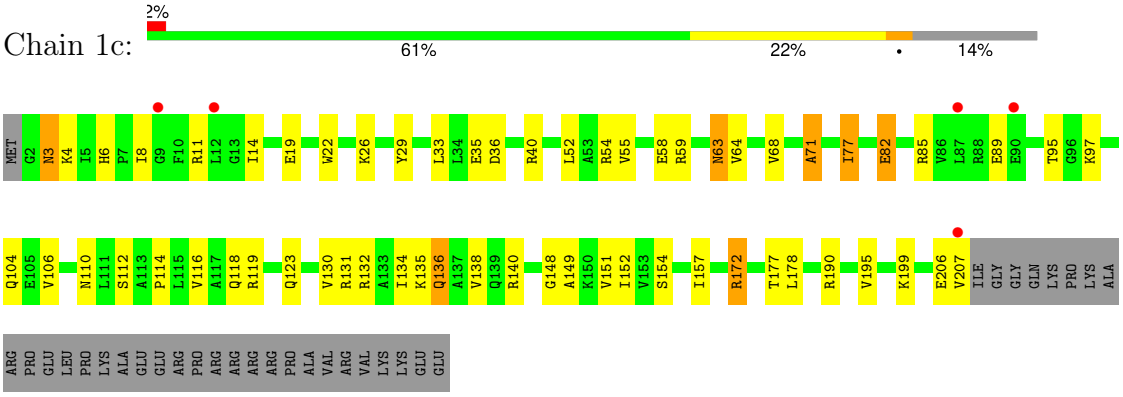
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



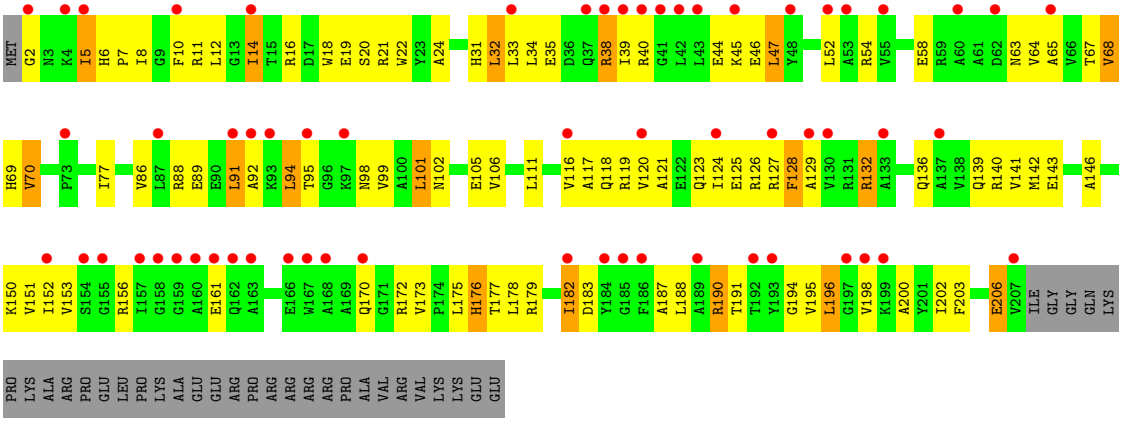
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



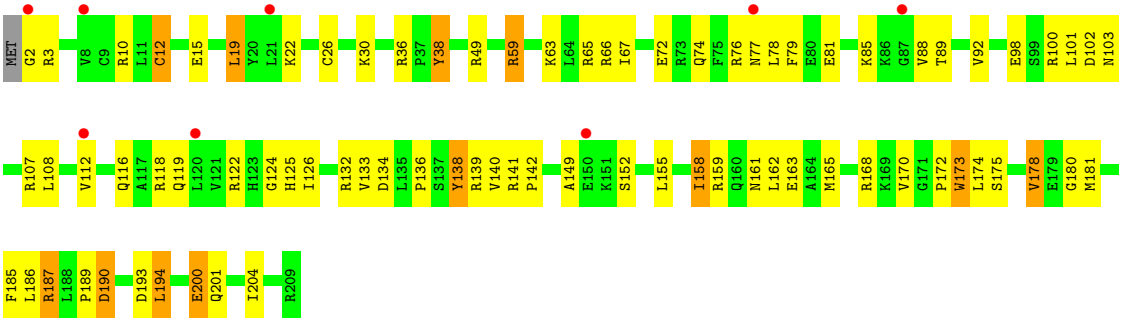
• Molecule 34: 30S ribosomal protein S3

Chain 2c:



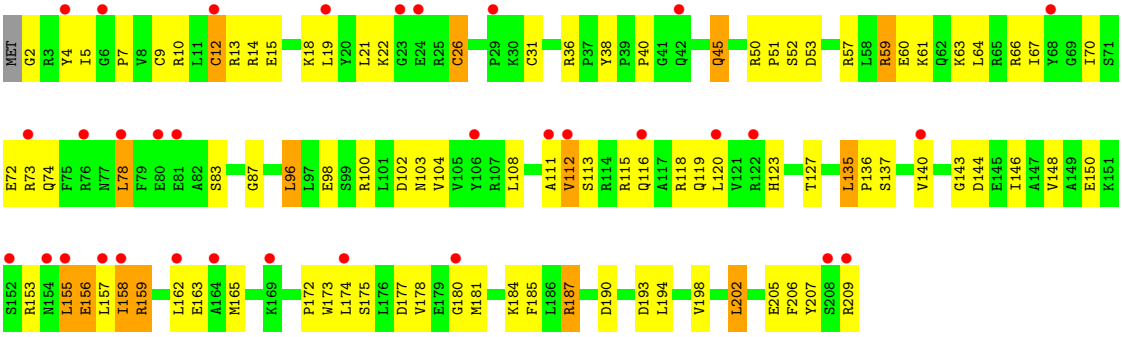
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



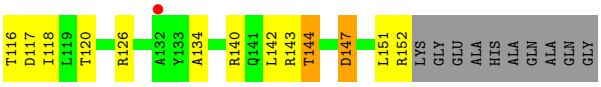
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



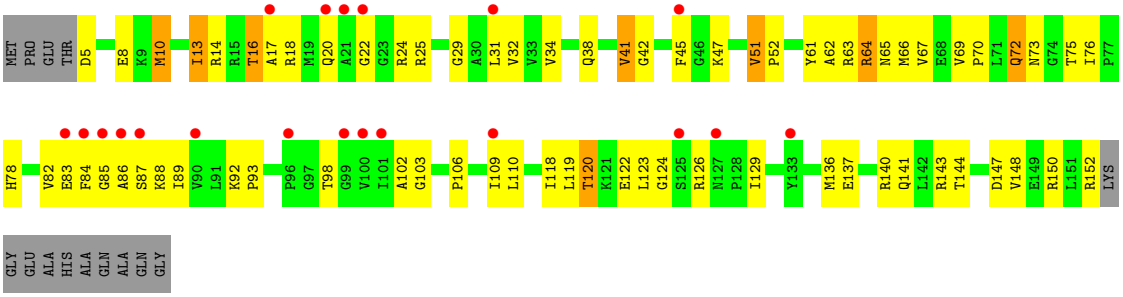
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



• Molecule 36: 30S ribosomal protein S5

Chain 2e:

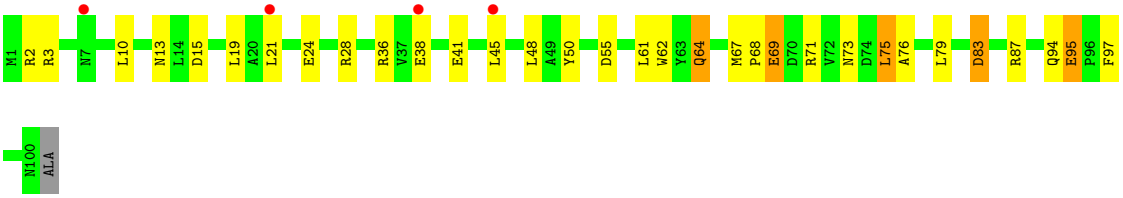


• Molecule 37: 30S ribosomal protein S6

Chain 1f:

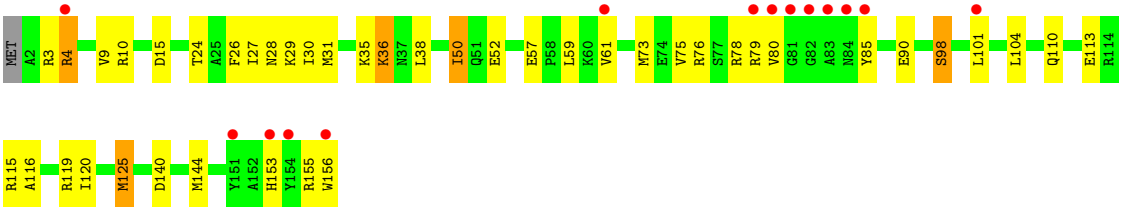
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



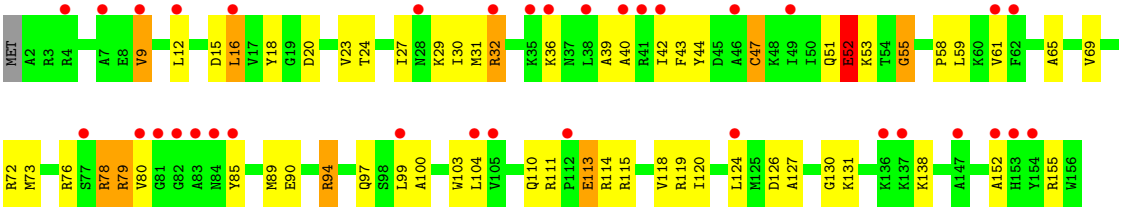
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



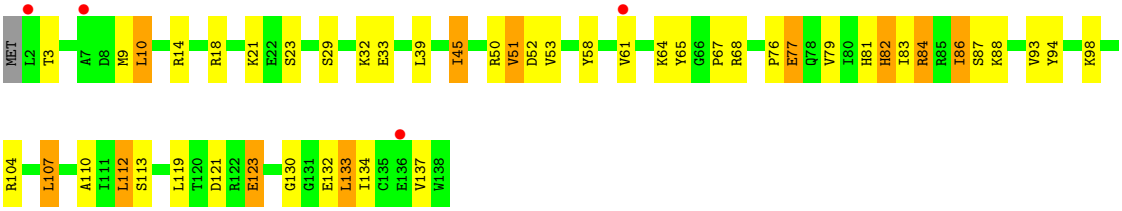
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



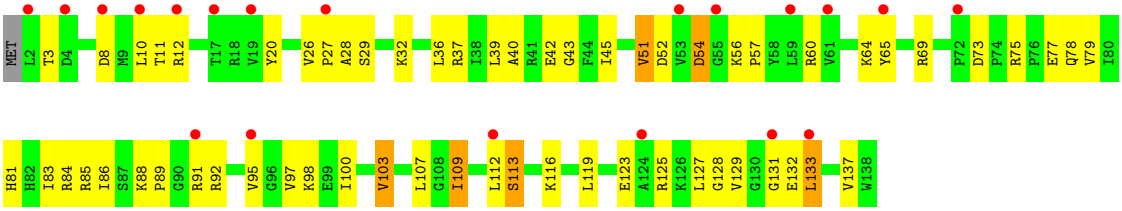
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



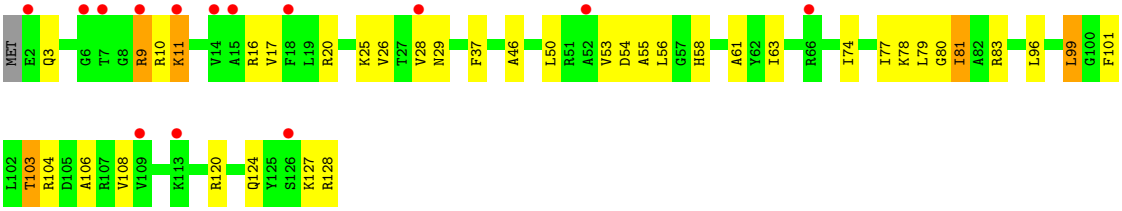
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



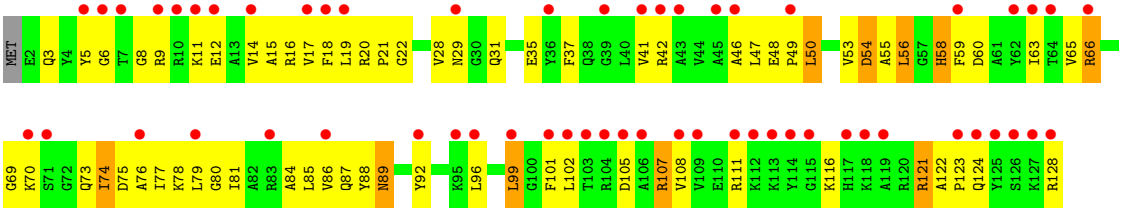
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



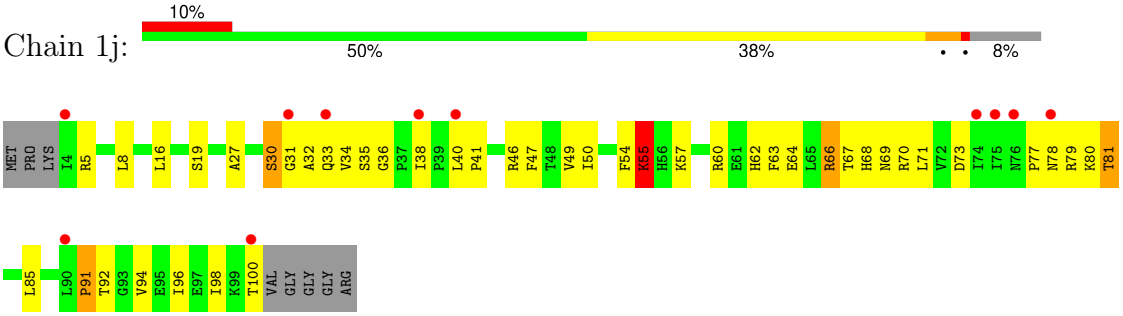
• Molecule 40: 30S ribosomal protein S9

Chain 2i:



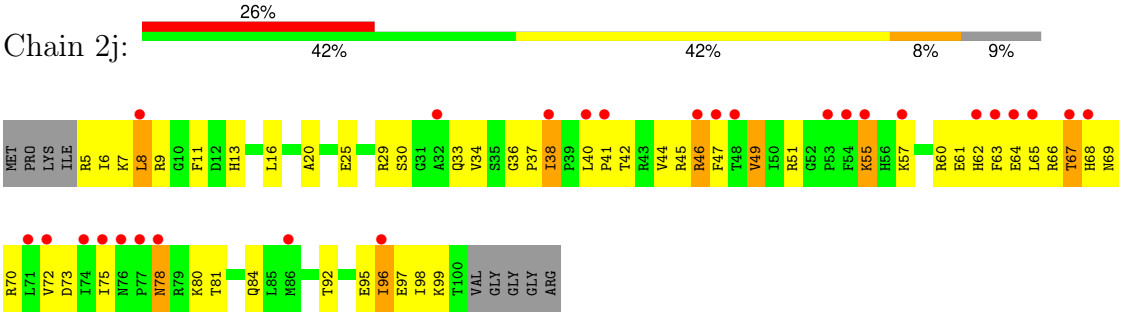
• Molecule 41: 30S ribosomal protein S10

Chain 1j:



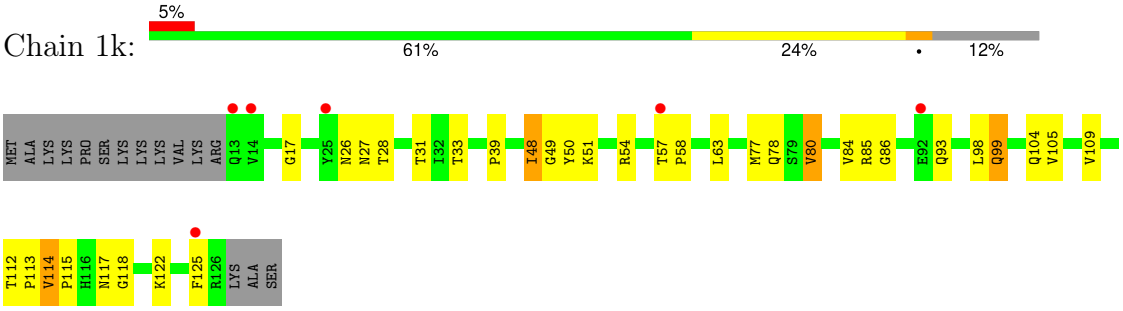
• Molecule 41: 30S ribosomal protein S10

Chain 2j:



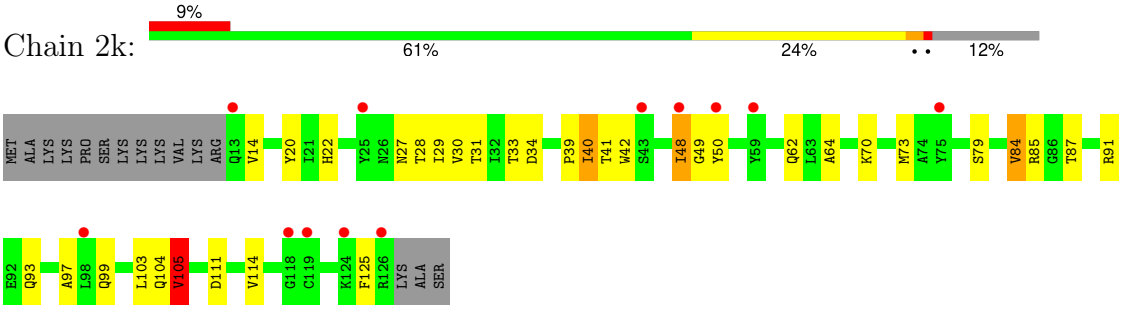
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



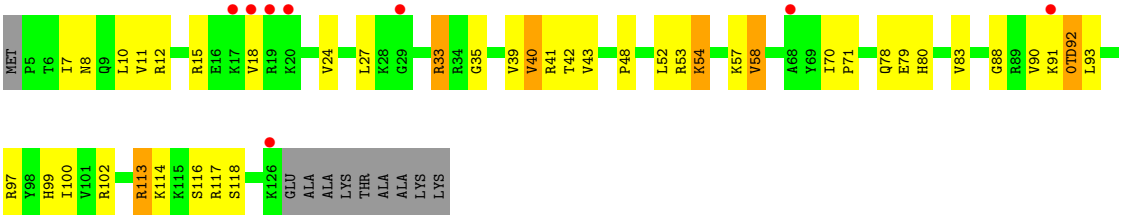
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



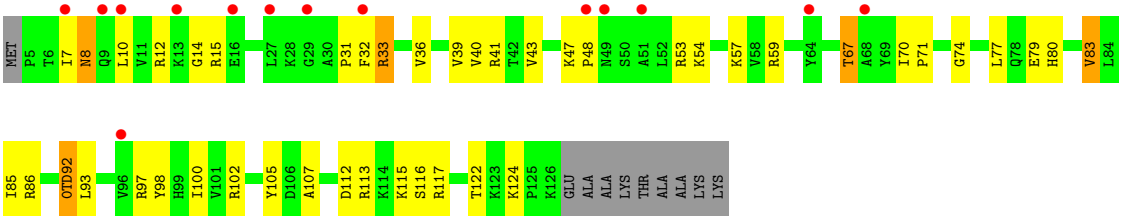
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



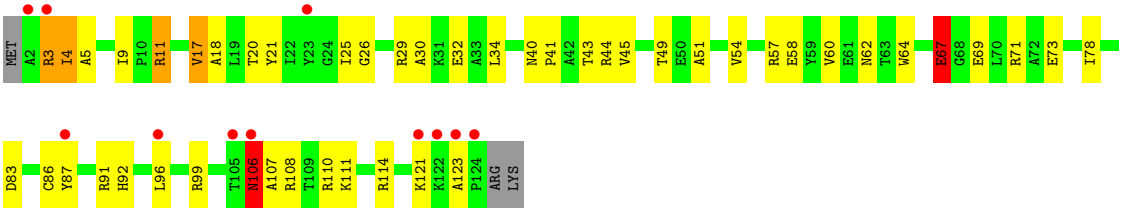
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



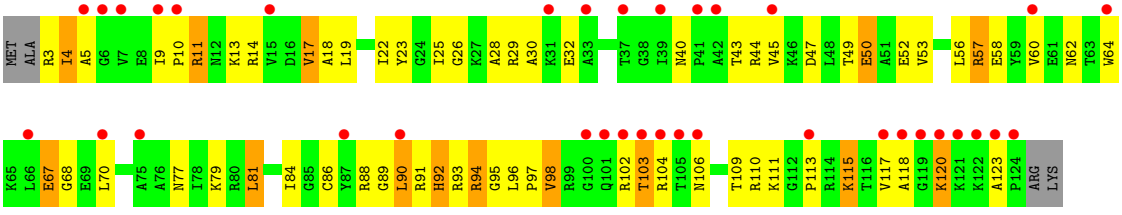
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



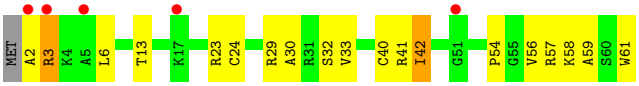
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



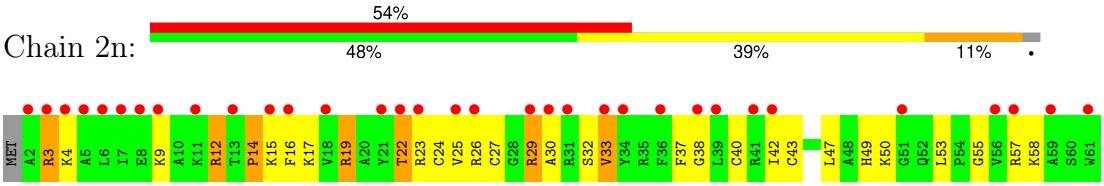
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



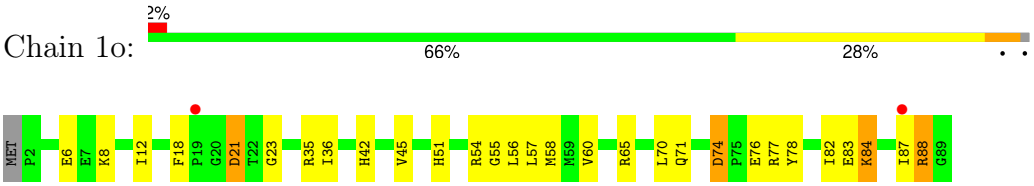
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:



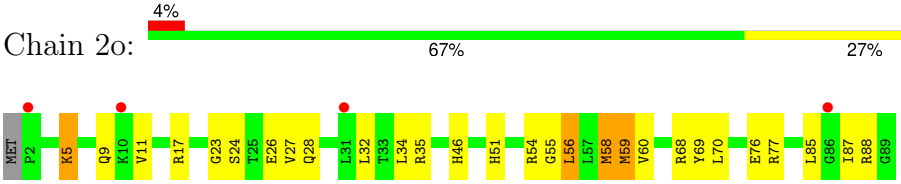
• Molecule 46: 30S ribosomal protein S15

Chain 1o:



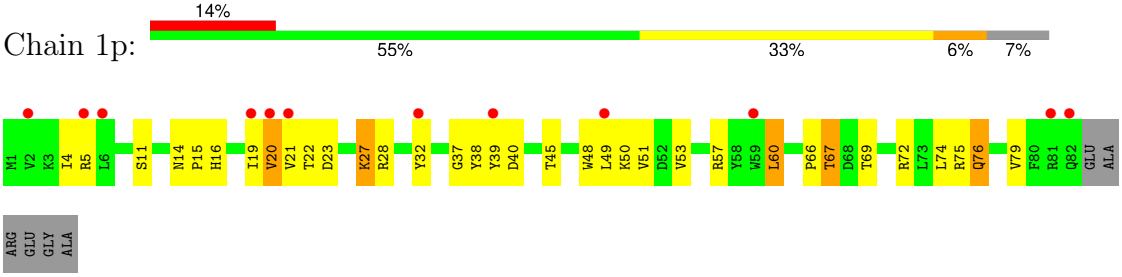
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



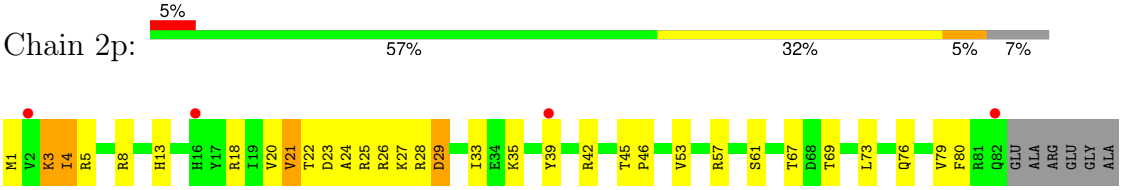
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



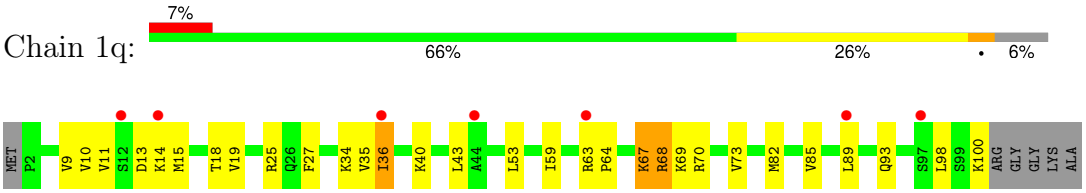
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



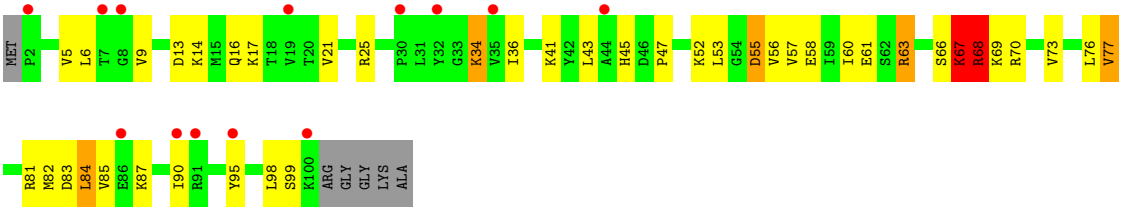
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



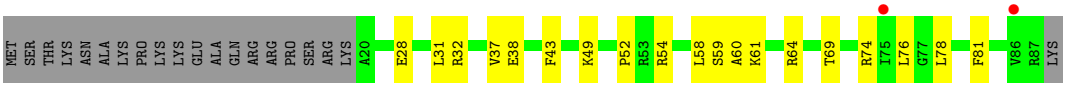
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



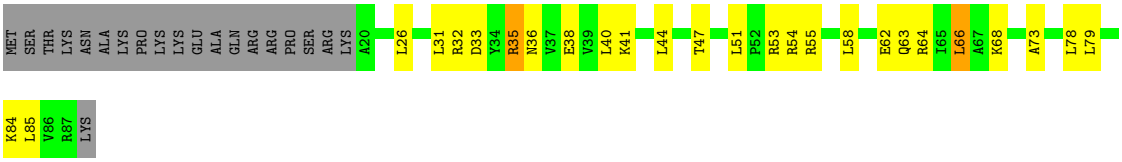
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



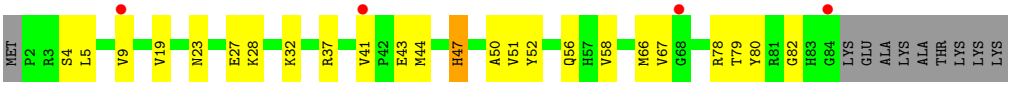
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



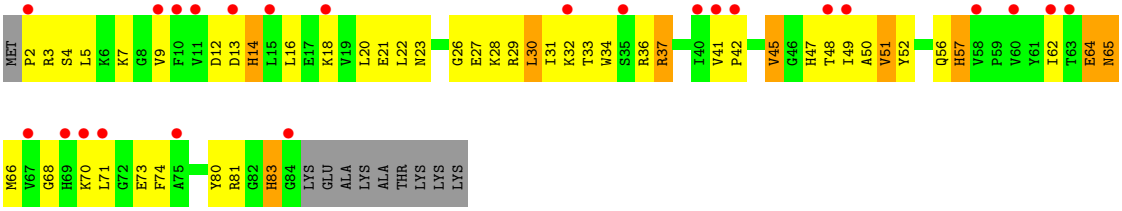
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



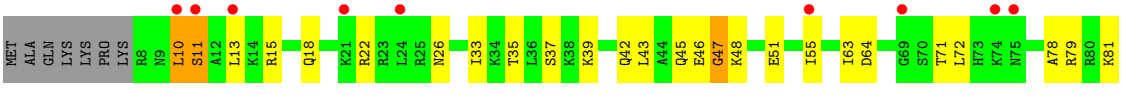
• Molecule 50: 30S ribosomal protein S19

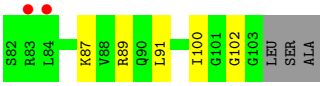
Chain 2s:



• Molecule 51: 30S ribosomal protein S20

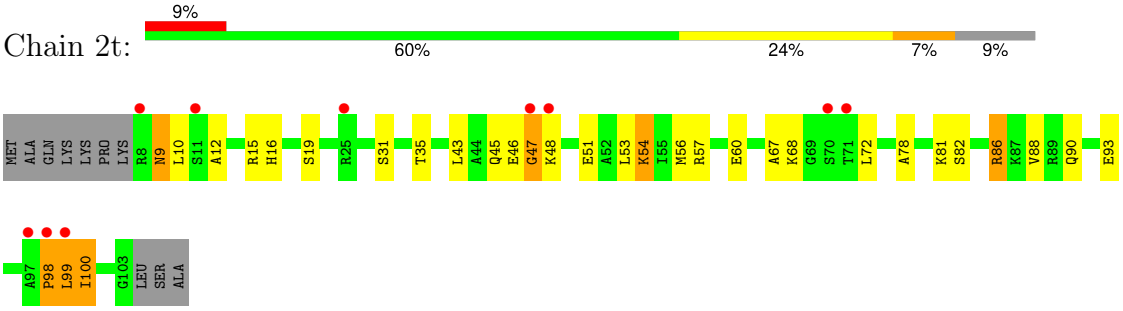
Chain 1t:





• Molecule 51: 30S ribosomal protein S20

Chain 2t:

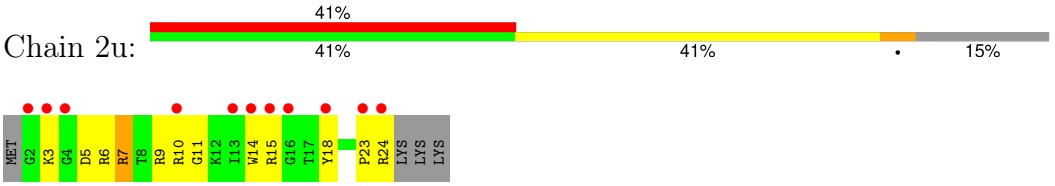


• Molecule 52: 30S ribosomal protein Thx

Chain 1u:

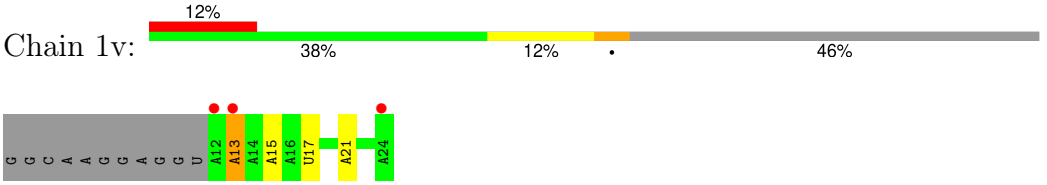
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



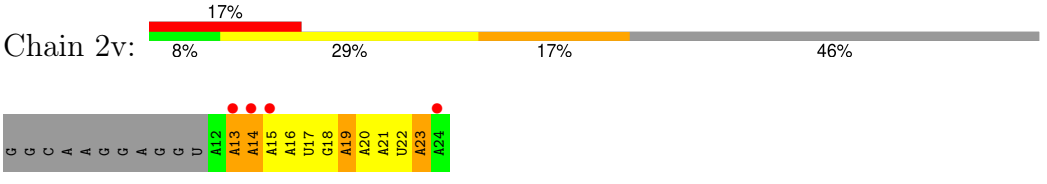
• Molecule 53: MET-LYS-mRNA

Chain 1v:



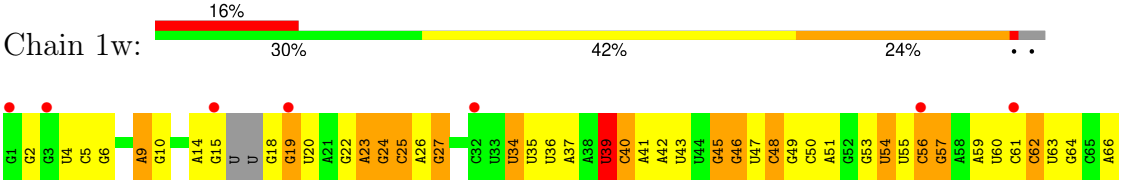
• Molecule 53: MET-LYS-mRNA

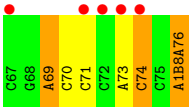
Chain 2v:



• Molecule 54: A-site Aminoacyl-tRNA Lys-tRNAlys

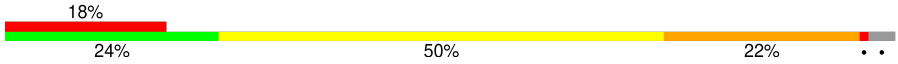
Chain 1w:

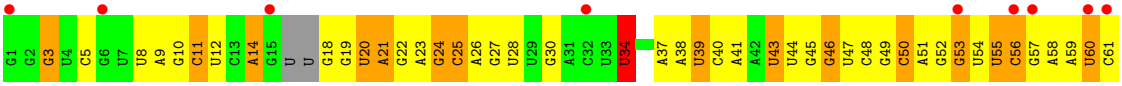


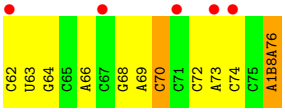


• Molecule 54: A-site Aminoacyl-tRNA Lys-tRNAlys

Chain 2w:

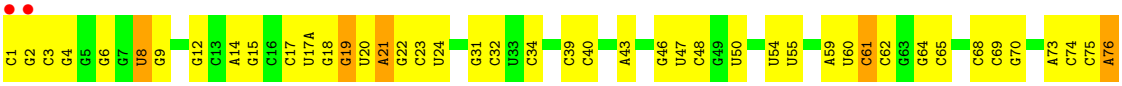






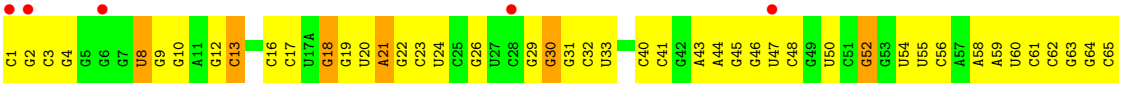
• Molecule 55: P-site Peptidyl-tRNA fMRC-tRNAcys RNA-part

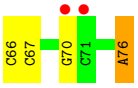
Chain 1x:



• Molecule 55: P-site Peptidyl-tRNA fMRC-tRNAcys RNA-part

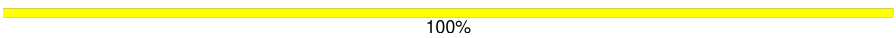
Chain 2x:





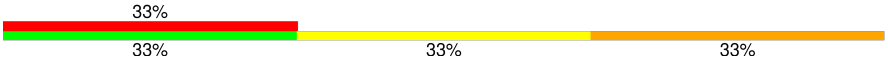
• Molecule 56: P-site Peptidyl-tRNA fMRC-tRNAcys Peptide-part

Chain 1z:



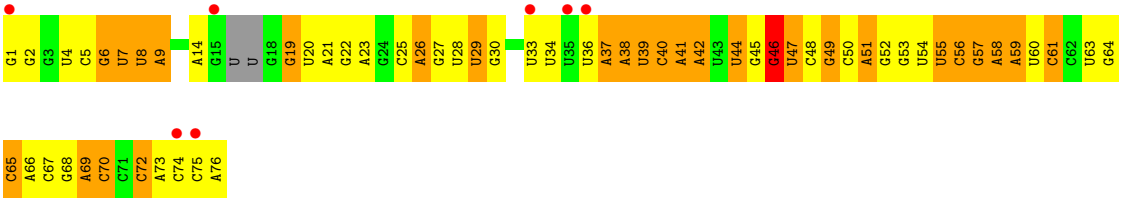
• Molecule 56: P-site Peptidyl-tRNA fMRC-tRNAcys Peptide-part

Chain 2z:



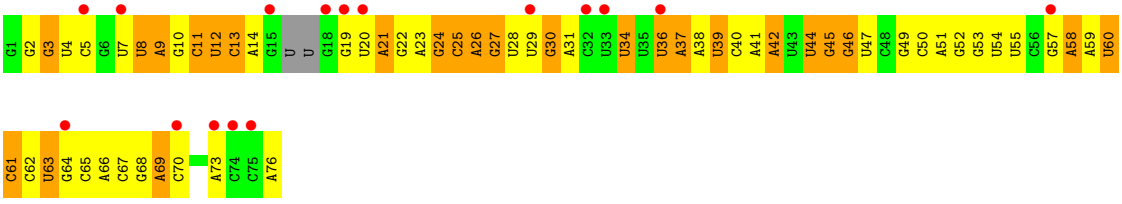
• Molecule 57: E-site Deacylated tRNAlys

Chain 1y:



• Molecule 57: E-site Deacylated tRNAlys

Chain 2y:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	210.04Å 447.59Å 618.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	124.58 – 2.80 124.58 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (124.58-2.80) 99.2 (124.58-2.80)	Depositor EDS
R_{merge}	0.31	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.23 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.17.1	Depositor
R, R_{free}	0.229 , 0.281 0.229 , 0.280	Depositor DCC
R_{free} test set	70928 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	53.7	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 54.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	299377	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FME, G7M, OMU, MA6, 5MU, A1B8A, UR3, 4OC, OMC, M2G, T6A, U8U, TEL, 8AN, K, OMG, SF4, 2MG, 4SU, 2MA, 5MC, PSU, MG, ZN, 0TD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1A	0.27	1/69011 (0.0%)	0.46	1/107720 (0.0%)
1	2A	0.21	0/67295	0.40	1/105042 (0.0%)
2	1B	0.21	0/2882	0.40	0/4494
2	2B	0.19	0/2879	0.38	0/4487
3	1D	0.28	0/2186	0.52	0/2944
3	2D	0.23	0/2186	0.47	0/2944
4	1E	0.26	0/1592	0.50	0/2149
4	2E	0.24	0/1592	0.45	0/2149
5	1F	0.24	0/1619	0.48	0/2193
5	2F	0.21	0/1615	0.47	0/2188
6	1G	0.22	0/1448	0.46	0/1957
6	2G	0.20	0/1453	0.46	0/1963
7	1H	0.22	0/1356	0.41	0/1834
7	2H	0.21	0/1356	0.41	0/1834
8	1I	0.20	0/1112	0.43	0/1514
8	2I	0.19	0/1079	0.40	0/1475
9	1N	0.25	0/1144	0.45	0/1543
9	2N	0.19	0/1144	0.38	0/1543
10	1O	0.25	0/943	0.49	0/1269
10	2O	0.23	0/943	0.48	0/1269
11	1P	0.26	0/1152	0.52	0/1533
11	2P	0.21	0/1152	0.51	0/1533
12	1Q	0.27	0/1143	0.48	0/1527
12	2Q	0.21	0/1143	0.45	0/1527
13	1R	0.26	0/982	0.49	0/1312
13	2R	0.24	0/982	0.53	0/1312
14	1S	0.23	0/883	0.46	0/1176
14	2S	0.20	0/880	0.47	0/1172
15	1T	0.25	0/1105	0.53	1/1477 (0.1%)
15	2T	0.20	0/1097	0.45	0/1468
16	1U	0.26	0/977	0.46	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.19	0/977	0.39	0/1301
17	1V	0.24	0/782	0.44	0/1049
17	2V	0.19	0/782	0.42	0/1049
18	1W	0.26	0/897	0.45	0/1205
18	2W	0.22	0/897	0.43	0/1205
19	1X	0.27	0/764	0.55	0/1025
19	2X	0.24	0/764	0.52	0/1025
20	1Y	0.22	0/819	0.48	0/1095
20	2Y	0.21	0/819	0.43	0/1095
21	1Z	0.22	0/1267	0.47	0/1717
21	2Z	0.21	0/1299	0.42	0/1763
22	10	0.25	0/662	0.47	0/881
22	20	0.23	0/662	0.46	0/881
23	11	0.24	0/762	0.43	0/1014
23	21	0.22	0/762	0.44	0/1014
24	12	0.24	0/590	0.45	0/781
24	22	0.20	0/590	0.42	0/781
25	13	0.23	0/474	0.45	0/635
25	23	0.18	0/469	0.39	0/630
26	14	0.22	0/565	0.54	0/761
26	24	0.22	0/545	0.55	0/737
27	15	0.25	0/469	0.51	0/635
27	25	0.23	0/469	0.46	0/635
28	16	0.26	0/460	0.44	0/613
28	26	0.20	0/456	0.40	0/608
29	17	0.26	0/426	0.51	0/561
29	27	0.24	0/426	0.50	0/561
30	18	0.27	0/525	0.49	0/691
30	28	0.21	0/525	0.42	0/691
31	19	0.26	0/310	0.53	0/407
31	29	0.20	0/310	0.40	0/407
32	1a	0.20	0/35795	0.38	0/55864
32	2a	0.19	1/35886 (0.0%)	0.38	1/56005 (0.0%)
33	1b	0.21	0/1881	0.48	0/2542
33	2b	0.29	1/1860 (0.1%)	0.51	0/2518
34	1c	0.19	0/1572	0.38	0/2126
34	2c	0.25	0/1566	0.51	1/2119 (0.0%)
35	1d	0.20	0/1685	0.44	0/2262
35	2d	0.20	0/1704	0.46	0/2284
36	1e	0.22	0/1145	0.49	0/1543
36	2e	0.21	0/1149	0.49	1/1548 (0.1%)
37	1f	0.22	0/823	0.41	0/1115
37	2f	0.21	0/829	0.40	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.19	0/1250	0.41	0/1679
38	2g	0.19	0/1254	0.44	0/1683
39	1h	0.20	0/1108	0.42	0/1494
39	2h	0.19	0/1108	0.44	0/1494
40	1i	0.21	0/1002	0.50	0/1346
40	2i	0.20	0/997	0.44	0/1343
41	1j	0.19	0/722	0.49	0/982
41	2j	0.22	0/727	0.44	0/988
42	1k	0.20	0/844	0.44	0/1145
42	2k	0.17	0/848	0.42	0/1149
43	1l	0.21	0/937	0.44	0/1260
43	2l	0.21	0/937	0.45	0/1260
44	1m	0.21	0/969	0.47	0/1302
44	2m	0.26	0/961	0.50	0/1291
45	1n	0.18	0/501	0.44	0/664
45	2n	0.20	0/501	0.45	0/664
46	1o	0.19	0/739	0.42	0/985
46	2o	0.19	0/739	0.41	0/985
47	1p	0.21	0/697	0.49	0/939
47	2p	0.21	0/693	0.49	0/935
48	1q	0.18	0/836	0.41	0/1117
48	2q	0.21	0/836	0.47	0/1117
49	1r	0.19	0/560	0.42	0/746
49	2r	0.21	0/560	0.44	0/746
50	1s	0.20	0/667	0.48	0/900
50	2s	0.24	0/661	0.56	0/893
51	1t	0.19	0/730	0.43	0/965
51	2t	0.21	0/729	0.49	0/965
52	1u	0.20	0/203	0.51	0/266
52	2u	0.23	0/203	0.42	0/266
53	1v	0.23	0/319	0.38	0/495
53	2v	0.24	0/319	0.44	0/495
54	1w	0.30	2/1593 (0.1%)	0.38	0/2474
54	2w	0.36	2/1593 (0.1%)	0.54	0/2474
55	1x	0.25	0/1723	0.40	0/2684
55	2x	0.25	1/1723 (0.1%)	0.39	0/2684
56	1z	0.50	0/16	0.68	0/19
56	2z	0.35	0/16	0.79	0/19
57	1y	0.30	0/1618	0.43	0/2513
57	2y	0.32	2/1618 (0.1%)	0.48	0/2513
All	All	0.23	10/316807 (0.0%)	0.43	6/474290 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	2F	0	1
29	27	0	1
33	1b	0	2
All	All	0	4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	2b	10	LEU	CA-C	6.23	1.61	1.52
57	2y	46	G7M	O3'-P	5.51	1.61	1.56
54	2w	46	G7M	O3'-P	5.39	1.61	1.56
54	1w	46	G7M	O3'-P	5.38	1.61	1.56
54	2w	37	T6A	O3'-P	5.26	1.61	1.56
1	1A	2552	OMU	O3'-P	5.13	1.61	1.56
54	1w	37	T6A	O3'-P	5.08	1.61	1.56
57	2y	37	T6A	O3'-P	5.05	1.61	1.56
55	2x	8	4SU	O3'-P	5.04	1.61	1.56
32	2a	527	G7M	O3'-P	5.01	1.61	1.56

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	2c	94	LEU	N-CA-C	-8.65	104.76	114.62
36	2e	109	ILE	N-CA-C	-6.80	104.98	112.80
1	1A	1992	G	C2'-C3'-O3'	6.36	119.04	109.50
1	2A	1992	G	C2'-C3'-O3'	6.10	118.65	109.50
15	1T	129	ARG	N-CA-C	-5.74	106.89	112.97
32	2a	1263	C	N1-C2-O2	5.15	134.36	118.90

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	1b	126	GLU	Peptide
33	1b	130	ARG	Peptide
29	27	46	VAL	Peptide
5	2F	20	LEU	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31193	700	0
1	2A	60322	0	30424	798	0
2	1B	2577	0	1304	30	0
2	2B	2575	0	1303	56	0
3	1D	2136	0	2218	51	0
3	2D	2136	0	2218	57	0
4	1E	1559	0	1618	40	0
4	2E	1559	0	1618	37	0
5	1F	1584	0	1625	52	0
5	2F	1580	0	1619	61	0
6	1G	1423	0	1436	49	0
6	2G	1428	0	1438	66	0
7	1H	1330	0	1407	28	0
7	2H	1330	0	1407	39	0
8	1I	1097	0	1140	29	0
8	2I	1064	0	1082	34	0
9	1N	1117	0	1184	22	0
9	2N	1117	0	1184	18	0
10	1O	933	0	996	24	0
10	2O	933	0	996	24	0
11	1P	1135	0	1212	37	0
11	2P	1135	0	1212	38	0
12	1Q	1122	0	1179	35	0
12	2Q	1122	0	1179	46	0
13	1R	968	0	1033	22	0
13	2R	968	0	1033	24	0
14	1S	873	0	927	26	0
14	2S	870	0	923	60	0
15	1T	1091	0	1151	33	0
15	2T	1083	0	1136	30	0
16	1U	959	0	1018	22	0
16	2U	959	0	1019	31	0
17	1V	771	0	829	8	0
17	2V	771	0	830	21	0
18	1W	886	0	940	27	0
18	2W	886	0	940	17	0
19	1X	750	0	814	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	25	0
20	1Y	806	0	881	20	0
20	2Y	806	0	881	22	0
21	1Z	1240	0	1240	39	0
21	2Z	1271	0	1273	49	0
22	10	653	0	674	12	0
22	20	653	0	674	20	0
23	11	755	0	826	17	0
23	21	755	0	826	23	0
24	12	588	0	643	9	0
24	22	588	0	643	22	0
25	13	469	0	518	15	0
25	23	464	0	514	16	0
26	14	552	0	533	18	0
26	24	532	0	503	27	0
27	15	455	0	465	6	0
27	25	455	0	465	10	0
28	16	453	0	473	13	0
28	26	449	0	469	14	0
29	17	418	0	467	11	0
29	27	418	0	467	15	0
30	18	517	0	582	14	0
30	28	517	0	582	18	0
31	19	307	0	335	6	0
31	29	307	0	335	10	0
32	1a	32246	0	16293	454	0
32	2a	32327	0	16338	577	0
33	1b	1846	0	1867	53	0
33	2b	1825	0	1828	81	0
34	1c	1548	0	1535	40	0
34	2c	1542	0	1517	75	0
35	1d	1655	0	1672	56	0
35	2d	1674	0	1713	71	0
36	1e	1129	0	1185	35	0
36	2e	1133	0	1191	47	0
37	1f	810	0	804	16	0
37	2f	816	0	808	17	0
38	1g	1231	0	1238	28	0
38	2g	1235	0	1249	37	0
39	1h	1088	0	1126	30	0
39	2h	1088	0	1126	42	0
40	1i	983	0	986	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	978	0	966	52	0
41	1j	709	0	650	34	0
41	2j	714	0	672	35	0
42	1k	829	0	825	17	0
42	2k	833	0	834	17	0
43	1l	932	0	981	27	0
43	2l	932	0	981	27	0
44	1m	958	0	1002	30	0
44	2m	950	0	988	50	0
45	1n	492	0	529	20	0
45	2n	492	0	529	25	0
46	1o	728	0	760	16	0
46	2o	728	0	760	27	0
47	1p	681	0	697	27	0
47	2p	677	0	686	25	0
48	1q	823	0	891	17	0
48	2q	823	0	891	26	0
49	1r	555	0	618	13	0
49	2r	555	0	618	12	0
50	1s	652	0	662	10	0
50	2s	646	0	644	40	0
51	1t	728	0	798	22	0
51	2t	727	0	796	19	0
52	1u	199	0	208	7	0
52	2u	199	0	208	11	0
53	1v	283	0	141	6	0
53	2v	283	0	141	9	0
54	1w	1599	0	800	31	0
54	2w	1599	0	801	48	0
55	1x	1646	0	839	20	0
55	2x	1646	0	839	32	0
56	1z	27	0	28	1	0
56	2z	27	0	28	5	0
57	1y	1577	0	799	39	0
57	2y	1577	0	798	38	0
58	10	11	0	0	0	0
58	11	5	0	0	0	0
58	12	2	0	0	0	0
58	13	4	0	0	0	0
58	14	1	0	0	0	0
58	15	8	0	0	0	0
58	16	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	17	7	0	0	0	0
58	18	6	0	0	0	0
58	19	1	0	0	0	0
58	1A	1080	0	0	0	0
58	1B	40	0	0	0	0
58	1D	12	0	0	0	0
58	1E	12	0	0	0	0
58	1F	11	0	0	0	0
58	1G	5	0	0	0	0
58	1N	6	0	0	0	0
58	1O	4	0	0	0	0
58	1P	9	0	0	0	0
58	1Q	7	0	0	0	0
58	1R	7	0	0	0	0
58	1S	1	0	0	0	0
58	1T	2	0	0	0	0
58	1U	10	0	0	0	0
58	1V	8	0	0	0	0
58	1W	7	0	0	0	0
58	1X	5	0	0	0	0
58	1Y	2	0	0	0	0
58	1Z	3	0	0	0	0
58	1a	209	0	0	0	0
58	1b	1	0	0	0	0
58	1d	1	0	0	0	0
58	1e	1	0	0	0	0
58	1f	2	0	0	0	0
58	1l	2	0	0	0	0
58	1m	1	0	0	0	0
58	1n	2	0	0	0	0
58	1p	2	0	0	0	0
58	1t	1	0	0	0	0
58	1v	1	0	0	0	0
58	1w	5	0	0	0	0
58	1x	12	0	0	0	0
58	20	2	0	0	0	0
58	21	4	0	0	0	0
58	23	3	0	0	0	0
58	25	3	0	0	0	0
58	27	3	0	0	0	0
58	28	2	0	0	0	0
58	2A	824	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	2B	19	0	0	0	0
58	2D	8	0	0	0	0
58	2E	7	0	0	0	0
58	2F	6	0	0	0	0
58	2G	1	0	0	0	0
58	2N	1	0	0	0	0
58	2O	2	0	0	0	0
58	2P	2	0	0	0	0
58	2Q	2	0	0	0	0
58	2R	2	0	0	0	0
58	2T	3	0	0	0	0
58	2U	1	0	0	0	0
58	2V	2	0	0	0	0
58	2W	4	0	0	0	0
58	2X	2	0	0	0	0
58	2Y	1	0	0	0	0
58	2Z	1	0	0	0	0
58	2a	211	0	0	0	0
58	2d	2	0	0	0	0
58	2e	1	0	0	0	0
58	2f	1	0	0	0	0
58	2g	1	0	0	0	0
58	2j	1	0	0	0	0
58	2k	1	0	0	0	0
58	2l	4	0	0	0	0
58	2q	2	0	0	1	0
58	2r	1	0	0	0	0
58	2t	1	0	0	0	0
58	2v	3	0	0	0	0
58	2w	2	0	0	0	0
58	2x	5	0	0	0	0
59	1A	1	0	0	0	0
59	2A	1	0	0	0	0
60	1A	58	0	65	4	0
60	2A	58	0	65	4	0
61	14	1	0	0	0	0
61	15	1	0	0	0	0
61	16	1	0	0	0	0
61	19	1	0	0	0	0
61	1Y	1	0	0	0	0
61	1n	1	0	0	0	0
61	24	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	25	1	0	0	0	0
61	26	1	0	0	0	0
61	29	1	0	0	0	0
61	2Y	1	0	0	0	0
61	2n	1	0	0	0	0
62	1d	8	0	0	1	0
62	2d	8	0	0	2	0
63	10	13	0	0	1	0
63	11	9	0	0	0	0
63	12	4	0	0	0	0
63	13	4	0	0	0	0
63	15	6	0	0	0	0
63	16	2	0	0	0	0
63	17	5	0	0	0	0
63	18	9	0	0	2	0
63	1A	1780	0	0	101	0
63	1B	57	0	0	3	0
63	1D	24	0	0	1	0
63	1E	22	0	0	3	0
63	1F	14	0	0	3	0
63	1G	2	0	0	0	0
63	1H	2	0	0	0	0
63	1I	1	0	0	0	0
63	1N	7	0	0	0	0
63	1O	4	0	0	0	0
63	1P	19	0	0	1	0
63	1Q	6	0	0	0	0
63	1R	13	0	0	3	0
63	1S	4	0	0	0	0
63	1T	11	0	0	0	0
63	1U	10	0	0	1	0
63	1V	9	0	0	0	0
63	1W	10	0	0	2	0
63	1X	4	0	0	0	0
63	1Y	1	0	0	0	0
63	1Z	1	0	0	0	0
63	1a	226	0	0	22	0
63	1b	1	0	0	0	0
63	1e	2	0	0	0	0
63	1l	7	0	0	0	0
63	1m	1	0	0	0	0
63	1n	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	1q	2	0	0	0	0
63	1v	5	0	0	0	0
63	1w	5	0	0	1	0
63	1x	3	0	0	0	0
63	1y	1	0	0	1	0
63	20	3	0	0	0	0
63	21	5	0	0	1	0
63	25	1	0	0	1	0
63	27	2	0	0	0	0
63	28	2	0	0	1	0
63	29	1	0	0	0	0
63	2A	850	0	0	79	0
63	2B	16	0	0	1	0
63	2D	18	0	0	2	0
63	2E	10	0	0	1	0
63	2F	12	0	0	0	0
63	2N	1	0	0	0	0
63	2O	1	0	0	0	0
63	2P	1	0	0	0	0
63	2Q	1	0	0	0	0
63	2R	2	0	0	0	0
63	2T	4	0	0	0	0
63	2U	2	0	0	0	0
63	2W	2	0	0	0	0
63	2X	2	0	0	0	0
63	2Z	1	0	0	0	0
63	2a	148	0	0	21	0
63	2d	1	0	0	0	0
63	2e	1	0	0	0	0
63	2i	1	0	0	0	0
63	2l	5	0	0	0	0
63	2p	2	0	0	0	0
63	2t	2	0	0	0	0
63	2v	1	0	0	0	0
63	2w	4	0	0	1	0
63	2x	4	0	0	0	0
All	All	299377	0	196882	4932	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (4932) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1082:U:H3	1:1A:1086:A:N6	1.23	1.34
54:2w:51:A:N6	54:2w:63:U:H3	1.46	1.14
57:2y:10:G:H1	57:2y:25:C:N4	1.47	1.11
1:2A:2503:2MA:H8	56:2z:2:ARG:HH12	1.17	1.04
54:2w:51:A:H3'	54:2w:64:G:H21	1.17	1.03
1:1A:1082:U:O4	1:1A:1086:A:N1	1.95	0.98
1:1A:1057:A:H61	1:1A:1081:U:H3	1.12	0.97
54:2w:51:A:N6	54:2w:63:U:N3	2.07	0.96
1:1A:2128:C:H42	1:1A:2160:G:H1	0.98	0.96
1:1A:792:G:O6	63:1A:4103:HOH:O	1.83	0.94
32:2a:1399:C:H4'	32:2a:1400:5MC:H5'	1.51	0.93
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.49	0.92
32:1a:1004:A:N6	32:1a:1037:C:N3	2.18	0.91
53:1v:21:A:N1	54:1w:34:U8U:O4	2.06	0.89
1:1A:2128:C:N4	1:1A:2160:G:H1	1.69	0.89
1:1A:2427:C:OP1	63:1A:4104:HOH:O	1.90	0.89
54:1w:50:C:H42	54:1w:64:G:H1	1.19	0.88
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.08	0.88
54:2w:51:A:H3'	54:2w:64:G:N2	1.89	0.88
54:1w:27:G:H1	54:1w:43:U:H3	1.19	0.87
34:1c:82:GLU:HG3	34:1c:85:ARG:HH21	1.37	0.87
1:1A:1780:A:N7	63:1A:4119:HOH:O	2.08	0.87
54:2w:51:A:N1	54:2w:63:U:O4	2.08	0.87
57:2y:10:G:N2	57:2y:25:C:N3	2.22	0.86
5:2F:64:ILE:HD11	5:2F:75:HIS:HB2	1.57	0.86
1:1A:668:G:N7	63:1A:4120:HOH:O	2.08	0.86
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.09	0.85
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.10	0.84
1:2A:948:G:OP1	63:2A:3905:HOH:O	1.96	0.84
1:2A:1689:A:H62	1:2A:1698:A:H2	1.25	0.84
1:2A:2057:A:OP2	63:2A:3904:HOH:O	1.95	0.84
1:2A:2138:C:H42	1:2A:2153:G:H1	1.27	0.83
41:2j:47:PHE:HB2	41:2j:63:PHE:HB2	1.58	0.83
1:1A:1071:G:O6	1:1A:1100:C:N4	2.12	0.82
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.11	0.82
32:2a:1182:G:H4'	32:2a:1183:A:H5'	1.61	0.82
44:2m:123:ALA:HB3	54:2w:39:PSU:H4'	1.61	0.82
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.10	0.82
1:1A:2136:C:N3	1:1A:2155:G:C2	2.48	0.82
1:2A:827:U:OP1	63:2A:3906:HOH:O	1.97	0.82
33:2b:91:PRO:HG2	33:2b:155:LEU:HB2	1.60	0.82
57:2y:9:A:N3	57:2y:45:G:N2	2.27	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2713:A:OP1	13:1R:14:SER:OG	1.98	0.82
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.10	0.82
1:1A:2499:C:OP1	63:1A:4105:HOH:O	1.97	0.82
3:1D:180:GLY:HA3	3:1D:275:LYS:HB3	1.60	0.82
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.62	0.82
26:24:53:GLU:HG2	26:24:55:ARG:H	1.44	0.82
22:20:10:THR:HG22	22:20:12:ASN:H	1.43	0.81
1:1A:1056:G:H5"	1:1A:1057:A:H5'	1.61	0.81
15:1T:77:PRO:HG2	15:1T:80:SER:HB2	1.63	0.81
48:1q:64:PRO:HB3	48:1q:70:ARG:HH11	1.45	0.81
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	1.62	0.81
1:1A:1865:G:OP1	63:1A:4108:HOH:O	1.99	0.81
1:1A:2136:C:N3	1:1A:2155:G:N2	2.28	0.81
1:2A:962:G:OP1	63:2A:3905:HOH:O	1.99	0.81
42:2k:48:ILE:O	42:2k:50:TYR:N	2.14	0.81
1:1A:1332:G:OP1	63:1A:4106:HOH:O	1.98	0.80
1:1A:2096:U:H3	1:1A:2193:G:H1	1.29	0.80
34:2c:63:ASN:HB3	34:2c:98:ASN:HD22	1.46	0.80
40:2i:14:VAL:HG23	40:2i:66:ARG:HG3	1.62	0.80
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.63	0.80
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.62	0.80
1:2A:1604:C:OP1	63:2A:3907:HOH:O	1.98	0.80
40:2i:15:ALA:HB2	40:2i:65:VAL:HG23	1.63	0.80
32:2a:1183:A:H3'	32:2a:1184:G:H5"	1.64	0.80
1:1A:376:C:OP1	63:1A:4107:HOH:O	1.99	0.80
1:1A:1082:U:N3	1:1A:1086:A:N6	2.04	0.80
1:1A:2037:G:O6	63:1A:4109:HOH:O	1.99	0.80
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.64	0.80
41:2j:8:LEU:HB3	41:2j:96:ILE:HG23	1.64	0.80
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.11	0.79
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.31	0.79
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.64	0.79
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.64	0.79
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.15	0.79
3:1D:8:PRO:HB3	3:1D:14:ARG:HG2	1.65	0.79
32:2a:708:C:H2'	32:2a:709:G:H8	1.47	0.79
32:1a:975:A:H4'	32:1a:976:G:H5"	1.65	0.79
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.65	0.79
32:2a:1271:G:N2	32:2a:1272:G:N7	2.31	0.78
1:1A:1671:U:O4	63:1A:4110:HOH:O	2.01	0.78
1:1A:2550:G:OP1	63:1A:4110:HOH:O	2.00	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:34:GLU:HA	44:2m:57:ARG:HH21	1.48	0.78
1:1A:2136:C:N4	1:1A:2155:G:N1	2.31	0.78
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.66	0.78
26:14:55:ARG:H	26:14:56:VAL:HA	1.47	0.78
37:2f:2:ARG:HE	37:2f:69:GLU:HG2	1.47	0.78
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.16	0.78
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.66	0.78
1:2A:2497:A:O2'	63:2A:3908:HOH:O	2.01	0.78
41:1j:27:ALA:HA	41:1j:81:THR:HG21	1.64	0.78
5:2F:103:LYS:HA	5:2F:106:ARG:HD3	1.64	0.78
50:2s:20:LEU:HD23	50:2s:23:ASN:HD22	1.49	0.78
47:1p:48:TRP:HH2	47:1p:76:GLN:HE22	1.32	0.78
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.16	0.78
57:2y:12:U:H3	57:2y:23:A:H61	1.30	0.78
54:2w:3:G:H1	54:2w:70:C:H42	1.30	0.77
1:1A:882:G:H1	1:1A:894:C:H42	1.32	0.77
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.30	0.77
57:2y:22:G:N7	57:2y:46:G7M:N2	2.31	0.77
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.16	0.77
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.65	0.77
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.65	0.77
1:2A:2615:U:OP1	63:2A:3909:HOH:O	2.03	0.77
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.66	0.77
12:2Q:20:ALA:HB2	21:2Z:79:ARG:HE	1.49	0.77
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.18	0.77
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.17	0.77
1:1A:84:A:H5"	20:1Y:8:LYS:HG2	1.68	0.76
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.48	0.76
32:2a:1272:G:N2	32:2a:1273:G:N7	2.34	0.76
1:1A:2226:C:OP2	63:1A:4111:HOH:O	2.03	0.76
32:2a:299:G:O6	63:2a:3301:HOH:O	2.03	0.76
1:1A:1009:A:OP2	9:1N:37:LYS:NZ	2.17	0.76
1:1A:2038:G:O6	63:1A:4113:HOH:O	2.04	0.76
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.68	0.76
1:1A:2430:A:OP1	63:1A:4114:HOH:O	2.04	0.76
32:1a:674:G:H2'	32:1a:675:A:H8	1.51	0.76
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.18	0.76
18:2W:25:ARG:NH2	18:2W:74:ALA:O	2.18	0.76
32:2a:1014:A:H1'	50:2s:34:TRP:HB2	1.67	0.76
32:1a:1363(A):A:H4'	32:1a:1364:U:H2'	1.67	0.76
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.49	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1W:92:ARG:NH2	63:1W:301:HOH:O	2.19	0.75
1:1A:1139:G:OP2	9:1N:70:LYS:NZ	2.19	0.75
1:2A:2592:G:OP1	63:2A:3910:HOH:O	2.04	0.75
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.18	0.75
1:1A:1269:A:N7	63:1A:4166:HOH:O	2.20	0.75
26:14:16:CYS:SG	26:14:17:GLY:N	2.60	0.75
47:1p:11:SER:HB2	47:1p:14:ASN:HB3	1.67	0.75
14:2S:25:ARG:HB3	14:2S:40:ILE:HB	1.68	0.75
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.51	0.75
1:1A:2682:U:O2'	15:1T:58:ASN:ND2	2.20	0.75
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.19	0.75
1:1A:2541:A:OP2	63:1A:4115:HOH:O	2.04	0.75
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.68	0.75
3:1D:260:ARG:HH22	3:1D:266:SER:HB2	1.52	0.75
1:2A:1434:A:H61	1:2A:1558:A:H62	1.35	0.75
1:1A:1633:G:OP2	63:1A:4112:HOH:O	2.04	0.74
35:1d:88:VAL:HA	36:1e:97:GLY:HA3	1.69	0.74
35:1d:133:VAL:HG11	35:1d:138:TYR:HD1	1.52	0.74
32:1a:1027:C:C2	32:1a:1034:G:N2	2.54	0.74
1:2A:253:C:OP2	30:28:5:LYS:NZ	2.19	0.74
19:2X:63:LYS:HG2	19:2X:72:LYS:HG3	1.69	0.74
33:2b:91:PRO:HG3	33:2b:154:LEU:HB2	1.69	0.74
33:2b:214:ILE:HG22	33:2b:215:LEU:HD23	1.69	0.74
45:2n:12:ARG:HH21	45:2n:14:PRO:HB3	1.52	0.74
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.68	0.74
1:2A:2711:A:N3	63:2A:3963:HOH:O	2.21	0.74
2:2B:41:U:H5	6:2G:70:VAL:H	1.35	0.74
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.19	0.74
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.04	0.74
40:2i:17:VAL:HG11	40:2i:81:ILE:HG12	1.68	0.74
35:1d:26:CYS:HB3	62:1d:302:SF4:S1	2.27	0.74
54:1w:34:U8U:O4	54:1w:34:U8U:N	2.21	0.74
32:2a:1133:G:H1	32:2a:1141:C:H42	1.32	0.74
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.68	0.74
2:2B:48:A:OP2	14:2S:30:ARG:NH2	2.21	0.74
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.70	0.74
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.21	0.74
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.68	0.73
6:1G:59:GLU:OE2	6:1G:153:ARG:NH2	2.21	0.73
1:2A:1603:A:OP1	63:2A:3915:HOH:O	2.06	0.73
32:2a:953:G:H5'	32:2a:965:A:H61	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.06	0.73
21:1Z:119:GLU:N	21:1Z:171:ILE:O	2.21	0.73
32:2a:558:G:OP1	63:2a:3301:HOH:O	2.05	0.73
32:2a:1080:A:H5'	36:2e:14:ARG:HH21	1.50	0.73
1:2A:1812:A:OP2	63:2A:3911:HOH:O	2.05	0.73
1:2A:1021:A:H62	1:2A:1141:U:H3	1.36	0.73
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.22	0.73
32:2a:677:U:H3	32:2a:713:G:H22	1.37	0.73
32:2a:1264:C:H42	32:2a:1271:G:H1	1.34	0.73
1:1A:1041:C:H42	1:1A:1114:G:H1	1.35	0.73
1:1A:1971:A:OP1	63:1A:4116:HOH:O	2.06	0.73
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.21	0.73
32:2a:1289:A:OP1	52:2u:10:ARG:NH2	2.21	0.73
32:1a:1118:C:OP1	40:1i:104:ARG:NH1	2.20	0.73
8:1I:101:LEU:HD22	8:1I:107:VAL:HB	1.71	0.72
1:2A:450:G:O6	63:2A:3913:HOH:O	2.06	0.72
1:2A:731:C:OP1	63:2A:3912:HOH:O	2.05	0.72
44:2m:3:ARG:HB3	44:2m:9:ILE:H	1.53	0.72
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	1.71	0.72
32:2a:562:C:H1'	43:2l:15:ARG:HB3	1.71	0.72
33:2b:189:ASP:N	33:2b:189:ASP:OD1	2.21	0.72
1:2A:2712(A):A:OP2	63:2A:3917:HOH:O	2.07	0.72
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.22	0.72
35:2d:12:CYS:HB3	35:2d:19:LEU:H	1.55	0.72
1:1A:2292:C:OP1	14:1S:17:ARG:NH1	2.23	0.72
1:2A:2100:G:H1	1:2A:2189:U:H3	1.35	0.72
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.54	0.72
6:1G:161:THR:HG23	6:1G:163:ALA:H	1.54	0.72
1:2A:2419:U:O4	63:2A:3914:HOH:O	2.06	0.72
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	1.71	0.72
32:1a:200:G:H1	32:1a:217:C:H42	1.37	0.72
32:2a:601:C:H2'	32:2a:602:A:H8	1.53	0.72
35:2d:15:GLU:OE2	35:2d:59:ARG:NH1	2.22	0.72
32:2a:830:G:H5"	33:2b:22:LYS:HE2	1.70	0.72
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.53	0.72
1:1A:1263:U:OP1	27:15:16:ARG:NH1	2.23	0.71
7:1H:46:GLU:HB2	7:1H:49:VAL:HG12	1.72	0.71
1:2A:1647:G:OP1	63:2A:3918:HOH:O	2.08	0.71
32:2a:953:G:N7	44:2m:104:ARG:NH2	2.38	0.71
50:2s:49:ILE:HG22	50:2s:62:ILE:HD11	1.70	0.71
1:1A:692:C:O2'	3:1D:38:LYS:NZ	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:664:G:H22	32:1a:741:G:H1	1.38	0.71
33:1b:83:MET:HB3	33:1b:234:PRO:HG3	1.72	0.71
32:2a:1089:G:H1	32:2a:1096:C:H42	1.37	0.71
34:2c:44:GLU:HA	34:2c:52:LEU:HD23	1.71	0.71
1:1A:365:C:OP2	63:1A:4121:HOH:O	2.08	0.71
1:2A:2011:U:OP1	18:2W:42:ARG:NH1	2.23	0.71
1:2A:2503:2MA:H8	56:2z:2:ARG:NH1	2.01	0.71
8:2I:45:LYS:O	8:2I:49:ALA:N	2.24	0.71
8:1I:70:GLU:O	8:1I:74:ASN:ND2	2.23	0.71
32:1a:190:U:H2'	32:1a:191:G:H8	1.56	0.71
32:1a:812:C:N3	63:1a:1921:HOH:O	2.22	0.71
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.71	0.71
24:22:41:ILE:HG13	24:22:43:GLN:HG2	1.73	0.71
32:2a:673:G:H2'	32:2a:674:G:C8	2.24	0.71
1:1A:1014:U:OP2	63:1A:4117:HOH:O	2.07	0.71
11:1P:63:PRO:HB2	30:18:30:ARG:HH21	1.54	0.71
1:2A:83:G:H1	1:2A:102:G:HO2'	1.35	0.71
1:2A:963:U:OP2	63:2A:3905:HOH:O	2.08	0.71
32:2a:598:U:O4	63:2a:3302:HOH:O	2.06	0.71
32:1a:136:C:H42	32:1a:227:G:H1	1.38	0.71
32:1a:1505:G:OP2	63:1a:1901:HOH:O	2.08	0.71
39:2h:97:VAL:HG21	39:2h:128:GLY:HA2	1.73	0.71
1:1A:202:U:OP1	63:1A:4118:HOH:O	2.07	0.71
1:1A:2790:A:H5'	1:1A:2893:G:H21	1.56	0.71
21:1Z:93:ASP:HA	21:1Z:131:ARG:HH12	1.54	0.71
54:1w:50:C:N4	54:1w:64:G:H1	1.88	0.71
28:16:13:CYS:SG	28:16:47:THR:HG21	2.31	0.71
30:18:29:LYS:O	63:18:201:HOH:O	2.09	0.71
57:1y:63:U:H2'	57:1y:64:G:C8	2.25	0.71
32:1a:946:A:OP1	44:1m:114:ARG:NH2	2.23	0.70
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.24	0.70
21:2Z:77:ASP:OD1	21:2Z:80:ARG:NH1	2.24	0.70
32:2a:964:A:O2'	41:2j:55:LYS:NZ	2.23	0.70
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.73	0.70
45:2n:22:THR:HB	45:2n:33:VAL:HG11	1.72	0.70
46:2o:24:SER:HB3	46:2o:27:VAL:HG23	1.73	0.70
1:1A:248:G:OP1	63:1A:4122:HOH:O	2.09	0.70
1:1A:253:C:OP2	30:18:5:LYS:NZ	2.23	0.70
1:1A:855:G:N7	63:1A:4185:HOH:O	2.23	0.70
40:2i:5:TYR:O	40:2i:87:GLN:NE2	2.24	0.70
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1004:A:H5"	32:2a:1024:G:H22	1.57	0.70
32:1a:1499:A:OP2	63:1a:1901:HOH:O	2.09	0.70
2:1B:99:G:OP2	63:1B:301:HOH:O	2.10	0.70
1:2A:1452:A:OP2	63:2A:3920:HOH:O	2.10	0.70
41:2j:44:VAL:HG22	41:2j:66:ARG:HG2	1.72	0.70
57:2y:10:G:H1	57:2y:25:C:H42	0.75	0.70
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.74	0.70
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.73	0.70
11:1P:39:LYS:HB2	11:1P:45:LEU:HD13	1.73	0.70
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.24	0.70
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.74	0.70
1:2A:1012:U:OP1	16:2U:75:ASN:ND2	2.22	0.70
1:2A:1627:G:OP2	63:2A:3923:HOH:O	2.10	0.70
1:2A:1648:C:OP1	63:2A:3918:HOH:O	2.10	0.70
1:1A:1027:A:N3	63:1A:4196:HOH:O	2.25	0.69
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.24	0.69
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.74	0.69
28:16:9:LEU:HD13	28:16:51:GLU:HG3	1.74	0.69
1:2A:1782:C:OP1	63:2A:3925:HOH:O	2.10	0.69
4:2E:119:ARG:HD3	4:2E:160:TYR:HB2	1.73	0.69
1:2A:2062:A:OP1	63:2A:3921:HOH:O	2.10	0.69
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.26	0.69
24:22:35:LEU:HD23	24:22:50:ILE:HG12	1.74	0.69
1:1A:192:C:OP1	63:1A:4125:HOH:O	2.10	0.69
1:1A:1013:C:OP2	63:1A:4117:HOH:O	2.11	0.69
34:1c:172:ARG:NH2	34:1c:206:GLU:OE2	2.25	0.69
1:2A:1604:C:OP2	63:2A:3915:HOH:O	2.11	0.69
32:2a:839:U:H3'	32:2a:840:C:H5'	1.75	0.69
1:1A:1057:A:N6	1:1A:1081:U:H3	1.89	0.69
1:2A:2499:C:OP2	63:2A:3922:HOH:O	2.10	0.69
32:2a:596:C:OP2	63:2a:3302:HOH:O	2.10	0.69
53:2v:14:A:N6	57:2y:34:U8U:S2	2.65	0.69
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.26	0.69
45:2n:26:ARG:HD3	45:2n:43:CYS:HB3	1.73	0.69
1:1A:1770:G:OP1	63:1A:4131:HOH:O	2.11	0.69
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.74	0.69
2:2B:93:G:OP1	21:2Z:79:ARG:NH2	2.26	0.69
4:2E:127:ASP:OD2	63:2E:401:HOH:O	2.10	0.69
32:2a:11:G:H1	32:2a:23:C:H42	1.41	0.69
32:2a:543:C:OP2	35:2d:10:ARG:NH2	2.25	0.69
53:2v:21:A:N1	54:2w:34:U8U:O4	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:120:U:OP2	63:1A:4128:HOH:O	2.11	0.69
32:1a:1025:U:O2	32:1a:1036:G:O6	2.11	0.69
1:2A:601:C:O2'	5:2F:104:LYS:NZ	2.24	0.69
1:2A:2165:G:H1	1:2A:2171:A:H8	1.40	0.69
54:2w:63:U:H2'	54:2w:64:G:H8	1.58	0.69
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.74	0.69
40:2i:50:LEU:HD13	40:2i:56:LEU:HA	1.75	0.69
1:1A:1267:U:OP1	63:1A:4127:HOH:O	2.11	0.68
1:1A:1315:C:OP2	63:1A:4106:HOH:O	2.10	0.68
1:1A:2575:C:OP2	63:1A:4129:HOH:O	2.11	0.68
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.25	0.68
36:2e:65:ASN:HD21	36:2e:140:ARG:HH21	1.41	0.68
1:1A:198:C:OP1	63:1A:4124:HOH:O	2.10	0.68
4:1E:176:ILE:HB	4:1E:181:LEU:HB2	1.74	0.68
1:2A:854:G:H2'	1:2A:855:G:H8	1.58	0.68
13:2R:118:GLU:CD	13:2R:118:GLU:H	2.01	0.68
34:2c:190:ARG:NE	34:2c:190:ARG:O	2.26	0.68
41:2j:8:LEU:HD11	41:2j:20:ALA:HB2	1.73	0.68
26:14:55:ARG:N	26:14:56:VAL:HA	2.08	0.68
11:1P:50:ARG:HH21	30:18:7:HIS:HD2	1.41	0.68
16:1U:75:ASN:OD1	16:1U:78:THR:OG1	2.10	0.68
1:2A:1828:G:OP1	63:2A:3926:HOH:O	2.11	0.68
12:1Q:78:PRO:HG2	12:1Q:81:VAL:HG11	1.75	0.68
1:2A:1159:U:H2'	1:2A:1160:G:H8	1.59	0.68
1:2A:1600:C:OP1	19:2X:58:HIS:NE2	2.23	0.68
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.26	0.68
1:1A:1174:A:H4'	1:1A:1175:U:OP1	1.93	0.68
40:1i:26:VAL:HG12	40:1i:61:ALA:HB3	1.74	0.68
39:1h:110:ALA:HB3	39:1h:121:ASP:HB3	1.75	0.68
32:2a:768:A:OP2	63:2a:3303:HOH:O	2.11	0.68
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.59	0.68
32:2a:1123:A:H4'	41:2j:37:PRO:HD2	1.76	0.68
34:2c:117:ALA:HB2	34:2c:200:ALA:HB2	1.76	0.68
1:1A:744:G:OP1	63:1A:4123:HOH:O	2.10	0.68
32:1a:352:C:OP2	63:1a:1902:HOH:O	2.11	0.68
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.75	0.68
57:1y:9:A:H5'	57:1y:46:G7M:H1'	1.76	0.68
1:2A:2295:C:H5	14:2S:13:ARG:HH22	1.42	0.68
1:1A:816:C:OP2	63:1A:4126:HOH:O	2.10	0.68
18:1W:24:ILE:HA	18:1W:27:LYS:HG3	1.76	0.68
40:2i:128:ARG:NH2	55:2x:33:U:OP2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2543:G:N7	63:1A:4211:HOH:O	2.26	0.67
39:2h:20:TYR:HE2	39:2h:75:ARG:HD2	1.57	0.67
43:2l:54:LYS:HB3	43:2l:70:ILE:HD12	1.76	0.67
55:2x:40:C:H2'	55:2x:41:C:H6	1.59	0.67
32:1a:583:A:OP2	63:1a:1904:HOH:O	2.12	0.67
32:1a:624:C:H2'	32:1a:625:G:H8	1.57	0.67
43:2l:8:ASN:OD1	48:2q:34:LYS:NZ	2.26	0.67
32:1a:636:U:H2'	32:1a:637:G:H8	1.59	0.67
32:1a:953:G:H5'	32:1a:965:A:H61	1.59	0.67
57:2y:26:A:N6	57:2y:45:G:O6	2.28	0.67
1:1A:1245:G:OP1	11:1P:13:ASN:ND2	2.26	0.67
2:2B:22:U:H3	2:2B:61:G:H1	1.40	0.67
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.26	0.67
32:1a:13:U:OP1	63:1a:1903:HOH:O	2.12	0.67
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.75	0.67
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.26	0.67
32:1a:79:G:H1	32:1a:90:U:H3	1.38	0.67
1:2A:2299:G:N1	1:2A:2318:G:N7	2.43	0.67
32:2a:601:C:H2'	32:2a:602:A:C8	2.29	0.67
32:2a:815:A:N7	32:2a:1509:C:O2'	2.27	0.67
44:2m:4:ILE:HD13	44:2m:22:ILE:HG13	1.76	0.67
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.26	0.67
1:2A:422:A:OP2	63:2A:3927:HOH:O	2.13	0.67
30:28:30:ARG:NH1	63:28:201:HOH:O	2.27	0.67
35:2d:153:ARG:HD3	35:2d:181:MET:HG3	1.76	0.67
1:2A:2131:G:H4'	1:2A:2132:U:H3'	1.77	0.67
32:2a:1009:G:H22	32:2a:1021:G:H1'	1.58	0.67
32:2a:1162:C:H42	32:2a:1174:G:H1	1.43	0.67
1:1A:607:U:OP1	5:1F:102:PRO:HA	1.95	0.67
18:1W:68:ARG:HH12	18:1W:112:GLY:H	1.43	0.67
36:1e:78:HIS:HE1	36:1e:143:ARG:H	1.41	0.67
42:1k:33:THR:HA	42:1k:39:PRO:HA	1.75	0.67
1:2A:1253:A:OP1	63:2A:3929:HOH:O	2.13	0.67
2:2B:40:U:H1'	2:2B:45:A:H61	1.59	0.67
1:1A:952:G:OP1	12:1Q:16:ARG:NH2	2.28	0.67
13:1R:90:ARG:NH2	13:1R:118:GLU:OXT	2.27	0.67
57:1y:66:A:H2'	57:1y:67:C:C6	2.30	0.67
1:2A:469:G:O6	29:27:37:LYS:NZ	2.28	0.67
32:2a:1084:G:H3'	32:2a:1085:U:H2'	1.77	0.67
32:2a:1385:G:H2'	32:2a:1386:G:C8	2.30	0.67
1:1A:279:C:H42	1:1A:361:G:H1	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1352:U:OP2	63:1A:4133:HOH:O	2.13	0.66
32:1a:1179:A:H4'	40:1i:103:THR:HA	1.78	0.66
1:2A:951:C:OP1	63:2A:3928:HOH:O	2.13	0.66
26:24:15:ILE:O	26:24:33:VAL:N	2.29	0.66
32:2a:977:A:HO2'	32:2a:981:U:H3	1.42	0.66
34:2c:101:LEU:HD13	34:2c:102:ASN:H	1.60	0.66
1:2A:2637:U:H5"	4:2E:82:ARG:HH12	1.60	0.66
12:2Q:85:LYS:HG2	22:20:7:LEU:HB3	1.77	0.66
42:2k:85:ARG:NH2	42:2k:111:ASP:OD2	2.26	0.66
1:1A:792:G:OP2	63:1A:4135:HOH:O	2.13	0.66
1:1A:1054:A:H61	1:1A:1105:U:H3	1.44	0.66
4:1E:135:HIS:NE2	63:1E:401:HOH:O	2.28	0.66
9:1N:128:HIS:HE1	9:1N:135:PRO:HG2	1.59	0.66
5:2F:165:ARG:HG2	5:2F:168:ARG:HH21	1.61	0.66
1:1A:1054:A:N6	1:1A:1105:U:H3	1.94	0.66
11:1P:124:LYS:HA	11:1P:144:GLU:HB3	1.76	0.66
44:1m:4:ILE:HB	44:1m:57:ARG:HG3	1.78	0.66
1:2A:2104:G:H1	1:2A:2185:C:H42	1.42	0.66
1:2A:2138:C:N4	1:2A:2153:G:H1	1.91	0.66
6:2G:101:ILE:HD12	26:24:25:TYR:HB2	1.78	0.66
14:2S:62:LYS:HB3	14:2S:97:ARG:HD2	1.78	0.66
29:27:23:ARG:O	29:27:28:ARG:NH1	2.28	0.66
33:2b:70:PHE:HE2	33:2b:90:MET:HB2	1.60	0.66
1:2A:918:A:N3	2:2B:80:U:O2'	2.29	0.66
1:2A:1394:U:OP1	63:2A:3907:HOH:O	2.12	0.66
32:2a:661:G:H1	32:2a:744:C:H42	1.43	0.66
55:2x:8:4SU:O5'	55:2x:8:4SU:H6	1.95	0.66
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.77	0.66
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.28	0.66
1:2A:1785:A:N6	63:2A:3996:HOH:O	2.28	0.66
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.76	0.66
32:2a:1375:A:O2'	38:2g:29:LYS:NZ	2.23	0.66
32:1a:1054:C:OP2	63:1a:1906:HOH:O	2.14	0.66
32:1a:1329:A:H5"	44:1m:26:GLY:H	1.61	0.66
35:1d:101:LEU:HB2	35:1d:138:TYR:HB3	1.78	0.66
51:1t:22:ARG:O	51:1t:26:ASN:ND2	2.28	0.66
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.28	0.66
1:2A:2394:C:N3	57:2y:76:A:O2'	2.27	0.66
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.43	0.66
32:2a:1310:G:H5'	44:2m:77:ASN:HD21	1.61	0.66
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:33:THR:HA	42:2k:39:PRO:HA	1.76	0.66
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.29	0.66
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.29	0.65
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.77	0.65
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.78	0.65
32:2a:289:G:OP2	63:2a:3305:HOH:O	2.12	0.65
1:1A:1651:G:N7	63:1R:301:HOH:O	2.28	0.65
1:1A:2406:U:OP1	63:1A:4139:HOH:O	2.14	0.65
25:13:51:ALA:HA	25:13:54:VAL:HG12	1.78	0.65
32:1a:1267:C:O2	52:1u:20:LYS:NZ	2.29	0.65
26:24:26:SER:OG	26:24:27:THR:N	2.27	0.65
32:2a:547:A:OP1	63:2a:3304:HOH:O	2.12	0.65
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.31	0.65
1:2A:648:G:O2'	1:2A:2351:G:OP1	2.10	0.65
32:2a:9:G:H2'	32:2a:10:A:H8	1.61	0.65
1:1A:1186:G:OP1	63:1A:4138:HOH:O	2.14	0.65
1:2A:994:C:OP2	16:2U:54:LYS:NZ	2.27	0.65
32:2a:1244:C:H42	32:2a:1293:G:H1	1.44	0.65
54:2w:18:G:O2'	54:2w:57:G:N2	2.30	0.65
1:1A:272(J):C:H2'	1:1A:274:G:H8	1.61	0.65
1:1A:762:U:OP1	63:1A:4141:HOH:O	2.14	0.65
4:1E:143:ASN:HD22	4:1E:147:PRO:HD2	1.60	0.65
6:1G:33:ARG:O	6:1G:161:THR:OG1	2.11	0.65
7:1H:116:GLU:HG3	7:1H:117:PRO:HD2	1.79	0.65
32:1a:894:G:N7	63:1a:1930:HOH:O	2.29	0.65
1:2A:1376:C:OP2	63:2A:3930:HOH:O	2.14	0.65
1:2A:2624:G:N7	63:2A:4002:HOH:O	2.28	0.65
2:2B:3:C:H2'	2:2B:4:C:C6	2.31	0.65
21:1Z:77:ASP:OD2	21:1Z:80:ARG:NH1	2.30	0.65
1:2A:2632:A:HO2'	1:2A:2811:G:HO2'	1.40	0.65
32:2a:113:G:H1'	32:2a:354:G:H5'	1.78	0.65
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.14	0.65
1:1A:2337:G:OP1	63:1A:4142:HOH:O	2.15	0.65
3:1D:275:LYS:HG3	3:1D:276:LYS:HG3	1.79	0.65
1:2A:1271:G:OP2	63:2A:3918:HOH:O	2.14	0.65
1:2A:2430:A:OP2	63:2A:3906:HOH:O	2.13	0.65
7:2H:10:PRO:HA	7:2H:49:VAL:HG22	1.79	0.65
11:2P:2:LYS:HD3	11:2P:4:SER:H	1.62	0.65
32:2a:803:G:OP1	63:2a:3307:HOH:O	2.15	0.65
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.31	0.65
1:1A:2467:C:OP2	63:1A:4134:HOH:O	2.13	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:5:LEU:HD11	8:1I:12:LEU:HD13	1.78	0.65
15:1T:55:ASN:HD22	15:1T:58:ASN:HB2	1.61	0.65
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.32	0.65
41:1j:78:ASN:O	41:1j:80:LYS:N	2.29	0.65
1:2A:567:A:OP2	11:2P:29:LYS:NZ	2.28	0.65
1:2A:975:C:OP1	63:2A:3933:HOH:O	2.14	0.65
1:2A:2439:A:N6	55:2x:76:8AN:O1P	2.29	0.65
35:2d:57:ARG:NH1	35:2d:205:GLU:OE2	2.30	0.65
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	1.79	0.65
33:2b:104:ASN:OD1	33:2b:107:THR:OG1	2.14	0.65
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.29	0.65
32:1a:702:A:OP2	63:1a:1905:HOH:O	2.13	0.65
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.30	0.65
35:1d:79:PHE:HE1	35:1d:204:ILE:HG12	1.62	0.65
1:2A:1204:A:H2	1:2A:1241:A:H62	1.45	0.65
1:2A:1937:A:H1'	1:2A:1939:5MU:H72	1.79	0.65
1:1A:1764:G:N7	63:1A:4239:HOH:O	2.29	0.64
1:2A:1639:U:H2'	1:2A:1640:C:H5"	1.78	0.64
1:2A:1938:A:OP2	63:2A:3937:HOH:O	2.15	0.64
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.62	0.64
36:2e:84:PHE:O	36:2e:86:ALA:N	2.29	0.64
38:2g:9:VAL:HG23	38:2g:94:ARG:HH21	1.61	0.64
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.78	0.64
55:2x:23:C:H2'	55:2x:24:U:C6	2.32	0.64
1:1A:847:U:OP2	63:1A:4140:HOH:O	2.14	0.64
1:1A:956:G:O6	63:1A:4132:HOH:O	2.12	0.64
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	1.80	0.64
34:1c:36:ASP:OD1	34:1c:59:ARG:NH2	2.21	0.64
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.79	0.64
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.32	0.64
38:2g:111:ARG:NH1	38:2g:113:GLU:OE2	2.28	0.64
39:2h:69:ARG:NH2	39:2h:73:ASP:O	2.30	0.64
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.31	0.64
8:1I:45:LYS:HA	8:1I:48:GLU:HB2	1.80	0.64
32:1a:942:G:H21	40:1i:124:GLN:NE2	1.95	0.64
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.45	0.64
34:2c:136:GLN:O	34:2c:140:ARG:N	2.26	0.64
44:2m:91:ARG:HB2	44:2m:98:VAL:HG13	1.79	0.64
36:1e:84:PHE:HB2	36:1e:134:ALA:HB2	1.79	0.64
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.32	0.64
3:2D:166:GLN:HB2	3:2D:174:ILE:HG22	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.21	0.64
34:2c:125:GLU:O	34:2c:190:ARG:NH2	2.31	0.64
1:1A:2022:U:OP1	63:1A:4136:HOH:O	2.13	0.64
36:1e:53:LEU:HD23	36:1e:56:GLN:HE22	1.62	0.64
11:2P:63:PRO:HB2	30:28:30:ARG:HH21	1.62	0.64
32:2a:415:A:H3'	32:2a:416:G:H8	1.60	0.64
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.28	0.64
11:1P:96:THR:HG23	11:1P:99:LEU:HB3	1.78	0.64
14:1S:52:SER:HB2	14:1S:55:ALA:H	1.62	0.64
32:1a:1375:A:H4'	38:1g:29:LYS:HD3	1.79	0.64
1:2A:144:C:H2'	1:2A:145:G:H8	1.62	0.64
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.33	0.64
52:2u:6:ARG:HD3	52:2u:15:ARG:HE	1.62	0.64
1:1A:135:G:N7	63:1A:4236:HOH:O	2.29	0.64
43:1l:52:LEU:O	43:1l:54:LYS:NZ	2.31	0.64
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.80	0.64
1:1A:2573:C:OP1	63:1A:4129:HOH:O	2.14	0.64
7:1H:3:ARG:NE	7:1H:3:ARG:HA	2.12	0.64
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.33	0.64
7:2H:3:ARG:HH22	7:2H:65:HIS:HB3	1.62	0.64
37:2f:97:PHE:HB2	49:2r:32:ARG:HE	1.63	0.64
1:1A:322:A:OP1	5:1F:168:ARG:HD3	1.98	0.64
1:1A:588:U:H2'	1:1A:589:C:C6	2.33	0.64
1:1A:998:C:OP1	63:1A:4143:HOH:O	2.15	0.64
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.33	0.64
1:2A:2268:A:OP1	63:2A:3938:HOH:O	2.15	0.64
5:2F:124:LEU:HB3	5:2F:193:VAL:HG22	1.79	0.64
21:2Z:23:LYS:HD2	21:2Z:40:ASP:HA	1.80	0.64
55:1x:61:C:H2'	55:1x:62:C:C6	2.33	0.64
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.31	0.64
27:25:41:PRO:O	27:25:44:THR:OG1	2.14	0.64
32:1a:504:C:OP1	63:1a:1909:HOH:O	2.16	0.63
15:2T:29:ARG:NH2	15:2T:46:GLU:OE1	2.30	0.63
32:2a:1289:A:H5'	52:2u:10:ARG:HH22	1.63	0.63
57:2y:12:U:H3	57:2y:23:A:N6	1.96	0.63
32:1a:1503:A:N3	53:1v:13:A:N6	2.46	0.63
1:2A:2010:G:O6	63:2A:3931:HOH:O	2.14	0.63
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.28	0.63
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.30	0.63
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.79	0.63
32:1a:674:G:H2'	32:1a:675:A:C8	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.32	0.63
1:2A:2705:A:OP2	63:2A:3936:HOH:O	2.15	0.63
32:2a:1275:A:H3'	32:2a:1276:G:H8	1.64	0.63
39:2h:83:ILE:HG13	39:2h:137:VAL:HG22	1.80	0.63
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.30	0.63
7:1H:159:GLU:HG3	7:1H:169:VAL:HG11	1.80	0.63
12:1Q:18:LYS:O	12:1Q:98:LYS:NZ	2.30	0.63
27:25:2:ALA:N	63:25:201:HOH:O	2.30	0.63
1:1A:1168:G:O6	63:1A:4130:HOH:O	2.11	0.63
1:2A:1169:G:H22	1:2A:1180:C:H42	1.45	0.63
5:2F:33:LEU:HB3	11:2P:6:LEU:HD21	1.80	0.63
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.34	0.63
1:1A:1055:G:H1	1:1A:1104:C:H42	1.47	0.63
1:2A:120:U:OP2	63:2A:3939:HOH:O	2.15	0.63
8:2I:50:ARG:HA	8:2I:53:ALA:HB3	1.79	0.63
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.30	0.63
33:2b:54:THR:HG22	33:2b:199:TYR:HB3	1.81	0.63
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.33	0.63
6:2G:93:THR:OG1	6:2G:95:ARG:NH2	2.31	0.63
32:2a:993:G:H1	32:2a:1045:C:H42	1.46	0.63
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.31	0.63
44:1m:123:ALA:HB2	54:1w:39:PSU:H1'	1.80	0.63
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.31	0.63
24:22:7:ARG:HA	24:22:10:LEU:HD12	1.80	0.63
32:2a:944:G:OP1	63:2a:3308:HOH:O	2.16	0.63
47:2p:22:THR:HA	47:2p:33:ILE:HG13	1.81	0.63
1:1A:1666:G:O6	63:1A:4137:HOH:O	2.14	0.63
34:2c:52:LEU:HD13	34:2c:68:VAL:HG13	1.80	0.63
1:1A:2469:A:O3'	12:1Q:56:ARG:NH1	2.32	0.62
1:2A:2130:U:O2	1:2A:2134:A:O2'	2.16	0.62
2:2B:43:C:H5"	26:24:1:MET:HG2	1.80	0.62
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.80	0.62
32:2a:1479:C:H2'	32:2a:1480:G:H8	1.64	0.62
35:2d:155:LEU:HD22	35:2d:156:GLU:H	1.63	0.62
36:2e:82:VAL:HG11	36:2e:137:GLU:HG2	1.81	0.62
54:2w:11:C:H42	54:2w:24:G:H1	1.46	0.62
14:1S:14:VAL:O	14:1S:18:ILE:HG12	1.99	0.62
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.32	0.62
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.32	0.62
42:1k:48:ILE:O	42:1k:50:TYR:N	2.31	0.62
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:882:G:H22	1:2A:894:C:H42	1.47	0.62
1:2A:2134:A:O2'	1:2A:2159:G:N2	2.32	0.62
15:2T:108:ARG:NH1	32:2a:1464:G:OP1	2.32	0.62
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.32	0.62
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.31	0.62
32:2a:1270:C:OP2	52:2u:24:ARG:NH2	2.31	0.62
32:2a:297:G:N2	32:2a:300:A:OP2	2.33	0.62
32:2a:564:C:O2'	39:2h:91:ARG:NH2	2.22	0.62
46:2o:17:ARG:HD3	46:2o:77:ARG:HH21	1.64	0.62
1:1A:2683:C:H5'	15:1T:58:ASN:HD22	1.64	0.62
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.64	0.62
48:2q:53:LEU:HD11	48:2q:85:VAL:HG11	1.81	0.62
57:2y:8:U:O2'	57:2y:21:A:N1	2.32	0.62
57:2y:21:A:H62	57:2y:46:G7M:H1'	1.65	0.62
1:1A:1670:C:O2	4:1E:129:HIS:NE2	2.26	0.62
1:1A:2743:C:OP1	31:19:33:LYS:NZ	2.32	0.62
32:1a:636:U:H2'	32:1a:637:G:C8	2.34	0.62
32:2a:1263:C:N4	32:2a:1271:G:O6	2.33	0.62
34:2c:191:THR:OG1	34:2c:194:GLY:O	2.18	0.62
1:1A:1649:G:O2'	13:1R:107:ASP:OD2	2.15	0.62
1:1A:2762:G:OP2	63:1A:4144:HOH:O	2.16	0.62
32:1a:376:G:H5"	47:1p:5:ARG:HB3	1.80	0.62
32:1a:735:C:H2'	32:1a:736:C:H6	1.65	0.62
32:2a:753:A:OP1	46:2o:69:TYR:OH	2.16	0.62
32:2a:1237:C:H3'	32:2a:1336:C:H41	1.64	0.62
54:2w:3:G:H1	54:2w:70:C:N4	1.97	0.62
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.80	0.62
23:11:18:ILE:HG12	23:11:37:ILE:HG12	1.81	0.62
43:1l:27:LEU:HD23	43:1l:33:ARG:HB2	1.82	0.62
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.82	0.62
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.65	0.62
32:2a:501:C:H2'	32:2a:502:G:H8	1.64	0.62
1:1A:989:G:OP2	25:13:11:SER:OG	2.18	0.62
2:1B:41:U:H5	6:1G:70:VAL:H	1.45	0.62
32:1a:396:G:O2'	32:1a:398:C:OP1	2.13	0.62
37:1f:50:TYR:OH	49:1r:74:ARG:O	2.07	0.62
49:1r:52:PRO:HB2	49:1r:54:ARG:HG2	1.82	0.62
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.82	0.62
32:1a:1399:C:H4'	32:1a:1400:5MC:H5"	1.80	0.62
1:2A:925:C:H2'	1:2A:926:A:H8	1.63	0.62
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.81	0.62
33:2b:84:GLU:OE1	33:2b:87:ARG:NH1	2.33	0.62
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.65	0.62
51:2t:98:PRO:O	51:2t:99:LEU:HB2	2.00	0.62
6:1G:122:PRO:HB3	6:1G:170:ARG:HH12	1.65	0.61
7:1H:56:SER:OG	7:1H:57:ASP:N	2.29	0.61
1:2A:2006:C:OP2	63:2A:3942:HOH:O	2.16	0.61
1:2A:2123:G:H2'	1:2A:2124:G:C8	2.35	0.61
15:2T:16:ARG:HH21	15:2T:19:LEU:HD21	1.64	0.61
35:2d:111:ALA:HB1	35:2d:116:GLN:HG2	1.81	0.61
38:2g:126:ASP:O	38:2g:130:GLY:N	2.31	0.61
32:1a:404:U:OP1	35:1d:118:ARG:NH1	2.34	0.61
34:1c:19:GLU:HG3	34:1c:54:ARG:CZ	2.30	0.61
32:2a:70:G:H1	32:2a:99:U:H3	1.49	0.61
36:2e:152:ARG:HB3	39:2h:43:GLY:HA3	1.82	0.61
1:1A:1937:A:H1'	1:1A:1939:5MU:H72	1.82	0.61
6:2G:47:LYS:HD2	6:2G:48:GLU:H	1.65	0.61
34:2c:70:VAL:O	34:2c:106:VAL:N	2.25	0.61
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.81	0.61
43:1l:7:ILE:HD13	43:1l:10:LEU:HD12	1.81	0.61
48:1q:18:THR:OG1	48:1q:69:LYS:NZ	2.28	0.61
2:2B:7:G:N2	14:2S:38:GLN:HE22	1.98	0.61
7:2H:24:VAL:HG13	7:2H:37:VAL:HG11	1.81	0.61
26:24:24:THR:OG1	26:24:25:TYR:N	2.33	0.61
32:2a:736:C:H2'	32:2a:737:A:C8	2.35	0.61
1:1A:2114:A:N6	1:1A:2119:A:N7	2.48	0.61
32:1a:945:G:OP2	63:1a:1910:HOH:O	2.16	0.61
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.18	0.61
1:2A:2239:G:OP2	63:2A:3940:HOH:O	2.16	0.61
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.30	0.61
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.33	0.61
44:2m:4:ILE:HD12	44:2m:19:LEU:HD22	1.82	0.61
55:2x:29:G:H2'	55:2x:30:G:H8	1.65	0.61
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.00	0.61
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.19	0.61
6:2G:39:ILE:HD11	6:2G:155:MET:HG3	1.81	0.61
12:2Q:57:HIS:CE1	12:2Q:116:GLU:HG2	2.36	0.61
32:2a:107:G:H2'	32:2a:108:G:O4'	2.00	0.61
32:2a:406:G:H5'	35:2d:5:ILE:HD11	1.82	0.61
32:2a:1263:C:N3	32:2a:1272:G:O6	2.33	0.61
33:2b:230:VAL:HG22	33:2b:232:PRO:HD2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:8:ILE:C	34:2c:10:PHE:H	2.08	0.61
54:2w:20:U:H4'	54:2w:21:A:H5'	1.81	0.61
32:1a:673:G:H2'	32:1a:674:G:C8	2.35	0.61
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.83	0.61
43:1l:90:VAL:O	43:1l:92:0TD:N	2.34	0.61
44:1m:18:ALA:HA	44:1m:21:TYR:HD2	1.66	0.61
57:1y:1:G:H2'	57:1y:2:G:H8	1.66	0.61
1:2A:897:C:H5"	54:2w:56:C:OP1	2.00	0.61
4:2E:48:GLN:HE21	4:2E:78:LEU:HD22	1.65	0.61
7:2H:51:ARG:HH12	7:2H:53:GLU:HG3	1.65	0.61
26:24:49:PHE:O	26:24:51:ASP:N	2.34	0.61
41:2j:5:ARG:N	41:2j:99:LYS:O	2.34	0.61
32:1a:161:A:N1	32:1a:347:G:O2'	2.33	0.61
32:1a:1456:G:N2	51:1t:51:GLU:OE2	2.32	0.61
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.36	0.61
32:2a:64:G:H4'	32:2a:65:U:H3'	1.82	0.61
1:1A:2131:G:H5'	1:1A:2133:G:C8	2.35	0.61
32:1a:171:A:H2'	32:1a:172:A:C8	2.36	0.61
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.83	0.61
33:2b:88:ALA:HA	33:2b:223:ILE:HD11	1.83	0.61
36:2e:83:GLU:HA	36:2e:88:LYS:HA	1.81	0.61
1:2A:2131:G:N2	1:2A:2158:A:H62	1.99	0.61
7:2H:98:LEU:HD11	7:2H:125:VAL:H	1.65	0.61
31:29:16:VAL:HG22	31:29:25:VAL:HG22	1.82	0.61
32:2a:1058:G:H1	32:2a:1199:U:H3	1.48	0.61
33:2b:12:GLU:HB2	33:2b:213:LEU:HD21	1.82	0.61
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.36	0.60
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.82	0.60
32:1a:560:U:O2'	32:1a:561:U:OP2	2.15	0.60
32:1a:693:G:OP2	63:1a:1908:HOH:O	2.15	0.60
32:1a:1040:U:H2'	32:1a:1041:A:C8	2.36	0.60
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.73	0.60
32:1a:159:G:O2'	32:1a:161:A:N7	2.23	0.60
1:2A:1299:G:OP1	63:2A:3944:HOH:O	2.17	0.60
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.82	0.60
3:2D:123:ALA:HB1	3:2D:129:ASN:HD22	1.66	0.60
32:2a:695:A:H5'	57:2y:38:A:H4'	1.83	0.60
32:2a:1315:U:OP2	50:2s:7:LYS:NZ	2.32	0.60
34:2c:120:VAL:HA	34:2c:123:GLN:HB2	1.83	0.60
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.33	0.60
47:2p:1:MET:HG3	47:2p:3:LYS:HD3	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.82	0.60
1:2A:446:G:OP1	16:2U:3:ARG:NH1	2.34	0.60
1:2A:2343:C:H4'	1:2A:2373:G:O3'	2.01	0.60
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.66	0.60
28:26:10:LEU:HD23	28:26:22:ALA:HB2	1.82	0.60
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.67	0.60
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.36	0.60
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.34	0.60
1:1A:2255:G:OP2	63:1A:4146:HOH:O	2.16	0.60
36:2e:8:GLU:HG2	36:2e:34:VAL:HG23	1.83	0.60
50:2s:45:VAL:O	50:2s:47:HIS:ND1	2.33	0.60
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.35	0.60
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.37	0.60
16:2U:74:LEU:HD13	16:2U:79:PHE:HB2	1.82	0.60
32:2a:309:G:O2'	32:2a:607:A:N1	2.34	0.60
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	1.84	0.60
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.23	0.60
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.01	0.60
1:2A:821:A:N1	63:2A:4021:HOH:O	2.31	0.60
1:2A:2183:C:H2'	1:2A:2184:G:C8	2.36	0.60
32:2a:984:C:H2'	32:2a:985:C:H6	1.66	0.60
2:1B:66:A:H61	2:1B:108:U:H2'	1.67	0.60
32:1a:17:U:H2'	32:1a:18:C:C6	2.36	0.60
32:1a:1226:C:O2'	44:1m:111:LYS:NZ	2.34	0.60
1:2A:518:G:H4'	18:2W:18:ARG:HE	1.65	0.60
1:2A:1378:A:O2'	1:2A:1380:G:N7	2.29	0.60
1:2A:2127:G:H1	1:2A:2161:C:H42	1.48	0.60
3:2D:72:LYS:HB3	3:2D:75:ILE:HD12	1.84	0.60
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.36	0.60
32:1a:932:C:O3'	38:1g:4:ARG:NH2	2.34	0.60
1:2A:538:G:H2'	1:2A:539:G:H8	1.67	0.60
32:2a:1055:A:O2'	34:2c:156:ARG:NH2	2.35	0.60
1:1A:154(A):C:H42	1:1A:171:G:H1	1.49	0.60
1:1A:1252:G:OP2	63:1A:4147:HOH:O	2.17	0.60
13:1R:50:HIS:ND1	63:1R:303:HOH:O	2.30	0.60
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.84	0.60
1:2A:1951:U:O4	63:2A:3932:HOH:O	2.14	0.60
8:2I:77:LEU:HD21	8:2I:101:LEU:HB3	1.82	0.60
12:2Q:45:GLN:OE1	12:2Q:45:GLN:N	2.32	0.60
18:2W:11:ARG:NH1	18:2W:99:ARG:O	2.34	0.60
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:19:GLU:O	34:2c:40:ARG:NH2	2.35	0.60
42:2k:31:THR:HG23	42:2k:42:TRP:HB3	1.83	0.60
1:1A:882:G:H4'	54:1w:19:G:C6	2.37	0.60
1:2A:1645:G:H5"	1:2A:1646:C:H5'	1.84	0.60
1:2A:2712(A):A:OP1	63:2A:3943:HOH:O	2.17	0.60
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.82	0.60
33:2b:134:GLU:O	33:2b:138:LEU:HB2	2.01	0.60
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.37	0.59
11:1P:59:LEU:HD13	30:18:58:ILE:HD13	1.82	0.59
32:1a:186:C:H5'	51:1t:78:ALA:HB1	1.84	0.59
32:1a:642:A:N3	39:1h:113:SER:OG	2.29	0.59
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.37	0.59
1:2A:568:U:O4	63:2A:3934:HOH:O	2.14	0.59
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.37	0.59
1:2A:2242:G:OP1	63:2A:3941:HOH:O	2.16	0.59
2:2B:50:G:OP1	14:2S:63:THR:N	2.34	0.59
6:2G:135:LEU:HD22	6:2G:140:ILE:HD13	1.84	0.59
15:2T:127:ALA:C	15:2T:129:ARG:H	2.09	0.59
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.36	0.59
1:1A:2144:U:H3'	1:1A:2146:C:H42	1.66	0.59
8:1I:93:THR:HG22	8:1I:119:PRO:HB3	1.83	0.59
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.30	0.59
6:2G:96:ARG:HA	6:2G:99:MET:HE2	1.84	0.59
32:2a:1026:G:O6	32:2a:1036:G:N2	2.35	0.59
34:2c:183:ASP:HB3	34:2c:202:ILE:HB	1.84	0.59
43:2l:77:LEU:HD21	43:2l:107:ALA:HB2	1.84	0.59
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.30	0.59
32:1a:111:G:H5"	47:1p:27:LYS:HB3	1.84	0.59
41:1j:5:ARG:NH2	41:1j:73:ASP:OD2	2.34	0.59
1:2A:2466:C:H5"	31:29:6:SER:HB3	1.84	0.59
1:2A:2585:U:O4	54:2w:76:A1B8A:O2'	2.20	0.59
19:2X:10:ALA:O	19:2X:29:TRP:N	2.33	0.59
32:2a:516:PSU:O2	63:2a:3309:HOH:O	2.16	0.59
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.67	0.59
55:2x:52:G:H1	55:2x:62:C:H42	1.51	0.59
1:1A:1062:G:H22	1:1A:1077:A:H61	1.50	0.59
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.83	0.59
32:1a:1030(D):A:H3'	32:1a:1031:G:H4'	1.83	0.59
43:1l:70:ILE:HG12	43:1l:100:ILE:HD13	1.83	0.59
1:2A:1038:C:H42	1:2A:1117:G:H1	1.51	0.59
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:29:27:CYS:SG	31:29:28:GLU:N	2.75	0.59
32:2a:34:C:H2'	32:2a:35:G:C8	2.37	0.59
1:1A:2347:C:OP1	28:16:38:LYS:NZ	2.35	0.59
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.35	0.59
32:1a:999:C:H2'	32:1a:1000:U:O4'	2.02	0.59
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.36	0.59
23:21:52:ARG:NH2	23:21:57:GLU:OE1	2.36	0.59
32:2a:1517:G:H2'	32:2a:1518:MA6:H8	1.83	0.59
1:1A:2218:U:O4'	23:11:52:ARG:NH2	2.35	0.59
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.37	0.59
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.36	0.59
9:2N:123:TYR:HH	9:2N:130:HIS:HE2	1.49	0.59
19:2X:60:ARG:HH22	29:27:47:ARG:HH21	1.50	0.59
32:2a:1330:U:H4'	44:2m:23:TYR:CZ	2.38	0.59
32:2a:1385:G:H2'	32:2a:1386:G:H8	1.65	0.59
7:1H:124:GLU:HG3	7:1H:132:ARG:HB3	1.85	0.59
18:1W:13:SER:HB3	18:1W:16:LYS:HG3	1.83	0.59
32:1a:1373:G:H5"	38:1g:36:LYS:HD2	1.83	0.59
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.35	0.59
1:2A:2143:C:H42	1:2A:2148:G:H1	1.51	0.59
2:2B:70:C:H2'	2:2B:71:C:H6	1.68	0.59
32:2a:993:G:N7	32:2a:1213:A:N6	2.49	0.59
32:2a:1264:C:N4	32:2a:1271:G:H1	2.01	0.59
54:2w:63:U:H2'	54:2w:64:G:C8	2.37	0.59
1:1A:1399:C:OP1	19:1X:25:LYS:NZ	2.36	0.59
34:1c:19:GLU:HB3	34:1c:40:ARG:NH2	2.18	0.59
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.84	0.59
21:2Z:23:LYS:NZ	21:2Z:40:ASP:OD1	2.35	0.59
32:2a:376:G:H5"	47:2p:5:ARG:HB2	1.84	0.59
32:2a:771:G:O6	63:2a:3306:HOH:O	2.14	0.59
33:2b:30:ARG:HH21	33:2b:194:PRO:HB2	1.68	0.59
1:1A:1176:G:H21	1:1A:1178:C:P	2.25	0.59
1:1A:1325:G:OP1	63:1A:4149:HOH:O	2.17	0.59
54:1w:62:C:H2'	54:1w:63:U:C6	2.38	0.59
1:2A:862:G:OP2	63:2A:3945:HOH:O	2.17	0.59
1:2A:1604:C:O2'	1:2A:1610:A:N1	2.31	0.59
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.36	0.59
6:2G:63:ILE:HD13	6:2G:143:GLU:HB2	1.85	0.59
32:2a:539:A:H2'	32:2a:540:G:C8	2.37	0.59
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.21	0.59
39:2h:51:VAL:HG12	39:2h:52:ASP:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1143:A:OP2	63:1A:4148:HOH:O	2.17	0.59
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.36	0.59
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.36	0.59
32:1a:61:G:O6	63:1a:1912:HOH:O	2.17	0.59
32:1a:1025:U:C2	32:1a:1036:G:O6	2.55	0.59
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.17	0.59
35:1d:112:VAL:H	35:1d:116:GLN:NE2	2.01	0.59
39:1h:112:LEU:HA	39:1h:134:ILE:HG12	1.84	0.59
1:2A:302:C:OP2	20:2Y:73:ARG:NH1	2.36	0.59
1:2A:958:U:O2	2:2B:90:A:O2'	2.19	0.59
1:2A:1580:A:H3'	1:2A:1581:G:H8	1.67	0.59
55:2x:50:U:H3	55:2x:64:G:H1	1.49	0.59
1:1A:453:C:O2	1:1A:457:A:O2'	2.20	0.58
5:1F:11:VAL:HB	5:1F:18:ARG:HB2	1.84	0.58
5:1F:110:LEU:HD11	5:1F:181:LEU:HG	1.84	0.58
9:1N:128:HIS:CE1	9:1N:135:PRO:HG2	2.38	0.58
32:1a:45:U:H2'	32:1a:46:G:C8	2.37	0.58
1:2A:2393:A:H5"	11:2P:63:PRO:HB3	1.84	0.58
4:2E:176:ILE:HB	4:2E:181:LEU:HB2	1.84	0.58
1:1A:601:C:O2'	1:1A:605:C:OP1	2.18	0.58
47:1p:22:THR:OG1	47:1p:23:ASP:N	2.35	0.58
55:1x:73:A:H5"	55:1x:74:C:H5'	1.85	0.58
1:2A:124:G:OP1	1:2A:1376:C:O2'	2.15	0.58
1:2A:746:A:HO2'	1:2A:2611:U:HO2'	1.51	0.58
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.36	0.58
12:2Q:35:VAL:HG22	12:2Q:102:VAL:HG22	1.85	0.58
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.85	0.58
2:2B:119:G:H3'	2:2B:120:A:C8	2.39	0.58
23:21:56:GLN:HE22	23:21:87:PRO:HD3	1.67	0.58
32:2a:9:G:H2'	32:2a:10:A:C8	2.37	0.58
32:2a:56:U:H2'	32:2a:57:G:H8	1.68	0.58
34:2c:125:GLU:HB2	34:2c:190:ARG:HE	1.68	0.58
54:2w:76:A1B8A:OP1	63:2w:201:HOH:O	2.17	0.58
1:1A:1333:C:OP2	63:1A:4152:HOH:O	2.17	0.58
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.38	0.58
1:2A:468:G:N7	29:27:39:ARG:NH2	2.52	0.58
1:2A:805:G:OP1	63:2A:3947:HOH:O	2.17	0.58
1:2A:2318:G:H21	14:2S:3:ARG:HD3	1.68	0.58
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.85	0.58
32:2a:1076:C:OP1	33:2b:175:ARG:NH1	2.36	0.58
34:2c:123:GLN:HA	34:2c:126:ARG:CZ	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:70:LYS:HA	42:2k:73:MET:HE2	1.85	0.58
1:1A:2674:G:H4'	10:1O:30:ALA:HB2	1.85	0.58
11:1P:36:LYS:O	63:1P:301:HOH:O	2.16	0.58
19:1X:94:GLY:H	19:1X:95:LEU:C	2.10	0.58
32:1a:1292:U:H2'	32:1a:1293:G:C8	2.38	0.58
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.38	0.58
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.38	0.58
1:1A:1783:A:N7	63:1A:4269:HOH:O	2.32	0.58
1:1A:2419:U:H2'	1:1A:2420:C:C6	2.38	0.58
17:1V:55:ALA:HA	17:1V:101:GLY:HA3	1.85	0.58
1:2A:2378:A:O3'	14:2S:23:ARG:NH2	2.37	0.58
6:2G:112:PRO:HG3	26:24:43:TYR:HE1	1.69	0.58
18:2W:76:VAL:HG22	18:2W:103:ILE:HG23	1.86	0.58
32:2a:1106:G:H5"	34:2c:172:ARG:HB3	1.84	0.58
35:2d:50:ARG:HG2	35:2d:51:PRO:HD2	1.86	0.58
39:2h:10:LEU:HD13	39:2h:83:ILE:HG12	1.84	0.58
42:2k:22:HIS:CD2	42:2k:29:ILE:HD12	2.39	0.58
48:2q:66:SER:O	48:2q:68:ARG:N	2.37	0.58
1:1A:572:A:OP2	17:1V:78:LYS:NZ	2.36	0.58
1:2A:860:U:H1'	1:2A:2268:A:H5'	1.84	0.58
1:2A:2401:U:OP1	28:26:18:ARG:NH2	2.36	0.58
8:2I:123:LEU:HB2	8:2I:144:VAL:HB	1.85	0.58
32:2a:67:C:H2'	32:2a:68:G:C8	2.39	0.58
32:2a:1133:G:H1	32:2a:1141:C:N4	2.00	0.58
34:2c:125:GLU:HB2	34:2c:190:ARG:NE	2.18	0.58
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.86	0.58
34:1c:35:GLU:HG2	34:1c:59:ARG:HH22	1.68	0.58
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.15	0.58
49:1r:59:SER:OG	49:1r:60:ALA:N	2.36	0.58
1:2A:890:A:H2'	1:2A:892:G:H8	1.68	0.58
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.84	0.58
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.84	0.58
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.85	0.58
32:2a:1479:C:H2'	32:2a:1480:G:C8	2.38	0.58
44:2m:113:PRO:O	44:2m:115:LYS:NZ	2.36	0.58
1:1A:898:C:H2'	1:1A:899:A:H5'	1.85	0.58
3:1D:183:ARG:HG3	3:1D:270:ILE:HD13	1.86	0.58
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	1.86	0.58
32:1a:982:U:H5"	45:1n:6:LEU:HD11	1.85	0.58
36:1e:96:PRO:O	36:1e:98:THR:N	2.36	0.58
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:170:LEU:HD22	5:2F:172:TRP:HE1	1.69	0.58
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.85	0.58
32:2a:692:U:O2'	32:2a:694:A:N7	2.27	0.58
33:2b:114:ARG:O	33:2b:118:LEU:N	2.37	0.58
38:2g:73:MET:HB3	38:2g:90:GLU:HA	1.86	0.58
41:2j:69:ASN:O	41:2j:70:ARG:NH1	2.35	0.58
1:1A:2167:U:H2'	1:1A:2168:G:H4'	1.86	0.58
1:2A:2807:G:H1	1:2A:2892:A:H62	1.51	0.58
37:2f:76:ALA:HA	37:2f:79:LEU:HD12	1.85	0.58
54:2w:63:U:C2	54:2w:64:G:N7	2.72	0.58
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.86	0.57
1:1A:2136:C:C2	1:1A:2155:G:N2	2.72	0.57
1:1A:2347:C:O2'	28:16:21:TYR:OH	2.13	0.57
1:1A:2379:G:O2'	14:1S:17:ARG:NH2	2.37	0.57
3:1D:147:LEU:HD13	3:1D:155:LEU:HD21	1.86	0.57
25:13:7:LYS:HE3	25:13:34:GLU:HG2	1.84	0.57
33:1b:46:LYS:HA	33:1b:49:GLU:HB2	1.86	0.57
1:2A:854:G:H2'	1:2A:855:G:C8	2.38	0.57
32:2a:56:U:H2'	32:2a:57:G:C8	2.39	0.57
32:2a:1219:U:O2'	50:2s:34:TRP:HB3	2.04	0.57
32:2a:1271:G:C2	32:2a:1272:G:N7	2.72	0.57
40:2i:3:GLN:HG3	40:2i:20:ARG:HD2	1.86	0.57
4:1E:93:VAL:N	63:1E:402:HOH:O	2.36	0.57
5:1F:154:VAL:HG22	5:1F:191:ARG:HG3	1.86	0.57
28:16:11:LEU:HB2	28:16:21:TYR:HB2	1.86	0.57
1:2A:229:A:H2	1:2A:418:G:H4'	1.70	0.57
1:2A:994:C:O2	17:2V:10:LYS:NZ	2.36	0.57
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.21	0.57
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.38	0.57
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.22	0.57
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	1.86	0.57
2:1B:25:A:OP2	63:1B:302:HOH:O	2.17	0.57
32:1a:946:A:H2'	32:1a:947:G:C8	2.39	0.57
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.85	0.57
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	1.85	0.57
22:20:48:GLY:H	22:20:51:VAL:HB	1.70	0.57
57:2y:21:A:N6	57:2y:46:G7M:H1'	2.20	0.57
1:1A:1077:A:H2'	1:1A:1078:U:H4'	1.86	0.57
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.19	0.57
1:2A:721:C:H2'	1:2A:722:A:C8	2.39	0.57
1:2A:2122:U:H3	1:2A:2176:A:H61	1.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:38:VAL:HG12	6:2G:93:THR:HB	1.86	0.57
8:2I:9:LEU:HD21	8:2I:35:LEU:HD23	1.86	0.57
32:2a:664:G:H22	32:2a:741:G:H1	1.51	0.57
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.19	0.57
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.85	0.57
39:2h:78:GLN:O	39:2h:81:HIS:NE2	2.37	0.57
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.22	0.57
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.39	0.57
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.86	0.57
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.38	0.57
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.85	0.57
32:1a:987:G:H1	32:1a:1218:C:H42	1.51	0.57
1:2A:483:A:OP2	1:2A:484:C:N4	2.31	0.57
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.40	0.57
1:2A:2172:U:H4'	1:2A:2173:A:OP2	2.05	0.57
26:24:46:GLN:C	26:24:48:ARG:H	2.13	0.57
32:2a:560:U:H5'	32:2a:566:G:N2	2.20	0.57
32:2a:1005:A:H1'	32:2a:1025:U:H3	1.69	0.57
34:2c:129:ALA:HB3	34:2c:132:ARG:HD2	1.84	0.57
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.85	0.57
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.86	0.57
1:1A:910:A:C5	12:1Q:13:GLN:HG3	2.39	0.57
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.39	0.57
1:1A:2058:A:OP1	63:1A:4151:HOH:O	2.17	0.57
10:1O:88:ASN:ND2	10:1O:90:GLN:OE1	2.37	0.57
21:1Z:150:LEU:HD12	21:1Z:154:ASP:HB2	1.87	0.57
32:1a:13:U:O2'	63:1a:1914:HOH:O	2.18	0.57
34:1c:55:VAL:HG22	34:1c:68:VAL:HG22	1.85	0.57
1:2A:1927:A:H2'	1:2A:1928:A:C8	2.40	0.57
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.19	0.57
6:2G:114:ILE:HA	6:2G:140:ILE:HD11	1.85	0.57
9:2N:47:ALA:HB2	9:2N:112:LEU:HD11	1.86	0.57
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.36	0.57
33:2b:150:SER:OG	33:2b:151:GLY:N	2.34	0.57
35:2d:112:VAL:HG23	35:2d:113:SER:H	1.69	0.57
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD11	1.87	0.57
21:1Z:52:SER:O	21:1Z:54:HIS:N	2.37	0.57
38:1g:50:ILE:HD11	38:1g:125:MET:HG3	1.87	0.57
1:2A:140:G:N2	1:2A:1596:A:H4'	2.19	0.57
32:2a:375:U:OP1	47:2p:69:THR:OG1	2.22	0.57
49:2r:51:LEU:HB3	49:2r:55:ARG:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1087:G:H2'	1:1A:1089:G:C8	2.40	0.57
32:1a:352:C:O2'	32:1a:354:G:OP1	2.23	0.57
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.40	0.57
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.40	0.57
35:1d:178:VAL:C	35:1d:180:GLY:H	2.12	0.57
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.38	0.57
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.87	0.57
1:2A:144:C:H2'	1:2A:145:G:C8	2.40	0.57
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.20	0.57
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.40	0.57
39:2h:84:ARG:HH11	39:2h:86:ILE:HG12	1.69	0.57
1:1A:796:C:H2'	1:1A:797:C:C6	2.40	0.57
1:1A:1968:G:OP1	63:1A:4150:HOH:O	2.17	0.57
32:1a:920:U:H2'	32:1a:921:U:C6	2.40	0.57
32:1a:1226:C:H4'	50:1s:80:TYR:OH	2.05	0.57
33:1b:98:LEU:HG	33:1b:101:MET:HE3	1.85	0.57
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.05	0.57
15:2T:50:ILE:HG22	15:2T:102:ILE:HD11	1.87	0.57
54:2w:51:A:C3'	54:2w:64:G:H21	2.03	0.57
1:1A:811:U:OP1	63:1A:4153:HOH:O	2.18	0.57
21:1Z:126:VAL:HG12	21:1Z:128:VAL:HB	1.87	0.57
41:1j:16:LEU:HD22	41:1j:68:HIS:HB3	1.87	0.57
42:1k:48:ILE:O	42:1k:48:ILE:HG12	2.04	0.57
1:2A:832:G:H5'	11:2P:45:LEU:HD11	1.87	0.57
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.40	0.57
1:2A:2286:A:OP1	28:26:29:ASN:ND2	2.38	0.57
32:2a:1001(A):G:H2'	32:2a:1002:G:O4'	2.05	0.57
33:2b:149:LEU:HD23	33:2b:152:PHE:HB3	1.87	0.57
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.38	0.57
1:1A:826:U:OP1	63:1A:4104:HOH:O	2.18	0.56
1:1A:2124:G:H1	1:1A:2174:C:H42	1.52	0.56
32:1a:67:C:O2'	32:1a:171:A:N3	2.36	0.56
32:1a:150:C:H2'	32:1a:151:A:C8	2.39	0.56
32:1a:877:C:H5"	39:1h:88:LYS:HD3	1.87	0.56
1:2A:1230:C:H2'	1:2A:1231:G:H8	1.69	0.56
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.23	0.56
40:2i:65:VAL:HG21	40:2i:73:GLN:HB3	1.87	0.56
32:1a:150:C:H2'	32:1a:151:A:H8	1.68	0.56
32:1a:262:A:H2'	32:1a:263:A:C8	2.41	0.56
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.22	0.56
21:2Z:11:GLU:OE2	21:2Z:36:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.33	0.56
32:2a:1318:A:OP1	50:2s:3:ARG:NH2	2.28	0.56
35:2d:143:GLY:N	35:2d:185:PHE:O	2.33	0.56
37:2f:62:TRP:CH2	37:2f:64:GLN:HB2	2.40	0.56
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.87	0.56
45:2n:23:ARG:HH12	45:2n:30:ALA:HB2	1.70	0.56
1:1A:881:G:C2	1:1A:882:G:H1'	2.39	0.56
1:1A:1171:G:OP2	1:1A:1174:A:N6	2.39	0.56
1:1A:1918:A:N6	63:1A:4316:HOH:O	2.38	0.56
7:1H:3:ARG:HA	7:1H:3:ARG:HE	1.70	0.56
9:1N:30:ILE:HG23	9:1N:52:VAL:HG11	1.86	0.56
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.12	0.56
25:13:9:VAL:HG12	25:13:32:GLN:HE22	1.69	0.56
1:2A:370:G:OP1	1:2A:403:U:N3	2.28	0.56
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.37	0.56
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.40	0.56
39:2h:116:LYS:HD2	39:2h:129:VAL:HG11	1.87	0.56
42:2k:73:MET:HG2	42:2k:103:LEU:HD21	1.87	0.56
14:1S:36:TYR:CD1	14:1S:52:SER:HB3	2.40	0.56
18:1W:77:ASP:HB2	18:1W:102:HIS:HB2	1.87	0.56
32:1a:880:C:OP1	43:1l:8:ASN:ND2	2.36	0.56
41:1j:30:SER:HB3	41:1j:81:THR:HG23	1.87	0.56
51:1t:10:LEU:HD13	51:1t:11:SER:H	1.70	0.56
2:2B:37:C:O2	14:2S:95:HIS:NE2	2.38	0.56
14:2S:23:ARG:HG3	14:2S:24:LEU:N	2.19	0.56
14:2S:35:ILE:HD11	14:2S:101:LEU:HD13	1.86	0.56
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.38	0.56
32:2a:1159:U:O4'	32:2a:1182:G:N2	2.38	0.56
37:2f:41:GLU:OE1	49:2r:35:ARG:NH2	2.38	0.56
40:2i:28:VAL:HG13	40:2i:63:ILE:HB	1.86	0.56
44:2m:84:ILE:HG13	44:2m:86:CYS:HB2	1.87	0.56
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.06	0.56
2:1B:13:A:N1	2:1B:69:G:O2'	2.33	0.56
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.86	0.56
32:1a:376:G:O3'	47:1p:5:ARG:NH1	2.39	0.56
55:1x:61:C:H2'	55:1x:62:C:H6	1.70	0.56
1:2A:764:A:H5'	3:2D:210:GLY:HA2	1.87	0.56
4:2E:181:LEU:HD21	15:2T:6:LEU:HD22	1.88	0.56
6:2G:54:GLU:HA	6:2G:57:ALA:HB3	1.87	0.56
7:2H:45:VAL:HG22	7:2H:50:VAL:HG22	1.88	0.56
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:2q:82:MET:HA	48:2q:85:VAL:HB	1.87	0.56
1:1A:1068:G:H5”	1:1A:1069:A:OP2	2.05	0.56
1:1A:1359:A:H2’	1:1A:1360:A:H5’	1.88	0.56
1:1A:1636:C:H2’	1:1A:1637:A:C8	2.41	0.56
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.88	0.56
8:1I:87:LYS:HD3	8:1I:87:LYS:H	1.69	0.56
17:1V:60:GLU:HB2	17:1V:97:LYS:HE2	1.88	0.56
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	1.85	0.56
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.87	0.56
33:1b:131:PRO:O	33:1b:135:GLN:N	2.38	0.56
1:2A:2773:C:OP1	4:2E:166:THR:OG1	2.22	0.56
32:2a:643:C:O2’	39:2h:132:GLU:OE1	2.23	0.56
35:2d:18:LYS:HE3	35:2d:31:CYS:SG	2.45	0.56
36:2e:84:PHE:N	36:2e:87:SER:O	2.31	0.56
53:2v:14:A:H62	57:2y:34:U8U:HN3	1.53	0.56
1:1A:956:G:H2’	1:1A:957:A:H2’	1.88	0.56
1:1A:958:U:O2	2:1B:90:A:O2’	2.18	0.56
21:1Z:121:HIS:HE1	21:1Z:169:GLU:HG2	1.71	0.56
32:1a:176:C:H2’	32:1a:177:C:H6	1.69	0.56
32:1a:677:U:H3	32:1a:713:G:H22	1.53	0.56
32:1a:710:G:H5”	37:1f:54:LYS:HE2	1.87	0.56
54:1w:5:C:H2’	54:1w:6:G:C8	2.41	0.56
1:2A:2371:G:O6	63:2A:3935:HOH:O	2.14	0.56
1:2A:2482:G:O6	12:2Q:124:LYS:NZ	2.38	0.56
21:2Z:72:ARG:NH2	21:2Z:97:GLU:HB2	2.20	0.56
32:2a:937:A:N6	32:2a:1345:U:O4	2.39	0.56
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.41	0.56
1:1A:1325:G:OP1	1:1A:1647:G:O2’	2.20	0.56
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.52	0.56
1:2A:1507:A:O2’	1:2A:1508:A:O5’	2.21	0.56
1:2A:2293:C:H5”	14:2S:89:ARG:NH2	2.21	0.56
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.33	0.56
34:2c:8:ILE:HD12	34:2c:16:ARG:HG2	1.86	0.56
36:2e:148:VAL:HG21	39:2h:107:LEU:HD22	1.88	0.56
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.88	0.56
52:2u:6:ARG:HB3	52:2u:15:ARG:HG3	1.88	0.56
57:2y:36:U:H2’	57:2y:37:T6A:O4’	2.06	0.56
11:1P:38:GLN:O	11:1P:39:LYS:HB3	2.05	0.56
32:1a:1278:U:H5’	32:1a:1279:A:O4’	2.05	0.56
32:1a:1435:G:H2’	32:1a:1436:U:C6	2.40	0.56
1:2A:668:G:H5’	1:2A:669:G:OP2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1316:G:H5'	32:2a:1360:A:H1'	1.88	0.56
32:2a:1515:C:H2'	32:2a:1516:G:H8	1.71	0.56
36:2e:51:VAL:HG13	36:2e:52:PRO:HD3	1.88	0.56
1:1A:1453:U:OP1	13:1R:77:ARG:NH1	2.39	0.56
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.88	0.56
1:1A:2611:U:C5	60:1A:4082:TEL:H352	2.41	0.56
18:1W:11:ARG:NH1	18:1W:99:ARG:O	2.38	0.56
32:1a:272:C:H2'	32:1a:273:A:H8	1.71	0.56
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	1.87	0.56
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.05	0.56
1:2A:2690:C:OP2	13:2R:14:SER:HB3	2.06	0.56
2:2B:7:G:H21	14:2S:38:GLN:NE2	2.02	0.56
32:2a:417:C:H2'	32:2a:418:C:C6	2.41	0.56
32:2a:1411:C:H2'	32:2a:1412:C:C6	2.41	0.56
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.37	0.56
1:1A:196:A:H2'	1:1A:196:A:N3	2.21	0.55
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HG3	1.88	0.55
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.89	0.55
1:2A:370:G:OP2	63:2A:3927:HOH:O	2.18	0.55
1:2A:2065:C:H2'	1:2A:2066:C:H6	1.72	0.55
2:2B:24:G:H4'	2:2B:25:A:N7	2.20	0.55
21:2Z:154:ASP:OD1	21:2Z:154:ASP:N	2.32	0.55
32:2a:782:A:OP1	63:2a:3310:HOH:O	2.18	0.55
32:2a:1254:C:H42	32:2a:1283:G:H1	1.54	0.55
36:2e:10:MET:HA	36:2e:32:VAL:HG22	1.87	0.55
1:1A:477:A:OP2	63:1A:4155:HOH:O	2.18	0.55
5:1F:95:ARG:HD3	5:1F:97:TYR:CZ	2.41	0.55
57:1y:68:G:H2'	57:1y:69:A:O4'	2.06	0.55
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.42	0.55
1:2A:2074:U:O4	63:2A:3949:HOH:O	2.17	0.55
32:2a:224:C:H2'	32:2a:225:C:H6	1.71	0.55
32:2a:1089:G:H1	32:2a:1096:C:N4	2.03	0.55
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.87	0.55
7:1H:28:GLY:HA3	7:1H:79:VAL:HB	1.88	0.55
32:1a:591:U:H2'	32:1a:592:G:C8	2.42	0.55
1:2A:2143:C:N4	1:2A:2148:G:H1	2.04	0.55
1:2A:2780:G:OP2	9:2N:118:LYS:NZ	2.34	0.55
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.23	0.55
7:2H:92:ILE:H	7:2H:92:ILE:HD12	1.70	0.55
11:2P:87:ASP:O	11:2P:90:ARG:NH1	2.38	0.55
23:21:65:SER:OG	23:21:66:HIS:ND1	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:130:A:H5'	48:2q:63:ARG:HH21	1.71	0.55
32:2a:1152:A:OP1	41:2j:70:ARG:NH2	2.39	0.55
1:1A:886:C:OP1	1:1A:886:C:H4'	2.03	0.55
1:1A:1062:G:H1	1:1A:1077:A:H61	1.55	0.55
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.41	0.55
1:1A:1800:C:OP1	3:1D:264:LYS:NZ	2.37	0.55
11:1P:29:LYS:HG2	11:1P:30:THR:HG23	1.88	0.55
32:1a:707:C:OP1	42:1k:85:ARG:NH1	2.40	0.55
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.71	0.55
44:1m:106:ASN:HA	44:1m:108:ARG:HG2	1.88	0.55
44:2m:88:ARG:O	44:2m:92:HIS:HB2	2.06	0.55
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.06	0.55
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.38	0.55
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.41	0.55
32:1a:112:G:OP2	47:1p:27:LYS:NZ	2.38	0.55
34:1c:35:GLU:OE2	34:1c:59:ARG:NH1	2.38	0.55
1:2A:2511:U:OP1	63:2A:3946:HOH:O	2.17	0.55
32:2a:1051:C:H2'	32:2a:1052:U:H6	1.71	0.55
35:2d:22:LYS:HG3	62:2d:303:SF4:S3	2.47	0.55
40:2i:55:ALA:HA	40:2i:58:HIS:CD2	2.42	0.55
1:1A:2117:A:O2'	1:1A:2118:U:H5"	2.07	0.55
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.88	0.55
32:1a:1327:C:OP2	52:1u:12:LYS:NZ	2.31	0.55
40:1i:77:ILE:O	40:1i:81:ILE:HG22	2.07	0.55
43:1l:42:THR:HG22	43:1l:54:LYS:HG3	1.87	0.55
10:2O:53:LYS:N	10:2O:56:ASP:OD2	2.26	0.55
32:2a:171:A:H2'	32:2a:172:A:C8	2.42	0.55
32:2a:404:U:H2'	32:2a:405:U:C6	2.42	0.55
46:2o:87:ILE:HG22	46:2o:88:ARG:H	1.70	0.55
57:2y:52:G:H1	57:2y:62:C:H42	1.55	0.55
32:1a:1125:U:O2	32:1a:1126:U:O2'	2.19	0.55
1:2A:83:G:N1	1:2A:102:G:O2'	2.33	0.55
1:2A:271(R):G:OP1	23:21:76:ARG:NE	2.40	0.55
1:2A:458:G:O2'	1:2A:469:G:O6	2.19	0.55
1:2A:492:A:H2'	1:2A:493:G:O4'	2.07	0.55
1:1A:1058:G:N2	1:1A:1081:U:O2	2.40	0.55
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.06	0.55
1:1A:1865:G:N2	1:1A:1877:A:OP2	2.35	0.55
4:1E:119:ARG:HD3	4:1E:160:TYR:HB2	1.88	0.55
5:1F:39:TRP:CH2	5:1F:106:ARG:HD3	2.41	0.55
32:1a:193:C:H2'	32:1a:194:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.55	0.55
1:2A:518:G:H4'	18:2W:18:ARG:NE	2.22	0.55
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.17	0.55
1:2A:1388:G:H2'	1:2A:1389:G:H8	1.72	0.55
21:2Z:130:PRO:HA	21:2Z:133:ILE:HD11	1.89	0.55
21:2Z:150:LEU:HB2	21:2Z:171:ILE:HD11	1.88	0.55
32:2a:222:U:H2'	32:2a:223:U:C6	2.41	0.55
32:2a:425:G:H4'	35:2d:45:GLN:HE22	1.70	0.55
34:2c:6:HIS:CE1	34:2c:8:ILE:HB	2.41	0.55
54:2w:25:C:H2'	54:2w:26:A:O4'	2.06	0.55
1:1A:671:C:N4	63:1A:4344:HOH:O	2.40	0.55
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.40	0.55
1:2A:861:A:N3	2:2B:79:C:O2'	2.38	0.55
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.25	0.55
1:2A:2324:C:H5"	1:2A:2325:G:H5'	1.87	0.55
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.05	0.55
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.20	0.55
15:2T:26:ASP:OD1	15:2T:92:GLY:N	2.38	0.55
32:2a:735:C:H2'	32:2a:736:C:H6	1.72	0.55
1:1A:783:A:O2'	1:1A:785:G:OP1	2.19	0.55
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.42	0.55
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.22	0.55
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.88	0.55
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.22	0.55
32:1a:444:C:H2'	32:1a:445:G:H8	1.72	0.55
32:1a:1241:G:OP1	38:1g:35:LYS:NZ	2.40	0.55
1:2A:1183:G:H5"	25:23:30:ARG:HH12	1.72	0.55
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.07	0.55
6:2G:68:PRO:HB2	6:2G:90:LEU:HB3	1.89	0.55
16:2U:88:ILE:HG22	16:2U:90:VAL:HG22	1.89	0.55
26:24:59:PHE:HE2	50:2s:64:GLU:HB2	1.72	0.55
32:2a:1138:G:C6	32:2a:1140:C:H1'	2.42	0.55
33:2b:97:TRP:HH2	33:2b:102:LEU:HG	1.72	0.55
39:2h:89:PRO:HA	39:2h:92:ARG:HE	1.72	0.55
1:1A:1062:G:C4	1:1A:1088:A:H2'	2.42	0.54
1:1A:2099:U:H3	1:1A:2190:G:H1	1.55	0.54
1:1A:2163:C:OP1	1:1A:2171:A:O2'	2.24	0.54
32:1a:67:C:H2'	32:1a:68:G:C8	2.42	0.54
32:1a:624:C:H2'	32:1a:625:G:C8	2.40	0.54
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.42	0.54
6:2G:59:GLU:OE1	6:2G:153:ARG:NH2	2.30	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:65:ARG:HH11	19:2X:70:LEU:HD21	1.73	0.54
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.41	0.54
4:1E:168:MET:HE2	4:1E:203:LYS:HG2	1.89	0.54
32:1a:626:U:H2'	32:1a:627:G:C8	2.42	0.54
32:1a:1006:C:N4	32:1a:1022:G:O6	2.41	0.54
32:1a:1498:UR3:O2'	53:1v:17:U:OP1	2.23	0.54
34:1c:110:ASN:HD22	34:1c:140:ARG:HB3	1.72	0.54
57:1y:41:A:H3'	57:1y:42:A:H8	1.71	0.54
1:2A:900:A:O2'	1:2A:901:A:OP1	2.23	0.54
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.42	0.54
32:2a:1154:G:H2'	32:2a:1155:G:C8	2.42	0.54
33:2b:8:LYS:HD2	33:2b:217:ARG:HB3	1.89	0.54
51:2t:82:SER:O	51:2t:86:ARG:HB2	2.06	0.54
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	1.89	0.54
33:1b:19:HIS:HE2	33:1b:206:ASP:HB2	1.73	0.54
33:1b:167:PRO:O	33:1b:171:ALA:N	2.41	0.54
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	1.88	0.54
41:1j:46:ARG:HB2	41:1j:46:ARG:HH11	1.72	0.54
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.39	0.54
1:2A:192:C:O2'	1:2A:802:A:N3	2.37	0.54
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.33	0.54
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.08	0.54
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.27	0.54
32:2a:442:C:H42	32:2a:492:G:H1	1.55	0.54
1:1A:251:A:C5	1:1A:252:G:H1'	2.42	0.54
1:1A:586:A:N1	1:1A:809:G:O2'	2.36	0.54
1:1A:839:U:H2'	1:1A:840:C:C6	2.42	0.54
1:1A:2128:C:N3	1:1A:2160:G:N2	2.45	0.54
1:1A:2135:A:H61	1:1A:2156:G:H4'	1.73	0.54
1:1A:2712:U:O2'	1:1A:2712(A):A:OP2	2.22	0.54
16:1U:36:ARG:NH2	63:1U:301:HOH:O	2.39	0.54
32:1a:1309:G:OP2	44:1m:99:ARG:NH2	2.40	0.54
38:1g:28:ASN:HA	38:1g:31:MET:HE3	1.90	0.54
1:2A:2123:G:H2'	1:2A:2124:G:H8	1.70	0.54
1:2A:2875:C:O2'	15:2T:2:ASN:OD1	2.25	0.54
2:2B:19:G:H2'	2:2B:20:C:O4'	2.07	0.54
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.39	0.54
21:2Z:70:LEU:HB2	21:2Z:91:LEU:HD21	1.89	0.54
32:2a:410:G:H21	32:2a:432:A:H62	1.55	0.54
32:2a:600:C:H2'	32:2a:601:C:C6	2.43	0.54
32:2a:985:C:H42	32:2a:1220:G:H1	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1272:G:N2	32:2a:1273:G:C5	2.76	0.54
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.08	0.54
32:1a:442:C:H42	32:1a:492:G:H1	1.55	0.54
41:1j:5:ARG:NE	41:1j:73:ASP:OD1	2.30	0.54
41:1j:64:GLU:OE2	41:1j:66:ARG:NE	2.39	0.54
49:1r:37:VAL:HG22	49:1r:78:LEU:HB3	1.89	0.54
1:2A:910:A:C5	12:2Q:13:GLN:HG3	2.42	0.54
1:2A:2131:G:H8	1:2A:2133:G:N3	2.06	0.54
21:2Z:123:ASP:N	21:2Z:123:ASP:OD1	2.41	0.54
32:2a:457:C:H2'	32:2a:458:C:C6	2.43	0.54
44:2m:29:ARG:HD3	44:2m:64:TRP:CE2	2.43	0.54
54:2w:43:U:H2'	54:2w:44:U:C6	2.42	0.54
1:1A:505:A:OP2	63:1A:4156:HOH:O	2.19	0.54
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.08	0.54
1:1A:2513:G:N2	4:1E:143:ASN:OD1	2.40	0.54
32:1a:343:U:O2'	32:1a:346:G:O6	2.23	0.54
32:1a:1086:U:H3	32:1a:1099:G:H22	1.55	0.54
1:2A:479:A:H4'	1:2A:480:A:OP1	2.07	0.54
3:2D:85:ASP:OD2	3:2D:88:ARG:NH1	2.31	0.54
8:2I:88:ILE:HD11	8:2I:123:LEU:HB3	1.88	0.54
12:2Q:2:LEU:O	12:2Q:70:PRO:HG2	2.07	0.54
15:2T:19:LEU:HD22	15:2T:86:ILE:HG13	1.89	0.54
19:2X:11:PRO:HA	19:2X:28:PHE:HA	1.89	0.54
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.23	0.54
34:2c:14:ILE:HG21	34:2c:178:LEU:HB3	1.89	0.54
54:2w:50:C:O2	54:2w:50:C:H2'	2.07	0.54
57:2y:8:U:O2'	57:2y:21:A:N6	2.39	0.54
1:1A:2245:U:H5"	1:1A:2246:G:H5'	1.89	0.54
11:1P:114:ILE:HG13	11:1P:130:PHE:CE1	2.43	0.54
32:1a:1166:G:N2	32:1a:1170:A:OP2	2.40	0.54
37:1f:70:ASP:OD1	37:1f:70:ASP:N	2.37	0.54
51:1t:42:GLN:HE21	51:1t:46:GLU:HG3	1.72	0.54
6:2G:37:VAL:HG13	6:2G:94:LEU:HB2	1.90	0.54
32:2a:22:G:H2'	32:2a:23:C:C6	2.42	0.54
32:2a:838:G:H1	32:2a:848:C:H42	1.55	0.54
32:2a:1118:C:N3	32:2a:1156:G:N2	2.54	0.54
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.43	0.54
32:1a:116:A:H61	32:1a:313:A:H1'	1.71	0.54
1:2A:1153:C:OP1	16:2U:76:TYR:OH	2.26	0.54
1:2A:1512:U:H2'	1:2A:1513:C:C6	2.43	0.54
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2117:A:N6	1:2A:2166:G:H1	2.05	0.54
8:2I:61:ARG:O	8:2I:65:ALA:N	2.40	0.54
16:2U:89:GLU:HB2	17:2V:50:PRO:HB3	1.89	0.54
32:1a:22:G:H4'	32:1a:885:G:C8	2.43	0.54
32:1a:222:U:H2'	32:1a:223:U:C6	2.43	0.54
36:1e:78:HIS:CE1	36:1e:143:ARG:H	2.24	0.54
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.32	0.54
1:2A:818:G:OP2	63:2A:3948:HOH:O	2.17	0.54
1:2A:1567:A:H5'	3:2D:58:HIS:CD2	2.43	0.54
3:2D:71:ASP:HB2	3:2D:103:ARG:HH12	1.72	0.54
6:2G:174:GLU:HA	6:2G:178:PHE:H	1.73	0.54
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.42	0.54
1:1A:458:G:C8	29:17:37:LYS:HG2	2.43	0.54
1:1A:2206:G:H5"	1:1A:2207:G:C5	2.43	0.54
16:1U:34:LYS:NZ	16:1U:37:GLU:OE1	2.40	0.54
32:1a:265:G:H2'	32:1a:267:C:H5	1.72	0.54
32:1a:417:C:H42	32:1a:426:G:H1	1.54	0.54
32:1a:475:G:H2'	32:1a:476:G:C8	2.43	0.54
47:1p:72:ARG:HA	47:1p:75:ARG:HB3	1.89	0.54
1:2A:752:A:H3'	29:27:1:MET:HE1	1.90	0.54
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.43	0.54
6:2G:123:ASN:OD1	6:2G:123:ASN:N	2.40	0.54
20:2Y:37:VAL:N	20:2Y:67:LEU:O	2.36	0.54
32:2a:457:C:H2'	32:2a:458:C:H6	1.73	0.54
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.40	0.54
32:2a:1114:C:H42	32:2a:1186:G:H1	1.56	0.54
36:2e:88:LYS:HD3	36:2e:123:LEU:HD12	1.89	0.54
1:1A:113:G:H5'	63:1A:4547:HOH:O	2.08	0.53
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.90	0.53
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.73	0.53
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.21	0.53
7:1H:105:LEU:HD12	7:1H:151:ILE:HD12	1.90	0.53
12:1Q:51:ARG:O	12:1Q:55:VAL:HG23	2.08	0.53
32:1a:79:G:N1	32:1a:90:U:N3	2.51	0.53
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.30	0.53
33:1b:102:LEU:HD23	33:1b:182:ILE:HD12	1.90	0.53
48:1q:34:LYS:HG2	48:1q:36:ILE:HG22	1.90	0.53
1:2A:674:G:H1'	5:2F:74:ARG:HD3	1.89	0.53
1:2A:987:G:O2'	1:2A:1000:A:N3	2.39	0.53
1:2A:2062:A:H61	56:2z:2:ARG:HH11	1.54	0.53
1:2A:2392:A:N3	11:2P:61:ARG:HG2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.41	0.53
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.89	0.53
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.90	0.53
21:2Z:72:ARG:HH22	21:2Z:97:GLU:HB2	1.74	0.53
32:2a:1109:C:H2'	32:2a:1110:A:O4'	2.08	0.53
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	1.90	0.53
45:2n:16:PHE:HB2	45:2n:19:ARG:HG3	1.89	0.53
54:2w:26:A:H2'	54:2w:27:G:C8	2.43	0.53
1:1A:1138:G:N3	9:1N:106:MET:HE2	2.23	0.53
1:1A:1213:A:N3	1:1A:1238:G:O2'	2.37	0.53
13:1R:15:SER:OG	63:1R:302:HOH:O	2.15	0.53
32:1a:200:G:H1	32:1a:217:C:N4	2.06	0.53
8:2I:40:THR:O	8:2I:44:LEU:N	2.39	0.53
32:2a:201:C:H42	32:2a:216:G:H1	1.55	0.53
32:2a:736:C:H2'	32:2a:737:A:H8	1.74	0.53
44:2m:10:PRO:HD2	44:2m:18:ALA:HB1	1.89	0.53
1:1A:370:G:OP2	63:1A:4162:HOH:O	2.19	0.53
1:1A:800:A:H8	1:1A:800:A:OP1	1.91	0.53
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.72	0.53
1:1A:2627:G:O2'	1:1A:2781:A:N1	2.33	0.53
32:1a:244:U:O2	63:1a:1907:HOH:O	2.15	0.53
32:1a:279:A:C5	48:1q:98:LEU:HD23	2.43	0.53
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.74	0.53
34:1c:19:GLU:HB3	34:1c:40:ARG:HH21	1.72	0.53
1:2A:918:A:O2'	2:2B:97:G:N2	2.40	0.53
1:2A:2119:A:N1	1:2A:2170:A:H2'	2.23	0.53
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.08	0.53
8:2I:55:ALA:HA	8:2I:58:LEU:HB3	1.90	0.53
16:2U:47:TYR:HA	16:2U:50:ARG:NH2	2.23	0.53
32:2a:707:C:H2'	32:2a:708:C:C6	2.43	0.53
32:2a:989:C:H1'	32:2a:1016:A:H2	1.73	0.53
32:2a:998:G:H1	32:2a:1043:C:H42	1.55	0.53
38:2g:76:ARG:HB3	38:2g:89:MET:HG3	1.91	0.53
1:1A:1062:G:H8	1:1A:1070:A:H4'	1.74	0.53
23:11:72:GLU:O	23:11:76:ARG:HG2	2.09	0.53
32:1a:276:G:O3'	48:1q:68:ARG:NH1	2.41	0.53
32:1a:328:C:H4'	32:1a:329:A:H5"	1.89	0.53
32:1a:737:A:H2'	32:1a:738:C:C6	2.44	0.53
1:2A:582:G:H2'	1:2A:583:G:C8	2.43	0.53
1:2A:1220:A:OP2	16:2U:19:LYS:NZ	2.34	0.53
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:133:LEU:HB3	3:2D:173:VAL:HG21	1.90	0.53
11:2P:56:SER:HB2	11:2P:61:ARG:HD2	1.90	0.53
32:2a:936:C:H2'	32:2a:937:A:O4'	2.08	0.53
32:2a:1226:C:H6	44:2m:103:THR:HB	1.74	0.53
33:2b:47:THR:O	33:2b:51:LEU:N	2.41	0.53
34:2c:156:ARG:HH21	34:2c:161:GLU:HA	1.72	0.53
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.89	0.53
43:2l:53:ARG:HD2	43:2l:93:LEU:HD21	1.91	0.53
1:1A:2168:G:N2	1:1A:2171:A:N7	2.56	0.53
1:1A:2503:2MA:C8	60:1A:4082:TEL:H572	2.39	0.53
6:1G:126:ASP:HB3	6:1G:130:ASN:H	1.73	0.53
11:1P:8:PRO:HB2	11:1P:12:ALA:HB3	1.89	0.53
1:2A:211:A:H2'	1:2A:212:G:O4'	2.08	0.53
1:2A:1183:G:H5"	25:23:30:ARG:HH22	1.73	0.53
32:2a:266:G:H2'	32:2a:266:G:N3	2.23	0.53
32:2a:976:G:P	45:2n:32:SER:H	2.31	0.53
32:2a:1255:G:O2'	32:2a:1258:G:N3	2.37	0.53
32:2a:1313:U:H5	50:2s:2:PRO:HG2	1.73	0.53
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.44	0.53
33:2b:8:LYS:HB3	33:2b:217:ARG:HE	1.72	0.53
35:2d:10:ARG:HA	35:2d:13:ARG:HB2	1.89	0.53
54:2w:26:A:H2'	54:2w:27:G:H8	1.74	0.53
57:2y:28:U:H3	57:2y:42:A:H61	1.55	0.53
1:1A:2252:G:N7	63:10:201:HOH:O	2.34	0.53
1:1A:2478:A:H5'	31:19:31:LYS:HD3	1.90	0.53
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.90	0.53
12:1Q:16:ARG:HG2	12:1Q:18:LYS:HG3	1.90	0.53
26:14:15:ILE:HG12	26:14:21:VAL:HG22	1.91	0.53
32:1a:1129:C:O2	32:1a:1130:A:N6	2.29	0.53
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.73	0.53
3:2D:231:HIS:O	63:2D:401:HOH:O	2.18	0.53
32:2a:418:C:H2'	32:2a:419:C:C6	2.44	0.53
32:2a:1401:G:OP1	53:2v:18:G:O2'	2.24	0.53
43:2l:74:GLY:O	43:2l:102:ARG:NH2	2.42	0.53
47:2p:23:ASP:OD2	47:2p:25:ARG:NH2	2.42	0.53
48:2q:66:SER:HB3	48:2q:69:LYS:HB2	1.90	0.53
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.09	0.53
1:1A:1252:G:N7	16:1U:36:ARG:NH1	2.53	0.53
6:1G:66:GLN:OE1	6:1G:98:ARG:NE	2.37	0.53
32:1a:1005:A:O2'	32:1a:1037:C:O2	2.27	0.53
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271(K):U:O2	8:2I:50:ARG:HD3	2.09	0.53
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.57	0.53
1:2A:1259:G:H2'	1:2A:1260:G:C8	2.44	0.53
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.09	0.53
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.07	0.53
1:2A:2701:C:H2'	1:2A:2702:U:H2'	1.91	0.53
30:28:52:LYS:O	30:28:56:GLU:HG3	2.08	0.53
32:2a:977:A:O2'	32:2a:981:U:N3	2.40	0.53
32:2a:1029:C:H1'	32:2a:1033:G:H22	1.73	0.53
32:2a:1312:G:H5'	50:2s:5:LEU:HD11	1.91	0.53
32:2a:1373:G:H5"	38:2g:36:LYS:HE2	1.91	0.53
40:2i:86:VAL:HG23	40:2i:96:LEU:HD12	1.90	0.53
1:1A:1062:G:P	1:1A:1070:A:H1'	2.49	0.53
1:1A:1111:A:N3	1:1A:1112:G:H1'	2.23	0.53
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.44	0.53
1:1A:1357:U:H2'	1:1A:1358:G:O4'	2.09	0.53
1:1A:1823:G:OP1	3:1D:54:ARG:NH1	2.42	0.53
5:1F:129:PHE:HB3	5:1F:132:VAL:HG13	1.90	0.53
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.24	0.53
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.09	0.53
43:1l:8:ASN:O	43:1l:12:ARG:HG3	2.09	0.53
1:2A:2130:U:H3	1:2A:2159:G:H1	1.57	0.53
1:2A:2483:C:H2'	1:2A:2484:G:O4'	2.09	0.53
1:2A:2782:G:OP2	63:2A:3952:HOH:O	2.19	0.53
32:2a:376:G:O3'	47:2p:5:ARG:NH1	2.38	0.53
32:2a:487:A:H2'	32:2a:488:C:O4'	2.09	0.53
32:2a:1206:G:H2'	32:2a:1207:2MG:O4'	2.09	0.53
57:2y:4:U:H2'	57:2y:5:C:H5'	1.91	0.53
1:1A:1371:G:O6	63:1A:4154:HOH:O	2.18	0.53
1:1A:2025:C:N4	63:1A:4359:HOH:O	2.41	0.53
32:1a:574:A:HO2'	32:1a:882:C:HO2'	1.54	0.53
43:1l:79:GLU:OE2	43:1l:80:HIS:NE2	2.42	0.53
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.08	0.53
6:2G:37:VAL:HG12	6:2G:99:MET:HB2	1.91	0.53
11:2P:88:LEU:HA	11:2P:91:PHE:HD2	1.74	0.53
36:2e:129:ILE:HD12	36:2e:129:ILE:H	1.73	0.53
54:2w:12:U:H3	54:2w:23:A:H61	1.57	0.53
1:1A:2064:C:H2'	1:1A:2065:C:C6	2.44	0.53
1:1A:2508:G:H5'	54:1w:74:C:H42	1.74	0.53
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.73	0.53
6:1G:18:GLU:HG3	6:1G:22:ARG:HD2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:135:C:H2'	32:1a:136:C:H5'	1.91	0.53
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.44	0.53
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.44	0.53
1:2A:81:G:H21	20:2Y:1:MET:HE3	1.74	0.53
1:2A:218:A:C2	1:2A:235:U:H4'	2.44	0.53
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.44	0.53
17:2V:25:LEU:N	17:2V:92:THR:OG1	2.41	0.53
26:24:44:THR:O	26:24:46:GLN:N	2.42	0.53
34:2c:88:ARG:HA	34:2c:91:LEU:HD13	1.90	0.53
38:2g:40:ALA:HB3	40:2i:41:VAL:HG21	1.91	0.53
1:1A:221:A:N1	1:1A:265:A:O2'	2.42	0.52
1:1A:530:G:N1	1:1A:2023:G:OP1	2.37	0.52
1:1A:1359:A:H2	1:1A:1372:U:O4	1.91	0.52
1:1A:2429:G:OP1	63:1A:4104:HOH:O	2.19	0.52
32:1a:1342:C:H2'	32:1a:1343:G:C8	2.44	0.52
38:1g:78:ARG:HH12	38:1g:155:ARG:C	2.17	0.52
1:2A:673:C:H5"	5:2F:81:PRO:HD2	1.90	0.52
1:2A:2130:U:H2'	1:2A:2158:A:N6	2.23	0.52
1:2A:2518:A:OP2	63:2A:3954:HOH:O	2.19	0.52
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.45	0.52
14:2S:11:LYS:HD2	14:2S:15:ARG:HH21	1.74	0.52
32:2a:984:C:H2'	32:2a:985:C:C6	2.44	0.52
32:2a:994:A:C5	32:2a:1216:G:H4'	2.45	0.52
32:2a:1002:G:H1	32:2a:1038:C:H42	1.57	0.52
35:2d:14:ARG:HB2	35:2d:40:PRO:HD2	1.90	0.52
46:2o:11:VAL:HG21	46:2o:34:LEU:HD13	1.90	0.52
1:1A:674:G:H1'	5:1F:74:ARG:HH11	1.73	0.52
5:1F:8:GLN:HE22	5:1F:21:ALA:HB2	1.74	0.52
32:1a:735:C:H2'	32:1a:736:C:C6	2.45	0.52
32:1a:757:U:H2'	32:1a:758:G:O4'	2.10	0.52
32:1a:1036:G:H3'	32:1a:1037:C:C6	2.44	0.52
32:1a:1095:U:P	32:1a:1108:G:H1	2.32	0.52
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.16	0.52
47:1p:53:VAL:HG13	47:1p:79:VAL:HG22	1.90	0.52
1:2A:271(D):G:H2'	1:2A:271(E):U:H6	1.74	0.52
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.43	0.52
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.23	0.52
5:2F:155:LEU:HB2	5:2F:189:THR:HG21	1.91	0.52
6:2G:63:ILE:HD11	6:2G:144:ILE:HG13	1.91	0.52
13:2R:104:ARG:HG3	13:2R:111:LEU:HD21	1.92	0.52
28:26:12:GLU:OE1	28:26:19:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1130:A:H5"	40:2i:18:PHE:CE2	2.44	0.52
32:2a:1310:G:H5'	44:2m:77:ASN:ND2	2.23	0.52
35:2d:108:LEU:HD21	35:2d:174:LEU:HB3	1.92	0.52
38:2g:16:LEU:HD21	40:2i:42:ARG:HG3	1.91	0.52
54:2w:51:A:N7	54:2w:64:G:H2'	2.24	0.52
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.43	0.52
35:1d:159:ARG:O	35:1d:163:GLU:N	2.42	0.52
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.38	0.52
1:2A:1529:G:O6	1:2A:1541:G:N2	2.42	0.52
1:2A:1580:A:H3'	1:2A:1581:G:C8	2.44	0.52
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.74	0.52
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.44	0.52
1:2A:2595:G:N7	63:2A:4031:HOH:O	2.33	0.52
1:2A:2657:A:O3'	7:2H:160:LYS:NZ	2.43	0.52
3:2D:137:PRO:O	3:2D:140:THR:OG1	2.15	0.52
6:2G:51:ARG:HD2	6:2G:52:ILE:H	1.74	0.52
24:22:32:LEU:HD11	24:22:50:ILE:HG23	1.92	0.52
26:24:58:ARG:HE	50:2s:68:GLY:H	1.55	0.52
32:2a:34:C:H2'	32:2a:35:G:H8	1.74	0.52
32:2a:524:G:H2'	32:2a:525:C:C6	2.44	0.52
33:2b:29:ALA:HA	33:2b:32:ILE:HD12	1.92	0.52
34:2c:118:GLN:HA	34:2c:121:ALA:HB3	1.91	0.52
36:2e:143:ARG:HH21	39:2h:77:GLU:CD	2.18	0.52
50:2s:65:ASN:OD1	50:2s:65:ASN:N	2.40	0.52
54:2w:51:A:N1	54:2w:63:U:C4	2.77	0.52
1:1A:1055:G:H2'	1:1A:1056:G:O4'	2.09	0.52
10:1O:10:VAL:HG11	10:1O:16:ALA:HB3	1.91	0.52
35:1d:12:CYS:HB3	35:1d:19:LEU:H	1.73	0.52
36:1e:143:ARG:NH2	39:1h:77:GLU:OE1	2.39	0.52
1:2A:724:U:H2'	1:2A:725:G:O4'	2.09	0.52
6:2G:41:GLN:O	6:2G:43:LEU:N	2.42	0.52
28:26:26:ASN:O	28:26:28:ARG:N	2.43	0.52
32:2a:991:U:C4	32:2a:1212:U:H1'	2.44	0.52
32:2a:1314:C:H2'	32:2a:1315:U:C6	2.44	0.52
32:2a:1363(A):A:H1'	32:2a:1365:G:N7	2.24	0.52
32:2a:1397:C:OP2	36:2e:24:ARG:NH2	2.41	0.52
32:2a:1507:A:OP2	53:2v:13:A:N6	2.42	0.52
33:2b:98:LEU:HB3	33:2b:101:MET:HG3	1.90	0.52
41:2j:64:GLU:OE2	41:2j:66:ARG:NE	2.41	0.52
1:1A:451:C:OP2	63:1A:4157:HOH:O	2.19	0.52
6:1G:16:ARG:HH22	6:1G:31:VAL:HG11	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1W:46:PHE:O	18:1W:50:VAL:HG23	2.09	0.52
18:1W:68:ARG:NH1	18:1W:112:GLY:H	2.06	0.52
1:2A:745:G:H22	60:2A:3826:TEL:H51	1.75	0.52
1:2A:880:G:N2	1:2A:898:C:O2	2.42	0.52
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.10	0.52
1:2A:2295:C:H41	14:2S:13:ARG:NH1	2.08	0.52
19:2X:26:TYR:HB3	19:2X:92:LEU:HD12	1.92	0.52
37:2f:24:GLU:O	37:2f:28:ARG:N	2.29	0.52
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.44	0.52
1:1A:1532:C:H42	1:1A:1537:G:H1	1.57	0.52
1:1A:2154:G:C2	1:1A:2155:G:H1'	2.44	0.52
1:1A:2702:U:OP2	63:1A:4160:HOH:O	2.19	0.52
11:1P:100:LEU:HD22	11:1P:105:LEU:HD12	1.91	0.52
32:1a:299:G:H2'	32:1a:300:A:C8	2.45	0.52
32:1a:750:G:O2'	46:1o:21:ASP:OD1	2.26	0.52
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.10	0.52
40:1i:127:LYS:NZ	55:1x:34:C:OP2	2.35	0.52
54:1w:15:G:H22	54:1w:48:C:H42	1.57	0.52
57:1y:63:U:H2'	57:1y:64:G:H8	1.74	0.52
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.92	0.52
1:2A:1226:A:OP1	17:2V:84:LYS:NZ	2.32	0.52
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.45	0.52
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.17	0.52
21:2Z:31:ARG:HG3	21:2Z:32:HIS:CD2	2.44	0.52
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.43	0.52
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.39	0.52
1:1A:2125:G:N1	1:1A:2172:U:OP1	2.42	0.52
18:1W:58:ALA:HB1	18:1W:64:MET:HB2	1.92	0.52
32:1a:447:G:O6	32:1a:485:G:O2'	2.26	0.52
32:1a:646:U:H2'	32:1a:647:C:C6	2.44	0.52
32:1a:1038:C:H2'	32:1a:1039:C:C6	2.45	0.52
5:2F:28:ILE:HG22	5:2F:112:MET:HB3	1.92	0.52
5:2F:126:VAL:HG11	5:2F:142:TRP:HH2	1.75	0.52
15:2T:51:ARG:HG3	15:2T:98:LYS:HD2	1.92	0.52
15:2T:88:ILE:HG21	15:2T:91:ARG:CZ	2.40	0.52
26:24:59:PHE:CE2	50:2s:64:GLU:HB2	2.45	0.52
32:2a:735:C:H2'	32:2a:736:C:C6	2.43	0.52
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.56	0.52
49:2r:31:LEU:HD23	49:2r:31:LEU:H	1.75	0.52
51:2t:9:ASN:O	51:2t:10:LEU:HB2	2.09	0.52
54:2w:11:C:H2'	54:2w:12:U:C6	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:21:A:H61	55:2x:46:G:H2'	1.74	0.52
1:1A:568:U:O5'	1:1A:945:A:N6	2.43	0.52
32:1a:1224:G:OP1	63:1a:1916:HOH:O	2.19	0.52
41:1j:54:PHE:CE2	41:1j:55:LYS:HG2	2.44	0.52
1:2A:1336:A:H2'	1:2A:1337:G:H8	1.75	0.52
1:2A:1349:A:OP1	63:2A:3955:HOH:O	2.19	0.52
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.45	0.52
6:2G:112:PRO:HG3	26:24:43:TYR:CE1	2.45	0.52
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH1	2.25	0.52
32:2a:196:A:OP1	51:2t:68:LYS:NZ	2.27	0.52
32:2a:324:G:N1	32:2a:327:A:OP2	2.39	0.52
32:2a:1262:C:H2'	32:2a:1263:C:H5'	1.92	0.52
33:2b:8:LYS:HB3	33:2b:217:ARG:NE	2.25	0.52
35:2d:36:ARG:HD2	35:2d:38:TYR:OH	2.10	0.52
35:2d:74:GLN:O	35:2d:78:LEU:HB2	2.10	0.52
32:1a:377:G:H5'	47:1p:5:ARG:HH12	1.75	0.52
32:1a:475:G:H2'	32:1a:476:G:H8	1.75	0.52
32:1a:1025:U:O2	32:1a:1036:G:C6	2.63	0.52
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.09	0.52
57:1y:1:G:H2'	57:1y:2:G:C8	2.43	0.52
57:1y:4:U:H3	57:1y:69:A:H61	1.56	0.52
1:2A:195:A:H61	1:2A:198:C:H3'	1.75	0.52
1:2A:1777:U:H2'	1:2A:1778:U:C6	2.44	0.52
1:2A:1910:G:H2'	1:2A:1911:PSU:H6	1.73	0.52
1:2A:2702:U:H4'	1:2A:2703:C:OP1	2.10	0.52
2:2B:17:C:H2'	2:2B:18:G:O4'	2.09	0.52
3:2D:118:VAL:HG12	3:2D:129:ASN:ND2	2.25	0.52
32:2a:564:C:HO2'	39:2h:91:ARG:HH22	1.55	0.52
32:2a:1124:G:H4'	41:2j:38:ILE:HD11	1.91	0.52
32:2a:1263:C:C4	32:2a:1272:G:O6	2.63	0.52
44:2m:117:VAL:HG22	44:2m:118:ALA:H	1.75	0.52
1:2A:195:A:N7	63:2A:4035:HOH:O	2.34	0.52
1:2A:584:C:N4	63:2A:4073:HOH:O	2.40	0.52
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.24	0.52
46:2o:26:GLU:OE1	46:2o:77:ARG:NH2	2.42	0.52
1:1A:581:C:H2'	1:1A:582:G:H8	1.74	0.51
1:1A:1039:G:H1	1:1A:1116:C:H42	1.55	0.51
1:1A:1084:A:N3	1:1A:1105:U:O2'	2.35	0.51
6:1G:49:ASP:N	6:1G:49:ASP:OD1	2.43	0.51
30:18:42:ARG:NH1	63:18:202:HOH:O	2.39	0.51
32:1a:426:G:OP1	35:1d:36:ARG:NH1	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1342:C:H2'	32:1a:1343:G:H8	1.75	0.51
48:1q:15:MET:HE1	48:1q:43:LEU:HD22	1.91	0.51
2:2B:2:C:H2'	2:2B:3:C:C6	2.45	0.51
8:2I:37:VAL:HG12	8:2I:38:LEU:HD12	1.91	0.51
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	1.92	0.51
32:2a:1143:G:H2'	32:2a:1144:G:O4'	2.10	0.51
33:2b:103:THR:HG22	33:2b:180:LEU:HD21	1.91	0.51
1:1A:1235:G:OP1	63:1A:4156:HOH:O	2.19	0.51
1:1A:1342:A:OP2	63:1A:4159:HOH:O	2.19	0.51
1:1A:2012:G:OP2	18:1W:16:LYS:NZ	2.42	0.51
1:1A:2369:A:H2'	1:1A:2370:G:H8	1.75	0.51
3:1D:71:ASP:HB2	3:1D:103:ARG:HH12	1.74	0.51
32:1a:662:G:H2'	32:1a:663:A:C8	2.45	0.51
32:1a:977:A:O2'	32:1a:981:U:N3	2.42	0.51
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.44	0.51
1:2A:41:C:H2'	1:2A:42:G:H8	1.75	0.51
1:2A:601:C:O2'	1:2A:605:C:H5"	2.11	0.51
1:2A:801:G:O6	5:2F:53:THR:OG1	2.27	0.51
1:2A:1474:C:H2'	1:2A:1475:G:C8	2.45	0.51
1:2A:2303:G:H2'	1:2A:2304:G:O4'	2.10	0.51
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.45	0.51
28:26:6:ARG:HH21	28:26:24:GLU:HG3	1.73	0.51
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	1.92	0.51
32:2a:1515:C:H2'	32:2a:1516:G:C8	2.44	0.51
33:2b:12:GLU:O	33:2b:15:VAL:N	2.43	0.51
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.25	0.51
50:2s:28:LYS:HB3	50:2s:29:ARG:HA	1.91	0.51
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.92	0.51
57:2y:27:G:N2	57:2y:44:U:O2	2.44	0.51
1:1A:890:A:H2'	1:1A:892:G:O4'	2.10	0.51
5:1F:161:GLU:HG2	5:1F:164:ARG:NH2	2.26	0.51
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.29	0.51
6:1G:5:VAL:HG13	6:1G:8:LYS:HE2	1.91	0.51
32:1a:591:U:H2'	32:1a:592:G:H8	1.74	0.51
57:1y:55:PSU:C4	57:1y:57:G:H5'	2.45	0.51
1:2A:817:C:O2'	1:2A:839:U:H5"	2.10	0.51
1:2A:992:C:OP1	17:2V:74:LYS:NZ	2.31	0.51
1:2A:2538:C:H2'	1:2A:2539:C:H6	1.75	0.51
33:2b:42:ILE:HG21	33:2b:202:PRO:HB2	1.92	0.51
35:2d:57:ARG:HB3	35:2d:206:PHE:HB2	1.92	0.51
38:2g:18:TYR:HB3	38:2g:59:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:51:A:H61	54:2w:63:U:H3	0.62	0.51
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.10	0.51
25:13:39:ASP:OD1	25:13:44:ARG:NH1	2.44	0.51
32:1a:865:A:H2	32:1a:918:A:H4'	1.76	0.51
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.42	0.51
40:1i:46:ALA:HA	40:1i:78:LYS:HB2	1.91	0.51
54:1w:19:G:H1	54:1w:56:C:H42	1.57	0.51
57:1y:55:PSU:N3	57:1y:57:G:H5'	2.25	0.51
1:2A:943:U:OP2	63:2A:3953:HOH:O	2.19	0.51
13:2R:87:TYR:HB3	13:2R:90:ARG:HB3	1.91	0.51
14:2S:35:ILE:HG21	14:2S:66:ALA:HB2	1.93	0.51
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.29	0.51
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	1.92	0.51
48:2q:9:VAL:O	48:2q:21:VAL:HA	2.09	0.51
49:2r:73:ALA:HB3	49:2r:79:LEU:HD12	1.93	0.51
55:2x:17:C:OP2	55:2x:18:G:H5"	2.09	0.51
1:1A:302:C:OP2	20:1Y:73:ARG:NH2	2.43	0.51
43:1l:24:VAL:HB	43:1l:27:LEU:HD12	1.92	0.51
1:2A:84:A:H5'	20:2Y:8:LYS:HG2	1.92	0.51
2:2B:42:C:C2	6:2G:92:VAL:HA	2.46	0.51
6:2G:68:PRO:HA	6:2G:92:VAL:HB	1.92	0.51
10:2O:77:ILE:HD12	15:2T:74:ARG:HD2	1.91	0.51
13:2R:29:LEU:HD22	13:2R:79:LEU:HD13	1.91	0.51
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.92	0.51
24:22:14:ARG:O	24:22:67:LYS:NZ	2.35	0.51
26:24:53:GLU:HG2	26:24:55:ARG:N	2.21	0.51
32:2a:438:G:H4'	35:2d:123:HIS:CE1	2.45	0.51
32:2a:1258:G:H2'	32:2a:1259:C:C6	2.46	0.51
35:2d:78:LEU:HD21	35:2d:96:LEU:HB3	1.92	0.51
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.40	0.51
1:1A:1054:A:H3'	1:1A:1055:G:H8	1.74	0.51
1:1A:1062:G:H2'	1:1A:1063:G:C8	2.46	0.51
1:1A:2398:U:H2'	1:1A:2399:G:C8	2.45	0.51
1:1A:2398:U:H2'	1:1A:2399:G:H8	1.75	0.51
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.11	0.51
43:1l:39:VAL:HG11	43:1l:41:ARG:HH11	1.75	0.51
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.46	0.51
1:2A:2408:U:H2'	1:2A:2409:G:C8	2.46	0.51
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.91	0.51
12:2Q:122:GLY:HA2	12:2Q:125:LEU:HD12	1.93	0.51
20:2Y:2:ARG:NH1	20:2Y:4:LYS:HD3	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:643:C:H2'	32:2a:644:G:C8	2.46	0.51
32:2a:1189:C:P	41:2j:51:ARG:HH22	2.34	0.51
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.11	0.51
46:2o:55:GLY:HA2	46:2o:58:MET:HG3	1.91	0.51
50:2s:36:ARG:HG2	50:2s:51:VAL:HG12	1.93	0.51
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.25	0.51
1:1A:2429:G:N7	11:1P:56:SER:OG	2.41	0.51
1:1A:2470:G:O6	1:1A:2476:A:O2'	2.26	0.51
6:1G:3:LEU:O	6:1G:8:LYS:NZ	2.35	0.51
18:1W:92:ARG:NH1	63:1W:305:HOH:O	2.43	0.51
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.11	0.51
1:2A:848:G:H2'	1:2A:849:A:C8	2.45	0.51
1:2A:921:G:H4'	1:2A:2269:A:C5	2.46	0.51
6:2G:109:VAL:HG11	26:24:14:ILE:HG21	1.93	0.51
10:2O:88:ASN:HD21	10:2O:90:GLN:HB2	1.74	0.51
37:2f:68:PRO:HB2	37:2f:71:ARG:HG3	1.93	0.51
44:2m:19:LEU:HD11	44:2m:56:LEU:HD21	1.93	0.51
1:1A:2544:G:H1'	1:1A:2646:C:H4'	1.92	0.51
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.46	0.51
33:1b:73:THR:OG1	33:1b:170:GLU:OE1	2.29	0.51
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.11	0.51
35:1d:178:VAL:O	35:1d:180:GLY:N	2.44	0.51
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.46	0.51
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.11	0.51
1:2A:397:G:N7	63:2A:4038:HOH:O	2.34	0.51
1:2A:1614:A:P	1:2A:1614:A:H8	2.33	0.51
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.46	0.51
7:2H:98:LEU:HA	7:2H:103:LEU:HA	1.92	0.51
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.93	0.51
21:2Z:126:VAL:HB	21:2Z:161:VAL:HG23	1.93	0.51
32:2a:54:C:N4	32:2a:353:A:OP2	2.41	0.51
32:2a:533:A:OP1	63:2a:3309:HOH:O	2.19	0.51
32:2a:918:A:H2'	32:2a:919:A:C8	2.46	0.51
32:2a:1273:G:H5'	32:2a:1274:G:OP2	2.10	0.51
33:2b:54:THR:HA	33:2b:199:TYR:CD1	2.46	0.51
38:2g:42:ILE:HG22	38:2g:120:ILE:HD12	1.93	0.51
49:2r:36:ASN:O	49:2r:40:LEU:HG	2.10	0.51
1:1A:1028:A:H61	1:1A:1125:G:H2'	1.75	0.51
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.24	0.51
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.46	0.51
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:101:ARG:NH2	7:1H:121:ILE:O	2.34	0.51
32:1a:130:A:O2'	32:1a:131:C:O5'	2.25	0.51
32:1a:185:A:H2'	32:1a:186:C:C6	2.45	0.51
32:1a:1133:G:H1	32:1a:1141:C:H42	1.59	0.51
57:1y:25:C:H2'	57:1y:26:A:O4'	2.11	0.51
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.11	0.51
5:2F:104:LYS:HA	5:2F:107:LYS:HD2	1.91	0.51
13:2R:78:LYS:HE2	13:2R:83:ILE:HD11	1.93	0.51
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.91	0.51
25:23:6:VAL:HG13	25:23:54:VAL:HG13	1.93	0.51
32:2a:404:U:H2'	32:2a:405:U:H6	1.76	0.51
32:2a:714:G:H2'	32:2a:715:A:C8	2.45	0.51
32:2a:976:G:N7	32:2a:1359:C:H1'	2.26	0.51
32:2a:983:A:N1	32:2a:1222:G:N2	2.55	0.51
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.11	0.51
34:2c:119:ARG:HE	34:2c:140:ARG:CZ	2.23	0.51
34:2c:179:ARG:O	34:2c:206:GLU:HA	2.11	0.51
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	1.93	0.51
1:1A:192:C:O2'	1:1A:802:A:N3	2.40	0.51
1:1A:1062:G:H22	1:1A:1077:A:N6	2.09	0.51
1:1A:1073:A:OP2	1:1A:1096:A:H5'	2.11	0.51
1:1A:2079:U:O3'	23:11:35:THR:OG1	2.27	0.51
11:1P:50:ARG:HH21	30:18:7:HIS:CD2	2.24	0.51
32:1a:841:U:C4	32:1a:848:C:H1'	2.46	0.51
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.11	0.51
46:1o:70:LEU:HD23	46:1o:78:TYR:HA	1.93	0.51
1:2A:867:C:H2'	1:2A:868:U:H6	1.76	0.51
1:2A:1223:G:O6	17:2V:69:LYS:NZ	2.44	0.51
1:2A:2538:C:H2'	1:2A:2539:C:C6	2.46	0.51
11:2P:96:THR:O	11:2P:99:LEU:HB3	2.11	0.51
21:2Z:8:TYR:HB2	21:2Z:38:TYR:CE2	2.45	0.51
53:2v:19:A:H2'	53:2v:20:A:H8	1.76	0.51
54:2w:30:G:H1	54:2w:40:C:H42	1.59	0.51
1:1A:590:A:P	5:1F:95:ARG:HH21	2.33	0.50
1:1A:1038:C:H42	1:1A:1117:G:H1	1.60	0.50
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.75	0.50
38:1g:78:ARG:HH21	38:1g:79:ARG:NH1	2.09	0.50
1:2A:247:G:H4'	1:2A:386:G:C5	2.46	0.50
1:2A:925:C:H2'	1:2A:926:A:C8	2.43	0.50
1:2A:1671:U:OP2	63:2A:3956:HOH:O	2.19	0.50
2:2B:32:C:H2'	2:2B:33:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:64:ILE:HD12	5:2F:65:TRP:H	1.76	0.50
15:2T:102:ILE:HA	15:2T:105:LEU:HG	1.93	0.50
32:2a:1060:C:C5	34:2c:2:GLY:HA3	2.46	0.50
32:2a:1469:G:H2'	32:2a:1470:G:C8	2.46	0.50
38:2g:27:ILE:HA	38:2g:30:ILE:HB	1.92	0.50
40:2i:22:GLY:HA3	40:2i:60:ASP:OD2	2.11	0.50
1:1A:1986:A:OP1	63:1A:4164:HOH:O	2.19	0.50
1:1A:2032:G:OP2	1:1A:2454:G:O2'	2.23	0.50
6:1G:53:LEU:O	6:1G:57:ALA:N	2.40	0.50
15:1T:16:ARG:NH1	15:1T:83:ILE:O	2.33	0.50
32:1a:36:C:H1'	43:1l:118:SER:HB3	1.93	0.50
32:1a:373:A:H61	32:1a:391:G:H1'	1.76	0.50
46:1o:87:ILE:O	46:1o:88:ARG:HB3	2.12	0.50
1:2A:208:C:H2'	1:2A:209:C:C6	2.46	0.50
1:2A:774:A:H2'	1:2A:774:A:N3	2.26	0.50
1:2A:1203:G:OP2	1:2A:1204:A:O2'	2.25	0.50
1:2A:1633:G:OP2	63:2A:3957:HOH:O	2.19	0.50
1:2A:2104:G:H1	1:2A:2185:C:N4	2.09	0.50
1:2A:2110:G:C2	1:2A:2120:G:H1'	2.46	0.50
5:2F:165:ARG:HG2	5:2F:168:ARG:NH2	2.26	0.50
14:2S:64:GLU:O	14:2S:68:GLN:HG2	2.11	0.50
21:2Z:54:HIS:HB3	21:2Z:101:PRO:HD3	1.93	0.50
32:2a:296:U:O2'	32:2a:556:C:O2	2.28	0.50
32:2a:901:A:O2'	32:2a:1513:A:OP1	2.22	0.50
32:2a:1239:A:H4'	32:2a:1240:U:H5"	1.93	0.50
50:2s:32:LYS:HD2	50:2s:34:TRP:CZ3	2.46	0.50
1:1A:249:C:O2	30:18:12:LYS:NZ	2.30	0.50
1:1A:2028:U:H2'	1:1A:2029:G:O4'	2.10	0.50
1:1A:2277:G:OP2	22:10:10:THR:HG21	2.11	0.50
4:1E:32:PRO:HA	4:1E:90:THR:HA	1.93	0.50
6:1G:61:ALA:O	6:1G:65:GLY:N	2.39	0.50
21:1Z:5:LEU:HG	21:1Z:6:LYS:O	2.10	0.50
25:13:22:ALA:HB2	25:13:49:LYS:HD3	1.92	0.50
48:1q:64:PRO:HB3	48:1q:70:ARG:NH1	2.21	0.50
1:2A:627:A:N7	11:2P:84:ASN:ND2	2.58	0.50
1:2A:793:A:OP2	1:2A:2071:A:O2'	2.27	0.50
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.74	0.50
17:2V:5:VAL:HG13	17:2V:14:VAL:HG21	1.92	0.50
32:2a:17:U:H2'	32:2a:18:C:C6	2.46	0.50
32:2a:393:A:OP1	63:2a:3312:HOH:O	2.19	0.50
1:1A:2461:C:H2'	1:1A:2462:U:H6	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:163:C:H2'	32:1a:164:U:C6	2.47	0.50
32:1a:300:A:H1'	32:1a:565:U:O2	2.10	0.50
33:1b:12:GLU:C	33:1b:14:GLY:H	2.19	0.50
45:1n:24:CYS:HB2	45:1n:40:CYS:HB3	1.93	0.50
57:1y:69:A:H5'	57:1y:70:C:OP2	2.11	0.50
1:2A:285:C:H42	1:2A:356:G:H1	1.57	0.50
1:2A:531:C:H4'	1:2A:532:A:H5"	1.93	0.50
1:2A:652(A):A:H3'	1:2A:652(B):A:H5"	1.93	0.50
1:2A:903:C:H2'	1:2A:904:C:C6	2.47	0.50
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.76	0.50
4:2E:27:LEU:HD22	15:2T:1:MET:SD	2.51	0.50
32:2a:1411:C:H2'	32:2a:1412:C:H6	1.75	0.50
32:2a:1428:A:H5'	63:2a:3332:HOH:O	2.11	0.50
33:2b:21:ARG:HA	33:2b:39:ILE:HA	1.94	0.50
1:1A:652(C):G:N2	1:1A:653:A:H1'	2.26	0.50
1:1A:1609:A:N1	63:1A:4289:HOH:O	2.35	0.50
1:1A:2133:G:N1	1:1A:2157:G:H1'	2.27	0.50
12:1Q:20:ALA:HB2	21:1Z:79:ARG:HG3	1.93	0.50
15:1T:1:MET:HE2	15:1T:3:ARG:HG3	1.92	0.50
32:1a:181:G:H4'	32:1a:182:U:H5'	1.92	0.50
32:1a:222:U:H2'	32:1a:223:U:H6	1.76	0.50
32:1a:903:G:OP1	63:1a:1915:HOH:O	2.19	0.50
57:1y:51:A:H61	57:1y:63:U:H3	1.60	0.50
57:1y:57:G:H2'	57:1y:58:A:H5'	1.93	0.50
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	1.93	0.50
12:2Q:54:MET:HE1	12:2Q:104:PHE:HB3	1.94	0.50
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.12	0.50
24:22:3:LEU:O	24:22:7:ARG:HG3	2.12	0.50
32:2a:668:G:H21	46:2o:46:HIS:HE1	1.60	0.50
32:2a:749:C:H2'	32:2a:750:G:H8	1.75	0.50
34:2c:47:LEU:HB3	34:2c:52:LEU:HB2	1.94	0.50
43:2l:8:ASN:O	43:2l:12:ARG:HG3	2.11	0.50
1:1A:583:G:OP2	16:1U:10:ARG:NH1	2.43	0.50
5:1F:61:GLY:O	63:1F:402:HOH:O	2.19	0.50
32:1a:129(A):G:H4'	32:1a:130:A:H5"	1.92	0.50
32:1a:890:G:O2'	32:1a:906:G:O6	2.27	0.50
33:1b:115:LEU:HB2	33:1b:145:LEU:HD13	1.94	0.50
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.42	0.50
35:1d:190:ASP:H	35:1d:193:ASP:HB2	1.76	0.50
55:1x:15:G:H2'	55:1x:59:A:N1	2.27	0.50
1:2A:658:C:H2'	1:2A:659:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:746:A:H2'	1:2A:2612:C:H5"	1.94	0.50
1:2A:2150:U:H2'	1:2A:2151:G:H8	1.76	0.50
1:2A:2314:C:H5'	6:2G:38:VAL:HG21	1.94	0.50
5:2F:112:MET:HA	5:2F:115:ALA:HB3	1.93	0.50
15:2T:24:PRO:HA	15:2T:49:VAL:HG12	1.92	0.50
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.93	0.50
32:2a:708:C:H2'	32:2a:709:G:C8	2.37	0.50
33:2b:47:THR:HG23	33:2b:202:PRO:HD2	1.92	0.50
55:2x:10:G:N2	55:2x:26:G:H1'	2.26	0.50
1:1A:984:A:H5"	1:1A:985:C:H5	1.77	0.50
4:1E:52:LEU:O	4:1E:76:ARG:N	2.45	0.50
12:1Q:137:TYR:OH	21:1Z:45:ASP:OD1	2.28	0.50
26:14:15:ILE:HD12	26:14:32:TYR:HE1	1.77	0.50
32:1a:1366:C:H2'	32:1a:1367:C:C6	2.46	0.50
33:1b:71:VAL:HB	33:1b:164:VAL:HA	1.93	0.50
41:1j:19:SER:OG	41:1j:91:PRO:HD2	2.12	0.50
43:1l:48:PRO:HB3	53:1v:21:A:H4'	1.93	0.50
55:1x:75:C:H2'	55:1x:76:8AN:H1'	1.92	0.50
1:2A:2125:G:H1'	1:2A:2173:A:H61	1.75	0.50
2:2B:42:C:C4	2:2B:43:C:C4	3.00	0.50
6:2G:117:PHE:CE2	6:2G:119:GLY:HA2	2.46	0.50
32:2a:277:C:H5"	48:2q:68:ARG:NH2	2.27	0.50
32:2a:1048:G:N2	32:2a:1214:C:O2	2.42	0.50
41:2j:8:LEU:HG	41:2j:70:ARG:HB2	1.94	0.50
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.76	0.50
47:2p:53:VAL:HG22	47:2p:79:VAL:HG22	1.94	0.50
54:2w:50:C:H2'	54:2w:51:A:H5"	1.94	0.50
1:1A:64:A:O3'	19:1X:71:GLY:HA3	2.12	0.50
1:1A:581:C:H2'	1:1A:582:G:C8	2.47	0.50
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.46	0.50
2:1B:28:C:OP1	14:1S:36:TYR:OH	2.22	0.50
5:1F:123:LEU:HD13	5:1F:192:LEU:HD23	1.94	0.50
8:1I:2:LYS:HB2	8:1I:2:LYS:HZ2	1.76	0.50
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	1.93	0.50
32:1a:1414:U:H2'	32:1a:1415:G:H8	1.77	0.50
39:1h:29:SER:O	39:1h:33:GLU:HG3	2.12	0.50
49:1r:74:ARG:HD3	49:1r:81:PHE:CD1	2.47	0.50
1:2A:971:C:H2'	1:2A:972:G:O4'	2.12	0.50
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.11	0.50
1:2A:2832:U:OP2	63:2A:3950:HOH:O	2.18	0.50
3:2D:11:PRO:O	3:2D:14:ARG:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:2:LYS:HG2	11:2P:3:LEU:H	1.75	0.50
32:2a:105:G:O6	63:2a:3311:HOH:O	2.19	0.50
32:2a:298:A:N6	63:2a:3331:HOH:O	2.45	0.50
32:2a:501:C:H2'	32:2a:502:G:C8	2.45	0.50
34:2c:187:ALA:HB3	34:2c:198:VAL:HB	1.94	0.50
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.93	0.50
1:1A:2053:G:OP1	4:1E:144:ARG:HG3	2.12	0.50
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.94	0.50
14:1S:15:ARG:HE	14:1S:88:ASP:CG	2.19	0.50
20:1Y:43:ASN:HB3	20:1Y:65:ALA:HB3	1.94	0.50
32:1a:152:A:H61	32:1a:170:U:H1'	1.77	0.50
32:1a:429:U:O2'	35:1d:22:LYS:NZ	2.45	0.50
32:1a:718:G:O6	49:1r:74:ARG:NH1	2.45	0.50
33:1b:61:LEU:HD23	33:1b:66:GLY:HA3	1.94	0.50
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.30	0.50
39:1h:119:LEU:HB3	39:1h:123:GLU:HB3	1.92	0.50
48:1q:59:ILE:HG22	48:1q:73:VAL:HA	1.94	0.50
51:1t:63:ILE:HG21	51:1t:81:LYS:HG2	1.94	0.50
1:2A:212:G:H2'	1:2A:213:A:O4'	2.12	0.50
1:2A:924:C:H2'	1:2A:925:C:C6	2.47	0.50
1:2A:1970:A:OP1	63:2A:3959:HOH:O	2.20	0.50
11:2P:85:LEU:HA	11:2P:88:LEU:HD12	1.94	0.50
32:2a:5:U:H3	35:2d:87:GLY:H	1.59	0.50
32:2a:360:A:H2'	32:2a:361:G:C8	2.47	0.50
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.43	0.50
32:2a:1154:G:H2'	32:2a:1155:G:H8	1.76	0.50
35:2d:4:TYR:OH	35:2d:7:PRO:O	2.28	0.50
1:1A:570:G:H2'	1:1A:2030:A:N7	2.27	0.49
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.47	0.49
5:1F:155:LEU:HB3	5:1F:192:LEU:HD12	1.94	0.49
6:1G:17:PRO:HA	6:1G:20:ILE:HD12	1.93	0.49
32:1a:1517:G:H3'	32:1a:1518:MA6:H8	1.94	0.49
55:1x:68:C:H2'	55:1x:69:C:C6	2.47	0.49
57:1y:56:C:H2'	57:1y:57:G:O4'	2.12	0.49
1:2A:96:G:H4'	24:22:48:HIS:NE2	2.27	0.49
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.46	0.49
1:2A:265:A:H1'	1:2A:266:G:O4'	2.12	0.49
1:2A:879:G:H3'	1:2A:880:G:H8	1.77	0.49
5:2F:196:LEU:O	5:2F:200:GLU:N	2.40	0.49
6:2G:116:ASP:CG	44:2m:68:GLY:HA3	2.37	0.49
21:2Z:79:ARG:HD2	21:2Z:80:ARG:NH2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.47	0.49
32:2a:593:G:H1	32:2a:646:U:H3	1.59	0.49
32:2a:643:C:H2'	32:2a:644:G:H8	1.76	0.49
33:2b:213:LEU:HD23	33:2b:214:ILE:HD12	1.93	0.49
34:2c:111:LEU:HD22	34:2c:146:ALA:HB2	1.93	0.49
38:2g:12:LEU:H	38:2g:12:LEU:HD12	1.77	0.49
1:1A:1468:C:OP1	63:1A:4165:HOH:O	2.20	0.49
1:1A:2393:A:H5"	11:1P:63:PRO:HB3	1.95	0.49
12:1Q:85:LYS:HD3	22:10:7:LEU:HD22	1.93	0.49
15:1T:106:SER:O	15:1T:110:ILE:HG13	2.12	0.49
32:1a:1445:C:H42	32:1a:1457:G:H1	1.59	0.49
34:1c:71:ALA:HA	34:1c:106:VAL:HG21	1.94	0.49
35:1d:165:MET:SD	35:1d:168:ARG:HD2	2.52	0.49
43:1l:35:GLY:HA3	43:1l:58:VAL:HG12	1.92	0.49
51:1t:33:ILE:O	51:1t:37:SER:OG	2.16	0.49
1:2A:2136:C:N3	1:2A:2155:G:N2	2.55	0.49
6:2G:38:VAL:HA	6:2G:93:THR:HA	1.94	0.49
32:2a:840:C:H4'	32:2a:841:U:OP1	2.12	0.49
32:2a:986:A:N3	50:2s:52:TYR:OH	2.43	0.49
32:2a:1079:G:OP2	32:2a:1079:G:H8	1.95	0.49
38:2g:44:TYR:HA	38:2g:47:CYS:HB2	1.94	0.49
41:2j:40:LEU:HB2	41:2j:69:ASN:HB2	1.93	0.49
50:2s:18:LYS:HD3	50:2s:31:ILE:HG21	1.94	0.49
1:1A:218:A:H2	1:1A:235:U:H4'	1.77	0.49
1:1A:620:G:N3	1:1A:620:G:H5'	2.26	0.49
1:1A:2067:G:N7	63:1A:4290:HOH:O	2.35	0.49
6:1G:126:ASP:OD2	6:1G:130:ASN:ND2	2.35	0.49
32:1a:524:G:H2'	32:1a:525:C:C6	2.47	0.49
32:1a:996:A:H2'	32:1a:997:U:C6	2.47	0.49
1:2A:97:C:OP1	24:22:2:LYS:NZ	2.44	0.49
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.76	0.49
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.11	0.49
6:2G:165:THR:HG22	6:2G:168:GLU:HG3	1.93	0.49
14:2S:80:LEU:O	14:2S:82:ILE:N	2.45	0.49
19:2X:5:TYR:CE2	24:22:30:ARG:HB3	2.47	0.49
26:24:46:GLN:O	26:24:48:ARG:N	2.43	0.49
32:2a:500:G:H2'	32:2a:501:C:C6	2.46	0.49
32:2a:715:A:H2'	32:2a:716:A:C8	2.46	0.49
32:2a:868:C:H2'	32:2a:869:G:O4'	2.12	0.49
32:2a:1371:G:O3'	40:2i:69:GLY:HA3	2.12	0.49
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:91:LEU:O	34:2c:95:THR:N	2.44	0.49
51:2t:56:MET:O	51:2t:60:GLU:N	2.38	0.49
57:2y:60:U:H3'	57:2y:61:C:C6	2.47	0.49
1:1A:652(C):G:H1	1:1A:652(V):C:H42	1.60	0.49
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.48	0.49
32:1a:772:U:C2	32:1a:773:G:C8	3.00	0.49
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.48	0.49
40:1i:53:VAL:O	40:1i:55:ALA:N	2.45	0.49
54:1w:25:C:H2'	54:1w:26:A:O4'	2.12	0.49
1:2A:529:A:H62	1:2A:2041:U:H3	1.60	0.49
1:2A:1011:G:OP1	16:2U:77:SER:OG	2.29	0.49
1:2A:1865:G:N2	1:2A:1877:A:OP2	2.45	0.49
1:2A:2320:A:H1'	1:2A:2321:G:N1	2.28	0.49
4:2E:119:ARG:HG2	4:2E:120:TRP:CD1	2.47	0.49
5:2F:153:SER:HB2	5:2F:190:GLU:H	1.77	0.49
11:2P:136:GLU:HG3	11:2P:137:LYS:H	1.76	0.49
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.12	0.49
34:2c:18:TRP:HH2	45:2n:57:ARG:HG3	1.78	0.49
35:2d:116:GLN:CD	35:2d:157:LEU:HD21	2.37	0.49
40:2i:3:GLN:HA	40:2i:20:ARG:HG3	1.93	0.49
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.94	0.49
32:1a:580:U:H2'	32:1a:581:G:O4'	2.12	0.49
34:1c:95:THR:C	34:1c:97:LYS:H	2.20	0.49
1:2A:731:C:OP2	63:2A:3951:HOH:O	2.19	0.49
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.43	0.49
1:2A:1364:G:P	23:21:3:LYS:HG3	2.52	0.49
1:2A:2127:G:H1	1:2A:2161:C:N4	2.11	0.49
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.13	0.49
9:2N:103:VAL:O	9:2N:107:LEU:HG	2.12	0.49
32:2a:194:C:H2'	32:2a:195:A:H5"	1.95	0.49
32:2a:1466:C:H2'	32:2a:1467:G:O4'	2.12	0.49
36:2e:20:GLN:OE1	36:2e:25:ARG:NH1	2.45	0.49
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.13	0.49
42:2k:62:GLN:HB2	42:2k:93:GLN:HG3	1.94	0.49
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.93	0.49
1:1A:218:A:C2	1:1A:235:U:H4'	2.48	0.49
1:1A:740:U:OP2	63:1A:4163:HOH:O	2.19	0.49
1:1A:858:U:O2	1:1A:2268:A:H2'	2.13	0.49
1:1A:989:G:H4'	1:1A:990:A:OP1	2.11	0.49
1:1A:1946:U:H2'	1:1A:1947:C:C6	2.48	0.49
4:1E:29:GLY:HA3	63:1E:402:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:98:LEU:HG	7:1H:125:VAL:HG23	1.93	0.49
20:1Y:8:LYS:HD3	20:1Y:97:ARG:NH1	2.27	0.49
33:1b:185:ILE:HB	33:1b:199:TYR:HB2	1.94	0.49
57:1y:26:A:H61	57:1y:44:U:H3	1.59	0.49
5:2F:132:VAL:HG11	5:2F:163:VAL:HA	1.93	0.49
7:2H:26:VAL:HG12	7:2H:79:VAL:HG21	1.95	0.49
8:2I:26:ALA:HA	8:2I:30:LEU:HB2	1.94	0.49
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	1.94	0.49
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.11	0.49
32:2a:256:U:H2'	32:2a:257:G:C8	2.48	0.49
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.44	0.49
46:2o:24:SER:O	46:2o:28:GLN:HG3	2.12	0.49
57:2y:10:G:O6	57:2y:45:G:N1	2.46	0.49
1:1A:428:A:H8	1:1A:428:A:OP2	1.96	0.49
1:1A:657:U:H2'	1:1A:658:C:C6	2.48	0.49
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.48	0.49
32:1a:1366:C:O2'	41:1j:60:ARG:NH2	2.42	0.49
34:1c:132:ARG:O	34:1c:136:GLN:HG3	2.12	0.49
38:1g:76:ARG:HD3	38:1g:156:TRP:CZ2	2.47	0.49
41:1j:78:ASN:C	41:1j:80:LYS:H	2.20	0.49
45:1n:29:ARG:HD2	45:1n:42:ILE:HD11	1.95	0.49
57:1y:72:C:H2'	57:1y:73:A:O4'	2.13	0.49
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.13	0.49
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.48	0.49
1:2A:1192:G:H2'	1:2A:1193:G:H8	1.78	0.49
1:2A:1890:A:OP2	63:2A:3958:HOH:O	2.19	0.49
5:2F:126:VAL:HG11	5:2F:142:TRP:CH2	2.48	0.49
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.95	0.49
12:2Q:30:GLY:HA3	12:2Q:107:ALA:HB2	1.95	0.49
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.53	0.49
20:2Y:79:CYS:SG	20:2Y:81:LYS:HG3	2.53	0.49
32:2a:43:C:H2'	32:2a:44:G:O4'	2.13	0.49
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.47	0.49
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.48	0.49
1:1A:11:G:C2'	1:1A:12:U:H5'	2.43	0.49
1:1A:38:A:H2'	1:1A:39:C:C6	2.48	0.49
1:1A:484:C:H2'	1:1A:485:C:C6	2.48	0.49
1:1A:922:U:H2'	1:1A:923:C:C6	2.48	0.49
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.31	0.49
1:1A:2133:G:H1	1:1A:2157:G:H1'	1.78	0.49
1:1A:2314:C:H2'	1:1A:2315:G:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:62:TYR:HA	3:1D:87:ASN:OD1	2.13	0.49
6:1G:121:ASN:O	6:1G:131:TYR:OH	2.30	0.49
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.38	0.49
19:1X:72:LYS:NZ	19:1X:75:ASP:OD1	2.38	0.49
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	1.94	0.49
23:11:71:TYR:O	23:11:75:GLU:HG2	2.12	0.49
32:1a:375:U:OP1	47:1p:69:THR:OG1	2.24	0.49
32:1a:1004:A:H8	32:1a:1005:A:H4'	1.77	0.49
33:1b:33:TYR:N	33:1b:41:ILE:O	2.36	0.49
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.61	0.49
1:2A:882:G:H22	1:2A:894:C:N4	2.09	0.49
1:2A:1230:C:H2'	1:2A:1231:G:C8	2.48	0.49
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.39	0.49
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.13	0.49
1:2A:2515:C:H2'	1:2A:2516:G:C8	2.48	0.49
9:2N:58:ASP:N	9:2N:58:ASP:OD1	2.46	0.49
23:21:19:GLN:HB3	23:21:35:THR:HG23	1.95	0.49
32:2a:1371:G:OP1	40:2i:12:GLU:HB3	2.13	0.49
42:2k:79:SER:HA	42:2k:104:GLN:HB3	1.95	0.49
1:1A:27:G:N2	1:1A:512:G:H1'	2.28	0.49
1:1A:2197:U:H1'	1:1A:2198:A:C8	2.48	0.49
1:1A:2667:C:H2'	1:1A:2668:G:O4'	2.13	0.49
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.95	0.49
10:1O:120:GLU:OE1	15:1T:67:SER:OG	2.26	0.49
15:1T:92:GLY:O	15:1T:120:ARG:NH2	2.46	0.49
23:11:5:CYS:HA	23:11:46:LEU:HD11	1.95	0.49
32:1a:437:U:H5"	35:1d:155:LEU:HD11	1.95	0.49
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.48	0.49
38:1g:153:HIS:HE1	42:1k:57:THR:HG22	1.78	0.49
39:1h:14:ARG:NH2	39:1h:83:ILE:O	2.30	0.49
42:1k:78:GLN:O	42:1k:104:GLN:N	2.39	0.49
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.95	0.49
1:2A:537:C:H2'	1:2A:538:G:C8	2.48	0.49
1:2A:859:G:H5'	1:2A:2268:A:O2'	2.12	0.49
1:2A:2031:A:N3	1:2A:2455:G:O2'	2.38	0.49
1:2A:2108:C:H2'	1:2A:2109:U:H6	1.77	0.49
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.36	0.49
4:2E:54:GLN:HB2	4:2E:76:ARG:HG2	1.95	0.49
4:2E:55:ASN:HD22	4:2E:58:ARG:HG3	1.78	0.49
4:2E:55:ASN:HB3	4:2E:58:ARG:HG3	1.94	0.49
20:2Y:52:SER:OG	20:2Y:55:TYR:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:20:U:H2'	32:2a:21:G:O4'	2.13	0.49
32:2a:235:C:H2'	32:2a:236:G:C8	2.48	0.49
32:2a:997:U:H3	32:2a:1044:A:H61	1.60	0.49
46:2o:87:ILE:HG22	46:2o:88:ARG:N	2.28	0.49
1:1A:1051:G:H2'	1:1A:1052:C:O4'	2.13	0.49
1:1A:2250:G:OP1	12:1Q:85:LYS:NZ	2.31	0.49
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.48	0.49
12:1Q:89:ASN:HB2	55:1x:1:C:N3	2.28	0.49
39:1h:83:ILE:HG13	39:1h:137:VAL:HG22	1.94	0.49
54:1w:19:G:N2	54:1w:56:C:N3	2.60	0.49
1:2A:185:U:H2'	1:2A:186:G:C8	2.48	0.49
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.46	0.49
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.13	0.49
1:2A:2280:G:O2'	1:2A:2388:A:N1	2.40	0.49
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.37	0.49
5:2F:80:ALA:HB3	5:2F:83:PHE:HD2	1.76	0.49
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.44	0.49
32:2a:359:U:H2'	32:2a:360:A:H8	1.77	0.49
32:2a:372:C:O2'	63:2a:3313:HOH:O	2.20	0.49
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.95	0.49
32:2a:920:U:H2'	32:2a:921:U:C6	2.48	0.49
32:2a:993:G:H1	32:2a:1045:C:N4	2.10	0.49
32:2a:1095:U:H2'	32:2a:1096:C:O4'	2.12	0.49
33:2b:118:LEU:HB3	33:2b:142:LEU:HD12	1.95	0.49
40:2i:50:LEU:O	40:2i:54:ASP:N	2.46	0.49
51:2t:90:GLN:HA	51:2t:93:GLU:HG3	1.95	0.49
1:1A:1417:C:H2'	1:1A:1418:G:O4'	2.12	0.48
1:1A:1509(A):A:H3'	1:1A:1509(B):A:H8	1.78	0.48
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.13	0.48
4:1E:9:VAL:HG13	15:1T:3:ARG:HG2	1.94	0.48
10:1O:68:GLU:OE1	10:1O:78:ARG:NH1	2.46	0.48
23:11:50:ARG:HE	23:11:50:ARG:HB2	1.32	0.48
32:1a:235:C:H2'	32:1a:236:G:H8	1.76	0.48
32:1a:1266:G:N2	32:1a:1269:A:OP2	2.40	0.48
33:1b:28:PHE:HD2	33:1b:32:ILE:HG13	1.77	0.48
1:2A:1003:G:O2'	1:2A:1010:A:N1	2.39	0.48
1:2A:1153:C:H5'	16:2U:76:TYR:HE2	1.77	0.48
1:2A:1388:G:H2'	1:2A:1389:G:C8	2.48	0.48
1:2A:1388:G:H4'	1:2A:1525:G:O2'	2.13	0.48
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.13	0.48
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2319:G:N2	14:2S:3:ARG:HE	2.11	0.48
12:2Q:31:ASP:O	12:2Q:134:ARG:N	2.46	0.48
21:2Z:97:GLU:HB3	21:2Z:125:LEU:HD11	1.95	0.48
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.27	0.48
32:2a:1289:A:P	52:2u:9:ARG:HH22	2.36	0.48
33:2b:185:ILE:HG22	33:2b:199:TYR:CB	2.42	0.48
38:2g:115:ARG:O	38:2g:119:ARG:HG3	2.13	0.48
43:2l:79:GLU:HG2	43:2l:80:HIS:CE1	2.48	0.48
1:1A:247:G:H4'	1:1A:386:G:C5	2.47	0.48
1:1A:271(R):G:H4'	23:11:80:LEU:HD11	1.95	0.48
1:1A:1580:A:OP2	1:1A:1580:A:H8	1.96	0.48
1:1A:1769:G:O2'	1:1A:1958:C:OP1	2.22	0.48
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.14	0.48
6:1G:21:ARG:HG2	6:1G:21:ARG:HH11	1.78	0.48
12:1Q:78:PRO:HD3	55:1x:1:C:C2	2.48	0.48
32:1a:444:C:H2'	32:1a:445:G:C8	2.48	0.48
32:1a:1198:G:O6	63:1a:1913:HOH:O	2.17	0.48
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.13	0.48
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.48	0.48
40:1i:28:VAL:HG21	40:1i:37:PHE:CE2	2.48	0.48
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.14	0.48
1:2A:752:A:OP1	29:27:3:ARG:NH2	2.42	0.48
1:2A:1721:G:H8	1:2A:1741:A:H62	1.60	0.48
12:2Q:53:ALA:HB1	12:2Q:120:ILE:HG22	1.96	0.48
19:2X:72:LYS:NZ	19:2X:75:ASP:OD1	2.38	0.48
23:21:32:LYS:O	63:21:201:HOH:O	2.20	0.48
32:2a:1029:C:N4	32:2a:1032:G:H1	2.11	0.48
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.48	0.48
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.13	0.48
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.46	0.48
55:2x:59:A:H2'	55:2x:60:U:H5'	1.95	0.48
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.48	0.48
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.37	0.48
2:1B:7:G:H5'	14:1S:29:PHE:CE2	2.48	0.48
10:1O:75:SER:OG	15:1T:74:ARG:NH1	2.47	0.48
12:1Q:43:THR:HG22	12:1Q:94:VAL:HG12	1.95	0.48
25:13:6:VAL:HG12	25:13:28:LEU:HD11	1.94	0.48
28:16:6:ARG:NH1	28:16:24:GLU:OE2	2.40	0.48
32:1a:176:C:H2'	32:1a:177:C:C6	2.48	0.48
32:1a:341:C:H2'	32:1a:342:C:C6	2.48	0.48
39:1h:94:TYR:HE1	39:1h:132:GLU:HB2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:92:HIS:HA	44:1m:110:ARG:NH2	2.28	0.48
44:1m:107:ALA:HB3	44:1m:111:LYS:HD3	1.94	0.48
1:2A:1186:G:H2'	1:2A:1187:G:O4'	2.13	0.48
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.48	0.48
21:2Z:79:ARG:HB2	21:2Z:80:ARG:NH1	2.29	0.48
24:22:13:ALA:HA	24:22:16:LEU:HG	1.95	0.48
32:2a:1162:C:N4	32:2a:1174:G:H1	2.08	0.48
33:2b:178:ARG:NH1	33:2b:196:LEU:O	2.47	0.48
40:2i:37:PHE:HE1	40:2i:70:LYS:HB3	1.77	0.48
1:1A:383:U:H2'	1:1A:385:C:H5	1.79	0.48
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.14	0.48
11:1P:106:LEU:HD22	11:1P:112:LEU:HD13	1.95	0.48
1:2A:250:G:H2'	1:2A:251:A:C8	2.48	0.48
1:2A:956:G:H2'	1:2A:957:A:H2'	1.96	0.48
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.49	0.48
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.13	0.48
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.95	0.48
3:2D:211:ARG:O	3:2D:215:LEU:HG	2.12	0.48
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.96	0.48
5:2F:139:PHE:CG	5:2F:167:ALA:HB2	2.48	0.48
18:2W:43:GLY:O	18:2W:47:VAL:HG23	2.13	0.48
32:2a:224:C:H2'	32:2a:225:C:C6	2.47	0.48
34:2c:121:ALA:HB1	34:2c:188:LEU:O	2.12	0.48
50:2s:12:ASP:O	50:2s:14:HIS:N	2.41	0.48
1:1A:1828:G:H8	1:1A:1828:G:OP2	1.96	0.48
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.79	0.48
8:1I:1:MET:HE1	8:1I:27:ARG:HH22	1.79	0.48
25:13:16:PRO:HB2	25:13:18:ASP:OD1	2.13	0.48
32:1a:189(B):C:H2'	32:1a:189(C):C:C6	2.48	0.48
57:1y:29:U:H2'	57:1y:30:G:C8	2.47	0.48
1:2A:515:A:H1'	1:2A:581:C:H1'	1.96	0.48
1:2A:957:A:OP1	12:2Q:76:LYS:HG3	2.13	0.48
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.48	0.48
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.29	0.48
1:2A:1363:C:O2'	1:2A:1809:A:N3	2.40	0.48
8:2I:87:LYS:HA	8:2I:122:GLU:HA	1.95	0.48
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.48	0.48
9:2N:53:VAL:HG22	9:2N:121:LYS:HB2	1.96	0.48
21:2Z:121:HIS:N	21:2Z:171:ILE:O	2.46	0.48
30:28:28:GLY:O	30:28:36:LYS:NZ	2.45	0.48
32:2a:22:G:H4'	32:2a:885:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:131:C:O2'	32:2a:262:A:N3	2.38	0.48
32:2a:390:C:H2'	32:2a:391:G:C8	2.48	0.48
32:2a:523:A:H61	43:2l:92:0TD:CG	2.26	0.48
32:2a:973:G:H3'	32:2a:974:A:H5"	1.96	0.48
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.29	0.48
51:2t:16:HIS:O	51:2t:19:SER:OG	2.24	0.48
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.25	0.48
1:1A:1779:U:H2'	63:1A:4269:HOH:O	2.14	0.48
1:1A:2469:A:O2'	12:1Q:56:ARG:NH1	2.46	0.48
5:1F:51:THR:O	5:1F:93:LYS:NZ	2.45	0.48
8:1I:9:LEU:HB3	8:1I:12:LEU:HB3	1.95	0.48
15:1T:127:ALA:C	15:1T:129:ARG:H	2.20	0.48
21:1Z:121:HIS:HB2	21:1Z:171:ILE:HG22	1.95	0.48
32:1a:56:U:H2'	32:1a:57:G:C8	2.48	0.48
32:1a:757:U:O2'	32:1a:879:C:O2	2.30	0.48
32:1a:865:A:C2	32:1a:918:A:H4'	2.49	0.48
1:2A:27:G:N2	1:2A:512:G:H1'	2.28	0.48
1:2A:41:C:H2'	1:2A:42:G:C8	2.48	0.48
1:2A:171:G:H2'	1:2A:172:C:C6	2.49	0.48
1:2A:700:G:H2'	1:2A:701:G:O4'	2.14	0.48
1:2A:879:G:H3'	1:2A:880:G:C8	2.49	0.48
1:2A:894:C:O2'	1:2A:895:U:H5"	2.14	0.48
1:2A:2295:C:H41	14:2S:13:ARG:HH12	1.60	0.48
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.44	0.48
2:2B:28:C:OP1	14:2S:31:SER:OG	2.19	0.48
5:2F:107:LYS:HG2	5:2F:108:LYS:N	2.28	0.48
20:2Y:13:VAL:HB	20:2Y:72:VAL:HG13	1.95	0.48
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.47	0.48
32:2a:221:C:H2'	32:2a:222:U:H6	1.78	0.48
32:2a:501:C:H1'	32:2a:549:C:H1'	1.94	0.48
32:2a:1226:C:O2'	44:2m:111:LYS:NZ	2.43	0.48
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.31	0.48
39:2h:20:TYR:CE2	39:2h:75:ARG:HD2	2.45	0.48
1:1A:862:G:H2'	1:1A:863:A:O4'	2.13	0.48
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.12	0.48
29:17:19:ARG:O	29:17:23:ARG:HG3	2.13	0.48
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.95	0.48
33:1b:12:GLU:O	33:1b:15:VAL:HG22	2.13	0.48
34:1c:114:PRO:O	34:1c:118:GLN:NE2	2.47	0.48
35:1d:107:ARG:NH2	35:1d:194:LEU:HD11	2.29	0.48
38:1g:79:ARG:NH2	38:1g:80:VAL:HG22	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:312:G:H4'	1:2A:331:A:N3	2.28	0.48
1:2A:570:G:H2'	1:2A:2030:A:C5	2.48	0.48
1:2A:815:C:H2'	1:2A:816:C:H6	1.78	0.48
1:2A:1169:G:N2	1:2A:1170:G:O6	2.45	0.48
1:2A:1472:A:N6	1:2A:1519:G:H1'	2.29	0.48
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.78	0.48
5:2F:64:ILE:HD12	5:2F:65:TRP:N	2.28	0.48
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.13	0.48
12:2Q:89:ASN:HB2	55:2x:1:C:N3	2.28	0.48
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.14	0.48
32:2a:447:G:O6	32:2a:485:G:O2'	2.30	0.48
32:2a:662:G:H2'	32:2a:663:A:C8	2.48	0.48
32:2a:1181:G:H4'	32:2a:1182:G:OP1	2.12	0.48
32:2a:1244:C:N4	32:2a:1293:G:H1	2.09	0.48
35:2d:175:SER:OG	35:2d:184:LYS:HB2	2.13	0.48
36:2e:65:ASN:HD21	36:2e:140:ARG:NH2	2.08	0.48
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.13	0.48
41:2j:30:SER:O	41:2j:81:THR:OG1	2.20	0.48
47:2p:39:TYR:CG	47:2p:73:LEU:HD21	2.49	0.48
54:2w:11:C:N4	54:2w:24:G:H1	2.09	0.48
1:1A:1441:G:H2'	1:1A:1442:G:H8	1.79	0.48
1:1A:2136:C:N4	1:1A:2155:G:C6	2.76	0.48
1:1A:2317:C:H2'	1:1A:2318:G:O4'	2.13	0.48
1:1A:2419:U:H2'	1:1A:2420:C:H6	1.77	0.48
1:1A:2846:G:N7	63:1A:4294:HOH:O	2.35	0.48
3:1D:60:ARG:HD3	3:1D:87:ASN:ND2	2.28	0.48
5:1F:161:GLU:O	5:1F:165:ARG:HG3	2.13	0.48
8:1I:17:GLN:HG2	8:1I:18:VAL:H	1.79	0.48
8:1I:48:GLU:O	8:1I:52:ARG:NH2	2.47	0.48
12:1Q:43:THR:OG1	12:1Q:46:GLN:HG3	2.13	0.48
32:1a:1255:G:H1	32:1a:1282:C:H42	1.62	0.48
33:1b:19:HIS:HA	33:1b:39:ILE:HG23	1.95	0.48
57:1y:53:G:H1	57:1y:61:C:H42	1.60	0.48
1:2A:752:A:P	29:27:3:ARG:HH22	2.36	0.48
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.13	0.48
1:2A:2138:C:H2'	1:2A:2139:C:O4'	2.14	0.48
3:2D:73:VAL:HG22	3:2D:120:GLY:HA2	1.96	0.48
9:2N:35:ARG:HB2	9:2N:37:LYS:HG3	1.96	0.48
21:2Z:98:MET:O	21:2Z:126:VAL:HG22	2.13	0.48
21:2Z:128:VAL:HG12	21:2Z:129:SER:H	1.79	0.48
32:2a:444:C:H2'	32:2a:445:G:H8	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:792:A:H4'	32:2a:793:U:O5'	2.14	0.48
32:2a:1343:G:O2'	40:2i:121:ARG:HD2	2.13	0.48
32:2a:1477:C:H2'	32:2a:1478:C:H6	1.78	0.48
33:2b:92:TYR:CE2	33:2b:151:GLY:HA3	2.48	0.48
48:2q:45:HIS:CD2	48:2q:47:PRO:HG3	2.48	0.48
1:1A:582:G:H2'	1:1A:583:G:C8	2.49	0.48
1:1A:907:U:O2'	12:1Q:101:ARG:NH2	2.46	0.48
1:1A:1266:G:O4'	18:1W:15:ARG:NH2	2.45	0.48
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.47	0.48
1:1A:1500:G:O2'	3:1D:100:GLY:O	2.25	0.48
1:1A:2147:G:H3'	1:1A:2147:G:N3	2.29	0.48
1:1A:2505:G:O6	1:1A:2576:G:H2'	2.14	0.48
15:1T:35:LYS:HG3	15:1T:40:THR:HG22	1.95	0.48
15:1T:55:ASN:ND2	15:1T:58:ASN:HB2	2.29	0.48
15:1T:126:ALA:O	15:1T:129:ARG:HB2	2.13	0.48
35:1d:108:LEU:HD21	35:1d:174:LEU:HB3	1.96	0.48
35:1d:173:TRP:HA	35:1d:187:ARG:HE	1.79	0.48
37:1f:30:LEU:HB3	37:1f:35:ALA:HB3	1.95	0.48
39:1h:112:LEU:HB3	39:1h:133:LEU:HA	1.96	0.48
40:1i:17:VAL:HG11	40:1i:81:ILE:N	2.29	0.48
1:2A:118:A:N3	1:2A:178:G:H1'	2.28	0.48
1:2A:1263:U:H1'	27:25:10:LYS:HG3	1.95	0.48
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.40	0.48
3:2D:206:LEU:O	3:2D:211:ARG:HD3	2.14	0.48
6:2G:108:ASN:O	6:2G:112:PRO:HG2	2.14	0.48
8:2I:72:LEU:HD12	8:2I:140:LEU:HD21	1.94	0.48
32:2a:528:C:H5'	32:2a:529:G:OP2	2.14	0.48
32:2a:737:A:H1'	37:2f:73:ASN:HD21	1.77	0.48
32:2a:913:A:H4'	32:2a:914:A:O5'	2.14	0.48
32:2a:1227:A:H3'	32:2a:1227:A:N3	2.28	0.48
43:2l:83:VAL:HG22	43:2l:100:ILE:HG23	1.95	0.48
1:1A:139(A):G:O6	63:1A:4158:HOH:O	2.19	0.48
1:1A:774:A:N7	1:1A:787:U:O2'	2.46	0.48
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.49	0.48
1:1A:971:C:O2'	1:1A:983:A:N3	2.46	0.48
1:1A:1614:A:P	1:1A:1614:A:H8	2.36	0.48
1:1A:2360:A:H2'	1:1A:2361:A:O4'	2.13	0.48
2:1B:11:C:H3'	2:1B:12:C:C6	2.49	0.48
7:1H:118:PRO:HD2	7:1H:121:ILE:HB	1.96	0.48
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.96	0.48
16:1U:34:LYS:HA	16:1U:34:LYS:HD2	1.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:1:MET:HE1	24:12:26:ARG:HH21	1.78	0.48
32:1a:272:C:H2'	32:1a:273:A:C8	2.49	0.48
32:1a:1246:C:H42	32:1a:1291:G:H1	1.60	0.48
35:1d:142:PRO:HA	35:1d:185:PHE:HD2	1.79	0.48
1:2A:2135:A:C8	1:2A:2136:C:H5	2.31	0.48
1:2A:2515:C:H2'	1:2A:2516:G:H8	1.78	0.48
1:2A:2811:G:N2	1:2A:2891:G:H1'	2.28	0.48
5:2F:130:ALA:H	5:2F:142:TRP:CD1	2.32	0.48
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.96	0.48
25:23:6:VAL:HG22	25:23:56:VAL:HG13	1.96	0.48
32:2a:11:G:H1	32:2a:23:C:N4	2.09	0.48
33:2b:90:MET:HE2	33:2b:226:ARG:HH12	1.78	0.48
34:2c:22:TRP:HZ3	34:2c:24:ALA:HB2	1.79	0.48
35:2d:158:ILE:H	35:2d:158:ILE:HG12	1.52	0.48
40:2i:31:GLN:HB3	40:2i:35:GLU:CD	2.39	0.48
44:2m:50:GLU:HA	44:2m:53:VAL:HG22	1.94	0.48
44:2m:89:GLY:O	44:2m:93:ARG:HG3	2.13	0.48
46:2o:54:ARG:O	46:2o:58:MET:HG2	2.13	0.48
1:1A:191:A:H2'	1:1A:192:C:C6	2.49	0.47
1:1A:1226:A:OP1	16:1U:16:LYS:NZ	2.43	0.47
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.29	0.47
1:1A:2134:A:N7	1:1A:2156:G:O2'	2.46	0.47
1:1A:2167:U:C2'	1:1A:2168:G:H4'	2.44	0.47
2:1B:78:A:H2'	2:1B:79:C:O4'	2.14	0.47
37:1f:18:GLN:HA	37:1f:21:LEU:HG	1.96	0.47
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.94	0.47
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	1.96	0.47
41:1j:50:ILE:HD11	41:1j:57:LYS:HD3	1.95	0.47
44:1m:29:ARG:HA	44:1m:32:GLU:HB2	1.96	0.47
1:2A:108:U:H2'	1:2A:109:G:H8	1.78	0.47
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.49	0.47
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.13	0.47
19:2X:94:GLY:N	19:2X:95:LEU:HB2	2.29	0.47
20:2Y:28:LYS:N	20:2Y:38:ILE:O	2.46	0.47
21:2Z:171:ILE:HG13	21:2Z:172:ALA:H	1.77	0.47
28:26:8:LYS:HD3	30:28:34:TRP:CD2	2.49	0.47
32:2a:328:C:H4'	32:2a:329:A:H5'	1.95	0.47
33:2b:57:PHE:HB2	33:2b:199:TYR:CZ	2.49	0.47
33:2b:215:LEU:HA	33:2b:218:ALA:HB3	1.97	0.47
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.14	0.47
34:2c:183:ASP:N	34:2c:202:ILE:O	2.38	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:11:LYS:HA	40:2i:108:VAL:HG12	1.96	0.47
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.49	0.47
17:1V:30:GLY:N	17:1V:61:VAL:O	2.33	0.47
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.29	0.47
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.82	0.47
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.47	0.47
1:2A:300:A:P	20:2Y:86:ARG:HH12	2.37	0.47
1:2A:646:A:H2'	1:2A:647:G:O4'	2.14	0.47
1:2A:1474:C:H2'	1:2A:1475:G:H8	1.79	0.47
6:2G:86:MET:H	6:2G:86:MET:HG3	1.41	0.47
8:2I:102:SER:HA	8:2I:107:VAL:O	2.15	0.47
12:2Q:27:VAL:N	12:2Q:138:ASP:OD1	2.47	0.47
29:27:5:TRP:CD1	29:27:7:PRO:HD3	2.48	0.47
32:2a:1010:G:N2	32:2a:1020:U:H1'	2.29	0.47
32:2a:1122:U:N3	32:2a:1123:A:N7	2.62	0.47
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.29	0.47
1:1A:2203:U:O2'	1:1A:2205:C:H5'	2.14	0.47
1:1A:2723:C:OP1	13:1R:3:HIS:ND1	2.34	0.47
9:1N:24:GLY:O	9:1N:28:THR:HG23	2.15	0.47
15:1T:45:PHE:CE1	15:1T:65:LYS:HD3	2.49	0.47
15:1T:111:ARG:HH21	32:1a:1463:C:P	2.38	0.47
18:1W:37:ARG:HD2	18:1W:38:TYR:CE2	2.49	0.47
28:16:12:GLU:OE1	28:16:52:VAL:HG11	2.13	0.47
36:1e:99:GLY:N	36:1e:117:ASP:OD1	2.41	0.47
51:1t:64:ASP:OD2	51:1t:81:LYS:HD3	2.14	0.47
1:2A:989:G:OP2	25:23:11:SER:OG	2.31	0.47
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.14	0.47
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.14	0.47
3:2D:123:ALA:O	3:2D:131:LEU:HD21	2.14	0.47
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.96	0.47
8:2I:87:LYS:HE3	8:2I:87:LYS:HB3	1.52	0.47
22:20:25:ARG:HA	22:20:25:ARG:HD3	1.56	0.47
24:22:29:LYS:HE2	24:22:57:ILE:HG21	1.95	0.47
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.79	0.47
40:2i:50:LEU:HA	40:2i:53:VAL:HG22	1.95	0.47
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.95	0.47
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.50	0.47
7:1H:126:PRO:HD2	7:1H:130:ARG:O	2.14	0.47
32:1a:143:A:O2'	32:1a:144:G:OP2	2.32	0.47
32:1a:250:A:H4'	32:1a:251:G:O5'	2.13	0.47
32:1a:409:G:H1	32:1a:433:C:H42	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:643:C:H2'	32:1a:644:G:H8	1.79	0.47
32:1a:824:C:H2'	32:1a:825:G:C8	2.49	0.47
34:1c:112:SER:O	34:1c:116:VAL:HG23	2.14	0.47
55:1x:3:C:H42	55:1x:70:G:H1	1.63	0.47
1:2A:855:G:O2'	22:20:27:GLU:OE2	2.23	0.47
1:2A:858:U:O2	1:2A:2268:A:H2'	2.14	0.47
1:2A:918:A:C2	2:2B:81:G:H5'	2.49	0.47
1:2A:2161:C:H2'	1:2A:2162:G:O4'	2.14	0.47
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.14	0.47
12:2Q:7:MET:HE2	12:2Q:7:MET:HA	1.96	0.47
24:22:30:ARG:O	24:22:34:GLU:HG3	2.14	0.47
32:2a:1063:C:H3'	32:2a:1064:G:H2'	1.97	0.47
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.49	0.47
32:2a:1459:C:OP1	51:2t:31:SER:OG	2.18	0.47
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.54	0.47
55:2x:29:G:H2'	55:2x:30:G:C8	2.47	0.47
1:1A:271(K):U:O4'	8:1I:50:ARG:NH2	2.47	0.47
1:1A:271(P):C:H2'	1:1A:271(Q):G:O4'	2.14	0.47
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.30	0.47
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.50	0.47
6:1G:5:VAL:HG22	6:1G:8:LYS:H	1.79	0.47
8:1I:141:LYS:HE2	8:1I:141:LYS:HB2	1.79	0.47
13:1R:22:ARG:HG2	13:1R:69:ASP:HB3	1.95	0.47
32:1a:1136:U:H5"	32:1a:1137:C:C2	2.50	0.47
32:1a:1186:G:H21	45:1n:61:TRP:C	2.23	0.47
32:1a:1226:C:H4'	50:1s:80:TYR:CZ	2.50	0.47
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.15	0.47
33:1b:32:ILE:HD13	33:1b:40:HIS:HD2	1.79	0.47
35:1d:194:LEU:HA	35:1d:194:LEU:HD13	1.69	0.47
41:1j:16:LEU:HD22	41:1j:68:HIS:CB	2.44	0.47
47:1p:5:ARG:NH2	47:1p:28:ARG:HA	2.28	0.47
54:1w:18:G:O2'	54:1w:57:G:N1	2.36	0.47
2:2B:105:A:H3'	2:2B:106:G:O4'	2.15	0.47
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.96	0.47
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.39	0.47
23:21:6:GLU:HG3	23:21:61:ARG:O	2.14	0.47
28:26:6:ARG:NH2	28:26:24:GLU:HG3	2.30	0.47
32:2a:396:G:O2'	32:2a:398:C:OP1	2.28	0.47
32:2a:416:G:H1	32:2a:427:U:H3	1.63	0.47
32:2a:1190:G:H5'	34:2c:176:HIS:HE1	1.73	0.47
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:150:GLU:HA	35:2d:153:ARG:HG3	1.97	0.47
36:2e:144:THR:OG1	36:2e:147:ASP:OD1	2.32	0.47
37:2f:13:ASN:ND2	37:2f:55:ASP:OD2	2.46	0.47
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	1.95	0.47
1:1A:1686:C:H2'	1:1A:1687:G:O4'	2.15	0.47
1:1A:2136:C:N4	1:1A:2155:G:H1	2.10	0.47
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.50	0.47
1:1A:2684:U:OP1	15:1T:53:ARG:HD3	2.15	0.47
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.47	0.47
31:19:8:LYS:O	31:19:34:GLN:NE2	2.36	0.47
32:1a:189(K):U:H2'	32:1a:189(L):G:H8	1.75	0.47
32:1a:269:C:H2'	32:1a:270:A:C8	2.49	0.47
32:1a:730:G:C5	32:1a:731:G:H1'	2.50	0.47
36:1e:80:ILE:HG22	36:1e:91:LEU:HB2	1.96	0.47
38:1g:116:ALA:O	38:1g:119:ARG:N	2.48	0.47
39:1h:53:VAL:HB	39:1h:58:TYR:CE2	2.50	0.47
41:1j:5:ARG:O	41:1j:98:ILE:HA	2.15	0.47
50:1s:44:MET:O	50:1s:47:HIS:ND1	2.43	0.47
1:2A:1001:A:H2'	1:2A:1002:G:O4'	2.15	0.47
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.13	0.47
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.47	0.47
32:2a:129(A):G:N2	32:2a:189(F):U:H5"	2.29	0.47
33:2b:162:ILE:HG12	33:2b:184:VAL:HG22	1.96	0.47
38:2g:78:ARG:HE	38:2g:79:ARG:HG3	1.80	0.47
41:2j:7:LYS:HG2	41:2j:9:ARG:CZ	2.44	0.47
1:1A:530:G:H4'	1:1A:531:C:OP1	2.14	0.47
1:1A:699:A:H2'	1:1A:700:G:O4'	2.15	0.47
1:1A:912:C:OP1	12:1Q:8:LYS:NZ	2.48	0.47
1:1A:960:A:C8	1:1A:962:G:C8	3.02	0.47
1:1A:1054:A:H3'	1:1A:1055:G:C8	2.50	0.47
1:1A:1364:G:OP2	23:11:3:LYS:HG3	2.15	0.47
1:1A:1720:U:H2'	1:1A:1721:G:O4'	2.15	0.47
1:1A:1952:A:C6	1:1A:1953:A:N1	2.82	0.47
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.15	0.47
2:1B:24:G:N7	2:1B:56:G:H2'	2.30	0.47
10:1O:16:ALA:HB2	10:1O:52:VAL:HG21	1.97	0.47
13:1R:56:LYS:NZ	13:1R:90:ARG:O	2.46	0.47
14:1S:65:VAL:O	14:1S:69:VAL:HG12	2.14	0.47
18:1W:97:LYS:HE2	18:1W:99:ARG:NH2	2.29	0.47
25:13:12:PRO:HB2	25:13:20:LYS:HG2	1.96	0.47
32:1a:112:G:P	47:1p:27:LYS:HZ2	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:130:A:C8	48:1q:63:ARG:HD3	2.49	0.47
32:1a:1117:G:H5"	40:1i:104:ARG:NH1	2.29	0.47
32:1a:1124:G:OP1	41:1j:36:GLY:N	2.41	0.47
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.24	0.47
35:1d:172:PRO:C	35:1d:174:LEU:H	2.23	0.47
37:1f:80:ARG:NH1	37:1f:88:VAL:O	2.48	0.47
45:1n:40:CYS:SG	45:1n:42:ILE:HG13	2.55	0.47
47:1p:40:ASP:HB3	47:1p:48:TRP:CB	2.45	0.47
1:2A:142:A:HO2'	1:2A:1407:C:HO2'	1.55	0.47
1:2A:667:U:H1'	30:28:2:PRO:HD2	1.97	0.47
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.15	0.47
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.44	0.47
2:2B:90:A:N7	2:2B:91:C:H1'	2.30	0.47
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.96	0.47
7:2H:144:VAL:O	7:2H:148:ILE:HG13	2.15	0.47
8:2I:38:LEU:O	8:2I:40:THR:N	2.46	0.47
32:2a:7:G:H5'	32:2a:298:A:O4'	2.15	0.47
32:2a:693:G:H2'	32:2a:694:A:C8	2.49	0.47
32:2a:1026:G:N2	32:2a:1027:C:O4'	2.47	0.47
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.50	0.47
32:2a:1400:5MC:H6	32:2a:1400:5MC:H5"	1.79	0.47
35:2d:10:ARG:HB2	35:2d:40:PRO:HG3	1.96	0.47
35:2d:36:ARG:HB3	35:2d:38:TYR:CE2	2.49	0.47
39:2h:12:ARG:NH1	39:2h:27:PRO:HD3	2.28	0.47
51:2t:67:ALA:HA	51:2t:72:LEU:O	2.14	0.47
55:2x:66:C:H2'	55:2x:67:C:O4'	2.14	0.47
56:2z:2:ARG:H	56:2z:2:ARG:HG2	1.62	0.47
1:1A:86:C:H4'	1:1A:104:U:H1'	1.97	0.47
1:1A:2314:C:H2'	1:1A:2315:G:C8	2.50	0.47
5:1F:122:LYS:HB3	5:1F:191:ARG:HB3	1.97	0.47
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.60	0.47
14:1S:71:ARG:H	14:1S:71:ARG:HG2	1.40	0.47
20:1Y:10:GLY:HA2	20:1Y:27:VAL:HB	1.97	0.47
29:17:24:THR:O	29:17:28:ARG:HG3	2.14	0.47
32:1a:240:C:H2'	32:1a:241:C:H6	1.79	0.47
32:1a:1048:G:OP1	45:1n:3:ARG:HB3	2.14	0.47
47:1p:38:TYR:O	47:1p:49:LEU:HD22	2.15	0.47
1:2A:959:A:N3	1:2A:2457:U:O2'	2.48	0.47
1:2A:2378:A:H4'	14:2S:23:ARG:HH12	1.80	0.47
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.50	0.47
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:16:G:O2'	2:2B:17:C:H5'	2.15	0.47
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	1.97	0.47
6:2G:167:GLU:OE1	6:2G:167:GLU:N	2.47	0.47
8:2I:121:LYS:HD2	8:2I:121:LYS:HA	1.59	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.15	0.47
30:28:26:LYS:HD2	30:28:48:PHE:CD2	2.50	0.47
32:2a:6:G:N2	36:2e:98:THR:HG23	2.30	0.47
32:2a:114:U:H2'	32:2a:115:G:C8	2.50	0.47
32:2a:430:A:H2'	32:2a:431:A:O4'	2.14	0.47
32:2a:1442:G:O2'	32:2a:1442(B):A:N7	2.45	0.47
32:2a:1490:C:H2'	32:2a:1491:G:O4'	2.15	0.47
35:2d:159:ARG:O	35:2d:163:GLU:HB2	2.15	0.47
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.29	0.47
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.95	0.47
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.11	0.47
1:1A:1065:U:H1'	1:1A:1074:G:C2	2.50	0.47
1:1A:2054:A:OP1	1:1A:2055:C:O2'	2.28	0.47
3:1D:182:LEU:HD23	3:1D:182:LEU:HA	1.80	0.47
4:1E:32:PRO:HB3	4:1E:90:THR:HG22	1.96	0.47
5:1F:179:GLU:N	5:1F:179:GLU:OE1	2.47	0.47
32:1a:737:A:H2'	32:1a:738:C:H6	1.78	0.47
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.47	0.47
55:1x:50:U:H3	55:1x:64:G:H1	1.61	0.47
1:2A:1686:C:H2'	1:2A:1687:G:O4'	2.15	0.47
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.29	0.47
6:2G:20:ILE:HA	6:2G:25:TYR:HD2	1.80	0.47
6:2G:166:ASP:O	6:2G:170:ARG:N	2.47	0.47
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.88	0.47
35:2d:153:ARG:NH1	35:2d:180:GLY:O	2.48	0.47
39:2h:51:VAL:HG11	39:2h:60:ARG:HH21	1.80	0.47
41:2j:57:LYS:O	41:2j:60:ARG:NH2	2.45	0.47
45:2n:3:ARG:HD3	45:2n:3:ARG:HA	1.42	0.47
50:2s:28:LYS:HB3	50:2s:29:ARG:CA	2.45	0.47
52:2u:3:LYS:HB3	52:2u:14:TRP:CG	2.49	0.47
54:2w:50:C:C2	54:2w:51:A:C2	3.03	0.47
1:1A:295:G:OP1	20:1Y:1:MET:HB3	2.14	0.47
1:1A:2340:G:H2'	1:1A:2341:G:H8	1.79	0.47
1:1A:2849:U:OP2	15:1T:95:ARG:NH1	2.48	0.47
13:1R:9:LYS:O	13:1R:17:ARG:HD3	2.14	0.47
32:1a:789:U:O2'	32:1a:791:G:N7	2.40	0.47
35:1d:63:LYS:O	35:1d:67:ILE:N	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:79:ARG:HD2	38:1g:80:VAL:N	2.30	0.47
40:1i:9:ARG:HB2	40:1i:9:ARG:HH11	1.79	0.47
54:1w:76:A1B8A:N	55:1x:76:8AN:H2'	2.30	0.47
57:1y:47:U:H2'	57:1y:50:C:OP1	2.15	0.47
1:2A:605:C:O2	1:2A:657:U:O2'	2.30	0.47
2:2B:49:C:OP1	14:2S:97:ARG:HB3	2.15	0.47
4:2E:104:VAL:HG22	4:2E:198:VAL:HG13	1.97	0.47
7:2H:26:VAL:O	7:2H:79:VAL:HG11	2.14	0.47
14:2S:15:ARG:NH1	14:2S:88:ASP:OD2	2.47	0.47
19:2X:14:SER:C	19:2X:16:LYS:H	2.22	0.47
22:20:27:GLU:HB2	22:20:69:PHE:HD1	1.79	0.47
22:20:51:VAL:HG22	22:20:81:VAL:HG23	1.97	0.47
32:2a:730:G:O6	46:2o:51:HIS:NE2	2.47	0.47
32:2a:744:C:H4'	32:2a:852:G:O2'	2.15	0.47
32:2a:841:U:C4	32:2a:848:C:H1'	2.49	0.47
32:2a:1071:C:H42	32:2a:1104:G:H1	1.63	0.47
38:2g:100:ALA:O	38:2g:104:LEU:HG	2.14	0.47
8:1I:101:LEU:O	8:1I:106:GLY:N	2.48	0.46
9:1N:66:LYS:O	9:1N:70:LYS:HB3	2.15	0.46
32:1a:376:G:OP2	47:1p:67:THR:HG21	2.15	0.46
32:1a:381:C:H2'	32:1a:382:A:O4'	2.14	0.46
32:1a:663:A:O3'	49:1r:64:ARG:NH2	2.47	0.46
32:1a:719:C:H1'	49:1r:49:LYS:HB3	1.96	0.46
32:1a:973:G:N3	41:1j:54:PHE:HE1	2.13	0.46
32:1a:1531:A:H8	32:1a:1531:A:O5'	1.98	0.46
38:1g:78:ARG:HD3	38:1g:156:TRP:CZ3	2.50	0.46
57:1y:59:A:H3'	57:1y:60:U:C6	2.50	0.46
57:1y:74:C:H2'	57:1y:75:C:C6	2.50	0.46
1:2A:7:G:H2'	1:2A:8:A:C8	2.51	0.46
1:2A:922:U:H2'	1:2A:923:C:C6	2.49	0.46
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.30	0.46
4:2E:179:GLU:HG3	15:2T:9:LEU:HD21	1.97	0.46
10:2O:76:ALA:O	15:2T:74:ARG:HG3	2.14	0.46
14:2S:35:ILE:HD13	14:2S:66:ALA:HB1	1.97	0.46
16:2U:105:VAL:HG13	17:2V:45:THR:HG23	1.97	0.46
32:2a:620:C:H2'	32:2a:621:A:O4'	2.15	0.46
32:2a:821:G:H2'	32:2a:822:C:C6	2.50	0.46
32:2a:865:A:H5'	32:2a:1078:U:C5	2.50	0.46
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.80	0.46
32:2a:1329:A:O2'	44:2m:70:LEU:HD21	2.15	0.46
32:2a:1342:C:H2'	32:2a:1343:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:12:GLU:HA	33:2b:213:LEU:HD11	1.97	0.46
35:2d:100:ARG:NH2	35:2d:102:ASP:OD2	2.48	0.46
35:2d:172:PRO:HB2	35:2d:187:ARG:NH2	2.31	0.46
41:2j:8:LEU:HD12	41:2j:16:LEU:HD22	1.96	0.46
46:2o:5:LYS:H	46:2o:5:LYS:HG3	1.37	0.46
55:2x:23:C:H2'	55:2x:24:U:H6	1.80	0.46
1:1A:287:C:H2'	1:1A:288:C:H6	1.81	0.46
1:1A:639:U:H2'	1:1A:640:C:C6	2.50	0.46
1:1A:859:G:O2'	1:1A:916:G:O6	2.34	0.46
2:1B:6:C:H2'	2:1B:7:G:O4'	2.15	0.46
10:1O:38:VAL:HG13	10:1O:87:ILE:HD11	1.97	0.46
12:1Q:16:ARG:HG3	12:1Q:17:LEU:H	1.80	0.46
21:1Z:30:ASN:HA	21:1Z:89:PHE:HE1	1.81	0.46
32:1a:518:C:H4'	32:1a:519:C:H5"	1.97	0.46
32:1a:1036:G:H5"	32:1a:1037:C:C5	2.50	0.46
33:1b:19:HIS:NE2	33:1b:206:ASP:HB2	2.30	0.46
35:1d:65:ARG:NH1	35:1d:72:GLU:HB2	2.30	0.46
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.97	0.46
1:2A:2252:G:O6	22:20:4:LYS:HD3	2.15	0.46
1:2A:2818:G:OP1	1:2A:2837:G:O2'	2.27	0.46
7:2H:51:ARG:NH1	7:2H:53:GLU:HG3	2.29	0.46
21:2Z:97:GLU:HA	21:2Z:126:VAL:O	2.15	0.46
32:2a:533:A:O2'	32:2a:535:A:OP2	2.27	0.46
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.79	0.46
32:2a:1134:G:N1	32:2a:1135:U:H1'	2.30	0.46
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.80	0.46
35:2d:172:PRO:HB2	35:2d:187:ARG:HH21	1.81	0.46
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.15	0.46
1:1A:2105:C:H2'	1:1A:2106:G:H8	1.80	0.46
2:1B:43:C:H5"	26:14:1:MET:HG3	1.97	0.46
2:1B:58:A:OP2	63:1B:303:HOH:O	2.19	0.46
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.48	0.46
11:1P:85:LEU:HG	11:1P:115:LEU:O	2.15	0.46
20:1Y:76:CYS:HA	20:1Y:106:LEU:HD12	1.97	0.46
24:12:10:LEU:HB3	24:12:14:ARG:NH1	2.31	0.46
32:1a:7:G:O2'	36:1e:120:THR:O	2.33	0.46
32:1a:646:U:H2'	32:1a:647:C:H6	1.80	0.46
32:1a:664:G:N2	32:1a:741:G:H1	2.08	0.46
32:1a:925:G:H1'	32:1a:1502:A:C4	2.51	0.46
32:1a:1255:G:O2'	32:1a:1258:G:N3	2.46	0.46
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.96	0.46
57:1y:36:U:C2	57:1y:37:T6A:H1'	2.49	0.46
1:2A:185:U:H2'	1:2A:186:G:H8	1.79	0.46
1:2A:1791:A:N6	1:2A:1828:G:O2'	2.46	0.46
1:2A:1908:C:O2'	55:2x:12:G:H5"	2.16	0.46
32:2a:555:C:H2'	32:2a:556:C:C6	2.50	0.46
32:2a:865:A:H5'	32:2a:1078:U:H5	1.80	0.46
32:2a:995:C:O2	45:2n:4:LYS:NZ	2.41	0.46
32:2a:1265:G:C4	32:2a:1271:G:N2	2.82	0.46
32:2a:1431:C:H42	32:2a:1469:G:H1	1.62	0.46
33:2b:28:PHE:CG	33:2b:190:THR:HA	2.50	0.46
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.97	0.46
44:2m:13:LYS:O	44:2m:45:VAL:N	2.43	0.46
49:2r:53:ARG:HG2	49:2r:63:GLN:HE21	1.80	0.46
57:2y:29:U:H2'	57:2y:30:G:O4'	2.14	0.46
1:1A:405:U:O5'	1:1A:405:U:H6	1.98	0.46
1:1A:759:G:OP1	63:1A:4169:HOH:O	2.20	0.46
1:1A:864:G:O2'	1:1A:865:C:H5'	2.15	0.46
1:1A:2056:G:OP2	63:1A:4170:HOH:O	2.21	0.46
3:1D:20:ASP:OD2	3:1D:22:SER:OG	2.34	0.46
5:1F:102:PRO:O	5:1F:106:ARG:HG3	2.16	0.46
23:11:3:LYS:HB2	23:11:61:ARG:HH12	1.79	0.46
32:1a:527:G7M:O2'	32:1a:535:A:N1	2.40	0.46
32:1a:1518:MA6:H93	32:1a:1519:MA6:C9	2.45	0.46
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.51	0.46
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.98	0.46
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.15	0.46
1:2A:749:C:OP2	63:2A:3964:HOH:O	2.21	0.46
2:2B:2:C:N4	2:2B:119:G:O6	2.48	0.46
2:2B:42:C:O2	6:2G:92:VAL:HG23	2.16	0.46
13:2R:98:LEU:HB2	13:2R:113:LEU:HD11	1.96	0.46
14:2S:87:PHE:HB2	14:2S:112:PHE:CE1	2.50	0.46
32:2a:834:C:H2'	32:2a:835:U:H6	1.80	0.46
38:2g:126:ASP:HB3	38:2g:131:LYS:C	2.40	0.46
50:2s:33:THR:HG21	50:2s:49:ILE:HD11	1.98	0.46
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.80	0.46
1:1A:1857:G:C6	1:1A:1858:G:C6	3.04	0.46
1:1A:2369:A:H2'	1:1A:2370:G:C8	2.50	0.46
14:1S:19:LYS:O	14:1S:22:GLY:N	2.43	0.46
25:13:35:ARG:HE	25:13:37:LEU:HD21	1.80	0.46
26:14:68:ARG:HD3	26:14:68:ARG:HA	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:186:C:H2'	32:1a:187:C:C6	2.50	0.46
32:1a:643:C:H2'	32:1a:644:G:C8	2.51	0.46
37:1f:36:ARG:HB3	37:1f:36:ARG:CZ	2.44	0.46
39:1h:110:ALA:N	39:1h:121:ASP:OD1	2.43	0.46
41:1j:49:VAL:HG11	45:1n:41:ARG:O	2.15	0.46
43:1l:42:THR:HA	43:1l:53:ARG:O	2.15	0.46
50:1s:41:VAL:HG12	50:1s:43:GLU:H	1.79	0.46
57:1y:19:G:OP1	57:1y:60:U:N3	2.46	0.46
1:2A:307:G:H21	1:2A:330:A:H62	1.64	0.46
1:2A:1259:G:H2'	1:2A:1260:G:H8	1.79	0.46
16:2U:52:ARG:HA	16:2U:55:ARG:HD3	1.97	0.46
32:2a:301:G:H2'	32:2a:302:G:H8	1.80	0.46
33:2b:46:LYS:O	33:2b:50:GLU:HB2	2.15	0.46
34:2c:22:TRP:CH2	34:2c:32:LEU:HB3	2.51	0.46
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.51	0.46
36:2e:18:ARG:N	36:2e:25:ARG:O	2.47	0.46
40:2i:92:TYR:O	40:2i:96:LEU:HB2	2.16	0.46
45:2n:53:LEU:HD23	45:2n:53:LEU:HA	1.63	0.46
1:1A:1079:C:N4	1:1A:1088:A:O4'	2.47	0.46
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.50	0.46
5:1F:155:LEU:HD11	5:1F:176:LEU:HD12	1.98	0.46
12:1Q:68:ILE:HD13	12:1Q:103:MET:HG2	1.97	0.46
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.48	0.46
26:14:63:TYR:N	26:14:64:GLY:HA2	2.30	0.46
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.98	0.46
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.98	0.46
1:2A:1464:C:O2'	1:2A:1528:A:N3	2.47	0.46
1:2A:2066:C:C2'	1:2A:2067:G:H5'	2.45	0.46
1:2A:2472:G:N2	1:2A:2477:C:H5"	2.31	0.46
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.15	0.46
32:2a:825:G:H2'	32:2a:826:C:C6	2.51	0.46
32:2a:975:A:H4'	32:2a:976:G:H5"	1.97	0.46
32:2a:1284:C:H3'	32:2a:1285:A:H8	1.80	0.46
32:2a:1353:G:H2'	32:2a:1354:C:C6	2.50	0.46
34:2c:54:ARG:HB2	34:2c:69:HIS:CG	2.51	0.46
40:2i:9:ARG:HG2	40:2i:14:VAL:HA	1.97	0.46
40:2i:37:PHE:CE1	40:2i:70:LYS:HB3	2.50	0.46
50:2s:32:LYS:HB2	50:2s:57:HIS:CE1	2.50	0.46
1:1A:606:U:H4'	1:1A:658:C:H4'	1.98	0.46
1:1A:2389:G:H5"	1:1A:2390:U:O4'	2.15	0.46
7:1H:57:ASP:O	7:1H:62:LYS:HD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.98	0.46
12:1Q:109:VAL:HG22	12:1Q:113:GLN:OE1	2.16	0.46
14:1S:87:PHE:CE1	14:1S:102:ALA:HB2	2.50	0.46
15:1T:113:LYS:HD3	15:1T:113:LYS:HA	1.79	0.46
18:1W:29:LEU:HD22	18:1W:69:LEU:HD12	1.97	0.46
21:1Z:52:SER:O	21:1Z:52:SER:OG	2.31	0.46
23:11:18:ILE:HG12	23:11:37:ILE:CG1	2.45	0.46
32:1a:659:U:H2'	32:1a:660:G:O4'	2.16	0.46
32:1a:1003:G:N3	32:1a:1004:A:H2	2.12	0.46
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.50	0.46
47:1p:49:LEU:HD11	47:1p:51:VAL:HG23	1.98	0.46
55:1x:19:G:H5"	55:1x:60:U:O4	2.15	0.46
1:2A:995:C:O2	9:2N:3:THR:OG1	2.26	0.46
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.50	0.46
1:2A:1561:G:H2'	1:2A:1562:A:C8	2.50	0.46
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.50	0.46
1:2A:2361:A:OP2	30:28:26:LYS:NZ	2.46	0.46
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.80	0.46
3:2D:222:ARG:NH2	63:2D:405:HOH:O	2.48	0.46
5:2F:135:LYS:HB3	5:2F:138:GLU:HG3	1.97	0.46
9:2N:115:ARG:HA	9:2N:118:LYS:HD2	1.98	0.46
15:2T:99:LEU:O	15:2T:101:PHE:N	2.48	0.46
32:2a:644:G:H5'	39:2h:92:ARG:HH22	1.81	0.46
34:2c:46:GLU:CD	34:2c:46:GLU:H	2.24	0.46
1:1A:829:A:N7	1:1A:2248:C:H5'	2.30	0.46
1:1A:1068:G:H2'	1:1A:1096:A:H1'	1.96	0.46
1:1A:2287:A:C8	1:1A:2289:G:C8	3.03	0.46
1:1A:2639:A:H2'	1:1A:2640:G:O4'	2.16	0.46
4:1E:18:ASP:OD2	15:1T:33:LYS:NZ	2.39	0.46
5:1F:75:HIS:ND1	63:1F:401:HOH:O	2.13	0.46
7:1H:22:GLY:C	7:1H:23:ARG:HG3	2.40	0.46
32:1a:667:G:H4'	46:1o:51:HIS:ND1	2.31	0.46
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.16	0.46
1:2A:81:G:H1	1:2A:105:C:H42	1.64	0.46
1:2A:855:G:H2'	1:2A:856:C:C6	2.51	0.46
1:2A:1902:C:OP1	3:2D:242:ARG:HD2	2.16	0.46
4:2E:29:GLY:H	4:2E:180:ASN:HB3	1.81	0.46
8:2I:84:GLY:O	8:2I:86:THR:N	2.42	0.46
11:2P:63:PRO:HB2	30:28:30:ARG:NH2	2.30	0.46
13:2R:33:ARG:NH1	27:25:57:VAL:O	2.38	0.46
21:2Z:121:HIS:ND1	21:2Z:123:ASP:O	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:547:A:OP2	35:2d:2:GLY:N	2.49	0.46
32:2a:1206:G:C6	32:2a:1207:2MG:C5	3.04	0.46
32:2a:1261:A:H5'	32:2a:1283:G:O3'	2.16	0.46
32:2a:1353:G:H2'	32:2a:1354:C:H6	1.81	0.46
40:2i:17:VAL:HG13	40:2i:63:ILE:HG12	1.98	0.46
54:2w:18:G:H5'	54:2w:60:U:O2'	2.16	0.46
1:1A:656:G:H2'	1:1A:657:U:O4'	2.16	0.46
1:1A:876:C:H2'	1:1A:877:U:C6	2.51	0.46
1:1A:1740:G:H2'	1:1A:1741:A:C8	2.51	0.46
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.79	0.46
2:1B:17:C:H2'	2:1B:18:G:O4'	2.16	0.46
29:17:29:LYS:O	29:17:33:ARG:HB2	2.16	0.46
32:1a:901:A:O5'	32:1a:901:A:H8	1.99	0.46
35:1d:122:ARG:HD2	35:1d:122:ARG:HA	1.64	0.46
35:1d:124:GLY:C	35:1d:126:ILE:H	2.23	0.46
45:1n:3:ARG:HD3	45:1n:3:ARG:HA	1.65	0.46
48:1q:13:ASP:HA	48:1q:19:VAL:HG12	1.98	0.46
55:1x:64:G:H2'	55:1x:65:C:C6	2.51	0.46
57:1y:7:U:O2'	57:1y:49:G:OP2	2.19	0.46
1:2A:414:C:H4'	1:2A:1879:C:O2	2.16	0.46
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.51	0.46
1:2A:1153:C:H5'	16:2U:76:TYR:CE2	2.50	0.46
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.16	0.46
1:2A:2088:G:H2'	1:2A:2089:U:O4'	2.15	0.46
7:2H:126:PRO:HG2	7:2H:130:ARG:HH21	1.81	0.46
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.81	0.46
32:2a:778:G:H2'	32:2a:779:C:O4'	2.15	0.46
32:2a:1005:A:H3'	32:2a:1006:C:C6	2.51	0.46
32:2a:1152:A:H5'	41:2j:13:HIS:CD2	2.51	0.46
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.32	0.46
32:2a:1414:U:H3	32:2a:1486:G:H1	1.64	0.46
33:2b:97:TRP:CH2	33:2b:102:LEU:HG	2.51	0.46
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	1.98	0.46
1:1A:662:G:OP1	11:1P:16:ARG:NE	2.49	0.46
1:1A:1478:G:O2'	1:1A:1558:A:N7	2.49	0.46
1:1A:1682:G:C2	1:1A:1757:U:H1'	2.51	0.46
1:1A:1791:A:H5'	3:1D:206:LEU:HD12	1.98	0.46
1:1A:1833:U:O2'	1:1A:1969:A:N1	2.47	0.46
1:1A:2366:A:H2'	1:1A:2367:G:O4'	2.15	0.46
32:1a:353:A:H5'	32:1a:353:A:H8	1.81	0.46
32:1a:1191:A:OP1	34:1c:4:LYS:NZ	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1258:G:H8	32:1a:1258:G:OP2	1.98	0.46
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	1.98	0.46
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.98	0.46
1:2A:902:C:H2'	1:2A:903:C:C6	2.52	0.46
1:2A:1847:A:H4'	1:2A:1848:A:OP2	2.16	0.46
1:2A:2108:C:H2'	1:2A:2109:U:C6	2.51	0.46
1:2A:2371:G:O2'	28:26:46:HIS:ND1	2.46	0.46
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.60	0.46
9:2N:1:MET:HE2	16:2U:93:LYS:HG2	1.97	0.46
32:2a:698:G:H2'	32:2a:699:C:C6	2.51	0.46
35:2d:102:ASP:HB3	35:2d:136:PRO:HB3	1.97	0.46
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.50	0.45
1:1A:535:C:O3'	16:1U:53:ARG:NH1	2.48	0.45
1:1A:1036:G:OP2	7:1H:59:ARG:HD2	2.16	0.45
3:1D:118:VAL:HG22	3:1D:119:ALA:H	1.81	0.45
32:1a:337:C:H2'	32:1a:338:A:C8	2.50	0.45
32:1a:1005:A:OP2	32:1a:1024:G:N2	2.49	0.45
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.17	0.45
32:1a:1148:U:O4'	40:1i:16:ARG:HD2	2.16	0.45
32:1a:1292:U:H2'	32:1a:1293:G:H8	1.78	0.45
45:1n:58:LYS:HB3	45:1n:58:LYS:HE3	1.74	0.45
1:2A:559:G:H22	16:2U:49:HIS:CE1	2.34	0.45
1:2A:709:U:H2'	1:2A:710:G:C8	2.51	0.45
1:2A:1443:G:H1	1:2A:1548:C:H42	1.65	0.45
1:2A:2271:G:OP1	22:20:18:ALA:HB1	2.15	0.45
1:2A:2564:A:OP1	1:2A:2648:C:H4'	2.16	0.45
3:2D:76:PRO:HA	3:2D:118:VAL:HG23	1.99	0.45
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.98	0.45
14:2S:94:TYR:CE2	14:2S:99:LYS:HG3	2.51	0.45
21:2Z:10:ARG:NH2	21:2Z:26:GLY:O	2.49	0.45
23:21:52:ARG:HA	23:21:56:GLN:O	2.16	0.45
32:2a:301:G:H2'	32:2a:302:G:C8	2.51	0.45
32:2a:757:U:H2'	32:2a:758:G:O4'	2.16	0.45
32:2a:1295:G:H21	32:2a:1302:U:H3	1.62	0.45
34:2c:38:ARG:HE	34:2c:38:ARG:HB2	1.30	0.45
36:2e:16:THR:OG1	36:2e:17:ALA:N	2.49	0.45
39:2h:84:ARG:NH1	39:2h:86:ILE:HG12	2.31	0.45
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.16	0.45
1:1A:467:G:OP1	29:17:33:ARG:HD2	2.16	0.45
1:1A:888:C:O2	44:1m:83:ASP:HA	2.15	0.45
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1971:A:C4	3:1D:241:PRO:HD3	2.50	0.45
1:1A:2017:U:H4'	27:15:8:LYS:O	2.17	0.45
1:1A:2718:G:OP1	15:1T:100:TYR:HD2	1.99	0.45
4:1E:18:ASP:N	4:1E:18:ASP:OD1	2.49	0.45
9:1N:137:LYS:NZ	9:1N:139:GLU:OE2	2.40	0.45
32:1a:289:G:OP2	63:1a:1919:HOH:O	2.21	0.45
32:1a:1239:A:H62	32:1a:1299:A:N6	2.15	0.45
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.51	0.45
33:1b:91:PRO:HG3	33:1b:154:LEU:HB3	1.98	0.45
48:1q:10:VAL:HG13	48:1q:19:VAL:HB	1.98	0.45
1:2A:251:A:C5	1:2A:252:G:H1'	2.51	0.45
1:2A:613:G:O2'	1:2A:614(C):A:N1	2.45	0.45
1:2A:2712:U:OP1	1:2A:2714:G:H4'	2.16	0.45
2:2B:6:C:H42	2:2B:115:G:H1	1.64	0.45
11:2P:2:LYS:HG2	11:2P:3:LEU:N	2.31	0.45
12:2Q:42:ILE:HD13	12:2Q:125:LEU:HD22	1.98	0.45
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.98	0.45
13:2R:36:THR:HG22	13:2R:37:THR:N	2.31	0.45
23:21:83:GLU:OE1	23:21:83:GLU:N	2.42	0.45
25:23:10:LYS:HB3	25:23:53:LEU:HD23	1.98	0.45
26:24:57:GLU:HA	26:24:58:ARG:HA	1.61	0.45
32:2a:259:G:H1	32:2a:267:C:H42	1.63	0.45
32:2a:957:U:H2'	32:2a:959:A:OP2	2.17	0.45
37:2f:48:LEU:HB3	37:2f:50:TYR:O	2.15	0.45
38:2g:32:ARG:HB3	38:2g:32:ARG:NH1	2.31	0.45
1:1A:254:G:H4'	1:1A:384:U:H5'	1.98	0.45
1:1A:302:C:H2'	1:1A:303:U:H6	1.82	0.45
1:1A:586:A:H5'	5:1F:89:VAL:HG21	1.97	0.45
1:1A:730:C:H3'	63:1A:4441:HOH:O	2.16	0.45
1:1A:1058:G:H1	1:1A:1080:C:H42	1.63	0.45
1:1A:1568:G:H5'	3:1D:60:ARG:HA	1.99	0.45
1:1A:1826:G:H4'	3:1D:242:ARG:CZ	2.47	0.45
1:1A:2151:G:H2'	1:1A:2152:G:C8	2.51	0.45
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.34	0.45
1:1A:2424:C:O2	1:1A:2429:G:O2'	2.27	0.45
1:1A:2475:C:H42	1:1A:2529:G:H22	1.64	0.45
1:1A:2477:C:N4	31:19:10:ILE:HG23	2.30	0.45
8:1I:117:GLU:HG3	8:1I:118:LYS:H	1.81	0.45
19:1X:8:ILE:O	24:12:36:ARG:NH2	2.50	0.45
32:1a:162:A:N7	32:1a:163:C:H1'	2.31	0.45
32:1a:600:C:H2'	32:1a:601:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:939:G:C6	32:1a:940:C:C4	3.05	0.45
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.52	0.45
32:1a:1264:C:H2'	32:1a:1265:G:H8	1.81	0.45
33:1b:174:VAL:HG13	33:1b:184:VAL:HG11	1.98	0.45
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	1.98	0.45
36:1e:151:LEU:HD11	39:1h:77:GLU:OE2	2.16	0.45
1:2A:208:C:H2'	1:2A:209:C:H6	1.81	0.45
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.51	0.45
1:2A:1913:A:H4'	1:2A:1914:C:O5'	2.15	0.45
1:2A:2262:U:OP2	22:20:16:SER:OG	2.31	0.45
1:2A:2318:G:H21	14:2S:3:ARG:CD	2.28	0.45
1:2A:2355:C:O2	22:20:39:ARG:NH2	2.48	0.45
1:2A:2749:A:H1'	7:2H:63:SER:OG	2.16	0.45
5:2F:47:GLY:HA3	5:2F:95:ARG:O	2.17	0.45
6:2G:179:PRO:HB2	26:24:42:PHE:CE2	2.50	0.45
7:2H:22:GLY:C	7:2H:37:VAL:HG22	2.40	0.45
12:2Q:18:LYS:HE3	12:2Q:18:LYS:HB2	1.85	0.45
12:2Q:73:PRO:HG3	12:2Q:93:TYR:HE1	1.82	0.45
14:2S:88:ASP:OD1	14:2S:90:GLY:N	2.49	0.45
32:2a:288:A:H2'	32:2a:289:G:H4'	1.99	0.45
32:2a:683:G:H2'	32:2a:684:A:C8	2.51	0.45
32:2a:775:G:H2'	32:2a:776:G:O4'	2.17	0.45
33:2b:110:GLN:O	33:2b:110:GLN:HG2	2.16	0.45
46:2o:85:LEU:HB3	46:2o:87:ILE:HG13	1.99	0.45
57:2y:38:A:H2'	57:2y:39:PSU:O4'	2.16	0.45
1:1A:709:U:H2'	1:1A:710:G:C8	2.51	0.45
1:1A:784:A:C8	1:1A:792:G:C5	3.05	0.45
1:1A:1023:U:O2'	1:1A:1122:G:H5'	2.17	0.45
8:1I:77:LEU:HD22	8:1I:101:LEU:HG	1.99	0.45
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.51	0.45
20:1Y:2:ARG:HE	20:1Y:2:ARG:HB3	1.54	0.45
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.39	0.45
32:1a:1273:G:H3'	32:1a:1274:G:H8	1.81	0.45
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.99	0.45
34:1c:22:TRP:CH2	45:1n:54:PRO:HG2	2.52	0.45
40:1i:50:LEU:HD23	40:1i:81:ILE:HD11	1.97	0.45
1:2A:459:U:H5"	29:27:40:TRP:CD2	2.52	0.45
1:2A:1288:U:O4	13:2R:106:GLY:HA3	2.17	0.45
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.52	0.45
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.82	0.45
1:2A:1811:G:H3'	63:2A:3911:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2018:G:P	27:25:9:LYS:HZ3	2.39	0.45
1:2A:2552:OMU:H6	1:2A:2552:OMU:O5'	2.17	0.45
1:2A:2748:A:N3	7:2H:63:SER:HB3	2.31	0.45
6:2G:41:GLN:HG2	6:2G:154:GLY:O	2.16	0.45
13:2R:13:HIS:CE1	13:2R:15:SER:HB3	2.50	0.45
41:2j:36:GLY:O	41:2j:38:ILE:HD12	2.15	0.45
44:2m:91:ARG:HA	44:2m:96:LEU:HB2	1.98	0.45
1:1A:11:G:H2'	1:1A:12:U:H5'	1.98	0.45
1:1A:18:C:H2'	1:1A:19:C:C6	2.51	0.45
1:1A:484:C:OP1	20:1Y:51:VAL:HG22	2.17	0.45
1:1A:577:G:C6	1:1A:578:A:C6	3.05	0.45
1:1A:1359:A:C2	1:1A:1372:U:O4	2.69	0.45
1:1A:1557:C:H5"	1:1A:1558:A:OP2	2.16	0.45
5:1F:164:ARG:O	5:1F:168:ARG:HB3	2.15	0.45
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.39	0.45
20:1Y:47:LYS:HB3	20:1Y:61:ILE:HG22	1.98	0.45
32:1a:623:C:H2'	32:1a:624:C:O4'	2.17	0.45
32:1a:901:A:C5	32:1a:902:G:H1'	2.51	0.45
32:1a:1118:C:H2'	32:1a:1119:C:C6	2.51	0.45
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.97	0.45
34:1c:14:ILE:HD12	34:1c:178:LEU:HD22	1.97	0.45
42:1k:54:ARG:H	42:1k:54:ARG:HG3	1.47	0.45
1:2A:191:A:H2'	1:2A:192:C:C6	2.51	0.45
1:2A:614(A):U:O5'	1:2A:614(A):U:H6	2.00	0.45
1:2A:852:G:C6	1:2A:926:A:C6	3.05	0.45
1:2A:1117:G:H2'	1:2A:1118:C:H6	1.82	0.45
1:2A:1710:C:H2'	1:2A:1711:C:C6	2.50	0.45
1:2A:1784:A:H4'	1:2A:1785:A:O5'	2.17	0.45
1:2A:2238:G:H5"	63:2A:4265:HOH:O	2.16	0.45
1:2A:2343:C:O3'	1:2A:2373:G:H4'	2.16	0.45
1:2A:2786:U:H2'	1:2A:2787:C:H6	1.82	0.45
1:2A:2892:A:H2'	1:2A:2893:G:H5'	1.98	0.45
2:2B:7:G:H2'	2:2B:8:U:O4'	2.17	0.45
5:2F:13:SER:HB3	5:2F:127:GLU:HB2	1.97	0.45
6:2G:12:TYR:HA	6:2G:16:ARG:HG3	1.98	0.45
6:2G:108:ASN:O	26:24:36:CYS:HA	2.16	0.45
8:2I:69:LYS:HE2	8:2I:69:LYS:HB2	1.76	0.45
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HG2	2.31	0.45
20:2Y:90:LEU:H	20:2Y:90:LEU:HD12	1.80	0.45
32:2a:537:G:H5"	43:2l:113:ARG:NH1	2.32	0.45
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.98	0.45
47:2p:57:ARG:O	47:2p:61:SER:N	2.50	0.45
1:1A:1045:A:OP1	1:1A:1046:A:H3'	2.17	0.45
1:1A:2633:G:H2'	1:1A:2634:G:O4'	2.17	0.45
1:1A:2723:C:O3'	13:1R:1:MET:HE1	2.17	0.45
8:1I:44:LEU:HA	8:1I:44:LEU:HD12	1.72	0.45
22:10:29:GLN:O	22:10:67:VAL:HG23	2.16	0.45
31:19:2:LYS:HE2	31:19:31:LYS:O	2.16	0.45
32:1a:253:U:H2'	32:1a:254:G:C8	2.52	0.45
32:1a:1118:C:H2'	32:1a:1119:C:H6	1.82	0.45
44:1m:30:ALA:O	44:1m:34:LEU:HG	2.16	0.45
1:2A:10:G:O2'	1:2A:2801(A):A:N7	2.44	0.45
1:2A:614:U:H2'	1:2A:614(A):U:O4'	2.16	0.45
1:2A:1161:C:H4'	17:2V:8:GLY:HA2	1.99	0.45
1:2A:1697:G:OP2	1:2A:1698:A:O2'	2.28	0.45
1:2A:1745:C:H2'	1:2A:1745(A):C:O4'	2.17	0.45
1:2A:1817:G:C6	1:2A:1818:U:C4	3.04	0.45
1:2A:1910:G:H2'	1:2A:1911:PSU:C6	2.50	0.45
1:2A:2637:U:H5"	4:2E:82:ARG:NH1	2.29	0.45
2:2B:29:A:O2'	2:2B:58:A:N1	2.47	0.45
7:2H:24:VAL:HG21	7:2H:72:ILE:HD12	1.99	0.45
26:24:62:ARG:HA	26:24:62:ARG:NE	2.32	0.45
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.52	0.45
34:2c:173:VAL:HG22	34:2c:203:PHE:HB2	1.99	0.45
38:2g:69:VAL:HA	38:2g:138:LYS:HD3	1.98	0.45
1:1A:1056:G:H21	1:1A:1103:A:H62	1.64	0.45
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.99	0.45
15:1T:116:ALA:HB1	15:1T:121:ILE:HD11	1.99	0.45
32:1a:264:U:H4'	48:1q:63:ARG:HD2	1.98	0.45
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.29	0.45
32:1a:864:A:OP1	63:1a:1917:HOH:O	2.20	0.45
1:2A:26:G:H1'	1:2A:514:A:N6	2.32	0.45
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.15	0.45
1:2A:1187:G:H8	1:2A:1187:G:OP2	2.00	0.45
2:2B:18:G:H2'	2:2B:19:G:C8	2.51	0.45
2:2B:49:C:H2'	2:2B:50:G:C8	2.51	0.45
11:2P:49:ARG:HA	30:28:57:ARG:HB3	1.99	0.45
18:2W:65:LEU:HD23	18:2W:65:LEU:HA	1.75	0.45
32:2a:834:C:H2'	32:2a:835:U:C6	2.52	0.45
32:2a:1049:U:OP1	45:2n:3:ARG:HB2	2.16	0.45
32:2a:1147:C:O2	40:2i:16:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:126:GLU:OE1	33:2b:126:GLU:N	2.45	0.45
34:2c:34:LEU:HG	34:2c:38:ARG:HH22	1.82	0.45
37:2f:95:GLU:H	37:2f:95:GLU:HG2	1.45	0.45
41:2j:47:PHE:N	41:2j:63:PHE:O	2.41	0.45
1:1A:1055:G:H1	1:1A:1104:C:N4	2.12	0.45
1:1A:1310:G:OP2	29:17:9:ARG:NE	2.50	0.45
1:1A:2409:G:C6	1:1A:2410:G:C5	3.05	0.45
1:1A:2432:A:H5"	63:1y:101:HOH:O	2.17	0.45
2:1B:90:A:N7	2:1B:91:C:H1'	2.32	0.45
20:1Y:61:ILE:HD12	20:1Y:61:ILE:HA	1.65	0.45
32:1a:131:C:H2'	32:1a:132:C:C6	2.52	0.45
32:1a:748:C:H4'	32:1a:749:C:O5'	2.16	0.45
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.52	0.45
1:2A:25:U:C4	1:2A:26:G:C6	3.05	0.45
1:2A:538:G:H2'	1:2A:539:G:C8	2.51	0.45
1:2A:576:U:H2'	1:2A:577:G:C8	2.51	0.45
1:2A:728:G:H5"	3:2D:13:ARG:NH2	2.31	0.45
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.52	0.45
1:2A:1497:U:H5"	1:2A:1498:C:H5	1.81	0.45
1:2A:2227:A:H5"	3:2D:263:ARG:NH1	2.32	0.45
9:2N:28:THR:OG1	9:2N:29:LYS:N	2.49	0.45
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.17	0.45
17:2V:1:MET:HG2	17:2V:43:GLU:OE1	2.17	0.45
17:2V:2:PHE:CZ	17:2V:41:GLY:HA3	2.51	0.45
26:24:64:GLY:C	26:24:66:SER:H	2.24	0.45
32:2a:255:G:H2'	32:2a:256:U:C6	2.52	0.45
32:2a:1329:A:H5"	44:2m:26:GLY:H	1.81	0.45
32:2a:1329:A:H5'	44:2m:29:ARG:NE	2.32	0.45
35:2d:194:LEU:HD23	35:2d:194:LEU:HA	1.79	0.45
40:2i:77:ILE:O	40:2i:81:ILE:HG13	2.16	0.45
43:2l:10:LEU:HD21	43:2l:15:ARG:HE	1.82	0.45
43:2l:41:ARG:HE	43:2l:43:VAL:HG22	1.82	0.45
44:2m:49:THR:O	44:2m:53:VAL:HG13	2.16	0.45
50:2s:13:ASP:HA	50:2s:16:LEU:HB3	1.99	0.45
55:2x:40:C:H2'	55:2x:41:C:C6	2.45	0.45
57:2y:22:G:N7	57:2y:46:G7M:C2	2.80	0.45
1:1A:26:G:C6	1:1A:27:G:N1	2.85	0.45
1:1A:184:C:H2'	1:1A:185:U:C6	2.52	0.45
1:1A:632:A:H2'	1:1A:633:A:C8	2.52	0.45
1:1A:672:C:OP1	63:1A:4168:HOH:O	2.20	0.45
1:1A:717:G:H2'	1:1A:718:A:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.99	0.45
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.17	0.45
1:1A:2749:A:H1'	7:1H:63:SER:OG	2.17	0.45
5:1F:129:PHE:HB3	5:1F:132:VAL:CG1	2.47	0.45
8:1I:107:VAL:HG12	8:1I:109:ILE:HG12	1.99	0.45
13:1R:37:THR:OG1	13:1R:40:LYS:HG3	2.17	0.45
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.99	0.45
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.52	0.45
32:1a:413:G:H21	32:1a:428:G:H1'	1.80	0.45
32:1a:1176:A:H2'	32:1a:1177:G:C8	2.52	0.45
36:1e:42:GLY:HA2	36:1e:65:ASN:O	2.17	0.45
57:1y:22:G:H2'	57:1y:23:A:C8	2.52	0.45
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.52	0.45
1:2A:776:G:N7	1:2A:793:A:O2'	2.49	0.45
1:2A:2156:G:H2'	1:2A:2157:G:C2	2.51	0.45
1:2A:2296:U:P	14:2S:9:ARG:HH22	2.38	0.45
32:2a:789:U:O2'	32:2a:791:G:N7	2.43	0.45
32:2a:1002:G:H2'	32:2a:1003:G:H4'	1.98	0.45
32:2a:1067:A:H8	32:2a:1067:A:O5'	2.00	0.45
32:2a:1226:C:C6	44:2m:103:THR:HB	2.50	0.45
32:2a:1367:C:H5'	41:2j:60:ARG:HH12	1.82	0.45
34:2c:18:TRP:NE1	45:2n:53:LEU:O	2.47	0.45
34:2c:88:ARG:O	34:2c:91:LEU:HB2	2.17	0.45
36:2e:41:VAL:O	36:2e:66:MET:HA	2.17	0.45
38:2g:20:ASP:HB3	38:2g:23:VAL:HB	1.98	0.45
46:2o:58:MET:HG2	46:2o:58:MET:H	1.46	0.45
50:2s:66:MET:HB2	50:2s:74:PHE:CZ	2.52	0.45
1:1A:245:G:O5'	11:1P:73:GLY:HA2	2.16	0.45
1:1A:687:C:H5"	29:17:2:LYS:HE2	1.99	0.45
1:1A:1059:G:H2'	1:1A:1060:U:C5	2.52	0.45
1:1A:1668:A:H4'	1:1A:1669:A:O5'	2.16	0.45
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.32	0.45
1:1A:2721:A:N3	63:1A:4298:HOH:O	2.36	0.45
6:1G:3:LEU:HD12	26:14:25:TYR:CZ	2.52	0.45
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.17	0.45
26:14:16:CYS:HB2	26:14:36:CYS:HB3	1.99	0.45
32:1a:652:U:O4	32:1a:752:G:O2'	2.31	0.45
32:1a:859:A:H2'	32:1a:860:A:O4'	2.17	0.45
32:1a:1058:G:H2'	32:1a:1059:C:O4'	2.17	0.45
33:1b:100:GLY:N	33:1b:176:GLU:OE2	2.45	0.45
33:1b:174:VAL:HG13	33:1b:184:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.17	0.45
39:1h:94:TYR:CE1	39:1h:132:GLU:HB2	2.51	0.45
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.52	0.45
1:2A:1821:A:H2'	1:2A:1822:G:C8	2.51	0.45
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.17	0.45
1:2A:2359:C:H2'	1:2A:2360:A:O4'	2.17	0.45
2:2B:2:C:H2'	2:2B:3:C:H6	1.82	0.45
2:2B:72:G:O2'	2:2B:105:A:N6	2.50	0.45
5:2F:117:ARG:NH2	5:2F:189:THR:O	2.48	0.45
8:2I:48:GLU:HG3	8:2I:52:ARG:NH1	2.32	0.45
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.16	0.45
15:2T:99:LEU:O	15:2T:102:ILE:HG12	2.17	0.45
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.57	0.45
32:2a:1004:A:N3	32:2a:1038:C:C2	2.85	0.45
32:2a:1347:G:H5"	40:2i:107:ARG:HB3	1.99	0.45
38:2g:120:ILE:O	38:2g:124:LEU:HB2	2.17	0.45
48:2q:55:ASP:OD1	48:2q:55:ASP:N	2.49	0.45
48:2q:57:VAL:HA	48:2q:77:VAL:HG23	1.99	0.45
1:1A:531:C:C5	1:1A:2035:G:C2	3.05	0.44
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.52	0.44
1:1A:2630:G:H21	1:1A:2892:A:H1'	1.81	0.44
1:1A:2801(A):A:N3	1:1A:2895:U:H1'	2.32	0.44
5:1F:12:LEU:HB2	5:1F:124:LEU:HD11	1.97	0.44
5:1F:33:LEU:HB3	11:1P:6:LEU:HD21	1.99	0.44
13:1R:12:ARG:HG2	13:1R:16:HIS:CG	2.52	0.44
25:13:7:LYS:HG2	25:13:9:VAL:HG13	1.98	0.44
32:1a:664:G:OP1	49:1r:64:ARG:NE	2.45	0.44
32:1a:1275:A:H2'	32:1a:1276:G:O4'	2.17	0.44
32:1a:1402:4OC:H2'	32:1a:1403:C:O4'	2.16	0.44
33:1b:30:ARG:HG3	33:1b:31:TYR:CD1	2.52	0.44
35:1d:149:ALA:HB3	35:1d:152:SER:HB2	1.98	0.44
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.17	0.44
54:1w:40:C:H2'	54:1w:41:A:H8	1.81	0.44
1:2A:68:G:H2'	1:2A:69:C:O4'	2.17	0.44
1:2A:307:G:N1	1:2A:310:A:OP2	2.49	0.44
1:2A:606:U:H4'	1:2A:658:C:H4'	1.99	0.44
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.82	0.44
1:2A:1876:A:H2'	1:2A:1877:A:H8	1.81	0.44
1:2A:2011:U:H2'	1:2A:2012:G:O4'	2.17	0.44
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.82	0.44
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2649:U:H2'	1:2A:2650:U:C6	2.52	0.44
6:2G:45:GLU:H	6:2G:45:GLU:HG2	1.53	0.44
30:28:52:LYS:HG2	30:28:56:GLU:OE2	2.17	0.44
32:2a:968:A:C4	32:2a:1062:U:H4'	2.52	0.44
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.50	0.44
32:2a:1493:A:O2'	53:2v:19:A:H1'	2.18	0.44
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.99	0.44
39:2h:54:ASP:HB3	39:2h:56:LYS:HD2	1.97	0.44
1:1A:286:C:H2'	1:1A:287:C:C6	2.53	0.44
1:1A:536:A:H2'	1:1A:537:C:C6	2.52	0.44
1:1A:673:C:H5"	5:1F:81:PRO:HD2	1.99	0.44
1:1A:882:G:H1	1:1A:894:C:N4	2.07	0.44
1:1A:1594:G:H2'	1:1A:1595:G:O4'	2.17	0.44
2:1B:4:C:H2'	2:1B:5:C:O4'	2.17	0.44
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.52	0.44
10:1O:86:ILE:HG22	10:1O:94:ARG:HD3	2.00	0.44
14:1S:110:LEU:HA	14:1S:110:LEU:HD12	1.76	0.44
26:14:7:PRO:HB2	26:14:27:THR:CG2	2.48	0.44
32:1a:270:A:H2'	32:1a:271:C:O4'	2.17	0.44
32:1a:1128:C:H4'	32:1a:1148:U:O2	2.18	0.44
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.53	0.44
54:1w:76:A1B8A:OP1	63:1w:201:HOH:O	2.21	0.44
1:2A:416:C:H2'	1:2A:417:C:C6	2.52	0.44
1:2A:466:A:OP1	29:27:34:ARG:NH1	2.50	0.44
1:2A:918:A:C6	1:2A:919:G:H1'	2.52	0.44
1:2A:1142(A):A:H4'	9:2N:25:ARG:HH22	1.81	0.44
1:2A:1441:G:O3'	1:2A:1628:G:H5"	2.17	0.44
1:2A:1853:A:N3	1:2A:2233:U:O2'	2.42	0.44
1:2A:1878:G:H2'	1:2A:1879:C:C6	2.52	0.44
1:2A:1967:C:OP1	63:2A:3965:HOH:O	2.21	0.44
1:2A:2010:G:H5"	18:2W:42:ARG:HB2	1.99	0.44
1:2A:2838:G:C6	1:2A:2839:G:C5	3.06	0.44
2:2B:10:C:H2'	2:2B:11:C:H6	1.82	0.44
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.51	0.44
18:2W:12:ILE:O	18:2W:101:SER:OG	2.31	0.44
22:20:52:GLY:O	22:20:59:LEU:HA	2.17	0.44
31:29:26:ILE:H	31:29:26:ILE:HG13	1.67	0.44
32:2a:256:U:OP1	48:2q:17:LYS:NZ	2.39	0.44
32:2a:953:G:H1	32:2a:1228:C:H42	1.64	0.44
32:2a:977:A:O3'	32:2a:980:C:N4	2.50	0.44
32:2a:1278:U:H5'	32:2a:1279:A:OP1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:10:LEU:HD11	37:2f:61:LEU:HD12	1.98	0.44
1:1A:636:G:O2'	1:1A:638:G:O2'	2.28	0.44
1:1A:705:A:C2	1:1A:727:A:H1'	2.52	0.44
1:1A:784:A:H5"	63:1A:4103:HOH:O	2.16	0.44
1:1A:832:G:H5'	11:1P:45:LEU:HD11	1.99	0.44
1:1A:2014:A:N1	63:1A:4293:HOH:O	2.35	0.44
2:1B:66:A:N6	2:1B:108:U:H2'	2.31	0.44
4:1E:40:GLU:CD	4:1E:40:GLU:H	2.25	0.44
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.53	0.44
33:1b:60:ASP:HA	33:1b:63:MET:HE3	1.99	0.44
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.16	0.44
40:1i:3:GLN:HE21	40:1i:20:ARG:NH2	2.15	0.44
40:1i:9:ARG:HD2	40:1i:104:ARG:NH1	2.32	0.44
41:1j:16:LEU:CD2	41:1j:70:ARG:HG2	2.48	0.44
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.33	0.44
47:1p:57:ARG:HH21	47:1p:79:VAL:HA	1.82	0.44
1:2A:1169:G:H22	1:2A:1180:C:N4	2.14	0.44
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.52	0.44
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.16	0.44
1:2A:2136:C:N4	1:2A:2155:G:N1	2.64	0.44
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.17	0.44
1:2A:2823:A:OP1	4:2E:113:PHE:HB2	2.16	0.44
4:2E:54:GLN:OE1	4:2E:55:ASN:N	2.48	0.44
4:2E:113:PHE:HA	4:2E:159:HIS:HD2	1.81	0.44
6:2G:38:VAL:HG22	6:2G:158:ALA:HB3	1.99	0.44
13:2R:36:THR:HG22	13:2R:37:THR:H	1.82	0.44
14:2S:26:LEU:HD22	14:2S:87:PHE:HD1	1.82	0.44
32:2a:15:G:H2'	32:2a:16:A:C8	2.52	0.44
32:2a:1066:C:H2'	32:2a:1067:A:C8	2.52	0.44
32:2a:1304:G:C6	32:2a:1305:G:N1	2.85	0.44
33:2b:188:ALA:O	33:2b:202:PRO:HA	2.17	0.44
33:2b:207:ALA:O	33:2b:211:ILE:HG13	2.17	0.44
38:2g:99:LEU:HD22	38:2g:103:TRP:CZ2	2.53	0.44
41:2j:46:ARG:HA	41:2j:64:GLU:HA	2.00	0.44
55:2x:3:C:H42	55:2x:70:G:H1	1.65	0.44
57:2y:2:G:H2'	57:2y:3:G:O4'	2.17	0.44
1:1A:373:U:O2	1:1A:423:A:H2	2.00	0.44
1:1A:2618:G:H21	4:1E:150:VAL:HG21	1.82	0.44
5:1F:64:ILE:HD11	5:1F:75:HIS:HB2	2.00	0.44
5:1F:135:LYS:HB2	5:1F:138:GLU:HG3	1.99	0.44
10:1O:70:LYS:HE2	10:1O:70:LYS:HB3	1.79	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.49	0.44
14:1S:51:ALA:HB1	14:1S:69:VAL:HG23	2.00	0.44
14:1S:83:LYS:HD2	14:1S:111:GLU:OE2	2.17	0.44
21:1Z:28:MET:O	21:1Z:34:ASN:HA	2.17	0.44
23:11:46:LEU:O	23:11:47:GLN:NE2	2.50	0.44
32:1a:108:G:C6	51:1t:15:ARG:HD2	2.52	0.44
32:1a:182:U:C4	32:1a:183:G:H1'	2.53	0.44
32:1a:737:A:H5"	37:1f:92:LYS:HG3	1.98	0.44
32:1a:974:A:OP1	45:1n:29:ARG:NH2	2.50	0.44
32:1a:1146:A:H2'	32:1a:1147:C:O4'	2.17	0.44
32:1a:1366:C:H2'	32:1a:1367:C:H6	1.82	0.44
34:1c:130:VAL:HG11	34:1c:157:ILE:HG12	2.00	0.44
34:1c:131:ARG:NH2	34:1c:135:LYS:HE3	2.33	0.44
35:1d:173:TRP:O	35:1d:186:LEU:HB2	2.17	0.44
43:1l:40:VAL:HG21	43:1l:78:GLN:HA	2.00	0.44
1:2A:921:G:C6	1:2A:922:U:C4	3.06	0.44
1:2A:947:G:H2'	1:2A:948:G:C8	2.52	0.44
1:2A:1365:A:OP2	23:21:3:LYS:HG2	2.17	0.44
1:2A:1902:C:H5'	3:2D:246:PRO:HD3	1.99	0.44
1:2A:2141:G:H2'	1:2A:2142:C:O4'	2.18	0.44
1:2A:2689:U:P	1:2A:2719:G:H22	2.39	0.44
12:2Q:1:MET:N	12:2Q:1:MET:HE3	2.32	0.44
32:2a:176:C:H2'	32:2a:177:C:C6	2.52	0.44
32:2a:504:C:H42	32:2a:541:G:H1	1.65	0.44
33:2b:97:TRP:CD1	33:2b:172:ILE:HB	2.53	0.44
34:2c:20:SER:OG	34:2c:40:ARG:NH1	2.50	0.44
35:2d:22:LYS:HG2	62:2d:303:SF4:S4	2.57	0.44
47:2p:28:ARG:HG2	47:2p:29:ASP:OD1	2.17	0.44
1:1A:181:A:H1'	1:1A:435:C:H5'	2.00	0.44
1:1A:588:U:O4	1:1A:670:A:H1'	2.17	0.44
1:1A:668:G:H5'	1:1A:669:G:OP2	2.17	0.44
1:1A:774:A:N3	1:1A:774:A:H2'	2.33	0.44
1:1A:889:C:H2'	1:1A:889:C:OP2	2.17	0.44
1:1A:1052:C:H2'	1:1A:1053:C:H6	1.83	0.44
1:1A:2386:C:H2'	1:1A:2387:U:C6	2.52	0.44
4:1E:47:VAL:HG23	4:1E:84:PHE:HB3	1.99	0.44
21:1Z:30:ASN:OD1	21:1Z:33:LEU:HG	2.18	0.44
21:1Z:72:ARG:HD3	21:1Z:72:ARG:HA	1.63	0.44
32:1a:690:G:C6	32:1a:691:G:C6	3.06	0.44
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.53	0.44
33:1b:101:MET:C	33:1b:102:LEU:HD12	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:23:A:H3'	54:1w:24:G:H8	1.82	0.44
54:1w:50:C:N3	54:1w:64:G:N2	2.56	0.44
1:2A:881:G:N2	54:2w:56:C:N3	2.65	0.44
1:2A:910:A:N1	1:2A:2277:G:H1'	2.32	0.44
1:2A:1152:C:H4'	16:2U:77:SER:HA	2.00	0.44
1:2A:1252:G:N2	16:2U:37:GLU:OE2	2.49	0.44
1:2A:1942:5MC:H4'	54:2w:72:C:P	2.57	0.44
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.35	0.44
1:2A:2342:C:O2'	1:2A:2374:C:H5"	2.17	0.44
3:2D:136:ILE:O	3:2D:168:ARG:NH2	2.51	0.44
7:2H:15:VAL:HG13	7:2H:27:LYS:O	2.18	0.44
7:2H:56:SER:HB2	7:2H:61:HIS:ND1	2.32	0.44
12:2Q:32:TYR:OH	12:2Q:111:GLU:OE1	2.23	0.44
12:2Q:78:PRO:HD3	55:2x:1:C:N3	2.31	0.44
14:2S:34:HIS:HB3	14:2S:53:SER:HB3	2.00	0.44
32:2a:143:A:O3'	32:2a:144:G:H8	2.00	0.44
32:2a:889:A:H8	32:2a:889:A:OP1	2.01	0.44
32:2a:994:A:N7	32:2a:1216:G:H4'	2.32	0.44
32:2a:1100:C:C2	32:2a:1102:A:H5'	2.52	0.44
35:2d:177:ASP:OD1	35:2d:180:GLY:N	2.50	0.44
45:2n:4:LYS:HB3	45:2n:4:LYS:HE2	1.74	0.44
49:2r:38:GLU:HA	49:2r:41:LYS:HE2	1.99	0.44
53:2v:22:U:H2'	53:2v:23:A:H8	1.82	0.44
57:2y:60:U:H3'	57:2y:61:C:C5	2.53	0.44
1:1A:483:A:H1'	20:1Y:59:GLY:O	2.17	0.44
1:1A:973:A:H8	1:1A:973:A:OP1	2.00	0.44
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.53	0.44
4:1E:31:CYS:HB3	4:1E:49:LEU:HD13	2.00	0.44
6:1G:21:ARG:HA	6:1G:21:ARG:NE	2.31	0.44
16:1U:82:GLY:HA3	16:1U:113:ALA:HB1	1.99	0.44
32:1a:153:C:H2'	32:1a:154:C:C6	2.53	0.44
32:1a:510:A:N3	32:1a:543:C:H1'	2.33	0.44
35:1d:15:GLU:OE1	35:1d:59:ARG:NH1	2.50	0.44
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.50	0.44
41:1j:47:PHE:HB2	41:1j:63:PHE:HB2	1.98	0.44
47:1p:4:ILE:HB	47:1p:66:PRO:HA	2.00	0.44
57:1y:38:A:H2'	57:1y:39:PSU:O4'	2.18	0.44
1:2A:84:A:N1	1:2A:98:G:O2'	2.40	0.44
1:2A:686:G:N2	1:2A:788:A:H61	2.14	0.44
1:2A:1026:U:H4'	1:2A:1027:A:OP1	2.18	0.44
1:2A:1423:G:H2'	1:2A:1424:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1714:G:H2'	1:2A:1717:G:H8	1.82	0.44
1:2A:1908:C:O2	55:2x:12:G:H4'	2.18	0.44
1:2A:2768:C:H2'	1:2A:2769:C:O4'	2.18	0.44
2:2B:66:A:N6	2:2B:108:U:H3'	2.32	0.44
4:2E:117:MET:HB3	4:2E:117:MET:HE2	1.72	0.44
11:2P:138:LEU:HG	11:2P:143:GLY:HA3	2.00	0.44
12:2Q:79:LEU:HD23	12:2Q:79:LEU:HA	1.82	0.44
32:2a:67:C:H2'	32:2a:68:G:H8	1.80	0.44
32:2a:359:U:H2'	32:2a:360:A:C8	2.52	0.44
32:2a:962:C:H2'	32:2a:963:G:H8	1.82	0.44
32:2a:1326:C:H5"	52:2u:18:TYR:O	2.18	0.44
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.33	0.44
32:2a:1350:A:H2'	32:2a:1351:U:C6	2.53	0.44
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.47	0.44
36:2e:5:ASP:N	36:2e:5:ASP:OD1	2.51	0.44
36:2e:70:PRO:HG2	36:2e:144:THR:HG23	2.00	0.44
39:2h:20:TYR:OH	39:2h:75:ARG:HB3	2.18	0.44
41:2j:49:VAL:HG13	41:2j:61:GLU:HB3	1.99	0.44
50:2s:22:LEU:O	50:2s:26:GLY:N	2.49	0.44
1:1A:11:G:N7	63:1A:4296:HOH:O	2.36	0.44
1:1A:143(A):C:H2'	1:1A:144:C:H6	1.82	0.44
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.52	0.44
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.17	0.44
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.18	0.44
5:1F:57:VAL:HG13	5:1F:59:TYR:H	1.83	0.44
6:1G:48:GLU:O	6:1G:50:ALA:N	2.51	0.44
12:1Q:14:ARG:HB3	12:1Q:41:TRP:HH2	1.82	0.44
12:1Q:135:ASP:O	12:1Q:139:GLU:HG3	2.17	0.44
12:1Q:138:ASP:OD2	21:1Z:81:ARG:NH1	2.50	0.44
13:1R:2:ARG:O	13:1R:5:LYS:HG3	2.18	0.44
18:1W:4:LYS:HD2	18:1W:6:ILE:HD11	1.99	0.44
24:12:1:MET:N	24:12:52:ASP:OD2	2.39	0.44
32:1a:640:A:HO2'	32:1a:641:U:H5'	1.83	0.44
33:1b:112:VAL:O	33:1b:116:GLU:N	2.43	0.44
33:1b:125:PRO:O	33:1b:127:ILE:N	2.50	0.44
34:1c:110:ASN:ND2	34:1c:140:ARG:HB3	2.32	0.44
1:2A:108:U:H2'	1:2A:109:G:C8	2.53	0.44
1:2A:747:U:O2	1:2A:2014:A:H1'	2.16	0.44
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.53	0.44
1:2A:1814:G:C6	1:2A:1815:A:C6	3.06	0.44
1:2A:2290:G:O2'	1:2A:2381:C:H1'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:91:SER:HB2	8:2I:119:PRO:HB2	2.00	0.44
15:2T:127:ALA:C	15:2T:129:ARG:N	2.74	0.44
19:2X:26:TYR:O	19:2X:81:VAL:HG22	2.18	0.44
32:2a:794:A:OP1	63:2a:3310:HOH:O	2.21	0.44
32:2a:1077:G:N2	32:2a:1079:G:H3'	2.32	0.44
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.18	0.44
33:2b:16:HIS:CE1	33:2b:203:GLY:HA2	2.52	0.44
57:2y:29:U:H3	57:2y:41:A:H61	1.64	0.44
1:1A:29:U:H2'	1:1A:30:G:C8	2.53	0.44
1:1A:396:G:H1'	23:11:42:GLN:HB3	1.99	0.44
1:1A:900:A:H2'	1:1A:901:A:O4'	2.18	0.44
1:1A:1069:A:H4'	1:1A:1070:A:H5"	1.99	0.44
1:1A:1827:C:C2'	1:1A:1828:G:H5'	2.48	0.44
1:1A:2086:U:H2'	1:1A:2087:G:H8	1.82	0.44
1:1A:2629:A:H1'	1:1A:2630:G:C5'	2.47	0.44
1:1A:2660:A:H2'	1:1A:2661:G:O4'	2.18	0.44
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.17	0.44
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.77	0.44
21:1Z:4:ARG:NH2	21:1Z:60:GLU:OE2	2.42	0.44
32:1a:21:G:H2'	32:1a:22:G:C8	2.53	0.44
32:1a:266:G:H2'	32:1a:266:G:N3	2.32	0.44
33:1b:143:GLU:O	33:1b:147:LYS:N	2.49	0.44
34:1c:119:ARG:HH11	34:1c:123:GLN:HE21	1.66	0.44
42:1k:17:GLY:O	42:1k:80:VAL:HA	2.18	0.44
51:1t:45:GLN:HB2	51:1t:91:LEU:HD13	2.00	0.44
1:2A:340:A:H2'	1:2A:341:G:O4'	2.18	0.44
1:2A:639:U:H2'	1:2A:640:C:C6	2.53	0.44
1:2A:1022:G:N2	1:2A:1142(A):A:H2	2.16	0.44
1:2A:1462:C:H4'	1:2A:2703:C:H5'	2.00	0.44
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.53	0.44
10:2O:17:ARG:HA	10:2O:17:ARG:HD3	1.66	0.44
22:20:51:VAL:HG21	22:20:79:VAL:O	2.18	0.44
23:21:73:LEU:HD23	23:21:73:LEU:HA	1.89	0.44
24:22:65:ASN:O	24:22:69:ARG:HB2	2.18	0.44
25:23:18:ASP:N	25:23:18:ASP:OD1	2.51	0.44
32:2a:1010:G:C2	32:2a:1020:U:H1'	2.53	0.44
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.17	0.44
32:2a:1469:G:H2'	32:2a:1470:G:H8	1.83	0.44
34:2c:5:ILE:HD12	34:2c:5:ILE:HA	1.78	0.44
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.99	0.44
47:2p:3:LYS:HA	47:2p:3:LYS:HD2	1.54	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:31:ILE:HG22	50:2s:32:LYS:O	2.18	0.44
51:2t:57:ARG:HH12	51:2t:100:ILE:HD12	1.81	0.44
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.18	0.44
57:2y:68:G:H2'	57:2y:69:A:H5"	2.00	0.44
1:1A:651:G:OP1	30:18:19:SER:OG	2.32	0.44
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.83	0.44
1:1A:1477:A:C2	1:1A:1515:G:C2	3.06	0.44
1:1A:2582:G:OP2	63:1A:4173:HOH:O	2.21	0.44
2:1B:78:A:C2	2:1B:100:A:C4	3.05	0.44
2:1B:83:G:OP1	25:13:19:GLN:NE2	2.41	0.44
32:1a:908:A:H2'	32:1a:909:A:C8	2.53	0.44
32:1a:1197:G:OP2	63:1a:1906:HOH:O	2.21	0.44
32:1a:1308:U:H3'	44:1m:99:ARG:HH21	1.83	0.44
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	1.98	0.44
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.99	0.44
1:2A:579:G:H2'	1:2A:580:C:C6	2.53	0.44
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.52	0.44
1:2A:666:G:H2'	1:2A:667:U:C6	2.53	0.44
1:2A:1792:G:H2'	1:2A:1793:C:H6	1.83	0.44
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.53	0.44
6:2G:15:VAL:HG13	6:2G:175:LEU:HD12	2.00	0.44
10:2O:1:MET:HG3	10:2O:67:LYS:HG2	1.99	0.44
13:2R:10:LEU:HD23	13:2R:10:LEU:HA	1.81	0.44
20:2Y:102:CYS:SG	20:2Y:104:GLY:N	2.90	0.44
27:25:9:LYS:HA	27:25:9:LYS:HD3	1.71	0.44
32:2a:173:U:H5"	32:2a:197:A:O4'	2.18	0.44
32:2a:403:C:OP2	35:2d:74:GLN:NE2	2.51	0.44
32:2a:945:G:N2	32:2a:1334:G:O2'	2.51	0.44
34:2c:116:VAL:HG21	34:2c:202:ILE:HD11	2.00	0.44
35:2d:22:LYS:O	35:2d:113:SER:HB3	2.18	0.44
41:2j:11:PHE:CE1	41:2j:67:THR:HB	2.53	0.44
51:2t:53:LEU:O	51:2t:57:ARG:HG3	2.16	0.44
1:1A:36:G:N3	1:1A:450:G:O2'	2.51	0.43
1:1A:478:A:C6	1:1A:480:A:C6	3.06	0.43
1:1A:863:A:OP1	12:1Q:22:LYS:HG3	2.18	0.43
1:1A:969:U:H2'	1:1A:970:C:C6	2.52	0.43
1:1A:1072:C:O5'	1:1A:1072:C:H6	2.01	0.43
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.33	0.43
10:1O:64:ARG:NH1	10:1O:101:PRO:O	2.34	0.43
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.58	0.43
23:11:82:LEU:HA	23:11:85:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:14:ARG:O	24:12:67:LYS:NZ	2.36	0.43
32:1a:1290:G:H2'	32:1a:1291:G:H8	1.83	0.43
40:1i:106:ALA:O	40:1i:108:VAL:HG13	2.18	0.43
51:1t:39:LYS:HG2	51:1t:55:ILE:HG21	1.99	0.43
1:2A:134:C:H42	1:2A:145:G:H1	1.65	0.43
1:2A:479:A:N3	1:2A:481:G:H5"	2.33	0.43
1:2A:2694:G:C6	1:2A:2695:C:C4	3.06	0.43
3:2D:118:VAL:HG12	3:2D:129:ASN:HD21	1.81	0.43
3:2D:170:GLY:C	3:2D:172:TYR:H	2.25	0.43
14:2S:15:ARG:HB3	14:2S:19:LYS:HE3	2.00	0.43
17:2V:56:SER:HB3	17:2V:100:ARG:HD2	1.98	0.43
32:2a:126:G:OP1	32:2a:605:U:O2'	2.36	0.43
32:2a:620:C:C2	35:2d:135:LEU:HG	2.53	0.43
32:2a:683:G:C6	32:2a:684:A:C6	3.06	0.43
32:2a:999:C:H2'	32:2a:1000:U:C6	2.53	0.43
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.52	0.43
32:2a:1263:C:H3'	32:2a:1263:C:H6	1.82	0.43
33:2b:70:PHE:HB2	33:2b:92:TYR:HB3	1.99	0.43
34:2c:6:HIS:HD2	34:2c:7:PRO:HD2	1.82	0.43
40:2i:17:VAL:HG22	40:2i:63:ILE:HD13	2.00	0.43
45:2n:47:LEU:HA	45:2n:50:LYS:HB2	2.00	0.43
1:1A:228:A:H8	1:1A:228:A:H3'	1.84	0.43
1:1A:831:G:N2	11:1P:53:GLY:O	2.51	0.43
1:1A:839:U:H2'	1:1A:840:C:H6	1.83	0.43
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.52	0.43
1:1A:1762:A:H2'	63:1A:5565:HOH:O	2.17	0.43
1:1A:2059:A:N1	60:1A:4082:TEL:H573	2.33	0.43
1:1A:2301:C:H2'	1:1A:2302:G:C8	2.54	0.43
2:1B:54:G:H2'	2:1B:55:U:C6	2.53	0.43
7:1H:17:VAL:HG21	7:1H:50:VAL:HG21	1.99	0.43
11:1P:100:LEU:HA	11:1P:100:LEU:HD23	1.76	0.43
12:1Q:81:VAL:HG12	22:10:5:LYS:HD3	1.99	0.43
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG21	2.00	0.43
32:1a:258:G:H2'	32:1a:259:G:H8	1.83	0.43
32:1a:881:G:P	43:1l:12:ARG:HH22	2.41	0.43
32:1a:987:G:H1	32:1a:1218:C:N4	2.16	0.43
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.45	0.43
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.99	0.43
36:1e:7:GLU:HG2	36:1e:112:LEU:HD21	2.00	0.43
37:1f:6:VAL:HG13	37:1f:90:VAL:HG22	2.00	0.43
57:1y:29:U:H2'	57:1y:30:G:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:287:C:H2'	1:2A:288:C:C6	2.53	0.43
1:2A:1882:C:H2'	1:2A:1883:G:O4'	2.18	0.43
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.18	0.43
32:2a:1227:A:C8	50:2s:83:HIS:HB3	2.53	0.43
32:2a:1317:C:N4	45:2n:19:ARG:HH21	2.16	0.43
33:2b:70:PHE:CE2	33:2b:90:MET:HB2	2.46	0.43
44:2m:14:ARG:HB2	44:2m:17:VAL:HG23	1.99	0.43
1:1A:27:G:C2	1:1A:512:G:N3	2.86	0.43
1:1A:674:G:O2'	5:1F:74:ARG:HD3	2.18	0.43
1:1A:781:A:H2'	1:1A:1777:U:O2'	2.18	0.43
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.48	0.43
1:1A:2577:A:OP2	27:15:3:LYS:NZ	2.43	0.43
3:1D:108:PRO:HD2	3:1D:111:LEU:HD22	1.99	0.43
14:1S:106:ARG:HE	14:1S:112:PHE:C	2.26	0.43
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.19	0.43
22:10:32:ARG:H	22:10:35:ASN:ND2	2.16	0.43
32:1a:40:C:H2'	32:1a:41:G:H8	1.83	0.43
32:1a:854:G:H3'	32:1a:871:U:O4	2.18	0.43
32:1a:872:A:C8	32:1a:874:G:C8	3.06	0.43
36:1e:72:GLN:O	36:1e:75:THR:HG22	2.17	0.43
37:1f:100:ASN:HB2	49:1r:28:GLU:HA	2.00	0.43
39:1h:9:MET:SD	39:1h:32:LYS:HB3	2.58	0.43
47:1p:40:ASP:HB3	47:1p:48:TRP:HB2	1.99	0.43
1:2A:222:A:H3'	1:2A:421:U:H5'	2.00	0.43
1:2A:782:A:N7	3:2D:221:VAL:HG21	2.34	0.43
1:2A:958:U:OP1	12:2Q:74:TYR:OH	2.25	0.43
1:2A:1018:C:H2'	1:2A:1019:U:C6	2.53	0.43
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.53	0.43
1:2A:1815:A:C6	1:2A:1817:G:C6	3.07	0.43
4:2E:179:GLU:HB2	4:2E:181:LEU:HG	2.00	0.43
6:2G:84:LYS:HB2	6:2G:84:LYS:HE3	1.88	0.43
6:2G:99:MET:O	6:2G:103:LEU:HG	2.17	0.43
14:2S:19:LYS:C	14:2S:21:THR:H	2.25	0.43
14:2S:33:LYS:HG2	14:2S:34:HIS:CD2	2.52	0.43
32:2a:233:C:H2'	32:2a:234:C:H6	1.83	0.43
32:2a:381:C:H2'	32:2a:382:A:O4'	2.19	0.43
32:2a:399:G:H2'	32:2a:400:C:C6	2.53	0.43
32:2a:792:A:H1'	32:2a:794:A:N7	2.33	0.43
32:2a:998:G:H1	32:2a:1043:C:N4	2.15	0.43
32:2a:1004:A:C6	32:2a:1037:C:H1'	2.53	0.43
32:2a:1254:C:OP1	41:2j:45:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.53	0.43
39:2h:91:ARG:HB2	43:2l:7:ILE:HG13	1.99	0.43
47:2p:4:ILE:HG23	47:2p:21:VAL:HG12	2.00	0.43
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.18	0.43
50:2s:12:ASP:OD2	50:2s:37:ARG:NH1	2.51	0.43
51:2t:12:ALA:HA	51:2t:15:ARG:HB2	2.00	0.43
1:1A:142(A):C:H2'	1:1A:143:G:O4'	2.17	0.43
1:1A:1438:U:O2'	1:1A:1439:A:H5'	2.18	0.43
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.53	0.43
1:1A:2801(A):A:H1'	1:1A:2895:U:C1'	2.48	0.43
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.51	0.43
4:1E:119:ARG:HG2	4:1E:120:TRP:CD1	2.53	0.43
10:1O:24:VAL:HA	10:1O:39:ILE:HG22	2.00	0.43
12:1Q:10:ARG:HH11	12:1Q:11:LYS:HE3	1.84	0.43
19:1X:93:GLU:H	19:1X:93:GLU:HG2	1.66	0.43
32:1a:44:G:C2	32:1a:45:U:H1'	2.54	0.43
32:1a:626:U:H2'	32:1a:627:G:H8	1.82	0.43
32:1a:714:G:H2'	32:1a:715:A:C8	2.54	0.43
35:1d:81:GLU:OE2	35:1d:139:ARG:NH1	2.30	0.43
36:1e:78:HIS:HE1	36:1e:143:ARG:N	2.12	0.43
36:1e:112:LEU:HD23	36:1e:112:LEU:HA	1.86	0.43
38:1g:27:ILE:HA	38:1g:30:ILE:HD12	1.99	0.43
38:1g:76:ARG:HD3	38:1g:156:TRP:HZ2	1.83	0.43
1:2A:28:A:H1'	1:2A:513:A:C2	2.53	0.43
1:2A:229:A:H5'	1:2A:230:U:OP1	2.18	0.43
1:2A:1434:A:N6	1:2A:1558:A:H62	2.10	0.43
18:2W:88:ARG:HA	18:2W:88:ARG:HD2	1.75	0.43
21:2Z:52:SER:C	21:2Z:54:HIS:H	2.26	0.43
21:2Z:128:VAL:HG22	21:2Z:161:VAL:HA	2.00	0.43
25:23:40:THR:HG22	25:23:42:ALA:H	1.83	0.43
27:25:52:TYR:O	27:25:55:ARG:HG2	2.19	0.43
32:2a:711:G:O2'	32:2a:712:A:H5'	2.18	0.43
32:2a:1320:C:OP1	50:2s:70:LYS:HG3	2.19	0.43
36:2e:102:ALA:HB2	36:2e:120:THR:HG21	2.00	0.43
39:2h:100:ILE:HD12	39:2h:125:ARG:HG3	2.00	0.43
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.18	0.43
48:2q:53:LEU:HD21	48:2q:82:MET:HE1	1.99	0.43
49:2r:31:LEU:HB2	49:2r:66:LEU:HD12	2.00	0.43
50:2s:33:THR:H	50:2s:57:HIS:CE1	2.37	0.43
1:1A:484:C:H2'	1:1A:485:C:H6	1.84	0.43
1:1A:1268:A:C2	1:1A:2013:A:C4	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1338:G:O2'	1:1A:1393:A:N1	2.46	0.43
1:1A:1936:A:C2	1:1A:1945:G:C6	3.07	0.43
1:1A:2252:G:O6	22:10:4:LYS:HD2	2.18	0.43
63:1A:4776:HOH:O	5:1F:74:ARG:HG3	2.17	0.43
2:1B:95:C:H2'	2:1B:96:U:C6	2.53	0.43
6:1G:120:LEU:N	6:1G:179:PRO:O	2.46	0.43
7:1H:26:VAL:HG12	7:1H:79:VAL:HG21	2.01	0.43
18:1W:12:ILE:O	18:1W:101:SER:OG	2.34	0.43
21:1Z:31:ARG:HB3	21:1Z:31:ARG:HH11	1.84	0.43
29:17:12:ARG:CZ	29:17:44:PRO:HB3	2.49	0.43
32:1a:938:A:C6	32:1a:939:G:C5	3.06	0.43
32:1a:1277:C:O2'	32:1a:1279:A:H8	2.01	0.43
32:1a:1355:G:H2'	32:1a:1356:G:H8	1.84	0.43
35:1d:74:GLN:O	35:1d:78:LEU:HG	2.18	0.43
42:1k:99:GLN:H	42:1k:99:GLN:HG3	1.50	0.43
46:1o:18:PHE:CE2	46:1o:21:ASP:HB2	2.53	0.43
1:2A:29:U:H2'	1:2A:30:G:C8	2.54	0.43
1:2A:117:G:OP2	1:2A:119:A:O2'	2.28	0.43
1:2A:179:G:C6	1:2A:180:G:C5	3.07	0.43
1:2A:375:C:H2'	1:2A:376:C:C6	2.53	0.43
1:2A:728:G:H1'	3:2D:10:THR:HG21	2.00	0.43
1:2A:1147:C:C2'	1:2A:1148:A:H5'	2.48	0.43
1:2A:2393:A:H2'	1:2A:2394:C:O4'	2.18	0.43
1:2A:2424:C:O2	1:2A:2429:G:O2'	2.19	0.43
2:2B:43:C:O2	6:2G:95:ARG:NH2	2.50	0.43
10:2O:90:GLN:HB3	10:2O:92:GLU:HG3	2.00	0.43
19:2X:94:GLY:CA	19:2X:95:LEU:HB2	2.49	0.43
32:2a:89:C:H2'	32:2a:90:U:O4'	2.18	0.43
32:2a:1207:2MG:C2'	32:2a:1208:C:H5'	2.49	0.43
36:2e:63:ARG:HA	36:2e:66:MET:HE1	2.00	0.43
40:2i:19:LEU:HD12	40:2i:84:ALA:HB3	2.01	0.43
54:2w:23:A:H3'	54:2w:24:G:H8	1.84	0.43
1:1A:359:A:H2'	1:1A:360:G:O4'	2.18	0.43
1:1A:690:G:H2'	1:1A:691:C:C6	2.54	0.43
1:1A:957:A:N1	1:1A:2458:G:H4'	2.34	0.43
1:1A:2431:U:OP2	63:1A:4174:HOH:O	2.21	0.43
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.54	0.43
6:1G:73:ALA:HB3	6:1G:85:GLY:H	1.83	0.43
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.19	0.43
12:1Q:84:GLY:O	12:1Q:85:LYS:HB2	2.17	0.43
22:10:82:ARG:HE	22:10:82:ARG:HB2	1.63	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:37:PHE:O	24:12:41:ILE:HG12	2.18	0.43
32:1a:390:C:H2'	32:1a:391:G:C8	2.54	0.43
32:1a:516:PSU:O2'	32:1a:519:C:N3	2.46	0.43
32:1a:1201:A:H4'	32:1a:1202:G:O5'	2.19	0.43
32:1a:1426:C:H2'	32:1a:1427:U:C6	2.54	0.43
35:1d:138:TYR:C	35:1d:138:TYR:CD2	2.97	0.43
37:1f:44:GLY:HA2	37:1f:59:TYR:CZ	2.54	0.43
41:1j:85:LEU:HD23	41:1j:85:LEU:HA	1.83	0.43
57:1y:40:C:H2'	57:1y:41:A:O4'	2.18	0.43
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.53	0.43
1:2A:1714:G:H2'	1:2A:1717:G:C8	2.52	0.43
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.18	0.43
1:2A:2572:A:OP1	1:2A:2574:G:O2'	2.34	0.43
5:2F:24:LEU:HD21	5:2F:114:VAL:HG23	2.00	0.43
6:2G:5:VAL:HG11	6:2G:101:ILE:HD13	1.99	0.43
14:2S:10:ARG:NH2	14:2S:91:PRO:O	2.52	0.43
19:2X:90:GLU:C	19:2X:92:LEU:H	2.27	0.43
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.33	0.43
32:2a:404:U:OP1	35:2d:118:ARG:NH2	2.48	0.43
32:2a:874:G:H2'	32:2a:875:C:C6	2.54	0.43
32:2a:957:U:O2'	32:2a:959:A:N7	2.39	0.43
32:2a:1002:G:N3	32:2a:1003:G:H1'	2.34	0.43
32:2a:1229:A:O3'	55:2x:30:G:H5"	2.18	0.43
32:2a:1367:C:H5'	41:2j:60:ARG:NH1	2.33	0.43
32:2a:1502:A:C8	32:2a:1505:G:N2	2.87	0.43
34:2c:86:VAL:O	34:2c:89:GLU:HB3	2.19	0.43
57:2y:52:G:H1	57:2y:62:C:N4	2.15	0.43
1:1A:228:A:H2'	1:1A:230:U:H1'	2.01	0.43
1:1A:252:G:OP1	11:1P:50:ARG:NH1	2.42	0.43
1:1A:828:U:H4'	1:1A:831:G:N1	2.33	0.43
1:1A:1041:C:N4	1:1A:1114:G:H1	2.08	0.43
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.19	0.43
1:1A:2712:U:OP1	1:1A:2714:G:H4'	2.18	0.43
4:1E:98:PRO:HA	4:1E:172:VAL:HG12	2.01	0.43
10:1O:12:ASP:OD1	10:1O:14:THR:OG1	2.36	0.43
14:1S:71:ARG:O	14:1S:75:GLU:N	2.41	0.43
32:1a:253:U:H2'	32:1a:254:G:H8	1.84	0.43
32:1a:510:A:OP2	35:1d:49:ARG:NH1	2.52	0.43
32:1a:1068:G:N2	32:1a:1191:A:N3	2.48	0.43
41:1j:35:SER:HB3	41:1j:73:ASP:CB	2.47	0.43
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1035:U:H2'	1:2A:1036:G:H8	1.83	0.43
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.19	0.43
1:2A:2109:U:C2'	1:2A:2110:G:H5'	2.49	0.43
1:2A:2134:A:H2'	1:2A:2134:A:N3	2.33	0.43
1:2A:2224:G:H4'	1:2A:2226:C:C2	2.53	0.43
1:2A:2306:C:N4	6:2G:42:GLY:O	2.51	0.43
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.53	0.43
1:2A:2571:C:H5"	1:2A:2572:A:H5"	2.01	0.43
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.19	0.43
7:2H:51:ARG:NH1	7:2H:51:ARG:HB3	2.33	0.43
17:2V:37:VAL:HG22	17:2V:57:VAL:HG23	2.00	0.43
18:2W:13:SER:O	18:2W:17:VAL:HG23	2.18	0.43
21:2Z:10:ARG:NE	21:2Z:37:VAL:O	2.52	0.43
32:2a:583:A:H2'	32:2a:584:G:O4'	2.18	0.43
32:2a:691:G:H2'	32:2a:692:U:C6	2.53	0.43
32:2a:1027:C:N3	32:2a:1035:A:H1'	2.33	0.43
32:2a:1499:A:H8	32:2a:1519:MA6:H2	1.84	0.43
47:2p:26:ARG:HG3	47:2p:27:LYS:N	2.33	0.43
55:2x:43:A:H2'	55:2x:44:A:C8	2.54	0.43
1:1A:783:A:N3	1:1A:783:A:H2'	2.34	0.43
1:1A:1173:G:OP2	1:1A:1173:G:H2'	2.18	0.43
1:1A:2144:U:H3'	1:1A:2146:C:N4	2.31	0.43
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.54	0.43
3:1D:72:LYS:HD3	3:1D:97:TYR:CE1	2.53	0.43
3:1D:133:LEU:N	3:1D:189:CYS:O	2.45	0.43
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.29	0.43
18:1W:1:MET:HE3	18:1W:2:GLU:O	2.17	0.43
32:1a:185:A:O2'	51:1t:81:LYS:NZ	2.51	0.43
32:1a:964:A:O2'	41:1j:55:LYS:HD3	2.18	0.43
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.53	0.43
32:1a:1461:G:H2'	32:1a:1462:G:C8	2.54	0.43
34:1c:63:ASN:OD1	34:1c:63:ASN:N	2.51	0.43
34:1c:134:ILE:O	34:1c:138:VAL:HG23	2.19	0.43
34:1c:134:ILE:HG23	34:1c:151:VAL:HB	2.01	0.43
38:1g:98:SER:HA	38:1g:101:LEU:HD12	2.01	0.43
40:1i:9:ARG:H	40:1i:79:LEU:HD23	1.84	0.43
51:1t:11:SER:O	51:1t:11:SER:OG	2.33	0.43
52:1u:5:ASP:C	52:1u:7:ARG:H	2.25	0.43
1:2A:143:G:H2'	1:2A:143(A):C:H6	1.83	0.43
1:2A:154(A):C:H42	1:2A:171:G:H1	1.65	0.43
1:2A:271(F):C:H2'	1:2A:271(G):C:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:686:G:H21	1:2A:788:A:H61	1.66	0.43
1:2A:852:G:C6	1:2A:853:G:C6	3.06	0.43
1:2A:856:C:O2'	1:2A:857:C:OP1	2.34	0.43
1:2A:869:G:C2	1:2A:909:A:C2	3.07	0.43
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.84	0.43
1:2A:2143:C:H2'	1:2A:2144:U:O4'	2.18	0.43
1:2A:2885:C:O2'	27:25:34:PRO:HG3	2.19	0.43
3:2D:171:ASP:O	3:2D:187:GLY:N	2.46	0.43
4:2E:179:GLU:HG3	15:2T:9:LEU:CD2	2.49	0.43
8:2I:93:THR:HG22	8:2I:94:ALA:H	1.83	0.43
8:2I:104:GLN:HB3	8:2I:105:HIS:ND1	2.34	0.43
11:2P:139:LYS:C	11:2P:141:ALA:H	2.26	0.43
12:2Q:54:MET:HE3	12:2Q:64:ILE:HG23	1.99	0.43
32:2a:109:A:C6	32:2a:326:G:C6	3.06	0.43
32:2a:352:C:H4'	32:2a:354:G:OP1	2.19	0.43
32:2a:642:A:N3	39:2h:113:SER:OG	2.50	0.43
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.23	0.43
32:2a:1347:G:H22	32:2a:1374:A:P	2.42	0.43
33:2b:95:GLN:HG3	33:2b:147:LYS:HG2	2.00	0.43
41:2j:7:LYS:HG3	41:2j:70:ARG:O	2.19	0.43
47:2p:28:ARG:HG2	47:2p:28:ARG:HH11	1.83	0.43
1:1A:843:G:H1	1:1A:935:C:H42	1.66	0.43
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.19	0.43
1:1A:2138:C:N3	1:1A:2154:G:N1	2.67	0.43
1:1A:2292:C:H42	1:1A:2340:G:H1	1.66	0.43
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.19	0.43
1:1A:2732:G:H3'	1:1A:2733:A:O4'	2.19	0.43
11:1P:64:LYS:O	30:18:30:ARG:NH2	2.52	0.43
13:1R:86:ARG:NH2	13:1R:117:VAL:O	2.52	0.43
23:11:70:VAL:O	23:11:73:LEU:HB2	2.19	0.43
32:1a:998:G:C6	32:1a:1044:A:C6	3.07	0.43
32:1a:1108:G:O6	63:1a:1911:HOH:O	2.16	0.43
32:1a:1288:A:N1	32:1a:1371:G:H1'	2.34	0.43
35:1d:161:ASN:O	35:1d:165:MET:HG2	2.19	0.43
41:1j:46:ARG:HB2	41:1j:46:ARG:NH1	2.34	0.43
48:1q:27:PHE:CZ	48:1q:36:ILE:HD11	2.54	0.43
54:1w:63:U:H2'	54:1w:64:G:C8	2.54	0.43
1:2A:686:G:H8	29:27:6:GLN:O	2.01	0.43
1:2A:1028:A:N3	1:2A:2486:G:O2'	2.46	0.43
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.54	0.43
1:2A:1503:U:H2'	1:2A:1504:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1688:U:H2'	1:2A:1698:A:N6	2.34	0.43
1:2A:2062:A:C2	56:2z:1:FME:HA	2.54	0.43
1:2A:2070:G:H2'	1:2A:2071:A:H8	1.81	0.43
2:2B:58:A:H3'	2:2B:59:A:H8	1.83	0.43
7:2H:51:ARG:NH2	7:2H:53:GLU:OE2	2.49	0.43
21:2Z:61:LEU:HB2	21:2Z:65:GLN:HB2	2.00	0.43
32:2a:551:U:H2'	32:2a:552:U:C6	2.54	0.43
32:2a:657:G:O2'	46:2o:28:GLN:HG2	2.19	0.43
32:2a:1077:G:H5'	32:2a:1078:U:OP2	2.18	0.43
32:2a:1255:G:P	41:2j:45:ARG:HH22	2.42	0.43
32:2a:1347:G:N1	32:2a:1374:A:OP2	2.38	0.43
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.54	0.43
36:2e:13:ILE:HA	36:2e:29:GLY:O	2.18	0.43
38:2g:52:GLU:H	38:2g:52:GLU:HG2	1.48	0.43
38:2g:69:VAL:HG21	38:2g:104:LEU:HD21	2.01	0.43
40:2i:85:LEU:HA	40:2i:88:TYR:HB3	2.00	0.43
47:2p:1:MET:O	47:2p:24:ALA:N	2.35	0.43
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.19	0.43
1:1A:851:U:O2'	25:13:42:ALA:O	2.37	0.43
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.18	0.43
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.19	0.43
7:1H:41:MET:HE3	7:1H:64:LEU:HB2	2.00	0.43
21:1Z:52:SER:O	21:1Z:53:ILE:HG12	2.19	0.43
21:1Z:59:LEU:HD11	21:1Z:88:PHE:CG	2.54	0.43
21:1Z:155:LEU:HD23	21:1Z:155:LEU:HA	1.86	0.43
30:18:52:LYS:N	30:18:53:PRO:HD2	2.34	0.43
32:1a:456:C:C2'	32:1a:457:C:H5'	2.49	0.43
32:1a:575:G:O2'	32:1a:821:G:H5'	2.19	0.43
33:1b:78:GLN:O	33:1b:81:VAL:HG12	2.19	0.43
38:1g:78:ARG:HG3	38:1g:79:ARG:H	1.84	0.43
39:1h:87:SER:HB2	39:1h:93:VAL:H	1.83	0.43
43:1l:7:ILE:O	43:1l:11:VAL:HG23	2.19	0.43
46:1o:36:ILE:HG23	46:1o:56:LEU:HD11	2.01	0.43
54:1w:5:C:H2'	54:1w:6:G:H8	1.83	0.43
1:2A:300:A:OP2	20:2Y:86:ARG:NH1	2.52	0.43
1:2A:783:A:OP2	63:2A:3966:HOH:O	2.22	0.43
1:2A:1498:C:O4'	1:2A:1577:C:H4'	2.19	0.43
1:2A:1833:U:H2'	1:2A:1834:U:C6	2.54	0.43
1:2A:2113:U:H3	1:2A:2169:A:H62	1.66	0.43
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.80	0.43
7:2H:30:LYS:HB2	7:2H:79:VAL:C	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:4:ILE:HA	8:2I:17:GLN:O	2.19	0.43
14:2S:68:GLN:O	14:2S:72:ALA:N	2.48	0.43
28:26:32:ASN:OD1	28:26:32:ASN:N	2.52	0.43
29:27:12:ARG:CZ	29:27:44:PRO:HB3	2.49	0.43
32:2a:103:C:O2'	32:2a:172:A:N1	2.38	0.43
33:2b:28:PHE:CD2	33:2b:190:THR:HA	2.54	0.43
33:2b:37:ASN:C	33:2b:39:ILE:H	2.25	0.43
38:2g:115:ARG:HH11	38:2g:118:VAL:HG21	1.82	0.43
39:2h:98:LYS:HE2	39:2h:98:LYS:HB2	1.85	0.43
42:2k:84:VAL:HG11	42:2k:91:ARG:HD2	2.01	0.43
44:2m:3:ARG:NH2	44:2m:11:ARG:HE	2.16	0.43
45:2n:32:SER:O	45:2n:40:CYS:HA	2.18	0.43
50:2s:42:PRO:O	50:2s:45:VAL:HG12	2.19	0.43
1:1A:1967:C:H2'	1:1A:1968:G:H5'	2.01	0.42
6:1G:47:LYS:O	6:1G:86:MET:HE2	2.18	0.42
14:1S:36:TYR:HD1	14:1S:52:SER:HB3	1.84	0.42
21:1Z:157:LEU:HD13	21:1Z:161:VAL:HG23	2.01	0.42
23:11:67:ILE:N	23:11:68:PRO:HD2	2.33	0.42
25:13:10:LYS:NZ	25:13:15:TYR:OH	2.38	0.42
32:1a:749:C:H2'	32:1a:750:G:H8	1.84	0.42
32:1a:1198:G:O2'	41:1j:55:LYS:NZ	2.50	0.42
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.53	0.42
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.19	0.42
32:1a:1376:U:OP1	38:1g:98:SER:HB3	2.18	0.42
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	2.00	0.42
40:1i:99:LEU:HD12	40:1i:101:PHE:CE2	2.54	0.42
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.36	0.42
50:1s:52:TYR:HA	50:1s:56:GLN:O	2.19	0.42
1:2A:81:G:N7	63:2A:4051:HOH:O	2.37	0.42
1:2A:582:G:H2'	1:2A:583:G:H8	1.83	0.42
1:2A:634:C:H2'	1:2A:635:C:C6	2.54	0.42
1:2A:1330:C:OP1	63:2A:3960:HOH:O	2.20	0.42
1:2A:1423:G:H2'	1:2A:1424:G:C8	2.53	0.42
1:2A:1913:A:C8	32:2a:1494:G:H4'	2.54	0.42
1:2A:1923:U:O2'	55:2x:12:G:N3	2.52	0.42
6:2G:37:VAL:CG1	6:2G:99:MET:HB2	2.49	0.42
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.43	0.42
7:2H:121:ILE:HD13	7:2H:121:ILE:HA	1.87	0.42
7:2H:127:GLU:H	7:2H:127:GLU:HG2	1.77	0.42
12:2Q:30:GLY:O	12:2Q:134:ARG:HD3	2.19	0.42
26:24:22:ILE:HG22	26:24:24:THR:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:266:G:H5”	32:2a:268:C:H41	1.84	0.42
32:2a:1004:A:N1	32:2a:1037:C:H1’	2.34	0.42
32:2a:1018:C:H2’	32:2a:1019:C:O4’	2.18	0.42
32:2a:1079:G:H5’	36:2e:45:PHE:HE2	1.83	0.42
33:2b:16:HIS:ND1	33:2b:204:ASN:HB2	2.34	0.42
33:2b:83:MET:HE3	33:2b:83:MET:HB2	1.93	0.42
38:2g:23:VAL:HG13	38:2g:43:PHE:CE2	2.54	0.42
57:2y:67:C:H2’	57:2y:68:G:C8	2.54	0.42
1:1A:55:G:O2’	1:1A:127:A:N1	2.51	0.42
1:1A:228:A:H3’	1:1A:228:A:C8	2.54	0.42
1:1A:278:A:P	1:1A:278:A:H8	2.42	0.42
1:1A:469:G:O6	29:17:37:LYS:NZ	2.48	0.42
1:1A:727:A:OP1	1:1A:1431:U:O2’	2.35	0.42
1:1A:2243:U:H2’	1:1A:2244:U:C6	2.55	0.42
1:1A:2259:G:C8	1:1A:2427:C:C4	3.07	0.42
1:1A:2286:A:H4’	1:1A:2287:A:O4’	2.19	0.42
1:1A:2397:G:C6	1:1A:2398:U:C4	3.07	0.42
6:1G:64:THR:HB	6:1G:94:LEU:HD21	2.00	0.42
10:1O:111:PHE:HB3	10:1O:114:ILE:HG13	2.00	0.42
16:1U:110:VAL:O	16:1U:114:LYS:HG3	2.19	0.42
19:1X:60:ARG:HE	19:1X:60:ARG:HB3	1.60	0.42
21:1Z:21:ALA:O	21:1Z:23:LYS:NZ	2.51	0.42
32:1a:40:C:H2’	32:1a:41:G:C8	2.54	0.42
32:1a:911:U:H2’	32:1a:912:C:C6	2.54	0.42
32:1a:1039:C:H2’	32:1a:1040:U:H6	1.81	0.42
46:1o:71:GLN:HA	46:1o:78:TYR:HB2	2.01	0.42
51:1t:10:LEU:HD22	51:1t:10:LEU:HA	1.85	0.42
1:2A:537:C:H2’	1:2A:538:G:H8	1.84	0.42
1:2A:1015:G:H2’	1:2A:1016:G:C8	2.52	0.42
1:2A:1035:U:H5”	7:2H:59:ARG:HD3	2.01	0.42
1:2A:1183:G:H5”	25:23:30:ARG:NH1	2.34	0.42
1:2A:2356:C:P	22:20:24:LYS:HZ2	2.39	0.42
1:2A:2619:C:OP1	4:2E:152:LYS:HE3	2.19	0.42
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.18	0.42
12:2Q:41:TRP:HB3	12:2Q:94:VAL:HB	2.00	0.42
14:2S:80:LEU:HD23	14:2S:80:LEU:HA	1.80	0.42
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.19	0.42
21:2Z:73:GLN:H	21:2Z:87:ASP:HB2	1.84	0.42
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.53	0.42
32:2a:189(B):C:H2’	32:2a:189(C):C:C6	2.54	0.42
32:2a:414:A:H2’	32:2a:415:A:O4’	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:654:G:H2'	32:2a:655:A:O4'	2.19	0.42
32:2a:1004:A:H8	32:2a:1025:U:O4	2.02	0.42
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	2.01	0.42
43:2l:41:ARG:HH12	43:2l:57:LYS:NZ	2.17	0.42
54:2w:14:A:C4	54:2w:22:G:C2	3.07	0.42
54:2w:55:PSU:O2'	54:2w:57:G:N7	2.50	0.42
1:1A:123:G:H2'	1:1A:124:G:O4'	2.19	0.42
1:1A:569:U:C4	1:1A:570:G:C6	3.08	0.42
1:1A:1504:C:H2'	1:1A:1505:C:C6	2.54	0.42
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.19	0.42
3:1D:96:HIS:CD2	3:1D:102:LYS:HG2	2.55	0.42
4:1E:37:ARG:HA	4:1E:42:ASP:OD2	2.19	0.42
6:1G:100:TRP:O	6:1G:104:GLU:N	2.48	0.42
12:1Q:18:LYS:HE3	12:1Q:18:LYS:HB2	1.83	0.42
15:1T:11:GLU:HG2	15:1T:57:PHE:CD2	2.54	0.42
23:11:3:LYS:HB3	23:11:4:VAL:H	1.51	0.42
26:14:7:PRO:HB2	26:14:27:THR:HG21	2.01	0.42
32:1a:502:G:H2'	32:1a:503:C:O4'	2.20	0.42
32:1a:692:U:H1'	32:1a:695:A:N7	2.34	0.42
36:1e:34:VAL:O	36:1e:41:VAL:HA	2.19	0.42
1:2A:524:U:H2'	1:2A:525:U:C6	2.54	0.42
1:2A:1003:G:N2	1:2A:1153:C:C2	2.87	0.42
1:2A:2556:C:H2'	1:2A:2557:G:O4'	2.18	0.42
6:2G:66:GLN:OE1	6:2G:98:ARG:NE	2.52	0.42
6:2G:179:PRO:HG3	26:24:43:TYR:CE2	2.54	0.42
11:2P:2:LYS:HD3	11:2P:4:SER:N	2.32	0.42
13:2R:8:ARG:O	13:2R:17:ARG:HD2	2.20	0.42
25:23:8:LEU:O	25:23:32:GLN:N	2.33	0.42
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.34	0.42
32:2a:157:G:H1	32:2a:164:U:H3	1.66	0.42
32:2a:413:G:H21	32:2a:428:G:H1'	1.83	0.42
32:2a:519:C:H2'	32:2a:520:A:O4'	2.19	0.42
32:2a:819:A:H4'	32:2a:820:U:OP2	2.19	0.42
32:2a:946:A:H2'	32:2a:947:G:C8	2.54	0.42
32:2a:1217:C:H2'	32:2a:1218:C:O4'	2.20	0.42
34:2c:16:ARG:HD2	34:2c:16:ARG:HA	1.85	0.42
36:2e:10:MET:H	36:2e:10:MET:HG2	1.42	0.42
36:2e:62:ALA:C	36:2e:64:ARG:H	2.27	0.42
38:2g:113:GLU:HG3	38:2g:119:ARG:HG2	2.01	0.42
41:2j:6:ILE:HB	41:2j:72:VAL:O	2.18	0.42
43:2l:97:ARG:HB2	43:2l:98:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2o:87:ILE:O	46:2o:88:ARG:HB3	2.19	0.42
50:2s:71:LEU:HD23	50:2s:71:LEU:HA	1.89	0.42
1:1A:239:U:H2'	1:1A:240:G:O4'	2.19	0.42
1:1A:527:C:OP1	63:1A:4175:HOH:O	2.21	0.42
1:1A:729:G:C5	3:1D:208:LYS:HB2	2.53	0.42
1:1A:776:G:N2	1:1A:2241:A:OP1	2.51	0.42
1:1A:897:C:H2'	1:1A:898:C:C6	2.54	0.42
1:1A:1568:G:H4'	3:1D:59:LYS:HG2	2.00	0.42
1:1A:2105:C:H2'	1:1A:2106:G:C8	2.55	0.42
1:1A:2516:G:C6	1:1A:2517:C:C4	3.07	0.42
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.54	0.42
3:1D:168:ARG:HA	3:1D:173:VAL:HA	2.01	0.42
6:1G:23:PHE:CZ	6:1G:168:GLU:HA	2.55	0.42
10:1O:48:PRO:CB	32:1a:1422:G:H5"	2.49	0.42
22:10:53:MET:HA	22:10:58:THR:O	2.19	0.42
28:16:17:LYS:HE3	28:16:17:LYS:HB3	1.89	0.42
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.20	0.42
44:1m:67:GLU:O	44:1m:71:ARG:HB2	2.20	0.42
51:1t:43:LEU:HD22	51:1t:48:LYS:HD2	2.02	0.42
1:2A:62:C:H42	1:2A:93:G:H1	1.67	0.42
1:2A:287:C:H2'	1:2A:288:C:H6	1.83	0.42
1:2A:901:A:H2'	1:2A:902:C:O4'	2.20	0.42
1:2A:966:G:C6	1:2A:967:C:C4	3.07	0.42
1:2A:1364:G:N7	23:21:3:LYS:HD2	2.34	0.42
1:2A:2059:A:N1	60:2A:3826:TEL:H573	2.33	0.42
1:2A:2106:G:H2'	1:2A:2107:C:O4'	2.18	0.42
1:2A:2122:U:H3	1:2A:2176:A:N6	2.17	0.42
1:2A:2133:G:C2	1:2A:2157:G:C6	3.07	0.42
1:2A:2625:G:H2'	1:2A:2626:C:O4'	2.19	0.42
1:2A:2637:U:C4	1:2A:2638:G:C6	3.07	0.42
2:2B:43:C:H2'	2:2B:45:A:N7	2.34	0.42
3:2D:2:ALA:N	3:2D:200:ASP:OD2	2.52	0.42
3:2D:145:VAL:HG13	3:2D:191:ALA:HB2	2.02	0.42
5:2F:139:PHE:CD1	5:2F:167:ALA:HB2	2.54	0.42
7:2H:3:ARG:NH2	7:2H:5:GLY:H	2.17	0.42
11:2P:84:ASN:OD1	11:2P:117:GLU:N	2.39	0.42
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.34	0.42
32:2a:1040:U:H2'	32:2a:1041:A:C8	2.54	0.42
32:2a:1074:G:H4'	33:2b:103:THR:O	2.19	0.42
32:2a:1457:G:H5"	51:2t:35:THR:HG21	2.00	0.42
34:2c:33:LEU:HD22	45:2n:37:PHE:HD1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:111:LEU:HD23	34:2c:141:VAL:HG13	2.02	0.42
39:2h:20:TYR:HD1	39:2h:65:TYR:CD1	2.38	0.42
43:2l:79:GLU:HG2	43:2l:80:HIS:ND1	2.34	0.42
51:2t:54:LYS:HA	51:2t:57:ARG:CZ	2.49	0.42
54:2w:18:G:H4'	54:2w:60:U:C4	2.55	0.42
1:1A:1789:A:H5"	3:1D:220:HIS:O	2.19	0.42
3:1D:34:VAL:HG12	3:1D:63:ARG:HG3	2.02	0.42
5:1F:64:ILE:HD12	5:1F:65:TRP:CZ3	2.54	0.42
15:1T:73:GLU:OE2	15:1T:103:ARG:NE	2.52	0.42
18:1W:65:LEU:HD23	18:1W:65:LEU:HA	1.80	0.42
21:1Z:150:LEU:O	21:1Z:171:ILE:HG12	2.18	0.42
28:16:11:LEU:HD23	28:16:11:LEU:HA	1.90	0.42
32:1a:190:U:H2'	32:1a:191:G:C8	2.45	0.42
32:1a:424:G:H2'	32:1a:425:G:H8	1.84	0.42
32:1a:648:A:H2'	32:1a:649:G:H8	1.85	0.42
32:1a:1223:C:OP2	50:1s:78:ARG:NH2	2.52	0.42
38:1g:113:GLU:N	38:1g:113:GLU:OE2	2.53	0.42
47:1p:74:LEU:HG	47:1p:79:VAL:HG21	2.01	0.42
54:1w:18:G:N2	54:1w:57:G:H2'	2.35	0.42
1:2A:79:G:H2'	1:2A:80:G:H8	1.85	0.42
1:2A:196:A:O2'	1:2A:805:G:O6	2.37	0.42
1:2A:262:A:H2'	1:2A:263:C:O4'	2.20	0.42
1:2A:302:C:P	20:2Y:73:ARG:HH12	2.41	0.42
1:2A:863:A:H2'	1:2A:864:G:C8	2.54	0.42
1:2A:1213:A:H2'	1:2A:1214:A:C8	2.55	0.42
1:2A:1617:C:OP2	63:2A:3967:HOH:O	2.22	0.42
1:2A:2557:G:H2'	1:2A:2558:C:H6	1.83	0.42
1:2A:2762:G:H2'	1:2A:2763:G:O4'	2.19	0.42
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.55	0.42
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	2.00	0.42
5:2F:65:TRP:CZ2	5:2F:75:HIS:HD2	2.37	0.42
14:2S:19:LYS:O	14:2S:21:THR:N	2.52	0.42
19:2X:92:LEU:HD23	19:2X:92:LEU:HA	1.75	0.42
32:2a:135:C:O2	47:2p:1:MET:HB3	2.20	0.42
32:2a:427:U:H3'	32:2a:428:G:H2'	2.01	0.42
32:2a:673:G:O3'	37:2f:87:ARG:NH2	2.52	0.42
32:2a:747:C:H5"	32:2a:748:C:OP2	2.18	0.42
33:2b:158:LEU:HD23	33:2b:182:ILE:HD11	2.01	0.42
34:2c:67:THR:HG23	34:2c:102:ASN:HB3	2.02	0.42
34:2c:195:VAL:C	34:2c:196:LEU:HD23	2.44	0.42
35:2d:57:ARG:HD3	35:2d:202:LEU:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.18	0.42
36:2e:136:MET:O	36:2e:140:ARG:HG3	2.20	0.42
40:2i:16:ARG:HH21	40:2i:18:PHE:HZ	1.67	0.42
41:2j:42:THR:HG23	41:2j:68:HIS:HA	2.02	0.42
43:2l:47:LYS:HA	43:2l:48:PRO:HA	1.76	0.42
44:2m:120:LYS:NZ	54:2w:41:A:H5'	2.34	0.42
45:2n:16:PHE:HD2	45:2n:19:ARG:HD2	1.85	0.42
1:1A:782:A:H1'	63:1A:5044:HOH:O	2.20	0.42
1:1A:1908:C:O2	55:1x:12:G:H4'	2.19	0.42
1:1A:2422:A:O4'	57:1y:76:A:N6	2.52	0.42
1:1A:2492:U:H2'	1:1A:2493:U:H6	1.85	0.42
1:1A:2641:G:OP1	9:1N:83:LYS:HD3	2.20	0.42
5:1F:170:LEU:HD13	5:1F:172:TRP:CZ2	2.55	0.42
6:1G:60:LEU:HD12	6:1G:60:LEU:HA	1.88	0.42
8:1I:38:LEU:O	8:1I:40:THR:HG23	2.20	0.42
9:1N:120:LEU:HG	9:1N:122:VAL:HG23	2.00	0.42
11:1P:28:GLY:O	11:1P:30:THR:N	2.53	0.42
32:1a:192:U:H2'	32:1a:193:C:H6	1.84	0.42
32:1a:530:G:O6	53:1v:21:A:H1'	2.18	0.42
32:1a:665:A:H2'	32:1a:732:C:O2	2.19	0.42
32:1a:744:C:O2'	32:1a:851:G:N2	2.52	0.42
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.19	0.42
32:1a:1349:A:C2	32:1a:1374:A:C4	3.08	0.42
35:1d:173:TRP:CD1	35:1d:173:TRP:N	2.87	0.42
36:1e:74:GLY:C	36:1e:116:THR:HG22	2.45	0.42
47:1p:15:PRO:O	47:1p:16:HIS:ND1	2.52	0.42
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	2.02	0.42
56:1z:1:FME:C	56:1z:3:CYS:H	2.33	0.42
1:2A:932:G:H4'	1:2A:933:A:O5'	2.20	0.42
1:2A:1179:C:H2'	1:2A:1180:C:C6	2.54	0.42
1:2A:1246:A:OP1	5:2F:38:ARG:NH2	2.33	0.42
1:2A:1512:U:H2'	1:2A:1513:C:H6	1.84	0.42
1:2A:1790:C:H5"	1:2A:1791:A:OP1	2.20	0.42
1:2A:2118:U:H5	1:2A:2148:G:N3	2.18	0.42
2:2B:80:U:H2'	2:2B:81:G:C8	2.55	0.42
5:2F:164:ARG:HD2	5:2F:176:LEU:O	2.20	0.42
6:2G:114:ILE:HB	6:2G:117:PHE:HD1	1.85	0.42
6:2G:150:ASP:CG	6:2G:151:ALA:H	2.27	0.42
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.55	0.42
20:2Y:2:ARG:HH12	20:2Y:4:LYS:HD3	1.83	0.42
21:2Z:91:LEU:HB3	21:2Z:130:PRO:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:20:53:MET:HG3	22:20:59:LEU:HD23	2.00	0.42
32:2a:509:A:H4'	32:2a:510:A:OP1	2.19	0.42
32:2a:953:G:H5'	32:2a:965:A:N6	2.27	0.42
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.19	0.42
40:2i:75:ASP:HA	40:2i:78:LYS:HB3	2.00	0.42
57:2y:11:C:H2'	57:2y:12:U:C6	2.54	0.42
1:1A:876:C:H2'	1:1A:877:U:H6	1.84	0.42
1:1A:1697:G:OP2	1:1A:1698:A:O2'	2.20	0.42
1:1A:1844:C:H2'	1:1A:1845:G:H8	1.84	0.42
1:1A:2095:C:H2'	1:1A:2096:U:O4'	2.19	0.42
1:1A:2127:G:H2'	1:1A:2128:C:C6	2.55	0.42
2:1B:57:A:H1'	6:1G:29:TRP:HB2	2.02	0.42
6:1G:105:LYS:NZ	26:14:25:TYR:O	2.34	0.42
11:1P:2:LYS:HG2	11:1P:3:LEU:N	2.35	0.42
11:1P:83:VAL:O	11:1P:114:ILE:HA	2.20	0.42
26:14:49:PHE:HB3	26:14:50:VAL:H	1.49	0.42
32:1a:1151:A:O2'	32:1a:1152:A:O5'	2.36	0.42
33:1b:76:GLN:HB3	33:1b:208:ILE:HG22	2.01	0.42
35:1d:3:ARG:HD3	35:1d:118:ARG:NH1	2.35	0.42
36:1e:90:VAL:O	36:1e:120:THR:HA	2.20	0.42
40:1i:10:ARG:O	40:1i:11:LYS:C	2.63	0.42
44:1m:25:ILE:HD11	44:1m:60:VAL:HG13	2.02	0.42
44:1m:51:ALA:HA	44:1m:54:VAL:HG22	2.01	0.42
54:1w:10:G:O6	54:1w:25:C:N3	2.53	0.42
57:1y:19:G:P	57:1y:60:U:H3	2.42	0.42
1:2A:807:U:C2	1:2A:808:G:C8	3.07	0.42
1:2A:2166:G:H3'	1:2A:2167:U:H5"	2.00	0.42
1:2A:2784:C:H2'	1:2A:2785:C:H6	1.84	0.42
1:2A:2864:G:OP1	15:2T:119:LYS:HD3	2.19	0.42
5:2F:197:ASP:O	5:2F:201:VAL:HG23	2.19	0.42
6:2G:121:ASN:HB3	6:2G:124:SER:HB2	2.01	0.42
8:2I:48:GLU:HG3	8:2I:52:ARG:HH12	1.84	0.42
12:2Q:78:PRO:HG2	12:2Q:81:VAL:HG11	2.00	0.42
28:26:26:ASN:C	28:26:28:ARG:H	2.27	0.42
30:28:15:LYS:O	30:28:23:VAL:HG12	2.20	0.42
32:2a:790:A:H61	32:2a:1498:UR3:P	2.43	0.42
32:2a:1097:C:H1'	32:2a:1170:A:H1'	2.00	0.42
35:2d:59:ARG:NH1	35:2d:59:ARG:HA	2.34	0.42
35:2d:148:VAL:HB	35:2d:181:MET:HB3	2.02	0.42
36:2e:103:GLY:O	36:2e:106:PRO:HD2	2.20	0.42
36:2e:143:ARG:NE	39:2h:77:GLU:OE2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:110:ARG:HA	44:2m:110:ARG:HD2	1.90	0.42
46:2o:59:MET:HE3	46:2o:59:MET:HB2	1.94	0.42
55:2x:21:A:N6	55:2x:46:G:H2'	2.34	0.42
1:1A:443:A:N6	5:1F:41:LEU:O	2.47	0.42
1:1A:539:G:H2'	1:1A:540:C:C6	2.55	0.42
1:1A:764:A:H5"	3:1D:210:GLY:HA2	2.01	0.42
1:1A:817:C:O2'	1:1A:839:U:H5"	2.19	0.42
1:1A:2145:C:OP2	1:1A:2146:C:N4	2.52	0.42
1:1A:2336:A:H61	22:10:43:THR:CG2	2.33	0.42
1:1A:2784:C:H2'	1:1A:2785:C:H6	1.85	0.42
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.20	0.42
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.55	0.42
9:1N:39:ARG:HH21	9:1N:41:ASP:CG	2.27	0.42
11:1P:112:LEU:O	11:1P:128:HIS:HB2	2.20	0.42
26:14:62:ARG:C	26:14:63:TYR:CG	2.97	0.42
32:1a:6:G:H1	36:1e:98:THR:HG21	1.85	0.42
32:1a:1290:G:C4	32:1a:1291:G:C8	3.08	0.42
34:1c:52:LEU:HD21	34:1c:55:VAL:HG23	2.02	0.42
34:1c:77:ILE:H	34:1c:77:ILE:HG12	1.60	0.42
34:1c:85:ARG:O	34:1c:89:GLU:HB2	2.19	0.42
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.78	0.42
44:1m:108:ARG:HA	44:1m:108:ARG:HD3	1.79	0.42
51:1t:72:LEU:HD23	51:1t:72:LEU:HA	1.88	0.42
54:1w:4:U:H3	54:1w:69:A:H61	1.68	0.42
1:2A:272(G):C:H42	1:2A:363(C):G:H1	1.68	0.42
1:2A:1233:C:H2'	1:2A:1234:U:C6	2.54	0.42
1:2A:2591:C:OP1	3:2D:239:ARG:HB2	2.20	0.42
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.35	0.42
2:2B:16:G:C6	2:2B:69:G:C2	3.08	0.42
13:2R:75:LEU:HD12	13:2R:75:LEU:HA	1.87	0.42
32:2a:656:C:HO2'	46:2o:28:GLN:CD	2.15	0.42
32:2a:707:C:H4'	42:2k:20:TYR:CD2	2.55	0.42
32:2a:859:A:H2'	32:2a:860:A:O4'	2.19	0.42
32:2a:1208:C:H2'	32:2a:1209:C:O4'	2.20	0.42
32:2a:1434:A:H2'	32:2a:1435:G:O4'	2.20	0.42
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.19	0.42
33:2b:41:ILE:HD13	33:2b:41:ILE:HA	1.83	0.42
38:2g:51:GLN:HB2	38:2g:58:PRO:HG3	2.02	0.42
39:2h:103:VAL:HG11	39:2h:109:ILE:C	2.45	0.42
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.54	0.42
43:2l:102:ARG:H	43:2l:102:ARG:HG2	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:58:LEU:HD22	49:2r:62:GLU:HB3	2.02	0.42
1:1A:1232:G:C6	1:1A:1233:C:C4	3.08	0.42
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.55	0.42
3:1D:120:GLY:HA2	3:1D:190:TYR:OH	2.20	0.42
4:1E:117:MET:HE2	4:1E:117:MET:HB3	1.76	0.42
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.37	0.42
8:1I:130:TYR:N	8:1I:138:ILE:O	2.39	0.42
28:16:38:LYS:HB2	28:16:49:HIS:CE1	2.54	0.42
29:17:46:VAL:O	29:17:48:LYS:NZ	2.53	0.42
32:1a:1260:C:O5'	32:1a:1284:C:H4'	2.19	0.42
32:1a:1457:G:H2'	32:1a:1458:G:C8	2.55	0.42
33:1b:83:MET:CB	33:1b:234:PRO:HG3	2.48	0.42
34:1c:138:VAL:HG13	34:1c:149:ALA:HB3	2.01	0.42
36:1e:65:ASN:OD1	36:1e:140:ARG:NH2	2.53	0.42
37:1f:38:GLU:HB2	37:1f:64:GLN:HG2	2.00	0.42
42:1k:51:LYS:HD3	42:1k:51:LYS:HA	1.87	0.42
57:1y:51:A:H2'	57:1y:52:G:C8	2.54	0.42
57:1y:58:A:N6	57:1y:61:C:C2	2.87	0.42
1:2A:471:A:H2'	1:2A:472:A:O4'	2.20	0.42
1:2A:815:C:H2'	1:2A:816:C:C6	2.55	0.42
1:2A:1151:G:H4'	16:2U:81:HIS:ND1	2.35	0.42
1:2A:2347:C:OP1	28:26:38:LYS:NZ	2.50	0.42
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.46	0.42
5:2F:78:ILE:HA	5:2F:83:PHE:CD2	2.55	0.42
7:2H:45:VAL:HA	7:2H:49:VAL:O	2.20	0.42
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.76	0.42
12:2Q:3:MET:HE3	12:2Q:3:MET:HB2	1.90	0.42
19:2X:5:TYR:CD2	24:22:30:ARG:HB3	2.55	0.42
25:23:16:PRO:HB2	25:23:18:ASP:OD1	2.20	0.42
32:2a:662:G:O2'	32:2a:836:G:OP1	2.35	0.42
32:2a:878:G:OP1	39:2h:88:LYS:HB3	2.20	0.42
32:2a:1240:U:H4'	32:2a:1241:G:OP2	2.18	0.42
34:2c:8:ILE:O	34:2c:12:LEU:HG	2.20	0.42
34:2c:12:LEU:HB3	34:2c:18:TRP:CH2	2.55	0.42
34:2c:31:HIS:O	34:2c:35:GLU:HB3	2.20	0.42
34:2c:176:HIS:CD2	34:2c:176:HIS:N	2.87	0.42
37:2f:83:ASP:OD1	37:2f:83:ASP:N	2.52	0.42
46:2o:70:LEU:HD11	46:2o:77:ARG:HB2	2.02	0.42
48:2q:9:VAL:HA	48:2q:55:ASP:O	2.19	0.42
54:2w:51:A:N6	54:2w:63:U:C2	2.83	0.42
1:1A:303:U:H2'	1:1A:304:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:526:A:O2'	1:1A:2043:C:O2	2.32	0.42
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.20	0.42
1:1A:1395:A:N3	63:1A:4301:HOH:O	2.37	0.42
1:1A:2052:G:C8	4:1E:141:ILE:HD11	2.55	0.42
1:1A:2124:G:H1	1:1A:2174:C:N4	2.18	0.42
1:1A:2140:C:H2'	1:1A:2141:G:C8	2.55	0.42
3:1D:230:ASP:OD1	63:1D:401:HOH:O	2.22	0.42
11:1P:119:GLU:OE1	25:23:3:ARG:HD3	2.20	0.42
14:1S:67:ARG:O	14:1S:71:ARG:HG2	2.19	0.42
19:1X:72:LYS:HE3	19:1X:73:ARG:O	2.20	0.42
21:1Z:158:PRO:HD2	21:1Z:161:VAL:HG21	2.01	0.42
24:12:10:LEU:O	24:12:14:ARG:HG3	2.20	0.42
24:12:16:LEU:O	24:12:67:LYS:NZ	2.53	0.42
32:1a:418:C:H1'	32:1a:540:G:O2'	2.19	0.42
32:1a:447:G:H8	32:1a:447:G:O5'	2.03	0.42
32:1a:485:G:O2'	32:1a:486:U:OP2	2.38	0.42
32:1a:722:A:N6	32:1a:724:G:C2	2.88	0.42
32:1a:792:A:H1'	32:1a:794:A:N7	2.35	0.42
32:1a:1120:G:H2'	32:1a:1121:U:H6	1.84	0.42
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.55	0.42
33:1b:172:ILE:HA	33:1b:175:ARG:NH1	2.35	0.42
35:1d:138:TYR:C	35:1d:138:TYR:HD2	2.28	0.42
35:1d:174:LEU:HD23	35:1d:185:PHE:HA	2.02	0.42
1:2A:242:G:H8	30:28:4:MET:O	2.02	0.42
1:2A:918:A:H2	2:2B:81:G:H5'	1.85	0.42
1:2A:964:C:O2'	1:2A:2273:A:N3	2.39	0.42
1:2A:1359:A:C2	1:2A:1372:U:O4	2.73	0.42
1:2A:1790:C:H4'	3:2D:209:ALA:HB2	2.02	0.42
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.50	0.42
1:2A:1913:A:N6	54:2w:38:A:H5'	2.35	0.42
1:2A:2600:A:N6	63:2A:4121:HOH:O	2.53	0.42
2:2B:50:G:P	14:2S:62:LYS:HB2	2.60	0.42
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.48	0.42
3:2D:97:TYR:O	3:2D:100:GLY:N	2.45	0.42
6:2G:120:LEU:HD13	6:2G:120:LEU:HA	1.89	0.42
7:2H:105:LEU:HB2	7:2H:113:VAL:HB	2.00	0.42
8:2I:77:LEU:HB3	8:2I:142:VAL:HG13	2.01	0.42
11:2P:45:LEU:HA	11:2P:45:LEU:HD12	1.81	0.42
16:2U:28:ARG:NH1	16:2U:38:THR:OG1	2.52	0.42
19:2X:11:PRO:CB	19:2X:92:LEU:HD21	2.50	0.42
20:2Y:54:LYS:C	20:2Y:56:PRO:HD3	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:5:LEU:O	21:2Z:59:LEU:HA	2.20	0.42
22:20:28:GLY:HA2	22:20:66:VAL:HG13	2.02	0.42
24:22:41:ILE:H	24:22:41:ILE:HG12	1.69	0.42
31:29:6:SER:O	31:29:6:SER:OG	2.31	0.42
32:2a:227:G:H2'	32:2a:228:A:O4'	2.20	0.42
32:2a:825:G:N2	39:2h:11:THR:HG21	2.35	0.42
32:2a:959:A:H5"	32:2a:960:U:OP2	2.20	0.42
32:2a:1079:G:H2'	32:2a:1080:A:C8	2.55	0.42
32:2a:1209:C:O2'	32:2a:1214:C:N4	2.52	0.42
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.85	0.42
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.34	0.42
32:2a:1378:C:C2	32:2a:1379:G:H1'	2.55	0.42
36:2e:89:ILE:HD12	36:2e:89:ILE:HA	1.88	0.42
36:2e:110:LEU:HD13	36:2e:118:ILE:HG12	2.00	0.42
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.35	0.42
47:2p:53:VAL:HG13	47:2p:79:VAL:HG13	2.02	0.42
48:2q:13:ASP:HB2	58:2q:202:MG:MG	1.45	0.42
54:2w:18:G:HO2'	54:2w:57:G:N2	2.18	0.42
1:1A:10:G:H1'	1:1A:2801(A):A:C2	2.54	0.41
1:1A:827:U:O2	1:1A:2246:G:H4'	2.20	0.41
1:1A:1426:G:O2'	1:1A:1572:A:N6	2.49	0.41
1:1A:2391:G:O6	1:1A:2425:A:H8	2.03	0.41
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.35	0.41
3:1D:9:TYR:CE1	3:1D:13:ARG:HG3	2.55	0.41
7:1H:96:ALA:N	7:1H:128:PRO:O	2.52	0.41
12:1Q:59:ARG:C	12:1Q:61:GLY:H	2.28	0.41
15:1T:55:ASN:ND2	15:1T:55:ASN:O	2.53	0.41
18:1W:6:ILE:HA	18:1W:103:ILE:O	2.20	0.41
21:1Z:48:PHE:HE1	21:1Z:71:VAL:HG11	1.85	0.41
32:1a:411:A:O2'	32:1a:413:G:H5'	2.20	0.41
32:1a:503:C:OP2	43:1l:116:SER:OG	2.31	0.41
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.47	0.41
35:1d:36:ARG:HB2	35:1d:38:TYR:CZ	2.56	0.41
36:1e:91:LEU:HB3	36:1e:118:ILE:HD11	2.01	0.41
38:1g:78:ARG:HA	38:1g:78:ARG:HD2	1.81	0.41
46:1o:82:ILE:HG13	46:1o:83:GLU:N	2.35	0.41
57:1y:6:G:C6	57:1y:7:U:C4	3.08	0.41
1:2A:311:A:C6	1:2A:328:U:C4	3.08	0.41
1:2A:732:C:H2'	1:2A:733:G:O4'	2.20	0.41
1:2A:1324:G:O2'	1:2A:1326:U:OP2	2.38	0.41
1:2A:2193:G:C4	1:2A:2194:G:C8	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2308:G:O2'	1:2A:2310:A:N7	2.40	0.41
1:2A:2343:C:H5'	1:2A:2374:C:OP1	2.20	0.41
1:2A:2417:C:H2'	1:2A:2418:A:H8	1.85	0.41
2:2B:38:C:O4'	14:2S:95:HIS:NE2	2.53	0.41
7:2H:88:LEU:HD23	7:2H:130:ARG:HG3	2.02	0.41
12:2Q:48:GLU:O	12:2Q:52:VAL:HG23	2.19	0.41
18:2W:11:ARG:HD3	18:2W:82:LEU:HD12	2.02	0.41
25:23:26:LEU:HD21	25:23:46:ASN:HB2	2.00	0.41
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.55	0.41
32:2a:37:U:O2'	32:2a:547:A:N1	2.48	0.41
32:2a:1008:C:N3	32:2a:1021:G:N2	2.66	0.41
32:2a:1157:A:C5	32:2a:1180:A:C6	3.07	0.41
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.36	0.41
32:2a:1265:G:C2	32:2a:1271:G:C2	3.08	0.41
33:2b:13:ALA:C	33:2b:15:VAL:H	2.27	0.41
38:2g:31:MET:HA	38:2g:39:ALA:HB2	2.02	0.41
44:2m:23:TYR:H	44:2m:67:GLU:HG2	1.85	0.41
1:1A:657:U:H2'	1:1A:658:C:H6	1.84	0.41
1:1A:887:A:H1'	1:1A:889:C:OP1	2.20	0.41
1:1A:1991:U:H2'	1:1A:1992:G:H5"	2.02	0.41
1:1A:2056:G:C2	1:1A:2057:A:C8	3.08	0.41
1:1A:2630:G:N3	1:1A:2892:A:O2'	2.53	0.41
3:1D:130:ALA:C	3:1D:131:LEU:HD12	2.45	0.41
6:1G:77:ILE:HG12	6:1G:82:LEU:HB3	2.02	0.41
32:1a:263:A:OP2	51:1t:79:ARG:NH1	2.53	0.41
32:1a:408:A:H2'	32:1a:409:G:O4'	2.19	0.41
32:1a:540:G:H2'	32:1a:541:G:O4'	2.20	0.41
32:1a:838:G:H1	32:1a:848:C:H42	1.68	0.41
32:1a:1030(D):A:C3'	32:1a:1031:G:H4'	2.49	0.41
32:1a:1202:G:O2'	45:1n:29:ARG:HG3	2.20	0.41
35:1d:102:ASP:HB3	35:1d:136:PRO:HB3	2.01	0.41
39:1h:82:HIS:CE1	39:1h:84:ARG:HB2	2.54	0.41
57:1y:4:U:H3	57:1y:69:A:N6	2.17	0.41
1:2A:1280:G:N2	1:2A:1291:C:C2	2.88	0.41
1:2A:1364:G:C8	23:21:3:LYS:HD2	2.55	0.41
1:2A:2027:G:H2'	1:2A:2028:U:O4'	2.20	0.41
1:2A:2186:G:C2	1:2A:2187:G:C8	3.08	0.41
1:2A:2249:U:N3	1:2A:2253:G:OP2	2.46	0.41
1:2A:2408:U:H2'	1:2A:2409:G:H8	1.84	0.41
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.55	0.41
7:2H:26:VAL:O	7:2H:32:GLU:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:5:LEU:HD22	8:2I:9:LEU:HD13	2.01	0.41
12:2Q:21:THR:HA	12:2Q:98:LYS:HD3	2.01	0.41
23:21:5:CYS:SG	23:21:62:VAL:HG23	2.60	0.41
32:2a:8:A:N6	35:2d:209:ARG:HB2	2.35	0.41
32:2a:66:G:OP1	32:2a:66:G:H8	2.03	0.41
32:2a:181:G:N2	32:2a:182:U:O4	2.33	0.41
32:2a:219:C:C4	32:2a:220:G:C8	3.08	0.41
32:2a:363:A:C5	43:2l:31:PRO:HD2	2.55	0.41
32:2a:1345:U:OP2	63:2a:3314:HOH:O	2.22	0.41
35:2d:162:LEU:HG	35:2d:181:MET:SD	2.60	0.41
36:2e:61:TYR:HA	36:2e:64:ARG:HG3	2.01	0.41
39:2h:40:ALA:C	39:2h:42:GLU:H	2.28	0.41
43:2l:7:ILE:HG22	48:2q:34:LYS:HD2	2.02	0.41
44:2m:28:ALA:C	44:2m:30:ALA:H	2.28	0.41
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.52	0.41
1:1A:1045:A:H8	1:1A:1111:A:N6	2.17	0.41
1:1A:1153:C:N4	1:1A:1154:G:C6	2.89	0.41
1:1A:2375:G:O2'	1:1A:2377:A:N7	2.41	0.41
5:1F:160:ASN:O	5:1F:164:ARG:HG3	2.20	0.41
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	2.02	0.41
21:1Z:8:TYR:HB2	21:1Z:38:TYR:CE2	2.56	0.41
31:19:2:LYS:HD3	31:19:4:ARG:NH2	2.35	0.41
32:1a:92:C:H2'	32:1a:93:G:C8	2.55	0.41
32:1a:870:U:H4'	32:1a:871:U:H5"	2.02	0.41
32:1a:1079:G:C6	32:1a:1080:A:N6	2.89	0.41
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.20	0.41
32:1a:1445:C:N4	32:1a:1457:G:H1	2.18	0.41
34:1c:6:HIS:CD2	34:1c:8:ILE:HB	2.55	0.41
36:1e:74:GLY:CA	36:1e:116:THR:HG22	2.50	0.41
39:1h:18:ARG:NH2	39:1h:81:HIS:O	2.50	0.41
42:1k:58:PRO:O	42:1k:93:GLN:HG2	2.20	0.41
44:1m:40:ASN:HB3	44:1m:43:THR:OG1	2.20	0.41
48:1q:85:VAL:O	48:1q:89:LEU:HG	2.20	0.41
1:2A:79:G:H2'	1:2A:80:G:C8	2.56	0.41
1:2A:109:G:H2'	1:2A:110:G:O4'	2.20	0.41
1:2A:995:C:H5"	16:2U:54:LYS:HG3	2.01	0.41
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.54	0.41
1:2A:2690:C:N4	1:2A:2713:A:H1'	2.36	0.41
3:2D:255:LYS:HD3	3:2D:255:LYS:HA	1.94	0.41
5:2F:40:GLN:NE2	5:2F:182:ASN:HB2	2.35	0.41
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:11:TYR:OH	6:2G:16:ARG:HD3	2.20	0.41
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	2.02	0.41
14:2S:94:TYR:CZ	14:2S:99:LYS:HG3	2.55	0.41
21:2Z:40:ASP:OD2	21:2Z:42:VAL:HG13	2.19	0.41
24:22:23:LYS:O	24:22:26:ARG:N	2.53	0.41
24:22:67:LYS:HA	24:22:67:LYS:HD3	1.86	0.41
32:2a:237:C:H5"	48:2q:25:ARG:CZ	2.50	0.41
32:2a:343:U:H2'	32:2a:345:C:C5	2.54	0.41
32:2a:565:U:OP2	32:2a:566:G:O2'	2.35	0.41
33:2b:24:TRP:H	33:2b:24:TRP:HD1	1.68	0.41
36:2e:42:GLY:HA2	36:2e:65:ASN:O	2.20	0.41
40:2i:116:LYS:HA	40:2i:123:PRO:HD3	2.02	0.41
41:2j:78:ASN:O	41:2j:80:LYS:N	2.52	0.41
43:2l:32:PHE:O	43:2l:33:ARG:HD3	2.20	0.41
44:2m:81:LEU:H	44:2m:81:LEU:HG	1.63	0.41
44:2m:90:LEU:O	44:2m:94:ARG:HB2	2.21	0.41
45:2n:15:LYS:HB3	45:2n:15:LYS:HE2	1.74	0.41
51:2t:43:LEU:HD13	51:2t:51:GLU:HG3	2.02	0.41
54:2w:10:G:H2'	54:2w:11:C:C6	2.55	0.41
55:2x:64:G:H2'	55:2x:65:C:H6	1.85	0.41
1:1A:511:U:H4'	1:1A:1235:G:H4'	2.02	0.41
1:1A:511:U:O4	1:1A:512:G:N1	2.52	0.41
1:1A:764:A:O4'	3:1D:213:ARG:HG3	2.20	0.41
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.20	0.41
1:1A:1907:G:C6	1:1A:1908:C:C4	3.08	0.41
3:1D:177:LEU:HD12	3:1D:181:GLU:HG2	2.02	0.41
6:1G:11:TYR:O	6:1G:16:ARG:HG3	2.19	0.41
13:1R:100:LEU:HD21	13:1R:113:LEU:HD23	2.03	0.41
32:1a:203:U:O2	32:1a:216:G:N1	2.53	0.41
32:1a:1206:G:H2'	32:1a:1207:2MG:O4'	2.20	0.41
32:1a:1430:C:H2'	32:1a:1431:C:C6	2.56	0.41
35:1d:178:VAL:C	35:1d:180:GLY:N	2.78	0.41
38:1g:15:ASP:HB3	38:1g:24:THR:HG23	2.02	0.41
40:1i:79:LEU:O	40:1i:83:ARG:HG3	2.21	0.41
42:1k:112:THR:O	42:1k:114:VAL:HG12	2.20	0.41
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.19	0.41
1:2A:1740:G:H2'	1:2A:1741:A:C8	2.56	0.41
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.36	0.41
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.54	0.41
12:2Q:140:ALA:C	12:2Q:141:GLN:HG2	2.45	0.41
13:2R:98:LEU:H	13:2R:113:LEU:HD12	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:61:ASN:O	14:2S:65:VAL:HG13	2.20	0.41
32:2a:184:G:H2'	32:2a:185:A:H8	1.85	0.41
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.51	0.41
32:2a:1005:A:H3'	32:2a:1006:C:H6	1.84	0.41
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.55	0.41
33:2b:188:ALA:HB1	33:2b:192:SER:HB2	2.01	0.41
41:2j:65:LEU:HD12	41:2j:65:LEU:HA	1.89	0.41
44:2m:79:LYS:HE3	44:2m:79:LYS:HB3	1.82	0.41
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.45	0.41
54:2w:51:A:C4	54:2w:64:G:C2	3.09	0.41
55:2x:43:A:C2	55:2x:44:A:C4	3.08	0.41
57:2y:63:U:H2'	57:2y:64:G:C8	2.55	0.41
1:1A:518:G:H4'	18:1W:18:ARG:NE	2.35	0.41
1:1A:1043:C:H2'	1:1A:1044:G:H8	1.85	0.41
1:1A:1176:G:N2	1:1A:1178:C:O5'	2.47	0.41
1:1A:1508:A:O2'	1:1A:1509:C:OP1	2.29	0.41
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.20	0.41
1:1A:1790:C:H5"	1:1A:1791:A:OP1	2.20	0.41
1:1A:2390:U:P	30:18:35:GLN:HE22	2.43	0.41
1:1A:2804:C:H2'	1:1A:2805:G:C8	2.54	0.41
6:1G:148:MET:H	6:1G:148:MET:HG3	1.65	0.41
21:1Z:121:HIS:CE1	21:1Z:169:GLU:HG2	2.54	0.41
24:12:63:VAL:HA	24:12:66:GLU:HB2	2.02	0.41
32:1a:482:A:H2'	32:1a:483:C:O4'	2.20	0.41
32:1a:597:G:C6	32:1a:598:U:C2	3.08	0.41
32:1a:648:A:H2'	32:1a:649:G:C8	2.56	0.41
32:1a:993:G:H2'	32:1a:995:C:H41	1.84	0.41
32:1a:1202:G:C4	45:1n:42:ILE:HD12	2.55	0.41
32:1a:1347:G:O2'	32:1a:1373:G:O6	2.29	0.41
35:1d:112:VAL:H	35:1d:116:GLN:HE21	1.66	0.41
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	2.01	0.41
39:1h:67:PRO:O	39:1h:76:PRO:HB3	2.20	0.41
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.65	0.41
44:1m:69:GLU:O	44:1m:73:GLU:N	2.51	0.41
49:1r:43:PHE:CZ	49:1r:58:LEU:HD11	2.56	0.41
50:1s:51:VAL:O	50:1s:58:VAL:N	2.39	0.41
51:1t:39:LYS:HE3	51:1t:39:LYS:HB2	1.95	0.41
57:1y:65:C:H2'	57:1y:66:A:C8	2.55	0.41
1:2A:855:G:C6	1:2A:856:C:N4	2.89	0.41
1:2A:892:G:H3'	1:2A:893:C:H5"	2.01	0.41
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:75:G:H5'	2:2B:76:G:OP2	2.21	0.41
3:2D:96:HIS:CD2	3:2D:102:LYS:HG2	2.55	0.41
10:2O:63:VAL:HG23	10:2O:64:ARG:HG3	2.01	0.41
11:2P:135:LEU:HD23	11:2P:135:LEU:HA	1.83	0.41
17:2V:56:SER:HB3	17:2V:100:ARG:HB2	2.02	0.41
25:23:44:ARG:O	25:23:48:GLU:HG2	2.19	0.41
32:2a:925:G:H1'	32:2a:1502:A:C4	2.56	0.41
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.21	0.41
32:2a:1201:A:H4'	32:2a:1202:G:O5'	2.20	0.41
32:2a:1401:G:H2'	32:2a:1402:4OC:O4'	2.20	0.41
35:2d:135:LEU:C	35:2d:137:SER:H	2.28	0.41
37:2f:3:ARG:NE	37:2f:38:GLU:OE1	2.53	0.41
38:2g:152:ALA:O	38:2g:155:ARG:HD3	2.20	0.41
39:2h:95:VAL:HG22	39:2h:131:GLY:O	2.20	0.41
51:2t:10:LEU:HD12	51:2t:10:LEU:HA	1.85	0.41
57:2y:58:A:C2	57:2y:60:U:H2'	2.55	0.41
1:1A:27:G:O2'	1:1A:28:A:OP2	2.38	0.41
1:1A:262:A:H2'	1:1A:263:C:O4'	2.20	0.41
1:1A:443:A:H5"	1:1A:444:C:OP1	2.20	0.41
1:1A:724:U:H2'	1:1A:725:G:O4'	2.20	0.41
1:1A:787:U:OP2	63:1A:4179:HOH:O	2.22	0.41
1:1A:1152:C:H1'	16:1U:77:SER:HB3	2.03	0.41
1:1A:1709:U:H2'	1:1A:1710:C:C6	2.56	0.41
1:1A:2431:U:H2'	1:1A:2433:A:OP2	2.21	0.41
2:1B:2:C:H2'	2:1B:3:C:C6	2.55	0.41
6:1G:99:MET:O	6:1G:103:LEU:HB2	2.20	0.41
9:1N:12:ARG:HG2	9:1N:50:ASP:CG	2.45	0.41
10:1O:19:ILE:HB	10:1O:41:ALA:HB1	2.02	0.41
21:1Z:100:VAL:HG11	21:1Z:134:PRO:HG2	2.02	0.41
26:14:15:ILE:HB	26:14:32:TYR:CD1	2.55	0.41
32:1a:109:A:H2'	32:1a:326:G:N2	2.35	0.41
32:1a:1329:A:N7	52:1u:7:ARG:NH2	2.68	0.41
32:1a:1346:A:O2'	38:1g:10:ARG:NH2	2.52	0.41
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	2.03	0.41
43:1l:40:VAL:HG21	43:1l:78:GLN:C	2.46	0.41
1:2A:459:U:H4'	29:27:40:TRP:CZ3	2.55	0.41
1:2A:614(C):A:H4'	1:2A:615:G:OP1	2.21	0.41
1:2A:787:U:H5"	1:2A:788:A:H5'	2.03	0.41
1:2A:879:G:N3	1:2A:879:G:H2'	2.35	0.41
1:2A:1149:G:H2'	1:2A:1150:C:H6	1.84	0.41
1:2A:1607:C:H5"	1:2A:1608:A:H5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.55	0.41
1:2A:2345:G:OP2	28:26:38:LYS:NZ	2.51	0.41
1:2A:2721:A:OP1	63:2A:3968:HOH:O	2.22	0.41
2:2B:102:A:OP2	63:2B:301:HOH:O	2.22	0.41
3:2D:71:ASP:CB	3:2D:103:ARG:HH12	2.33	0.41
7:2H:43:VAL:HG22	7:2H:52:VAL:HG22	2.01	0.41
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.55	0.41
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.40	0.41
14:2S:25:ARG:HH11	14:2S:40:ILE:HG21	1.85	0.41
15:2T:33:LYS:HE2	15:2T:40:THR:HG21	2.02	0.41
16:2U:88:ILE:HD13	17:2V:47:VAL:HG11	2.02	0.41
22:20:68:GLU:HB2	22:20:80:HIS:HB2	2.02	0.41
23:21:64:ALA:HA	23:21:67:ILE:HG13	2.02	0.41
30:28:33:ASN:HA	30:28:36:LYS:HG3	2.01	0.41
32:2a:35:G:H1	32:2a:549:C:H42	1.68	0.41
32:2a:189(B):C:C2	32:2a:189(J):G:C2	3.08	0.41
32:2a:674:G:H2'	32:2a:675:A:C8	2.56	0.41
32:2a:1194:U:H4'	36:2e:22:GLY:HA3	2.03	0.41
32:2a:1260:C:P	32:2a:1284:C:H4'	2.61	0.41
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.56	0.41
33:2b:212:GLN:OE1	33:2b:216:SER:HB2	2.21	0.41
39:2h:36:LEU:HD23	39:2h:39:LEU:HD12	2.02	0.41
43:2l:57:LYS:HA	43:2l:67:THR:HA	2.02	0.41
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.85	0.41
48:2q:84:LEU:O	48:2q:87:LYS:HB2	2.21	0.41
50:2s:33:THR:HG22	50:2s:50:ALA:O	2.21	0.41
54:2w:55:PSU:H2'	54:2w:56:C:H5"	2.02	0.41
57:2y:13:C:N3	57:2y:23:A:N6	2.69	0.41
1:1A:24:G:H2'	1:1A:25:U:O4'	2.20	0.41
1:1A:287:C:H2'	1:1A:288:C:C6	2.55	0.41
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.36	0.41
1:1A:1007:C:OP1	9:1N:37:LYS:NZ	2.53	0.41
1:1A:1108:U:H2'	1:1A:1109:C:O4'	2.21	0.41
60:1A:4082:TEL:H332	60:1A:4082:TEL:H19	1.67	0.41
4:1E:7:VAL:HG23	4:1E:51:PHE:HE2	1.86	0.41
6:1G:16:ARG:NH2	6:1G:31:VAL:HG11	2.34	0.41
6:1G:132:ASN:HA	6:1G:157:ILE:O	2.21	0.41
11:1P:95:VAL:HB	11:1P:125:VAL:HG12	2.02	0.41
15:1T:11:GLU:OE2	15:1T:57:PHE:HB3	2.20	0.41
15:1T:50:ILE:HA	15:1T:99:LEU:HD12	2.02	0.41
16:1U:33:ARG:O	16:1U:37:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:139:VAL:HG12	21:1Z:140:ASP:H	1.86	0.41
32:1a:399:G:H2'	32:1a:400:C:C6	2.56	0.41
32:1a:1003:G:OP1	32:1a:1003:G:H4'	2.20	0.41
32:1a:1299:A:H2'	32:1a:1299:A:N3	2.35	0.41
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.56	0.41
36:1e:78:HIS:CE1	36:1e:142:LEU:HA	2.55	0.41
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.56	0.41
1:2A:2136:C:O2'	1:2A:2137:C:O4'	2.38	0.41
1:2A:2513:G:N2	4:2E:143:ASN:OD1	2.54	0.41
12:2Q:134:ARG:NH2	21:2Z:122:ARG:HE	2.18	0.41
14:2S:62:LYS:O	14:2S:65:VAL:HG22	2.21	0.41
32:2a:200:G:H2'	32:2a:201:C:O4'	2.21	0.41
32:2a:941:G:H2'	32:2a:942:G:O4'	2.21	0.41
32:2a:1265:G:C6	32:2a:1266:G:C5	3.09	0.41
33:2b:119:GLU:HG3	33:2b:142:LEU:HD11	2.01	0.41
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.20	0.41
1:1A:7:G:H2'	1:1A:8:A:O4'	2.20	0.41
1:1A:320:A:H4'	1:1A:322:A:N7	2.36	0.41
1:1A:740:U:H2'	1:1A:741:G:C8	2.55	0.41
1:1A:1047:G:H2'	1:1A:1110:G:N1	2.36	0.41
1:1A:1340:U:OP1	19:1X:16:LYS:HE2	2.20	0.41
1:1A:1712:C:H2'	1:1A:1713:U:O4'	2.20	0.41
1:1A:2533:A:H2'	1:1A:2534:A:O4'	2.20	0.41
1:1A:2612:C:O5'	27:15:2:ALA:HB3	2.21	0.41
1:1A:2888:C:H2'	1:1A:2889:C:H6	1.86	0.41
4:1E:147:PRO:HB2	4:1E:149:ARG:HG2	2.03	0.41
7:1H:149:ARG:HH12	7:1H:167:GLU:CD	2.28	0.41
8:1I:130:TYR:O	8:1I:138:ILE:N	2.50	0.41
11:1P:126:VAL:HG12	11:1P:148:LEU:HD13	2.02	0.41
13:1R:38:VAL:HG22	13:1R:112:ALA:HB2	2.02	0.41
32:1a:402:G:C6	32:1a:403:C:C4	3.09	0.41
32:1a:457:C:H2'	32:1a:458:C:C6	2.56	0.41
32:1a:666:G:C2	32:1a:741:G:C4	3.09	0.41
32:1a:971:G:N2	32:1a:1363(A):A:OP2	2.43	0.41
32:1a:1084:G:C5	32:1a:1085:U:C4	3.08	0.41
40:1i:55:ALA:HA	40:1i:58:HIS:CD2	2.56	0.41
43:1l:113:ARG:HG3	43:1l:114:LYS:N	2.35	0.41
1:2A:30:G:C5	1:2A:31:C:C4	3.09	0.41
1:2A:234:C:H2'	1:2A:235:U:C6	2.55	0.41
1:2A:251:A:C4	1:2A:252:G:H1'	2.55	0.41
1:2A:390:A:H4'	1:2A:391:G:H5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1005:C:H2'	1:2A:1006:C:H6	1.86	0.41
1:2A:1288:U:C2	1:2A:1327:C:O2	2.74	0.41
1:2A:1654:A:OP1	13:2R:1:MET:N	2.41	0.41
1:2A:1882:C:H5"	23:21:26:ARG:NH1	2.36	0.41
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.21	0.41
5:2F:53:THR:N	5:2F:56:GLU:OE1	2.36	0.41
6:2G:4:ASP:HA	6:2G:8:LYS:NZ	2.36	0.41
7:2H:136:ILE:H	7:2H:136:ILE:HG13	1.43	0.41
17:2V:55:ALA:HA	17:2V:101:GLY:HA2	2.01	0.41
21:2Z:4:ARG:HH21	21:2Z:60:GLU:CD	2.29	0.41
28:26:26:ASN:C	28:26:28:ARG:N	2.79	0.41
32:2a:186:C:H5'	51:2t:78:ALA:HB1	2.03	0.41
32:2a:532:A:H2	34:2c:156:ARG:HH22	1.62	0.41
32:2a:656:C:H2'	32:2a:657:G:O4'	2.20	0.41
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.20	0.41
32:2a:1376:U:P	38:2g:94:ARG:HH12	2.44	0.41
34:2c:18:TRP:NE1	45:2n:55:GLY:H	2.19	0.41
34:2c:120:VAL:O	34:2c:124:ILE:HG12	2.21	0.41
39:2h:107:LEU:HD23	39:2h:107:LEU:HA	1.90	0.41
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.21	0.41
57:2y:46:G7M:H8	57:2y:46:G7M:H2'	1.83	0.41
1:1A:312:G:H4'	1:1A:331:A:C2	2.56	0.41
1:1A:571:A:N6	1:1A:2499:C:O3'	2.54	0.41
1:1A:729:G:O2'	63:1A:4177:HOH:O	2.21	0.41
1:1A:1062:G:C8	1:1A:1070:A:H4'	2.55	0.41
1:1A:1274:A:N3	1:1A:1297:C:H1'	2.36	0.41
1:1A:1580:A:H5"	1:1A:1581:G:OP2	2.20	0.41
1:1A:1971:A:C2	3:1D:241:PRO:HD3	2.56	0.41
1:1A:2118:U:H4'	1:1A:2119:A:OP1	2.20	0.41
1:1A:2165:G:N1	1:1A:2171:A:H8	2.19	0.41
1:1A:2860:A:N7	1:1A:2861:G:H1'	2.36	0.41
4:1E:54:GLN:OE1	4:1E:55:ASN:N	2.51	0.41
5:1F:39:TRP:HB2	5:1F:99:TYR:CZ	2.56	0.41
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.39	0.41
5:1F:144:LYS:HB3	5:1F:144:LYS:HE3	1.78	0.41
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	2.03	0.41
8:1I:38:LEU:HD23	8:1I:38:LEU:N	2.36	0.41
8:1I:52:ARG:CZ	8:1I:52:ARG:HB2	2.51	0.41
8:1I:123:LEU:HA	8:1I:144:VAL:HG23	2.03	0.41
12:1Q:89:ASN:HB2	55:1x:1:C:C2	2.55	0.41
16:1U:101:ARG:O	16:1U:103:PRO:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:26:TYR:O	19:1X:81:VAL:HG23	2.21	0.41
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	2.02	0.41
21:1Z:99:TYR:HA	21:1Z:124:ILE:O	2.21	0.41
25:13:4:LEU:O	25:13:36:VAL:HA	2.21	0.41
28:16:35:GLU:OE1	28:16:50:ARG:NH2	2.48	0.41
32:1a:39:G:C6	32:1a:40:C:C4	3.09	0.41
32:1a:383:A:C5	32:1a:384:G:H1'	2.56	0.41
32:1a:405:U:O4	35:1d:2:GLY:N	2.53	0.41
32:1a:542:G:P	35:1d:10:ARG:HH22	2.43	0.41
32:1a:925:G:C2	32:1a:927:G:C8	3.09	0.41
32:1a:975:A:H5'	32:1a:975:A:H8	1.85	0.41
32:1a:987:G:H2'	32:1a:988:G:C8	2.56	0.41
32:1a:1041:A:H2'	32:1a:1042:G:O4'	2.21	0.41
32:1a:1150:U:H4'	41:1j:41:PRO:HG3	2.03	0.41
32:1a:1168:A:H8	32:1a:1168:A:OP1	2.03	0.41
32:1a:1305:G:OP2	52:1u:2:GLY:N	2.54	0.41
32:1a:1348:U:H4'	40:1i:120:ARG:HD2	2.03	0.41
33:1b:166:ASP:HB3	33:1b:169:LYS:HB2	2.01	0.41
34:1c:138:VAL:HG22	34:1c:151:VAL:HG23	2.03	0.41
35:1d:200:GLU:OE1	35:1d:201:GLN:N	2.54	0.41
42:1k:86:GLY:N	42:1k:112:THR:OG1	2.41	0.41
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.21	0.41
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.20	0.41
47:1p:39:TYR:CD1	47:1p:49:LEU:HD23	2.54	0.41
47:1p:60:LEU:HA	47:1p:60:LEU:HD12	1.80	0.41
54:1w:9:A:O2'	54:1w:45:G:N2	2.53	0.41
57:1y:7:U:O2'	57:1y:8:U:H5'	2.20	0.41
1:2A:196:A:N3	1:2A:196:A:H2'	2.36	0.41
1:2A:332:A:O2'	1:2A:334:C:OP2	2.29	0.41
1:2A:586:A:N1	1:2A:809:G:O2'	2.36	0.41
1:2A:776:G:N2	1:2A:2241:A:OP1	2.52	0.41
1:2A:867:C:H2'	1:2A:868:U:C6	2.53	0.41
1:2A:908:C:OP1	12:2Q:22:LYS:HE2	2.21	0.41
1:2A:1388:G:H1	1:2A:1399:C:H42	1.67	0.41
1:2A:1448:G:H1'	1:2A:1528:A:N1	2.36	0.41
1:2A:2019:A:N7	27:25:9:LYS:HE3	2.36	0.41
1:2A:2110:G:N1	1:2A:2120:G:H1'	2.36	0.41
1:2A:2293:C:H42	1:2A:2339:G:H1	1.68	0.41
1:2A:2370:G:C6	1:2A:2371:G:C6	3.09	0.41
1:2A:2469:A:C2	1:2A:2470:G:H1'	2.56	0.41
2:2B:56:G:H4'	2:2B:57:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:146:GLU:HG2	3:2D:152:GLY:C	2.46	0.41
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.54	0.41
4:2E:181:LEU:HD23	4:2E:181:LEU:HA	1.83	0.41
5:2F:23:ASP:O	5:2F:24:LEU:HD12	2.20	0.41
5:2F:126:VAL:HG22	5:2F:194:MET:O	2.21	0.41
7:2H:58:GLU:HG2	7:2H:60:ARG:H	1.86	0.41
8:2I:4:ILE:HG23	8:2I:18:VAL:HG22	2.02	0.41
10:2O:23:ARG:NH2	10:2O:28:SER:O	2.54	0.41
10:2O:34:THR:OG1	10:2O:35:VAL:N	2.54	0.41
10:2O:104:ARG:NH1	10:2O:104:ARG:HB2	2.35	0.41
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.21	0.41
15:2T:64:ARG:NH1	15:2T:73:GLU:OE2	2.54	0.41
20:2Y:55:TYR:CZ	20:2Y:61:ILE:HG13	2.56	0.41
22:20:69:PHE:CE2	22:20:79:VAL:HG22	2.55	0.41
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.86	0.41
25:23:54:VAL:HG12	25:23:56:VAL:HG22	2.03	0.41
26:24:40:HIS:O	26:24:44:THR:HG22	2.21	0.41
32:2a:120:A:C6	32:2a:122:G:C2	3.09	0.41
32:2a:404:U:P	35:2d:118:ARG:HH21	2.43	0.41
32:2a:407:G:OP1	35:2d:115:ARG:HD3	2.21	0.41
32:2a:485:G:H1’	32:2a:486:U:H5	1.85	0.41
32:2a:591:U:H2’	32:2a:592:G:C8	2.55	0.41
32:2a:664:G:P	49:2r:64:ARG:HH21	2.43	0.41
32:2a:983:A:H1’	32:2a:1049:U:O2	2.20	0.41
32:2a:1005:A:H5”	32:2a:1006:C:H5	1.86	0.41
32:2a:1010:G:N2	32:2a:1020:U:O2’	2.54	0.41
32:2a:1271:G:C2	32:2a:1272:G:C5	3.09	0.41
33:2b:16:HIS:O	33:2b:18:GLY:N	2.54	0.41
34:2c:8:ILE:C	34:2c:10:PHE:N	2.76	0.41
35:2d:18:LYS:NZ	35:2d:26:CYS:O	2.36	0.41
35:2d:144:ASP:O	35:2d:146:ILE:HG13	2.20	0.41
38:2g:114:ARG:HB2	38:2g:115:ARG:NH2	2.36	0.41
40:2i:48:GLU:N	40:2i:49:PRO:CD	2.84	0.41
40:2i:58:HIS:ND1	40:2i:58:HIS:N	2.69	0.41
40:2i:88:TYR:CD2	40:2i:89:ASN:HB2	2.55	0.41
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.85	0.41
41:2j:13:HIS:HB3	41:2j:68:HIS:CE1	2.56	0.41
45:2n:24:CYS:HA	45:2n:38:GLY:O	2.21	0.41
48:2q:83:ASP:OD1	48:2q:83:ASP:N	2.52	0.41
48:2q:95:TYR:O	48:2q:98:LEU:N	2.50	0.41
50:2s:18:LYS:HA	50:2s:21:GLU:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:64:G:H2'	55:2x:65:C:C6	2.56	0.41
57:2y:9:A:N6	57:2y:24:G:N7	2.68	0.41
1:1A:878:A:H2'	1:1A:879:G:H5'	2.03	0.41
1:1A:1003:G:O2'	1:1A:1010:A:N1	2.51	0.41
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.20	0.41
1:1A:2552:OMU:O5'	1:1A:2552:OMU:H6	2.21	0.41
1:1A:2822:G:OP1	63:1A:4172:HOH:O	2.21	0.41
6:1G:67:LYS:HD3	26:14:5:ILE:HD12	2.03	0.41
8:1I:1:MET:HE1	8:1I:27:ARG:NH2	2.36	0.41
13:1R:12:ARG:HG2	13:1R:16:HIS:ND1	2.36	0.41
16:1U:17:ILE:HG13	16:1U:32:PHE:HE1	1.86	0.41
21:1Z:52:SER:C	21:1Z:54:HIS:N	2.78	0.41
33:1b:41:ILE:HD13	33:1b:41:ILE:HA	1.91	0.41
34:1c:29:TYR:O	34:1c:33:LEU:N	2.54	0.41
34:1c:52:LEU:HD11	34:1c:55:VAL:HG23	2.02	0.41
35:1d:158:ILE:O	35:1d:162:LEU:N	2.46	0.41
47:1p:19:ILE:N	47:1p:37:GLY:O	2.54	0.41
54:1w:34:U8U:H2'	54:1w:35:U:O4'	2.21	0.41
55:1x:21:A:H61	55:1x:46:G:H2'	1.85	0.41
1:2A:271(K):U:O2	8:2I:50:ARG:NH2	2.54	0.41
1:2A:453:C:O2	1:2A:457:A:O2'	2.38	0.41
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.31	0.41
1:2A:640:C:H42	1:2A:648:G:H1	1.67	0.41
1:2A:715:G:C4	46:2o:56:LEU:HD21	2.56	0.41
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.54	0.41
1:2A:1688:U:H1'	1:2A:1701:A:C6	2.55	0.41
1:2A:2335:A:O2'	1:2A:2336:A:H5"	2.21	0.41
1:2A:2836:U:C4	1:2A:2883:A:N6	2.88	0.41
3:2D:66:ASP:OD2	3:2D:103:ARG:NH1	2.54	0.41
7:2H:24:VAL:HG13	7:2H:37:VAL:CG1	2.50	0.41
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.56	0.41
9:2N:83:LYS:HE2	9:2N:83:LYS:HB2	1.94	0.41
19:2X:90:GLU:C	19:2X:92:LEU:N	2.79	0.41
21:2Z:94:GLU:H	21:2Z:94:GLU:HG3	1.60	0.41
26:24:16:CYS:HB3	26:24:19:GLY:H	1.85	0.41
32:2a:472:A:H5"	47:2p:80:PHE:HB3	2.03	0.41
33:2b:27:LYS:HB3	33:2b:194:PRO:HD2	2.03	0.41
33:2b:67:THR:HG21	33:2b:155:LEU:HD12	2.03	0.41
33:2b:192:SER:O	33:2b:194:PRO:HD3	2.21	0.41
34:2c:182:ILE:H	34:2c:182:ILE:HG12	1.62	0.41
35:2d:12:CYS:HB3	35:2d:19:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:63:LYS:O	35:2d:67:ILE:HG13	2.21	0.41
36:2e:143:ARG:HB3	36:2e:147:ASP:HB2	2.02	0.41
50:2s:32:LYS:HD2	50:2s:34:TRP:HZ3	1.84	0.41
50:2s:33:THR:H	50:2s:57:HIS:HE1	1.69	0.41
53:2v:16:A:H2'	53:2v:17:U:O4'	2.21	0.41
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.36	0.40
1:1A:1070:A:H5"	1:1A:1072:C:OP1	2.21	0.40
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.37	0.40
1:1A:2629:A:H1'	1:1A:2630:G:H5"	2.03	0.40
2:1B:2:C:H2'	2:1B:3:C:H6	1.85	0.40
4:1E:11:MET:HE2	4:1E:11:MET:HB3	1.96	0.40
7:1H:87:LEU:HD23	7:1H:87:LEU:HA	1.90	0.40
8:1I:17:GLN:HG2	8:1I:18:VAL:N	2.36	0.40
9:1N:15:LEU:HB2	9:1N:135:PRO:HB2	2.03	0.40
16:1U:89:GLU:HB2	17:1V:50:PRO:HB3	2.04	0.40
32:1a:827:U:H5"	32:1a:828:A:OP2	2.21	0.40
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	2.03	0.40
38:1g:144:MET:HE2	38:1g:144:MET:HB3	1.89	0.40
43:1l:39:VAL:HB	43:1l:57:LYS:HE2	2.01	0.40
46:1o:82:ILE:C	46:1o:84:LYS:H	2.29	0.40
47:1p:39:TYR:HD1	47:1p:49:LEU:HD23	1.85	0.40
53:1v:21:A:N1	54:1w:34:U8U:C4	2.81	0.40
54:1w:15:G:H22	54:1w:48:C:N4	2.20	0.40
1:2A:56:A:H2'	1:2A:57:C:O4'	2.20	0.40
1:2A:422:A:H2'	1:2A:423:A:C8	2.57	0.40
1:2A:468:G:OP2	29:27:37:LYS:HE3	2.21	0.40
1:2A:577:G:C6	1:2A:578:A:C6	3.09	0.40
1:2A:675:A:N3	1:2A:2443:C:O2'	2.45	0.40
1:2A:1557:C:H5"	1:2A:1558:A:OP2	2.21	0.40
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.36	0.40
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.56	0.40
1:2A:2807:G:C2	1:2A:2808:U:H1'	2.56	0.40
6:2G:41:GLN:O	6:2G:43:LEU:HD22	2.21	0.40
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.21	0.40
10:2O:88:ASN:ND2	10:2O:90:GLN:HB2	2.36	0.40
10:2O:119:PRO:HB2	15:2T:68:TYR:CE2	2.56	0.40
13:2R:99:LYS:HA	13:2R:112:ALA:HA	2.02	0.40
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.21	0.40
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.50	0.40
31:29:3:VAL:HA	31:29:35:ARG:O	2.21	0.40
32:2a:46:G:H2'	32:2a:366:C:C5	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:486:U:H2'	32:2a:487:A:C8	2.56	0.40
32:2a:920:U:H2'	32:2a:921:U:H6	1.86	0.40
32:2a:1212:U:H5'	32:2a:1213:A:C8	2.56	0.40
32:2a:1316:G:H5"	45:2n:17:LYS:HE3	2.03	0.40
32:2a:1329:A:OP2	52:2u:7:ARG:NH2	2.53	0.40
33:2b:172:ILE:H	33:2b:172:ILE:HG13	1.59	0.40
34:2c:127:ARG:HH12	34:2c:191:THR:HG22	1.87	0.40
44:2m:96:LEU:C	44:2m:110:ARG:HG2	2.45	0.40
50:2s:20:LEU:HD23	50:2s:20:LEU:HA	1.94	0.40
55:2x:61:C:H2'	55:2x:62:C:C6	2.56	0.40
1:1A:271(N):U:O2'	1:1A:271(O):C:H5'	2.21	0.40
1:1A:445:C:OP1	16:1U:2:PRO:HA	2.21	0.40
1:1A:647:G:O5'	1:1A:647:G:H8	2.04	0.40
1:1A:978:G:C2	1:1A:986:C:C2	3.09	0.40
1:1A:1038:C:N4	1:1A:1117:G:H1	2.19	0.40
1:1A:1695:G:N7	3:1D:14:ARG:NH2	2.67	0.40
2:1B:29:A:H2'	2:1B:30:C:C6	2.56	0.40
8:1I:6:LEU:C	8:1I:15:VAL:HG23	2.46	0.40
9:1N:25:ARG:O	9:1N:29:LYS:NZ	2.53	0.40
9:1N:138:LEU:HD23	9:1N:138:LEU:HA	1.83	0.40
12:1Q:3:MET:HE3	12:1Q:3:MET:HB2	1.98	0.40
13:1R:94:TYR:C	13:1R:117:VAL:HG23	2.46	0.40
16:1U:85:LYS:HE2	16:1U:85:LYS:HB3	1.57	0.40
18:1W:68:ARG:NH1	18:1W:111:HIS:HA	2.36	0.40
32:1a:599:C:H4'	39:1h:130:GLY:C	2.45	0.40
32:1a:883:C:N4	32:1a:884:U:O4	2.54	0.40
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.21	0.40
32:1a:1279:A:H5"	32:1a:1280:A:OP1	2.21	0.40
32:1a:1284:C:H3'	32:1a:1285:A:C8	2.56	0.40
32:1a:1401:G:H2'	32:1a:1402:4OC:O4'	2.21	0.40
39:1h:39:LEU:HB2	39:1h:45:ILE:HD11	2.03	0.40
44:1m:121:LYS:HB2	54:1w:40:C:H5"	2.03	0.40
54:1w:61:C:H3'	54:1w:62:C:H5"	2.03	0.40
55:1x:23:C:H2'	55:1x:24:U:C6	2.57	0.40
55:1x:39:C:H2'	55:1x:40:C:C6	2.56	0.40
1:2A:557:U:H2'	1:2A:558:G:C8	2.57	0.40
1:2A:2379:G:H4'	14:2S:21:THR:HG21	2.03	0.40
3:2D:208:LYS:HG3	3:2D:210:GLY:H	1.86	0.40
12:2Q:111:GLU:OE1	12:2Q:133:ARG:NH2	2.54	0.40
16:2U:61:TRP:CZ2	16:2U:93:LYS:HG3	2.56	0.40
21:2Z:35:ARG:HD2	21:2Z:35:ARG:HA	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:21:77:ALA:C	23:21:79:GLY:H	2.28	0.40
32:2a:575:G:O2'	32:2a:821:G:H5'	2.21	0.40
32:2a:599:C:H2'	32:2a:600:C:C6	2.56	0.40
32:2a:762:C:H2'	32:2a:763:G:C8	2.56	0.40
32:2a:772:U:H2'	32:2a:773:G:O4'	2.21	0.40
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.31	0.40
33:2b:10:LEU:HD12	33:2b:10:LEU:HA	1.82	0.40
36:2e:136:MET:HE3	36:2e:136:MET:HB3	1.89	0.40
39:2h:103:VAL:HG11	39:2h:109:ILE:O	2.21	0.40
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.86	0.40
47:2p:45:THR:HA	47:2p:46:PRO:HD3	1.87	0.40
55:2x:44:A:C6	55:2x:45:G:C6	3.09	0.40
1:1A:238:C:C2	1:1A:260:G:C2	3.10	0.40
1:1A:906:G:H2'	1:1A:907:U:O4'	2.22	0.40
1:1A:1485:G:H1	1:1A:1504:C:H42	1.68	0.40
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.56	0.40
1:1A:1812:A:O2'	3:1D:45:ASN:N	2.51	0.40
1:1A:2051:A:H5'	1:1A:2578:G:O4'	2.21	0.40
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.56	0.40
1:1A:2146:C:O2	1:1A:2147:G:N1	2.54	0.40
18:1W:87:PRO:O	18:1W:88:ARG:HD2	2.21	0.40
28:16:38:LYS:HE3	28:16:38:LYS:HB3	1.96	0.40
32:1a:313:A:H2'	32:1a:314:C:C6	2.55	0.40
32:1a:413:G:N2	32:1a:428:G:H1'	2.37	0.40
32:1a:601:C:H2'	32:1a:602:A:C8	2.56	0.40
32:1a:691:G:O2'	32:1a:797:C:H4'	2.20	0.40
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.54	0.40
32:1a:1438:G:H2'	32:1a:1439:C:C6	2.57	0.40
33:1b:233:SER:HB2	33:1b:234:PRO:HD2	2.03	0.40
36:1e:78:HIS:CE1	36:1e:142:LEU:HD23	2.57	0.40
37:1f:36:ARG:HB2	37:1f:66:GLU:O	2.21	0.40
38:1g:73:MET:HE3	38:1g:73:MET:HB3	1.82	0.40
39:1h:10:LEU:H	39:1h:10:LEU:HG	1.63	0.40
45:1n:6:LEU:HD23	45:1n:6:LEU:HA	1.93	0.40
1:2A:393:C:H2'	1:2A:394:A:H8	1.86	0.40
1:2A:773:U:O2'	3:2D:48:ARG:HD3	2.22	0.40
1:2A:843:G:N2	1:2A:936:C:C2	2.90	0.40
1:2A:1031:G:N3	31:29:36:GLN:NE2	2.65	0.40
1:2A:1116:C:H2'	1:2A:1117:G:H8	1.85	0.40
1:2A:2335:A:C8	1:2A:2337:G:C5	3.10	0.40
60:2A:3826:TEL:H112	60:2A:3826:TEL:O18	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:2A:3826:TEL:H19	60:2A:3826:TEL:H332	1.63	0.40
3:2D:58:HIS:O	3:2D:60:ARG:HG3	2.21	0.40
6:2G:133:LEU:HG	6:2G:157:ILE:HB	2.03	0.40
8:2I:1:MET:N	8:2I:20:ASP:OD1	2.28	0.40
11:2P:39:LYS:HB2	11:2P:45:LEU:HD13	2.03	0.40
12:2Q:60:ARG:HH21	54:2w:53:G:P	2.44	0.40
12:2Q:132:VAL:HG21	21:2Z:81:ARG:HH21	1.86	0.40
16:2U:80:ILE:HD13	16:2U:80:ILE:HA	1.93	0.40
21:2Z:23:LYS:HB3	21:2Z:38:TYR:CD1	2.56	0.40
21:2Z:98:MET:HE2	21:2Z:98:MET:HB2	1.86	0.40
21:2Z:151:HIS:HB3	21:2Z:152:ALA:H	1.74	0.40
32:2a:179:A:H2'	32:2a:180:U:C6	2.56	0.40
32:2a:485:G:O2'	32:2a:486:U:OP2	2.40	0.40
32:2a:545:C:H5'	35:2d:72:GLU:HB2	2.02	0.40
32:2a:676:A:N6	63:2a:3341:HOH:O	2.55	0.40
32:2a:1032:G:H2'	32:2a:1033:G:O4'	2.20	0.40
32:2a:1472:U:H2'	32:2a:1473:A:O4'	2.22	0.40
34:2c:92:ALA:C	34:2c:94:LEU:H	2.29	0.40
42:2k:87:THR:HA	42:2k:91:ARG:CZ	2.52	0.40
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	2.03	0.40
47:2p:39:TYR:CD2	47:2p:73:LEU:HD21	2.56	0.40
48:2q:81:ARG:HA	48:2q:81:ARG:HD2	1.73	0.40
1:1A:17:G:H2'	1:1A:18:C:C6	2.55	0.40
1:1A:489:G:H2'	1:1A:491:G:O4'	2.21	0.40
1:1A:1353:A:H62	1:1A:1377:G:H2'	1.85	0.40
1:1A:1441:G:H2'	1:1A:1442:G:C8	2.56	0.40
1:1A:1815:A:H8	1:1A:1815:A:OP1	2.04	0.40
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.36	0.40
5:1F:45:ARG:NH2	63:1F:403:HOH:O	2.55	0.40
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	2.02	0.40
20:1Y:81:LYS:HE2	20:1Y:101:LYS:HD2	2.02	0.40
32:1a:691:G:P	42:1k:26:ASN:HD22	2.44	0.40
32:1a:1355:G:H2'	32:1a:1356:G:C8	2.57	0.40
33:1b:160:ASP:O	33:1b:183:PRO:HD2	2.22	0.40
35:1d:155:LEU:O	35:1d:158:ILE:HG13	2.22	0.40
42:1k:115:PRO:HB2	42:1k:118:GLY:H	1.87	0.40
44:1m:96:LEU:HD23	44:1m:96:LEU:HA	1.93	0.40
57:1y:67:C:H2'	57:1y:68:G:C8	2.56	0.40
1:2A:511:U:H4'	1:2A:1235:G:H4'	2.03	0.40
1:2A:511:U:O4	1:2A:512:G:N1	2.55	0.40
1:2A:1427:A:H4'	1:2A:1428:C:O5'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1945:G:H2'	1:2A:1946:U:C6	2.57	0.40
1:2A:2291:U:H5"	1:2A:2380:C:O2'	2.21	0.40
1:2A:2489:G:C6	1:2A:2490:G:N1	2.90	0.40
6:2G:140:ILE:HG22	6:2G:141:PHE:CD2	2.56	0.40
14:2S:24:LEU:HD23	14:2S:24:LEU:HA	1.86	0.40
17:2V:4:ILE:HA	17:2V:12:TYR:O	2.22	0.40
17:2V:85:LYS:HE2	17:2V:85:LYS:HB2	1.74	0.40
19:2X:5:TYR:CZ	24:22:30:ARG:HB3	2.56	0.40
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.57	0.40
32:2a:259:G:H2'	32:2a:260:G:O4'	2.21	0.40
32:2a:302:G:N3	32:2a:556:C:H4'	2.36	0.40
32:2a:392:G:H5'	47:2p:13:HIS:CE1	2.56	0.40
32:2a:688:G:H2'	32:2a:689:C:H6	1.86	0.40
32:2a:1046:A:H3'	32:2a:1047:G:H8	1.86	0.40
32:2a:1116:C:H2'	32:2a:1117:G:C8	2.56	0.40
32:2a:1202:G:C6	45:2n:42:ILE:HG21	2.57	0.40
35:2d:9:CYS:O	35:2d:13:ARG:HG3	2.21	0.40
40:2i:88:TYR:HD2	40:2i:89:ASN:HB2	1.87	0.40
55:2x:31:G:N3	55:2x:31:G:H2'	2.36	0.40
1:1A:760:G:H2'	1:1A:761:A:O4'	2.21	0.40
1:1A:1526:G:C6	1:1A:1527:G:C2	3.10	0.40
1:1A:1702:G:H2'	1:1A:1703:G:O4'	2.21	0.40
1:1A:2662:A:H8	1:1A:2662:A:O5'	2.03	0.40
4:1E:101:ARG:HB2	4:1E:201:THR:HG21	2.04	0.40
11:1P:56:SER:HB2	11:1P:61:ARG:HD2	2.03	0.40
15:1T:27:THR:HB	15:1T:90:GLN:HB3	2.03	0.40
28:16:39:TYR:HA	28:16:46:HIS:HA	2.04	0.40
32:1a:43:C:H2'	32:1a:44:G:O4'	2.21	0.40
32:1a:192:U:H2'	32:1a:193:C:C6	2.57	0.40
32:1a:452:A:O2'	32:1a:453:A:H5"	2.21	0.40
32:1a:659:U:C2	32:1a:660:G:C8	3.09	0.40
32:1a:942:G:H21	40:1i:124:GLN:HE22	1.68	0.40
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.21	0.40
32:1a:1268:A:H2'	32:1a:1269:A:C8	2.56	0.40
33:1b:82:ARG:NH1	33:1b:150:SER:OG	2.55	0.40
43:1l:53:ARG:HD2	43:1l:93:LEU:HD11	2.04	0.40
45:1n:6:LEU:HD22	45:1n:23:ARG:HH21	1.86	0.40
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.21	0.40
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.56	0.40
1:2A:2597:G:H2'	1:2A:2598:A:C8	2.57	0.40
3:2D:79:VAL:HA	3:2D:95:LEU:HD23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:155:LEU:HD22	5:2F:185:ASP:O	2.21	0.40
5:2F:185:ASP:HA	5:2F:188:ARG:HB2	2.02	0.40
30:28:23:VAL:CG2	30:28:47:LYS:HB3	2.51	0.40
32:2a:324:G:N2	32:2a:326:G:H3'	2.37	0.40
32:2a:406:G:H21	35:2d:119:GLN:NE2	2.20	0.40
32:2a:663:A:H2'	32:2a:664:G:O4'	2.21	0.40
32:2a:922:G:N3	32:2a:1398:A:H2	2.20	0.40
36:2e:76:ILE:O	36:2e:93:PRO:HB3	2.22	0.40
37:2f:69:GLU:C	37:2f:71:ARG:H	2.30	0.40
38:2g:138:LYS:HE2	38:2g:138:LYS:HB3	1.95	0.40
48:2q:66:SER:O	48:2q:69:LYS:N	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	1D	273/276 (99%)	246 (90%)	25 (9%)	2 (1%)	19 48
3	2D	273/276 (99%)	245 (90%)	28 (10%)	0	100 100
4	1E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	25 56
4	2E	202/206 (98%)	182 (90%)	17 (8%)	3 (2%)	8 29
5	1F	201/210 (96%)	190 (94%)	10 (5%)	1 (0%)	25 56
5	2F	201/210 (96%)	186 (92%)	13 (6%)	2 (1%)	13 39
6	1G	179/182 (98%)	152 (85%)	25 (14%)	2 (1%)	12 37
6	2G	179/182 (98%)	155 (87%)	18 (10%)	6 (3%)	3 11
7	1H	172/180 (96%)	158 (92%)	13 (8%)	1 (1%)	22 51
7	2H	172/180 (96%)	149 (87%)	21 (12%)	2 (1%)	11 34
8	1I	144/148 (97%)	123 (85%)	20 (14%)	1 (1%)	19 48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
8	2I	144/148 (97%)	119 (83%)	22 (15%)	3 (2%)	5 20
9	1N	138/140 (99%)	130 (94%)	8 (6%)	0	100 100
9	2N	138/140 (99%)	122 (88%)	14 (10%)	2 (1%)	9 30
10	1O	120/122 (98%)	112 (93%)	8 (7%)	0	100 100
10	2O	120/122 (98%)	103 (86%)	15 (12%)	2 (2%)	7 26
11	1P	147/150 (98%)	130 (88%)	14 (10%)	3 (2%)	6 21
11	2P	147/150 (98%)	124 (84%)	19 (13%)	4 (3%)	4 15
12	1Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
12	2Q	139/141 (99%)	125 (90%)	14 (10%)	0	100 100
13	1R	116/118 (98%)	111 (96%)	4 (3%)	1 (1%)	14 42
13	2R	116/118 (98%)	108 (93%)	7 (6%)	1 (1%)	14 42
14	1S	108/112 (96%)	102 (94%)	6 (6%)	0	100 100
14	2S	108/112 (96%)	93 (86%)	11 (10%)	4 (4%)	2 9
15	1T	129/146 (88%)	120 (93%)	9 (7%)	0	100 100
15	2T	129/146 (88%)	116 (90%)	11 (8%)	2 (2%)	8 27
16	1U	114/118 (97%)	114 (100%)	0	0	100 100
16	2U	114/118 (97%)	111 (97%)	3 (3%)	0	100 100
17	1V	99/101 (98%)	88 (89%)	9 (9%)	2 (2%)	6 21
17	2V	99/101 (98%)	87 (88%)	10 (10%)	2 (2%)	6 21
18	1W	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
18	2W	110/113 (97%)	107 (97%)	3 (3%)	0	100 100
19	1X	93/96 (97%)	88 (95%)	4 (4%)	1 (1%)	12 37
19	2X	93/96 (97%)	83 (89%)	8 (9%)	2 (2%)	5 20
20	1Y	105/110 (96%)	100 (95%)	5 (5%)	0	100 100
20	2Y	105/110 (96%)	98 (93%)	7 (7%)	0	100 100
21	1Z	148/206 (72%)	129 (87%)	14 (10%)	5 (3%)	3 11
21	2Z	156/206 (76%)	128 (82%)	22 (14%)	6 (4%)	2 9
22	10	81/85 (95%)	78 (96%)	3 (4%)	0	100 100
22	20	81/85 (95%)	73 (90%)	7 (9%)	1 (1%)	11 34
23	11	95/98 (97%)	91 (96%)	4 (4%)	0	100 100
23	21	95/98 (97%)	88 (93%)	6 (6%)	1 (1%)	12 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
24	12	68/72 (94%)	65 (96%)	3 (4%)	0	100 100
24	22	68/72 (94%)	63 (93%)	5 (7%)	0	100 100
25	13	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
25	23	57/60 (95%)	52 (91%)	4 (7%)	1 (2%)	7 24
26	14	67/71 (94%)	49 (73%)	15 (22%)	3 (4%)	2 7
26	24	67/71 (94%)	47 (70%)	17 (25%)	3 (4%)	2 7
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
27	25	57/60 (95%)	48 (84%)	9 (16%)	0	100 100
28	16	51/54 (94%)	48 (94%)	3 (6%)	0	100 100
28	26	51/54 (94%)	45 (88%)	5 (10%)	1 (2%)	6 21
29	17	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
30	18	62/65 (95%)	60 (97%)	2 (3%)	0	100 100
30	28	62/65 (95%)	55 (89%)	7 (11%)	0	100 100
31	19	35/37 (95%)	34 (97%)	1 (3%)	0	100 100
31	29	35/37 (95%)	30 (86%)	5 (14%)	0	100 100
33	1b	229/256 (90%)	195 (85%)	26 (11%)	8 (4%)	3 10
33	2b	229/256 (90%)	177 (77%)	45 (20%)	7 (3%)	3 12
34	1c	204/239 (85%)	184 (90%)	19 (9%)	1 (0%)	25 56
34	2c	204/239 (85%)	170 (83%)	32 (16%)	2 (1%)	13 39
35	1d	206/209 (99%)	180 (87%)	24 (12%)	2 (1%)	13 39
35	2d	206/209 (99%)	176 (85%)	29 (14%)	1 (0%)	25 56
36	1e	146/162 (90%)	130 (89%)	12 (8%)	4 (3%)	4 15
36	2e	146/162 (90%)	128 (88%)	14 (10%)	4 (3%)	4 15
37	1f	98/101 (97%)	91 (93%)	6 (6%)	1 (1%)	13 39
37	2f	98/101 (97%)	90 (92%)	8 (8%)	0	100 100
38	1g	153/156 (98%)	130 (85%)	22 (14%)	1 (1%)	19 48
38	2g	153/156 (98%)	133 (87%)	16 (10%)	4 (3%)	4 16
39	1h	135/138 (98%)	125 (93%)	10 (7%)	0	100 100
39	2h	135/138 (98%)	118 (87%)	16 (12%)	1 (1%)	19 48
40	1i	125/128 (98%)	109 (87%)	14 (11%)	2 (2%)	8 27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
40	2i	125/128 (98%)	106 (85%)	17 (14%)	2 (2%)	8 27
41	1j	95/105 (90%)	78 (82%)	11 (12%)	6 (6%)	1 3
41	2j	94/105 (90%)	77 (82%)	14 (15%)	3 (3%)	3 12
42	1k	112/129 (87%)	100 (89%)	10 (9%)	2 (2%)	7 24
42	2k	112/129 (87%)	96 (86%)	14 (12%)	2 (2%)	7 24
43	1l	119/132 (90%)	108 (91%)	10 (8%)	1 (1%)	16 44
43	2l	119/132 (90%)	107 (90%)	10 (8%)	2 (2%)	7 26
44	1m	121/126 (96%)	104 (86%)	15 (12%)	2 (2%)	7 26
44	2m	120/126 (95%)	100 (83%)	19 (16%)	1 (1%)	16 44
45	1n	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
45	2n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	7 26
46	1o	86/89 (97%)	76 (88%)	9 (10%)	1 (1%)	11 34
46	2o	86/89 (97%)	81 (94%)	5 (6%)	0	100 100
47	1p	80/88 (91%)	68 (85%)	12 (15%)	0	100 100
47	2p	80/88 (91%)	70 (88%)	10 (12%)	0	100 100
48	1q	97/105 (92%)	86 (89%)	11 (11%)	0	100 100
48	2q	97/105 (92%)	85 (88%)	10 (10%)	2 (2%)	5 20
49	1r	66/88 (75%)	59 (89%)	7 (11%)	0	100 100
49	2r	66/88 (75%)	61 (92%)	5 (8%)	0	100 100
50	1s	81/93 (87%)	69 (85%)	12 (15%)	0	100 100
50	2s	81/93 (87%)	63 (78%)	15 (18%)	3 (4%)	2 9
51	1t	94/106 (89%)	86 (92%)	5 (5%)	3 (3%)	3 12
51	2t	94/106 (89%)	81 (86%)	9 (10%)	4 (4%)	2 7
52	1u	21/27 (78%)	18 (86%)	3 (14%)	0	100 100
52	2u	21/27 (78%)	19 (90%)	1 (5%)	1 (5%)	2 6
56	1z	1/3 (33%)	0	1 (100%)	0	100 100
56	2z	1/3 (33%)	0	1 (100%)	0	100 100
All	All	11372/12134 (94%)	10129 (89%)	1098 (10%)	145 (1%)	10 32

All (145) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA

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Mol	Chain	Res	Type
6	1G	181	ARG
7	1H	126	PRO
21	1Z	53	ILE
26	14	49	PHE
33	1b	17	PHE
36	1e	96	PRO
41	1j	79	ARG
42	1k	49	GLY
44	1m	67	GLU
6	2G	96	ARG
8	2I	10	GLU
14	2S	81	GLY
21	2Z	93	ASP
26	24	45	GLY
26	24	50	VAL
33	2b	17	PHE
42	2k	49	GLY
45	2n	14	PRO
48	2q	67	LYS
19	1X	94	GLY
21	1Z	93	ASP
21	1Z	163	LEU
26	14	45	GLY
26	14	47	GLN
33	1b	129	GLU
35	1d	173	TRP
36	1e	97	GLY
40	1i	11	LYS
40	1i	54	ASP
41	1j	55	LYS
43	1l	91	LYS
51	1t	47	GLY
51	1t	100	ILE
5	2F	130	ALA
6	2G	42	GLY
6	2G	126	ASP
7	2H	92	ILE
11	2P	36	LYS
14	2S	84	GLN
15	2T	100	TYR
33	2b	123	ALA
36	2e	85	GLY

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Mol	Chain	Res	Type
48	2q	68	ARG
50	2s	57	HIS
51	2t	47	GLY
6	1G	43	LEU
11	1P	29	LYS
11	1P	38	GLN
17	1V	79	VAL
33	1b	20	GLU
33	1b	126	GLU
34	1c	71	ALA
38	1g	4	ARG
44	1m	106	ASN
51	1t	102	GLY
4	2E	52	LEU
4	2E	69	LYS
6	2G	47	LYS
6	2G	104	GLU
7	2H	46	GLU
8	2I	117	GLU
11	2P	29	LYS
17	2V	79	VAL
28	26	27	LYS
33	2b	87	ARG
33	2b	202	PRO
38	2g	55	GLY
51	2t	99	LEU
4	1E	52	LEU
11	1P	45	LEU
13	1R	11	ASN
17	1V	53	GLU
21	1Z	51	ALA
33	1b	13	ALA
33	1b	124	SER
35	1d	125	HIS
36	1e	85	GLY
41	1j	30	SER
41	1j	33	GLN
4	2E	144	ARG
8	2I	39	ALA
9	2N	2	LYS
11	2P	38	GLN
11	2P	45	LEU

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Mol	Chain	Res	Type
14	2S	20	ARG
14	2S	79	ALA
15	2T	95	ARG
19	2X	94	GLY
21	2Z	158	PRO
23	21	78	LYS
26	24	47	GLN
33	2b	20	GLU
38	2g	85	TYR
39	2h	133	LEU
40	2i	121	ARG
41	2j	78	ASN
43	2l	105	TYR
51	2t	98	PRO
3	1D	263	ARG
33	1b	125	PRO
10	2O	5	GLN
13	2R	107	ASP
19	2X	15	GLU
21	2Z	104	PHE
21	2Z	171	ILE
33	2b	119	GLU
36	2e	124	GLY
36	2e	141	GLN
38	2g	52	GLU
38	2g	80	VAL
41	2j	75	ILE
42	2k	105	VAL
50	2s	81	ARG
51	2t	9	ASN
21	1Z	168	GLU
36	1e	69	VAL
37	1f	70	ASP
41	1j	77	PRO
5	2F	195	ASP
40	2i	56	LEU
44	2m	90	LEU
50	2s	9	VAL
3	1D	3	VAL
41	1j	91	PRO
46	1o	23	GLY
21	2Z	146	ILE

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Mol	Chain	Res	Type
22	20	30	VAL
35	2d	112	VAL
41	2j	41	PRO
43	2l	14	GLY
42	1k	105	VAL
6	2G	88	ILE
8	1I	145	VAL
33	1b	131	PRO
9	2N	49	GLY
10	2O	43	VAL
33	2b	231	GLU
34	2c	64	VAL
34	2c	99	VAL
25	23	59	VAL
36	2e	69	VAL
52	2u	23	PRO
21	2Z	165	VAL
17	2V	50	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	1D	215/218 (99%)	204 (95%)	11 (5%)	20 51
3	2D	215/218 (99%)	201 (94%)	14 (6%)	14 40
4	1E	164/166 (99%)	148 (90%)	16 (10%)	6 21
4	2E	164/166 (99%)	154 (94%)	10 (6%)	15 43
5	1F	160/166 (96%)	144 (90%)	16 (10%)	6 20
5	2F	159/166 (96%)	137 (86%)	22 (14%)	3 10
6	1G	143/156 (92%)	126 (88%)	17 (12%)	4 14
6	2G	143/156 (92%)	119 (83%)	24 (17%)	1 6
7	1H	144/148 (97%)	125 (87%)	19 (13%)	3 11
7	2H	144/148 (97%)	125 (87%)	19 (13%)	3 11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
8	1I	113/124 (91%)	84 (74%)	29 (26%)	0 1
8	2I	105/124 (85%)	81 (77%)	24 (23%)	0 2
9	1N	118/119 (99%)	106 (90%)	12 (10%)	6 19
9	2N	118/119 (99%)	107 (91%)	11 (9%)	7 23
10	1O	100/100 (100%)	93 (93%)	7 (7%)	12 36
10	2O	100/100 (100%)	92 (92%)	8 (8%)	10 30
11	1P	115/116 (99%)	105 (91%)	10 (9%)	8 26
11	2P	115/116 (99%)	103 (90%)	12 (10%)	5 18
12	1Q	111/111 (100%)	101 (91%)	10 (9%)	8 25
12	2Q	111/111 (100%)	96 (86%)	15 (14%)	3 10
13	1R	101/101 (100%)	94 (93%)	7 (7%)	13 37
13	2R	101/101 (100%)	99 (98%)	2 (2%)	50 81
14	1S	86/88 (98%)	73 (85%)	13 (15%)	2 8
14	2S	85/88 (97%)	69 (81%)	16 (19%)	1 4
15	1T	115/127 (91%)	108 (94%)	7 (6%)	15 43
15	2T	113/127 (89%)	107 (95%)	6 (5%)	19 49
16	1U	93/94 (99%)	83 (89%)	10 (11%)	5 17
16	2U	93/94 (99%)	87 (94%)	6 (6%)	14 40
17	1V	80/82 (98%)	74 (92%)	6 (8%)	11 33
17	2V	80/82 (98%)	68 (85%)	12 (15%)	2 8
18	1W	90/92 (98%)	86 (96%)	4 (4%)	24 56
18	2W	90/92 (98%)	81 (90%)	9 (10%)	6 20
19	1X	77/78 (99%)	72 (94%)	5 (6%)	14 40
19	2X	77/78 (99%)	70 (91%)	7 (9%)	7 24
20	1Y	85/91 (93%)	73 (86%)	12 (14%)	3 9
20	2Y	85/91 (93%)	73 (86%)	12 (14%)	3 9
21	1Z	135/179 (75%)	113 (84%)	22 (16%)	2 6
21	2Z	137/179 (76%)	109 (80%)	28 (20%)	1 3
22	10	65/67 (97%)	63 (97%)	2 (3%)	35 69
22	20	65/67 (97%)	64 (98%)	1 (2%)	60 86
23	11	80/83 (96%)	74 (92%)	6 (8%)	11 33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
23	21	80/83 (96%)	71 (89%)	9 (11%)	4 16
24	12	65/67 (97%)	58 (89%)	7 (11%)	5 17
24	22	65/67 (97%)	55 (85%)	10 (15%)	2 7
25	13	51/52 (98%)	44 (86%)	7 (14%)	3 10
25	23	50/52 (96%)	44 (88%)	6 (12%)	4 14
26	14	59/63 (94%)	47 (80%)	12 (20%)	1 3
26	24	53/63 (84%)	44 (83%)	9 (17%)	1 5
27	15	50/52 (96%)	44 (88%)	6 (12%)	4 14
27	25	50/52 (96%)	48 (96%)	2 (4%)	27 60
28	16	51/52 (98%)	47 (92%)	4 (8%)	10 31
28	26	50/52 (96%)	40 (80%)	10 (20%)	1 3
29	17	41/42 (98%)	38 (93%)	3 (7%)	11 34
29	27	41/42 (98%)	37 (90%)	4 (10%)	6 21
30	18	54/55 (98%)	50 (93%)	4 (7%)	11 33
30	28	54/55 (98%)	51 (94%)	3 (6%)	17 47
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 71
31	29	34/34 (100%)	31 (91%)	3 (9%)	8 26
33	1b	192/220 (87%)	169 (88%)	23 (12%)	4 14
33	2b	187/220 (85%)	145 (78%)	42 (22%)	1 2
34	1c	142/188 (76%)	129 (91%)	13 (9%)	7 24
34	2c	140/188 (74%)	114 (81%)	26 (19%)	1 4
35	1d	169/181 (93%)	147 (87%)	22 (13%)	3 11
35	2d	173/181 (96%)	148 (86%)	25 (14%)	2 8
36	1e	113/123 (92%)	99 (88%)	14 (12%)	4 13
36	2e	114/123 (93%)	99 (87%)	15 (13%)	3 11
37	1f	84/90 (93%)	73 (87%)	11 (13%)	3 11
37	2f	85/90 (94%)	74 (87%)	11 (13%)	3 11
38	1g	119/127 (94%)	101 (85%)	18 (15%)	2 8
38	2g	120/127 (94%)	104 (87%)	16 (13%)	3 10
39	1h	114/119 (96%)	98 (86%)	16 (14%)	3 9
39	2h	114/119 (96%)	100 (88%)	14 (12%)	4 13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
40	1i	90/99 (91%)	82 (91%)	8 (9%)	8 25
40	2i	89/99 (90%)	76 (85%)	13 (15%)	2 8
41	1j	66/92 (72%)	58 (88%)	8 (12%)	4 13
41	2j	69/92 (75%)	52 (75%)	17 (25%)	0 2
42	1k	82/99 (83%)	69 (84%)	13 (16%)	2 7
42	2k	83/99 (84%)	74 (89%)	9 (11%)	5 17
43	1l	96/108 (89%)	87 (91%)	9 (9%)	7 23
43	2l	96/108 (89%)	83 (86%)	13 (14%)	3 10
44	1m	93/101 (92%)	83 (89%)	10 (11%)	5 17
44	2m	92/101 (91%)	72 (78%)	20 (22%)	1 2
45	1n	49/50 (98%)	42 (86%)	7 (14%)	2 9
45	2n	49/50 (98%)	40 (82%)	9 (18%)	1 4
46	1o	78/80 (98%)	69 (88%)	9 (12%)	4 15
46	2o	78/80 (98%)	72 (92%)	6 (8%)	10 31
47	1p	69/74 (93%)	61 (88%)	8 (12%)	4 15
47	2p	68/74 (92%)	60 (88%)	8 (12%)	4 14
48	1q	94/97 (97%)	84 (89%)	10 (11%)	5 18
48	2q	94/97 (97%)	74 (79%)	20 (21%)	1 3
49	1r	59/77 (77%)	56 (95%)	3 (5%)	20 51
49	2r	59/77 (77%)	49 (83%)	10 (17%)	1 5
50	1s	69/80 (86%)	58 (84%)	11 (16%)	2 7
50	2s	67/80 (84%)	54 (81%)	13 (19%)	1 4
51	1t	70/82 (85%)	65 (93%)	5 (7%)	12 35
51	2t	70/82 (85%)	64 (91%)	6 (9%)	8 27
52	1u	18/22 (82%)	17 (94%)	1 (6%)	17 47
52	2u	18/22 (82%)	17 (94%)	1 (6%)	17 47
56	1z	2/2 (100%)	1 (50%)	1 (50%)	0 0
56	2z	2/2 (100%)	1 (50%)	1 (50%)	0 0
All	All	9307/10068 (92%)	8193 (88%)	1114 (12%)	4 14

All (1114) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	115	GLN
3	1D	174	ILE
3	1D	181	GLU
3	1D	189	CYS
3	1D	229	VAL
3	1D	242	ARG
3	1D	260	ARG
3	1D	266	SER
3	1D	273	ARG
3	1D	275	LYS
4	1E	12	THR
4	1E	18	ASP
4	1E	33	VAL
4	1E	38	THR
4	1E	41	LYS
4	1E	45	THR
4	1E	47	VAL
4	1E	55	ASN
4	1E	73	GLU
4	1E	87	GLU
4	1E	93	VAL
4	1E	116	VAL
4	1E	119	ARG
4	1E	154	LYS
4	1E	166	THR
4	1E	184	VAL
5	1F	17	ARG
5	1F	24	LEU
5	1F	33	LEU
5	1F	37	VAL
5	1F	39	TRP
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	82	ILE
5	1F	88	VAL
5	1F	132	VAL
5	1F	158	THR
5	1F	162	LEU
5	1F	165	ARG
5	1F	168	ARG
5	1F	183	VAL

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Mol	Chain	Res	Type
6	1G	5	VAL
6	1G	7	LEU
6	1G	21	ARG
6	1G	31	VAL
6	1G	43	LEU
6	1G	49	ASP
6	1G	60	LEU
6	1G	77	ILE
6	1G	79	ASN
6	1G	108	ASN
6	1G	133	LEU
6	1G	139	LEU
6	1G	140	ILE
6	1G	148	MET
6	1G	149	VAL
6	1G	159	VAL
6	1G	161	THR
7	1H	3	ARG
7	1H	17	VAL
7	1H	23	ARG
7	1H	24	VAL
7	1H	37	VAL
7	1H	49	VAL
7	1H	56	SER
7	1H	58	GLU
7	1H	77	LYS
7	1H	84	SER
7	1H	85	LYS
7	1H	92	ILE
7	1H	106	THR
7	1H	116	GLU
7	1H	119	GLU
7	1H	127	GLU
7	1H	132	ARG
7	1H	133	VAL
7	1H	134	SER
8	1I	2	LYS
8	1I	9	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	27	ARG
8	1I	37	VAL

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Mol	Chain	Res	Type
8	1I	38	LEU
8	1I	41	GLU
8	1I	44	LEU
8	1I	60	GLU
8	1I	64	GLU
8	1I	75	LEU
8	1I	76	THR
8	1I	79	ILE
8	1I	81	VAL
8	1I	86	THR
8	1I	87	LYS
8	1I	91	SER
8	1I	92	VAL
8	1I	95	LYS
8	1I	101	LEU
8	1I	102	SER
8	1I	108	THR
8	1I	109	ILE
8	1I	114	LEU
8	1I	116	LEU
8	1I	133	HIS
8	1I	141	LYS
8	1I	142	VAL
9	1N	1	MET
9	1N	5	VAL
9	1N	8	GLN
9	1N	9	VAL
9	1N	10	GLU
9	1N	46	VAL
9	1N	60	ILE
9	1N	62	VAL
9	1N	63	THR
9	1N	68	GLU
9	1N	131	GLN
9	1N	136	GLU
10	1O	21	CYS
10	1O	31	LYS
10	1O	35	VAL
10	1O	39	ILE
10	1O	75	SER
10	1O	114	ILE
10	1O	120	GLU

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Mol	Chain	Res	Type
11	1P	1	MET
11	1P	15	ARG
11	1P	47	ASP
11	1P	96	THR
11	1P	98	GLU
11	1P	99	LEU
11	1P	101	VAL
11	1P	114	ILE
11	1P	119	GLU
11	1P	148	LEU
12	1Q	7	MET
12	1Q	8	LYS
12	1Q	16	ARG
12	1Q	77	LYS
12	1Q	81	VAL
12	1Q	91	GLU
12	1Q	98	LYS
12	1Q	109	VAL
12	1Q	127	ILE
12	1Q	133	ARG
13	1R	14	SER
13	1R	15	SER
13	1R	30	THR
13	1R	36	THR
13	1R	91	GLN
13	1R	102	GLU
13	1R	114	VAL
14	1S	13	ARG
14	1S	14	VAL
14	1S	36	TYR
14	1S	46	VAL
14	1S	50	SER
14	1S	52	SER
14	1S	56	LEU
14	1S	57	LYS
14	1S	69	VAL
14	1S	71	ARG
14	1S	78	LEU
14	1S	80	LEU
14	1S	110	LEU
15	1T	8	LYS
15	1T	23	ARG

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Mol	Chain	Res	Type
15	1T	28	VAL
15	1T	34	VAL
15	1T	84	GLN
15	1T	96	ARG
15	1T	128	GLU
16	1U	29	SER
16	1U	34	LYS
16	1U	74	LEU
16	1U	77	SER
16	1U	78	THR
16	1U	83	LEU
16	1U	84	LYS
16	1U	95	LEU
16	1U	110	VAL
16	1U	111	GLU
17	1V	15	GLU
17	1V	46	VAL
17	1V	51	VAL
17	1V	79	VAL
17	1V	82	ARG
17	1V	92	THR
18	1W	6	ILE
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
19	1X	23	GLU
19	1X	43	VAL
19	1X	50	LYS
19	1X	52	VAL
19	1X	81	VAL
20	1Y	1	MET
20	1Y	2	ARG
20	1Y	9	LYS
20	1Y	44	ILE
20	1Y	55	TYR
20	1Y	61	ILE
20	1Y	72	VAL
20	1Y	86	ARG
20	1Y	91	GLU
20	1Y	99	CYS
20	1Y	106	LEU
20	1Y	107	ASP

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Mol	Chain	Res	Type
21	1Z	18	LEU
21	1Z	28	MET
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	46	LYS
21	1Z	53	ILE
21	1Z	56	VAL
21	1Z	61	LEU
21	1Z	92	SER
21	1Z	96	VAL
21	1Z	132	ASN
21	1Z	135	GLU
21	1Z	139	VAL
21	1Z	140	ASP
21	1Z	146	ILE
21	1Z	148	ASP
21	1Z	153	SER
21	1Z	154	ASP
21	1Z	162	GLU
21	1Z	169	GLU
21	1Z	170	THR
21	1Z	171	ILE
22	10	4	LYS
22	10	10	THR
23	11	3	LYS
23	11	37	ILE
23	11	40	ARG
23	11	51	VAL
23	11	59	THR
23	11	78	LYS
24	12	35	LEU
24	12	40	SER
24	12	41	ILE
24	12	53	LEU
24	12	55	ARG
24	12	65	ASN
24	12	69	ARG
25	13	29	ARG
25	13	32	GLN
25	13	37	LEU
25	13	40	THR
25	13	54	VAL

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Mol	Chain	Res	Type
25	13	56	VAL
25	13	60	GLU
26	14	5	ILE
26	14	22	ILE
26	14	27	THR
26	14	31	ILE
26	14	49	PHE
26	14	52	THR
26	14	53	GLU
26	14	56	VAL
26	14	63	TYR
26	14	67	TYR
26	14	68	ARG
26	14	69	LYS
27	15	6	VAL
27	15	26	THR
27	15	40	LYS
27	15	55	ARG
27	15	58	LEU
27	15	60	VAL
28	16	5	VAL
28	16	19	ARG
28	16	37	ARG
28	16	47	THR
29	17	1	MET
29	17	4	THR
29	17	43	THR
30	18	14	VAL
30	18	43	GLN
30	18	49	VAL
30	18	52	LYS
31	19	9	ARG
33	1b	8	LYS
33	1b	12	GLU
33	1b	17	PHE
33	1b	21	ARG
33	1b	23	ARG
33	1b	35	GLU
33	1b	39	ILE
33	1b	64	ARG
33	1b	69	LEU
33	1b	80	ILE

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Mol	Chain	Res	Type
33	1b	83	MET
33	1b	108	ILE
33	1b	110	GLN
33	1b	115	LEU
33	1b	133	LYS
33	1b	157	ARG
33	1b	160	ASP
33	1b	170	GLU
33	1b	185	ILE
33	1b	187	LEU
33	1b	196	LEU
33	1b	208	ILE
33	1b	212	GLN
34	1c	3	ASN
34	1c	26	LYS
34	1c	63	ASN
34	1c	64	VAL
34	1c	77	ILE
34	1c	82	GLU
34	1c	104	GLN
34	1c	136	GLN
34	1c	154	SER
34	1c	172	ARG
34	1c	190	ARG
34	1c	195	VAL
34	1c	207	VAL
35	1d	12	CYS
35	1d	19	LEU
35	1d	38	TYR
35	1d	59	ARG
35	1d	76	ARG
35	1d	77	ASN
35	1d	85	LYS
35	1d	89	THR
35	1d	92	VAL
35	1d	100	ARG
35	1d	132	ARG
35	1d	138	TYR
35	1d	140	VAL
35	1d	141	ARG
35	1d	158	ILE
35	1d	170	VAL

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Mol	Chain	Res	Type
35	1d	175	SER
35	1d	178	VAL
35	1d	187	ARG
35	1d	190	ASP
35	1d	194	LEU
35	1d	200	GLU
36	1e	11	ILE
36	1e	12	LEU
36	1e	20	GLN
36	1e	31	LEU
36	1e	33	VAL
36	1e	34	VAL
36	1e	41	VAL
36	1e	47	LYS
36	1e	53	LEU
36	1e	56	GLN
36	1e	73	ASN
36	1e	79	GLU
36	1e	144	THR
36	1e	147	ASP
37	1f	19	LEU
37	1f	21	LEU
37	1f	36	ARG
37	1f	45	LEU
37	1f	55	ASP
37	1f	64	GLN
37	1f	65	VAL
37	1f	70	ASP
37	1f	72	VAL
37	1f	75	LEU
37	1f	78	GLU
38	1g	9	VAL
38	1g	36	LYS
38	1g	38	LEU
38	1g	50	ILE
38	1g	52	GLU
38	1g	57	GLU
38	1g	59	LEU
38	1g	61	VAL
38	1g	75	VAL
38	1g	85	TYR
38	1g	90	GLU

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Mol	Chain	Res	Type
38	1g	98	SER
38	1g	104	LEU
38	1g	110	GLN
38	1g	115	ARG
38	1g	120	ILE
38	1g	125	MET
38	1g	140	ASP
39	1h	3	THR
39	1h	10	LEU
39	1h	23	SER
39	1h	45	ILE
39	1h	50	ARG
39	1h	51	VAL
39	1h	61	VAL
39	1h	77	GLU
39	1h	82	HIS
39	1h	84	ARG
39	1h	86	ILE
39	1h	98	LYS
39	1h	107	LEU
39	1h	112	LEU
39	1h	123	GLU
39	1h	133	LEU
40	1i	9	ARG
40	1i	25	LYS
40	1i	29	ASN
40	1i	81	ILE
40	1i	96	LEU
40	1i	99	LEU
40	1i	103	THR
40	1i	128	ARG
41	1j	34	VAL
41	1j	38	ILE
41	1j	55	LYS
41	1j	66	ARG
41	1j	67	THR
41	1j	81	THR
41	1j	94	VAL
41	1j	100	THR
42	1k	31	THR
42	1k	48	ILE
42	1k	63	LEU

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Mol	Chain	Res	Type
42	1k	77	MET
42	1k	80	VAL
42	1k	84	VAL
42	1k	98	LEU
42	1k	99	GLN
42	1k	109	VAL
42	1k	114	VAL
42	1k	117	ASN
42	1k	122	LYS
42	1k	125	PHE
43	1l	18	VAL
43	1l	33	ARG
43	1l	40	VAL
43	1l	43	VAL
43	1l	54	LYS
43	1l	58	VAL
43	1l	83	VAL
43	1l	97	ARG
43	1l	113	ARG
44	1m	3	ARG
44	1m	4	ILE
44	1m	11	ARG
44	1m	17	VAL
44	1m	49	THR
44	1m	64	TRP
44	1m	67	GLU
44	1m	78	ILE
44	1m	86	CYS
44	1m	106	ASN
45	1n	3	ARG
45	1n	13	THR
45	1n	32	SER
45	1n	33	VAL
45	1n	42	ILE
45	1n	56	VAL
45	1n	57	ARG
46	1o	6	GLU
46	1o	21	ASP
46	1o	42	HIS
46	1o	45	VAL
46	1o	57	LEU
46	1o	74	ASP

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Mol	Chain	Res	Type
46	1o	76	GLU
46	1o	84	LYS
46	1o	88	ARG
47	1p	20	VAL
47	1p	21	VAL
47	1p	27	LYS
47	1p	45	THR
47	1p	50	LYS
47	1p	60	LEU
47	1p	67	THR
47	1p	76	GLN
48	1q	9	VAL
48	1q	11	VAL
48	1q	14	LYS
48	1q	25	ARG
48	1q	35	VAL
48	1q	36	ILE
48	1q	67	LYS
48	1q	68	ARG
48	1q	93	GLN
48	1q	100	LYS
49	1r	31	LEU
49	1r	38	GLU
49	1r	76	LEU
50	1s	5	LEU
50	1s	9	VAL
50	1s	19	VAL
50	1s	23	ASN
50	1s	27	GLU
50	1s	28	LYS
50	1s	37	ARG
50	1s	47	HIS
50	1s	66	MET
50	1s	67	VAL
50	1s	79	THR
51	1t	10	LEU
51	1t	11	SER
51	1t	13	LEU
51	1t	71	THR
51	1t	89	ARG
52	1u	20	LYS
56	1z	2	ARG

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Mol	Chain	Res	Type
3	2D	3	VAL
3	2D	27	THR
3	2D	35	LYS
3	2D	38	LYS
3	2D	73	VAL
3	2D	113	VAL
3	2D	118	VAL
3	2D	140	THR
3	2D	176	ARG
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	266	SER
3	2D	275	LYS
4	2E	41	LYS
4	2E	45	THR
4	2E	61	ARG
4	2E	116	VAL
4	2E	119	ARG
4	2E	134	ILE
4	2E	150	VAL
4	2E	171	GLU
4	2E	175	VAL
4	2E	184	VAL
5	2F	12	LEU
5	2F	15	SER
5	2F	28	ILE
5	2F	33	LEU
5	2F	36	VAL
5	2F	41	LEU
5	2F	48	THR
5	2F	64	ILE
5	2F	70	THR
5	2F	95	ARG
5	2F	96	ASP
5	2F	107	LYS
5	2F	108	LYS
5	2F	114	VAL
5	2F	153	SER
5	2F	157	VAL
5	2F	158	THR
5	2F	161	GLU

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Mol	Chain	Res	Type
5	2F	183	VAL
5	2F	186	ILE
5	2F	191	ARG
5	2F	203	GLN
6	2G	8	LYS
6	2G	20	ILE
6	2G	26	GLN
6	2G	41	GLN
6	2G	43	LEU
6	2G	45	GLU
6	2G	47	LYS
6	2G	51	ARG
6	2G	53	LEU
6	2G	62	LEU
6	2G	66	GLN
6	2G	77	ILE
6	2G	86	MET
6	2G	88	ILE
6	2G	92	VAL
6	2G	99	MET
6	2G	111	LEU
6	2G	120	LEU
6	2G	123	ASN
6	2G	130	ASN
6	2G	138	GLN
6	2G	140	ILE
6	2G	149	VAL
6	2G	172	LEU
7	2H	3	ARG
7	2H	7	LEU
7	2H	37	VAL
7	2H	49	VAL
7	2H	51	ARG
7	2H	58	GLU
7	2H	65	HIS
7	2H	67	LEU
7	2H	70	THR
7	2H	85	LYS
7	2H	103	LEU
7	2H	106	THR
7	2H	115	VAL
7	2H	119	GLU

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Mol	Chain	Res	Type
7	2H	127	GLU
7	2H	133	VAL
7	2H	136	ILE
7	2H	149	ARG
7	2H	153	LYS
8	2I	4	ILE
8	2I	6	LEU
8	2I	15	VAL
8	2I	38	LEU
8	2I	42	SER
8	2I	44	LEU
8	2I	51	ILE
8	2I	58	LEU
8	2I	61	ARG
8	2I	68	LEU
8	2I	77	LEU
8	2I	78	THR
8	2I	81	VAL
8	2I	82	ARG
8	2I	86	THR
8	2I	87	LYS
8	2I	104	GLN
8	2I	107	VAL
8	2I	114	LEU
8	2I	117	GLU
8	2I	136	VAL
8	2I	139	GLN
8	2I	140	LEU
8	2I	144	VAL
9	2N	22	THR
9	2N	28	THR
9	2N	38	HIS
9	2N	43	THR
9	2N	46	VAL
9	2N	48	MET
9	2N	62	VAL
9	2N	65	LYS
9	2N	84	LYS
9	2N	85	ILE
9	2N	131	GLN
10	2O	35	VAL
10	2O	38	VAL

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Mol	Chain	Res	Type
10	2O	52	VAL
10	2O	58	VAL
10	2O	77	ILE
10	2O	96	THR
10	2O	108	GLU
10	2O	113	LYS
11	2P	3	LEU
11	2P	6	LEU
11	2P	7	ARG
11	2P	30	THR
11	2P	45	LEU
11	2P	56	SER
11	2P	68	GLN
11	2P	77	ARG
11	2P	90	ARG
11	2P	96	THR
11	2P	123	LEU
11	2P	133	SER
12	2Q	1	MET
12	2Q	5	ARG
12	2Q	7	MET
12	2Q	12	GLN
12	2Q	54	MET
12	2Q	85	LYS
12	2Q	90	VAL
12	2Q	103	MET
12	2Q	109	VAL
12	2Q	116	GLU
12	2Q	123	HIS
12	2Q	133	ARG
12	2Q	134	ARG
12	2Q	135	ASP
12	2Q	141	GLN
13	2R	24	GLN
13	2R	73	VAL
14	2S	5	THR
14	2S	9	ARG
14	2S	13	ARG
14	2S	19	LYS
14	2S	20	ARG
14	2S	28	VAL
14	2S	35	ILE

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Mol	Chain	Res	Type
14	2S	36	TYR
14	2S	43	GLU
14	2S	49	VAL
14	2S	57	LYS
14	2S	63	THR
14	2S	78	LEU
14	2S	85	VAL
14	2S	98	VAL
14	2S	101	LEU
15	2T	39	ARG
15	2T	54	ARG
15	2T	63	VAL
15	2T	89	VAL
15	2T	90	GLN
15	2T	96	ARG
16	2U	9	VAL
16	2U	17	ILE
16	2U	90	VAL
16	2U	95	LEU
16	2U	110	VAL
16	2U	117	GLN
17	2V	1	MET
17	2V	7	THR
17	2V	14	VAL
17	2V	19	LYS
17	2V	25	LEU
17	2V	33	VAL
17	2V	49	THR
17	2V	73	SER
17	2V	79	VAL
17	2V	85	LYS
17	2V	93	GLU
17	2V	98	GLU
18	2W	10	VAL
18	2W	11	ARG
18	2W	17	VAL
18	2W	18	ARG
18	2W	27	LYS
18	2W	59	VAL
18	2W	63	ASP
18	2W	67	ASP
18	2W	96	ILE

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Mol	Chain	Res	Type
19	2X	1	MET
19	2X	18	TYR
19	2X	43	VAL
19	2X	57	LEU
19	2X	75	ASP
19	2X	80	ILE
19	2X	92	LEU
20	2Y	2	ARG
20	2Y	12	THR
20	2Y	19	LYS
20	2Y	30	VAL
20	2Y	42	VAL
20	2Y	44	ILE
20	2Y	49	VAL
20	2Y	62	GLU
20	2Y	72	VAL
20	2Y	88	LYS
20	2Y	89	PHE
20	2Y	99	CYS
21	2Z	6	LYS
21	2Z	18	LEU
21	2Z	28	MET
21	2Z	35	ARG
21	2Z	36	LYS
21	2Z	42	VAL
21	2Z	47	VAL
21	2Z	50	GLN
21	2Z	56	VAL
21	2Z	70	LEU
21	2Z	71	VAL
21	2Z	80	ARG
21	2Z	82	ARG
21	2Z	84	GLU
21	2Z	91	LEU
21	2Z	98	MET
21	2Z	121	HIS
21	2Z	123	ASP
21	2Z	128	VAL
21	2Z	136	PHE
21	2Z	144	LEU
21	2Z	145	GLU
21	2Z	154	ASP

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Mol	Chain	Res	Type
21	2Z	155	LEU
21	2Z	157	LEU
21	2Z	161	VAL
21	2Z	163	LEU
21	2Z	169	GLU
22	20	55	ARG
23	21	4	VAL
23	21	26	ARG
23	21	30	VAL
23	21	35	THR
23	21	40	ARG
23	21	41	ARG
23	21	46	LEU
23	21	69	LYS
23	21	82	LEU
24	22	19	VAL
24	22	21	LEU
24	22	25	VAL
24	22	29	LYS
24	22	38	GLN
24	22	41	ILE
24	22	44	LEU
24	22	50	ILE
24	22	53	LEU
24	22	62	THR
25	23	31	LEU
25	23	34	GLU
25	23	35	ARG
25	23	54	VAL
25	23	56	VAL
25	23	59	VAL
26	24	26	SER
26	24	31	ILE
26	24	33	VAL
26	24	35	VAL
26	24	49	PHE
26	24	56	VAL
26	24	63	TYR
26	24	68	ARG
26	24	69	LYS
27	25	57	VAL
27	25	59	GLU

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Mol	Chain	Res	Type
28	26	5	VAL
28	26	9	LEU
28	26	14	THR
28	26	15	GLU
28	26	32	ASN
28	26	34	LEU
28	26	40	CYS
28	26	45	LYS
28	26	48	VAL
28	26	50	ARG
29	27	1	MET
29	27	24	THR
29	27	36	GLN
29	27	41	ARG
30	28	4	MET
30	28	50	LEU
30	28	62	LEU
31	29	4	ARG
31	29	6	SER
31	29	26	ILE
33	2b	8	LYS
33	2b	9	GLU
33	2b	11	LEU
33	2b	12	GLU
33	2b	16	HIS
33	2b	47	THR
33	2b	48	MET
33	2b	55	PHE
33	2b	58	ILE
33	2b	61	LEU
33	2b	67	THR
33	2b	68	ILE
33	2b	71	VAL
33	2b	76	GLN
33	2b	93	VAL
33	2b	94	ASN
33	2b	96	ARG
33	2b	107	THR
33	2b	110	GLN
33	2b	117	GLU
33	2b	118	LEU
33	2b	127	ILE

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Mol	Chain	Res	Type
33	2b	136	VAL
33	2b	138	LEU
33	2b	141	GLU
33	2b	144	ARG
33	2b	149	LEU
33	2b	150	SER
33	2b	154	LEU
33	2b	155	LEU
33	2b	157	ARG
33	2b	163	PHE
33	2b	172	ILE
33	2b	179	LYS
33	2b	180	LEU
33	2b	185	ILE
33	2b	189	ASP
33	2b	196	LEU
33	2b	210	SER
33	2b	213	LEU
33	2b	215	LEU
33	2b	230	VAL
34	2c	5	ILE
34	2c	14	ILE
34	2c	21	ARG
34	2c	32	LEU
34	2c	38	ARG
34	2c	39	ILE
34	2c	45	LYS
34	2c	47	LEU
34	2c	68	VAL
34	2c	70	VAL
34	2c	77	ILE
34	2c	91	LEU
34	2c	101	LEU
34	2c	105	GLU
34	2c	128	PHE
34	2c	132	ARG
34	2c	150	LYS
34	2c	151	VAL
34	2c	152	ILE
34	2c	153	VAL
34	2c	175	LEU
34	2c	176	HIS

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Mol	Chain	Res	Type
34	2c	182	ILE
34	2c	190	ARG
34	2c	196	LEU
34	2c	206	GLU
35	2d	12	CYS
35	2d	21	LEU
35	2d	26	CYS
35	2d	45	GLN
35	2d	52	SER
35	2d	53	ASP
35	2d	59	ARG
35	2d	60	GLU
35	2d	70	ILE
35	2d	78	LEU
35	2d	83	SER
35	2d	96	LEU
35	2d	120	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	155	LEU
35	2d	156	GLU
35	2d	158	ILE
35	2d	159	ARG
35	2d	165	MET
35	2d	178	VAL
35	2d	187	ARG
35	2d	190	ASP
35	2d	193	ASP
35	2d	202	LEU
36	2e	10	MET
36	2e	13	ILE
36	2e	16	THR
36	2e	31	LEU
36	2e	38	GLN
36	2e	41	VAL
36	2e	47	LYS
36	2e	51	VAL
36	2e	64	ARG
36	2e	67	VAL
36	2e	72	GLN
36	2e	73	ASN
36	2e	78	HIS

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Mol	Chain	Res	Type
36	2e	120	THR
36	2e	150	ARG
37	2f	15	ASP
37	2f	19	LEU
37	2f	21	LEU
37	2f	36	ARG
37	2f	45	LEU
37	2f	64	GLN
37	2f	69	GLU
37	2f	75	LEU
37	2f	83	ASP
37	2f	94	GLN
37	2f	95	GLU
38	2g	9	VAL
38	2g	15	ASP
38	2g	16	LEU
38	2g	24	THR
38	2g	32	ARG
38	2g	47	CYS
38	2g	52	GLU
38	2g	53	LYS
38	2g	61	VAL
38	2g	72	ARG
38	2g	78	ARG
38	2g	79	ARG
38	2g	94	ARG
38	2g	97	GLN
38	2g	110	GLN
38	2g	113	GLU
39	2h	3	THR
39	2h	8	ASP
39	2h	26	VAL
39	2h	37	ARG
39	2h	45	ILE
39	2h	51	VAL
39	2h	54	ASP
39	2h	85	ARG
39	2h	103	VAL
39	2h	109	ILE
39	2h	112	LEU
39	2h	113	SER
39	2h	127	LEU

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Mol	Chain	Res	Type
39	2h	133	LEU
40	2i	29	ASN
40	2i	47	LEU
40	2i	50	LEU
40	2i	54	ASP
40	2i	58	HIS
40	2i	66	ARG
40	2i	74	ILE
40	2i	89	ASN
40	2i	99	LEU
40	2i	102	LEU
40	2i	105	ASP
40	2i	107	ARG
40	2i	111	ARG
41	2j	8	LEU
41	2j	25	GLU
41	2j	29	ARG
41	2j	33	GLN
41	2j	34	VAL
41	2j	38	ILE
41	2j	46	ARG
41	2j	49	VAL
41	2j	55	LYS
41	2j	62	HIS
41	2j	67	THR
41	2j	73	ASP
41	2j	84	GLN
41	2j	95	GLU
41	2j	96	ILE
41	2j	97	GLU
41	2j	98	ILE
42	2k	14	VAL
42	2k	30	VAL
42	2k	40	ILE
42	2k	41	THR
42	2k	48	ILE
42	2k	84	VAL
42	2k	105	VAL
42	2k	114	VAL
42	2k	125	PHE
43	2l	8	ASN
43	2l	33	ARG

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Mol	Chain	Res	Type
43	2l	36	VAL
43	2l	39	VAL
43	2l	40	VAL
43	2l	59	ARG
43	2l	67	THR
43	2l	83	VAL
43	2l	85	ILE
43	2l	86	ARG
43	2l	112	ASP
43	2l	116	SER
43	2l	122	THR
44	2m	4	ILE
44	2m	11	ARG
44	2m	17	VAL
44	2m	25	ILE
44	2m	32	GLU
44	2m	47	ASP
44	2m	50	GLU
44	2m	52	GLU
44	2m	57	ARG
44	2m	60	VAL
44	2m	67	GLU
44	2m	81	LEU
44	2m	92	HIS
44	2m	94	ARG
44	2m	98	VAL
44	2m	102	ARG
44	2m	103	THR
44	2m	106	ASN
44	2m	115	LYS
44	2m	120	LYS
45	2n	3	ARG
45	2n	9	LYS
45	2n	12	ARG
45	2n	19	ARG
45	2n	22	THR
45	2n	25	VAL
45	2n	29	ARG
45	2n	33	VAL
45	2n	58	LYS
46	2o	5	LYS
46	2o	32	LEU

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Mol	Chain	Res	Type
46	2o	56	LEU
46	2o	58	MET
46	2o	59	MET
46	2o	76	GLU
47	2p	3	LYS
47	2p	4	ILE
47	2p	20	VAL
47	2p	21	VAL
47	2p	29	ASP
47	2p	42	ARG
47	2p	67	THR
47	2p	76	GLN
48	2q	5	VAL
48	2q	14	LYS
48	2q	34	LYS
48	2q	36	ILE
48	2q	41	LYS
48	2q	43	LEU
48	2q	52	LYS
48	2q	55	ASP
48	2q	56	VAL
48	2q	60	ILE
48	2q	61	GLU
48	2q	63	ARG
48	2q	67	LYS
48	2q	68	ARG
48	2q	70	ARG
48	2q	73	VAL
48	2q	77	VAL
48	2q	84	LEU
48	2q	90	ILE
48	2q	99	SER
49	2r	26	LEU
49	2r	35	ARG
49	2r	44	LEU
49	2r	47	THR
49	2r	54	ARG
49	2r	66	LEU
49	2r	68	LYS
49	2r	78	LEU
49	2r	84	LYS
49	2r	85	LEU

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Mol	Chain	Res	Type
50	2s	14	HIS
50	2s	27	GLU
50	2s	30	LEU
50	2s	37	ARG
50	2s	41	VAL
50	2s	45	VAL
50	2s	48	THR
50	2s	51	VAL
50	2s	56	GLN
50	2s	64	GLU
50	2s	65	ASN
50	2s	73	GLU
50	2s	83	HIS
51	2t	45	GLN
51	2t	46	GLU
51	2t	54	LYS
51	2t	86	ARG
51	2t	88	VAL
51	2t	100	ILE
52	2u	7	ARG
56	2z	2	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (146) such sidechains are listed below:

Mol	Chain	Res	Type
5	1F	8	GLN
5	1F	69	HIS
5	1F	133	ASN
5	1F	203	GLN
9	1N	94	HIS
9	1N	128	HIS
10	1O	89	ASN
12	1Q	57	HIS
13	1R	61	HIS
13	1R	71	GLN
14	1S	95	HIS
15	1T	55	ASN
15	1T	58	ASN
16	1U	117	GLN
18	1W	111	HIS
19	1X	31	HIS
19	1X	82	GLN

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Mol	Chain	Res	Type
21	1Z	121	HIS
21	1Z	151	HIS
22	10	35	ASN
22	10	70	GLN
24	12	38	GLN
24	12	48	HIS
24	12	65	ASN
24	12	70	GLN
25	13	32	GLN
26	14	40	HIS
26	14	60	GLN
30	18	35	GLN
31	19	20	HIS
33	1b	40	HIS
33	1b	135	GLN
34	1c	6	HIS
34	1c	69	HIS
34	1c	118	GLN
34	1c	123	GLN
35	1d	77	ASN
35	1d	116	GLN
35	1d	119	GLN
35	1d	123	HIS
35	1d	125	HIS
36	1e	20	GLN
36	1e	56	GLN
36	1e	78	HIS
36	1e	141	GLN
37	1f	57	GLN
37	1f	73	ASN
37	1f	100	ASN
38	1g	28	ASN
38	1g	106	GLN
38	1g	148	ASN
39	1h	82	HIS
40	1i	3	GLN
40	1i	34	ASN
40	1i	38	GLN
40	1i	58	HIS
40	1i	124	GLN
41	1j	56	HIS
41	1j	68	HIS

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Mol	Chain	Res	Type
42	1k	38	ASN
42	1k	104	GLN
43	1l	99	HIS
44	1m	77	ASN
46	1o	9	GLN
46	1o	46	HIS
46	1o	71	GLN
47	1p	76	GLN
48	1q	93	GLN
49	1r	63	GLN
50	1s	83	HIS
51	1t	42	GLN
51	1t	75	ASN
51	1t	90	GLN
3	2D	87	ASN
3	2D	126	GLN
3	2D	129	ASN
4	2E	48	GLN
4	2E	55	ASN
5	2F	40	GLN
5	2F	69	HIS
5	2F	75	HIS
5	2F	133	ASN
7	2H	111	HIS
7	2H	147	ASN
9	2N	8	GLN
10	2O	88	ASN
10	2O	90	GLN
12	2Q	12	GLN
12	2Q	57	HIS
12	2Q	123	HIS
13	2R	24	GLN
14	2S	38	GLN
15	2T	43	GLN
15	2T	58	ASN
15	2T	79	HIS
15	2T	90	GLN
16	2U	72	HIS
16	2U	94	ASN
16	2U	117	GLN
17	2V	64	HIS
17	2V	80	GLN

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Mol	Chain	Res	Type
19	2X	31	HIS
21	2Z	50	GLN
21	2Z	73	GLN
21	2Z	151	HIS
22	20	17	GLN
22	20	70	GLN
23	21	56	GLN
24	22	38	GLN
24	22	56	GLN
26	24	40	HIS
33	2b	94	ASN
33	2b	110	GLN
33	2b	135	GLN
34	2c	98	ASN
35	2d	116	GLN
35	2d	119	GLN
35	2d	129	ASN
36	2e	65	ASN
36	2e	127	ASN
36	2e	141	GLN
37	2f	57	GLN
37	2f	73	ASN
37	2f	100	ASN
38	2g	28	ASN
38	2g	106	GLN
40	2i	31	GLN
40	2i	34	ASN
40	2i	87	GLN
40	2i	117	HIS
41	2j	13	HIS
41	2j	62	HIS
42	2k	22	HIS
42	2k	99	GLN
42	2k	116	HIS
44	2m	77	ASN
46	2o	50	HIS
48	2q	45	HIS
49	2r	63	GLN
50	2s	23	ASN
50	2s	57	HIS
50	2s	69	HIS
50	2s	83	HIS

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Mol	Chain	Res	Type
51	2t	16	HIS
51	2t	42	GLN
51	2t	90	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	527 (18%)	24 (0%)
1	2A	2791/2915 (95%)	532 (19%)	24 (0%)
2	1B	119/121 (98%)	15 (12%)	0
2	2B	118/121 (97%)	28 (23%)	0
32	1a	1497/1521 (98%)	281 (18%)	0
32	2a	1501/1521 (98%)	364 (24%)	0
53	1v	12/24 (50%)	2 (16%)	0
53	2v	12/24 (50%)	5 (41%)	0
54	1w	71/76 (93%)	33 (46%)	0
54	2w	71/76 (93%)	34 (47%)	0
55	1x	75/77 (97%)	17 (22%)	0
55	2x	75/77 (97%)	17 (22%)	0
57	1y	72/76 (94%)	34 (47%)	0
57	2y	72/76 (94%)	38 (52%)	0
All	All	9350/9620 (97%)	1927 (20%)	48 (0%)

All (1927) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	10	G
1	1A	12	U
1	1A	15	G
1	1A	29	U
1	1A	34	C
1	1A	36	G
1	1A	45	C
1	1A	50	U
1	1A	55	G
1	1A	61	G
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	78	A
1	1A	84	A

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Mol	Chain	Res	Type
1	1A	94	C
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	139(A)	G
1	1A	145	G
1	1A	154	G
1	1A	154(A)	C
1	1A	173	G
1	1A	182	A
1	1A	196	A
1	1A	198	C
1	1A	199	A
1	1A	205	G
1	1A	214	G
1	1A	215	G
1	1A	216	A
1	1A	221	A
1	1A	222	A
1	1A	223	A
1	1A	225	A
1	1A	228	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	265	A
1	1A	267	C
1	1A	271(J)	C
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	271(O)	C
1	1A	271(P)	C
1	1A	271(R)	G
1	1A	272(B)	G
1	1A	272(I)	U
1	1A	275	G
1	1A	279	C
1	1A	311	A

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Mol	Chain	Res	Type
1	1A	329	G
1	1A	330	A
1	1A	331	A
1	1A	338	G
1	1A	352	G
1	1A	357	A
1	1A	363	G
1	1A	363(A)	A
1	1A	363(B)	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	418	G
1	1A	428	A
1	1A	443	A
1	1A	444	C
1	1A	448	U
1	1A	449	A
1	1A	454	A
1	1A	455	C
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	494	G
1	1A	504	U
1	1A	505	A
1	1A	508	G
1	1A	509	C
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	586	A
1	1A	593	G
1	1A	603	A

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Mol	Chain	Res	Type
1	1A	604	G
1	1A	607	U
1	1A	614(A)	U
1	1A	614(B)	G
1	1A	615	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(D)	C
1	1A	652(F)	G
1	1A	652(T)	C
1	1A	654	A
1	1A	669	G
1	1A	686	G
1	1A	717	G
1	1A	726	G
1	1A	730	C
1	1A	732	C
1	1A	740	U
1	1A	746	A
1	1A	747	U
1	1A	762	U
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	783	A
1	1A	784	A
1	1A	785	G
1	1A	789	A
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	819	A
1	1A	827	U
1	1A	828	U
1	1A	830	G
1	1A	832	G
1	1A	859	G
1	1A	866	A
1	1A	879	G
1	1A	880	G

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Mol	Chain	Res	Type
1	1A	883	G
1	1A	884	C
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	895	U
1	1A	896	A
1	1A	897	C
1	1A	898	C
1	1A	907	U
1	1A	910	A
1	1A	915	C
1	1A	931	G
1	1A	932	G
1	1A	938	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C
1	1A	963	U
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	985	C
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1025	G
1	1A	1026	U
1	1A	1030	G
1	1A	1033	U
1	1A	1034	G
1	1A	1038	C
1	1A	1039	G
1	1A	1040	C
1	1A	1043	C
1	1A	1044	G
1	1A	1046	A

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Mol	Chain	Res	Type
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1055	G
1	1A	1058	G
1	1A	1063	G
1	1A	1065	U
1	1A	1068	G
1	1A	1069	A
1	1A	1071	G
1	1A	1073	A
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U
1	1A	1079	C
1	1A	1083	U
1	1A	1086	A
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	G
1	1A	1092	C
1	1A	1094	U
1	1A	1097	U
1	1A	1099	G
1	1A	1101	U
1	1A	1109	C
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G
1	1A	1116	C
1	1A	1117	G
1	1A	1130	U
1	1A	1131	G
1	1A	1135	C
1	1A	1136	G
1	1A	1142	U
1	1A	1149	G
1	1A	1169	G
1	1A	1171	G
1	1A	1173	G

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Mol	Chain	Res	Type
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1218	C
1	1A	1237	A
1	1A	1244	G
1	1A	1247	A
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1319	G
1	1A	1320	C
1	1A	1341	U
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1379	A
1	1A	1384	A
1	1A	1385	G
1	1A	1391	U
1	1A	1395	A
1	1A	1396	U
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1439	A
1	1A	1445	A
1	1A	1450	G
1	1A	1455	G
1	1A	1461	G
1	1A	1467	C
1	1A	1482	G
1	1A	1490	A

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Mol	Chain	Res	Type
1	1A	1493	C
1	1A	1494	A
1	1A	1505	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1539	G
1	1A	1543	C
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1647	G
1	1A	1648	C
1	1A	1664	A
1	1A	1674	G
1	1A	1678	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1718	G
1	1A	1719	G
1	1A	1722	A
1	1A	1739	U
1	1A	1743	C
1	1A	1746	G
1	1A	1757	U
1	1A	1758	G
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G

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Mol	Chain	Res	Type
1	1A	1816	G
1	1A	1819	A
1	1A	1828	G
1	1A	1829	A
1	1A	1839	G
1	1A	1847	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1914	C
1	1A	1921	G
1	1A	1929	G
1	1A	1930	G
1	1A	1935	G
1	1A	1936	A
1	1A	1937	A
1	1A	1938	A
1	1A	1941	C
1	1A	1955	U
1	1A	1963	U
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1983	C
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A
1	1A	2039	C
1	1A	2043	C
1	1A	2049	G
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A

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Mol	Chain	Res	Type
1	1A	2069	G
1	1A	2093	G
1	1A	2096	U
1	1A	2098	U
1	1A	2100	G
1	1A	2101	G
1	1A	2102	U
1	1A	2108	C
1	1A	2110	G
1	1A	2111	C
1	1A	2112	G
1	1A	2113	U
1	1A	2114	A
1	1A	2115	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2120	G
1	1A	2121	G
1	1A	2122	U
1	1A	2123	G
1	1A	2126	A
1	1A	2127	G
1	1A	2129	C
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2136	C
1	1A	2137	C
1	1A	2140	C
1	1A	2142	C
1	1A	2144	U
1	1A	2146	C
1	1A	2150	U
1	1A	2151	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G

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Mol	Chain	Res	Type
1	1A	2160	G
1	1A	2161	C
1	1A	2166	G
1	1A	2167	U
1	1A	2168	G
1	1A	2169	A
1	1A	2170	A
1	1A	2171	A
1	1A	2172	U
1	1A	2173	A
1	1A	2175	C
1	1A	2180	U
1	1A	2184	G
1	1A	2186	G
1	1A	2187	G
1	1A	2189	U
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2219	G
1	1A	2225	A
1	1A	2234	G
1	1A	2235	G
1	1A	2238	G
1	1A	2239	G
1	1A	2240	C
1	1A	2268	A
1	1A	2269	A
1	1A	2273	A
1	1A	2279	G
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2296	U
1	1A	2305	A
1	1A	2308	G
1	1A	2312	U
1	1A	2314	C
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G

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Mol	Chain	Res	Type
1	1A	2335	A
1	1A	2336	A
1	1A	2343	C
1	1A	2347	C
1	1A	2350	C
1	1A	2354	G
1	1A	2361	A
1	1A	2379	G
1	1A	2383	G
1	1A	2385	C
1	1A	2391	G
1	1A	2396	G
1	1A	2406	U
1	1A	2410	G
1	1A	2422	A
1	1A	2423	U
1	1A	2424	C
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2434	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2470	G
1	1A	2476	A
1	1A	2478	A
1	1A	2490	G
1	1A	2491	U
1	1A	2492	U
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2529	G
1	1A	2535	G
1	1A	2550	G
1	1A	2554	U
1	1A	2556	C
1	1A	2566	A

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Mol	Chain	Res	Type
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2582	G
1	1A	2601	C
1	1A	2602	A
1	1A	2608	G
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2686	G
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2718	G
1	1A	2721	A
1	1A	2726	U
1	1A	2732	G
1	1A	2733	A
1	1A	2758	A
1	1A	2765	A
1	1A	2766	G
1	1A	2769	C
1	1A	2778	A
1	1A	2780	G
1	1A	2789	C
1	1A	2790	A
1	1A	2791	C
1	1A	2792	G
1	1A	2793	G
1	1A	2794	C
1	1A	2802	G
1	1A	2805	G
1	1A	2820	A
1	1A	2821	A

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Mol	Chain	Res	Type
1	1A	2833	G
1	1A	2834	G
1	1A	2835	A
1	1A	2872	G
1	1A	2873	A
1	1A	2880	C
1	1A	2886	G
1	1A	2894	G
2	1B	13	A
2	1B	21	G
2	1B	24	G
2	1B	25	A
2	1B	30	C
2	1B	32	C
2	1B	35	U
2	1B	42	C
2	1B	45	A
2	1B	56	G
2	1B	63	G
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	5	U
32	1a	7	G
32	1a	9	G
32	1a	39	G
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	54	C
32	1a	61	G
32	1a	70	G
32	1a	77	G
32	1a	79	G
32	1a	91	C
32	1a	92	C
32	1a	93	G
32	1a	101	A
32	1a	116	A
32	1a	120	A
32	1a	121	C

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Mol	Chain	Res	Type
32	1a	131	C
32	1a	143	A
32	1a	144	G
32	1a	150	C
32	1a	151	A
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	179	A
32	1a	182	U
32	1a	189	G
32	1a	189(B)	C
32	1a	189(G)	G
32	1a	189(H)	G
32	1a	189(J)	G
32	1a	195	A
32	1a	197	A
32	1a	199	G
32	1a	200	G
32	1a	201	C
32	1a	203	U
32	1a	204	U
32	1a	219	C
32	1a	231	G
32	1a	247	G
32	1a	251	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	318	G
32	1a	321	A
32	1a	328	C
32	1a	329	A
32	1a	332	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	382	A
32	1a	384	G
32	1a	390	C

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Mol	Chain	Res	Type
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	407	G
32	1a	412	A
32	1a	413	G
32	1a	422	C
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	431	A
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	453	A
32	1a	457	C
32	1a	461	A
32	1a	470	C
32	1a	471	G
32	1a	482	A
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	506	G
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	519	C
32	1a	528	C
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	550	G
32	1a	559	A
32	1a	561	U
32	1a	564	C
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C

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Mol	Chain	Res	Type
32	1a	617	G
32	1a	619	U
32	1a	628	G
32	1a	630	G
32	1a	631	G
32	1a	634	C
32	1a	639	G
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	671	G
32	1a	673	G
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	723	U
32	1a	724	G
32	1a	734	G
32	1a	749	C
32	1a	755	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	806	C
32	1a	815	A
32	1a	817	C
32	1a	821	G
32	1a	827	U
32	1a	828	A
32	1a	838	G
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	852	G
32	1a	870	U
32	1a	873	A
32	1a	874	G
32	1a	885	G
32	1a	902	G
32	1a	914	A
32	1a	916	G

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Mol	Chain	Res	Type
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	936	C
32	1a	939	G
32	1a	942	G
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	995	C
32	1a	996	A
32	1a	997	U
32	1a	1000	U
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1008	C
32	1a	1009	G
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1037	C
32	1a	1038	C
32	1a	1041	A

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Mol	Chain	Res	Type
32	1a	1042	G
32	1a	1044	A
32	1a	1045	C
32	1a	1053	G
32	1a	1081	G
32	1a	1084	G
32	1a	1085	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1108	G
32	1a	1118	C
32	1a	1124	G
32	1a	1125	U
32	1a	1126	U
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1140	C
32	1a	1146	A
32	1a	1152	A
32	1a	1158	C
32	1a	1159	U
32	1a	1181	G
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1200	C
32	1a	1201	A
32	1a	1202	G
32	1a	1208	C
32	1a	1212	U
32	1a	1213	A
32	1a	1214	C
32	1a	1225	A
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1246	C
32	1a	1250	A
32	1a	1253	G

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Mol	Chain	Res	Type
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1263	C
32	1a	1270	C
32	1a	1275	A
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1312	G
32	1a	1319	A
32	1a	1320	C
32	1a	1323	G
32	1a	1331	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1350	A
32	1a	1353	G
32	1a	1363	C
32	1a	1364	U
32	1a	1365	G
32	1a	1370	G
32	1a	1379	G
32	1a	1397	C
32	1a	1400	5MC
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1458	G
32	1a	1487	G
32	1a	1492	A

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Mol	Chain	Res	Type
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1517	G
32	1a	1519	MA6
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
53	1v	13	A
53	1v	15	A
54	1w	2	G
54	1w	9	A
54	1w	14	A
54	1w	19	G
54	1w	20	U
54	1w	22	G
54	1w	23	A
54	1w	24	G
54	1w	25	C
54	1w	27	G
54	1w	36	U
54	1w	39	PSU
54	1w	40	C
54	1w	42	A
54	1w	45	G
54	1w	46	G7M
54	1w	47	U
54	1w	48	C
54	1w	49	G
54	1w	51	A
54	1w	53	G
54	1w	54	5MU
54	1w	56	C
54	1w	57	G
54	1w	59	A
54	1w	60	U
54	1w	62	C
54	1w	66	A
54	1w	69	A
54	1w	70	C

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Mol	Chain	Res	Type
54	1w	71	C
54	1w	73	A
54	1w	74	C
55	1x	2	G
55	1x	4	G
55	1x	6	G
55	1x	9	G
55	1x	14	A
55	1x	17	C
55	1x	17(A)	U
55	1x	18	G
55	1x	19	G
55	1x	20	U
55	1x	21	A
55	1x	22	G
55	1x	31	G
55	1x	43	A
55	1x	47	U
55	1x	48	C
55	1x	61	C
57	1y	5	C
57	1y	6	G
57	1y	7	U
57	1y	8	U
57	1y	9	A
57	1y	14	A
57	1y	19	G
57	1y	20	U
57	1y	21	A
57	1y	26	A
57	1y	27	G
57	1y	28	U
57	1y	29	U
57	1y	33	U
57	1y	38	A
57	1y	40	C
57	1y	41	A
57	1y	42	A
57	1y	44	U
57	1y	45	G
57	1y	46	G7M
57	1y	47	U

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Mol	Chain	Res	Type
57	1y	48	C
57	1y	49	G
57	1y	51	A
57	1y	56	C
57	1y	57	G
57	1y	58	A
57	1y	59	A
57	1y	61	C
57	1y	65	C
57	1y	69	A
57	1y	70	C
57	1y	72	C
1	2A	8	A
1	2A	15	G
1	2A	33	U
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	64	A
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	78	A
1	2A	79	G
1	2A	84	A
1	2A	90	U
1	2A	94	C
1	2A	95	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	125	G
1	2A	143	G
1	2A	147	U
1	2A	154(A)	C
1	2A	157	U
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	200	U
1	2A	205	G
1	2A	215	G

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Mol	Chain	Res	Type
1	2A	216	A
1	2A	222	A
1	2A	228	A
1	2A	229	A
1	2A	230	U
1	2A	233	A
1	2A	248	G
1	2A	266	G
1	2A	271(C)	C
1	2A	271(J)	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	271(W)	G
1	2A	272	G
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	311	A
1	2A	317	G
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	331	A
1	2A	333	G
1	2A	335	C
1	2A	342	G
1	2A	346	A
1	2A	352	G
1	2A	354	G
1	2A	363	G
1	2A	372	G
1	2A	386	G
1	2A	391	G
1	2A	396	G
1	2A	404	C
1	2A	405	U
1	2A	411	G
1	2A	412	A

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Mol	Chain	Res	Type
1	2A	421	U
1	2A	434	U
1	2A	444	C
1	2A	454	A
1	2A	456	C
1	2A	457	A
1	2A	481	G
1	2A	494	G
1	2A	496	G
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	583	G
1	2A	588	U
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(U)	G
1	2A	652(V)	C
1	2A	669	G
1	2A	686	G
1	2A	715	G
1	2A	717	G
1	2A	726	G

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Mol	Chain	Res	Type
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	774	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	811	U
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	832	G
1	2A	847	U
1	2A	857	C
1	2A	859	G
1	2A	864	G
1	2A	869	G
1	2A	873	G
1	2A	874	G
1	2A	878	A
1	2A	879	G
1	2A	880	G
1	2A	882	G
1	2A	883	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	894	C
1	2A	895	U
1	2A	896	A
1	2A	897	C
1	2A	900	A

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Mol	Chain	Res	Type
1	2A	901	A
1	2A	907	U
1	2A	910	A
1	2A	914	C
1	2A	915	C
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	961	C
1	2A	968	G
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	989	G
1	2A	996	A
1	2A	999	U
1	2A	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1020	A
1	2A	1021	A
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1027	A
1	2A	1033	U
1	2A	1037	G
1	2A	1038	C
1	2A	1039	G
1	2A	1040	C
1	2A	1041	C
1	2A	1042	G
1	2A	1043	C
1	2A	1114	G
1	2A	1116	C
1	2A	1126	A
1	2A	1129	A

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Mol	Chain	Res	Type
1	2A	1130	U
1	2A	1131	G
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142	U
1	2A	1142(A)	A
1	2A	1148	A
1	2A	1151	G
1	2A	1155	A
1	2A	1167	U
1	2A	1169	G
1	2A	1170	G
1	2A	1171	G
1	2A	1205	U
1	2A	1210	A
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1221	C
1	2A	1230	C
1	2A	1236	G
1	2A	1253	A
1	2A	1256	G
1	2A	1268	A
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1309	G
1	2A	1314	C
1	2A	1333	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1370	C
1	2A	1378	A
1	2A	1380	G

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Mol	Chain	Res	Type
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1388	G
1	2A	1395	A
1	2A	1403	C
1	2A	1416	G
1	2A	1417	C
1	2A	1419	A
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1472	A
1	2A	1482	G
1	2A	1486	A
1	2A	1490	A
1	2A	1493	C
1	2A	1496	A
1	2A	1497	U
1	2A	1506	C
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1514	U
1	2A	1531	C
1	2A	1532	C
1	2A	1547	C
1	2A	1558	A
1	2A	1559	G
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1581	G
1	2A	1584	C

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Mol	Chain	Res	Type
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1628	G
1	2A	1636	C
1	2A	1640	C
1	2A	1648	C
1	2A	1653	G
1	2A	1654	A
1	2A	1667	G
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1714	G
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1745(A)	C
1	2A	1746	G
1	2A	1756	G
1	2A	1758	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1786	A
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1820	U
1	2A	1829	A
1	2A	1847	A
1	2A	1848	A
1	2A	1861	G
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C

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Mol	Chain	Res	Type
1	2A	1916	A
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1964	G
1	2A	1966	A
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1975	G
1	2A	1984	G
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2039	C
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2067	G
1	2A	2069	G
1	2A	2077	A
1	2A	2101	G
1	2A	2108	C
1	2A	2109	U
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2113	U
1	2A	2115	G
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U

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Mol	Chain	Res	Type
1	2A	2120	G
1	2A	2122	U
1	2A	2124	G
1	2A	2125	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2137	C
1	2A	2138	C
1	2A	2142	C
1	2A	2143	C
1	2A	2145	C
1	2A	2149	G
1	2A	2150	U
1	2A	2151	G
1	2A	2154	G
1	2A	2157	G
1	2A	2158	A
1	2A	2159	G
1	2A	2161	C
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2171	A
1	2A	2172	U
1	2A	2173	A
1	2A	2174	C
1	2A	2175	C
1	2A	2176	A
1	2A	2178	C
1	2A	2181	G
1	2A	2184	G
1	2A	2185	C
1	2A	2186	G
1	2A	2188	C

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Mol	Chain	Res	Type
1	2A	2189	U
1	2A	2198	A
1	2A	2202	C
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2222	G
1	2A	2225	A
1	2A	2239	G
1	2A	2249	U
1	2A	2267	A
1	2A	2275	C
1	2A	2277	G
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2288	A
1	2A	2293	C
1	2A	2298	A
1	2A	2305	A
1	2A	2307	G
1	2A	2308	G
1	2A	2311	A
1	2A	2318	G
1	2A	2320	A
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2340	G
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2358	G
1	2A	2366	A
1	2A	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2388	A
1	2A	2396	G
1	2A	2398	U
1	2A	2400	G

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Mol	Chain	Res	Type
1	2A	2406	U
1	2A	2410	G
1	2A	2417	C
1	2A	2422	A
1	2A	2424	C
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2440	C
1	2A	2441	C
1	2A	2442	C
1	2A	2448	A
1	2A	2449	U
1	2A	2469	A
1	2A	2474	C
1	2A	2476	A
1	2A	2480	C
1	2A	2481	G
1	2A	2490	G
1	2A	2491	U
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2507	C
1	2A	2518	A
1	2A	2520	C
1	2A	2529	G
1	2A	2549	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2569	G
1	2A	2578	G
1	2A	2582	G
1	2A	2586	C
1	2A	2602	A
1	2A	2609	U
1	2A	2610	C
1	2A	2611	U
1	2A	2612	C

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Mol	Chain	Res	Type
1	2A	2615	U
1	2A	2629	A
1	2A	2630	G
1	2A	2634	G
1	2A	2646	C
1	2A	2654	A
1	2A	2670	A
1	2A	2686	G
1	2A	2689	U
1	2A	2690	C
1	2A	2691	C
1	2A	2702	U
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2739	U
1	2A	2748	A
1	2A	2754	U
1	2A	2759	G
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2770	G
1	2A	2778	A
1	2A	2780	G
1	2A	2793	G
1	2A	2805	G
1	2A	2808	U
1	2A	2820	A
1	2A	2821	A
1	2A	2835	A
1	2A	2872	G
1	2A	2880	C
1	2A	2886	G
1	2A	2892	A
1	2A	2893	G
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	3	C

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Mol	Chain	Res	Type
2	2B	5	C
2	2B	8	U
2	2B	9	G
2	2B	13	A
2	2B	15	A
2	2B	17	C
2	2B	20	C
2	2B	21	G
2	2B	24	G
2	2B	26	A
2	2B	30	C
2	2B	32	C
2	2B	44	G
2	2B	45	A
2	2B	53	A
2	2B	59	A
2	2B	65	C
2	2B	67	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G
2	2B	91	C
2	2B	106	G
2	2B	110	G
2	2B	116	G
32	2a	7	G
32	2a	9	G
32	2a	14	U
32	2a	15	G
32	2a	22	G
32	2a	24	U
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	52	G
32	2a	65	U
32	2a	66	G
32	2a	73	G

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Mol	Chain	Res	Type
32	2a	76	C
32	2a	79	G
32	2a	80	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	125	U
32	2a	131	C
32	2a	142	G
32	2a	143	A
32	2a	144	G
32	2a	151	A
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(E)	U
32	2a	189(G)	G
32	2a	189(H)	G
32	2a	189(L)	G
32	2a	190	U
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	220	G
32	2a	229	U
32	2a	245	C
32	2a	247	G
32	2a	250	A
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	321	A
32	2a	328	C

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Mol	Chain	Res	Type
32	2a	332	G
32	2a	338	A
32	2a	341	C
32	2a	344	A
32	2a	346	G
32	2a	350	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	384	G
32	2a	388	G
32	2a	397	A
32	2a	398	C
32	2a	404	U
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	414	A
32	2a	415	A
32	2a	422	C
32	2a	424	G
32	2a	429	U
32	2a	435	C
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	477	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	508	C
32	2a	509	A
32	2a	510	A

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Mol	Chain	Res	Type
32	2a	511	C
32	2a	517	G
32	2a	518	C
32	2a	521	G
32	2a	524	G
32	2a	527	G7M
32	2a	531	U
32	2a	532	A
32	2a	536	C
32	2a	547	A
32	2a	559	A
32	2a	564	C
32	2a	568	G
32	2a	572	A
32	2a	573	A
32	2a	575	G
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	598	U
32	2a	601	C
32	2a	630	G
32	2a	638	G
32	2a	639	G
32	2a	649	G
32	2a	653	A
32	2a	657	G
32	2a	665	A
32	2a	671	G
32	2a	687	A
32	2a	688	G
32	2a	702	A
32	2a	708	C
32	2a	712	A
32	2a	721	G
32	2a	723	U
32	2a	729	A
32	2a	731	G
32	2a	738	C
32	2a	746	A
32	2a	747	C
32	2a	748	C

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Mol	Chain	Res	Type
32	2a	749	C
32	2a	755	G
32	2a	760	G
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	787	A
32	2a	790	A
32	2a	793	U
32	2a	794	A
32	2a	805	C
32	2a	816	A
32	2a	817	C
32	2a	818	G
32	2a	821	G
32	2a	828	A
32	2a	834	C
32	2a	835	U
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	857	C
32	2a	858	G
32	2a	859	A
32	2a	864	A
32	2a	872	A
32	2a	873	A
32	2a	897	C
32	2a	902	G
32	2a	914	A
32	2a	916	G
32	2a	923	A
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	932	C
32	2a	933	G
32	2a	934	C
32	2a	942	G
32	2a	951	G
32	2a	958	A
32	2a	960	U

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Mol	Chain	Res	Type
32	2a	961	U
32	2a	969	A
32	2a	971	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	979	C
32	2a	982	U
32	2a	984	C
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	997	U
32	2a	1000	U
32	2a	1001	A
32	2a	1002	G
32	2a	1003	G
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1007	C
32	2a	1008	C
32	2a	1009	G
32	2a	1016	A
32	2a	1020	U
32	2a	1021	G
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1030(D)	A
32	2a	1031	G
32	2a	1035	A
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U

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Mol	Chain	Res	Type
32	2a	1045	C
32	2a	1050	G
32	2a	1053	G
32	2a	1054	C
32	2a	1055	A
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1071	C
32	2a	1073	U
32	2a	1079	G
32	2a	1084	G
32	2a	1085	U
32	2a	1086	U
32	2a	1092	A
32	2a	1093	A
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1105	A
32	2a	1108	G
32	2a	1109	C
32	2a	1113	C
32	2a	1117	G
32	2a	1121	U
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1142	G
32	2a	1143	G
32	2a	1145	C
32	2a	1146	A
32	2a	1147	C
32	2a	1152	A
32	2a	1155	G
32	2a	1157	A

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Mol	Chain	Res	Type
32	2a	1159	U
32	2a	1160	G
32	2a	1172	C
32	2a	1181	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1190	G
32	2a	1194	U
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1208	C
32	2a	1211	U
32	2a	1213	A
32	2a	1214	C
32	2a	1215	G
32	2a	1219	U
32	2a	1227	A
32	2a	1233	G
32	2a	1237	C
32	2a	1238	A
32	2a	1246	C
32	2a	1247	U
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1262	C
32	2a	1263	C
32	2a	1272	G
32	2a	1273	G
32	2a	1275	A
32	2a	1279	A
32	2a	1280	A
32	2a	1283	G
32	2a	1285	A
32	2a	1287	A
32	2a	1289	A
32	2a	1299	A
32	2a	1300	G
32	2a	1301	U

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Mol	Chain	Res	Type
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1311	G
32	2a	1312	G
32	2a	1313	U
32	2a	1320	C
32	2a	1322	C
32	2a	1323	G
32	2a	1336	C
32	2a	1337	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1358	U
32	2a	1363	C
32	2a	1363(A)	A
32	2a	1368	G
32	2a	1379	G
32	2a	1381	U
32	2a	1398	A
32	2a	1400	5MC
32	2a	1401	G
32	2a	1404	5MC
32	2a	1406	U
32	2a	1410	G
32	2a	1411	C
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1442(B)	A
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G
32	2a	1460	A
32	2a	1475	G
32	2a	1492	A
32	2a	1494	G
32	2a	1499	A
32	2a	1503	A

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Mol	Chain	Res	Type
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
32	2a	1508	G
32	2a	1517	G
32	2a	1519	MA6
32	2a	1520	G
32	2a	1528	U
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	13	A
53	2v	14	A
53	2v	15	A
53	2v	19	A
53	2v	23	A
54	2w	3	G
54	2w	5	C
54	2w	8	U
54	2w	9	A
54	2w	11	C
54	2w	14	A
54	2w	19	G
54	2w	20	U
54	2w	21	A
54	2w	24	G
54	2w	25	C
54	2w	28	U
54	2w	34	U8U
54	2w	43	U
54	2w	45	G
54	2w	46	G7M
54	2w	47	U
54	2w	48	C
54	2w	49	G
54	2w	50	C
54	2w	52	G
54	2w	53	G
54	2w	56	C
54	2w	58	A
54	2w	59	A

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Mol	Chain	Res	Type
54	2w	60	U
54	2w	61	C
54	2w	62	C
54	2w	66	A
54	2w	68	G
54	2w	69	A
54	2w	70	C
54	2w	73	A
54	2w	74	C
55	2x	2	G
55	2x	4	G
55	2x	9	G
55	2x	13	C
55	2x	16	C
55	2x	18	G
55	2x	19	G
55	2x	20	U
55	2x	21	A
55	2x	22	G
55	2x	30	G
55	2x	47	U
55	2x	48	C
55	2x	52	G
55	2x	56	C
55	2x	58	A
55	2x	63	G
57	2y	3	G
57	2y	7	U
57	2y	8	U
57	2y	9	A
57	2y	11	C
57	2y	12	U
57	2y	13	C
57	2y	14	A
57	2y	19	G
57	2y	20	U
57	2y	21	A
57	2y	24	G
57	2y	25	C
57	2y	26	A
57	2y	27	G
57	2y	30	G

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Mol	Chain	Res	Type
57	2y	31	A
57	2y	36	U
57	2y	40	C
57	2y	42	A
57	2y	44	U
57	2y	45	G
57	2y	47	U
57	2y	49	G
57	2y	50	C
57	2y	51	A
57	2y	53	G
57	2y	57	G
57	2y	58	A
57	2y	59	A
57	2y	60	U
57	2y	61	C
57	2y	63	U
57	2y	65	C
57	2y	66	A
57	2y	69	A
57	2y	70	C
57	2y	73	A

All (48) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	221	A
1	1A	266	G
1	1A	271(K)	U
1	1A	278	A
1	1A	548	A
1	1A	746	A
1	1A	774	A
1	1A	1033	U
1	1A	1047	G
1	1A	1139	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1442	G
1	1A	1508	A

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Mol	Chain	Res	Type
1	1A	1663	C
1	1A	1992	G
1	1A	2145	C
1	1A	2183	C
1	1A	2406	U
1	1A	2430	A
1	1A	2629	A
1	1A	2689	U
1	2A	196	A
1	2A	229	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	752	A
1	2A	827	U
1	2A	856	C
1	2A	900	A
1	2A	1026	U
1	2A	1210	A
1	2A	1379	A
1	2A	1442	G
1	2A	1530	C
1	2A	1602	U
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2119	A
1	2A	2126	A
1	2A	2156	G
1	2A	2406	U
1	2A	2689	U

5.4 Non-standard residues in protein, DNA, RNA chains (i)

86 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection.

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
54	G7M	2w	46	54	20,26,27	1.19	1 (5%)	16,39,42	0.82	0
1	5MU	2A	1939	1,58	19,22,23	1.39	4 (21%)	27,32,35	2.24	6 (22%)
32	4OC	1a	1402	32	20,23,24	0.73	0	25,32,35	1.04	2 (8%)
1	PSU	2A	1911	1	18,21,22	1.42	3 (16%)	21,30,33	2.06	3 (14%)
43	0TD	2l	92	43	8,9,10	4.49	2 (25%)	6,11,13	7.26	2 (33%)
55	PSU	2x	55	55	18,21,22	1.33	2 (11%)	21,30,33	2.13	4 (19%)
55	5MC	2x	32	55	19,22,23	1.56	3 (15%)	26,32,35	1.18	3 (11%)
54	PSU	1w	39	54	18,21,22	1.37	2 (11%)	21,30,33	2.04	4 (19%)
57	PSU	1y	55	57	18,21,22	1.44	2 (11%)	21,30,33	1.89	3 (14%)
55	5MC	1x	32	55	19,22,23	1.81	3 (15%)	26,32,35	1.19	2 (7%)
32	G7M	2a	527	58,32	20,26,27	1.21	2 (10%)	16,39,42	0.53	0
32	UR3	2a	1498	58,32	19,22,23	0.98	0	26,32,35	1.77	4 (15%)
32	PSU	2a	516	58,32	18,21,22	1.39	3 (16%)	21,30,33	2.17	6 (28%)
32	M2G	1a	966	32	20,27,28	1.31	3 (15%)	19,40,43	1.02	2 (10%)
55	8AN	2x	76	58,55	17,24,25	1.26	3 (17%)	13,35,38	3.30	3 (23%)
57	PSU	1y	39	57	18,21,22	1.50	3 (16%)	21,30,33	1.73	3 (14%)
57	T6A	1y	37	57	17,24,35	0.82	1 (5%)	16,35,52	1.22	2 (12%)
57	PSU	2y	39	57	18,21,22	1.37	2 (11%)	21,30,33	1.85	4 (19%)
32	5MC	1a	1407	32	19,22,23	1.63	3 (15%)	26,32,35	1.17	2 (7%)
32	PSU	1a	516	58,32	18,21,22	1.38	2 (11%)	21,30,33	2.05	4 (19%)
57	T6A	2y	37	57,32	17,24,35	0.80	0	16,35,52	1.24	2 (12%)
1	2MA	2A	2503	1,58	18,25,26	0.65	0	20,37,40	1.87	4 (20%)
32	5MC	1a	1404	32	19,22,23	1.74	3 (15%)	26,32,35	1.15	3 (11%)
54	PSU	2w	39	54	18,21,22	1.43	2 (11%)	21,30,33	1.70	3 (14%)
1	5MU	2A	1915	1	19,22,23	1.47	5 (26%)	27,32,35	2.02	5 (18%)
54	T6A	2w	37	53,54	26,34,35	1.03	1 (3%)	28,49,52	1.94	5 (17%)
54	5MU	1w	54	54	19,22,23	1.43	4 (21%)	27,32,35	2.24	6 (22%)
32	2MG	1a	1207	32	18,26,27	0.98	1 (5%)	16,38,41	1.51	4 (25%)
54	U8U	2w	34	53,54	20,24,25	1.40	3 (15%)	22,34,37	1.37	4 (18%)
55	4SU	2x	8	55	18,21,22	2.20	6 (33%)	25,30,33	1.50	7 (28%)
54	PSU	2w	55	58,54	18,21,22	1.35	2 (11%)	21,30,33	1.99	4 (19%)
32	MA6	1a	1519	32	19,26,27	1.01	2 (10%)	18,38,41	2.06	3 (16%)
57	5MU	1y	54	57	19,22,23	1.41	5 (26%)	27,32,35	2.25	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
54	U8U	1w	34	53,54	20,24,25	1.40	3 (15%)	22,34,37	1.71	4 (18%)
56	FME	1z	1	56	8,9,10	1.04	0	8,9,11	0.81	0
32	MA6	2a	1518	32	19,26,27	1.00	2 (10%)	18,38,41	1.89	3 (16%)
57	U8U	1y	34	57	17,21,25	1.50	3 (17%)	21,30,37	1.45	3 (14%)
54	G7M	1w	46	54	20,26,27	1.23	1 (5%)	16,39,42	0.66	0
1	PSU	2A	1917	1	18,21,22	1.39	2 (11%)	21,30,33	2.11	4 (19%)
32	UR3	1a	1498	32	19,22,23	1.07	1 (5%)	26,32,35	1.82	5 (19%)
56	FME	2z	1	56	8,9,10	1.00	0	8,9,11	0.78	0
1	5MU	1A	1915	1	19,22,23	1.42	6 (31%)	27,32,35	2.16	7 (25%)
1	5MC	1A	1942	1	19,22,23	1.63	3 (15%)	26,32,35	1.10	2 (7%)
57	5MU	2y	54	57	19,22,23	1.43	5 (26%)	27,32,35	2.12	7 (25%)
32	MA6	2a	1519	32	19,26,27	0.99	1 (5%)	18,38,41	1.85	3 (16%)
57	G7M	1y	46	57	20,26,27	1.36	2 (10%)	16,39,42	0.59	0
1	OMU	2A	2552	1,58	19,22,23	1.22	3 (15%)	25,31,34	1.69	5 (20%)
1	OMG	2A	2251	1,55	19,26,27	0.87	1 (5%)	21,38,41	1.16	2 (9%)
32	M2G	2a	966	32	20,27,28	1.44	3 (15%)	19,40,43	0.98	2 (10%)
57	G7M	2y	46	57	20,26,27	1.32	1 (5%)	16,39,42	0.74	0
1	5MC	2A	1942	1	19,22,23	1.74	3 (15%)	26,32,35	1.18	2 (7%)
32	5MC	1a	1400	32	19,22,23	1.76	3 (15%)	26,32,35	1.19	3 (11%)
1	5MC	2A	1962	1,58	19,22,23	1.54	3 (15%)	26,32,35	1.15	2 (7%)
1	2MA	1A	2503	1,58	18,25,26	0.66	0	20,37,40	2.12	4 (20%)
1	OMC	2A	1920	1	19,22,23	0.77	0	25,31,34	0.86	1 (4%)
1	PSU	1A	1917	1	18,21,22	1.39	3 (16%)	21,30,33	2.08	3 (14%)
1	PSU	1A	2605	1,58	18,21,22	1.31	4 (22%)	21,30,33	1.92	4 (19%)
32	MA6	1a	1518	32	19,26,27	1.02	2 (10%)	18,38,41	1.86	3 (16%)
1	PSU	1A	1911	1	18,21,22	1.41	3 (16%)	21,30,33	2.01	4 (19%)
32	5MC	1a	967	32	19,22,23	1.44	3 (15%)	26,32,35	1.11	2 (7%)
55	5MU	2x	54	55	19,22,23	1.42	6 (31%)	27,32,35	2.25	7 (25%)
32	G7M	1a	527	58,32	20,26,27	1.20	1 (5%)	16,39,42	0.64	0
32	5MC	2a	1400	32	19,22,23	1.72	3 (15%)	26,32,35	1.21	4 (15%)
54	A1B8A	1w	76	54	26,33,34	1.24	3 (11%)	23,46,49	1.74	3 (13%)
55	5MU	1x	54	55	19,22,23	1.48	5 (26%)	27,32,35	1.74	5 (18%)
55	PSU	1x	55	55	18,21,22	1.35	2 (11%)	21,30,33	1.98	3 (14%)
32	4OC	2a	1402	58,32	20,23,24	0.76	0	25,32,35	1.06	2 (8%)
55	4SU	1x	8	55	18,21,22	2.34	5 (27%)	25,30,33	1.59	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	OMU	1A	2552	1,58	19,22,23	1.22	3 (15%)	25,31,34	1.89	5 (20%)
54	PSU	1w	55	54	18,21,22	1.35	2 (11%)	21,30,33	1.94	4 (19%)
1	PSU	2A	2605	1	18,21,22	1.39	3 (16%)	21,30,33	2.01	3 (14%)
32	5MC	2a	1404	32	19,22,23	1.70	3 (15%)	26,32,35	1.15	2 (7%)
54	A1B8A	2w	76	54	26,33,34	1.19	3 (11%)	23,46,49	1.66	2 (8%)
1	OMC	1A	1920	1	19,22,23	0.81	0	25,31,34	0.97	0
1	5MC	1A	1962	1,58	19,22,23	1.64	3 (15%)	26,32,35	1.19	3 (11%)
54	5MU	2w	54	54	19,22,23	1.52	5 (26%)	27,32,35	1.60	7 (25%)
1	OMG	1A	2251	1,58,55	19,26,27	0.94	1 (5%)	21,38,41	1.17	2 (9%)
32	2MG	2a	1207	32	18,26,27	0.95	1 (5%)	16,38,41	1.26	2 (12%)
1	5MU	1A	1939	1,58	19,22,23	1.41	4 (21%)	27,32,35	2.26	6 (22%)
57	U8U	2y	34	57,53	17,21,25	1.64	3 (17%)	21,30,37	1.47	3 (14%)
43	0TD	1l	92	43	8,9,10	4.68	1 (12%)	6,11,13	1.85	2 (33%)
32	5MC	2a	967	58,32	19,22,23	1.71	3 (15%)	26,32,35	1.19	3 (11%)
57	PSU	2y	55	57	18,21,22	1.32	2 (11%)	21,30,33	2.21	4 (19%)
54	T6A	1w	37	54	26,34,35	0.97	1 (3%)	28,49,52	1.79	5 (17%)
55	8AN	1x	76	55	17,24,25	1.24	1 (5%)	13,35,38	4.29	3 (23%)
32	5MC	2a	1407	32	19,22,23	1.65	3 (15%)	26,32,35	1.11	2 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	G7M	2w	46	54	-	3/3/25/26	0/3/3/3
1	5MU	2A	1939	1,58	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	1/9/29/30	0/2/2/2
1	PSU	2A	1911	1	-	2/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	3/7/12/14	-
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
54	PSU	1w	39	54	-	2/7/25/26	0/2/2/2
57	PSU	1y	55	57	-	2/7/25/26	0/2/2/2
55	5MC	1x	32	55	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	58,32	-	2/3/25/26	0/3/3/3
32	UR3	2a	1498	58,32	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	PSU	2a	516	58,32	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/7/29/30	0/3/3/3
55	8AN	2x	76	58,55	-	3/3/25/26	0/3/3/3
57	PSU	1y	39	57	-	0/7/25/26	0/2/2/2
57	T6A	1y	37	57	-	1/3/25/42	0/3/3/3
57	PSU	2y	39	57	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	58,32	-	0/7/25/26	0/2/2/2
57	T6A	2y	37	57,32	-	0/3/25/42	0/3/3/3
1	2MA	2A	2503	1,58	-	2/3/25/26	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	1/7/25/26	0/2/2/2
54	T6A	2w	37	53,54	-	7/19/41/42	0/3/3/3
54	5MU	1w	54	54	-	2/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/5/27/28	0/3/3/3
54	U8U	2w	34	53,54	-	3/10/28/29	0/2/2/2
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
54	PSU	2w	55	58,54	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/7/29/30	0/3/3/3
57	5MU	1y	54	57	-	0/7/25/26	0/2/2/2
54	U8U	1w	34	53,54	-	2/10/28/29	0/2/2/2
56	FME	1z	1	56	-	5/7/9/11	-
32	MA6	2a	1518	32	-	0/7/29/30	0/3/3/3
57	U8U	1y	34	57	-	0/7/25/29	0/2/2/2
54	G7M	1w	46	54	-	2/3/25/26	0/3/3/3
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
56	FME	2z	1	56	-	3/7/9/11	-
1	5MU	1A	1915	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
57	5MU	2y	54	57	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	3/7/29/30	0/3/3/3
57	G7M	1y	46	57	-	1/3/25/26	0/3/3/3
1	OMU	2A	2552	1,58	-	0/9/27/28	0/2/2/2
1	OMG	2A	2251	1,55	-	1/5/27/28	0/3/3/3
32	M2G	2a	966	32	-	0/7/29/30	0/3/3/3
57	G7M	2y	46	57	-	0/3/25/26	0/3/3/3
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
1	5MC	2A	1962	1,58	-	1/7/25/26	0/2/2/2
1	2MA	1A	2503	1,58	-	3/3/25/26	0/3/3/3
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	1,58	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/7/29/30	0/3/3/3
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	58,32	-	2/3/25/26	0/3/3/3
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
54	A1B8A	1w	76	54	-	3/16/38/39	0/3/3/3
55	5MU	1x	54	55	-	0/7/25/26	0/2/2/2
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	58,32	-	2/9/29/30	0/2/2/2
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	1,58	-	0/9/27/28	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	2/7/25/26	0/2/2/2
54	A1B8A	2w	76	54	-	3/16/38/39	0/3/3/3
1	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2
1	5MC	1A	1962	1,58	-	0/7/25/26	0/2/2/2
54	5MU	2w	54	54	-	1/7/25/26	0/2/2/2
1	OMG	1A	2251	1,58,55	-	0/5/27/28	0/3/3/3
32	2MG	2a	1207	32	-	0/5/27/28	0/3/3/3
1	5MU	1A	1939	1,58	-	0/7/25/26	0/2/2/2
57	U8U	2y	34	57,53	-	0/7/25/29	0/2/2/2
43	0TD	1l	92	43	-	4/7/12/14	-
32	5MC	2a	967	58,32	-	0/7/25/26	0/2/2/2
57	PSU	2y	55	57	-	0/7/25/26	0/2/2/2
54	T6A	1w	37	54	-	6/19/41/42	0/3/3/3
55	8AN	1x	76	55	-	3/3/25/26	0/3/3/3
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2

All (206) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.80	1.69	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.16	1.70	1.82
55	1x	32	5MC	C5-C4	6.59	1.49	1.44
32	1a	1400	5MC	C5-C4	6.51	1.49	1.44
32	1a	1404	5MC	C5-C4	6.43	1.49	1.44
32	2a	1400	5MC	C5-C4	6.43	1.49	1.44
1	2A	1942	5MC	C5-C4	6.34	1.48	1.44
32	2a	967	5MC	C5-C4	6.23	1.48	1.44
32	2a	1404	5MC	C5-C4	6.17	1.48	1.44
1	1A	1962	5MC	C5-C4	6.07	1.48	1.44
32	1a	1407	5MC	C5-C4	5.97	1.48	1.44
32	2a	1407	5MC	C5-C4	5.97	1.48	1.44
1	1A	1942	5MC	C5-C4	5.95	1.48	1.44
55	1x	8	4SU	C4-N3	-5.80	1.31	1.37
55	2x	32	5MC	C5-C4	5.51	1.48	1.44
55	2x	8	4SU	C4-N3	-5.33	1.32	1.37
1	2A	1962	5MC	C5-C4	5.23	1.48	1.44
55	1x	8	4SU	C4-S4	-4.99	1.59	1.68
32	1a	967	5MC	C5-C4	4.88	1.47	1.44
57	2y	34	U8U	C2-S2	-4.75	1.60	1.67
55	2x	8	4SU	C4-S4	-4.69	1.60	1.68
54	1w	34	U8U	C2-S2	-4.68	1.60	1.67
54	2w	34	U8U	C2-S2	-4.65	1.60	1.67
32	2a	966	M2G	C2-N3	4.41	1.36	1.30
57	2y	46	G7M	C5-C4	4.24	1.47	1.39
54	1w	76	A1B8A	O4'-C1'	4.23	1.46	1.40
57	1y	39	PSU	C6-C5	4.19	1.39	1.35
57	1y	34	U8U	C2-S2	-4.18	1.61	1.67
57	1y	55	PSU	C6-C5	4.18	1.39	1.35
57	1y	46	G7M	C5-C4	3.94	1.47	1.39
54	2w	55	PSU	C6-C5	3.90	1.39	1.35
54	2w	39	PSU	C6-C5	3.86	1.39	1.35
54	1w	55	PSU	C6-C5	3.82	1.39	1.35
57	2y	39	PSU	C6-C5	3.79	1.39	1.35
57	2y	55	PSU	C6-C5	3.78	1.39	1.35
54	1w	46	G7M	C5-C4	3.77	1.46	1.39
32	1a	527	G7M	C5-C4	3.77	1.46	1.39
1	2A	1917	PSU	C6-C5	3.71	1.39	1.35
32	1a	516	PSU	C6-C5	3.67	1.39	1.35
32	2a	527	G7M	C5-C4	3.67	1.46	1.39
55	1x	8	4SU	C2-N3	-3.66	1.31	1.38
32	1a	966	M2G	C2-N3	3.63	1.35	1.30
54	2w	76	A1B8A	O4'-C1'	3.61	1.45	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	46	G7M	C5-C4	3.58	1.46	1.39
32	2a	516	PSU	C6-C5	3.57	1.39	1.35
1	1A	1917	PSU	C6-C5	3.49	1.39	1.35
1	2A	2605	PSU	C6-C5	3.45	1.39	1.35
55	1x	8	4SU	C5-C4	-3.45	1.38	1.42
1	2A	1911	PSU	C6-C5	3.42	1.39	1.35
1	1A	1911	PSU	C6-C5	3.41	1.39	1.35
55	1x	55	PSU	C6-C5	3.35	1.39	1.35
55	2x	55	PSU	C6-C5	3.34	1.39	1.35
54	1w	39	PSU	C6-C5	3.34	1.39	1.35
55	2x	8	4SU	C5-C4	-3.32	1.38	1.42
1	1A	1939	5MU	C6-C5	3.21	1.39	1.34
55	1x	32	5MC	C6-C5	3.19	1.39	1.34
54	2w	37	T6A	C6-C5	3.15	1.49	1.44
54	2w	76	A1B8A	C6-C5	-3.12	1.31	1.43
55	1x	54	5MU	C4-N3	-3.11	1.33	1.38
55	2x	8	4SU	C2-N3	-3.10	1.32	1.38
54	2w	54	5MU	C6-C5	3.07	1.39	1.34
54	2w	54	5MU	C2-N1	3.05	1.43	1.38
1	1A	2552	OMU	C4-N3	-3.02	1.33	1.38
32	2a	966	M2G	C2-N2	2.98	1.40	1.35
32	2a	1404	5MC	C6-C5	2.94	1.39	1.34
54	1w	54	5MU	C6-C5	2.94	1.39	1.34
1	2A	1915	5MU	C6-C5	2.93	1.39	1.34
1	2A	1962	5MC	C6-C5	2.93	1.39	1.34
55	1x	54	5MU	C6-C5	2.92	1.39	1.34
57	1y	39	PSU	C4-N3	-2.90	1.33	1.38
54	1w	34	U8U	C4-N3	-2.86	1.33	1.38
55	2x	54	5MU	C6-C5	2.85	1.39	1.34
1	2A	1942	5MC	C6-C5	2.84	1.39	1.34
57	1y	54	5MU	C6-C5	2.84	1.39	1.34
32	1a	1498	UR3	C2-N1	2.84	1.42	1.38
32	1a	1400	5MC	C6-C5	2.83	1.39	1.34
1	1A	1942	5MC	C6-C5	2.82	1.39	1.34
57	2y	34	U8U	C4-N3	-2.82	1.33	1.38
55	2x	32	5MC	C6-C5	2.82	1.39	1.34
1	1A	2605	PSU	C4-N3	-2.81	1.33	1.38
57	1y	54	5MU	C4-C5	2.81	1.49	1.44
32	1a	966	M2G	C2-N2	2.78	1.40	1.35
57	2y	54	5MU	C6-C5	2.78	1.39	1.34
1	2A	2605	PSU	C4-N3	-2.77	1.33	1.38
1	1A	1915	5MU	C6-C5	2.76	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	1911	PSU	C4-N3	-2.75	1.33	1.38
1	2A	2552	OMU	C4-N3	-2.74	1.33	1.38
32	1a	1404	5MC	C6-C5	2.74	1.39	1.34
1	1A	1939	5MU	C4-N3	-2.73	1.33	1.38
32	2a	967	5MC	C6-C5	2.72	1.39	1.34
1	1A	1917	PSU	C4-N3	-2.72	1.33	1.38
54	1w	76	A1B8A	C6-C5	-2.71	1.33	1.43
55	2x	54	5MU	C4-C5	2.69	1.49	1.44
1	2A	1915	5MU	C4-N3	-2.69	1.33	1.38
1	2A	1915	5MU	C2-N1	2.68	1.42	1.38
1	1A	2251	OMG	C6-N1	-2.67	1.33	1.37
1	2A	1911	PSU	C4-N3	-2.64	1.33	1.38
54	2w	54	5MU	C4-N3	-2.63	1.33	1.38
54	2w	39	PSU	C4-N3	-2.63	1.33	1.38
1	2A	1939	5MU	C6-C5	2.63	1.38	1.34
1	1A	1939	5MU	C2-N3	-2.62	1.33	1.38
54	1w	37	T6A	C6-C5	2.62	1.48	1.44
32	1a	1207	2MG	C6-N1	-2.61	1.33	1.37
54	1w	39	PSU	C4-N3	-2.60	1.34	1.38
57	1y	34	U8U	C4-N3	-2.60	1.34	1.38
54	2w	34	U8U	C4-N3	-2.60	1.34	1.38
1	2A	1939	5MU	C4-N3	-2.60	1.34	1.38
57	2y	54	5MU	C4-C5	2.59	1.49	1.44
57	1y	46	G7M	C6-N1	-2.59	1.33	1.37
57	2y	54	5MU	C2-N1	2.57	1.42	1.38
1	2A	2251	OMG	C6-N1	-2.56	1.33	1.37
1	2A	1917	PSU	C4-N3	-2.56	1.34	1.38
1	1A	1915	5MU	C4-N3	-2.56	1.34	1.38
32	2a	1407	5MC	C6-C5	2.55	1.38	1.34
55	2x	76	8AN	C6-C5	-2.55	1.33	1.43
55	2x	54	5MU	C4-N3	-2.55	1.34	1.38
55	2x	55	PSU	C4-N3	-2.54	1.34	1.38
1	1A	1962	5MC	C6-N1	-2.54	1.33	1.38
54	1w	54	5MU	C2-N1	2.54	1.42	1.38
57	2y	34	U8U	C5-C4	2.53	1.49	1.43
32	1a	1407	5MC	C6-C5	2.53	1.38	1.34
32	1a	966	M2G	C6-N1	-2.52	1.33	1.37
55	1x	54	5MU	C2-N3	-2.52	1.33	1.38
55	2x	76	8AN	O4'-C1'	2.52	1.44	1.40
55	1x	76	8AN	C5-N7	-2.50	1.30	1.39
32	1a	1519	MA6	C6-C5	-2.49	1.41	1.44
32	1a	967	5MC	C6-C5	2.48	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	1939	5MU	C6-N1	-2.47	1.33	1.38
32	2a	516	PSU	C4-N3	-2.47	1.34	1.38
57	2y	54	5MU	C4-N3	-2.46	1.34	1.38
1	1A	1915	5MU	C4-C5	2.46	1.48	1.44
54	2w	54	5MU	O2-C2	2.46	1.27	1.23
32	1a	967	5MC	C6-N1	-2.46	1.33	1.38
57	2y	39	PSU	C4-N3	-2.45	1.34	1.38
57	1y	55	PSU	C4-N3	-2.45	1.34	1.38
54	1w	54	5MU	C4-C5	2.45	1.48	1.44
54	2w	55	PSU	C4-N3	-2.44	1.34	1.38
57	1y	54	5MU	C2-N1	2.44	1.42	1.38
32	2a	966	M2G	C6-N1	-2.43	1.34	1.37
32	2a	516	PSU	O4'-C1'	-2.43	1.40	1.43
55	1x	8	4SU	O2-C2	2.42	1.27	1.23
32	1a	1518	MA6	C6-C5	-2.41	1.41	1.44
32	2a	1400	5MC	C6-C5	2.40	1.38	1.34
32	1a	516	PSU	C4-N3	-2.39	1.34	1.38
57	1y	34	U8U	C5-C4	2.39	1.48	1.43
1	2A	1942	5MC	C6-N1	-2.37	1.34	1.38
1	1A	1915	5MU	C2-N1	2.36	1.42	1.38
1	2A	1915	5MU	C4-C5	2.35	1.48	1.44
32	1a	1400	5MC	C6-N1	-2.34	1.34	1.38
32	2a	527	G7M	C6-N1	-2.33	1.34	1.37
32	2a	1518	MA6	C6-C5	-2.33	1.41	1.44
54	1w	54	5MU	C4-N3	-2.33	1.34	1.38
54	1w	55	PSU	C4-N3	-2.33	1.34	1.38
55	2x	8	4SU	O2-C2	2.32	1.27	1.23
1	2A	1962	5MC	C6-N1	-2.32	1.34	1.38
1	1A	2552	OMU	C2-N3	-2.31	1.33	1.38
1	2A	1939	5MU	C4-C5	2.31	1.48	1.44
55	1x	55	PSU	C4-N3	-2.31	1.34	1.38
1	1A	2605	PSU	C2-N1	-2.29	1.33	1.36
57	1y	39	PSU	C2-N3	-2.28	1.33	1.37
55	2x	8	4SU	C2-N1	2.26	1.42	1.38
57	2y	55	PSU	C4-N3	-2.26	1.34	1.38
54	2w	34	U8U	C6-N1	-2.25	1.34	1.38
32	2a	1519	MA6	C6-C5	-2.24	1.41	1.44
55	2x	76	8AN	C5-N7	-2.24	1.31	1.39
32	1a	1404	5MC	C6-N1	-2.23	1.34	1.38
32	2a	1400	5MC	C6-N1	-2.23	1.34	1.38
1	1A	1942	5MC	C6-N1	-2.23	1.34	1.38
1	1A	1939	5MU	C4-C5	2.23	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	967	5MC	C6-N1	-2.19	1.34	1.38
54	1w	34	U8U	C6-N1	-2.19	1.34	1.38
57	1y	54	5MU	C4-N3	-2.19	1.34	1.38
1	1A	2605	PSU	C6-C5	2.18	1.37	1.35
32	2a	1207	2MG	C6-N1	-2.17	1.34	1.37
1	1A	2605	PSU	C2-N3	-2.17	1.33	1.37
32	2a	1404	5MC	C6-N1	-2.17	1.34	1.38
1	2A	1915	5MU	C6-N1	-2.17	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.17	1.34	1.38
55	1x	54	5MU	C4-C5	2.16	1.48	1.44
54	1w	76	A1B8A	C5-N7	-2.16	1.32	1.39
1	2A	2552	OMU	C5-C4	-2.15	1.39	1.43
43	2l	92	0TD	CB-CA	2.15	1.55	1.54
54	2w	76	A1B8A	C5-N7	-2.14	1.32	1.39
32	1a	1407	5MC	C6-N1	-2.14	1.34	1.38
55	1x	54	5MU	C6-N1	-2.14	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.14	1.34	1.38
54	2w	54	5MU	C4-C5	2.13	1.48	1.44
55	2x	54	5MU	C2-N1	2.13	1.41	1.38
55	1x	32	5MC	C6-N1	-2.13	1.34	1.38
1	2A	2552	OMU	C2-N3	-2.12	1.34	1.38
1	1A	1915	5MU	C2-N3	-2.11	1.34	1.38
57	1y	37	T6A	C2-N3	2.11	1.35	1.32
57	2y	54	5MU	C6-N1	-2.11	1.34	1.38
55	2x	32	5MC	C6-N1	-2.11	1.34	1.38
1	1A	2552	OMU	C5-C4	-2.07	1.39	1.43
32	2a	1518	MA6	C6-N1	2.06	1.35	1.32
1	1A	1911	PSU	C2-N3	-2.05	1.34	1.37
57	1y	54	5MU	C6-N1	-2.05	1.34	1.38
1	1A	1962	5MC	C6-C5	2.05	1.38	1.34
1	2A	2605	PSU	C2-N3	-2.03	1.34	1.37
55	2x	54	5MU	C2-N3	-2.02	1.34	1.38
1	2A	1911	PSU	C2-N1	-2.02	1.34	1.36
32	1a	1519	MA6	C6-N1	2.01	1.35	1.32
32	1a	1518	MA6	C6-N1	2.01	1.35	1.32
1	1A	1917	PSU	C2-N3	-2.00	1.34	1.37
55	2x	54	5MU	C6-N1	-2.00	1.34	1.38

All (278) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	2l	92	0TD	CSB-SB-CB	-17.58	70.76	102.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1x	76	8AN	O4'-C1'-N9	10.95	123.27	108.75
55	1x	76	8AN	C4'-O4'-C1'	-8.54	102.10	109.92
55	2x	76	8AN	C4'-O4'-C1'	-7.60	102.97	109.92
1	1A	2503	2MA	C2-N3-C4	7.47	121.49	115.46
32	2a	1498	UR3	C4-N3-C2	-6.93	119.00	124.58
32	1a	1498	UR3	C4-N3-C2	-6.88	119.05	124.58
54	1w	37	T6A	C2-N1-C6	6.86	121.92	116.60
54	2w	37	T6A	C2-N1-C6	6.86	121.92	116.60
54	1w	76	A1B8A	N3-C2-N1	-6.81	119.42	128.67
57	2y	55	PSU	N1-C2-N3	6.74	122.28	115.17
1	2A	1917	PSU	N1-C2-N3	6.71	122.25	115.17
54	2w	76	A1B8A	N3-C2-N1	-6.53	119.81	128.67
1	2A	1911	PSU	N1-C2-N3	6.51	122.03	115.17
55	2x	76	8AN	N3-C2-N1	-6.49	119.86	128.67
55	2x	55	PSU	N1-C2-N3	6.47	121.99	115.17
54	1w	39	PSU	N1-C2-N3	6.46	121.98	115.17
1	1A	1917	PSU	N1-C2-N3	6.42	121.94	115.17
32	2a	516	PSU	N1-C2-N3	6.41	121.93	115.17
1	2A	2605	PSU	N1-C2-N3	6.30	121.81	115.17
55	1x	76	8AN	N3-C2-N1	-6.29	120.13	128.67
32	1a	516	PSU	N1-C2-N3	6.24	121.75	115.17
55	1x	55	PSU	N1-C2-N3	6.15	121.66	115.17
1	1A	1911	PSU	N1-C2-N3	6.09	121.59	115.17
1	2A	2503	2MA	C2-N3-C4	6.04	120.34	115.46
55	2x	76	8AN	O4'-C1'-N9	6.03	116.73	108.75
57	1y	55	PSU	N1-C2-N3	5.98	121.47	115.17
54	1w	55	PSU	N1-C2-N3	5.84	121.32	115.17
32	1a	1519	MA6	N3-C2-N1	-5.71	120.92	128.67
1	1A	2605	PSU	N1-C2-N3	5.65	121.13	115.17
57	1y	54	5MU	C4-N3-C2	-5.64	119.94	127.34
32	2a	1518	MA6	N3-C2-N1	-5.62	121.04	128.67
55	2x	54	5MU	N3-C2-N1	5.61	122.20	114.89
55	2x	54	5MU	C4-N3-C2	-5.59	120.01	127.34
54	2w	55	PSU	N1-C2-N3	5.59	121.06	115.17
1	1A	1939	5MU	N3-C2-N1	5.58	122.16	114.89
54	1w	54	5MU	C4-N3-C2	-5.56	120.05	127.34
1	2A	1939	5MU	C4-N3-C2	-5.55	120.06	127.34
57	1y	39	PSU	N1-C2-N3	5.52	121.00	115.17
32	1a	1519	MA6	C2-N1-C6	5.52	122.25	116.84
1	1A	1939	5MU	C4-N3-C2	-5.50	120.13	127.34
57	2y	39	PSU	N1-C2-N3	5.49	120.96	115.17
54	2w	39	PSU	N1-C2-N3	5.40	120.87	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1915	5MU	N3-C2-N1	5.36	121.87	114.89
57	1y	54	5MU	N3-C2-N1	5.29	121.78	114.89
32	2a	1519	MA6	N3-C2-N1	-5.26	121.54	128.67
1	1A	1915	5MU	N3-C2-N1	5.24	121.72	114.89
1	1A	1915	5MU	C4-N3-C2	-5.23	120.48	127.34
1	2A	1939	5MU	N3-C2-N1	5.17	121.63	114.89
54	1w	54	5MU	N3-C2-N1	5.17	121.62	114.89
57	2y	54	5MU	C4-N3-C2	-5.13	120.61	127.34
57	2y	34	U8U	C2-N3-C4	-5.12	121.02	127.33
1	1A	2552	OMU	N3-C2-N1	5.11	121.54	114.89
57	2y	54	5MU	N3-C2-N1	5.11	121.54	114.89
32	1a	1518	MA6	N3-C2-N1	-4.98	121.92	128.67
1	2A	1915	5MU	C4-N3-C2	-4.91	120.91	127.34
32	1a	1518	MA6	C2-N1-C6	4.90	121.65	116.84
54	1w	54	5MU	C5-C4-N3	4.86	119.55	115.32
54	1w	34	U8U	C5-C4-N3	4.81	122.54	115.21
1	1A	1939	5MU	C5-C4-N3	4.79	119.49	115.32
57	1y	54	5MU	C5-C4-N3	4.78	119.47	115.32
1	1A	2552	OMU	C4-N3-C2	-4.64	120.85	126.61
54	1w	54	5MU	O4-C4-C5	-4.63	119.62	124.92
57	1y	34	U8U	C2-N3-C4	-4.57	121.70	127.33
1	1A	1915	5MU	C5-C4-N3	4.57	119.30	115.32
55	2x	55	PSU	C4-N3-C2	-4.54	120.11	126.37
55	2x	54	5MU	C5-C4-N3	4.50	119.24	115.32
57	2y	55	PSU	C4-N3-C2	-4.50	120.17	126.37
32	2a	1518	MA6	C2-N1-C6	4.49	121.24	116.84
1	2A	2552	OMU	C4-N3-C2	-4.47	121.06	126.61
1	1A	1939	5MU	O4-C4-C5	-4.43	119.85	124.92
1	1A	1939	5MU	C5-C6-N1	-4.41	118.52	123.31
1	2A	1911	PSU	O2-C2-N1	-4.38	118.28	122.79
1	2A	1939	5MU	O4-C4-C5	-4.38	119.91	124.92
57	2y	54	5MU	C5-C4-N3	4.37	119.12	115.32
55	1x	54	5MU	N3-C2-N1	4.36	120.57	114.89
1	2A	1939	5MU	C5-C6-N1	-4.36	118.58	123.31
1	2A	1939	5MU	C5-C4-N3	4.29	119.05	115.32
32	2a	516	PSU	C4-N3-C2	-4.28	120.47	126.37
1	2A	1917	PSU	C4-N3-C2	-4.26	120.50	126.37
57	1y	54	5MU	O4-C4-C5	-4.24	120.06	124.92
57	2y	55	PSU	O2-C2-N1	-4.23	118.43	122.79
54	1w	34	U8U	O4-C4-C5	-4.20	117.64	124.71
54	2w	55	PSU	C4-N3-C2	-4.13	120.68	126.37
54	2w	37	T6A	N6-C10-N11	4.12	119.44	113.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1917	PSU	C4-N3-C2	-4.10	120.72	126.37
32	1a	516	PSU	O2-C2-N1	-4.09	118.57	122.79
1	2A	2552	OMU	N3-C2-N1	4.08	120.21	114.89
54	1w	39	PSU	C4-N3-C2	-4.02	120.83	126.37
1	1A	2605	PSU	C4-N3-C2	-4.02	120.84	126.37
1	1A	1915	5MU	O4-C4-C5	-4.02	120.32	124.92
54	1w	54	5MU	C5-C6-N1	-3.99	118.98	123.31
1	1A	1911	PSU	C4-N3-C2	-3.98	120.89	126.37
32	2a	1519	MA6	C2-N1-C6	3.97	120.74	116.84
32	1a	516	PSU	C4-N3-C2	-3.95	120.92	126.37
1	2A	2605	PSU	C4-N3-C2	-3.94	120.95	126.37
57	2y	54	5MU	O4-C4-C5	-3.92	120.44	124.92
55	1x	54	5MU	C4-N3-C2	-3.89	122.24	127.34
55	1x	8	4SU	C6-C5-C4	-3.88	116.59	119.95
55	2x	54	5MU	C5-C6-N1	-3.85	119.13	123.31
1	1A	2552	OMU	O2-C2-N1	-3.83	117.81	122.80
54	1w	55	PSU	C4-N3-C2	-3.81	121.12	126.37
54	1w	39	PSU	O2-C2-N1	-3.79	118.88	122.79
55	1x	55	PSU	C4-N3-C2	-3.78	121.16	126.37
1	2A	1915	5MU	C5-C4-N3	3.78	118.61	115.32
1	1A	1942	5MC	C5-C6-N1	-3.74	119.25	123.31
55	1x	55	PSU	O2-C2-N1	-3.74	118.93	122.79
55	2x	55	PSU	O2-C2-N1	-3.71	118.96	122.79
1	2A	1942	5MC	C5-C6-N1	-3.71	119.28	123.31
1	2A	1911	PSU	C4-N3-C2	-3.71	121.27	126.37
32	2a	516	PSU	O2-C2-N1	-3.67	119.00	122.79
55	2x	54	5MU	O4-C4-C5	-3.64	120.75	124.92
54	1w	37	T6A	N3-C2-N1	-3.63	123.75	128.67
1	1A	1911	PSU	O2-C2-N1	-3.61	119.06	122.79
54	2w	54	5MU	O4-C4-C5	-3.61	120.79	124.92
57	1y	54	5MU	C5-C6-N1	-3.58	119.42	123.31
55	1x	54	5MU	C5-C4-N3	3.58	118.43	115.32
1	1A	2605	PSU	O2-C2-N1	-3.57	119.11	122.79
57	2y	39	PSU	C4-N3-C2	-3.57	121.46	126.37
32	2a	1404	5MC	C5-C6-N1	-3.56	119.44	123.31
1	2A	1917	PSU	O2-C2-N1	-3.56	119.12	122.79
54	2w	37	T6A	N3-C2-N1	-3.55	123.85	128.67
54	2w	54	5MU	C5-C4-N3	3.55	118.41	115.32
55	1x	8	4SU	C5-C4-N3	3.54	118.04	114.75
1	2A	1915	5MU	O4-C4-C5	-3.53	120.88	124.92
54	2w	34	U8U	C1'-N1-C6	-3.53	115.35	121.15
55	1x	32	5MC	C5-C6-N1	-3.52	119.49	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	1y	55	PSU	C4-N3-C2	-3.51	121.53	126.37
1	2A	1962	5MC	C5-C6-N1	-3.49	119.52	123.31
1	2A	2552	OMU	C5-C4-N3	3.48	119.67	114.80
54	2w	34	U8U	C5-C4-N3	3.45	120.48	115.21
54	1w	34	U8U	C1'-N1-C6	-3.45	115.47	121.15
55	1x	54	5MU	C5-C6-N1	-3.45	119.56	123.31
1	1A	1917	PSU	O2-C2-N1	-3.43	119.25	122.79
32	1a	1400	5MC	C5-C6-N1	-3.40	119.62	123.31
57	1y	37	T6A	N3-C2-N1	-3.40	124.06	128.67
57	2y	37	T6A	N3-C2-N1	-3.40	124.06	128.67
54	1w	55	PSU	O2-C2-N1	-3.39	119.30	122.79
32	2a	1407	5MC	C5-C6-N1	-3.37	119.65	123.31
55	2x	54	5MU	O2-C2-N1	-3.35	118.44	122.80
54	2w	54	5MU	N3-C2-N1	3.33	119.22	114.89
32	1a	1404	5MC	C5-C6-N1	-3.32	119.70	123.31
32	1a	1207	2MG	C8-N7-C5	3.28	108.14	102.55
57	2y	54	5MU	C5-C6-N1	-3.28	119.75	123.31
1	1A	2251	OMG	C8-N7-C5	3.28	108.13	102.55
32	1a	1498	UR3	C5-C4-N3	3.25	119.31	115.04
43	1l	92	0TD	CSB-SB-CB	3.23	108.18	102.36
32	1a	967	5MC	C5-C6-N1	-3.20	119.84	123.31
55	2x	8	4SU	C6-C5-C4	-3.20	117.18	119.95
32	2a	1498	UR3	C5-C4-N3	3.19	119.24	115.04
1	2A	1915	5MU	C5-C6-N1	-3.18	119.86	123.31
55	2x	8	4SU	C5-C4-N3	3.17	117.70	114.75
32	2a	1519	MA6	C4-C5-N7	-3.17	105.99	109.34
1	1A	1915	5MU	C5-C6-N1	-3.17	119.87	123.31
32	2a	967	5MC	C5-C6-N1	-3.17	119.87	123.31
1	1A	1962	5MC	C5-C6-N1	-3.16	119.88	123.31
54	2w	34	U8U	O4-C4-C5	-3.12	119.46	124.71
54	1w	76	A1B8A	C4'-O4'-C1'	-3.12	107.07	109.92
55	2x	8	4SU	C1'-N1-C2	3.10	123.16	117.59
55	1x	8	4SU	O2-C2-N1	3.10	126.83	122.80
55	1x	8	4SU	S4-C4-N3	-3.10	116.97	120.20
54	2w	54	5MU	C4-N3-C2	-3.10	123.28	127.34
1	1A	1939	5MU	O2-C2-N1	-3.08	118.78	122.80
55	2x	32	5MC	C5-C6-N1	-3.08	119.97	123.31
32	1a	1207	2MG	N1-C2-N2	3.05	119.68	116.56
55	1x	32	5MC	C5-C4-N3	-3.04	118.64	121.75
32	1a	1407	5MC	C5-C6-N1	-3.02	120.03	123.31
57	1y	54	5MU	O2-C2-N1	-3.02	118.86	122.80
54	2w	55	PSU	C6-C5-C4	-3.02	116.14	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	1y	55	PSU	O2-C2-N1	-3.00	119.69	122.79
1	2A	2251	OMG	C8-N7-C5	2.99	107.64	102.55
57	1y	34	U8U	C5-C4-N3	2.99	118.98	114.80
1	1A	2552	OMU	C5-C4-N3	2.99	118.98	114.80
1	2A	2503	2MA	C2-N1-C6	2.95	122.64	118.10
32	1a	1407	5MC	C5-C4-N3	-2.94	118.74	121.75
1	2A	2605	PSU	O2-C2-N1	-2.93	119.77	122.79
57	1y	39	PSU	C4-N3-C2	-2.92	122.35	126.37
57	2y	34	U8U	C5-C4-N3	2.92	118.88	114.80
55	2x	32	5MC	C5-C4-N3	-2.90	118.78	121.75
1	2A	2552	OMU	O2-C2-N1	-2.90	119.03	122.80
55	1x	54	5MU	O4-C4-C5	-2.89	121.61	124.92
54	2w	37	T6A	C4-C5-N7	-2.88	106.29	109.34
54	2w	76	A1B8A	C4-C5-N7	-2.88	106.29	109.34
32	1a	1400	5MC	C5-C4-N3	-2.86	118.82	121.75
1	1A	2503	2MA	C2-N1-C6	2.86	122.50	118.10
1	2A	1939	5MU	O2-C2-N1	-2.86	119.08	122.80
32	2a	1400	5MC	C5-C6-N1	-2.85	120.22	123.31
32	2a	1207	2MG	C8-N7-C5	2.84	107.39	102.55
54	2w	39	PSU	C4-N3-C2	-2.83	122.47	126.37
32	2a	1404	5MC	C5-C4-N3	-2.83	118.85	121.75
1	2A	1942	5MC	C5-C4-N3	-2.83	118.86	121.75
32	1a	1518	MA6	C4-C5-N7	-2.82	106.36	109.34
32	2a	1402	4OC	CM4-N4-C4	-2.81	116.96	122.45
1	2A	1962	5MC	C5-C4-N3	-2.78	118.91	121.75
32	1a	966	M2G	C8-N7-C5	2.76	107.24	102.55
32	2a	1518	MA6	C4-C5-N7	-2.75	106.43	109.34
32	2a	516	PSU	O4'-C1'-C2'	2.74	108.95	105.15
54	2w	55	PSU	O2-C2-N1	-2.72	119.98	122.79
57	2y	37	T6A	C4-C5-N7	-2.72	106.46	109.34
32	1a	1402	4OC	C6-C5-C4	2.69	120.25	117.00
32	2a	1407	5MC	C5-C4-N3	-2.67	119.02	121.75
32	2a	966	M2G	C8-N7-C5	2.67	107.10	102.55
55	2x	8	4SU	O2-C2-N1	2.67	126.27	122.80
32	2a	1400	5MC	C5-C4-N3	-2.64	119.05	121.75
54	2w	37	T6A	N6-C6-N1	2.63	121.67	118.71
54	1w	34	U8U	C5-C6-N1	-2.60	119.43	122.94
55	1x	8	4SU	C1'-N1-C2	2.60	122.25	117.59
32	1a	1404	5MC	C5-C4-N3	-2.58	119.11	121.75
55	2x	55	PSU	C5-C6-N1	-2.58	118.56	122.14
57	1y	37	T6A	C4-C5-N7	-2.57	106.62	109.34
57	1y	39	PSU	O2-C2-N3	-2.57	117.30	121.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1962	5MC	C5-C4-N3	-2.56	119.13	121.75
57	1y	34	U8U	O4-C4-C5	-2.56	120.74	125.16
32	1a	1498	UR3	C6-N1-C2	-2.55	119.71	121.80
1	2A	2552	OMU	O4-C4-C5	-2.55	120.77	125.16
32	1a	1498	UR3	C1'-N1-C2	2.53	121.19	117.04
54	1w	54	5MU	O2-C2-N1	-2.51	119.52	122.80
1	1A	1962	5MC	CM5-C5-C6	-2.50	119.46	122.85
32	1a	1519	MA6	C4-C5-N7	-2.50	106.69	109.34
32	1a	967	5MC	C5-C4-N3	-2.48	119.21	121.75
54	2w	39	PSU	O2-C2-N1	-2.48	120.23	122.79
54	2w	54	5MU	C5-C6-N1	-2.46	120.64	123.31
54	1w	37	T6A	N6-C10-N11	2.46	117.15	113.77
54	1w	37	T6A	C4-C5-N7	-2.45	106.75	109.34
32	1a	1498	UR3	C3U-N3-C2	2.41	121.53	117.33
57	2y	54	5MU	O2-C2-N1	-2.40	119.67	122.80
1	1A	1942	5MC	C5-C4-N3	-2.40	119.29	121.75
32	2a	1207	2MG	N1-C2-N2	2.40	119.01	116.56
55	2x	32	5MC	O2-C2-N3	-2.39	118.56	122.33
32	2a	1400	5MC	C1'-N1-C6	-2.38	117.22	121.15
1	1A	1915	5MU	O2-C2-N1	-2.37	119.72	122.80
32	1a	1207	2MG	N2-C2-N3	-2.37	117.50	120.51
55	2x	8	4SU	C6-N1-C2	-2.35	118.14	121.00
54	2w	54	5MU	C1'-N1-C2	2.33	121.78	117.59
1	1A	1911	PSU	C6-C5-C4	-2.33	116.61	118.17
1	1A	1915	5MU	C5M-C5-C4	2.32	121.25	118.78
1	1A	2251	OMG	C5-C6-N1	2.30	118.46	114.07
1	2A	2251	OMG	CM2-O2'-C2'	-2.30	108.57	114.47
32	2a	967	5MC	C5-C4-N3	-2.30	119.40	121.75
57	2y	34	U8U	O4-C4-C5	-2.29	121.20	125.16
1	2A	2503	2MA	C5-C6-N1	-2.29	118.14	120.84
1	1A	2552	OMU	O4-C4-C5	-2.28	121.23	125.16
43	1l	92	0TD	OD2-CG-CB	2.27	118.05	113.15
32	1a	1400	5MC	O2-C2-N3	-2.25	118.78	122.33
32	2a	967	5MC	C1'-N1-C6	-2.25	117.45	121.15
1	1A	2503	2MA	C4-C5-N7	-2.25	106.96	109.34
54	1w	37	T6A	N6-C6-N1	2.23	121.22	118.71
1	2A	1917	PSU	C5-C6-N1	-2.23	119.05	122.14
55	2x	8	4SU	S4-C4-N3	-2.21	117.89	120.20
57	2y	54	5MU	C5M-C5-C4	2.18	121.11	118.78
1	2A	2503	2MA	O4'-C1'-N9	-2.16	105.89	108.75
32	1a	516	PSU	O4'-C1'-C2'	2.14	108.11	105.15
32	2a	1498	UR3	C3U-N3-C4	2.13	120.82	117.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	1402	4OC	O2-C2-N3	-2.11	119.00	122.33
1	1A	2503	2MA	N3-C2-N1	-2.11	122.07	125.77
32	1a	1402	4OC	O2-C2-N3	-2.11	119.00	122.33
57	2y	55	PSU	C5-C6-N1	-2.10	119.22	122.14
57	2y	39	PSU	C6-C5-C4	-2.10	116.75	118.17
54	1w	39	PSU	C5-C6-N1	-2.09	119.23	122.14
32	1a	1404	5MC	CM5-C5-C6	-2.09	120.03	122.85
57	1y	54	5MU	C5M-C5-C4	2.09	121.01	118.78
1	2A	1920	OMC	O2-C2-N3	-2.08	119.05	122.33
54	1w	76	A1B8A	C4-C5-N7	-2.08	107.14	109.34
32	2a	516	PSU	C3'-C2'-C1'	2.06	104.12	101.69
1	1A	2605	PSU	C5-C6-N1	-2.06	119.28	122.14
54	2w	54	5MU	C1'-N1-C6	-2.06	117.76	121.15
32	2a	966	M2G	C5-C6-N1	2.05	117.99	114.07
54	2w	34	U8U	C5-C6-N1	-2.04	120.19	122.94
32	2a	1400	5MC	CM5-C5-C6	-2.03	120.10	122.85
32	2a	1498	UR3	C1'-N1-C2	2.03	120.36	117.04
32	1a	966	M2G	C5-C6-N1	2.02	117.92	114.07
43	2l	92	0TD	OD2-CG-CB	2.02	117.51	113.15
32	1a	1207	2MG	CM2-N2-C2	-2.02	119.32	123.65
32	2a	516	PSU	C5-C6-N1	-2.01	119.34	122.14
55	2x	8	4SU	O2-C2-N3	-2.01	117.77	121.49
57	2y	39	PSU	O2-C2-N1	-2.01	120.71	122.79
54	1w	55	PSU	C6-C5-C4	-2.01	116.82	118.17
55	2x	54	5MU	C5M-C5-C4	2.00	120.92	118.78

There are no chirality outliers.

All (87) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1400	5MC	O4'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
43	1l	92	0TD	O-C-CA-CB
43	1l	92	0TD	CG-CB-SB-CSB
55	1x	76	8AN	C4'-C5'-O5'-P
32	2a	1519	MA6	O4'-C4'-C5'-O5'
43	2l	92	0TD	SB-CB-CG-OD2
54	2w	34	U8U	C5-C-N-CA
54	1w	37	T6A	O10-C10-N6-C6
54	1w	37	T6A	N11-C10-N6-C6
54	1w	37	T6A	N11-C12-C13-ODA

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Mol	Chain	Res	Type	Atoms
54	1w	37	T6A	N11-C12-C13-ODB
54	1w	37	T6A	C14-C12-C13-ODA
54	1w	37	T6A	C14-C12-C13-ODB
54	2w	37	T6A	C5-C6-N6-C10
54	2w	37	T6A	O10-C10-N6-C6
54	2w	37	T6A	N11-C10-N6-C6
54	1w	39	PSU	O4'-C4'-C5'-O5'
54	1w	46	G7M	O4'-C4'-C5'-O5'
54	2w	46	G7M	O4'-C4'-C5'-O5'
54	1w	76	A1B8A	O-C-CA-CB
54	1w	76	A1B8A	N3'-C-CA-CB
54	2w	76	A1B8A	O4'-C4'-C5'-O5'
56	1z	1	FME	O1-CN-N-CA
56	1z	1	FME	CB-CA-N-CN
56	1z	1	FME	N-CA-CB-CG
56	1z	1	FME	O-C-CA-CB
56	2z	1	FME	O1-CN-N-CA
56	2z	1	FME	O-C-CA-CB
55	2x	76	8AN	C3'-C4'-C5'-O5'
54	2w	76	A1B8A	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
54	2w	46	G7M	C3'-C4'-C5'-O5'
54	2w	37	T6A	N6-C10-N11-C12
56	2z	1	FME	CA-CB-CG-SD
54	2w	34	U8U	C3'-C4'-C5'-O5'
54	2w	34	U8U	O4'-C4'-C5'-O5'
54	2w	76	A1B8A	C-CA-CB-CG
32	1a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
54	1w	39	PSU	C3'-C4'-C5'-O5'
54	1w	46	G7M	C3'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
55	2x	76	8AN	O4'-C4'-C5'-O5'
32	2a	1404	5MC	O4'-C4'-C5'-O5'
54	1w	54	5MU	O4'-C4'-C5'-O5'
1	2A	1911	PSU	O4'-C4'-C5'-O5'
32	2a	1404	5MC	C3'-C4'-C5'-O5'
54	2w	37	T6A	O10-C10-N11-C12
54	1w	54	5MU	C3'-C4'-C5'-O5'
54	2w	37	T6A	C13-C12-C14-C15
54	1w	34	U8U	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	2A	2251	OMG	C1'-C2'-O2'-CM2
32	1a	1402	4OC	O4'-C4'-C5'-O5'
55	1x	76	8AN	O4'-C4'-C5'-O5'
54	2w	37	T6A	N1-C6-N6-C10
56	1z	1	FME	C-CA-CB-CG
1	2A	1915	5MU	O4'-C4'-C5'-O5'
54	1w	34	U8U	C3'-C4'-C5'-O5'
55	1x	76	8AN	C3'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
54	2w	46	G7M	C4'-C5'-O5'-P
55	2x	76	8AN	C4'-C5'-O5'-P
1	2A	1962	5MC	O4'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD1
43	2l	92	0TD	SB-CB-CG-OD1
32	1a	1519	MA6	C4'-C5'-O5'-P
1	1A	2503	2MA	O4'-C4'-C5'-O5'
57	1y	46	G7M	C4'-C5'-O5'-P
57	1y	55	PSU	O4'-C1'-C5-C4
32	2a	1402	4OC	C3'-C4'-C5'-O5'
1	2A	2503	2MA	O4'-C4'-C5'-O5'
43	1l	92	0TD	CA-CB-SB-CSB
1	1A	2503	2MA	C4'-C5'-O5'-P
57	1y	55	PSU	O4'-C1'-C5-C6
43	2l	92	0TD	CG-CB-SB-CSB
57	1y	37	T6A	C4'-C5'-O5'-P
1	2A	2503	2MA	C4'-C5'-O5'-P
32	2a	1519	MA6	C4'-C5'-O5'-P
1	1A	2503	2MA	C3'-C4'-C5'-O5'
1	2A	1911	PSU	C3'-C4'-C5'-O5'
1	1A	1920	OMC	C2'-C1'-N1-C2
54	1w	76	A1B8A	CG-CD-CE-NZ
32	1a	527	G7M	C4'-C5'-O5'-P
54	2w	54	5MU	C2'-C1'-N1-C2

There are no ring outliers.

48 monomers are involved in 72 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1939	5MU	2	0
32	1a	1402	4OC	3	0
1	2A	1911	PSU	2	0
43	2l	92	0TD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	1w	39	PSU	1	0
57	1y	55	PSU	2	0
32	2a	1498	UR3	1	0
32	2a	516	PSU	1	0
55	2x	76	8AN	1	0
57	1y	39	PSU	1	0
57	1y	37	T6A	1	0
57	2y	39	PSU	1	0
32	1a	516	PSU	1	0
57	2y	37	T6A	1	0
1	2A	2503	2MA	2	0
54	2w	39	PSU	1	0
32	1a	1207	2MG	1	0
54	2w	34	U8U	1	0
55	2x	8	4SU	1	0
54	2w	55	PSU	2	0
32	1a	1519	MA6	2	0
54	1w	34	U8U	4	0
56	1z	1	FME	1	0
32	2a	1518	MA6	2	0
32	1a	1498	UR3	1	0
56	2z	1	FME	1	0
32	2a	1519	MA6	3	0
57	1y	46	G7M	1	0
1	2A	2552	OMU	1	0
57	2y	46	G7M	5	0
1	2A	1942	5MC	1	0
32	1a	1400	5MC	1	0
1	1A	2503	2MA	1	0
1	1A	1917	PSU	1	0
32	1a	1518	MA6	3	0
32	1a	527	G7M	1	0
32	2a	1400	5MC	2	0
54	1w	76	A1B8A	2	0
32	2a	1402	4OC	2	0
55	1x	8	4SU	1	0
1	1A	2552	OMU	1	0
32	2a	1404	5MC	2	0
54	2w	76	A1B8A	2	0
32	2a	1207	2MG	3	0
1	1A	1939	5MU	1	0
57	2y	34	U8U	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
43	1l	92	0TD	1	0
55	1x	76	8AN	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2677 ligands modelled in this entry, 2673 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
62	SF4	2d	303	35	0,12,12	-	-	-		
62	SF4	1d	302	35	0,12,12	-	-	-		
60	TEL	2A	3826	-	58,62,62	1.30	4 (6%)	74,92,92	1.88	14 (18%)
60	TEL	1A	4082	-	58,62,62	1.36	5 (8%)	74,92,92	1.54	8 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	SF4	2d	303	35	-	-	0/6/5/5
62	SF4	1d	302	35	-	-	0/6/5/5
60	TEL	2A	3826	-	-	9/73/108/108	0/4/5/5
60	TEL	1A	4082	-	-	10/73/108/108	0/4/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	1A	4082	TEL	O5-C10	5.74	1.44	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	2A	3826	TEL	O5-C10	5.43	1.44	1.35
60	1A	4082	TEL	O9-C15	5.08	1.45	1.34
60	2A	3826	TEL	O9-C15	5.01	1.45	1.34
60	1A	4082	TEL	O5-C2	-3.43	1.42	1.47
60	2A	3826	TEL	O5-C2	-3.00	1.43	1.47
60	1A	4082	TEL	O9-C4	-2.74	1.41	1.46
60	2A	3826	TEL	C36-N31	-2.48	1.34	1.38
60	1A	4082	TEL	C36-N31	-2.46	1.34	1.38

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
60	2A	3826	TEL	O9-C15-C21	9.28	120.09	110.93
60	1A	4082	TEL	O9-C15-C21	6.60	117.44	110.93
60	1A	4082	TEL	C17-C11-N6	-5.90	104.31	113.25
60	2A	3826	TEL	C17-C11-N6	-5.71	104.59	113.25
60	2A	3826	TEL	C4-O9-C15	-3.81	111.55	118.20
60	2A	3826	TEL	C8-C4-C2	-3.56	110.32	115.23
60	2A	3826	TEL	O20-C15-C21	-3.52	120.09	124.65
60	1A	4082	TEL	C4-O9-C15	-3.21	112.60	118.20
60	2A	3826	TEL	C28-C24-C19	-3.05	111.13	116.10
60	2A	3826	TEL	C56-N52-C47	2.85	121.84	116.85
60	1A	4082	TEL	O20-C15-C21	-2.51	121.39	124.65
60	2A	3826	TEL	O5-C2-C1	2.45	111.12	106.80
60	1A	4082	TEL	C28-C24-C19	-2.42	112.15	116.10
60	1A	4082	TEL	O9-C4-C2	2.37	110.84	105.48
60	2A	3826	TEL	O18-C13-C19	-2.37	117.01	121.30
60	2A	3826	TEL	O5-C10-N6	-2.37	107.97	109.86
60	2A	3826	TEL	O9-C15-O20	-2.29	119.81	123.95
60	2A	3826	TEL	O9-C4-C2	2.27	110.61	105.48
60	2A	3826	TEL	C38-O32-C28	2.27	122.12	117.51
60	1A	4082	TEL	O5-C10-O16	2.26	125.26	122.54
60	2A	3826	TEL	O9-C4-C8	2.08	111.24	107.36
60	1A	4082	TEL	C25-C21-C15	-2.07	106.29	110.34

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	1A	4082	TEL	C1-C2-C4-C8
60	1A	4082	TEL	O5-C2-C4-C8
60	1A	4082	TEL	O5-C2-C4-O9

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Mol	Chain	Res	Type	Atoms
60	1A	4082	TEL	C24-C28-O32-C38
60	1A	4082	TEL	C33-C28-O32-C38
60	1A	4082	TEL	C34-C28-O32-C38
60	2A	3826	TEL	C1-C2-C4-C8
60	2A	3826	TEL	O5-C2-C4-C8
60	2A	3826	TEL	C24-C28-O32-C38
60	2A	3826	TEL	C33-C28-O32-C38
60	2A	3826	TEL	C34-C28-O32-C38
60	2A	3826	TEL	N6-C11-C17-C22
60	1A	4082	TEL	N6-C3-C7-C12
60	2A	3826	TEL	O32-C28-C34-C30
60	2A	3826	TEL	C23-C19-C24-C28
60	1A	4082	TEL	C1-C2-C4-O9
60	1A	4082	TEL	C3-C2-C4-C8
60	1A	4082	TEL	C3-C2-C4-O9
60	2A	3826	TEL	C3-C2-C4-C8

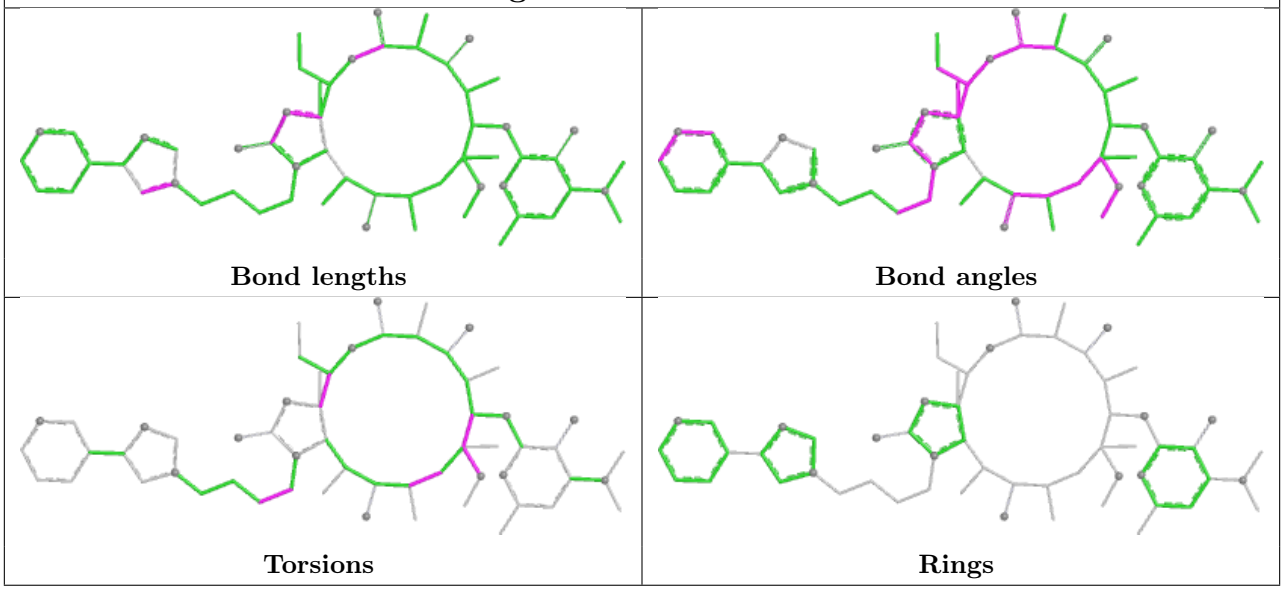
There are no ring outliers.

4 monomers are involved in 11 short contacts:

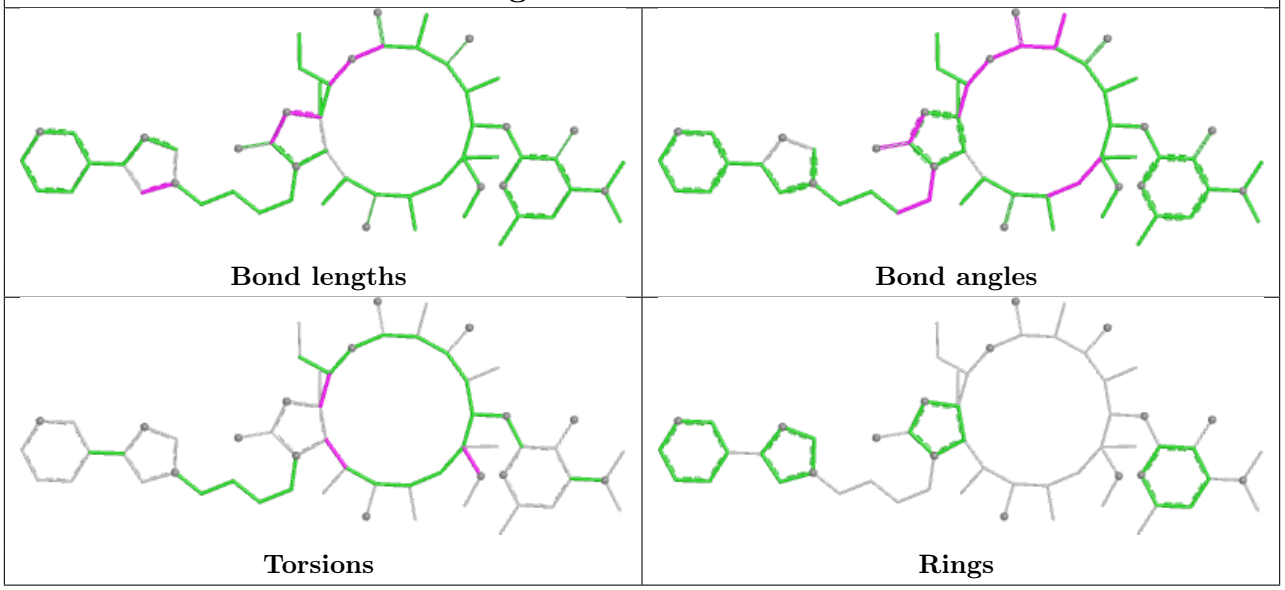
Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	2d	303	SF4	2	0
62	1d	302	SF4	1	0
60	2A	3826	TEL	4	0
60	1A	4082	TEL	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand TEL 2A 3826



Ligand TEL 1A 4082



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	1A	2860/2915 (98%)	-0.10	110 (3%) 44 36	17, 35, 97, 108	0
1	2A	2789/2915 (95%)	0.35	96 (3%) 48 40	30, 58, 93, 107	0
2	1B	120/121 (99%)	-0.06	1 (0%) 82 77	28, 50, 62, 85	0
2	2B	120/121 (99%)	1.27	21 (17%) 5 4	58, 82, 91, 99	0
3	1D	275/276 (99%)	-0.07	3 (1%) 77 71	17, 34, 49, 76	0
3	2D	275/276 (99%)	0.34	5 (1%) 67 60	30, 51, 65, 86	0
4	1E	204/206 (99%)	-0.01	0 100 100	18, 42, 62, 80	0
4	2E	204/206 (99%)	0.38	5 (2%) 58 49	29, 56, 70, 83	0
5	1F	203/210 (96%)	0.01	0 100 100	19, 43, 69, 82	0
5	2F	203/210 (96%)	0.46	2 (0%) 79 73	32, 66, 79, 88	0
6	1G	181/182 (99%)	0.42	7 (3%) 44 36	39, 56, 73, 85	0
6	2G	181/182 (99%)	1.35	36 (19%) 3 3	71, 81, 89, 95	0
7	1H	174/180 (96%)	0.16	2 (1%) 77 71	35, 52, 64, 75	0
7	2H	174/180 (96%)	0.91	11 (6%) 27 21	68, 81, 89, 95	0
8	1I	146/148 (98%)	0.75	5 (3%) 48 40	42, 72, 82, 89	0
8	2I	146/148 (98%)	0.90	15 (10%) 13 10	55, 73, 84, 87	0
9	1N	140/140 (100%)	0.02	0 100 100	25, 40, 60, 75	0
9	2N	140/140 (100%)	0.89	10 (7%) 23 18	43, 65, 76, 81	0
10	1O	122/122 (100%)	-0.06	0 100 100	25, 40, 55, 60	0
10	2O	122/122 (100%)	0.29	0 100 100	41, 53, 67, 75	0
11	1P	149/150 (99%)	0.28	1 (0%) 84 79	20, 45, 67, 77	0
11	2P	149/150 (99%)	0.63	7 (4%) 37 30	38, 67, 79, 87	0
12	1Q	141/141 (100%)	0.02	2 (1%) 73 66	25, 40, 54, 68	0
12	2Q	141/141 (100%)	1.13	14 (9%) 14 11	47, 66, 77, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.06	0 100 100	21, 35, 51, 66	0
13	2R	118/118 (100%)	0.29	0 100 100	35, 49, 62, 68	0
14	1S	110/112 (98%)	0.17	0 100 100	36, 48, 60, 63	0
14	2S	110/112 (98%)	1.21	21 (19%) 4 4	63, 74, 83, 86	0
15	1T	131/146 (89%)	0.29	2 (1%) 71 64	34, 46, 68, 79	0
15	2T	131/146 (89%)	0.36	2 (1%) 71 64	44, 57, 71, 81	0
16	1U	116/118 (98%)	-0.09	1 (0%) 81 75	22, 32, 49, 66	0
16	2U	116/118 (98%)	0.63	2 (1%) 69 61	45, 64, 75, 83	0
17	1V	101/101 (100%)	-0.07	0 100 100	22, 43, 60, 70	0
17	2V	101/101 (100%)	0.76	3 (2%) 52 44	43, 73, 81, 85	0
18	1W	112/113 (99%)	-0.26	0 100 100	25, 33, 49, 73	0
18	2W	112/113 (99%)	0.47	2 (1%) 67 60	36, 50, 67, 85	0
19	1X	95/96 (98%)	-0.07	1 (1%) 77 71	26, 37, 58, 74	0
19	2X	95/96 (98%)	0.90	8 (8%) 18 14	48, 59, 73, 79	0
20	1Y	107/110 (97%)	0.21	3 (2%) 55 46	36, 48, 67, 77	0
20	2Y	107/110 (97%)	1.25	15 (14%) 7 7	61, 71, 79, 82	0
21	1Z	154/206 (74%)	0.49	7 (4%) 39 31	42, 60, 83, 88	0
21	2Z	160/206 (77%)	1.08	18 (11%) 11 9	70, 80, 89, 95	0
22	10	83/85 (97%)	0.35	8 (9%) 15 11	26, 36, 62, 78	0
22	20	83/85 (97%)	1.18	11 (13%) 8 7	51, 65, 75, 91	0
23	11	97/98 (98%)	0.15	1 (1%) 79 73	25, 42, 65, 70	0
23	21	97/98 (98%)	0.53	3 (3%) 51 43	36, 56, 74, 78	0
24	12	70/72 (97%)	-0.05	0 100 100	35, 47, 59, 68	0
24	22	70/72 (97%)	0.67	0 100 100	56, 69, 75, 77	0
25	13	59/60 (98%)	-0.04	0 100 100	28, 38, 56, 63	0
25	23	59/60 (98%)	0.59	0 100 100	54, 67, 77, 82	0
26	14	69/71 (97%)	0.63	4 (5%) 30 23	52, 74, 88, 94	0
26	24	69/71 (97%)	1.01	6 (8%) 17 13	74, 87, 93, 99	0
27	15	59/60 (98%)	-0.20	0 100 100	20, 36, 50, 62	0
27	25	59/60 (98%)	0.26	0 100 100	34, 51, 64, 74	0
28	16	53/54 (98%)	-0.01	1 (1%) 66 58	30, 40, 57, 61	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.87	4 (7%) 22 16	46, 60, 69, 76	0
29	17	48/49 (97%)	-0.12	1 (2%) 63 55	21, 28, 53, 58	0
29	27	48/49 (97%)	0.20	3 (6%) 27 21	31, 41, 59, 66	0
30	18	64/65 (98%)	-0.01	1 (1%) 70 63	24, 33, 40, 49	0
30	28	64/65 (98%)	0.66	1 (1%) 70 63	47, 55, 62, 66	0
31	19	37/37 (100%)	-0.05	1 (2%) 56 47	28, 37, 56, 59	0
31	29	37/37 (100%)	1.29	4 (10%) 12 9	59, 69, 77, 87	0
32	1a	1488/1521 (97%)	0.44	31 (2%) 63 55	31, 65, 92, 106	0
32	2a	1491/1521 (98%)	0.91	124 (8%) 19 14	50, 80, 97, 106	0
33	1b	231/256 (90%)	0.73	21 (9%) 16 12	62, 76, 84, 91	0
33	2b	231/256 (90%)	1.46	55 (23%) 2 3	74, 86, 92, 95	0
34	1c	206/239 (86%)	0.39	5 (2%) 59 51	52, 69, 80, 90	0
34	2c	206/239 (86%)	1.48	61 (29%) 1 2	74, 85, 90, 94	0
35	1d	208/209 (99%)	0.54	8 (3%) 44 36	55, 67, 77, 80	0
35	2d	208/209 (99%)	1.18	33 (15%) 6 5	65, 75, 83, 91	0
36	1e	148/162 (91%)	0.54	1 (0%) 84 79	50, 62, 71, 83	0
36	2e	148/162 (91%)	1.03	20 (13%) 8 7	69, 79, 85, 89	0
37	1f	100/101 (99%)	0.35	0 100 100	49, 64, 75, 79	0
37	2f	100/101 (99%)	0.72	4 (4%) 43 35	60, 72, 80, 83	0
38	1g	155/156 (99%)	0.83	14 (9%) 17 12	57, 70, 84, 99	0
38	2g	155/156 (99%)	1.32	35 (22%) 3 3	73, 82, 88, 94	0
39	1h	137/138 (99%)	0.55	4 (2%) 54 45	55, 65, 72, 78	0
39	2h	137/138 (99%)	1.16	20 (14%) 7 6	69, 79, 84, 89	0
40	1i	127/128 (99%)	1.03	14 (11%) 12 9	50, 75, 84, 88	0
40	2i	127/128 (99%)	1.94	57 (44%) 1 1	74, 86, 91, 93	0
41	1j	97/105 (92%)	1.14	11 (11%) 11 9	51, 74, 85, 90	0
41	2j	96/105 (91%)	1.74	27 (28%) 2 2	75, 86, 92, 94	0
42	1k	114/129 (88%)	0.62	6 (5%) 33 26	39, 64, 77, 84	0
42	2k	114/129 (88%)	0.90	12 (10%) 13 10	63, 75, 83, 86	0
43	1l	121/132 (91%)	0.57	8 (6%) 26 19	45, 55, 66, 76	0
43	2l	121/132 (91%)	1.16	14 (11%) 11 9	53, 71, 78, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	123/126 (97%)	0.84	11 (8%) 17 13	54, 68, 78, 92	0
44	2m	122/126 (96%)	1.60	36 (29%) 1 2	71, 84, 89, 91	0
45	1n	60/61 (98%)	0.76	5 (8%) 19 14	56, 65, 75, 81	0
45	2n	60/61 (98%)	2.35	33 (55%) 0 0	77, 85, 89, 94	0
46	1o	88/89 (98%)	0.45	2 (2%) 61 52	50, 61, 73, 84	0
46	2o	88/89 (98%)	0.87	4 (4%) 39 31	62, 75, 82, 86	0
47	1p	82/88 (93%)	1.38	12 (14%) 7 6	57, 71, 78, 83	0
47	2p	82/88 (93%)	1.05	4 (4%) 36 28	57, 68, 76, 85	0
48	1q	99/105 (94%)	0.89	7 (7%) 23 18	53, 67, 75, 80	0
48	2q	99/105 (94%)	0.98	13 (13%) 8 7	63, 74, 81, 86	0
49	1r	68/88 (77%)	0.37	2 (2%) 54 45	53, 64, 73, 79	0
49	2r	68/88 (77%)	0.54	0 100 100	67, 76, 84, 87	0
50	1s	83/93 (89%)	0.70	4 (4%) 36 29	59, 70, 82, 93	0
50	2s	83/93 (89%)	1.76	24 (28%) 1 2	79, 86, 92, 93	0
51	1t	96/106 (90%)	0.81	11 (11%) 11 9	59, 70, 78, 86	0
51	2t	96/106 (90%)	0.89	10 (10%) 13 10	54, 69, 82, 84	0
52	1u	23/27 (85%)	1.23	3 (13%) 9 7	58, 64, 69, 76	0
52	2u	23/27 (85%)	2.21	11 (47%) 0 1	76, 81, 84, 89	0
53	1v	13/24 (54%)	1.34	3 (23%) 2 3	41, 77, 94, 95	0
53	2v	13/24 (54%)	1.68	4 (30%) 1 1	78, 91, 95, 97	0
54	1w	67/76 (88%)	1.29	12 (17%) 4 4	58, 96, 102, 104	0
54	2w	67/76 (88%)	1.52	14 (20%) 3 3	78, 99, 105, 106	0
55	1x	72/77 (93%)	0.44	2 (2%) 55 46	41, 65, 83, 84	0
55	2x	72/77 (93%)	1.10	7 (9%) 15 11	52, 82, 91, 97	0
56	1z	2/3 (66%)	0.69	0 100 100	43, 43, 43, 46	0
56	2z	2/3 (66%)	1.57	1 (50%) 0 1	53, 53, 53, 69	0
57	1y	68/76 (89%)	1.24	7 (10%) 13 10	54, 99, 105, 107	0
57	2y	68/76 (89%)	1.64	16 (23%) 2 3	69, 101, 106, 107	0
All	All	20884/21754 (96%)	0.52	1330 (6%) 27 20	17, 63, 91, 108	0

All (1330) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	2m	123	ALA	8.8
45	1n	2	ALA	8.5
38	1g	81	GLY	8.3
44	1m	123	ALA	7.3
44	1m	122	LYS	7.3
22	10	6	GLY	6.5
44	2m	124	PRO	6.4
22	20	5	LYS	6.3
44	2m	102	ARG	5.7
38	2g	80	VAL	5.7
44	1m	124	PRO	5.7
3	2D	276	LYS	5.6
22	10	8	GLY	5.5
40	2i	126	SER	5.5
1	2A	2112	G	5.4
1	2A	2147	G	5.4
22	10	7	LEU	5.4
1	1A	2115	G	5.4
39	2h	2	LEU	5.2
44	2m	122	LYS	5.1
52	2u	14	TRP	5.1
1	2A	2143	C	5.0
40	2i	14	VAL	5.0
1	1A	2121	G	5.0
45	2n	34	TYR	5.0
45	2n	29	ARG	4.9
41	2j	47	PHE	4.8
7	1H	2	SER	4.8
44	2m	121	LYS	4.8
43	2l	10	LEU	4.8
40	2i	36	TYR	4.7
1	1A	2133	G	4.7
45	2n	7	ILE	4.7
1	1A	2112	G	4.7
45	2n	33	VAL	4.6
38	1g	153	HIS	4.6
40	2i	103	THR	4.6
45	2n	11	LYS	4.6
1	2A	2145	C	4.5
15	1T	130	ALA	4.5
6	2G	159	VAL	4.5
21	2Z	146	ILE	4.5
34	2c	154	SER	4.5

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Mol	Chain	Res	Type	RSRZ
41	2j	55	LYS	4.5
45	2n	2	ALA	4.4
23	21	2	SER	4.4
34	2c	39	ILE	4.4
1	2A	2144	U	4.4
1	1A	1068	G	4.4
45	2n	39	LEU	4.3
32	1a	1531	A	4.3
43	1l	29	GLY	4.3
1	1A	2143	C	4.3
44	1m	121	LYS	4.3
34	2c	189	ALA	4.3
52	2u	16	GLY	4.3
3	1D	276	LYS	4.3
38	2g	153	HIS	4.3
15	1T	131	ALA	4.3
1	1A	2113	U	4.2
45	2n	30	ALA	4.2
1	2A	2133	G	4.2
1	2A	2146	C	4.2
1	1A	1096	A	4.2
22	20	6	GLY	4.2
38	1g	83	ALA	4.2
1	2A	2111	C	4.2
40	2i	11	LYS	4.1
51	1t	10	LEU	4.1
1	2A	2155	G	4.1
40	1i	9	ARG	4.1
40	2i	113	LYS	4.1
1	2A	2166	G	4.1
32	2a	1033	G	4.1
33	2b	202	PRO	4.1
40	2i	115	GLY	4.0
44	2m	105	THR	4.0
1	1A	2159	G	4.0
1	2A	2115	G	4.0
1	1A	1094	U	4.0
1	1A	2122	U	4.0
22	20	7	LEU	4.0
32	2a	1285	A	4.0
1	1A	2109	U	4.0
1	2A	2295	C	4.0

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Mol	Chain	Res	Type	RSRZ
50	2s	15	LEU	4.0
32	1a	1257	U	4.0
38	1g	82	GLY	4.0
1	1A	2145	C	3.9
38	1g	79	ARG	3.9
32	2a	1001(A)	G	3.9
14	2S	33	LYS	3.9
8	2I	20	ASP	3.9
50	2s	63	THR	3.9
41	2j	40	LEU	3.9
33	2b	131	PRO	3.9
45	2n	26	ARG	3.9
2	2B	23	G	3.9
32	2a	1354	C	3.9
35	2d	23	GLY	3.9
50	1s	84	GLY	3.9
21	2Z	174	VAL	3.8
33	2b	197	VAL	3.8
38	1g	80	VAL	3.8
35	1d	8	VAL	3.8
38	1g	156	TRP	3.8
45	2n	3	ARG	3.8
40	2i	49	PRO	3.8
22	20	9	SER	3.8
26	14	57	GLU	3.8
1	1A	1095	A	3.8
32	2a	1286	A	3.8
38	1g	154	TYR	3.8
40	2i	111	ARG	3.8
41	2j	54	PHE	3.8
12	2Q	30	GLY	3.8
28	26	5	VAL	3.8
1	2A	2168	G	3.8
32	2a	1036	G	3.8
32	2a	1356	G	3.8
52	2u	24	ARG	3.7
21	2Z	76	LEU	3.7
33	1b	133	LYS	3.7
45	1n	3	ARG	3.7
50	2s	62	ILE	3.7
39	2h	4	ASP	3.7
12	2Q	22	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
44	2m	33	ALA	3.7
33	1b	129	GLU	3.7
1	1A	2117	A	3.7
1	2A	2174	C	3.7
33	2b	152	PHE	3.7
1	1A	2131	G	3.7
1	2A	2110	G	3.7
45	2n	6	LEU	3.7
52	2u	15	ARG	3.7
40	2i	119	ALA	3.7
41	2j	63	PHE	3.7
9	2N	45	ASN	3.7
34	2c	55	VAL	3.7
1	1A	2110	G	3.7
32	2a	973	G	3.7
32	2a	1034	G	3.7
2	2B	55	U	3.7
43	2l	32	PHE	3.6
35	2d	154	ASN	3.6
54	1w	73	A	3.6
35	2d	209	ARG	3.6
32	2a	1202	G	3.6
41	2j	65	LEU	3.6
33	2b	165	VAL	3.6
6	2G	20	ILE	3.6
32	2a	1249	C	3.6
1	1A	2141	G	3.6
32	2a	1224	G	3.6
38	1g	4	ARG	3.6
1	2A	1536	C	3.6
41	2j	8	LEU	3.6
44	2m	120	LYS	3.6
40	2i	102	LEU	3.6
42	2k	124	LYS	3.6
21	1Z	141	VAL	3.5
45	2n	25	VAL	3.5
40	2i	7	THR	3.5
33	2b	121	LEU	3.5
47	1p	49	LEU	3.5
51	1t	24	LEU	3.5
14	2S	92	TYR	3.5
52	2u	13	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
3	2D	32	SER	3.5
33	2b	186	ALA	3.5
32	2a	1027	C	3.5
14	2S	32	LEU	3.5
40	2i	66	ARG	3.5
1	1A	2144	U	3.5
1	2A	2113	U	3.5
38	1g	84	ASN	3.5
20	2Y	1	MET	3.5
50	2s	84	GLY	3.4
32	2a	950	U	3.4
34	2c	87	LEU	3.4
1	2A	2114	A	3.4
2	2B	118	G	3.4
40	2i	5	TYR	3.4
22	10	5	LYS	3.4
15	2T	131	ALA	3.4
26	14	59	PHE	3.4
33	2b	187	LEU	3.4
21	2Z	81	ARG	3.4
40	2i	128	ARG	3.4
53	1v	12	A	3.4
38	2g	9	VAL	3.4
50	2s	41	VAL	3.4
41	1j	4	ILE	3.4
1	2A	2160	G	3.4
1	1A	885	C	3.4
32	2a	1114	C	3.4
6	2G	29	TRP	3.4
33	2b	196	LEU	3.4
1	1A	2142	C	3.4
1	1A	2174	C	3.4
1	2A	2136	C	3.4
54	1w	1	G	3.4
38	2g	32	ARG	3.3
32	2a	1149	C	3.3
32	2a	1260	C	3.3
36	2e	109	ILE	3.3
32	2a	1131	G	3.3
7	2H	2	SER	3.3
40	2i	123	PRO	3.3
50	2s	13	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
34	2c	124	ILE	3.3
50	2s	9	VAL	3.3
1	2A	2137	C	3.3
40	2i	6	GLY	3.3
43	2l	16	GLU	3.3
51	1t	69	GLY	3.3
1	1A	1078	U	3.3
8	2I	12	LEU	3.3
42	2k	25	TYR	3.3
1	2A	2159	G	3.3
44	2m	104	ARG	3.3
1	1A	2114	A	3.3
1	2A	2169	A	3.3
8	2I	18	VAL	3.3
50	2s	60	VAL	3.3
51	1t	13	LEU	3.3
40	2i	9	ARG	3.3
1	1A	1099	G	3.3
48	2q	32	TYR	3.2
22	10	2	ALA	3.2
1	1A	2111	C	3.2
1	1A	2803	C	3.2
47	1p	20	VAL	3.2
32	2a	1002	G	3.2
32	2a	1061	G	3.2
33	1b	18	GLY	3.2
33	2b	86	GLU	3.2
19	2X	69	TYR	3.2
1	1A	2130	U	3.2
32	2a	1038	C	3.2
33	2b	112	VAL	3.2
57	1y	75	C	3.2
32	2a	1290	G	3.2
54	2w	15	G	3.2
55	2x	70	G	3.2
19	2X	91	ALA	3.2
36	2e	17	ALA	3.2
51	1t	55	ILE	3.2
8	2I	3	VAL	3.2
54	1w	61	C	3.2
55	2x	1	C	3.2
1	1A	2169	A	3.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1363(A)	A	3.2
44	1m	87	TYR	3.2
1	1A	2149	G	3.2
1	2A	2148	G	3.2
1	2A	2156	G	3.2
6	2G	147	ASP	3.2
33	2b	203	GLY	3.2
34	2c	155	GLY	3.2
36	2e	85	GLY	3.2
34	2c	4	LYS	3.2
38	2g	62	PHE	3.2
1	1A	888	C	3.2
57	2y	32	C	3.2
33	2b	149	LEU	3.1
35	2d	155	LEU	3.1
40	2i	108	VAL	3.1
50	1s	9	VAL	3.1
1	1A	2119	A	3.1
32	1a	1030(D)	A	3.1
38	2g	77	SER	3.1
33	2b	97	TRP	3.1
41	1j	75	ILE	3.1
32	2a	1234	C	3.1
35	2d	112	VAL	3.1
38	2g	154	TYR	3.1
2	2B	53	A	3.1
32	2a	1236	A	3.1
34	2c	62	ASP	3.1
26	24	57	GLU	3.1
32	2a	1024	G	3.1
32	2a	1220	G	3.1
32	2a	1006	C	3.1
54	1w	56	C	3.1
40	2i	127	LYS	3.1
3	2D	275	LYS	3.1
43	2l	64	TYR	3.1
3	1D	176	ARG	3.1
30	18	46	ARG	3.1
45	2n	38	GLY	3.1
33	1b	17	PHE	3.1
4	2E	163	GLU	3.1
35	2d	111	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
12	2Q	79	LEU	3.0
34	1c	87	LEU	3.0
33	2b	7	VAL	3.0
14	2S	34	HIS	3.0
22	10	4	LYS	3.0
32	2a	1031	G	3.0
32	2a	1283	G	3.0
48	1q	12	SER	3.0
1	1A	2107	C	3.0
8	2I	117	GLU	3.0
32	2a	1532	U	3.0
34	2c	161	GLU	3.0
47	1p	19	ILE	3.0
32	2a	1001	A	3.0
32	2a	1250	A	3.0
12	2Q	18	LYS	3.0
51	1t	21	LYS	3.0
9	2N	69	GLN	3.0
45	2n	21	TYR	3.0
40	2i	18	PHE	3.0
8	2I	93	THR	3.0
41	2j	86	MET	3.0
7	2H	84	SER	3.0
42	1k	92	GLU	3.0
1	1A	2116	G	3.0
1	2A	2154	G	3.0
32	2a	1219	U	3.0
54	2w	1	G	3.0
54	2w	56	C	3.0
20	2Y	35	TYR	3.0
34	2c	2	GLY	3.0
6	2G	87	PRO	3.0
41	1j	76	ASN	3.0
41	2j	76	ASN	3.0
50	2s	49	ILE	3.0
47	1p	6	LEU	3.0
1	1A	2132	U	3.0
1	2A	2139	C	3.0
1	2A	2142	C	3.0
2	2B	54	G	3.0
29	17	47	ARG	3.0
39	2h	91	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
34	2c	53	ALA	3.0
34	2c	92	ALA	3.0
38	1g	61	VAL	3.0
33	2b	24	TRP	3.0
1	1A	1026	U	2.9
1	1A	1060	U	2.9
40	2i	83	ARG	2.9
51	2t	25	ARG	2.9
34	1c	9	GLY	2.9
34	2c	170	GLN	2.9
40	2i	63	ILE	2.9
1	1A	2135	A	2.9
45	2n	13	THR	2.9
33	2b	134	GLU	2.9
11	1P	15	ARG	2.9
12	2Q	39	PRO	2.9
6	2G	94	LEU	2.9
21	1Z	170	THR	2.9
32	2a	1116	C	2.9
39	1h	7	ALA	2.9
40	2i	45	ALA	2.9
1	2A	2123	G	2.9
32	2a	1355	G	2.9
53	2v	15	A	2.9
6	1G	180	PHE	2.9
32	1a	204	U	2.9
34	2c	158	GLY	2.9
44	2m	119	GLY	2.9
6	1G	152	LEU	2.9
41	1j	74	ILE	2.9
6	2G	48	GLU	2.9
33	2b	93	VAL	2.9
1	1A	2165	G	2.9
1	1A	2166	G	2.9
1	2A	882	G	2.9
1	2A	2157	G	2.9
1	2A	2319	G	2.9
20	2Y	17	SER	2.9
32	2a	1233	G	2.9
35	1d	2	GLY	2.9
3	2D	35	LYS	2.9
7	2H	128	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
34	2c	199	LYS	2.9
40	2i	99	LEU	2.9
41	2j	41	PRO	2.9
45	2n	4	LYS	2.9
45	2n	9	LYS	2.9
50	2s	32	LYS	2.9
6	1G	146	TYR	2.9
33	1b	188	ALA	2.9
33	1b	165	VAL	2.9
14	2S	97	ARG	2.9
40	2i	10	ARG	2.9
45	2n	57	ARG	2.9
1	2A	884	C	2.8
19	2X	28	PHE	2.8
20	2Y	34	LYS	2.8
34	2c	182	ILE	2.8
38	2g	81	GLY	2.8
41	2j	75	ILE	2.8
1	1A	2125	G	2.8
1	1A	2147	G	2.8
1	2A	2141	G	2.8
32	2a	1003	G	2.8
44	2m	101	GLN	2.8
47	2p	82	GLN	2.8
33	2b	34	ALA	2.8
34	2c	163	ALA	2.8
14	2S	7	TYR	2.8
43	1l	19	ARG	2.8
45	2n	23	ARG	2.8
1	1A	2136	C	2.8
55	1x	1	C	2.8
6	2G	50	ALA	2.8
12	2Q	121	ALA	2.8
32	2a	1150	U	2.8
1	1A	1093	G	2.8
1	2A	859	G	2.8
33	2b	168	THR	2.8
40	2i	101	PHE	2.8
31	29	15	LYS	2.8
43	1l	17	LYS	2.8
38	2g	38	LEU	2.8
11	2P	20	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
52	2u	4	GLY	2.8
1	1A	1064	C	2.8
1	2A	2170	A	2.8
1	2A	2294	C	2.8
1	2A	2310	A	2.8
1	2A	2753	A	2.8
2	2B	58	A	2.8
32	2a	1248	A	2.8
32	2a	1251	A	2.8
42	2k	126	ARG	2.8
35	2d	120	LEU	2.8
1	2A	883	G	2.8
32	2a	1021	G	2.8
32	2a	1032	G	2.8
32	2a	1216	G	2.8
42	2k	48	ILE	2.8
44	1m	106	ASN	2.8
36	2e	125	SER	2.8
21	2Z	141	VAL	2.8
44	2m	60	VAL	2.8
44	2m	117	VAL	2.8
1	1A	1057	A	2.8
1	2A	2117	A	2.8
32	2a	532	A	2.8
1	1A	1081	U	2.8
1	1A	2164	C	2.8
38	1g	85	TYR	2.8
57	2y	36	U	2.8
14	2S	5	THR	2.8
22	10	58	THR	2.8
41	1j	100	THR	2.8
21	1Z	146	ILE	2.8
8	2I	13	GLY	2.8
1	1A	2154	G	2.7
2	2B	61	G	2.7
32	1a	1023	G	2.7
45	2n	31	ARG	2.7
47	1p	5	ARG	2.7
47	1p	21	VAL	2.7
17	2V	73	SER	2.7
35	2d	208	SER	2.7
34	1c	90	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
34	2c	184	TYR	2.7
52	1u	18	TYR	2.7
1	2A	2132	U	2.7
7	2H	64	LEU	2.7
34	2c	95	THR	2.7
36	2e	31	LEU	2.7
45	2n	22	THR	2.7
50	2s	71	LEU	2.7
34	2c	5	ILE	2.7
1	2A	2128	C	2.7
41	2j	77	PRO	2.7
14	2S	3	ARG	2.7
40	2i	104	ARG	2.7
8	1I	146	ALA	2.7
9	2N	9	VAL	2.7
36	2e	20	GLN	2.7
22	20	4	LYS	2.7
1	2A	2116	G	2.7
54	2w	53	G	2.7
34	2c	52	LEU	2.7
34	2c	185	GLY	2.7
32	2a	1030(B)	C	2.7
37	2f	7	ASN	2.7
34	2c	60	ALA	2.7
34	2c	97	LYS	2.7
43	2l	9	GLN	2.7
34	2c	42	LEU	2.7
44	2m	9	ILE	2.7
8	2I	14	ASP	2.7
47	1p	32	TYR	2.7
22	10	3	HIS	2.7
41	2j	48	THR	2.7
1	1A	2118	U	2.7
1	1A	2123	G	2.7
35	2d	29	PRO	2.7
57	2y	57	G	2.7
48	2q	91	ARG	2.7
3	1D	275	LYS	2.7
8	2I	146	ALA	2.7
34	2c	137	ALA	2.7
35	1d	112	VAL	2.7
48	2q	100	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	1A	2146	C	2.7
1	1A	2161	C	2.7
35	1d	77	ASN	2.7
54	2w	32	C	2.7
45	2n	42	ILE	2.7
33	1b	9	GLU	2.7
8	2I	1	MET	2.7
20	2Y	5	MET	2.7
32	1a	1532	U	2.7
40	2i	42	ARG	2.6
41	2j	46	ARG	2.6
45	2n	41	ARG	2.6
55	2x	47	U	2.7
43	1l	91	LYS	2.6
39	2h	53	VAL	2.6
1	1A	2120	G	2.6
9	2N	47	ALA	2.6
32	1a	1001(A)	G	2.6
32	1a	1002	G	2.6
32	2a	1117	G	2.6
33	2b	237	ALA	2.6
38	2g	40	ALA	2.6
40	2i	46	ALA	2.6
45	2n	5	ALA	2.6
45	2n	61	TRP	2.6
32	2a	965	A	2.6
32	2a	974	A	2.6
32	2a	1289	A	2.6
41	2j	78	ASN	2.6
47	1p	82	GLN	2.6
41	1j	40	LEU	2.6
33	2b	41	ILE	2.6
33	2b	172	ILE	2.6
57	2y	74	C	2.6
40	2i	12	GLU	2.6
21	2Z	147	GLY	2.6
35	2d	68	TYR	2.6
33	2b	193	ASP	2.6
50	2s	2	PRO	2.6
38	2g	4	ARG	2.6
11	2P	76	LYS	2.6
1	2A	2109	U	2.6

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Mol	Chain	Res	Type	RSRZ
39	2h	95	VAL	2.6
40	2i	109	VAL	2.6
48	2q	19	VAL	2.6
6	1G	50	ALA	2.6
38	2g	99	LEU	2.6
39	2h	112	LEU	2.6
51	2t	99	LEU	2.6
1	1A	1077	A	2.6
1	1A	2158	A	2.6
32	2a	1252	A	2.6
32	2a	1287	A	2.6
38	2g	49	ILE	2.6
2	2B	24	G	2.6
32	2a	951	G	2.6
32	2a	1057	G	2.6
32	2a	1243	C	2.6
38	2g	85	TYR	2.6
40	1i	126	SER	2.6
43	2l	29	GLY	2.6
43	1l	20	LYS	2.6
6	2G	28	VAL	2.6
9	2N	46	VAL	2.6
21	2Z	86	VAL	2.6
48	2q	44	ALA	2.6
6	2G	139	LEU	2.6
33	2b	154	LEU	2.6
35	2d	157	LEU	2.6
41	2j	38	ILE	2.6
32	1a	1286	A	2.6
32	2a	1357	A	2.6
22	20	73	GLY	2.6
34	2c	159	GLY	2.6
1	1A	1087	G	2.6
32	2a	1026	G	2.6
32	2a	1370	G	2.6
35	2d	4	TYR	2.6
41	2j	67	THR	2.6
1	1A	154(A)	C	2.6
1	1A	2108	C	2.6
55	2x	28	C	2.6
33	2b	81	VAL	2.6
14	2S	80	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
38	2g	12	LEU	2.6
38	2g	16	LEU	2.6
38	2g	124	LEU	2.6
41	2j	71	LEU	2.6
44	1m	2	ALA	2.6
33	2b	127	ILE	2.6
38	2g	84	ASN	2.6
6	1G	48	GLU	2.6
45	2n	15	LYS	2.6
1	1A	1070	A	2.6
1	1A	2170	A	2.6
38	1g	151	TYR	2.6
47	2p	39	TYR	2.6
39	1h	61	VAL	2.6
44	2m	15	VAL	2.6
3	2D	61	LEU	2.6
39	1h	2	LEU	2.6
42	2k	98	LEU	2.6
43	1l	68	ALA	2.5
44	2m	66	LEU	2.6
1	2A	2100	G	2.5
1	2A	2138	C	2.5
2	2B	28	C	2.5
2	2B	119	G	2.5
32	2a	972	C	2.5
32	2a	1030(A)	G	2.5
32	2a	1241	G	2.5
32	2a	1384	C	2.5
57	1y	74	C	2.5
34	2c	152	ILE	2.5
50	2s	40	ILE	2.5
34	2c	162	GLN	2.5
57	1y	36	U	2.5
19	2X	33	LYS	2.5
50	2s	18	LYS	2.5
12	1Q	33	GLY	2.5
20	1Y	91	GLU	2.5
48	1q	63	ARG	2.5
35	2d	6	GLY	2.5
40	2i	39	GLY	2.5
20	2Y	45	VAL	2.5
34	1c	207	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	193	TYR	2.5
42	2k	75	TYR	2.5
44	1m	23	TYR	2.5
45	2n	18	VAL	2.5
48	2q	35	VAL	2.5
53	1v	13	A	2.5
6	2G	57	ALA	2.5
33	2b	161	ALA	2.5
16	1U	117	GLN	2.5
1	2A	2803	C	2.5
2	2B	27	C	2.5
32	2a	1028	C	2.5
1	1A	1059	G	2.5
32	1a	1036	G	2.5
32	2a	825	G	2.5
57	2y	33	U	2.5
19	2X	68	ARG	2.5
31	29	21	GLY	2.5
7	1H	105	LEU	2.5
23	11	2	SER	2.5
38	2g	42	ILE	2.5
6	2G	102	PHE	2.5
32	2a	1358	U	2.5
1	1A	2175	C	2.5
2	1B	88	C	2.5
23	21	28	GLY	2.5
32	1a	369	C	2.5
47	2p	16	HIS	2.5
34	2c	41	GLY	2.5
39	2h	131	GLY	2.5
48	2q	8	GLY	2.5
54	1w	67	C	2.5
43	2l	49	ASN	2.5
1	1A	1062	G	2.5
1	1A	2182	G	2.5
1	2A	1533	G	2.5
32	2a	731	G	2.5
32	2a	1489	G	2.5
39	2h	133	LEU	2.5
34	2c	192	THR	2.5
20	2Y	78	ALA	2.5
38	2g	152	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
5	2F	82	ILE	2.5
14	2S	35	ILE	2.5
41	2j	96	ILE	2.5
36	2e	84	PHE	2.5
34	2c	45	LYS	2.5
40	2i	105	ASP	2.5
40	2i	112	LYS	2.5
1	2A	529	A	2.5
1	2A	2173	A	2.5
33	2b	234	PRO	2.5
6	2G	85	GLY	2.5
26	24	17	GLY	2.5
21	2Z	145	GLU	2.5
32	1a	1000	U	2.5
38	1g	101	LEU	2.5
8	2I	11	ASN	2.5
33	2b	136	VAL	2.5
40	2i	29	ASN	2.5
1	1A	889	C	2.5
1	1A	1100	C	2.5
32	2a	1118	C	2.5
32	2a	1192	C	2.5
34	2c	65	ALA	2.5
38	2g	83	ALA	2.5
26	24	49	PHE	2.5
40	2i	92	TYR	2.5
1	2A	1042	G	2.4
1	2A	2127	G	2.4
1	2A	2151	G	2.4
1	2A	2893	G	2.4
32	1a	630	G	2.4
32	1a	1009	G	2.4
32	1a	1024	G	2.4
32	1a	1031	G	2.4
32	1a	1032	G	2.4
32	2a	971	G	2.4
32	2a	993	G	2.4
32	2a	1353	G	2.4
21	2Z	166	SER	2.4
52	1u	24	ARG	2.4
1	2A	1847	A	2.4
1	2A	2134	A	2.4

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Mol	Chain	Res	Type	RSRZ
1	2A	2158	A	2.4
2	2B	120	A	2.4
9	2N	68	GLU	2.4
35	1d	120	LEU	2.4
37	2f	21	LEU	2.4
39	2h	59	LEU	2.4
20	2Y	42	VAL	2.4
26	24	56	VAL	2.4
33	1b	7	VAL	2.4
34	2c	207	VAL	2.4
6	2G	55	LYS	2.4
33	2b	70	PHE	2.4
43	1l	126	LYS	2.4
1	1A	2177	C	2.4
1	2A	2108	C	2.4
40	2i	114	TYR	2.4
47	1p	39	TYR	2.4
48	2q	95	TYR	2.4
54	2w	71	C	2.4
20	2Y	2	ARG	2.4
9	2N	8	GLN	2.4
21	2Z	16	SER	2.4
48	1q	97	SER	2.4
1	1A	2151	G	2.4
1	2A	2323	G	2.4
32	2a	963	G	2.4
52	2u	23	PRO	2.4
36	2e	99	GLY	2.4
40	2i	117	HIS	2.4
12	2Q	102	VAL	2.4
20	1Y	3	VAL	2.4
34	2c	130	VAL	2.4
35	2d	140	VAL	2.4
2	2B	52	A	2.4
32	1a	1447	A	2.4
33	2b	200	ILE	2.4
6	2G	6	ALA	2.4
19	2X	34	ALA	2.4
50	2s	75	ALA	2.4
33	2b	67	THR	2.4
40	2i	125	TYR	2.4
44	2m	87	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
35	2d	76	ARG	2.4
1	1A	2188	C	2.4
32	2a	970	C	2.4
54	1w	71	C	2.4
54	2w	61	C	2.4
57	2y	75	C	2.4
33	2b	194	PRO	2.4
33	2b	192	SER	2.4
6	2G	173	LEU	2.4
6	2G	148	MET	2.4
34	2c	197	GLY	2.4
44	2m	6	GLY	2.4
41	2j	64	GLU	2.4
1	1A	2101	G	2.4
1	2A	10	G	2.4
1	2A	2120	G	2.4
32	2a	657	G	2.4
55	2x	2	G	2.4
38	2g	35	LYS	2.4
44	2m	31	LYS	2.4
20	2Y	36	ALA	2.4
34	2c	129	ALA	2.4
36	1e	132	ALA	2.4
45	1n	5	ALA	2.4
1	1A	899	A	2.4
1	1A	1963	U	2.4
1	1A	2167	U	2.4
2	2B	29	A	2.4
32	1a	609	A	2.4
32	1a	1035	A	2.4
32	2a	1020	U	2.4
12	2Q	10	ARG	2.4
29	27	41	ARG	2.4
36	2e	96	PRO	2.4
50	2s	42	PRO	2.4
8	1I	6	LEU	2.4
21	2Z	144	LEU	2.4
34	2c	91	LEU	2.4
32	2a	1217	C	2.4
32	2a	1362	C	2.4
57	2y	5	C	2.4
57	2y	70	C	2.4

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Mol	Chain	Res	Type	RSRZ
34	2c	120	VAL	2.4
40	1i	14	VAL	2.4
40	1i	28	VAL	2.4
45	2n	56	VAL	2.4
39	1h	136	GLU	2.4
20	2Y	44	ILE	2.4
33	1b	200	ILE	2.4
34	2c	14	ILE	2.4
34	2c	157	ILE	2.4
40	2i	95	LYS	2.4
48	1q	36	ILE	2.4
28	16	2	ALA	2.4
34	2c	160	ALA	2.4
44	2m	75	ALA	2.4
1	1A	173	G	2.4
1	1A	1056	G	2.4
1	1A	1097	U	2.4
1	1A	2189	U	2.4
1	1A	1088	A	2.4
1	1A	2790	A	2.4
1	2A	2181	G	2.4
21	2Z	80	ARG	2.4
32	1a	1003	G	2.4
35	2d	73	ARG	2.4
50	2s	48	THR	2.4
32	2a	1493	A	2.4
54	1w	3	G	2.4
33	2b	145	LEU	2.3
40	2i	19	LEU	2.3
42	2k	13	GLN	2.3
48	1q	89	LEU	2.3
12	2Q	123	HIS	2.3
16	2U	49	HIS	2.3
50	2s	69	HIS	2.3
40	2i	70	LYS	2.3
47	1p	2	VAL	2.3
6	2G	77	ILE	2.3
26	24	5	ILE	2.3
33	2b	231	GLU	2.3
1	1A	2128	C	2.3
1	1A	2129	C	2.3
54	2w	74	C	2.3

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Mol	Chain	Res	Type	RSRZ
33	2b	163	PHE	2.3
36	2e	45	PHE	2.3
44	2m	42	ALA	2.3
12	2Q	16	ARG	2.3
36	2e	127	ASN	2.3
1	2A	2189	U	2.3
7	2H	33	LEU	2.3
11	2P	110	TYR	2.3
38	2g	112	PRO	2.3
41	1j	90	LEU	2.3
1	1A	1098	A	2.3
1	1A	2171	A	2.3
44	2m	10	PRO	2.3
1	2A	652(U)	G	2.3
32	2a	1258	G	2.3
35	2d	42	GLN	2.3
41	1j	33	GLN	2.3
33	1b	19	HIS	2.3
33	2b	27	LYS	2.3
43	2l	13	LYS	2.3
45	1n	51	GLY	2.3
23	21	72	GLU	2.3
31	19	12	ASP	2.3
36	2e	87	SER	2.3
51	2t	70	SER	2.3
6	2G	171	ALA	2.3
7	2H	60	ARG	2.3
14	2S	20	ARG	2.3
1	1A	2137	C	2.3
1	2A	652(V)	C	2.3
32	1a	999	C	2.3
32	1a	1119	C	2.3
32	2a	1030	C	2.3
32	2a	1363	C	2.3
12	2Q	125	LEU	2.3
35	2d	12	CYS	2.3
52	2u	18	TYR	2.3
34	2c	37	GLN	2.3
36	2e	22	GLY	2.3
39	2h	19	VAL	2.3
43	1l	18	VAL	2.3
52	2u	2	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
53	2v	14	A	2.3
57	2y	73	A	2.3
33	2b	162	ILE	2.3
1	1A	880	G	2.3
1	1A	2104	G	2.3
32	1a	1033	G	2.3
32	1a	1034	G	2.3
32	2a	1222	G	2.3
34	2c	168	ALA	2.3
35	2d	164	ALA	2.3
40	1i	52	ALA	2.3
44	2m	118	ALA	2.3
31	29	19	ARG	2.3
33	1b	10	LEU	2.3
40	2i	79	LEU	2.3
1	2A	2129	C	2.3
1	2A	2804	C	2.3
33	2b	26	PRO	2.3
41	2j	53	PRO	2.3
48	2q	2	PRO	2.3
33	1b	22	LYS	2.3
40	2i	118	LYS	2.3
50	2s	70	LYS	2.3
33	2b	33	TYR	2.3
22	20	3	HIS	2.3
33	2b	71	VAL	2.3
38	2g	61	VAL	2.3
38	2g	105	VAL	2.3
41	2j	68	HIS	2.3
1	1A	229	A	2.3
34	2c	167	TRP	2.3
35	2d	24	GLU	2.3
37	2f	38	GLU	2.3
48	2q	86	GLU	2.3
20	1Y	2	ARG	2.3
34	2c	127	ARG	2.3
40	2i	71	SER	2.3
1	1A	2184	G	2.3
32	1a	1010	G	2.3
33	2b	221	LEU	2.3
34	2c	33	LEU	2.3
34	2c	43	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
35	2d	19	LEU	2.3
57	1y	15	G	2.3
34	2c	73	PRO	2.3
39	2h	17	THR	2.3
39	2h	27	PRO	2.3
40	2i	64	THR	2.3
48	1q	14	LYS	2.3
52	1u	23	PRO	2.3
1	1A	886	C	2.2
1	1A	1066	U	2.2
1	1A	2138	C	2.2
1	2A	1116	C	2.2
1	2A	2789	C	2.2
4	2E	184	VAL	2.2
19	2X	81	VAL	2.2
26	14	56	VAL	2.2
32	2a	1065	U	2.2
32	2a	1359	C	2.2
41	1j	38	ILE	2.2
41	2j	74	ILE	2.2
42	2k	119	CYS	2.2
50	1s	41	VAL	2.2
50	2s	58	VAL	2.2
57	1y	33	U	2.2
45	2n	16	PHE	2.2
8	1I	7	GLU	2.2
8	1I	117	GLU	2.2
9	2N	124	ALA	2.2
33	2b	30	ARG	2.2
40	1i	66	ARG	2.2
40	2i	106	ALA	2.2
45	2n	8	GLU	2.2
1	1A	1067	A	2.2
32	1a	1001	A	2.2
53	2v	24	A	2.2
14	2S	58	LEU	2.2
33	2b	158	LEU	2.2
35	1d	21	LEU	2.2
39	2h	8	ASP	2.2
44	2m	70	LEU	2.2
46	2o	31	LEU	2.2
51	1t	11	SER	2.2

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Mol	Chain	Res	Type	RSRZ
38	2g	36	LYS	2.2
5	2F	81	PRO	2.2
46	2o	2	PRO	2.2
6	2G	71	THR	2.2
40	1i	7	THR	2.2
42	1k	57	THR	2.2
44	1m	105	THR	2.2
1	2A	2101	G	2.2
6	2G	52	ILE	2.2
11	2P	26	GLY	2.2
14	2S	36	TYR	2.2
32	1a	1030(C)	G	2.2
32	2a	1156	G	2.2
33	1b	230	VAL	2.2
40	2i	17	VAL	2.2
43	2l	96	VAL	2.2
46	1o	87	ILE	2.2
49	1r	75	ILE	2.2
50	2s	11	VAL	2.2
54	2w	6	G	2.2
57	1y	1	G	2.2
57	2y	18	G	2.2
32	2a	1257	U	2.2
32	2a	1007	C	2.2
38	2g	41	ARG	2.2
51	1t	83	ARG	2.2
52	2u	10	ARG	2.2
54	1w	74	C	2.2
55	2x	71	C	2.2
44	2m	5	ALA	2.2
26	24	65	ASP	2.2
33	2b	22	LYS	2.2
35	2d	169	LYS	2.2
38	2g	136	LYS	2.2
51	1t	74	LYS	2.2
1	2A	2119	A	2.2
32	2a	975	A	2.2
32	2a	1225	A	2.2
54	2w	73	A	2.2
44	2m	103	THR	2.2
8	1I	142	VAL	2.2
20	2Y	37	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
20	2Y	104	GLY	2.2
40	2i	41	VAL	2.2
26	14	67	TYR	2.2
33	1b	33	TYR	2.2
51	1t	75	ASN	2.2
4	2E	96	PHE	2.2
1	1A	1065	U	2.2
1	1A	2150	U	2.2
1	1A	2181	G	2.2
1	2A	1026	U	2.2
1	2A	1030	G	2.2
1	2A	1816	G	2.2
2	2B	44	G	2.2
2	2B	50	G	2.2
4	2E	204	ALA	2.2
29	27	1	MET	2.2
32	2a	1053	G	2.2
32	2a	1124	G	2.2
32	2a	1125	U	2.2
33	2b	101	MET	2.2
40	2i	76	ALA	2.2
45	2n	59	ALA	2.2
57	2y	29	U	2.2
35	1d	150	GLU	2.2
20	2Y	31	LEU	2.2
1	1A	2179	C	2.2
32	2a	1203	C	2.2
32	2a	1270	C	2.2
46	2o	10	LYS	2.2
51	2t	48	LYS	2.2
7	2H	39	PRO	2.2
44	2m	41	PRO	2.2
21	1Z	171	ILE	2.2
32	1a	149	A	2.2
32	2a	1110	A	2.2
32	2a	1288	A	2.2
36	2e	101	ILE	2.2
40	2i	86	VAL	2.2
47	2p	2	VAL	2.2
48	2q	90	ILE	2.2
16	2U	73	GLY	2.2
33	2b	16	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
35	2d	116	GLN	2.2
6	1G	178	PHE	2.2
34	2c	38	ARG	2.2
35	2d	106	TYR	2.2
41	1j	78	ASN	2.2
51	2t	8	ARG	2.2
22	20	2	ALA	2.2
33	1b	34	ALA	2.2
33	2b	177	ALA	2.2
43	2l	68	ALA	2.2
17	2V	85	LYS	2.2
21	2Z	155	LEU	2.2
34	2c	93	LYS	2.2
35	2d	174	LEU	2.2
44	2m	90	LEU	2.2
52	2u	3	LYS	2.2
54	2w	60	U	2.2
1	1A	1058	G	2.2
1	1A	2160	G	2.2
1	1A	2168	G	2.2
1	2A	11	G	2.2
1	2A	2182	G	2.2
32	2a	27	G	2.2
39	2h	72	PRO	2.2
48	2q	30	PRO	2.2
57	2y	15	G	2.2
1	1A	884	C	2.2
1	1A	2140	C	2.2
1	2A	2140	C	2.2
1	2A	2175	C	2.2
1	2A	2188	C	2.2
32	2a	435	C	2.2
32	2a	1019	C	2.2
54	1w	32	C	2.2
54	1w	72	C	2.2
6	2G	140	ILE	2.2
6	2G	157	ILE	2.2
8	2I	88	ILE	2.2
17	2V	22	VAL	2.2
36	2e	100	VAL	2.2
40	1i	109	VAL	2.2
49	1r	86	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
35	2d	180	GLY	2.1
1	1A	896	A	2.1
6	1G	51	ARG	2.1
6	2G	128	ARG	2.1
32	2a	1531	A	2.1
40	2i	59	PHE	2.1
40	2i	124	GLN	2.1
53	2v	13	A	2.1
34	2c	48	TYR	2.1
40	2i	62	TYR	2.1
9	2N	102	ALA	2.1
12	2Q	20	ALA	2.1
28	26	11	LEU	2.1
33	1b	118	LEU	2.1
35	2d	78	LEU	2.1
36	2e	86	ALA	2.1
38	2g	7	ALA	2.1
38	2g	46	ALA	2.1
40	1i	113	LYS	2.1
33	2b	129	GLU	2.1
35	2d	80	GLU	2.1
44	2m	39	ILE	2.1
14	2S	46	VAL	2.1
33	1b	189	ASP	2.1
34	2c	116	VAL	2.1
50	2s	67	VAL	2.1
6	2G	76	SER	2.1
41	1j	31	GLY	2.1
51	2t	11	SER	2.1
1	1A	1092	C	2.1
1	2A	2104	G	2.1
1	2A	2301	C	2.1
1	2A	2339	G	2.1
2	2B	56	G	2.1
6	2G	83	ARG	2.1
6	2G	145	THR	2.1
12	1Q	5	ARG	2.1
14	2S	21	THR	2.1
21	2Z	170	THR	2.1
22	20	43	THR	2.1
32	1a	1026	G	2.1
32	2a	1087	G	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1127	G	2.1
32	2a	1128	C	2.1
32	2a	1254	C	2.1
32	2a	1361	G	2.1
34	2c	40	ARG	2.1
44	1m	3	ARG	2.1
44	2m	37	THR	2.1
48	2q	7	THR	2.1
54	1w	15	G	2.1
54	1w	19	G	2.1
54	2w	67	C	2.1
55	2x	6	G	2.1
57	2y	19	G	2.1
57	2y	64	G	2.1
33	1b	163	PHE	2.1
45	2n	36	PHE	2.1
50	2s	10	PHE	2.1
7	2H	138	LYS	2.1
6	2G	163	ALA	2.1
6	2G	172	LEU	2.1
15	2T	78	LEU	2.1
21	2Z	152	ALA	2.1
28	26	36	LEU	2.1
36	2e	133	TYR	2.1
40	2i	96	LEU	2.1
41	2j	57	LYS	2.1
32	2a	1004	A	2.1
32	2a	1005	A	2.1
42	2k	50	TYR	2.1
38	2g	28	ASN	2.1
35	2d	81	GLU	2.1
40	1i	2	GLU	2.1
44	2m	113	PRO	2.1
47	1p	59	TRP	2.1
8	2I	92	VAL	2.1
14	2S	98	VAL	2.1
39	2h	61	VAL	2.1
44	2m	45	VAL	2.1
6	2G	72	ARG	2.1
12	2Q	7	MET	2.1
30	28	28	GLY	2.1
35	1d	87	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
35	2d	122	ARG	2.1
39	2h	55	GLY	2.1
46	2o	86	GLY	2.1
21	2Z	121	HIS	2.1
34	2c	10	PHE	2.1
35	2d	152	SER	2.1
40	1i	18	PHE	2.1
50	2s	35	SER	2.1
51	2t	71	THR	2.1
14	2S	59	LYS	2.1
42	1k	13	GLN	2.1
14	2S	54	LEU	2.1
21	1Z	150	LEU	2.1
35	2d	162	LEU	2.1
39	2h	10	LEU	2.1
1	2A	2297	C	2.1
2	2B	4	C	2.1
32	1a	1028	C	2.1
32	2a	1109	C	2.1
32	2a	1244	C	2.1
32	2a	1366	C	2.1
39	2h	124	ALA	2.1
48	1q	44	ALA	2.1
54	2w	62	C	2.1
6	2G	146	TYR	2.1
1	1A	2100	G	2.1
1	2A	1115	G	2.1
54	2w	57	G	2.1
1	1A	1086	A	2.1
2	2B	57	A	2.1
32	2a	986	A	2.1
51	2t	98	PRO	2.1
19	2X	80	ILE	2.1
35	2d	158	ILE	2.1
43	2l	7	ILE	2.1
1	1A	1082	U	2.1
1	2A	1113	U	2.1
1	2A	2150	U	2.1
57	1y	35	U	2.1
19	1X	52	VAL	2.1
8	2I	34	GLY	2.1
18	2W	92	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
20	2Y	80	GLY	2.1
39	2h	12	ARG	2.1
47	1p	81	ARG	2.1
11	2P	35	HIS	2.1
34	2c	186	PHE	2.1
6	2G	162	THR	2.1
12	2Q	21	THR	2.1
6	2G	58	GLN	2.1
33	2b	11	LEU	2.1
34	1c	12	LEU	2.1
43	2l	27	LEU	2.1
51	1t	84	LEU	2.1
40	1i	15	ALA	2.1
40	2i	43	ALA	2.1
41	2j	32	ALA	2.1
33	2b	236	TYR	2.1
42	1k	25	TYR	2.1
1	1A	2794	C	2.1
2	2B	6	C	2.1
8	2I	10	GLU	2.1
32	2a	1018	C	2.1
32	2a	1045	C	2.1
34	2c	166	GLU	2.1
36	2e	83	GLU	2.1
7	2H	55	PRO	2.1
43	2l	48	PRO	2.1
46	1o	19	PRO	2.1
1	2A	916	G	2.1
1	2A	2124	G	2.1
1	2A	2801(A)	A	2.1
32	2a	1190	G	2.1
55	1x	2	G	2.1
31	29	23	VAL	2.1
41	2j	72	VAL	2.1
42	1k	14	VAL	2.1
32	2a	1364	U	2.1
57	2y	20	U	2.1
6	2G	24	GLY	2.1
11	2P	39	LYS	2.1
42	2k	118	GLY	2.1
45	2n	51	GLY	2.1
51	2t	47	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
21	1Z	104	PHE	2.1
21	2Z	88	PHE	2.1
14	2S	56	LEU	2.0
21	2Z	87	ASP	2.0
38	2g	147	ALA	2.0
51	2t	97	ALA	2.0
14	2S	61	ASN	2.0
33	2b	108	ILE	2.0
44	2m	106	ASN	2.0
1	2A	2474	C	2.0
2	2B	32	C	2.0
14	2S	14	VAL	2.0
32	2a	1137	C	2.0
32	2a	1214	C	2.0
22	20	11	ARG	2.0
29	27	47	ARG	2.0
33	1b	229	VAL	2.0
36	2e	90	VAL	2.0
44	2m	7	VAL	2.0
44	2m	64	TRP	2.0
38	2g	137	LYS	2.0
40	1i	11	LYS	2.0
45	1n	17	LYS	2.0
1	2A	2320	A	2.0
32	2a	26	A	2.0
32	2a	1092	A	2.0
42	1k	125	PHE	2.0
44	2m	100	GLY	2.0
50	1s	68	GLY	2.0
53	1v	24	A	2.0
56	2z	3	CYS	2.0
1	2A	271(K)	U	2.0
33	1b	11	LEU	2.0
1	1A	652(C)	G	2.0
1	2A	2149	G	2.0
32	2a	730	G	2.0
32	2a	1138	G	2.0
32	2a	1276	G	2.0
33	1b	40	HIS	2.0
41	2j	62	HIS	2.0
44	1m	96	LEU	2.0
57	2y	7	U	2.0

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Mol	Chain	Res	Type	RSRZ
11	2P	32	THR	2.0
34	2c	133	ALA	2.0
36	2e	21	ALA	2.0
43	2l	51	ALA	2.0
42	2k	43	SER	2.0
7	2H	94	TYR	2.0
39	2h	65	TYR	2.0
42	2k	59	TYR	2.0
21	1Z	120	ILE	2.0
33	2b	201	ILE	2.0
18	2W	60	ASN	2.0
6	2G	118	ARG	2.0
6	2G	160	VAL	2.0
28	26	28	ARG	2.0
34	2c	198	VAL	2.0
4	2E	186	GLY	2.0
7	2H	123	PHE	2.0
9	2N	51	PHE	2.0
22	20	76	GLY	2.0
37	2f	45	LEU	2.0
38	2g	82	GLY	2.0
38	2g	104	LEU	2.0
40	1i	6	GLY	2.0
1	1A	2178	C	2.0
1	2A	34	C	2.0
1	2A	885	C	2.0
32	2a	1314	C	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	PSU	2w	55	20/21	0.41	0.17	94,101,114,114	0
54	5MU	2w	54	21/22	0.43	0.18	86,98,102,109	0
57	G7M	2y	46	24/25	0.44	0.15	93,102,110,121	0
57	PSU	2y	55	20/21	0.51	0.16	94,102,106,116	0
57	U8U	1y	34	20/24	0.55	0.19	88,96,101,112	0
57	G7M	1y	46	24/25	0.56	0.12	91,100,105,115	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	PSU	1w	55	20/21	0.57	0.18	85,97,105,106	0
54	G7M	2w	46	24/25	0.58	0.14	92,100,105,110	0
57	T6A	1y	37	22/33	0.61	0.16	79,92,98,108	0
57	PSU	1y	39	20/21	0.64	0.13	91,97,105,111	0
57	T6A	2y	37	22/33	0.64	0.14	86,93,102,117	0
54	G7M	1w	46	24/25	0.65	0.13	86,95,103,104	0
54	T6A	2w	37	32/33	0.66	0.20	76,92,97,98	0
57	U8U	2y	34	20/24	0.68	0.17	96,104,112,115	0
57	PSU	2y	39	20/21	0.68	0.16	89,94,105,106	0
54	PSU	2w	39	20/21	0.69	0.17	85,93,99,104	0
57	5MU	2y	54	21/22	0.71	0.13	87,100,112,125	0
57	5MU	1y	54	21/22	0.71	0.12	92,100,102,113	0
57	PSU	1y	55	20/21	0.71	0.12	95,101,109,118	0
54	U8U	1w	34	23/24	0.72	0.22	76,83,91,105	0
55	5MU	2x	54	21/22	0.72	0.16	84,87,92,107	0
1	5MU	2A	1915	21/22	0.73	0.15	79,86,88,93	0
54	U8U	2w	34	23/24	0.73	0.20	80,92,99,108	0
54	5MU	1w	54	21/22	0.73	0.13	78,89,96,98	0
55	4SU	2x	8	20/21	0.77	0.15	79,85,90,96	0
55	PSU	2x	55	20/21	0.78	0.13	77,81,88,100	0
32	2MG	2a	1207	24/25	0.82	0.15	80,87,94,99	0
32	5MC	2a	1400	21/22	0.83	0.20	74,81,85,86	0
32	PSU	2a	516	20/21	0.83	0.12	80,87,94,94	0
32	M2G	2a	966	25/26	0.85	0.17	61,70,90,94	0
32	5MC	2a	967	21/22	0.85	0.16	71,77,87,89	0
32	G7M	2a	527	24/25	0.85	0.15	58,69,76,78	0
54	T6A	1w	37	32/33	0.85	0.14	67,76,83,84	0
1	PSU	2A	1911	20/21	0.86	0.12	62,70,80,83	0
54	A1B8A	2w	76	31/32	0.86	0.16	48,67,78,84	0
55	PSU	1x	55	20/21	0.87	0.11	57,66,75,81	0
1	OMC	2A	1920	21/22	0.87	0.14	54,71,78,78	0
43	0TD	2l	92	10/11	0.87	0.14	63,68,72,89	0
56	FME	2z	1	10/11	0.87	0.23	62,66,74,74	0
32	4OC	2a	1402	22/23	0.88	0.15	63,74,79,81	0
1	PSU	2A	1917	20/21	0.89	0.11	57,78,83,83	0
55	5MC	2x	32	21/22	0.89	0.14	70,74,79,83	0
54	PSU	1w	39	20/21	0.89	0.10	74,85,90,91	0
1	5MU	1A	1915	21/22	0.89	0.12	53,61,71,73	0
32	5MC	2a	1404	21/22	0.90	0.14	57,65,72,78	0
43	0TD	1l	92	10/11	0.90	0.12	50,54,57,66	0
32	PSU	1a	516	20/21	0.91	0.10	57,64,69,71	0
54	A1B8A	1w	76	31/32	0.91	0.13	31,48,58,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	8AN	1x	76	22/23	0.91	0.13	31,43,54,60	0
55	5MU	1x	54	21/22	0.91	0.11	65,72,79,85	0
1	5MC	2A	1962	21/22	0.92	0.13	40,53,60,70	0
1	PSU	1A	1917	20/21	0.92	0.11	41,54,63,66	0
56	FME	1z	1	10/11	0.92	0.20	41,52,67,68	0
55	8AN	2x	76	22/23	0.92	0.11	49,55,63,72	0
32	M2G	1a	966	25/26	0.93	0.14	37,48,57,61	0
1	5MC	2A	1942	21/22	0.93	0.12	39,62,73,78	0
55	4SU	1x	8	20/21	0.93	0.10	49,56,61,62	0
55	5MC	1x	32	21/22	0.93	0.13	41,52,57,66	0
32	2MG	1a	1207	24/25	0.93	0.10	59,65,73,76	0
32	5MC	2a	1407	21/22	0.93	0.12	59,64,69,72	0
32	MA6	2a	1518	24/25	0.93	0.13	58,68,72,77	0
32	MA6	2a	1519	24/25	0.93	0.15	60,69,76,78	0
32	MA6	1a	1519	24/25	0.93	0.13	36,39,42,51	0
1	5MC	1A	1942	21/22	0.94	0.10	36,46,53,55	0
32	UR3	2a	1498	21/22	0.94	0.11	55,65,71,74	0
32	G7M	1a	527	24/25	0.94	0.11	48,52,59,60	0
32	4OC	1a	1402	22/23	0.94	0.11	41,47,54,60	0
1	OMU	2A	2552	21/22	0.95	0.09	36,43,50,51	0
1	PSU	2A	2605	20/21	0.95	0.09	33,38,40,43	0
32	5MC	1a	1404	21/22	0.95	0.11	26,39,42,49	0
32	UR3	1a	1498	21/22	0.95	0.10	29,38,41,42	0
32	5MC	1a	967	21/22	0.95	0.11	45,52,57,59	0
1	OMG	2A	2251	24/25	0.95	0.10	34,39,44,45	0
1	PSU	1A	1911	20/21	0.96	0.08	38,48,53,56	0
1	OMC	1A	1920	21/22	0.96	0.10	29,48,53,54	0
1	5MU	2A	1939	21/22	0.96	0.09	32,36,40,43	0
32	MA6	1a	1518	24/25	0.97	0.09	27,37,42,46	0
32	5MC	1a	1400	21/22	0.97	0.10	41,47,52,58	0
1	2MA	2A	2503	23/24	0.97	0.08	27,31,35,36	0
32	5MC	1a	1407	21/22	0.97	0.09	26,38,41,42	0
1	5MC	1A	1962	21/22	0.97	0.07	23,36,41,46	0
1	5MU	1A	1939	21/22	0.98	0.06	23,27,32,36	0
1	OMG	1A	2251	24/25	0.98	0.07	19,24,29,34	0
1	2MA	1A	2503	23/24	0.98	0.07	16,20,25,26	0
1	OMU	1A	2552	21/22	0.98	0.07	21,29,33,37	0
1	PSU	1A	2605	20/21	0.98	0.06	17,28,30,31	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3787	1/1	0.59	0.18	71,71,71,71	0
58	MG	2A	3797	1/1	0.60	0.25	81,81,81,81	0
58	MG	2a	3185	1/1	0.60	0.20	89,89,89,89	0
58	MG	2a	3133	1/1	0.61	0.37	83,83,83,83	0
58	MG	2A	3758	1/1	0.61	0.15	76,76,76,76	0
58	MG	1a	1712	1/1	0.62	0.21	78,78,78,78	0
58	MG	2A	3546	1/1	0.62	0.22	53,53,53,53	0
58	MG	2a	3146	1/1	0.62	0.10	102,102,102,102	0
58	MG	1a	1695	1/1	0.62	0.18	73,73,73,73	0
58	MG	2A	3050	1/1	0.63	0.25	67,67,67,67	0
58	MG	2a	3190	1/1	0.63	0.16	89,89,89,89	0
58	MG	2A	3081	1/1	0.65	0.31	59,59,59,59	0
58	MG	2a	3036	1/1	0.65	0.24	69,69,69,69	0
58	MG	2a	3194	1/1	0.65	0.33	81,81,81,81	0
58	MG	1A	3882	1/1	0.66	0.25	26,26,26,26	0
58	MG	1A	3758	1/1	0.66	0.16	24,24,24,24	0
58	MG	1A	4066	1/1	0.67	0.22	78,78,78,78	0
58	MG	2A	3749	1/1	0.67	0.17	77,77,77,77	0
58	MG	2A	3567	1/1	0.68	0.21	82,82,82,82	0
58	MG	2A	3295	1/1	0.68	0.15	67,67,67,67	0
58	MG	2A	3458	1/1	0.69	0.25	61,61,61,61	0
58	MG	2A	3770	1/1	0.69	0.24	48,48,48,48	0
58	MG	1A	3436	1/1	0.69	0.19	60,60,60,60	0
58	MG	2a	3173	1/1	0.70	0.25	72,72,72,72	0
58	MG	2A	3541	1/1	0.70	0.15	59,59,59,59	0
58	MG	2A	3715	1/1	0.70	0.45	48,48,48,48	0
58	MG	1W	207	1/1	0.70	0.17	42,42,42,42	0
58	MG	21	101	1/1	0.71	0.17	76,76,76,76	0
58	MG	1A	3097	1/1	0.71	0.19	67,67,67,67	0
58	MG	1A	3515	1/1	0.71	0.13	63,63,63,63	0
58	MG	2A	3307	1/1	0.71	0.15	75,75,75,75	0
58	MG	2a	3098	1/1	0.72	0.18	87,87,87,87	0
58	MG	2a	3109	1/1	0.72	0.17	71,71,71,71	0
58	MG	2A	3323	1/1	0.72	0.29	81,81,81,81	0
58	MG	2A	3029	1/1	0.72	0.23	63,63,63,63	0
58	MG	2a	3163	1/1	0.72	0.19	75,75,75,75	0
58	MG	2A	3205	1/1	0.72	0.14	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3274	1/1	0.72	0.18	63,63,63,63	0
58	MG	1A	3456	1/1	0.72	0.16	63,63,63,63	0
58	MG	2A	3065	1/1	0.72	0.17	50,50,50,50	0
58	MG	2A	3246	1/1	0.73	0.26	76,76,76,76	0
58	MG	2A	3649	1/1	0.73	0.19	76,76,76,76	0
58	MG	2A	3415	1/1	0.73	0.11	61,61,61,61	0
58	MG	1A	3935	1/1	0.73	0.13	74,74,74,74	0
58	MG	1a	1751	1/1	0.73	0.16	73,73,73,73	0
58	MG	2A	3058	1/1	0.73	0.19	54,54,54,54	0
58	MG	1W	202	1/1	0.74	0.19	53,53,53,53	0
58	MG	2A	3728	1/1	0.74	0.19	60,60,60,60	0
58	MG	1A	3613	1/1	0.74	0.18	44,44,44,44	0
58	MG	1t	201	1/1	0.74	0.32	66,66,66,66	0
58	MG	2A	3296	1/1	0.74	0.28	70,70,70,70	0
58	MG	2A	3010	1/1	0.74	0.16	63,63,63,63	0
58	MG	2a	3181	1/1	0.74	0.23	70,70,70,70	0
58	MG	1B	205	1/1	0.74	0.30	68,68,68,68	0
58	MG	2a	3005	1/1	0.74	0.32	71,71,71,71	0
58	MG	2A	3653	1/1	0.74	0.32	85,85,85,85	0
58	MG	2l	202	1/1	0.74	0.26	71,71,71,71	0
58	MG	1A	3204	1/1	0.75	0.10	48,48,48,48	0
58	MG	2A	3220	1/1	0.75	0.24	59,59,59,59	0
58	MG	2A	3233	1/1	0.75	0.16	69,69,69,69	0
58	MG	1A	3812	1/1	0.75	0.14	29,29,29,29	0
58	MG	2A	3266	1/1	0.75	0.30	76,76,76,76	0
58	MG	1x	110	1/1	0.75	0.19	69,69,69,69	0
58	MG	2A	3719	1/1	0.75	0.13	61,61,61,61	0
58	MG	1A	4003	1/1	0.75	0.15	70,70,70,70	0
58	MG	1a	1643	1/1	0.75	0.25	70,70,70,70	0
58	MG	1a	1667	1/1	0.75	0.27	68,68,68,68	0
58	MG	1a	1692	1/1	0.75	0.20	63,63,63,63	0
58	MG	1A	4019	1/1	0.75	0.14	27,27,27,27	0
58	MG	2a	3210	1/1	0.75	0.21	80,80,80,80	0
58	MG	1A	3820	1/1	0.75	0.15	72,72,72,72	0
58	MG	2w	101	1/1	0.75	0.24	85,85,85,85	0
58	MG	1A	3815	1/1	0.76	0.14	46,46,46,46	0
58	MG	2a	3139	1/1	0.76	0.29	78,78,78,78	0
58	MG	2A	3252	1/1	0.76	0.15	61,61,61,61	0
58	MG	1B	213	1/1	0.76	0.19	56,56,56,56	0
58	MG	2a	3007	1/1	0.76	0.24	69,69,69,69	0
58	MG	2A	3647	1/1	0.76	0.19	62,62,62,62	0
58	MG	2a	3037	1/1	0.76	0.18	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2a	3064	1/1	0.76	0.35	60,60,60,60	0
58	MG	1a	1704	1/1	0.76	0.29	72,72,72,72	0
58	MG	1A	4077	1/1	0.76	0.16	39,39,39,39	0
58	MG	2a	3130	1/1	0.76	0.17	70,70,70,70	0
58	MG	2a	3132	1/1	0.76	0.09	73,73,73,73	0
58	MG	2A	3203	1/1	0.77	0.18	67,67,67,67	0
58	MG	2B	212	1/1	0.77	0.25	71,71,71,71	0
58	MG	1A	3424	1/1	0.77	0.31	44,44,44,44	0
58	MG	1A	3923	1/1	0.77	0.15	62,62,62,62	0
58	MG	2a	3160	1/1	0.77	0.16	74,74,74,74	0
58	MG	1A	3599	1/1	0.77	0.23	53,53,53,53	0
58	MG	2A	3408	1/1	0.77	0.33	79,79,79,79	0
58	MG	2a	3177	1/1	0.77	0.15	68,68,68,68	0
58	MG	1n	102	1/1	0.77	0.21	60,60,60,60	0
58	MG	2A	3440	1/1	0.77	0.10	58,58,58,58	0
58	MG	1A	3035	1/1	0.77	0.10	43,43,43,43	0
58	MG	1A	3371	1/1	0.77	0.13	42,42,42,42	0
58	MG	2a	3121	1/1	0.77	0.22	69,69,69,69	0
58	MG	2a	3124	1/1	0.77	0.25	71,71,71,71	0
58	MG	2A	3088	1/1	0.77	0.22	61,61,61,61	0
58	MG	2A	3279	1/1	0.78	0.23	69,69,69,69	0
58	MG	2A	3450	1/1	0.78	0.31	75,75,75,75	0
58	MG	2A	3281	1/1	0.78	0.26	66,66,66,66	0
58	MG	2A	3227	1/1	0.78	0.14	66,66,66,66	0
58	MG	2a	3175	1/1	0.78	0.16	84,84,84,84	0
58	MG	1A	3946	1/1	0.78	0.21	64,64,64,64	0
58	MG	1Y	201	1/1	0.78	0.09	73,73,73,73	0
58	MG	2A	3637	1/1	0.78	0.14	57,57,57,57	0
58	MG	2A	3812	1/1	0.78	0.15	64,64,64,64	0
58	MG	2a	3193	1/1	0.78	0.14	75,75,75,75	0
58	MG	1x	108	1/1	0.78	0.13	66,66,66,66	0
58	MG	20	101	1/1	0.78	0.15	70,70,70,70	0
58	MG	1x	109	1/1	0.78	0.17	61,61,61,61	0
58	MG	1A	3164	1/1	0.78	0.34	59,59,59,59	0
58	MG	2x	102	1/1	0.78	0.27	77,77,77,77	0
58	MG	1A	3130	1/1	0.79	0.11	71,71,71,71	0
58	MG	2A	3095	1/1	0.79	0.11	46,46,46,46	0
58	MG	1A	3425	1/1	0.79	0.24	55,55,55,55	0
58	MG	1a	1608	1/1	0.79	0.19	68,68,68,68	0
58	MG	1A	3321	1/1	0.79	0.11	52,52,52,52	0
58	MG	2A	3346	1/1	0.79	0.20	70,70,70,70	0
58	MG	2a	3092	1/1	0.79	0.10	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1656	1/1	0.79	0.17	61,61,61,61	0
58	MG	1A	3693	1/1	0.79	0.17	30,30,30,30	0
58	MG	2A	3244	1/1	0.79	0.15	53,53,53,53	0
58	MG	1A	3868	1/1	0.79	0.11	32,32,32,32	0
58	MG	1A	3702	1/1	0.79	0.12	20,20,20,20	0
58	MG	1A	3188	1/1	0.79	0.31	40,40,40,40	0
58	MG	1S	201	1/1	0.79	0.09	59,59,59,59	0
58	MG	1A	3777	1/1	0.79	0.19	65,65,65,65	0
58	MG	2A	3324	1/1	0.80	0.21	65,65,65,65	0
58	MG	1a	1615	1/1	0.80	0.22	47,47,47,47	0
58	MG	1a	1697	1/1	0.80	0.35	70,70,70,70	0
58	MG	1A	3358	1/1	0.80	0.29	43,43,43,43	0
58	MG	2A	3710	1/1	0.80	0.20	50,50,50,50	0
58	MG	2a	3170	1/1	0.80	0.32	78,78,78,78	0
58	MG	1A	3673	1/1	0.80	0.16	67,67,67,67	0
58	MG	1B	229	1/1	0.80	0.25	73,73,73,73	0
58	MG	1A	3721	1/1	0.80	0.24	63,63,63,63	0
58	MG	2A	3489	1/1	0.80	0.11	57,57,57,57	0
58	MG	2a	3094	1/1	0.80	0.25	78,78,78,78	0
58	MG	2A	3302	1/1	0.80	0.15	64,64,64,64	0
58	MG	2a	3100	1/1	0.80	0.16	60,60,60,60	0
58	MG	2A	3101	1/1	0.80	0.11	66,66,66,66	0
58	MG	2A	3126	1/1	0.80	0.12	57,57,57,57	0
58	MG	2j	201	1/1	0.80	0.30	73,73,73,73	0
58	MG	2A	3802	1/1	0.80	0.17	58,58,58,58	0
58	MG	2A	3625	1/1	0.80	0.30	79,79,79,79	0
58	MG	2B	204	1/1	0.80	0.23	69,69,69,69	0
58	MG	2a	3097	1/1	0.81	0.35	67,67,67,67	0
58	MG	1a	1660	1/1	0.81	0.20	75,75,75,75	0
58	MG	1A	3569	1/1	0.81	0.14	35,35,35,35	0
58	MG	2A	3260	1/1	0.81	0.23	55,55,55,55	0
58	MG	1A	3883	1/1	0.81	0.20	78,78,78,78	0
58	MG	2A	3754	1/1	0.81	0.17	56,56,56,56	0
58	MG	1A	3543	1/1	0.81	0.15	62,62,62,62	0
58	MG	2A	3466	1/1	0.81	0.18	63,63,63,63	0
58	MG	2A	3777	1/1	0.81	0.13	48,48,48,48	0
58	MG	1A	3687	1/1	0.81	0.14	48,48,48,48	0
58	MG	2A	3192	1/1	0.81	0.20	65,65,65,65	0
58	MG	2A	3804	1/1	0.81	0.19	60,60,60,60	0
58	MG	2A	3195	1/1	0.81	0.10	66,66,66,66	0
58	MG	2A	3559	1/1	0.81	0.17	65,65,65,65	0
58	MG	1A	3795	1/1	0.81	0.17	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3583	1/1	0.81	0.17	59,59,59,59	0
58	MG	20	102	1/1	0.81	0.19	73,73,73,73	0
58	MG	2A	3609	1/1	0.81	0.08	56,56,56,56	0
58	MG	2A	3299	1/1	0.81	0.23	72,72,72,72	0
58	MG	2A	3030	1/1	0.81	0.16	51,51,51,51	0
58	MG	2a	3010	1/1	0.81	0.17	63,63,63,63	0
58	MG	2A	3035	1/1	0.81	0.16	51,51,51,51	0
58	MG	1a	1634	1/1	0.81	0.12	62,62,62,62	0
58	MG	1A	3954	1/1	0.81	0.21	68,68,68,68	0
58	MG	2l	201	1/1	0.81	0.16	62,62,62,62	0
58	MG	2a	3080	1/1	0.81	0.27	71,71,71,71	0
58	MG	2A	3696	1/1	0.81	0.19	73,73,73,73	0
58	MG	1A	3870	1/1	0.81	0.14	50,50,50,50	0
58	MG	2A	3534	1/1	0.82	0.20	42,42,42,42	0
58	MG	1A	3796	1/1	0.82	0.17	47,47,47,47	0
58	MG	1A	4014	1/1	0.82	0.10	46,46,46,46	0
58	MG	2a	3034	1/1	0.82	0.34	77,77,77,77	0
58	MG	2A	3553	1/1	0.82	0.13	47,47,47,47	0
58	MG	1A	3459	1/1	0.82	0.27	43,43,43,43	0
58	MG	2A	3040	1/1	0.82	0.37	73,73,73,73	0
58	MG	2a	3071	1/1	0.82	0.33	68,68,68,68	0
58	MG	1A	4065	1/1	0.82	0.19	81,81,81,81	0
58	MG	2A	3584	1/1	0.82	0.18	64,64,64,64	0
58	MG	1A	3473	1/1	0.82	0.22	56,56,56,56	0
58	MG	2A	3062	1/1	0.82	0.13	69,69,69,69	0
58	MG	1A	3691	1/1	0.82	0.12	40,40,40,40	0
58	MG	1A	3495	1/1	0.82	0.11	40,40,40,40	0
58	MG	2A	3083	1/1	0.82	0.14	65,65,65,65	0
58	MG	1A	3701	1/1	0.82	0.16	50,50,50,50	0
58	MG	1B	218	1/1	0.82	0.11	57,57,57,57	0
58	MG	2a	3129	1/1	0.82	0.20	65,65,65,65	0
58	MG	2A	3096	1/1	0.82	0.11	61,61,61,61	0
58	MG	2A	3309	1/1	0.82	0.22	69,69,69,69	0
58	MG	1A	3317	1/1	0.82	0.20	53,53,53,53	0
58	MG	1a	1735	1/1	0.82	0.14	66,66,66,66	0
58	MG	2A	3182	1/1	0.82	0.17	61,61,61,61	0
58	MG	2A	3750	1/1	0.82	0.18	71,71,71,71	0
58	MG	2A	3388	1/1	0.82	0.11	50,50,50,50	0
58	MG	2A	3389	1/1	0.82	0.19	64,64,64,64	0
58	MG	2A	3391	1/1	0.82	0.21	56,56,56,56	0
58	MG	2A	3406	1/1	0.82	0.16	49,49,49,49	0
58	MG	1A	3158	1/1	0.82	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2a	3179	1/1	0.82	0.17	76,76,76,76	0
58	MG	1A	3027	1/1	0.82	0.29	74,74,74,74	0
58	MG	2a	3183	1/1	0.82	0.16	62,62,62,62	0
58	MG	1A	3595	1/1	0.82	0.13	47,47,47,47	0
58	MG	2a	3186	1/1	0.82	0.20	67,67,67,67	0
58	MG	2A	3811	1/1	0.82	0.13	74,74,74,74	0
58	MG	1A	3438	1/1	0.82	0.10	51,51,51,51	0
58	MG	2A	3817	1/1	0.82	0.13	67,67,67,67	0
58	MG	2a	3197	1/1	0.82	0.23	72,72,72,72	0
58	MG	2a	3204	1/1	0.82	0.35	72,72,72,72	0
58	MG	14	101	1/1	0.82	0.13	63,63,63,63	0
58	MG	2B	205	1/1	0.82	0.09	63,63,63,63	0
58	MG	1A	3293	1/1	0.82	0.27	71,71,71,71	0
58	MG	2A	3474	1/1	0.82	0.28	73,73,73,73	0
58	MG	1A	3980	1/1	0.82	0.13	23,23,23,23	0
58	MG	2A	3505	1/1	0.82	0.17	66,66,66,66	0
58	MG	2A	3721	1/1	0.83	0.20	65,65,65,65	0
58	MG	1a	1677	1/1	0.83	0.24	66,66,66,66	0
58	MG	2a	3096	1/1	0.83	0.19	62,62,62,62	0
58	MG	1A	3002	1/1	0.83	0.16	54,54,54,54	0
58	MG	2A	3008	1/1	0.83	0.18	51,51,51,51	0
58	MG	1A	3912	1/1	0.83	0.17	40,40,40,40	0
58	MG	2A	3287	1/1	0.83	0.23	66,66,66,66	0
58	MG	2a	3120	1/1	0.83	0.19	69,69,69,69	0
58	MG	1B	216	1/1	0.83	0.18	70,70,70,70	0
58	MG	2A	3526	1/1	0.83	0.13	60,60,60,60	0
58	MG	2A	3784	1/1	0.83	0.16	76,76,76,76	0
58	MG	2A	3149	1/1	0.83	0.18	57,57,57,57	0
58	MG	1a	1613	1/1	0.83	0.18	61,61,61,61	0
58	MG	2A	3185	1/1	0.83	0.40	73,73,73,73	0
58	MG	2A	3810	1/1	0.83	0.11	55,55,55,55	0
58	MG	2a	3141	1/1	0.83	0.18	62,62,62,62	0
58	MG	1A	3666	1/1	0.83	0.14	58,58,58,58	0
58	MG	1A	3060	1/1	0.83	0.20	50,50,50,50	0
58	MG	2A	3046	1/1	0.83	0.21	65,65,65,65	0
58	MG	2A	3047	1/1	0.83	0.13	59,59,59,59	0
58	MG	1a	1744	1/1	0.83	0.13	48,48,48,48	0
58	MG	2A	3384	1/1	0.83	0.11	46,46,46,46	0
58	MG	2W	201	1/1	0.83	0.15	57,57,57,57	0
58	MG	1B	232	1/1	0.83	0.11	86,86,86,86	0
58	MG	2A	3231	1/1	0.83	0.32	66,66,66,66	0
58	MG	1a	1768	1/1	0.83	0.20	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3648	1/1	0.83	0.17	72,72,72,72	0
58	MG	2A	3399	1/1	0.83	0.20	51,51,51,51	0
58	MG	2A	3651	1/1	0.83	0.10	57,57,57,57	0
58	MG	2a	3027	1/1	0.83	0.28	70,70,70,70	0
58	MG	1A	3368	1/1	0.83	0.20	53,53,53,53	0
58	MG	2A	3066	1/1	0.83	0.12	61,61,61,61	0
58	MG	1A	3457	1/1	0.83	0.11	57,57,57,57	0
58	MG	2a	3051	1/1	0.83	0.10	66,66,66,66	0
58	MG	2a	3052	1/1	0.83	0.22	83,83,83,83	0
58	MG	2A	3712	1/1	0.83	0.15	52,52,52,52	0
58	MG	1A	3955	1/1	0.83	0.12	60,60,60,60	0
58	MG	2A	3448	1/1	0.83	0.16	59,59,59,59	0
58	MG	2w	102	1/1	0.83	0.19	77,77,77,77	0
58	MG	2a	3090	1/1	0.83	0.12	63,63,63,63	0
58	MG	2A	3285	1/1	0.84	0.20	59,59,59,59	0
58	MG	1A	3810	1/1	0.84	0.14	32,32,32,32	0
58	MG	1A	3573	1/1	0.84	0.23	57,57,57,57	0
58	MG	2a	3040	1/1	0.84	0.23	65,65,65,65	0
58	MG	2a	3048	1/1	0.84	0.15	62,62,62,62	0
58	MG	1Q	204	1/1	0.84	0.07	47,47,47,47	0
58	MG	1A	3970	1/1	0.84	0.12	31,31,31,31	0
58	MG	2a	3060	1/1	0.84	0.21	68,68,68,68	0
58	MG	2A	3071	1/1	0.84	0.22	60,60,60,60	0
58	MG	2a	3065	1/1	0.84	0.15	61,61,61,61	0
58	MG	1A	3700	1/1	0.84	0.12	50,50,50,50	0
58	MG	1a	1731	1/1	0.84	0.13	81,81,81,81	0
58	MG	2a	3084	1/1	0.84	0.18	61,61,61,61	0
58	MG	2a	3085	1/1	0.84	0.18	77,77,77,77	0
58	MG	2A	3313	1/1	0.84	0.10	76,76,76,76	0
58	MG	1A	3323	1/1	0.84	0.18	44,44,44,44	0
58	MG	1A	3332	1/1	0.84	0.10	42,42,42,42	0
58	MG	1A	3496	1/1	0.84	0.13	48,48,48,48	0
58	MG	2A	3360	1/1	0.84	0.18	68,68,68,68	0
58	MG	1a	1757	1/1	0.84	0.15	59,59,59,59	0
58	MG	1a	1760	1/1	0.84	0.21	61,61,61,61	0
58	MG	2a	3105	1/1	0.84	0.24	75,75,75,75	0
58	MG	1A	3420	1/1	0.84	0.14	46,46,46,46	0
58	MG	1a	1776	1/1	0.84	0.16	56,56,56,56	0
58	MG	2A	3730	1/1	0.84	0.11	67,67,67,67	0
58	MG	1a	1795	1/1	0.84	0.21	66,66,66,66	0
58	MG	1A	3671	1/1	0.84	0.17	45,45,45,45	0
58	MG	1A	4068	1/1	0.84	0.14	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1w	101	1/1	0.84	0.10	69,69,69,69	0
58	MG	2A	3428	1/1	0.84	0.18	69,69,69,69	0
58	MG	2A	3775	1/1	0.84	0.18	39,39,39,39	0
58	MG	1a	1623	1/1	0.84	0.22	65,65,65,65	0
58	MG	2a	3145	1/1	0.84	0.11	82,82,82,82	0
58	MG	2A	3446	1/1	0.84	0.20	69,69,69,69	0
58	MG	1A	3270	1/1	0.84	0.21	59,59,59,59	0
58	MG	1a	1639	1/1	0.84	0.21	60,60,60,60	0
58	MG	1A	3561	1/1	0.84	0.10	54,54,54,54	0
58	MG	2a	3172	1/1	0.84	0.18	71,71,71,71	0
58	MG	1a	1648	1/1	0.84	0.31	64,64,64,64	0
58	MG	2a	3174	1/1	0.84	0.21	70,70,70,70	0
58	MG	1a	1649	1/1	0.84	0.26	57,57,57,57	0
58	MG	2A	3481	1/1	0.84	0.11	52,52,52,52	0
58	MG	1B	209	1/1	0.84	0.30	64,64,64,64	0
58	MG	2A	3819	1/1	0.84	0.14	66,66,66,66	0
58	MG	2A	3824	1/1	0.84	0.15	58,58,58,58	0
58	MG	2A	3502	1/1	0.84	0.20	57,57,57,57	0
58	MG	1A	3365	1/1	0.84	0.24	41,41,41,41	0
58	MG	2A	3513	1/1	0.84	0.13	54,54,54,54	0
58	MG	2B	215	1/1	0.84	0.23	75,75,75,75	0
58	MG	1A	3797	1/1	0.84	0.11	35,35,35,35	0
58	MG	1a	1675	1/1	0.84	0.17	66,66,66,66	0
58	MG	2A	3272	1/1	0.84	0.12	78,78,78,78	0
58	MG	1A	3947	1/1	0.84	0.15	17,17,17,17	0
58	MG	1a	1682	1/1	0.84	0.08	61,61,61,61	0
58	MG	2A	3052	1/1	0.84	0.16	76,76,76,76	0
58	MG	2A	3282	1/1	0.84	0.14	62,62,62,62	0
58	MG	2v	101	1/1	0.84	0.09	60,60,60,60	0
58	MG	2a	3017	1/1	0.84	0.18	63,63,63,63	0
58	MG	2A	3570	1/1	0.84	0.11	52,52,52,52	0
58	MG	2a	3032	1/1	0.84	0.19	80,80,80,80	0
58	MG	2x	104	1/1	0.84	0.27	74,74,74,74	0
58	MG	1a	1631	1/1	0.85	0.27	59,59,59,59	0
58	MG	1A	3189	1/1	0.85	0.17	57,57,57,57	0
58	MG	1A	3062	1/1	0.85	0.16	50,50,50,50	0
58	MG	2A	3581	1/1	0.85	0.16	57,57,57,57	0
58	MG	2a	3041	1/1	0.85	0.16	67,67,67,67	0
58	MG	2a	3046	1/1	0.85	0.18	81,81,81,81	0
58	MG	1a	1764	1/1	0.85	0.21	66,66,66,66	0
58	MG	1A	3871	1/1	0.85	0.12	23,23,23,23	0
58	MG	2A	3085	1/1	0.85	0.13	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1773	1/1	0.85	0.16	63,63,63,63	0
58	MG	1A	3878	1/1	0.85	0.12	22,22,22,22	0
58	MG	2A	3639	1/1	0.85	0.16	55,55,55,55	0
58	MG	1B	226	1/1	0.85	0.17	59,59,59,59	0
58	MG	2A	3098	1/1	0.85	0.14	58,58,58,58	0
58	MG	2A	3310	1/1	0.85	0.18	65,65,65,65	0
58	MG	2A	3311	1/1	0.85	0.17	78,78,78,78	0
58	MG	2A	3312	1/1	0.85	0.09	63,63,63,63	0
58	MG	1a	1797	1/1	0.85	0.13	66,66,66,66	0
58	MG	2A	3707	1/1	0.85	0.14	64,64,64,64	0
58	MG	2A	3318	1/1	0.85	0.13	57,57,57,57	0
58	MG	2A	3711	1/1	0.85	0.19	63,63,63,63	0
58	MG	2A	3319	1/1	0.85	0.26	72,72,72,72	0
58	MG	1A	3986	1/1	0.85	0.09	74,74,74,74	0
58	MG	2A	3142	1/1	0.85	0.26	67,67,67,67	0
58	MG	2A	3340	1/1	0.85	0.17	66,66,66,66	0
58	MG	2a	3115	1/1	0.85	0.26	69,69,69,69	0
58	MG	1A	3210	1/1	0.85	0.12	55,55,55,55	0
58	MG	2A	3158	1/1	0.85	0.19	68,68,68,68	0
58	MG	2A	3364	1/1	0.85	0.15	62,62,62,62	0
58	MG	2A	3383	1/1	0.85	0.16	51,51,51,51	0
58	MG	2A	3170	1/1	0.85	0.11	50,50,50,50	0
58	MG	2a	3131	1/1	0.85	0.34	76,76,76,76	0
58	MG	1A	3040	1/1	0.85	0.18	58,58,58,58	0
58	MG	1A	3894	1/1	0.85	0.12	52,52,52,52	0
58	MG	1V	201	1/1	0.85	0.30	30,30,30,30	0
58	MG	1A	4020	1/1	0.85	0.38	62,62,62,62	0
58	MG	2A	3400	1/1	0.85	0.21	43,43,43,43	0
58	MG	2A	3007	1/1	0.85	0.19	54,54,54,54	0
58	MG	1A	4025	1/1	0.85	0.12	28,28,28,28	0
58	MG	1A	4031	1/1	0.85	0.12	46,46,46,46	0
58	MG	2A	3223	1/1	0.85	0.15	59,59,59,59	0
58	MG	1A	3353	1/1	0.85	0.11	40,40,40,40	0
58	MG	2A	3444	1/1	0.85	0.30	59,59,59,59	0
58	MG	19	101	1/1	0.85	0.12	55,55,55,55	0
58	MG	1A	3669	1/1	0.85	0.15	47,47,47,47	0
58	MG	2A	3242	1/1	0.85	0.11	57,57,57,57	0
58	MG	2B	202	1/1	0.85	0.11	70,70,70,70	0
58	MG	2A	3037	1/1	0.85	0.15	39,39,39,39	0
58	MG	1a	1714	1/1	0.85	0.15	57,57,57,57	0
58	MG	2A	3251	1/1	0.85	0.23	60,60,60,60	0
58	MG	1a	1716	1/1	0.85	0.09	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2a	3189	1/1	0.85	0.26	61,61,61,61	0
58	MG	2D	302	1/1	0.85	0.14	51,51,51,51	0
58	MG	2A	3258	1/1	0.85	0.08	40,40,40,40	0
58	MG	1a	1729	1/1	0.85	0.16	57,57,57,57	0
58	MG	1A	3026	1/1	0.85	0.24	49,49,49,49	0
58	MG	2a	3201	1/1	0.85	0.26	54,54,54,54	0
58	MG	2A	3268	1/1	0.85	0.23	70,70,70,70	0
58	MG	2a	3206	1/1	0.85	0.17	69,69,69,69	0
58	MG	21	103	1/1	0.85	0.23	65,65,65,65	0
58	MG	2A	3269	1/1	0.85	0.32	63,63,63,63	0
58	MG	2a	3006	1/1	0.85	0.28	72,72,72,72	0
58	MG	1A	3753	1/1	0.85	0.10	19,19,19,19	0
58	MG	1a	1739	1/1	0.85	0.11	63,63,63,63	0
58	MG	1A	3570	1/1	0.85	0.11	32,32,32,32	0
58	MG	2a	3023	1/1	0.85	0.14	65,65,65,65	0
58	MG	2A	3552	1/1	0.85	0.17	65,65,65,65	0
58	MG	2A	3280	1/1	0.85	0.22	57,57,57,57	0
58	MG	2A	3375	1/1	0.86	0.21	50,50,50,50	0
58	MG	2a	3038	1/1	0.86	0.23	75,75,75,75	0
58	MG	1W	201	1/1	0.86	0.27	51,51,51,51	0
58	MG	1A	3462	1/1	0.86	0.12	50,50,50,50	0
58	MG	1A	3629	1/1	0.86	0.17	62,62,62,62	0
58	MG	2A	3663	1/1	0.86	0.14	46,46,46,46	0
58	MG	2A	3666	1/1	0.86	0.10	57,57,57,57	0
58	MG	1a	1779	1/1	0.86	0.22	56,56,56,56	0
58	MG	1A	3635	1/1	0.86	0.10	37,37,37,37	0
58	MG	2A	3074	1/1	0.86	0.17	65,65,65,65	0
58	MG	1Z	302	1/1	0.86	0.07	57,57,57,57	0
58	MG	2a	3070	1/1	0.86	0.30	73,73,73,73	0
58	MG	1A	3823	1/1	0.86	0.15	63,63,63,63	0
58	MG	1A	3207	1/1	0.86	0.22	57,57,57,57	0
58	MG	2A	3716	1/1	0.86	0.11	47,47,47,47	0
58	MG	2A	3267	1/1	0.86	0.14	67,67,67,67	0
58	MG	2a	3086	1/1	0.86	0.26	54,54,54,54	0
58	MG	2A	3417	1/1	0.86	0.14	65,65,65,65	0
58	MG	1a	1603	1/1	0.86	0.17	57,57,57,57	0
58	MG	1w	104	1/1	0.86	0.26	71,71,71,71	0
58	MG	2A	3735	1/1	0.86	0.28	66,66,66,66	0
58	MG	2A	3741	1/1	0.86	0.18	56,56,56,56	0
58	MG	1a	1701	1/1	0.86	0.12	58,58,58,58	0
58	MG	1A	3474	1/1	0.86	0.11	54,54,54,54	0
58	MG	2A	3275	1/1	0.86	0.23	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3449	1/1	0.86	0.28	53,53,53,53	0
58	MG	2A	3100	1/1	0.86	0.13	47,47,47,47	0
58	MG	1A	3482	1/1	0.86	0.30	54,54,54,54	0
58	MG	2A	3107	1/1	0.86	0.16	55,55,55,55	0
58	MG	2A	3120	1/1	0.86	0.24	66,66,66,66	0
58	MG	2A	3788	1/1	0.86	0.13	43,43,43,43	0
58	MG	2A	3004	1/1	0.86	0.28	58,58,58,58	0
58	MG	2A	3482	1/1	0.86	0.10	66,66,66,66	0
58	MG	2A	3486	1/1	0.86	0.23	75,75,75,75	0
58	MG	2A	3805	1/1	0.86	0.23	52,52,52,52	0
58	MG	1A	3377	1/1	0.86	0.13	55,55,55,55	0
58	MG	2A	3291	1/1	0.86	0.12	54,54,54,54	0
58	MG	1a	1617	1/1	0.86	0.10	55,55,55,55	0
58	MG	2A	3815	1/1	0.86	0.24	67,67,67,67	0
58	MG	2A	3508	1/1	0.86	0.17	62,62,62,62	0
58	MG	2A	3150	1/1	0.86	0.13	69,69,69,69	0
58	MG	2A	3821	1/1	0.86	0.15	65,65,65,65	0
58	MG	1a	1728	1/1	0.86	0.11	68,68,68,68	0
58	MG	2B	201	1/1	0.86	0.12	71,71,71,71	0
58	MG	2A	3022	1/1	0.86	0.21	54,54,54,54	0
58	MG	2B	203	1/1	0.86	0.15	66,66,66,66	0
58	MG	2A	3305	1/1	0.86	0.25	68,68,68,68	0
58	MG	2A	3543	1/1	0.86	0.15	61,61,61,61	0
58	MG	2A	3181	1/1	0.86	0.29	73,73,73,73	0
58	MG	2A	3550	1/1	0.86	0.16	65,65,65,65	0
58	MG	1B	225	1/1	0.86	0.20	45,45,45,45	0
58	MG	2E	305	1/1	0.86	0.10	26,26,26,26	0
58	MG	2P	202	1/1	0.86	0.18	62,62,62,62	0
58	MG	1A	3675	1/1	0.86	0.14	32,32,32,32	0
58	MG	1A	3686	1/1	0.86	0.09	25,25,25,25	0
58	MG	1a	1637	1/1	0.86	0.24	70,70,70,70	0
58	MG	2a	3195	1/1	0.86	0.11	65,65,65,65	0
58	MG	2A	3039	1/1	0.86	0.16	57,57,57,57	0
58	MG	1A	3574	1/1	0.86	0.21	38,38,38,38	0
58	MG	2A	3209	1/1	0.86	0.21	64,64,64,64	0
58	MG	2a	3205	1/1	0.86	0.21	69,69,69,69	0
58	MG	2A	3219	1/1	0.86	0.10	46,46,46,46	0
58	MG	2A	3590	1/1	0.86	0.12	19,19,19,19	0
58	MG	1E	308	1/1	0.86	0.11	29,29,29,29	0
58	MG	2A	3619	1/1	0.86	0.14	41,41,41,41	0
58	MG	2a	3018	1/1	0.86	0.20	62,62,62,62	0
58	MG	2l	204	1/1	0.86	0.12	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3431	1/1	0.86	0.20	46,46,46,46	0
58	MG	1A	3806	1/1	0.86	0.09	46,46,46,46	0
58	MG	2A	3229	1/1	0.86	0.13	67,67,67,67	0
58	MG	2A	3646	1/1	0.86	0.15	67,67,67,67	0
58	MG	1A	3170	1/1	0.86	0.13	45,45,45,45	0
58	MG	1a	1808	1/1	0.87	0.16	57,57,57,57	0
58	MG	1a	1809	1/1	0.87	0.23	70,70,70,70	0
58	MG	1B	203	1/1	0.87	0.14	47,47,47,47	0
58	MG	2A	3599	1/1	0.87	0.26	66,66,66,66	0
58	MG	2A	3604	1/1	0.87	0.14	60,60,60,60	0
58	MG	2a	3021	1/1	0.87	0.42	73,73,73,73	0
58	MG	2a	3022	1/1	0.87	0.15	68,68,68,68	0
58	MG	2A	3155	1/1	0.87	0.12	43,43,43,43	0
58	MG	2a	3025	1/1	0.87	0.26	72,72,72,72	0
58	MG	2a	3026	1/1	0.87	0.13	77,77,77,77	0
58	MG	1A	3578	1/1	0.87	0.12	41,41,41,41	0
58	MG	1A	3010	1/1	0.87	0.08	40,40,40,40	0
58	MG	2A	3634	1/1	0.87	0.28	71,71,71,71	0
58	MG	2a	3035	1/1	0.87	0.22	71,71,71,71	0
58	MG	2A	3636	1/1	0.87	0.18	69,69,69,69	0
58	MG	1A	3597	1/1	0.87	0.16	59,59,59,59	0
58	MG	1A	3485	1/1	0.87	0.15	55,55,55,55	0
58	MG	2A	3641	1/1	0.87	0.12	60,60,60,60	0
58	MG	2A	3184	1/1	0.87	0.17	57,57,57,57	0
58	MG	2a	3042	1/1	0.87	0.10	57,57,57,57	0
58	MG	2a	3044	1/1	0.87	0.11	52,52,52,52	0
58	MG	1A	3248	1/1	0.87	0.13	56,56,56,56	0
58	MG	1A	3929	1/1	0.87	0.14	30,30,30,30	0
58	MG	2a	3050	1/1	0.87	0.18	75,75,75,75	0
58	MG	1A	3931	1/1	0.87	0.18	61,61,61,61	0
58	MG	1a	1670	1/1	0.87	0.18	62,62,62,62	0
58	MG	2A	3357	1/1	0.87	0.27	70,70,70,70	0
58	MG	2A	3656	1/1	0.87	0.20	63,63,63,63	0
58	MG	1a	1673	1/1	0.87	0.21	60,60,60,60	0
58	MG	1A	3320	1/1	0.87	0.08	42,42,42,42	0
58	MG	2A	3368	1/1	0.87	0.13	58,58,58,58	0
58	MG	2A	3706	1/1	0.87	0.13	48,48,48,48	0
58	MG	2A	3371	1/1	0.87	0.16	46,46,46,46	0
58	MG	1A	3508	1/1	0.87	0.16	76,76,76,76	0
58	MG	1A	3639	1/1	0.87	0.12	48,48,48,48	0
58	MG	2A	3222	1/1	0.87	0.10	36,36,36,36	0
58	MG	2A	3713	1/1	0.87	0.14	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1686	1/1	0.87	0.24	59,59,59,59	0
58	MG	2A	3225	1/1	0.87	0.12	57,57,57,57	0
58	MG	1N	204	1/1	0.87	0.11	43,43,43,43	0
58	MG	1P	207	1/1	0.87	0.14	48,48,48,48	0
58	MG	2A	3230	1/1	0.87	0.18	78,78,78,78	0
58	MG	2a	3102	1/1	0.87	0.10	61,61,61,61	0
58	MG	2A	3729	1/1	0.87	0.15	61,61,61,61	0
58	MG	2A	3405	1/1	0.87	0.20	51,51,51,51	0
58	MG	2a	3114	1/1	0.87	0.15	62,62,62,62	0
58	MG	1A	3644	1/1	0.87	0.19	41,41,41,41	0
58	MG	1A	3653	1/1	0.87	0.13	25,25,25,25	0
58	MG	2A	3742	1/1	0.87	0.12	46,46,46,46	0
58	MG	2A	3743	1/1	0.87	0.11	65,65,65,65	0
58	MG	2a	3128	1/1	0.87	0.18	69,69,69,69	0
58	MG	2A	3409	1/1	0.87	0.20	46,46,46,46	0
58	MG	2A	3413	1/1	0.87	0.11	60,60,60,60	0
58	MG	2A	3234	1/1	0.87	0.07	56,56,56,56	0
58	MG	2A	3239	1/1	0.87	0.18	59,59,59,59	0
58	MG	2A	3760	1/1	0.87	0.11	64,64,64,64	0
58	MG	1A	3966	1/1	0.87	0.17	62,62,62,62	0
58	MG	2a	3140	1/1	0.87	0.18	59,59,59,59	0
58	MG	1A	3968	1/1	0.87	0.11	34,34,34,34	0
58	MG	1A	3800	1/1	0.87	0.13	54,54,54,54	0
58	MG	2A	3248	1/1	0.87	0.15	75,75,75,75	0
58	MG	2A	3249	1/1	0.87	0.15	44,44,44,44	0
58	MG	2A	3792	1/1	0.87	0.09	60,60,60,60	0
58	MG	2a	3164	1/1	0.87	0.22	63,63,63,63	0
58	MG	1A	3258	1/1	0.87	0.15	51,51,51,51	0
58	MG	1A	3261	1/1	0.87	0.08	44,44,44,44	0
58	MG	2A	3255	1/1	0.87	0.16	67,67,67,67	0
58	MG	1A	3544	1/1	0.87	0.12	36,36,36,36	0
58	MG	2A	3809	1/1	0.87	0.11	74,74,74,74	0
58	MG	2A	3468	1/1	0.87	0.09	54,54,54,54	0
58	MG	2A	3471	1/1	0.87	0.16	72,72,72,72	0
58	MG	10	108	1/1	0.87	0.12	49,49,49,49	0
58	MG	2A	3265	1/1	0.87	0.21	68,68,68,68	0
58	MG	2a	3184	1/1	0.87	0.24	70,70,70,70	0
58	MG	1A	3547	1/1	0.87	0.15	44,44,44,44	0
58	MG	15	107	1/1	0.87	0.22	33,33,33,33	0
58	MG	1A	3324	1/1	0.87	0.17	45,45,45,45	0
58	MG	1a	1602	1/1	0.87	0.21	58,58,58,58	0
58	MG	1a	1756	1/1	0.87	0.09	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3383	1/1	0.87	0.39	41,41,41,41	0
58	MG	1A	3854	1/1	0.87	0.10	31,31,31,31	0
58	MG	2a	3196	1/1	0.87	0.09	73,73,73,73	0
58	MG	2A	3516	1/1	0.87	0.23	65,65,65,65	0
58	MG	1A	3387	1/1	0.87	0.14	71,71,71,71	0
58	MG	1A	4060	1/1	0.87	0.18	54,54,54,54	0
58	MG	1A	3105	1/1	0.87	0.13	37,37,37,37	0
58	MG	1A	3333	1/1	0.87	0.18	67,67,67,67	0
58	MG	2a	3209	1/1	0.87	0.23	70,70,70,70	0
58	MG	1a	1627	1/1	0.87	0.18	66,66,66,66	0
58	MG	2F	303	1/1	0.87	0.14	67,67,67,67	0
58	MG	2A	3104	1/1	0.87	0.12	57,57,57,57	0
58	MG	2A	3289	1/1	0.87	0.11	48,48,48,48	0
58	MG	1A	3875	1/1	0.87	0.10	42,42,42,42	0
58	MG	1A	3577	1/1	0.87	0.20	53,53,53,53	0
58	MG	2A	3124	1/1	0.87	0.18	72,72,72,72	0
58	MG	1a	1806	1/1	0.87	0.31	54,54,54,54	0
58	MG	28	102	1/1	0.87	0.23	69,69,69,69	0
58	MG	2A	3141	1/1	0.87	0.13	51,51,51,51	0
58	MG	1A	3451	1/1	0.88	0.23	43,43,43,43	0
58	MG	1a	1661	1/1	0.88	0.16	69,69,69,69	0
58	MG	2A	3042	1/1	0.88	0.20	53,53,53,53	0
58	MG	1A	3874	1/1	0.88	0.09	23,23,23,23	0
58	MG	1A	3571	1/1	0.88	0.10	40,40,40,40	0
58	MG	2A	3049	1/1	0.88	0.15	63,63,63,63	0
58	MG	1A	3339	1/1	0.88	0.15	60,60,60,60	0
58	MG	1A	3024	1/1	0.88	0.24	55,55,55,55	0
58	MG	2A	3571	1/1	0.88	0.19	66,66,66,66	0
58	MG	2a	3019	1/1	0.88	0.13	59,59,59,59	0
58	MG	1A	3277	1/1	0.88	0.17	61,61,61,61	0
58	MG	2A	3061	1/1	0.88	0.17	52,52,52,52	0
58	MG	1a	1681	1/1	0.88	0.17	63,63,63,63	0
58	MG	1A	3891	1/1	0.88	0.17	51,51,51,51	0
58	MG	1A	3703	1/1	0.88	0.11	45,45,45,45	0
58	MG	1A	3911	1/1	0.88	0.14	68,68,68,68	0
58	MG	1a	1693	1/1	0.88	0.22	57,57,57,57	0
58	MG	1A	3713	1/1	0.88	0.10	72,72,72,72	0
58	MG	2A	3623	1/1	0.88	0.21	61,61,61,61	0
58	MG	1D	302	1/1	0.88	0.36	54,54,54,54	0
58	MG	2A	3630	1/1	0.88	0.16	56,56,56,56	0
58	MG	2A	3631	1/1	0.88	0.19	69,69,69,69	0
58	MG	2A	3297	1/1	0.88	0.18	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1D	306	1/1	0.88	0.10	35,35,35,35	0
58	MG	1A	3154	1/1	0.88	0.14	43,43,43,43	0
58	MG	2A	3304	1/1	0.88	0.15	63,63,63,63	0
58	MG	1F	308	1/1	0.88	0.09	44,44,44,44	0
58	MG	1F	311	1/1	0.88	0.11	47,47,47,47	0
58	MG	1A	3928	1/1	0.88	0.16	24,24,24,24	0
58	MG	1A	3463	1/1	0.88	0.15	46,46,46,46	0
58	MG	1A	3469	1/1	0.88	0.17	48,48,48,48	0
58	MG	1A	3598	1/1	0.88	0.10	17,17,17,17	0
58	MG	2A	3652	1/1	0.88	0.18	56,56,56,56	0
58	MG	1A	3302	1/1	0.88	0.14	37,37,37,37	0
58	MG	2a	3069	1/1	0.88	0.20	69,69,69,69	0
58	MG	2A	3109	1/1	0.88	0.17	48,48,48,48	0
58	MG	1V	203	1/1	0.88	0.75	36,36,36,36	0
58	MG	2a	3072	1/1	0.88	0.12	50,50,50,50	0
58	MG	1A	3311	1/1	0.88	0.12	39,39,39,39	0
58	MG	2a	3083	1/1	0.88	0.24	61,61,61,61	0
58	MG	2A	3671	1/1	0.88	0.08	65,65,65,65	0
58	MG	2A	3692	1/1	0.88	0.15	53,53,53,53	0
58	MG	1a	1750	1/1	0.88	0.18	65,65,65,65	0
58	MG	2A	3698	1/1	0.88	0.17	60,60,60,60	0
58	MG	1A	3315	1/1	0.88	0.11	53,53,53,53	0
58	MG	1A	3222	1/1	0.88	0.16	37,37,37,37	0
58	MG	2A	3348	1/1	0.88	0.16	65,65,65,65	0
58	MG	1A	3959	1/1	0.88	0.12	42,42,42,42	0
58	MG	2A	3358	1/1	0.88	0.10	66,66,66,66	0
58	MG	2a	3099	1/1	0.88	0.13	75,75,75,75	0
58	MG	1A	3075	1/1	0.88	0.14	57,57,57,57	0
58	MG	2A	3362	1/1	0.88	0.10	58,58,58,58	0
58	MG	1A	3399	1/1	0.88	0.14	55,55,55,55	0
58	MG	2A	3156	1/1	0.88	0.11	52,52,52,52	0
58	MG	13	104	1/1	0.88	0.16	58,58,58,58	0
58	MG	2A	3159	1/1	0.88	0.15	74,74,74,74	0
58	MG	2A	3161	1/1	0.88	0.18	76,76,76,76	0
58	MG	1A	3249	1/1	0.88	0.11	51,51,51,51	0
58	MG	2a	3123	1/1	0.88	0.27	56,56,56,56	0
58	MG	2A	3175	1/1	0.88	0.23	60,60,60,60	0
58	MG	2A	3740	1/1	0.88	0.10	72,72,72,72	0
58	MG	2A	3179	1/1	0.88	0.10	51,51,51,51	0
58	MG	1A	3979	1/1	0.88	0.10	20,20,20,20	0
58	MG	18	102	1/1	0.88	0.08	36,36,36,36	0
58	MG	2A	3183	1/1	0.88	0.14	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1793	1/1	0.88	0.18	55,55,55,55	0
58	MG	1a	1794	1/1	0.88	0.18	53,53,53,53	0
58	MG	2A	3757	1/1	0.88	0.16	72,72,72,72	0
58	MG	1A	3322	1/1	0.88	0.13	53,53,53,53	0
58	MG	1A	3981	1/1	0.88	0.13	39,39,39,39	0
58	MG	2A	3767	1/1	0.88	0.16	67,67,67,67	0
58	MG	2a	3158	1/1	0.88	0.28	77,77,77,77	0
58	MG	2A	3412	1/1	0.88	0.24	46,46,46,46	0
58	MG	1A	3533	1/1	0.88	0.10	55,55,55,55	0
58	MG	1A	3251	1/1	0.88	0.15	49,49,49,49	0
58	MG	2a	3169	1/1	0.88	0.27	57,57,57,57	0
58	MG	1A	4010	1/1	0.88	0.16	42,42,42,42	0
58	MG	2A	3211	1/1	0.88	0.22	57,57,57,57	0
58	MG	1n	101	1/1	0.88	0.31	57,57,57,57	0
58	MG	1A	3197	1/1	0.88	0.21	50,50,50,50	0
58	MG	2A	3445	1/1	0.88	0.21	55,55,55,55	0
58	MG	1A	3840	1/1	0.88	0.14	63,63,63,63	0
58	MG	1A	3846	1/1	0.88	0.26	40,40,40,40	0
58	MG	1w	102	1/1	0.88	0.10	78,78,78,78	0
58	MG	1A	3852	1/1	0.88	0.11	43,43,43,43	0
58	MG	1x	105	1/1	0.88	0.25	63,63,63,63	0
58	MG	2A	3463	1/1	0.88	0.26	60,60,60,60	0
58	MG	2A	3813	1/1	0.88	0.09	53,53,53,53	0
58	MG	2a	3187	1/1	0.88	0.29	68,68,68,68	0
58	MG	2a	3188	1/1	0.88	0.26	61,61,61,61	0
58	MG	1a	1628	1/1	0.88	0.13	64,64,64,64	0
58	MG	1a	1630	1/1	0.88	0.11	45,45,45,45	0
58	MG	1A	4029	1/1	0.88	0.16	46,46,46,46	0
58	MG	2A	3001	1/1	0.88	0.30	53,53,53,53	0
58	MG	1A	3853	1/1	0.88	0.09	49,49,49,49	0
58	MG	2A	3005	1/1	0.88	0.16	56,56,56,56	0
58	MG	2A	3006	1/1	0.88	0.16	39,39,39,39	0
58	MG	1A	3112	1/1	0.88	0.10	32,32,32,32	0
58	MG	2A	3490	1/1	0.88	0.18	59,59,59,59	0
58	MG	2A	3498	1/1	0.88	0.11	49,49,49,49	0
58	MG	1A	3864	1/1	0.88	0.14	45,45,45,45	0
58	MG	1a	1641	1/1	0.88	0.14	51,51,51,51	0
58	MG	2B	219	1/1	0.88	0.13	65,65,65,65	0
58	MG	1A	3866	1/1	0.88	0.12	30,30,30,30	0
58	MG	2A	3027	1/1	0.88	0.12	45,45,45,45	0
58	MG	1a	1644	1/1	0.88	0.24	66,66,66,66	0
58	MG	2O	201	1/1	0.88	0.22	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3267	1/1	0.88	0.23	62,62,62,62	0
58	MG	2T	202	1/1	0.88	0.23	70,70,70,70	0
58	MG	1A	3449	1/1	0.88	0.27	55,55,55,55	0
58	MG	2x	101	1/1	0.88	0.24	66,66,66,66	0
58	MG	2A	3539	1/1	0.88	0.16	46,46,46,46	0
58	MG	1A	4080	1/1	0.88	0.16	41,41,41,41	0
58	MG	2a	3031	1/1	0.89	0.30	58,58,58,58	0
58	MG	2A	3664	1/1	0.89	0.20	67,67,67,67	0
58	MG	1A	3129	1/1	0.89	0.15	33,33,33,33	0
58	MG	2A	3404	1/1	0.89	0.18	52,52,52,52	0
58	MG	2A	3683	1/1	0.89	0.09	65,65,65,65	0
58	MG	2A	3689	1/1	0.89	0.10	59,59,59,59	0
58	MG	11	102	1/1	0.89	0.14	56,56,56,56	0
58	MG	2a	3039	1/1	0.89	0.24	61,61,61,61	0
58	MG	1A	3181	1/1	0.89	0.22	34,34,34,34	0
58	MG	1A	3089	1/1	0.89	0.23	37,37,37,37	0
58	MG	2A	3701	1/1	0.89	0.24	45,45,45,45	0
58	MG	2a	3043	1/1	0.89	0.30	56,56,56,56	0
58	MG	2A	3702	1/1	0.89	0.15	62,62,62,62	0
58	MG	1A	3134	1/1	0.89	0.11	44,44,44,44	0
58	MG	1A	3592	1/1	0.89	0.12	39,39,39,39	0
58	MG	1A	4035	1/1	0.89	0.10	48,48,48,48	0
58	MG	2A	3055	1/1	0.89	0.17	54,54,54,54	0
58	MG	2A	3416	1/1	0.89	0.28	46,46,46,46	0
58	MG	2a	3056	1/1	0.89	0.17	51,51,51,51	0
58	MG	1A	4038	1/1	0.89	0.10	34,34,34,34	0
58	MG	2a	3061	1/1	0.89	0.15	63,63,63,63	0
58	MG	2A	3423	1/1	0.89	0.22	40,40,40,40	0
58	MG	2A	3426	1/1	0.89	0.25	57,57,57,57	0
58	MG	2a	3066	1/1	0.89	0.25	69,69,69,69	0
58	MG	2a	3068	1/1	0.89	0.11	76,76,76,76	0
58	MG	1A	3877	1/1	0.89	0.13	52,52,52,52	0
58	MG	1A	3259	1/1	0.89	0.14	54,54,54,54	0
58	MG	2A	3442	1/1	0.89	0.11	41,41,41,41	0
58	MG	2A	3063	1/1	0.89	0.18	49,49,49,49	0
58	MG	2a	3078	1/1	0.89	0.22	65,65,65,65	0
58	MG	1a	1609	1/1	0.89	0.15	57,57,57,57	0
58	MG	1A	3733	1/1	0.89	0.16	59,59,59,59	0
58	MG	1A	3059	1/1	0.89	0.12	39,39,39,39	0
58	MG	2A	3073	1/1	0.89	0.12	42,42,42,42	0
58	MG	1a	1759	1/1	0.89	0.08	58,58,58,58	0
58	MG	1A	4074	1/1	0.89	0.19	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3747	1/1	0.89	0.10	56,56,56,56	0
58	MG	2A	3082	1/1	0.89	0.18	75,75,75,75	0
58	MG	1A	3887	1/1	0.89	0.13	48,48,48,48	0
58	MG	2A	3753	1/1	0.89	0.13	57,57,57,57	0
58	MG	1a	1624	1/1	0.89	0.23	52,52,52,52	0
58	MG	1A	3263	1/1	0.89	0.19	56,56,56,56	0
58	MG	2A	3091	1/1	0.89	0.14	60,60,60,60	0
58	MG	2A	3759	1/1	0.89	0.13	65,65,65,65	0
58	MG	2a	3103	1/1	0.89	0.17	68,68,68,68	0
58	MG	2a	3104	1/1	0.89	0.11	60,60,60,60	0
58	MG	2A	3478	1/1	0.89	0.07	61,61,61,61	0
58	MG	1A	3418	1/1	0.89	0.21	55,55,55,55	0
58	MG	2a	3112	1/1	0.89	0.25	53,53,53,53	0
58	MG	1a	1629	1/1	0.89	0.22	52,52,52,52	0
58	MG	1a	1783	1/1	0.89	0.12	66,66,66,66	0
58	MG	2a	3119	1/1	0.89	0.40	71,71,71,71	0
58	MG	2A	3099	1/1	0.89	0.16	44,44,44,44	0
58	MG	1a	1787	1/1	0.89	0.17	65,65,65,65	0
58	MG	1A	3607	1/1	0.89	0.09	39,39,39,39	0
58	MG	1A	3054	1/1	0.89	0.11	52,52,52,52	0
58	MG	2a	3125	1/1	0.89	0.21	61,61,61,61	0
58	MG	2a	3126	1/1	0.89	0.20	47,47,47,47	0
58	MG	1B	211	1/1	0.89	0.15	58,58,58,58	0
58	MG	2A	3286	1/1	0.89	0.17	70,70,70,70	0
58	MG	1A	3625	1/1	0.89	0.12	48,48,48,48	0
58	MG	2A	3515	1/1	0.89	0.10	40,40,40,40	0
58	MG	2A	3113	1/1	0.89	0.11	68,68,68,68	0
58	MG	1B	215	1/1	0.89	0.16	67,67,67,67	0
58	MG	2a	3134	1/1	0.89	0.23	69,69,69,69	0
58	MG	1A	3626	1/1	0.89	0.12	59,59,59,59	0
58	MG	1A	3798	1/1	0.89	0.12	25,25,25,25	0
58	MG	1A	3325	1/1	0.89	0.26	48,48,48,48	0
58	MG	2a	3144	1/1	0.89	0.11	58,58,58,58	0
58	MG	1A	3934	1/1	0.89	0.09	56,56,56,56	0
58	MG	1A	3803	1/1	0.89	0.11	49,49,49,49	0
58	MG	2a	3154	1/1	0.89	0.21	75,75,75,75	0
58	MG	1A	3329	1/1	0.89	0.20	51,51,51,51	0
58	MG	1A	3509	1/1	0.89	0.08	49,49,49,49	0
58	MG	1A	3948	1/1	0.89	0.09	48,48,48,48	0
58	MG	2A	3558	1/1	0.89	0.20	63,63,63,63	0
58	MG	2a	3166	1/1	0.89	0.13	61,61,61,61	0
58	MG	1x	101	1/1	0.89	0.27	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1x	103	1/1	0.89	0.15	56,56,56,56	0
58	MG	1a	1663	1/1	0.89	0.13	66,66,66,66	0
58	MG	2A	3163	1/1	0.89	0.07	43,43,43,43	0
58	MG	2B	210	1/1	0.89	0.14	63,63,63,63	0
58	MG	2A	3164	1/1	0.89	0.13	68,68,68,68	0
58	MG	2B	214	1/1	0.89	0.26	66,66,66,66	0
58	MG	2A	3314	1/1	0.89	0.10	58,58,58,58	0
58	MG	1a	1664	1/1	0.89	0.16	58,58,58,58	0
58	MG	1A	3426	1/1	0.89	0.10	55,55,55,55	0
58	MG	2D	308	1/1	0.89	0.20	53,53,53,53	0
58	MG	2A	3592	1/1	0.89	0.15	56,56,56,56	0
58	MG	1a	1668	1/1	0.89	0.14	52,52,52,52	0
58	MG	2F	306	1/1	0.89	0.14	64,64,64,64	0
58	MG	2G	201	1/1	0.89	0.26	67,67,67,67	0
58	MG	1A	3522	1/1	0.89	0.29	64,64,64,64	0
58	MG	2A	3338	1/1	0.89	0.09	58,58,58,58	0
58	MG	1A	3162	1/1	0.89	0.44	31,31,31,31	0
58	MG	2A	3345	1/1	0.89	0.27	74,74,74,74	0
58	MG	1A	3542	1/1	0.89	0.15	37,37,37,37	0
58	MG	1A	3829	1/1	0.89	0.11	54,54,54,54	0
58	MG	1A	3084	1/1	0.89	0.17	36,36,36,36	0
58	MG	2A	3187	1/1	0.89	0.21	54,54,54,54	0
58	MG	2a	3203	1/1	0.89	0.19	62,62,62,62	0
58	MG	2A	3188	1/1	0.89	0.20	56,56,56,56	0
58	MG	1A	3335	1/1	0.89	0.15	38,38,38,38	0
58	MG	1A	3169	1/1	0.89	0.17	56,56,56,56	0
58	MG	1A	3450	1/1	0.89	0.11	37,37,37,37	0
58	MG	2a	3008	1/1	0.89	0.25	64,64,64,64	0
58	MG	2a	3211	1/1	0.89	0.18	68,68,68,68	0
58	MG	2A	3204	1/1	0.89	0.25	56,56,56,56	0
58	MG	1A	3985	1/1	0.89	0.12	63,63,63,63	0
58	MG	1A	3300	1/1	0.89	0.10	33,33,33,33	0
58	MG	1A	3861	1/1	0.89	0.30	40,40,40,40	0
58	MG	2t	201	1/1	0.89	0.19	49,49,49,49	0
58	MG	2A	3650	1/1	0.89	0.10	45,45,45,45	0
58	MG	1A	3356	1/1	0.89	0.11	48,48,48,48	0
58	MG	1a	1703	1/1	0.89	0.09	57,57,57,57	0
58	MG	2A	3038	1/1	0.89	0.14	61,61,61,61	0
58	MG	2A	3398	1/1	0.89	0.21	51,51,51,51	0
58	MG	1A	3228	1/1	0.89	0.08	38,38,38,38	0
58	MG	2a	3016	1/1	0.90	0.12	61,61,61,61	0
58	MG	1A	3099	1/1	0.90	0.20	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3621	1/1	0.90	0.13	53,53,53,53	0
58	MG	1X	105	1/1	0.90	0.08	43,43,43,43	0
58	MG	1A	3807	1/1	0.90	0.09	23,23,23,23	0
58	MG	2A	3608	1/1	0.90	0.14	37,37,37,37	0
58	MG	2A	3306	1/1	0.90	0.12	55,55,55,55	0
58	MG	1A	3489	1/1	0.90	0.08	58,58,58,58	0
58	MG	2A	3110	1/1	0.90	0.29	62,62,62,62	0
58	MG	1A	3491	1/1	0.90	0.16	52,52,52,52	0
58	MG	2a	3029	1/1	0.90	0.18	73,73,73,73	0
58	MG	2A	3117	1/1	0.90	0.10	67,67,67,67	0
58	MG	1a	1771	1/1	0.90	0.20	75,75,75,75	0
58	MG	2a	3033	1/1	0.90	0.18	75,75,75,75	0
58	MG	1A	3400	1/1	0.90	0.15	56,56,56,56	0
58	MG	1A	3001	1/1	0.90	0.08	30,30,30,30	0
58	MG	2A	3138	1/1	0.90	0.24	52,52,52,52	0
58	MG	1A	3132	1/1	0.90	0.10	33,33,33,33	0
58	MG	1A	3827	1/1	0.90	0.09	36,36,36,36	0
58	MG	2A	3644	1/1	0.90	0.14	41,41,41,41	0
58	MG	2A	3146	1/1	0.90	0.22	54,54,54,54	0
58	MG	2A	3335	1/1	0.90	0.11	46,46,46,46	0
58	MG	1a	1785	1/1	0.90	0.20	61,61,61,61	0
58	MG	1A	3107	1/1	0.90	0.14	52,52,52,52	0
58	MG	1A	3990	1/1	0.90	0.11	26,26,26,26	0
58	MG	1A	3995	1/1	0.90	0.11	40,40,40,40	0
58	MG	2a	3047	1/1	0.90	0.14	64,64,64,64	0
58	MG	1A	3830	1/1	0.90	0.10	72,72,72,72	0
58	MG	2A	3351	1/1	0.90	0.18	60,60,60,60	0
58	MG	2A	3353	1/1	0.90	0.16	56,56,56,56	0
58	MG	1A	3832	1/1	0.90	0.09	53,53,53,53	0
58	MG	1a	1800	1/1	0.90	0.31	66,66,66,66	0
58	MG	1a	1801	1/1	0.90	0.16	73,73,73,73	0
58	MG	2A	3667	1/1	0.90	0.08	71,71,71,71	0
58	MG	2A	3668	1/1	0.90	0.14	63,63,63,63	0
58	MG	1A	3647	1/1	0.90	0.09	22,22,22,22	0
58	MG	2A	3681	1/1	0.90	0.17	64,64,64,64	0
58	MG	2A	3363	1/1	0.90	0.12	71,71,71,71	0
58	MG	2A	3684	1/1	0.90	0.07	71,71,71,71	0
58	MG	2A	3168	1/1	0.90	0.09	64,64,64,64	0
58	MG	1A	3264	1/1	0.90	0.12	64,64,64,64	0
58	MG	2A	3173	1/1	0.90	0.09	31,31,31,31	0
58	MG	2a	3077	1/1	0.90	0.18	65,65,65,65	0
58	MG	1A	3657	1/1	0.90	0.07	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	4022	1/1	0.90	0.17	46,46,46,46	0
58	MG	1a	1622	1/1	0.90	0.08	56,56,56,56	0
58	MG	2A	3385	1/1	0.90	0.12	62,62,62,62	0
58	MG	1A	3227	1/1	0.90	0.17	51,51,51,51	0
58	MG	1A	3524	1/1	0.90	0.12	41,41,41,41	0
58	MG	2a	3088	1/1	0.90	0.09	45,45,45,45	0
58	MG	1A	3856	1/1	0.90	0.09	39,39,39,39	0
58	MG	2a	3091	1/1	0.90	0.11	62,62,62,62	0
58	MG	2A	3393	1/1	0.90	0.21	46,46,46,46	0
58	MG	1A	3141	1/1	0.90	0.11	18,18,18,18	0
58	MG	1w	105	1/1	0.90	0.14	80,80,80,80	0
58	MG	1A	3432	1/1	0.90	0.26	38,38,38,38	0
58	MG	1A	4046	1/1	0.90	0.08	41,41,41,41	0
58	MG	2A	3720	1/1	0.90	0.23	50,50,50,50	0
58	MG	2A	3193	1/1	0.90	0.22	63,63,63,63	0
58	MG	2A	3194	1/1	0.90	0.10	55,55,55,55	0
58	MG	1A	4048	1/1	0.90	0.14	50,50,50,50	0
58	MG	2A	3196	1/1	0.90	0.15	50,50,50,50	0
58	MG	2A	3411	1/1	0.90	0.11	45,45,45,45	0
58	MG	2A	3199	1/1	0.90	0.16	69,69,69,69	0
58	MG	2a	3111	1/1	0.90	0.07	79,79,79,79	0
58	MG	1A	3271	1/1	0.90	0.14	45,45,45,45	0
58	MG	1A	4064	1/1	0.90	0.09	48,48,48,48	0
58	MG	1A	3867	1/1	0.90	0.13	68,68,68,68	0
58	MG	2A	3745	1/1	0.90	0.09	55,55,55,55	0
58	MG	1A	3235	1/1	0.90	0.10	54,54,54,54	0
58	MG	1A	3288	1/1	0.90	0.11	37,37,37,37	0
58	MG	1A	3552	1/1	0.90	0.07	44,44,44,44	0
58	MG	1A	3237	1/1	0.90	0.14	55,55,55,55	0
58	MG	2A	3430	1/1	0.90	0.13	56,56,56,56	0
58	MG	2A	3435	1/1	0.90	0.07	57,57,57,57	0
58	MG	1A	4079	1/1	0.90	0.11	40,40,40,40	0
58	MG	1A	3297	1/1	0.90	0.26	46,46,46,46	0
58	MG	1A	3452	1/1	0.90	0.14	40,40,40,40	0
58	MG	2A	3764	1/1	0.90	0.12	62,62,62,62	0
58	MG	1A	3454	1/1	0.90	0.14	58,58,58,58	0
58	MG	2A	3023	1/1	0.90	0.16	50,50,50,50	0
58	MG	1A	3149	1/1	0.90	0.27	28,28,28,28	0
58	MG	1A	3098	1/1	0.90	0.11	39,39,39,39	0
58	MG	1A	3714	1/1	0.90	0.13	55,55,55,55	0
58	MG	2A	3456	1/1	0.90	0.13	51,51,51,51	0
58	MG	1A	3888	1/1	0.90	0.09	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3793	1/1	0.90	0.12	68,68,68,68	0
58	MG	1A	3575	1/1	0.90	0.26	63,63,63,63	0
58	MG	2a	3152	1/1	0.90	0.10	60,60,60,60	0
58	MG	1A	3892	1/1	0.90	0.35	36,36,36,36	0
58	MG	2a	3155	1/1	0.90	0.12	61,61,61,61	0
58	MG	2a	3156	1/1	0.90	0.10	67,67,67,67	0
58	MG	2A	3467	1/1	0.90	0.07	60,60,60,60	0
58	MG	1a	1674	1/1	0.90	0.12	50,50,50,50	0
58	MG	1A	3250	1/1	0.90	0.21	35,35,35,35	0
58	MG	2A	3472	1/1	0.90	0.17	54,54,54,54	0
58	MG	2A	3247	1/1	0.90	0.08	70,70,70,70	0
58	MG	1A	3749	1/1	0.90	0.08	16,16,16,16	0
58	MG	1A	3460	1/1	0.90	0.16	45,45,45,45	0
58	MG	2A	3814	1/1	0.90	0.14	61,61,61,61	0
58	MG	1A	3918	1/1	0.90	0.08	42,42,42,42	0
58	MG	1a	1685	1/1	0.90	0.26	39,39,39,39	0
58	MG	1B	234	1/1	0.90	0.12	58,58,58,58	0
58	MG	2A	3256	1/1	0.90	0.20	59,59,59,59	0
58	MG	2A	3493	1/1	0.90	0.13	65,65,65,65	0
58	MG	1a	1689	1/1	0.90	0.28	53,53,53,53	0
58	MG	2A	3501	1/1	0.90	0.13	53,53,53,53	0
58	MG	1B	235	1/1	0.90	0.10	50,50,50,50	0
58	MG	2A	3263	1/1	0.90	0.08	51,51,51,51	0
58	MG	1A	3582	1/1	0.90	0.24	60,60,60,60	0
58	MG	1a	1694	1/1	0.90	0.41	67,67,67,67	0
58	MG	1A	3768	1/1	0.90	0.15	54,54,54,54	0
58	MG	1E	301	1/1	0.90	0.20	43,43,43,43	0
58	MG	1E	305	1/1	0.90	0.10	59,59,59,59	0
58	MG	1A	3590	1/1	0.90	0.20	47,47,47,47	0
58	MG	2A	3536	1/1	0.90	0.15	38,38,38,38	0
58	MG	1E	312	1/1	0.90	0.07	51,51,51,51	0
58	MG	2A	3072	1/1	0.90	0.39	63,63,63,63	0
58	MG	1F	306	1/1	0.90	0.15	27,27,27,27	0
58	MG	2a	3200	1/1	0.90	0.17	61,61,61,61	0
58	MG	1A	3124	1/1	0.90	0.28	33,33,33,33	0
58	MG	1A	3788	1/1	0.90	0.10	53,53,53,53	0
58	MG	1a	1719	1/1	0.90	0.13	41,41,41,41	0
58	MG	1A	3253	1/1	0.90	0.09	69,69,69,69	0
58	MG	1A	3319	1/1	0.90	0.13	42,42,42,42	0
58	MG	1A	3385	1/1	0.90	0.08	47,47,47,47	0
58	MG	1A	3254	1/1	0.90	0.11	45,45,45,45	0
58	MG	2A	3568	1/1	0.90	0.15	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2g	201	1/1	0.90	0.19	76,76,76,76	0
58	MG	2A	3290	1/1	0.90	0.13	53,53,53,53	0
58	MG	2k	201	1/1	0.90	0.10	73,73,73,73	0
58	MG	1U	205	1/1	0.90	0.25	45,45,45,45	0
58	MG	2A	3579	1/1	0.90	0.10	24,24,24,24	0
58	MG	2l	203	1/1	0.90	0.14	74,74,74,74	0
58	MG	1A	3949	1/1	0.90	0.09	43,43,43,43	0
58	MG	2A	3582	1/1	0.90	0.21	61,61,61,61	0
58	MG	1A	3952	1/1	0.90	0.11	32,32,32,32	0
58	MG	1A	3394	1/1	0.90	0.16	44,44,44,44	0
58	MG	2A	3589	1/1	0.90	0.11	71,71,71,71	0
58	MG	2a	3011	1/1	0.90	0.29	63,63,63,63	0
58	MG	2a	3012	1/1	0.90	0.30	71,71,71,71	0
58	MG	2a	3015	1/1	0.90	0.19	70,70,70,70	0
59	K	2A	3418	1/1	0.90	0.12	74,74,74,74	0
61	ZN	24	501	1/1	0.90	0.14	128,128,128,128	0
58	MG	1A	3600	1/1	0.91	0.07	30,30,30,30	0
58	MG	2A	3600	1/1	0.91	0.11	46,46,46,46	0
58	MG	2A	3602	1/1	0.91	0.11	55,55,55,55	0
58	MG	1A	3256	1/1	0.91	0.14	46,46,46,46	0
58	MG	1A	3715	1/1	0.91	0.09	60,60,60,60	0
58	MG	2A	3320	1/1	0.91	0.19	63,63,63,63	0
58	MG	2A	3322	1/1	0.91	0.16	59,59,59,59	0
58	MG	2A	3620	1/1	0.91	0.18	51,51,51,51	0
58	MG	1A	3608	1/1	0.91	0.14	77,77,77,77	0
58	MG	2A	3152	1/1	0.91	0.10	45,45,45,45	0
58	MG	2A	3332	1/1	0.91	0.15	67,67,67,67	0
58	MG	2A	3333	1/1	0.91	0.10	62,62,62,62	0
58	MG	1A	3967	1/1	0.91	0.10	27,27,27,27	0
58	MG	2A	3336	1/1	0.91	0.07	61,61,61,61	0
58	MG	1A	3859	1/1	0.91	0.17	40,40,40,40	0
58	MG	1B	228	1/1	0.91	0.13	60,60,60,60	0
58	MG	2A	3343	1/1	0.91	0.21	53,53,53,53	0
58	MG	1A	3727	1/1	0.91	0.10	58,58,58,58	0
58	MG	2A	3160	1/1	0.91	0.28	51,51,51,51	0
58	MG	1b	301	1/1	0.91	0.15	71,71,71,71	0
58	MG	1A	3974	1/1	0.91	0.13	53,53,53,53	0
58	MG	1A	3312	1/1	0.91	0.13	54,54,54,54	0
58	MG	1a	1642	1/1	0.91	0.11	73,73,73,73	0
58	MG	1v	101	1/1	0.91	0.11	76,76,76,76	0
58	MG	2A	3359	1/1	0.91	0.09	55,55,55,55	0
58	MG	1A	3738	1/1	0.91	0.08	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3011	1/1	0.91	0.09	37,37,37,37	0
58	MG	2A	3662	1/1	0.91	0.15	59,59,59,59	0
58	MG	1a	1645	1/1	0.91	0.19	50,50,50,50	0
58	MG	2A	3180	1/1	0.91	0.26	69,69,69,69	0
58	MG	1A	3623	1/1	0.91	0.10	23,23,23,23	0
58	MG	2a	3055	1/1	0.91	0.26	60,60,60,60	0
58	MG	1D	312	1/1	0.91	0.10	35,35,35,35	0
58	MG	2A	3373	1/1	0.91	0.22	53,53,53,53	0
58	MG	1A	3398	1/1	0.91	0.10	39,39,39,39	0
58	MG	2a	3062	1/1	0.91	0.24	57,57,57,57	0
58	MG	2A	3673	1/1	0.91	0.17	65,65,65,65	0
58	MG	2A	3378	1/1	0.91	0.21	55,55,55,55	0
58	MG	1A	3273	1/1	0.91	0.13	35,35,35,35	0
58	MG	1x	106	1/1	0.91	0.20	49,49,49,49	0
58	MG	1A	3994	1/1	0.91	0.07	34,34,34,34	0
58	MG	1E	310	1/1	0.91	0.14	59,59,59,59	0
58	MG	2A	3693	1/1	0.91	0.12	54,54,54,54	0
58	MG	2A	3189	1/1	0.91	0.17	60,60,60,60	0
58	MG	2a	3073	1/1	0.91	0.09	64,64,64,64	0
58	MG	2a	3076	1/1	0.91	0.21	62,62,62,62	0
58	MG	2A	3191	1/1	0.91	0.13	57,57,57,57	0
58	MG	1E	311	1/1	0.91	0.20	51,51,51,51	0
58	MG	2A	3395	1/1	0.91	0.35	66,66,66,66	0
58	MG	2A	3705	1/1	0.91	0.09	47,47,47,47	0
58	MG	1A	3776	1/1	0.91	0.10	24,24,24,24	0
58	MG	1A	3343	1/1	0.91	0.14	39,39,39,39	0
58	MG	1A	3409	1/1	0.91	0.15	66,66,66,66	0
58	MG	1a	1671	1/1	0.91	0.26	70,70,70,70	0
58	MG	1A	3410	1/1	0.91	0.09	54,54,54,54	0
58	MG	1A	3643	1/1	0.91	0.17	35,35,35,35	0
58	MG	1P	206	1/1	0.91	0.13	56,56,56,56	0
58	MG	2A	3014	1/1	0.91	0.17	47,47,47,47	0
58	MG	2A	3718	1/1	0.91	0.21	54,54,54,54	0
58	MG	1A	3555	1/1	0.91	0.09	29,29,29,29	0
58	MG	1a	1679	1/1	0.91	0.17	60,60,60,60	0
58	MG	2A	3217	1/1	0.91	0.15	28,28,28,28	0
58	MG	1P	208	1/1	0.91	0.14	37,37,37,37	0
58	MG	2A	3028	1/1	0.91	0.17	78,78,78,78	0
58	MG	1Q	201	1/1	0.91	0.23	38,38,38,38	0
58	MG	1A	3413	1/1	0.91	0.25	54,54,54,54	0
58	MG	2A	3736	1/1	0.91	0.13	47,47,47,47	0
58	MG	1A	3349	1/1	0.91	0.13	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1687	1/1	0.91	0.28	51,51,51,51	0
58	MG	2A	3429	1/1	0.91	0.24	49,49,49,49	0
58	MG	1A	4027	1/1	0.91	0.09	47,47,47,47	0
58	MG	2A	3433	1/1	0.91	0.13	65,65,65,65	0
58	MG	2a	3118	1/1	0.91	0.15	57,57,57,57	0
58	MG	1A	3200	1/1	0.91	0.15	41,41,41,41	0
58	MG	2A	3438	1/1	0.91	0.11	60,60,60,60	0
58	MG	2A	3439	1/1	0.91	0.14	45,45,45,45	0
58	MG	1A	3471	1/1	0.91	0.08	44,44,44,44	0
58	MG	2A	3441	1/1	0.91	0.07	50,50,50,50	0
58	MG	1A	4032	1/1	0.91	0.16	51,51,51,51	0
58	MG	1A	3286	1/1	0.91	0.13	47,47,47,47	0
58	MG	2A	3235	1/1	0.91	0.08	55,55,55,55	0
58	MG	2A	3236	1/1	0.91	0.10	57,57,57,57	0
58	MG	2A	3762	1/1	0.91	0.10	41,41,41,41	0
58	MG	1A	3898	1/1	0.91	0.22	28,28,28,28	0
58	MG	2A	3241	1/1	0.91	0.16	62,62,62,62	0
58	MG	1A	3260	1/1	0.91	0.22	39,39,39,39	0
58	MG	2A	3774	1/1	0.91	0.10	30,30,30,30	0
58	MG	2A	3243	1/1	0.91	0.14	48,48,48,48	0
58	MG	1A	3364	1/1	0.91	0.31	51,51,51,51	0
58	MG	2A	3780	1/1	0.91	0.17	53,53,53,53	0
58	MG	2A	3461	1/1	0.91	0.17	52,52,52,52	0
58	MG	1A	4052	1/1	0.91	0.06	27,27,27,27	0
58	MG	2A	3054	1/1	0.91	0.17	58,58,58,58	0
58	MG	2a	3148	1/1	0.91	0.21	52,52,52,52	0
58	MG	1a	1707	1/1	0.91	0.23	54,54,54,54	0
58	MG	1a	1708	1/1	0.91	0.13	60,60,60,60	0
58	MG	2A	3059	1/1	0.91	0.12	58,58,58,58	0
58	MG	10	104	1/1	0.91	0.24	39,39,39,39	0
58	MG	10	105	1/1	0.91	0.13	44,44,44,44	0
58	MG	1A	3427	1/1	0.91	0.12	66,66,66,66	0
58	MG	10	109	1/1	0.91	0.11	48,48,48,48	0
58	MG	10	110	1/1	0.91	0.12	47,47,47,47	0
58	MG	1A	3684	1/1	0.91	0.07	26,26,26,26	0
58	MG	1A	3819	1/1	0.91	0.08	40,40,40,40	0
58	MG	1A	3488	1/1	0.91	0.05	57,57,57,57	0
58	MG	1a	1736	1/1	0.91	0.23	57,57,57,57	0
58	MG	15	105	1/1	0.91	0.07	56,56,56,56	0
58	MG	15	106	1/1	0.91	0.20	27,27,27,27	0
58	MG	1A	3430	1/1	0.91	0.12	43,43,43,43	0
58	MG	2A	3503	1/1	0.91	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	16	101	1/1	0.91	0.11	57,57,57,57	0
58	MG	2a	3180	1/1	0.91	0.17	71,71,71,71	0
58	MG	1a	1752	1/1	0.91	0.08	52,52,52,52	0
58	MG	2A	3089	1/1	0.91	0.12	52,52,52,52	0
58	MG	17	107	1/1	0.91	0.10	40,40,40,40	0
58	MG	1A	4069	1/1	0.91	0.10	56,56,56,56	0
58	MG	2A	3518	1/1	0.91	0.08	43,43,43,43	0
58	MG	2B	211	1/1	0.91	0.20	66,66,66,66	0
58	MG	2A	3521	1/1	0.91	0.16	62,62,62,62	0
58	MG	2A	3522	1/1	0.91	0.12	39,39,39,39	0
58	MG	1A	3115	1/1	0.91	0.11	39,39,39,39	0
58	MG	2A	3528	1/1	0.91	0.12	62,62,62,62	0
58	MG	2A	3284	1/1	0.91	0.09	56,56,56,56	0
58	MG	1A	4075	1/1	0.91	0.20	49,49,49,49	0
58	MG	1A	3295	1/1	0.91	0.15	52,52,52,52	0
58	MG	2E	307	1/1	0.91	0.17	59,59,59,59	0
58	MG	2a	3199	1/1	0.91	0.20	68,68,68,68	0
58	MG	2F	301	1/1	0.91	0.20	64,64,64,64	0
58	MG	1a	1765	1/1	0.91	0.14	64,64,64,64	0
58	MG	2A	3288	1/1	0.91	0.10	81,81,81,81	0
58	MG	1A	3072	1/1	0.91	0.11	20,20,20,20	0
58	MG	1a	1769	1/1	0.91	0.10	42,42,42,42	0
58	MG	1A	3133	1/1	0.91	0.09	43,43,43,43	0
58	MG	2Q	202	1/1	0.91	0.19	53,53,53,53	0
58	MG	2A	3292	1/1	0.91	0.08	44,44,44,44	0
58	MG	2V	202	1/1	0.91	0.21	55,55,55,55	0
58	MG	1a	1611	1/1	0.91	0.19	68,68,68,68	0
58	MG	1B	201	1/1	0.91	0.14	40,40,40,40	0
58	MG	1a	1777	1/1	0.91	0.13	48,48,48,48	0
58	MG	2A	3114	1/1	0.91	0.15	46,46,46,46	0
58	MG	1A	3837	1/1	0.91	0.13	34,34,34,34	0
58	MG	1A	3447	1/1	0.91	0.22	59,59,59,59	0
58	MG	2a	3003	1/1	0.91	0.07	72,72,72,72	0
58	MG	2a	3004	1/1	0.91	0.23	54,54,54,54	0
58	MG	1a	1619	1/1	0.91	0.20	53,53,53,53	0
58	MG	1A	3246	1/1	0.91	0.13	40,40,40,40	0
58	MG	2A	3127	1/1	0.91	0.14	53,53,53,53	0
58	MG	2A	3130	1/1	0.91	0.19	63,63,63,63	0
58	MG	2A	3132	1/1	0.91	0.15	64,64,64,64	0
58	MG	1a	1791	1/1	0.91	0.08	48,48,48,48	0
58	MG	2A	3139	1/1	0.91	0.10	41,41,41,41	0
58	MG	1A	3953	1/1	0.91	0.14	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3962	1/1	0.92	0.09	74,74,74,74	0
58	MG	2B	206	1/1	0.92	0.14	79,79,79,79	0
58	MG	2B	207	1/1	0.92	0.10	61,61,61,61	0
58	MG	2B	209	1/1	0.92	0.12	62,62,62,62	0
58	MG	10	111	1/1	0.92	0.07	44,44,44,44	0
58	MG	1A	3750	1/1	0.92	0.08	30,30,30,30	0
58	MG	11	103	1/1	0.92	0.10	36,36,36,36	0
58	MG	2B	213	1/1	0.92	0.15	64,64,64,64	0
58	MG	1A	3163	1/1	0.92	0.16	47,47,47,47	0
58	MG	2A	3464	1/1	0.92	0.20	51,51,51,51	0
58	MG	2B	216	1/1	0.92	0.12	59,59,59,59	0
58	MG	2B	217	1/1	0.92	0.11	72,72,72,72	0
58	MG	1A	3755	1/1	0.92	0.11	29,29,29,29	0
58	MG	2A	3210	1/1	0.92	0.22	42,42,42,42	0
58	MG	2D	304	1/1	0.92	0.22	48,48,48,48	0
58	MG	2D	305	1/1	0.92	0.24	67,67,67,67	0
58	MG	1f	202	1/1	0.92	0.08	65,65,65,65	0
58	MG	2E	302	1/1	0.92	0.08	54,54,54,54	0
58	MG	2E	304	1/1	0.92	0.09	50,50,50,50	0
58	MG	2A	3470	1/1	0.92	0.20	66,66,66,66	0
58	MG	2A	3212	1/1	0.92	0.17	59,59,59,59	0
58	MG	15	103	1/1	0.92	0.32	34,34,34,34	0
58	MG	1A	3757	1/1	0.92	0.09	36,36,36,36	0
58	MG	1A	3564	1/1	0.92	0.17	48,48,48,48	0
58	MG	1A	3278	1/1	0.92	0.12	37,37,37,37	0
58	MG	1A	3771	1/1	0.92	0.06	53,53,53,53	0
58	MG	2P	201	1/1	0.92	0.10	54,54,54,54	0
58	MG	16	102	1/1	0.92	0.25	57,57,57,57	0
58	MG	2A	3488	1/1	0.92	0.16	72,72,72,72	0
58	MG	1A	3344	1/1	0.92	0.23	54,54,54,54	0
58	MG	2T	203	1/1	0.92	0.15	56,56,56,56	0
58	MG	2A	3228	1/1	0.92	0.24	69,69,69,69	0
58	MG	2A	3491	1/1	0.92	0.12	46,46,46,46	0
58	MG	2W	202	1/1	0.92	0.11	55,55,55,55	0
58	MG	2A	3492	1/1	0.92	0.20	56,56,56,56	0
58	MG	1A	3441	1/1	0.92	0.09	41,41,41,41	0
58	MG	2A	3497	1/1	0.92	0.16	65,65,65,65	0
58	MG	1A	3783	1/1	0.92	0.11	17,17,17,17	0
58	MG	23	102	1/1	0.92	0.11	65,65,65,65	0
58	MG	1x	102	1/1	0.92	0.10	59,59,59,59	0
58	MG	1A	3346	1/1	0.92	0.08	37,37,37,37	0
58	MG	1x	104	1/1	0.92	0.14	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3282	1/1	0.92	0.18	22,22,22,22	0
58	MG	1a	1606	1/1	0.92	0.07	63,63,63,63	0
58	MG	2A	3237	1/1	0.92	0.07	57,57,57,57	0
58	MG	1A	3350	1/1	0.92	0.09	52,52,52,52	0
58	MG	2a	3009	1/1	0.92	0.20	66,66,66,66	0
58	MG	2A	3240	1/1	0.92	0.32	61,61,61,61	0
58	MG	1A	4002	1/1	0.92	0.14	59,59,59,59	0
58	MG	1A	3233	1/1	0.92	0.10	44,44,44,44	0
58	MG	2a	3013	1/1	0.92	0.13	58,58,58,58	0
58	MG	1x	111	1/1	0.92	0.27	58,58,58,58	0
58	MG	1A	3018	1/1	0.92	0.17	34,34,34,34	0
58	MG	1A	3579	1/1	0.92	0.07	54,54,54,54	0
58	MG	2A	3530	1/1	0.92	0.12	51,51,51,51	0
58	MG	1A	4017	1/1	0.92	0.12	40,40,40,40	0
58	MG	2a	3020	1/1	0.92	0.10	69,69,69,69	0
58	MG	1A	3580	1/1	0.92	0.06	39,39,39,39	0
58	MG	1A	3453	1/1	0.92	0.15	40,40,40,40	0
58	MG	1A	3291	1/1	0.92	0.13	39,39,39,39	0
58	MG	2a	3024	1/1	0.92	0.15	68,68,68,68	0
58	MG	1A	3361	1/1	0.92	0.26	32,32,32,32	0
58	MG	1A	3594	1/1	0.92	0.11	23,23,23,23	0
58	MG	2A	3018	1/1	0.92	0.13	68,68,68,68	0
58	MG	2A	3020	1/1	0.92	0.17	46,46,46,46	0
58	MG	1A	3168	1/1	0.92	0.08	28,28,28,28	0
58	MG	1A	3458	1/1	0.92	0.15	49,49,49,49	0
58	MG	2A	3026	1/1	0.92	0.07	39,39,39,39	0
58	MG	2A	3563	1/1	0.92	0.13	49,49,49,49	0
58	MG	2A	3566	1/1	0.92	0.15	38,38,38,38	0
58	MG	1A	3817	1/1	0.92	0.21	52,52,52,52	0
58	MG	1A	3818	1/1	0.92	0.19	55,55,55,55	0
58	MG	1a	1633	1/1	0.92	0.36	62,62,62,62	0
58	MG	1A	3238	1/1	0.92	0.23	36,36,36,36	0
58	MG	2A	3578	1/1	0.92	0.07	69,69,69,69	0
58	MG	2A	3270	1/1	0.92	0.15	56,56,56,56	0
58	MG	2A	3580	1/1	0.92	0.16	54,54,54,54	0
58	MG	2A	3034	1/1	0.92	0.15	36,36,36,36	0
58	MG	1A	4039	1/1	0.92	0.12	31,31,31,31	0
58	MG	1A	4041	1/1	0.92	0.10	50,50,50,50	0
58	MG	1A	3036	1/1	0.92	0.10	33,33,33,33	0
58	MG	1A	3370	1/1	0.92	0.10	49,49,49,49	0
58	MG	1A	3602	1/1	0.92	0.11	48,48,48,48	0
58	MG	1A	4056	1/1	0.92	0.13	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3044	1/1	0.92	0.14	55,55,55,55	0
58	MG	1A	3017	1/1	0.92	0.18	37,37,37,37	0
58	MG	1A	3374	1/1	0.92	0.09	45,45,45,45	0
58	MG	1A	3609	1/1	0.92	0.13	27,27,27,27	0
58	MG	2A	3605	1/1	0.92	0.16	48,48,48,48	0
58	MG	1a	1651	1/1	0.92	0.13	47,47,47,47	0
58	MG	1A	3470	1/1	0.92	0.09	35,35,35,35	0
58	MG	2A	3613	1/1	0.92	0.24	57,57,57,57	0
58	MG	2A	3615	1/1	0.92	0.11	44,44,44,44	0
58	MG	1A	4067	1/1	0.92	0.11	48,48,48,48	0
58	MG	1A	3839	1/1	0.92	0.22	41,41,41,41	0
58	MG	2A	3057	1/1	0.92	0.17	45,45,45,45	0
58	MG	2A	3293	1/1	0.92	0.17	41,41,41,41	0
58	MG	1A	3173	1/1	0.92	0.12	36,36,36,36	0
58	MG	1A	3472	1/1	0.92	0.15	48,48,48,48	0
58	MG	2a	3074	1/1	0.92	0.29	72,72,72,72	0
58	MG	2A	3632	1/1	0.92	0.13	48,48,48,48	0
58	MG	2A	3060	1/1	0.92	0.13	44,44,44,44	0
58	MG	2A	3298	1/1	0.92	0.45	54,54,54,54	0
58	MG	1A	3847	1/1	0.92	0.30	24,24,24,24	0
58	MG	1A	3849	1/1	0.92	0.08	44,44,44,44	0
58	MG	1A	3381	1/1	0.92	0.13	56,56,56,56	0
58	MG	1A	3174	1/1	0.92	0.14	35,35,35,35	0
58	MG	1A	3480	1/1	0.92	0.13	45,45,45,45	0
58	MG	2A	3067	1/1	0.92	0.31	69,69,69,69	0
58	MG	2A	3068	1/1	0.92	0.10	49,49,49,49	0
58	MG	1A	3041	1/1	0.92	0.11	42,42,42,42	0
58	MG	1A	3313	1/1	0.92	0.12	37,37,37,37	0
58	MG	1A	3047	1/1	0.92	0.06	26,26,26,26	0
58	MG	2a	3095	1/1	0.92	0.11	52,52,52,52	0
58	MG	1A	3862	1/1	0.92	0.15	29,29,29,29	0
58	MG	2A	3077	1/1	0.92	0.11	50,50,50,50	0
58	MG	2A	3654	1/1	0.92	0.18	67,67,67,67	0
58	MG	1A	3316	1/1	0.92	0.07	29,29,29,29	0
58	MG	1A	3108	1/1	0.92	0.13	30,30,30,30	0
58	MG	1A	3649	1/1	0.92	0.07	25,25,25,25	0
58	MG	1A	3650	1/1	0.92	0.09	51,51,51,51	0
58	MG	2A	3086	1/1	0.92	0.11	50,50,50,50	0
58	MG	1A	3492	1/1	0.92	0.09	36,36,36,36	0
58	MG	2A	3328	1/1	0.92	0.08	46,46,46,46	0
58	MG	1A	3191	1/1	0.92	0.11	33,33,33,33	0
58	MG	1A	3662	1/1	0.92	0.13	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3677	1/1	0.92	0.10	33,33,33,33	0
58	MG	2A	3679	1/1	0.92	0.13	58,58,58,58	0
58	MG	2a	3116	1/1	0.92	0.22	52,52,52,52	0
58	MG	1A	3664	1/1	0.92	0.09	29,29,29,29	0
58	MG	1A	3405	1/1	0.92	0.14	49,49,49,49	0
58	MG	2A	3337	1/1	0.92	0.28	60,60,60,60	0
58	MG	2A	3685	1/1	0.92	0.11	58,58,58,58	0
58	MG	1A	3497	1/1	0.92	0.12	43,43,43,43	0
58	MG	1A	3881	1/1	0.92	0.08	25,25,25,25	0
58	MG	1A	3498	1/1	0.92	0.09	49,49,49,49	0
58	MG	2A	3344	1/1	0.92	0.27	62,62,62,62	0
58	MG	1A	3503	1/1	0.92	0.07	29,29,29,29	0
58	MG	2A	3103	1/1	0.92	0.15	53,53,53,53	0
58	MG	1A	3408	1/1	0.92	0.13	49,49,49,49	0
58	MG	2A	3703	1/1	0.92	0.11	50,50,50,50	0
58	MG	1A	3677	1/1	0.92	0.09	25,25,25,25	0
58	MG	1A	3680	1/1	0.92	0.10	60,60,60,60	0
58	MG	2A	3354	1/1	0.92	0.12	43,43,43,43	0
58	MG	1a	1710	1/1	0.92	0.22	40,40,40,40	0
58	MG	1a	1711	1/1	0.92	0.11	44,44,44,44	0
58	MG	1A	3030	1/1	0.92	0.11	34,34,34,34	0
58	MG	2A	3116	1/1	0.92	0.21	47,47,47,47	0
58	MG	1A	3685	1/1	0.92	0.12	37,37,37,37	0
58	MG	1A	3152	1/1	0.92	0.13	40,40,40,40	0
58	MG	2A	3717	1/1	0.92	0.20	56,56,56,56	0
58	MG	1A	3899	1/1	0.92	0.23	26,26,26,26	0
58	MG	2A	3366	1/1	0.92	0.09	42,42,42,42	0
58	MG	1A	3904	1/1	0.92	0.12	40,40,40,40	0
58	MG	2A	3370	1/1	0.92	0.14	62,62,62,62	0
58	MG	1A	3910	1/1	0.92	0.09	61,61,61,61	0
58	MG	2A	3372	1/1	0.92	0.23	44,44,44,44	0
58	MG	1a	1730	1/1	0.92	0.13	45,45,45,45	0
58	MG	1F	309	1/1	0.92	0.16	45,45,45,45	0
58	MG	2A	3376	1/1	0.92	0.16	55,55,55,55	0
58	MG	2a	3168	1/1	0.92	0.18	42,42,42,42	0
58	MG	2A	3377	1/1	0.92	0.23	45,45,45,45	0
58	MG	2A	3136	1/1	0.92	0.24	57,57,57,57	0
58	MG	2A	3380	1/1	0.92	0.08	44,44,44,44	0
58	MG	2A	3382	1/1	0.92	0.35	53,53,53,53	0
58	MG	1A	3519	1/1	0.92	0.15	45,45,45,45	0
58	MG	1A	3521	1/1	0.92	0.24	47,47,47,47	0
58	MG	2a	3176	1/1	0.92	0.25	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3748	1/1	0.92	0.15	60,60,60,60	0
58	MG	2A	3140	1/1	0.92	0.14	64,64,64,64	0
58	MG	1O	203	1/1	0.92	0.11	51,51,51,51	0
58	MG	2A	3752	1/1	0.92	0.16	45,45,45,45	0
58	MG	2a	3182	1/1	0.92	0.22	53,53,53,53	0
58	MG	1A	3916	1/1	0.92	0.08	45,45,45,45	0
58	MG	1a	1749	1/1	0.92	0.19	59,59,59,59	0
58	MG	1A	3153	1/1	0.92	0.19	41,41,41,41	0
58	MG	1A	3699	1/1	0.92	0.09	35,35,35,35	0
58	MG	1A	3087	1/1	0.92	0.10	25,25,25,25	0
58	MG	2A	3153	1/1	0.92	0.35	63,63,63,63	0
58	MG	1a	1754	1/1	0.92	0.08	59,59,59,59	0
58	MG	2A	3402	1/1	0.92	0.15	50,50,50,50	0
58	MG	1A	3156	1/1	0.92	0.32	43,43,43,43	0
58	MG	1R	205	1/1	0.92	0.20	23,23,23,23	0
58	MG	1A	3930	1/1	0.92	0.08	62,62,62,62	0
58	MG	1U	201	1/1	0.92	0.17	35,35,35,35	0
58	MG	1a	1761	1/1	0.92	0.16	59,59,59,59	0
58	MG	1A	3534	1/1	0.92	0.14	54,54,54,54	0
58	MG	1A	3539	1/1	0.92	0.35	42,42,42,42	0
58	MG	2A	3167	1/1	0.92	0.14	61,61,61,61	0
58	MG	2a	3202	1/1	0.92	0.16	61,61,61,61	0
58	MG	1A	3704	1/1	0.92	0.10	38,38,38,38	0
58	MG	1V	206	1/1	0.92	0.13	48,48,48,48	0
58	MG	1A	3712	1/1	0.92	0.12	42,42,42,42	0
58	MG	2A	3799	1/1	0.92	0.15	35,35,35,35	0
58	MG	2A	3420	1/1	0.92	0.26	45,45,45,45	0
58	MG	1A	3219	1/1	0.92	0.15	53,53,53,53	0
58	MG	1A	3055	1/1	0.92	0.11	43,43,43,43	0
58	MG	2e	201	1/1	0.92	0.06	67,67,67,67	0
58	MG	1X	104	1/1	0.92	0.10	42,42,42,42	0
58	MG	1A	3330	1/1	0.92	0.09	39,39,39,39	0
58	MG	1A	3223	1/1	0.92	0.09	52,52,52,52	0
58	MG	1a	1784	1/1	0.92	0.11	67,67,67,67	0
58	MG	1A	3225	1/1	0.92	0.10	42,42,42,42	0
58	MG	1a	1786	1/1	0.92	0.17	54,54,54,54	0
58	MG	10	103	1/1	0.92	0.08	39,39,39,39	0
58	MG	1a	1790	1/1	0.92	0.14	68,68,68,68	0
58	MG	2A	3818	1/1	0.92	0.13	66,66,66,66	0
58	MG	2v	102	1/1	0.92	0.21	71,71,71,71	0
58	MG	1A	3554	1/1	0.92	0.10	36,36,36,36	0
58	MG	2A	3190	1/1	0.92	0.27	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3125	1/1	0.92	0.08	32,32,32,32	0
58	MG	10	107	1/1	0.92	0.09	48,48,48,48	0
58	MG	1A	3956	1/1	0.92	0.11	64,64,64,64	0
58	MG	2x	105	1/1	0.92	0.15	61,61,61,61	0
58	MG	1a	1796	1/1	0.92	0.28	59,59,59,59	0
58	MG	1A	3560	1/1	0.92	0.10	38,38,38,38	0
58	MG	1A	3116	1/1	0.93	0.11	43,43,43,43	0
58	MG	1A	3860	1/1	0.93	0.07	29,29,29,29	0
58	MG	2A	3238	1/1	0.93	0.10	57,57,57,57	0
58	MG	1A	3244	1/1	0.93	0.26	39,39,39,39	0
58	MG	2A	3011	1/1	0.93	0.11	48,48,48,48	0
58	MG	1A	4059	1/1	0.93	0.14	44,44,44,44	0
58	MG	2A	3016	1/1	0.93	0.19	54,54,54,54	0
58	MG	1A	3122	1/1	0.93	0.25	32,32,32,32	0
58	MG	1A	3247	1/1	0.93	0.07	50,50,50,50	0
58	MG	1A	3865	1/1	0.93	0.17	26,26,26,26	0
58	MG	1a	1638	1/1	0.93	0.14	43,43,43,43	0
58	MG	1A	3697	1/1	0.93	0.10	48,48,48,48	0
58	MG	1A	3461	1/1	0.93	0.12	40,40,40,40	0
58	MG	2E	306	1/1	0.93	0.13	44,44,44,44	0
58	MG	1A	3386	1/1	0.93	0.15	54,54,54,54	0
58	MG	1A	3326	1/1	0.93	0.10	51,51,51,51	0
58	MG	2F	302	1/1	0.93	0.09	52,52,52,52	0
58	MG	1A	4071	1/1	0.93	0.15	50,50,50,50	0
58	MG	1A	3467	1/1	0.93	0.08	41,41,41,41	0
58	MG	2A	3514	1/1	0.93	0.12	37,37,37,37	0
58	MG	1a	1647	1/1	0.93	0.06	51,51,51,51	0
58	MG	2A	3259	1/1	0.93	0.12	55,55,55,55	0
58	MG	2A	3036	1/1	0.93	0.18	49,49,49,49	0
58	MG	2Q	201	1/1	0.93	0.20	66,66,66,66	0
58	MG	2A	3519	1/1	0.93	0.12	48,48,48,48	0
58	MG	2R	201	1/1	0.93	0.10	50,50,50,50	0
58	MG	2T	201	1/1	0.93	0.10	52,52,52,52	0
58	MG	2A	3261	1/1	0.93	0.07	44,44,44,44	0
58	MG	2A	3262	1/1	0.93	0.07	72,72,72,72	0
58	MG	2V	201	1/1	0.93	0.28	46,46,46,46	0
58	MG	1A	3328	1/1	0.93	0.15	42,42,42,42	0
58	MG	1A	3093	1/1	0.93	0.13	38,38,38,38	0
58	MG	1A	3705	1/1	0.93	0.11	61,61,61,61	0
58	MG	2X	101	1/1	0.93	0.10	64,64,64,64	0
58	MG	2Z	301	1/1	0.93	0.16	80,80,80,80	0
58	MG	1a	1654	1/1	0.93	0.11	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1655	1/1	0.93	0.20	56,56,56,56	0
58	MG	2A	3043	1/1	0.93	0.06	64,64,64,64	0
58	MG	1A	3708	1/1	0.93	0.07	26,26,26,26	0
58	MG	2A	3542	1/1	0.93	0.09	41,41,41,41	0
58	MG	27	101	1/1	0.93	0.27	42,42,42,42	0
58	MG	27	103	1/1	0.93	0.15	41,41,41,41	0
58	MG	1a	1658	1/1	0.93	0.15	59,59,59,59	0
58	MG	2A	3273	1/1	0.93	0.09	45,45,45,45	0
58	MG	1A	4081	1/1	0.93	0.21	52,52,52,52	0
58	MG	2A	3048	1/1	0.93	0.11	67,67,67,67	0
58	MG	2A	3278	1/1	0.93	0.25	39,39,39,39	0
58	MG	2A	3557	1/1	0.93	0.12	33,33,33,33	0
58	MG	1A	3064	1/1	0.93	0.18	33,33,33,33	0
58	MG	1A	3331	1/1	0.93	0.08	46,46,46,46	0
58	MG	2A	3561	1/1	0.93	0.10	64,64,64,64	0
58	MG	2A	3051	1/1	0.93	0.18	55,55,55,55	0
58	MG	1A	3128	1/1	0.93	0.13	46,46,46,46	0
58	MG	1a	1666	1/1	0.93	0.22	57,57,57,57	0
58	MG	1A	3885	1/1	0.93	0.10	43,43,43,43	0
58	MG	1B	210	1/1	0.93	0.09	53,53,53,53	0
58	MG	1A	3069	1/1	0.93	0.08	42,42,42,42	0
58	MG	2A	3577	1/1	0.93	0.12	58,58,58,58	0
58	MG	1A	3587	1/1	0.93	0.17	52,52,52,52	0
58	MG	1A	3889	1/1	0.93	0.15	54,54,54,54	0
58	MG	1A	3724	1/1	0.93	0.13	48,48,48,48	0
58	MG	1A	3589	1/1	0.93	0.15	55,55,55,55	0
58	MG	1a	1676	1/1	0.93	0.19	47,47,47,47	0
58	MG	1B	221	1/1	0.93	0.08	41,41,41,41	0
58	MG	1A	3893	1/1	0.93	0.17	55,55,55,55	0
58	MG	1a	1680	1/1	0.93	0.23	74,74,74,74	0
58	MG	1A	3477	1/1	0.93	0.13	45,45,45,45	0
58	MG	2A	3591	1/1	0.93	0.16	23,23,23,23	0
58	MG	2a	3030	1/1	0.93	0.25	68,68,68,68	0
58	MG	2A	3070	1/1	0.93	0.14	22,22,22,22	0
58	MG	2A	3596	1/1	0.93	0.11	37,37,37,37	0
58	MG	2A	3597	1/1	0.93	0.15	56,56,56,56	0
58	MG	1A	3209	1/1	0.93	0.07	42,42,42,42	0
58	MG	2A	3300	1/1	0.93	0.13	59,59,59,59	0
58	MG	1A	3746	1/1	0.93	0.10	19,19,19,19	0
58	MG	1A	3747	1/1	0.93	0.15	41,41,41,41	0
58	MG	1A	3481	1/1	0.93	0.21	50,50,50,50	0
58	MG	1A	3336	1/1	0.93	0.07	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3080	1/1	0.93	0.09	46,46,46,46	0
58	MG	2A	3612	1/1	0.93	0.14	49,49,49,49	0
58	MG	2A	3308	1/1	0.93	0.10	55,55,55,55	0
58	MG	1a	1690	1/1	0.93	0.28	49,49,49,49	0
58	MG	1B	239	1/1	0.93	0.07	39,39,39,39	0
58	MG	1A	3752	1/1	0.93	0.10	40,40,40,40	0
58	MG	2A	3084	1/1	0.93	0.12	39,39,39,39	0
58	MG	1D	303	1/1	0.93	0.13	33,33,33,33	0
58	MG	2A	3628	1/1	0.93	0.29	60,60,60,60	0
58	MG	2A	3629	1/1	0.93	0.25	52,52,52,52	0
58	MG	1A	3914	1/1	0.93	0.14	53,53,53,53	0
58	MG	1D	310	1/1	0.93	0.08	33,33,33,33	0
58	MG	1a	1698	1/1	0.93	0.11	53,53,53,53	0
58	MG	2a	3057	1/1	0.93	0.07	58,58,58,58	0
58	MG	2a	3059	1/1	0.93	0.21	55,55,55,55	0
58	MG	1a	1700	1/1	0.93	0.08	54,54,54,54	0
58	MG	2A	3321	1/1	0.93	0.12	56,56,56,56	0
58	MG	1A	3046	1/1	0.93	0.06	34,34,34,34	0
58	MG	1A	3104	1/1	0.93	0.10	47,47,47,47	0
58	MG	2A	3097	1/1	0.93	0.20	55,55,55,55	0
58	MG	2A	3325	1/1	0.93	0.16	56,56,56,56	0
58	MG	2a	3067	1/1	0.93	0.14	59,59,59,59	0
58	MG	2A	3645	1/1	0.93	0.09	46,46,46,46	0
58	MG	2A	3327	1/1	0.93	0.13	54,54,54,54	0
58	MG	1A	3922	1/1	0.93	0.09	42,42,42,42	0
58	MG	2A	3331	1/1	0.93	0.13	47,47,47,47	0
58	MG	1A	3756	1/1	0.93	0.16	23,23,23,23	0
58	MG	1A	3301	1/1	0.93	0.13	37,37,37,37	0
58	MG	1A	3422	1/1	0.93	0.07	38,38,38,38	0
58	MG	1A	3028	1/1	0.93	0.11	19,19,19,19	0
58	MG	1A	3769	1/1	0.93	0.16	57,57,57,57	0
58	MG	2A	3105	1/1	0.93	0.14	45,45,45,45	0
58	MG	2a	3079	1/1	0.93	0.13	64,64,64,64	0
58	MG	2A	3339	1/1	0.93	0.09	47,47,47,47	0
58	MG	2A	3657	1/1	0.93	0.12	42,42,42,42	0
58	MG	2A	3106	1/1	0.93	0.15	54,54,54,54	0
58	MG	1A	3347	1/1	0.93	0.15	64,64,64,64	0
58	MG	1A	3348	1/1	0.93	0.10	51,51,51,51	0
58	MG	1A	3936	1/1	0.93	0.17	58,58,58,58	0
58	MG	1a	1725	1/1	0.93	0.09	40,40,40,40	0
58	MG	1a	1726	1/1	0.93	0.07	35,35,35,35	0
58	MG	1A	3937	1/1	0.93	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3940	1/1	0.93	0.10	52,52,52,52	0
58	MG	1O	204	1/1	0.93	0.09	59,59,59,59	0
58	MG	2A	3356	1/1	0.93	0.46	54,54,54,54	0
58	MG	1A	3305	1/1	0.93	0.10	39,39,39,39	0
58	MG	1A	3310	1/1	0.93	0.09	35,35,35,35	0
58	MG	1A	3784	1/1	0.93	0.10	12,12,12,12	0
58	MG	2A	3128	1/1	0.93	0.39	44,44,44,44	0
58	MG	2A	3687	1/1	0.93	0.10	62,62,62,62	0
58	MG	2A	3688	1/1	0.93	0.08	56,56,56,56	0
58	MG	2A	3129	1/1	0.93	0.08	42,42,42,42	0
58	MG	1A	3050	1/1	0.93	0.23	41,41,41,41	0
58	MG	2a	3106	1/1	0.93	0.20	65,65,65,65	0
58	MG	1Q	202	1/1	0.93	0.11	39,39,39,39	0
58	MG	2a	3110	1/1	0.93	0.26	53,53,53,53	0
58	MG	2A	3694	1/1	0.93	0.12	59,59,59,59	0
58	MG	2A	3365	1/1	0.93	0.06	42,42,42,42	0
58	MG	1a	1745	1/1	0.93	0.08	54,54,54,54	0
58	MG	2A	3700	1/1	0.93	0.10	46,46,46,46	0
58	MG	1A	3950	1/1	0.93	0.12	49,49,49,49	0
58	MG	1Q	207	1/1	0.93	0.10	34,34,34,34	0
58	MG	1A	3504	1/1	0.93	0.11	48,48,48,48	0
58	MG	1A	3624	1/1	0.93	0.07	38,38,38,38	0
58	MG	1A	3505	1/1	0.93	0.12	37,37,37,37	0
58	MG	1A	3506	1/1	0.93	0.10	44,44,44,44	0
58	MG	2A	3147	1/1	0.93	0.15	42,42,42,42	0
58	MG	1U	206	1/1	0.93	0.20	24,24,24,24	0
58	MG	1A	3627	1/1	0.93	0.08	21,21,21,21	0
58	MG	1V	202	1/1	0.93	0.37	39,39,39,39	0
58	MG	2A	3381	1/1	0.93	0.10	40,40,40,40	0
58	MG	1A	3016	1/1	0.93	0.12	43,43,43,43	0
58	MG	1A	3801	1/1	0.93	0.10	68,68,68,68	0
58	MG	1A	3964	1/1	0.93	0.12	69,69,69,69	0
58	MG	1A	3630	1/1	0.93	0.10	64,64,64,64	0
58	MG	2A	3386	1/1	0.93	0.24	51,51,51,51	0
58	MG	2a	3136	1/1	0.93	0.20	58,58,58,58	0
58	MG	1W	203	1/1	0.93	0.11	27,27,27,27	0
58	MG	2A	3723	1/1	0.93	0.08	41,41,41,41	0
58	MG	1A	3433	1/1	0.93	0.29	34,34,34,34	0
58	MG	2a	3142	1/1	0.93	0.11	81,81,81,81	0
58	MG	1A	3636	1/1	0.93	0.07	45,45,45,45	0
58	MG	1A	3638	1/1	0.93	0.13	38,38,38,38	0
58	MG	2A	3733	1/1	0.93	0.16	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3734	1/1	0.93	0.07	39,39,39,39	0
58	MG	1A	3971	1/1	0.93	0.07	30,30,30,30	0
58	MG	2A	3396	1/1	0.93	0.15	48,48,48,48	0
58	MG	2A	3738	1/1	0.93	0.09	52,52,52,52	0
58	MG	1a	1778	1/1	0.93	0.21	59,59,59,59	0
58	MG	1Y	202	1/1	0.93	0.27	46,46,46,46	0
58	MG	2a	3159	1/1	0.93	0.06	75,75,75,75	0
58	MG	1A	3973	1/1	0.93	0.11	48,48,48,48	0
58	MG	2a	3161	1/1	0.93	0.11	71,71,71,71	0
58	MG	1A	3143	1/1	0.93	0.08	57,57,57,57	0
58	MG	2A	3403	1/1	0.93	0.18	50,50,50,50	0
58	MG	1A	3360	1/1	0.93	0.08	33,33,33,33	0
58	MG	2A	3176	1/1	0.93	0.09	56,56,56,56	0
58	MG	1A	3439	1/1	0.93	0.12	46,46,46,46	0
58	MG	1A	3440	1/1	0.93	0.11	33,33,33,33	0
58	MG	1A	3314	1/1	0.93	0.08	31,31,31,31	0
58	MG	1A	3525	1/1	0.93	0.09	43,43,43,43	0
58	MG	1A	3988	1/1	0.93	0.06	25,25,25,25	0
58	MG	2A	3756	1/1	0.93	0.13	60,60,60,60	0
58	MG	1A	3651	1/1	0.93	0.10	42,42,42,42	0
58	MG	1A	3527	1/1	0.93	0.25	55,55,55,55	0
58	MG	1A	3828	1/1	0.93	0.18	48,48,48,48	0
58	MG	11	105	1/1	0.93	0.11	42,42,42,42	0
58	MG	2A	3419	1/1	0.93	0.20	25,25,25,25	0
58	MG	1A	3656	1/1	0.93	0.12	25,25,25,25	0
58	MG	1A	3530	1/1	0.93	0.09	40,40,40,40	0
58	MG	2A	3768	1/1	0.93	0.12	46,46,46,46	0
58	MG	2A	3424	1/1	0.93	0.13	49,49,49,49	0
58	MG	2A	3425	1/1	0.93	0.08	47,47,47,47	0
58	MG	1a	1802	1/1	0.93	0.22	51,51,51,51	0
58	MG	1A	4004	1/1	0.93	0.11	48,48,48,48	0
58	MG	1A	4006	1/1	0.93	0.10	61,61,61,61	0
58	MG	2A	3781	1/1	0.93	0.17	39,39,39,39	0
58	MG	2a	3191	1/1	0.93	0.18	64,64,64,64	0
58	MG	1A	4009	1/1	0.93	0.10	38,38,38,38	0
58	MG	2A	3431	1/1	0.93	0.13	38,38,38,38	0
58	MG	2A	3791	1/1	0.93	0.19	63,63,63,63	0
58	MG	2A	3432	1/1	0.93	0.14	60,60,60,60	0
58	MG	1A	3442	1/1	0.93	0.10	47,47,47,47	0
58	MG	1A	3833	1/1	0.93	0.10	44,44,44,44	0
58	MG	2A	3798	1/1	0.93	0.10	52,52,52,52	0
58	MG	1A	3834	1/1	0.93	0.14	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3446	1/1	0.93	0.46	40,40,40,40	0
58	MG	1A	3063	1/1	0.93	0.26	51,51,51,51	0
58	MG	18	106	1/1	0.93	0.23	66,66,66,66	0
58	MG	1A	4021	1/1	0.93	0.07	50,50,50,50	0
58	MG	1A	3232	1/1	0.93	0.11	51,51,51,51	0
58	MG	1A	4023	1/1	0.93	0.16	27,27,27,27	0
58	MG	1A	3184	1/1	0.93	0.05	53,53,53,53	0
58	MG	2A	3447	1/1	0.93	0.12	52,52,52,52	0
58	MG	2d	301	1/1	0.93	0.28	61,61,61,61	0
58	MG	2d	302	1/1	0.93	0.10	73,73,73,73	0
58	MG	1A	3187	1/1	0.93	0.11	27,27,27,27	0
58	MG	2f	201	1/1	0.93	0.10	58,58,58,58	0
58	MG	2A	3218	1/1	0.93	0.19	41,41,41,41	0
58	MG	1A	3090	1/1	0.93	0.14	42,42,42,42	0
58	MG	2A	3454	1/1	0.93	0.15	57,57,57,57	0
58	MG	1A	3851	1/1	0.93	0.12	47,47,47,47	0
58	MG	2A	3221	1/1	0.93	0.14	53,53,53,53	0
58	MG	1A	3373	1/1	0.93	0.10	27,27,27,27	0
58	MG	1a	1614	1/1	0.93	0.11	70,70,70,70	0
58	MG	1A	3272	1/1	0.93	0.09	37,37,37,37	0
58	MG	1A	4037	1/1	0.93	0.08	51,51,51,51	0
58	MG	1A	3376	1/1	0.93	0.16	47,47,47,47	0
58	MG	1A	3556	1/1	0.93	0.36	38,38,38,38	0
58	MG	1A	3857	1/1	0.93	0.11	33,33,33,33	0
58	MG	1A	4045	1/1	0.93	0.13	14,14,14,14	0
58	MG	2B	208	1/1	0.93	0.12	57,57,57,57	0
58	MG	1a	1625	1/1	0.93	0.12	52,52,52,52	0
58	MG	1a	1626	1/1	0.93	0.34	51,51,51,51	0
58	MG	1A	3858	1/1	0.93	0.18	40,40,40,40	0
58	MG	2A	3480	1/1	0.93	0.10	57,57,57,57	0
58	MG	1Z	303	1/1	0.94	0.12	52,52,52,52	0
58	MG	10	101	1/1	0.94	0.12	40,40,40,40	0
58	MG	1A	3403	1/1	0.94	0.12	56,56,56,56	0
58	MG	1a	1753	1/1	0.94	0.17	49,49,49,49	0
58	MG	1A	3475	1/1	0.94	0.40	58,58,58,58	0
58	MG	2A	3585	1/1	0.94	0.10	52,52,52,52	0
58	MG	2A	3587	1/1	0.94	0.12	52,52,52,52	0
58	MG	2W	203	1/1	0.94	0.06	35,35,35,35	0
58	MG	2W	204	1/1	0.94	0.10	58,58,58,58	0
58	MG	1a	1755	1/1	0.94	0.12	54,54,54,54	0
58	MG	1A	4026	1/1	0.94	0.07	30,30,30,30	0
58	MG	1A	3020	1/1	0.94	0.08	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3123	1/1	0.94	0.07	59,59,59,59	0
58	MG	2A	3593	1/1	0.94	0.09	46,46,46,46	0
58	MG	1a	1758	1/1	0.94	0.12	50,50,50,50	0
58	MG	1A	3478	1/1	0.94	0.19	52,52,52,52	0
58	MG	1A	3479	1/1	0.94	0.06	36,36,36,36	0
58	MG	1A	3032	1/1	0.94	0.09	32,32,32,32	0
58	MG	1A	3720	1/1	0.94	0.10	54,54,54,54	0
58	MG	2a	3002	1/1	0.94	0.20	59,59,59,59	0
58	MG	1A	3081	1/1	0.94	0.07	47,47,47,47	0
58	MG	1A	3340	1/1	0.94	0.08	37,37,37,37	0
58	MG	2A	3606	1/1	0.94	0.10	40,40,40,40	0
58	MG	11	104	1/1	0.94	0.12	57,57,57,57	0
58	MG	1a	1770	1/1	0.94	0.15	58,58,58,58	0
58	MG	2A	3611	1/1	0.94	0.07	36,36,36,36	0
58	MG	1A	3483	1/1	0.94	0.18	29,29,29,29	0
58	MG	1A	3731	1/1	0.94	0.08	41,41,41,41	0
58	MG	1A	3412	1/1	0.94	0.20	60,60,60,60	0
58	MG	2A	3616	1/1	0.94	0.15	32,32,32,32	0
58	MG	15	102	1/1	0.94	0.19	40,40,40,40	0
58	MG	2A	3144	1/1	0.94	0.15	53,53,53,53	0
58	MG	2A	3145	1/1	0.94	0.06	42,42,42,42	0
58	MG	2A	3352	1/1	0.94	0.11	55,55,55,55	0
58	MG	1A	3342	1/1	0.94	0.08	39,39,39,39	0
58	MG	1A	3886	1/1	0.94	0.10	37,37,37,37	0
58	MG	1A	3147	1/1	0.94	0.11	36,36,36,36	0
58	MG	1A	3056	1/1	0.94	0.09	30,30,30,30	0
58	MG	15	108	1/1	0.94	0.07	45,45,45,45	0
58	MG	1A	4057	1/1	0.94	0.11	52,52,52,52	0
58	MG	2A	3154	1/1	0.94	0.16	42,42,42,42	0
58	MG	1A	3151	1/1	0.94	0.23	29,29,29,29	0
58	MG	2A	3638	1/1	0.94	0.08	36,36,36,36	0
58	MG	17	101	1/1	0.94	0.14	56,56,56,56	0
58	MG	2A	3157	1/1	0.94	0.07	51,51,51,51	0
58	MG	2A	3643	1/1	0.94	0.11	53,53,53,53	0
58	MG	1A	3890	1/1	0.94	0.07	30,30,30,30	0
58	MG	1A	3192	1/1	0.94	0.47	41,41,41,41	0
58	MG	18	104	1/1	0.94	0.13	53,53,53,53	0
58	MG	1A	3193	1/1	0.94	0.08	44,44,44,44	0
58	MG	1A	3086	1/1	0.94	0.18	42,42,42,42	0
58	MG	1a	1601	1/1	0.94	0.09	51,51,51,51	0
58	MG	2A	3166	1/1	0.94	0.16	45,45,45,45	0
58	MG	1A	3306	1/1	0.94	0.10	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3351	1/1	0.94	0.11	39,39,39,39	0
58	MG	1A	3618	1/1	0.94	0.07	20,20,20,20	0
58	MG	1a	1803	1/1	0.94	0.21	58,58,58,58	0
58	MG	2A	3174	1/1	0.94	0.11	57,57,57,57	0
58	MG	1a	1805	1/1	0.94	0.39	54,54,54,54	0
58	MG	1a	1607	1/1	0.94	0.10	59,59,59,59	0
58	MG	2a	3045	1/1	0.94	0.16	76,76,76,76	0
58	MG	2A	3178	1/1	0.94	0.13	56,56,56,56	0
58	MG	1a	1807	1/1	0.94	0.30	63,63,63,63	0
58	MG	1A	3902	1/1	0.94	0.08	22,22,22,22	0
58	MG	2a	3049	1/1	0.94	0.20	50,50,50,50	0
58	MG	1A	3352	1/1	0.94	0.10	42,42,42,42	0
58	MG	1A	3906	1/1	0.94	0.07	32,32,32,32	0
58	MG	1d	301	1/1	0.94	0.25	63,63,63,63	0
58	MG	2a	3054	1/1	0.94	0.08	49,49,49,49	0
58	MG	2A	3390	1/1	0.94	0.18	46,46,46,46	0
58	MG	1a	1612	1/1	0.94	0.15	32,32,32,32	0
58	MG	2A	3678	1/1	0.94	0.10	56,56,56,56	0
58	MG	2A	3392	1/1	0.94	0.14	54,54,54,54	0
58	MG	2A	3680	1/1	0.94	0.11	54,54,54,54	0
58	MG	1m	3001	1/1	0.94	0.11	51,51,51,51	0
58	MG	2A	3394	1/1	0.94	0.14	39,39,39,39	0
58	MG	1A	3308	1/1	0.94	0.11	42,42,42,42	0
58	MG	1A	3198	1/1	0.94	0.06	37,37,37,37	0
58	MG	2A	3397	1/1	0.94	0.12	59,59,59,59	0
58	MG	1p	102	1/1	0.94	0.14	49,49,49,49	0
58	MG	1A	3357	1/1	0.94	0.12	32,32,32,32	0
58	MG	2A	3691	1/1	0.94	0.11	65,65,65,65	0
58	MG	1A	3437	1/1	0.94	0.07	28,28,28,28	0
58	MG	1A	3113	1/1	0.94	0.11	42,42,42,42	0
58	MG	1A	3628	1/1	0.94	0.08	13,13,13,13	0
58	MG	1w	103	1/1	0.94	0.06	81,81,81,81	0
58	MG	1A	3359	1/1	0.94	0.29	46,46,46,46	0
58	MG	2a	3075	1/1	0.94	0.12	59,59,59,59	0
58	MG	1B	207	1/1	0.94	0.21	46,46,46,46	0
58	MG	2A	3197	1/1	0.94	0.07	47,47,47,47	0
58	MG	1A	3042	1/1	0.94	0.11	30,30,30,30	0
58	MG	2A	3410	1/1	0.94	0.21	45,45,45,45	0
58	MG	2A	3704	1/1	0.94	0.07	68,68,68,68	0
58	MG	1A	3926	1/1	0.94	0.14	42,42,42,42	0
58	MG	1A	3632	1/1	0.94	0.07	36,36,36,36	0
58	MG	1A	3792	1/1	0.94	0.08	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3709	1/1	0.94	0.09	53,53,53,53	0
58	MG	2A	3414	1/1	0.94	0.16	57,57,57,57	0
58	MG	1A	3155	1/1	0.94	0.08	37,37,37,37	0
58	MG	1A	3362	1/1	0.94	0.10	63,63,63,63	0
58	MG	1A	3443	1/1	0.94	0.09	46,46,46,46	0
58	MG	2A	3714	1/1	0.94	0.09	51,51,51,51	0
58	MG	1B	219	1/1	0.94	0.08	36,36,36,36	0
58	MG	1A	3208	1/1	0.94	0.15	34,34,34,34	0
58	MG	1a	1636	1/1	0.94	0.18	43,43,43,43	0
58	MG	1B	222	1/1	0.94	0.10	40,40,40,40	0
58	MG	2A	3002	1/1	0.94	0.29	50,50,50,50	0
58	MG	1A	3642	1/1	0.94	0.10	36,36,36,36	0
58	MG	2a	3101	1/1	0.94	0.25	65,65,65,65	0
58	MG	2A	3427	1/1	0.94	0.24	52,52,52,52	0
58	MG	1A	3529	1/1	0.94	0.24	54,54,54,54	0
58	MG	1A	3034	1/1	0.94	0.33	24,24,24,24	0
58	MG	1A	3941	1/1	0.94	0.11	59,59,59,59	0
58	MG	2A	3226	1/1	0.94	0.14	45,45,45,45	0
58	MG	2A	3731	1/1	0.94	0.28	59,59,59,59	0
58	MG	1B	231	1/1	0.94	0.06	43,43,43,43	0
58	MG	1A	3646	1/1	0.94	0.08	36,36,36,36	0
58	MG	1A	3531	1/1	0.94	0.07	46,46,46,46	0
58	MG	2a	3113	1/1	0.94	0.19	52,52,52,52	0
58	MG	2A	3436	1/1	0.94	0.09	63,63,63,63	0
58	MG	1a	1646	1/1	0.94	0.23	40,40,40,40	0
58	MG	1A	3809	1/1	0.94	0.15	41,41,41,41	0
58	MG	2a	3117	1/1	0.94	0.24	49,49,49,49	0
58	MG	1B	236	1/1	0.94	0.11	55,55,55,55	0
58	MG	1A	3532	1/1	0.94	0.08	67,67,67,67	0
58	MG	1B	240	1/1	0.94	0.13	42,42,42,42	0
58	MG	2A	3744	1/1	0.94	0.08	59,59,59,59	0
58	MG	1A	3366	1/1	0.94	0.23	39,39,39,39	0
58	MG	1A	3021	1/1	0.94	0.07	36,36,36,36	0
58	MG	1A	3816	1/1	0.94	0.16	46,46,46,46	0
58	MG	1D	309	1/1	0.94	0.26	47,47,47,47	0
58	MG	2a	3127	1/1	0.94	0.19	42,42,42,42	0
58	MG	1A	3214	1/1	0.94	0.06	29,29,29,29	0
58	MG	2A	3751	1/1	0.94	0.16	63,63,63,63	0
58	MG	1A	3540	1/1	0.94	0.06	31,31,31,31	0
58	MG	2A	3031	1/1	0.94	0.12	49,49,49,49	0
58	MG	1A	3007	1/1	0.94	0.08	43,43,43,43	0
58	MG	1E	302	1/1	0.94	0.13	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3457	1/1	0.94	0.10	55,55,55,55	0
58	MG	1a	1665	1/1	0.94	0.22	48,48,48,48	0
58	MG	1A	3265	1/1	0.94	0.16	62,62,62,62	0
58	MG	2A	3462	1/1	0.94	0.13	60,60,60,60	0
58	MG	1A	3961	1/1	0.94	0.09	65,65,65,65	0
58	MG	1A	3822	1/1	0.94	0.08	38,38,38,38	0
58	MG	2a	3143	1/1	0.94	0.07	75,75,75,75	0
58	MG	2A	3250	1/1	0.94	0.09	54,54,54,54	0
58	MG	1A	3963	1/1	0.94	0.09	43,43,43,43	0
58	MG	2A	3041	1/1	0.94	0.14	57,57,57,57	0
58	MG	1A	3096	1/1	0.94	0.06	47,47,47,47	0
58	MG	2a	3149	1/1	0.94	0.14	66,66,66,66	0
58	MG	2a	3150	1/1	0.94	0.22	61,61,61,61	0
58	MG	1A	3455	1/1	0.94	0.14	50,50,50,50	0
58	MG	1A	3268	1/1	0.94	0.15	41,41,41,41	0
58	MG	2A	3473	1/1	0.94	0.08	55,55,55,55	0
58	MG	1A	3553	1/1	0.94	0.06	21,21,21,21	0
58	MG	2A	3476	1/1	0.94	0.21	47,47,47,47	0
58	MG	1A	3051	1/1	0.94	0.21	28,28,28,28	0
58	MG	1N	203	1/1	0.94	0.12	47,47,47,47	0
58	MG	1a	1678	1/1	0.94	0.07	56,56,56,56	0
58	MG	2a	3162	1/1	0.94	0.09	75,75,75,75	0
58	MG	1A	3674	1/1	0.94	0.06	32,32,32,32	0
58	MG	2A	3264	1/1	0.94	0.14	55,55,55,55	0
58	MG	1O	201	1/1	0.94	0.08	53,53,53,53	0
58	MG	2a	3167	1/1	0.94	0.21	50,50,50,50	0
58	MG	1A	3972	1/1	0.94	0.08	34,34,34,34	0
58	MG	1A	3380	1/1	0.94	0.27	26,26,26,26	0
58	MG	2A	3803	1/1	0.94	0.13	56,56,56,56	0
58	MG	1P	204	1/1	0.94	0.35	27,27,27,27	0
58	MG	1A	3066	1/1	0.94	0.13	41,41,41,41	0
58	MG	2A	3806	1/1	0.94	0.09	47,47,47,47	0
58	MG	1A	3835	1/1	0.94	0.11	37,37,37,37	0
58	MG	2A	3495	1/1	0.94	0.20	44,44,44,44	0
58	MG	2A	3496	1/1	0.94	0.05	27,27,27,27	0
58	MG	1a	1688	1/1	0.94	0.28	54,54,54,54	0
58	MG	1A	3557	1/1	0.94	0.16	30,30,30,30	0
58	MG	1P	209	1/1	0.94	0.11	46,46,46,46	0
58	MG	1A	3681	1/1	0.94	0.08	19,19,19,19	0
58	MG	1A	3982	1/1	0.94	0.13	16,16,16,16	0
58	MG	1A	3382	1/1	0.94	0.28	41,41,41,41	0
58	MG	1Q	206	1/1	0.94	0.08	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3226	1/1	0.94	0.25	52,52,52,52	0
58	MG	2A	3823	1/1	0.94	0.16	58,58,58,58	0
58	MG	1R	202	1/1	0.94	0.07	34,34,34,34	0
58	MG	2A	3283	1/1	0.94	0.13	54,54,54,54	0
58	MG	1A	3562	1/1	0.94	0.09	44,44,44,44	0
58	MG	1A	3053	1/1	0.94	0.14	44,44,44,44	0
58	MG	2a	3192	1/1	0.94	0.12	54,54,54,54	0
58	MG	1A	3690	1/1	0.94	0.08	19,19,19,19	0
58	MG	2A	3520	1/1	0.94	0.07	39,39,39,39	0
58	MG	1U	202	1/1	0.94	0.17	34,34,34,34	0
58	MG	1U	204	1/1	0.94	0.12	28,28,28,28	0
58	MG	1A	3274	1/1	0.94	0.15	48,48,48,48	0
58	MG	2A	3527	1/1	0.94	0.09	31,31,31,31	0
58	MG	2A	3079	1/1	0.94	0.08	47,47,47,47	0
58	MG	1A	4000	1/1	0.94	0.08	56,56,56,56	0
58	MG	1U	207	1/1	0.94	0.38	35,35,35,35	0
58	MG	2A	3535	1/1	0.94	0.11	40,40,40,40	0
58	MG	1U	210	1/1	0.94	0.07	41,41,41,41	0
58	MG	2A	3294	1/1	0.94	0.11	46,46,46,46	0
58	MG	2A	3540	1/1	0.94	0.07	57,57,57,57	0
58	MG	2a	3207	1/1	0.94	0.11	65,65,65,65	0
58	MG	2a	3208	1/1	0.94	0.08	63,63,63,63	0
58	MG	1A	3275	1/1	0.94	0.10	31,31,31,31	0
58	MG	1a	1715	1/1	0.94	0.17	50,50,50,50	0
58	MG	1A	3695	1/1	0.94	0.16	41,41,41,41	0
58	MG	1A	3696	1/1	0.94	0.09	46,46,46,46	0
58	MG	1a	1724	1/1	0.94	0.07	52,52,52,52	0
58	MG	2D	307	1/1	0.94	0.27	42,42,42,42	0
58	MG	1V	205	1/1	0.94	0.29	31,31,31,31	0
58	MG	2E	301	1/1	0.94	0.14	46,46,46,46	0
58	MG	1A	3131	1/1	0.94	0.29	47,47,47,47	0
58	MG	2A	3555	1/1	0.94	0.18	32,32,32,32	0
58	MG	2A	3556	1/1	0.94	0.17	46,46,46,46	0
58	MG	2A	3092	1/1	0.94	0.17	62,62,62,62	0
58	MG	1V	207	1/1	0.94	0.08	39,39,39,39	0
58	MG	1A	3698	1/1	0.94	0.11	54,54,54,54	0
58	MG	2q	202	1/1	0.94	0.07	71,71,71,71	0
58	MG	1A	3572	1/1	0.94	0.11	31,31,31,31	0
58	MG	1A	3102	1/1	0.94	0.08	42,42,42,42	0
58	MG	1A	3103	1/1	0.94	0.09	41,41,41,41	0
58	MG	1A	4018	1/1	0.94	0.07	39,39,39,39	0
58	MG	2N	201	1/1	0.94	0.07	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3175	1/1	0.94	0.16	31,31,31,31	0
58	MG	1a	1743	1/1	0.94	0.11	39,39,39,39	0
58	MG	1A	3863	1/1	0.94	0.33	25,25,25,25	0
58	MG	1A	3576	1/1	0.94	0.12	49,49,49,49	0
58	MG	2A	3316	1/1	0.94	0.12	62,62,62,62	0
60	TEL	2A	3826	58/58	0.94	0.14	27,41,47,55	0
58	MG	1A	3401	1/1	0.94	0.12	50,50,50,50	0
58	MG	1a	1717	1/1	0.95	0.17	76,76,76,76	0
58	MG	2A	3554	1/1	0.95	0.07	32,32,32,32	0
58	MG	1A	3136	1/1	0.95	0.12	30,30,30,30	0
58	MG	1a	1721	1/1	0.95	0.10	48,48,48,48	0
58	MG	1a	1722	1/1	0.95	0.06	57,57,57,57	0
58	MG	1A	4049	1/1	0.95	0.06	20,20,20,20	0
58	MG	1A	4051	1/1	0.95	0.09	51,51,51,51	0
58	MG	2A	3560	1/1	0.95	0.11	27,27,27,27	0
58	MG	1A	3138	1/1	0.95	0.07	35,35,35,35	0
58	MG	2A	3562	1/1	0.95	0.21	55,55,55,55	0
58	MG	2R	202	1/1	0.95	0.07	49,49,49,49	0
58	MG	1A	3372	1/1	0.95	0.07	45,45,45,45	0
58	MG	1A	3444	1/1	0.95	0.12	50,50,50,50	0
58	MG	1A	3224	1/1	0.95	0.17	35,35,35,35	0
58	MG	1A	3905	1/1	0.95	0.15	49,49,49,49	0
58	MG	1a	1732	1/1	0.95	0.13	50,50,50,50	0
58	MG	1a	1733	1/1	0.95	0.12	48,48,48,48	0
58	MG	2A	3573	1/1	0.95	0.15	45,45,45,45	0
58	MG	2A	3574	1/1	0.95	0.07	47,47,47,47	0
58	MG	1A	4063	1/1	0.95	0.18	48,48,48,48	0
58	MG	1A	3139	1/1	0.95	0.09	31,31,31,31	0
58	MG	1a	1738	1/1	0.95	0.19	42,42,42,42	0
58	MG	1A	3778	1/1	0.95	0.07	57,57,57,57	0
58	MG	1a	1740	1/1	0.95	0.09	46,46,46,46	0
58	MG	2A	3315	1/1	0.95	0.08	55,55,55,55	0
58	MG	1a	1741	1/1	0.95	0.14	35,35,35,35	0
58	MG	23	101	1/1	0.95	0.18	52,52,52,52	0
58	MG	2A	3317	1/1	0.95	0.16	36,36,36,36	0
58	MG	25	103	1/1	0.95	0.17	47,47,47,47	0
58	MG	1A	3781	1/1	0.95	0.07	16,16,16,16	0
58	MG	27	102	1/1	0.95	0.16	47,47,47,47	0
58	MG	1A	3633	1/1	0.95	0.10	28,28,28,28	0
58	MG	1A	3913	1/1	0.95	0.06	39,39,39,39	0
58	MG	1a	1748	1/1	0.95	0.15	43,43,43,43	0
58	MG	1A	3528	1/1	0.95	0.07	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3108	1/1	0.95	0.06	47,47,47,47	0
58	MG	11	101	1/1	0.95	0.30	33,33,33,33	0
58	MG	2A	3594	1/1	0.95	0.19	36,36,36,36	0
58	MG	1A	3915	1/1	0.95	0.08	51,51,51,51	0
58	MG	2A	3326	1/1	0.95	0.15	49,49,49,49	0
58	MG	2A	3598	1/1	0.95	0.12	41,41,41,41	0
58	MG	2A	3111	1/1	0.95	0.10	41,41,41,41	0
58	MG	1A	3785	1/1	0.95	0.13	37,37,37,37	0
58	MG	2A	3601	1/1	0.95	0.08	45,45,45,45	0
58	MG	2A	3329	1/1	0.95	0.09	58,58,58,58	0
58	MG	2a	3014	1/1	0.95	0.12	50,50,50,50	0
58	MG	2A	3330	1/1	0.95	0.06	63,63,63,63	0
58	MG	1A	3070	1/1	0.95	0.15	36,36,36,36	0
58	MG	2A	3115	1/1	0.95	0.23	58,58,58,58	0
58	MG	1A	3637	1/1	0.95	0.12	60,60,60,60	0
58	MG	12	101	1/1	0.95	0.07	37,37,37,37	0
58	MG	2A	3118	1/1	0.95	0.17	58,58,58,58	0
58	MG	12	102	1/1	0.95	0.12	36,36,36,36	0
58	MG	13	102	1/1	0.95	0.09	37,37,37,37	0
58	MG	1A	3178	1/1	0.95	0.10	27,27,27,27	0
58	MG	2A	3125	1/1	0.95	0.07	40,40,40,40	0
58	MG	2A	3617	1/1	0.95	0.19	64,64,64,64	0
58	MG	2A	3341	1/1	0.95	0.12	57,57,57,57	0
58	MG	1A	3180	1/1	0.95	0.05	30,30,30,30	0
58	MG	2a	3028	1/1	0.95	0.13	77,77,77,77	0
58	MG	2A	3622	1/1	0.95	0.11	46,46,46,46	0
58	MG	1A	3641	1/1	0.95	0.09	33,33,33,33	0
58	MG	1A	3229	1/1	0.95	0.15	29,29,29,29	0
58	MG	2A	3627	1/1	0.95	0.06	30,30,30,30	0
58	MG	1a	1762	1/1	0.95	0.16	62,62,62,62	0
58	MG	2A	3347	1/1	0.95	0.07	56,56,56,56	0
58	MG	15	104	1/1	0.95	0.21	38,38,38,38	0
58	MG	2A	3349	1/1	0.95	0.15	51,51,51,51	0
58	MG	2A	3350	1/1	0.95	0.09	49,49,49,49	0
58	MG	2A	3633	1/1	0.95	0.10	56,56,56,56	0
58	MG	2A	3131	1/1	0.95	0.12	31,31,31,31	0
58	MG	1A	3276	1/1	0.95	0.11	62,62,62,62	0
58	MG	2A	3135	1/1	0.95	0.13	43,43,43,43	0
58	MG	1a	1766	1/1	0.95	0.15	59,59,59,59	0
58	MG	1a	1767	1/1	0.95	0.09	57,57,57,57	0
58	MG	1A	3142	1/1	0.95	0.06	38,38,38,38	0
58	MG	1B	206	1/1	0.95	0.06	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3536	1/1	0.95	0.06	31,31,31,31	0
58	MG	1B	208	1/1	0.95	0.17	52,52,52,52	0
58	MG	2A	3143	1/1	0.95	0.14	59,59,59,59	0
58	MG	1A	3537	1/1	0.95	0.09	53,53,53,53	0
58	MG	1A	3805	1/1	0.95	0.09	33,33,33,33	0
58	MG	17	105	1/1	0.95	0.13	35,35,35,35	0
58	MG	1A	3384	1/1	0.95	0.09	62,62,62,62	0
58	MG	2A	3367	1/1	0.95	0.08	59,59,59,59	0
58	MG	1B	212	1/1	0.95	0.20	52,52,52,52	0
58	MG	1a	1782	1/1	0.95	0.09	75,75,75,75	0
58	MG	2A	3151	1/1	0.95	0.16	55,55,55,55	0
58	MG	2a	3058	1/1	0.95	0.21	60,60,60,60	0
58	MG	1A	3091	1/1	0.95	0.05	28,28,28,28	0
58	MG	18	105	1/1	0.95	0.07	32,32,32,32	0
58	MG	2A	3658	1/1	0.95	0.07	62,62,62,62	0
58	MG	2A	3659	1/1	0.95	0.13	46,46,46,46	0
58	MG	2A	3660	1/1	0.95	0.06	64,64,64,64	0
58	MG	2A	3374	1/1	0.95	0.20	41,41,41,41	0
58	MG	1A	3005	1/1	0.95	0.10	39,39,39,39	0
58	MG	1A	3944	1/1	0.95	0.06	31,31,31,31	0
58	MG	2A	3665	1/1	0.95	0.07	72,72,72,72	0
58	MG	1B	217	1/1	0.95	0.20	46,46,46,46	0
58	MG	1a	1788	1/1	0.95	0.11	38,38,38,38	0
58	MG	1A	3284	1/1	0.95	0.39	27,27,27,27	0
58	MG	2A	3669	1/1	0.95	0.05	60,60,60,60	0
58	MG	1A	3390	1/1	0.95	0.07	30,30,30,30	0
58	MG	1a	1604	1/1	0.95	0.10	60,60,60,60	0
58	MG	1a	1605	1/1	0.95	0.16	39,39,39,39	0
58	MG	2A	3162	1/1	0.95	0.06	36,36,36,36	0
58	MG	1A	3391	1/1	0.95	0.10	53,53,53,53	0
58	MG	1A	3658	1/1	0.95	0.08	32,32,32,32	0
58	MG	2A	3387	1/1	0.95	0.22	38,38,38,38	0
58	MG	2A	3165	1/1	0.95	0.12	36,36,36,36	0
58	MG	2a	3081	1/1	0.95	0.17	44,44,44,44	0
58	MG	1A	3550	1/1	0.95	0.08	38,38,38,38	0
58	MG	1a	1798	1/1	0.95	0.19	46,46,46,46	0
58	MG	2A	3686	1/1	0.95	0.11	36,36,36,36	0
58	MG	1a	1799	1/1	0.95	0.23	55,55,55,55	0
58	MG	2A	3169	1/1	0.95	0.08	32,32,32,32	0
58	MG	1A	3551	1/1	0.95	0.25	34,34,34,34	0
58	MG	2A	3171	1/1	0.95	0.10	50,50,50,50	0
58	MG	1a	1610	1/1	0.95	0.13	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2a	3093	1/1	0.95	0.07	64,64,64,64	0
58	MG	1A	3665	1/1	0.95	0.06	25,25,25,25	0
58	MG	1A	3236	1/1	0.95	0.29	42,42,42,42	0
58	MG	1a	1804	1/1	0.95	0.35	50,50,50,50	0
58	MG	1A	3395	1/1	0.95	0.09	38,38,38,38	0
58	MG	1A	3396	1/1	0.95	0.20	59,59,59,59	0
58	MG	1B	233	1/1	0.95	0.07	57,57,57,57	0
58	MG	1A	3957	1/1	0.95	0.08	57,57,57,57	0
58	MG	1A	3958	1/1	0.95	0.11	54,54,54,54	0
58	MG	1A	3397	1/1	0.95	0.08	44,44,44,44	0
58	MG	1A	3337	1/1	0.95	0.12	37,37,37,37	0
58	MG	1A	3338	1/1	0.95	0.08	35,35,35,35	0
58	MG	2A	3186	1/1	0.95	0.12	44,44,44,44	0
58	MG	2A	3708	1/1	0.95	0.13	45,45,45,45	0
58	MG	1A	3022	1/1	0.95	0.07	18,18,18,18	0
58	MG	1A	3118	1/1	0.95	0.14	39,39,39,39	0
58	MG	1A	3242	1/1	0.95	0.17	38,38,38,38	0
58	MG	1p	101	1/1	0.95	0.07	55,55,55,55	0
58	MG	1A	3682	1/1	0.95	0.09	35,35,35,35	0
58	MG	1A	3120	1/1	0.95	0.10	29,29,29,29	0
58	MG	1D	311	1/1	0.95	0.16	30,30,30,30	0
58	MG	1A	3078	1/1	0.95	0.07	35,35,35,35	0
58	MG	1A	3476	1/1	0.95	0.21	30,30,30,30	0
58	MG	1A	3079	1/1	0.95	0.05	29,29,29,29	0
58	MG	1E	303	1/1	0.95	0.05	21,21,21,21	0
58	MG	1A	3196	1/1	0.95	0.26	31,31,31,31	0
58	MG	2A	3200	1/1	0.95	0.11	59,59,59,59	0
58	MG	2A	3201	1/1	0.95	0.16	48,48,48,48	0
58	MG	2A	3724	1/1	0.95	0.22	62,62,62,62	0
58	MG	2A	3202	1/1	0.95	0.06	34,34,34,34	0
58	MG	1A	3006	1/1	0.95	0.10	43,43,43,43	0
58	MG	1A	3975	1/1	0.95	0.09	33,33,33,33	0
58	MG	1a	1640	1/1	0.95	0.21	42,42,42,42	0
58	MG	2A	3208	1/1	0.95	0.10	51,51,51,51	0
58	MG	1A	3848	1/1	0.95	0.07	48,48,48,48	0
58	MG	1A	3082	1/1	0.95	0.16	34,34,34,34	0
58	MG	1F	304	1/1	0.95	0.10	43,43,43,43	0
58	MG	1A	3417	1/1	0.95	0.07	36,36,36,36	0
58	MG	2A	3215	1/1	0.95	0.10	37,37,37,37	0
58	MG	1A	3157	1/1	0.95	0.11	24,24,24,24	0
58	MG	2a	3137	1/1	0.95	0.17	53,53,53,53	0
58	MG	1A	3984	1/1	0.95	0.06	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3419	1/1	0.95	0.16	54,54,54,54	0
58	MG	1x	112	1/1	0.95	0.20	60,60,60,60	0
58	MG	2A	3443	1/1	0.95	0.22	31,31,31,31	0
58	MG	1G	201	1/1	0.95	0.14	42,42,42,42	0
58	MG	1G	203	1/1	0.95	0.06	53,53,53,53	0
58	MG	2A	3003	1/1	0.95	0.17	48,48,48,48	0
58	MG	2A	3224	1/1	0.95	0.14	40,40,40,40	0
58	MG	1G	204	1/1	0.95	0.09	33,33,33,33	0
58	MG	1G	205	1/1	0.95	0.13	47,47,47,47	0
58	MG	1N	201	1/1	0.95	0.07	28,28,28,28	0
58	MG	1N	202	1/1	0.95	0.07	34,34,34,34	0
58	MG	2A	3455	1/1	0.95	0.13	53,53,53,53	0
58	MG	1a	1657	1/1	0.95	0.06	61,61,61,61	0
58	MG	1A	3307	1/1	0.95	0.19	54,54,54,54	0
58	MG	2a	3157	1/1	0.95	0.10	66,66,66,66	0
58	MG	1A	3486	1/1	0.95	0.28	40,40,40,40	0
58	MG	2A	3459	1/1	0.95	0.13	57,57,57,57	0
58	MG	2A	3013	1/1	0.95	0.22	44,44,44,44	0
58	MG	1N	205	1/1	0.95	0.10	57,57,57,57	0
58	MG	2A	3015	1/1	0.95	0.11	68,68,68,68	0
58	MG	1a	1662	1/1	0.95	0.13	43,43,43,43	0
58	MG	1A	3487	1/1	0.95	0.15	48,48,48,48	0
58	MG	1A	3581	1/1	0.95	0.10	36,36,36,36	0
58	MG	1A	3421	1/1	0.95	0.09	45,45,45,45	0
58	MG	2A	3776	1/1	0.95	0.13	44,44,44,44	0
58	MG	1P	201	1/1	0.95	0.14	31,31,31,31	0
58	MG	2A	3025	1/1	0.95	0.22	42,42,42,42	0
58	MG	2a	3171	1/1	0.95	0.15	64,64,64,64	0
58	MG	1A	3019	1/1	0.95	0.09	43,43,43,43	0
58	MG	1A	3309	1/1	0.95	0.20	55,55,55,55	0
58	MG	1A	3206	1/1	0.95	0.07	28,28,28,28	0
58	MG	1A	3255	1/1	0.95	0.11	43,43,43,43	0
58	MG	2A	3477	1/1	0.95	0.20	41,41,41,41	0
58	MG	1A	3043	1/1	0.95	0.31	34,34,34,34	0
58	MG	2A	3479	1/1	0.95	0.24	56,56,56,56	0
58	MG	1A	3044	1/1	0.95	0.16	33,33,33,33	0
58	MG	2A	3033	1/1	0.95	0.06	60,60,60,60	0
58	MG	2A	3800	1/1	0.95	0.10	27,27,27,27	0
58	MG	1A	3596	1/1	0.95	0.12	24,24,24,24	0
58	MG	2A	3485	1/1	0.95	0.10	48,48,48,48	0
58	MG	1A	3088	1/1	0.95	0.13	34,34,34,34	0
58	MG	2A	3487	1/1	0.95	0.10	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	4015	1/1	0.95	0.07	55,55,55,55	0
58	MG	1A	4016	1/1	0.95	0.07	47,47,47,47	0
58	MG	1R	201	1/1	0.95	0.12	37,37,37,37	0
58	MG	2A	3257	1/1	0.95	0.10	46,46,46,46	0
58	MG	1A	3716	1/1	0.95	0.07	42,42,42,42	0
58	MG	1R	203	1/1	0.95	0.06	38,38,38,38	0
58	MG	1R	204	1/1	0.95	0.31	48,48,48,48	0
58	MG	1A	3502	1/1	0.95	0.07	41,41,41,41	0
58	MG	1R	207	1/1	0.95	0.12	38,38,38,38	0
58	MG	1A	3165	1/1	0.95	0.12	40,40,40,40	0
58	MG	1T	202	1/1	0.95	0.10	41,41,41,41	0
58	MG	2a	3198	1/1	0.95	0.11	70,70,70,70	0
58	MG	1A	3872	1/1	0.95	0.08	27,27,27,27	0
58	MG	1A	3211	1/1	0.95	0.08	31,31,31,31	0
58	MG	1a	1691	1/1	0.95	0.14	36,36,36,36	0
58	MG	1A	3004	1/1	0.95	0.06	22,22,22,22	0
58	MG	2A	3509	1/1	0.95	0.07	40,40,40,40	0
58	MG	2A	3512	1/1	0.95	0.17	57,57,57,57	0
58	MG	1A	3604	1/1	0.95	0.10	35,35,35,35	0
58	MG	1A	3732	1/1	0.95	0.08	19,19,19,19	0
58	MG	2A	3271	1/1	0.95	0.15	40,40,40,40	0
58	MG	1A	3318	1/1	0.95	0.14	49,49,49,49	0
58	MG	1a	1696	1/1	0.95	0.24	50,50,50,50	0
58	MG	1U	208	1/1	0.95	0.13	32,32,32,32	0
58	MG	1A	3507	1/1	0.95	0.17	60,60,60,60	0
58	MG	1A	3745	1/1	0.95	0.07	54,54,54,54	0
58	MG	1A	3111	1/1	0.95	0.41	32,32,32,32	0
58	MG	2A	3525	1/1	0.95	0.09	40,40,40,40	0
58	MG	1a	1702	1/1	0.95	0.17	37,37,37,37	0
58	MG	1A	3611	1/1	0.95	0.11	40,40,40,40	0
58	MG	1V	204	1/1	0.95	0.07	27,27,27,27	0
58	MG	1a	1705	1/1	0.95	0.19	44,44,44,44	0
58	MG	1A	3367	1/1	0.95	0.19	50,50,50,50	0
58	MG	2D	301	1/1	0.95	0.18	49,49,49,49	0
58	MG	1A	3616	1/1	0.95	0.05	23,23,23,23	0
58	MG	2D	303	1/1	0.95	0.06	42,42,42,42	0
58	MG	2q	201	1/1	0.95	0.07	57,57,57,57	0
58	MG	1A	3510	1/1	0.95	0.08	42,42,42,42	0
58	MG	2r	101	1/1	0.95	0.14	52,52,52,52	0
58	MG	2A	3537	1/1	0.95	0.11	42,42,42,42	0
58	MG	2A	3069	1/1	0.95	0.09	41,41,41,41	0
58	MG	1A	3513	1/1	0.95	0.16	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2v	103	1/1	0.95	0.17	61,61,61,61	0
58	MG	1A	3221	1/1	0.95	0.07	33,33,33,33	0
58	MG	1a	1713	1/1	0.95	0.13	44,44,44,44	0
58	MG	2E	303	1/1	0.95	0.18	52,52,52,52	0
58	MG	1A	3516	1/1	0.95	0.15	38,38,38,38	0
58	MG	1A	3518	1/1	0.95	0.25	45,45,45,45	0
58	MG	2A	3547	1/1	0.95	0.08	46,46,46,46	0
58	MG	2A	3549	1/1	0.95	0.14	50,50,50,50	0
58	MG	2A	3076	1/1	0.95	0.09	48,48,48,48	0
58	MG	1X	102	1/1	0.95	0.08	37,37,37,37	0
58	MG	1A	4072	1/1	0.96	0.10	51,51,51,51	0
58	MG	1A	4073	1/1	0.96	0.06	40,40,40,40	0
58	MG	1A	3740	1/1	0.96	0.09	31,31,31,31	0
58	MG	1a	1772	1/1	0.96	0.10	40,40,40,40	0
58	MG	2A	3355	1/1	0.96	0.08	48,48,48,48	0
58	MG	2A	3603	1/1	0.96	0.21	55,55,55,55	0
58	MG	1A	3744	1/1	0.96	0.18	43,43,43,43	0
58	MG	1a	1774	1/1	0.96	0.11	44,44,44,44	0
58	MG	2Y	201	1/1	0.96	0.16	37,37,37,37	0
58	MG	1A	4076	1/1	0.96	0.19	46,46,46,46	0
58	MG	2A	3607	1/1	0.96	0.10	40,40,40,40	0
58	MG	1A	3517	1/1	0.96	0.09	37,37,37,37	0
58	MG	1A	4078	1/1	0.96	0.06	23,23,23,23	0
58	MG	21	102	1/1	0.96	0.22	53,53,53,53	0
58	MG	1A	3614	1/1	0.96	0.07	20,20,20,20	0
58	MG	1A	3077	1/1	0.96	0.07	41,41,41,41	0
58	MG	17	106	1/1	0.96	0.07	40,40,40,40	0
58	MG	25	102	1/1	0.96	0.10	49,49,49,49	0
58	MG	2A	3614	1/1	0.96	0.12	43,43,43,43	0
58	MG	1A	3617	1/1	0.96	0.06	30,30,30,30	0
58	MG	18	101	1/1	0.96	0.09	42,42,42,42	0
58	MG	1A	3901	1/1	0.96	0.12	30,30,30,30	0
58	MG	18	103	1/1	0.96	0.10	32,32,32,32	0
58	MG	2a	3001	1/1	0.96	0.10	57,57,57,57	0
58	MG	1B	202	1/1	0.96	0.12	38,38,38,38	0
58	MG	2A	3621	1/1	0.96	0.06	48,48,48,48	0
58	MG	1A	3378	1/1	0.96	0.18	25,25,25,25	0
58	MG	1A	3903	1/1	0.96	0.09	30,30,30,30	0
58	MG	1A	3327	1/1	0.96	0.05	26,26,26,26	0
58	MG	1A	3622	1/1	0.96	0.06	37,37,37,37	0
58	MG	1A	3754	1/1	0.96	0.12	26,26,26,26	0
58	MG	1A	3094	1/1	0.96	0.10	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3031	1/1	0.96	0.17	26,26,26,26	0
58	MG	1A	3177	1/1	0.96	0.10	31,31,31,31	0
58	MG	1A	3526	1/1	0.96	0.17	47,47,47,47	0
58	MG	1A	3760	1/1	0.96	0.07	12,12,12,12	0
58	MG	1B	214	1/1	0.96	0.18	65,65,65,65	0
58	MG	2A	3635	1/1	0.96	0.06	79,79,79,79	0
58	MG	1A	3765	1/1	0.96	0.10	21,21,21,21	0
58	MG	1A	3767	1/1	0.96	0.07	24,24,24,24	0
58	MG	1A	3145	1/1	0.96	0.20	28,28,28,28	0
58	MG	1A	3919	1/1	0.96	0.10	51,51,51,51	0
58	MG	1A	3008	1/1	0.96	0.08	17,17,17,17	0
58	MG	1B	220	1/1	0.96	0.10	34,34,34,34	0
58	MG	1A	3148	1/1	0.96	0.08	39,39,39,39	0
58	MG	1a	1616	1/1	0.96	0.08	63,63,63,63	0
58	MG	1A	3775	1/1	0.96	0.05	34,34,34,34	0
58	MG	1B	224	1/1	0.96	0.09	47,47,47,47	0
58	MG	1e	201	1/1	0.96	0.09	57,57,57,57	0
58	MG	1f	201	1/1	0.96	0.06	47,47,47,47	0
58	MG	1a	1620	1/1	0.96	0.10	59,59,59,59	0
58	MG	1A	3927	1/1	0.96	0.06	48,48,48,48	0
58	MG	1A	3334	1/1	0.96	0.10	46,46,46,46	0
58	MG	1B	227	1/1	0.96	0.09	55,55,55,55	0
58	MG	1A	3631	1/1	0.96	0.14	30,30,30,30	0
58	MG	2A	3655	1/1	0.96	0.05	42,42,42,42	0
58	MG	1A	3388	1/1	0.96	0.08	28,28,28,28	0
58	MG	1A	3780	1/1	0.96	0.10	54,54,54,54	0
58	MG	1A	3932	1/1	0.96	0.12	49,49,49,49	0
58	MG	1A	3933	1/1	0.96	0.08	52,52,52,52	0
58	MG	1A	3279	1/1	0.96	0.34	24,24,24,24	0
58	MG	1A	3230	1/1	0.96	0.06	29,29,29,29	0
58	MG	1a	1632	1/1	0.96	0.11	40,40,40,40	0
58	MG	1A	3037	1/1	0.96	0.09	21,21,21,21	0
58	MG	1B	237	1/1	0.96	0.07	55,55,55,55	0
58	MG	1a	1635	1/1	0.96	0.07	27,27,27,27	0
58	MG	1A	3535	1/1	0.96	0.27	23,23,23,23	0
58	MG	1A	3938	1/1	0.96	0.06	56,56,56,56	0
58	MG	1A	3786	1/1	0.96	0.05	36,36,36,36	0
58	MG	2A	3670	1/1	0.96	0.12	24,24,24,24	0
58	MG	1A	3185	1/1	0.96	0.06	63,63,63,63	0
58	MG	2A	3672	1/1	0.96	0.12	54,54,54,54	0
58	MG	1x	107	1/1	0.96	0.07	52,52,52,52	0
58	MG	2A	3674	1/1	0.96	0.07	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3943	1/1	0.96	0.08	51,51,51,51	0
58	MG	2A	3207	1/1	0.96	0.11	49,49,49,49	0
58	MG	1A	3234	1/1	0.96	0.10	33,33,33,33	0
58	MG	2A	3421	1/1	0.96	0.09	41,41,41,41	0
58	MG	2A	3422	1/1	0.96	0.18	34,34,34,34	0
58	MG	1A	3945	1/1	0.96	0.05	41,41,41,41	0
58	MG	1A	3790	1/1	0.96	0.09	29,29,29,29	0
58	MG	1A	3290	1/1	0.96	0.13	23,23,23,23	0
58	MG	1A	3794	1/1	0.96	0.28	25,25,25,25	0
58	MG	1A	3150	1/1	0.96	0.09	36,36,36,36	0
58	MG	1A	3541	1/1	0.96	0.06	35,35,35,35	0
58	MG	1A	3039	1/1	0.96	0.14	42,42,42,42	0
58	MG	1E	306	1/1	0.96	0.06	32,32,32,32	0
58	MG	1E	307	1/1	0.96	0.27	56,56,56,56	0
58	MG	1a	1652	1/1	0.96	0.14	42,42,42,42	0
58	MG	1a	1653	1/1	0.96	0.20	43,43,43,43	0
58	MG	2A	3695	1/1	0.96	0.09	35,35,35,35	0
58	MG	2A	3434	1/1	0.96	0.11	34,34,34,34	0
58	MG	1A	3645	1/1	0.96	0.15	37,37,37,37	0
58	MG	2A	3699	1/1	0.96	0.06	49,49,49,49	0
58	MG	1A	3100	1/1	0.96	0.15	23,23,23,23	0
58	MG	1A	3465	1/1	0.96	0.10	35,35,35,35	0
58	MG	1A	3545	1/1	0.96	0.21	42,42,42,42	0
58	MG	1F	302	1/1	0.96	0.10	34,34,34,34	0
58	MG	1A	3466	1/1	0.96	0.18	35,35,35,35	0
58	MG	2A	3017	1/1	0.96	0.07	38,38,38,38	0
58	MG	1A	3548	1/1	0.96	0.10	30,30,30,30	0
58	MG	1A	3345	1/1	0.96	0.12	48,48,48,48	0
58	MG	2A	3232	1/1	0.96	0.10	75,75,75,75	0
58	MG	2A	3021	1/1	0.96	0.11	62,62,62,62	0
58	MG	1A	3808	1/1	0.96	0.05	29,29,29,29	0
58	MG	1A	3468	1/1	0.96	0.04	44,44,44,44	0
58	MG	2a	3087	1/1	0.96	0.16	66,66,66,66	0
58	MG	1A	3402	1/1	0.96	0.12	35,35,35,35	0
58	MG	2a	3089	1/1	0.96	0.12	61,61,61,61	0
58	MG	1G	202	1/1	0.96	0.15	46,46,46,46	0
58	MG	2A	3451	1/1	0.96	0.08	50,50,50,50	0
58	MG	2A	3453	1/1	0.96	0.11	60,60,60,60	0
58	MG	1A	3811	1/1	0.96	0.08	31,31,31,31	0
58	MG	1A	3190	1/1	0.96	0.09	36,36,36,36	0
58	MG	1a	1669	1/1	0.96	0.32	59,59,59,59	0
58	MG	1A	3660	1/1	0.96	0.05	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3661	1/1	0.96	0.10	14,14,14,14	0
58	MG	1a	1672	1/1	0.96	0.07	48,48,48,48	0
58	MG	1A	3404	1/1	0.96	0.11	41,41,41,41	0
58	MG	2A	3245	1/1	0.96	0.15	43,43,43,43	0
58	MG	2A	3726	1/1	0.96	0.08	32,32,32,32	0
58	MG	1A	3127	1/1	0.96	0.29	29,29,29,29	0
58	MG	1A	3406	1/1	0.96	0.05	48,48,48,48	0
58	MG	2A	3465	1/1	0.96	0.05	48,48,48,48	0
58	MG	1A	3407	1/1	0.96	0.15	39,39,39,39	0
58	MG	2A	3732	1/1	0.96	0.07	49,49,49,49	0
58	MG	2a	3108	1/1	0.96	0.12	70,70,70,70	0
58	MG	1N	206	1/1	0.96	0.04	39,39,39,39	0
58	MG	1A	3821	1/1	0.96	0.22	35,35,35,35	0
58	MG	1A	3558	1/1	0.96	0.05	36,36,36,36	0
58	MG	1A	3976	1/1	0.96	0.08	38,38,38,38	0
58	MG	2A	3253	1/1	0.96	0.06	39,39,39,39	0
58	MG	1A	3559	1/1	0.96	0.20	29,29,29,29	0
58	MG	1A	3825	1/1	0.96	0.10	45,45,45,45	0
58	MG	1a	1684	1/1	0.96	0.15	30,30,30,30	0
58	MG	2A	3045	1/1	0.96	0.15	31,31,31,31	0
58	MG	1A	3826	1/1	0.96	0.13	36,36,36,36	0
58	MG	1A	3083	1/1	0.96	0.14	26,26,26,26	0
58	MG	1A	3067	1/1	0.96	0.09	42,42,42,42	0
58	MG	1A	3304	1/1	0.96	0.20	44,44,44,44	0
58	MG	1A	3676	1/1	0.96	0.12	28,28,28,28	0
58	MG	2A	3483	1/1	0.96	0.10	63,63,63,63	0
58	MG	1A	3411	1/1	0.96	0.09	56,56,56,56	0
58	MG	1A	3567	1/1	0.96	0.08	44,44,44,44	0
58	MG	1Q	205	1/1	0.96	0.08	33,33,33,33	0
58	MG	1A	3991	1/1	0.96	0.07	35,35,35,35	0
58	MG	2A	3056	1/1	0.96	0.10	65,65,65,65	0
58	MG	1A	3568	1/1	0.96	0.08	37,37,37,37	0
58	MG	1A	3194	1/1	0.96	0.19	27,27,27,27	0
58	MG	1A	3997	1/1	0.96	0.08	39,39,39,39	0
58	MG	1A	3999	1/1	0.96	0.06	69,69,69,69	0
58	MG	2A	3761	1/1	0.96	0.08	53,53,53,53	0
58	MG	1A	3836	1/1	0.96	0.11	57,57,57,57	0
58	MG	2A	3763	1/1	0.96	0.14	47,47,47,47	0
58	MG	1A	3683	1/1	0.96	0.12	39,39,39,39	0
58	MG	1A	3838	1/1	0.96	0.05	19,19,19,19	0
58	MG	2A	3277	1/1	0.96	0.13	44,44,44,44	0
58	MG	2A	3769	1/1	0.96	0.11	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3064	1/1	0.96	0.06	34,34,34,34	0
58	MG	1A	3195	1/1	0.96	0.08	17,17,17,17	0
58	MG	1A	4005	1/1	0.96	0.15	53,53,53,53	0
58	MG	1A	3415	1/1	0.96	0.08	29,29,29,29	0
58	MG	2a	3147	1/1	0.96	0.08	76,76,76,76	0
58	MG	2A	3506	1/1	0.96	0.15	42,42,42,42	0
58	MG	2A	3778	1/1	0.96	0.06	34,34,34,34	0
58	MG	1A	4007	1/1	0.96	0.07	52,52,52,52	0
58	MG	1A	3842	1/1	0.96	0.07	24,24,24,24	0
58	MG	2A	3782	1/1	0.96	0.09	44,44,44,44	0
58	MG	2A	3783	1/1	0.96	0.12	56,56,56,56	0
58	MG	2A	3510	1/1	0.96	0.06	48,48,48,48	0
58	MG	2A	3786	1/1	0.96	0.10	48,48,48,48	0
58	MG	1A	3845	1/1	0.96	0.10	46,46,46,46	0
58	MG	2A	3789	1/1	0.96	0.10	45,45,45,45	0
58	MG	1a	1709	1/1	0.96	0.06	43,43,43,43	0
58	MG	1A	3416	1/1	0.96	0.14	37,37,37,37	0
58	MG	1A	3085	1/1	0.96	0.08	39,39,39,39	0
58	MG	2A	3795	1/1	0.96	0.08	49,49,49,49	0
58	MG	1A	3688	1/1	0.96	0.07	27,27,27,27	0
58	MG	2a	3165	1/1	0.96	0.10	45,45,45,45	0
58	MG	2A	3517	1/1	0.96	0.16	42,42,42,42	0
58	MG	1U	209	1/1	0.96	0.28	30,30,30,30	0
58	MG	1A	3689	1/1	0.96	0.09	16,16,16,16	0
58	MG	2A	3801	1/1	0.96	0.10	33,33,33,33	0
58	MG	1A	3850	1/1	0.96	0.09	36,36,36,36	0
58	MG	1A	3033	1/1	0.96	0.36	28,28,28,28	0
58	MG	1A	3057	1/1	0.96	0.19	36,36,36,36	0
58	MG	2A	3524	1/1	0.96	0.09	27,27,27,27	0
58	MG	1a	1718	1/1	0.96	0.16	60,60,60,60	0
58	MG	1A	3199	1/1	0.96	0.29	42,42,42,42	0
58	MG	1a	1720	1/1	0.96	0.16	49,49,49,49	0
58	MG	1A	3159	1/1	0.96	0.07	25,25,25,25	0
58	MG	1A	3160	1/1	0.96	0.09	24,24,24,24	0
58	MG	2A	3087	1/1	0.96	0.06	32,32,32,32	0
58	MG	1a	1723	1/1	0.96	0.07	59,59,59,59	0
58	MG	1A	4024	1/1	0.96	0.09	28,28,28,28	0
58	MG	2A	3090	1/1	0.96	0.08	46,46,46,46	0
58	MG	1A	3423	1/1	0.96	0.18	29,29,29,29	0
58	MG	1A	3161	1/1	0.96	0.05	24,24,24,24	0
58	MG	2A	3820	1/1	0.96	0.10	42,42,42,42	0
58	MG	2A	3093	1/1	0.96	0.07	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3094	1/1	0.96	0.10	37,37,37,37	0
58	MG	1a	1727	1/1	0.96	0.06	34,34,34,34	0
58	MG	2A	3544	1/1	0.96	0.12	34,34,34,34	0
58	MG	1A	3493	1/1	0.96	0.08	28,28,28,28	0
58	MG	1W	204	1/1	0.96	0.07	40,40,40,40	0
58	MG	2A	3548	1/1	0.96	0.12	34,34,34,34	0
58	MG	1A	3048	1/1	0.96	0.05	24,24,24,24	0
58	MG	1X	101	1/1	0.96	0.06	35,35,35,35	0
58	MG	2A	3551	1/1	0.96	0.10	32,32,32,32	0
58	MG	1A	3110	1/1	0.96	0.06	31,31,31,31	0
58	MG	1A	3588	1/1	0.96	0.10	41,41,41,41	0
58	MG	1A	4033	1/1	0.96	0.06	15,15,15,15	0
58	MG	1A	3135	1/1	0.96	0.06	27,27,27,27	0
58	MG	1A	3429	1/1	0.96	0.16	36,36,36,36	0
58	MG	1Z	301	1/1	0.96	0.07	54,54,54,54	0
58	MG	1A	3500	1/1	0.96	0.13	29,29,29,29	0
58	MG	1A	3593	1/1	0.96	0.10	54,54,54,54	0
58	MG	1a	1742	1/1	0.96	0.15	44,44,44,44	0
58	MG	1A	3711	1/1	0.96	0.08	41,41,41,41	0
58	MG	2B	218	1/1	0.96	0.14	53,53,53,53	0
58	MG	1A	3073	1/1	0.96	0.17	26,26,26,26	0
58	MG	1A	3167	1/1	0.96	0.07	36,36,36,36	0
58	MG	1a	1747	1/1	0.96	0.12	37,37,37,37	0
58	MG	1A	3213	1/1	0.96	0.16	29,29,29,29	0
58	MG	10	106	1/1	0.96	0.10	47,47,47,47	0
58	MG	2A	3569	1/1	0.96	0.07	64,64,64,64	0
58	MG	1A	3015	1/1	0.96	0.06	38,38,38,38	0
58	MG	1A	3434	1/1	0.96	0.15	31,31,31,31	0
58	MG	2A	3119	1/1	0.96	0.18	46,46,46,46	0
58	MG	1A	3717	1/1	0.96	0.07	34,34,34,34	0
58	MG	2A	3576	1/1	0.96	0.10	43,43,43,43	0
58	MG	1A	4054	1/1	0.96	0.10	48,48,48,48	0
58	MG	2A	3334	1/1	0.96	0.09	58,58,58,58	0
58	MG	1A	4055	1/1	0.96	0.06	33,33,33,33	0
58	MG	1A	3876	1/1	0.96	0.09	42,42,42,42	0
58	MG	1A	3435	1/1	0.96	0.17	33,33,33,33	0
58	MG	1A	3266	1/1	0.96	0.11	55,55,55,55	0
58	MG	1A	3722	1/1	0.96	0.09	52,52,52,52	0
58	MG	2F	304	1/1	0.96	0.28	45,45,45,45	0
58	MG	1A	3215	1/1	0.96	0.07	39,39,39,39	0
58	MG	1A	3076	1/1	0.96	0.05	23,23,23,23	0
58	MG	2A	3342	1/1	0.96	0.17	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3588	1/1	0.96	0.12	56,56,56,56	0
58	MG	1A	3729	1/1	0.96	0.10	16,16,16,16	0
58	MG	1A	3511	1/1	0.96	0.07	30,30,30,30	0
58	MG	2A	3133	1/1	0.96	0.21	43,43,43,43	0
58	MG	13	103	1/1	0.96	0.11	49,49,49,49	0
58	MG	1A	3140	1/1	0.96	0.10	30,30,30,30	0
58	MG	1A	3375	1/1	0.96	0.19	55,55,55,55	0
60	TEL	1A	4082	58/58	0.96	0.10	18,25,33,38	0
58	MG	1A	3735	1/1	0.96	0.16	42,42,42,42	0
58	MG	1A	3171	1/1	0.96	0.07	41,41,41,41	0
58	MG	1A	3252	1/1	0.97	0.14	29,29,29,29	0
58	MG	1A	3292	1/1	0.97	0.07	43,43,43,43	0
58	MG	1A	3220	1/1	0.97	0.11	43,43,43,43	0
58	MG	2a	3053	1/1	0.97	0.13	43,43,43,43	0
58	MG	2A	3765	1/1	0.97	0.04	36,36,36,36	0
58	MG	1A	3694	1/1	0.97	0.08	36,36,36,36	0
58	MG	2A	3586	1/1	0.97	0.09	48,48,48,48	0
58	MG	1W	205	1/1	0.97	0.12	31,31,31,31	0
58	MG	1A	3873	1/1	0.97	0.11	32,32,32,32	0
58	MG	2A	3773	1/1	0.97	0.08	55,55,55,55	0
58	MG	1A	3106	1/1	0.97	0.11	25,25,25,25	0
58	MG	1A	3058	1/1	0.97	0.04	28,28,28,28	0
58	MG	1X	103	1/1	0.97	0.13	42,42,42,42	0
58	MG	2a	3063	1/1	0.97	0.13	57,57,57,57	0
58	MG	1A	3298	1/1	0.97	0.12	41,41,41,41	0
58	MG	1A	3978	1/1	0.97	0.10	31,31,31,31	0
58	MG	1A	3299	1/1	0.97	0.12	31,31,31,31	0
58	MG	1A	3563	1/1	0.97	0.15	36,36,36,36	0
58	MG	1A	3879	1/1	0.97	0.05	22,22,22,22	0
58	MG	2A	3121	1/1	0.97	0.12	53,53,53,53	0
58	MG	2A	3122	1/1	0.97	0.10	37,37,37,37	0
58	MG	2A	3785	1/1	0.97	0.13	36,36,36,36	0
58	MG	1A	3880	1/1	0.97	0.07	22,22,22,22	0
58	MG	1a	1683	1/1	0.97	0.10	48,48,48,48	0
58	MG	1A	3038	1/1	0.97	0.12	33,33,33,33	0
58	MG	1A	3565	1/1	0.97	0.08	46,46,46,46	0
58	MG	10	102	1/1	0.97	0.29	48,48,48,48	0
58	MG	1A	3566	1/1	0.97	0.06	35,35,35,35	0
58	MG	1A	3987	1/1	0.97	0.08	46,46,46,46	0
58	MG	1A	3884	1/1	0.97	0.10	29,29,29,29	0
58	MG	1A	3989	1/1	0.97	0.07	22,22,22,22	0
58	MG	1A	3514	1/1	0.97	0.07	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2a	3082	1/1	0.97	0.11	50,50,50,50	0
58	MG	1A	3109	1/1	0.97	0.05	22,22,22,22	0
58	MG	2A	3134	1/1	0.97	0.11	44,44,44,44	0
58	MG	1A	3176	1/1	0.97	0.20	33,33,33,33	0
58	MG	1A	3802	1/1	0.97	0.05	22,22,22,22	0
58	MG	2A	3137	1/1	0.97	0.10	38,38,38,38	0
58	MG	1A	3996	1/1	0.97	0.10	28,28,28,28	0
58	MG	1A	3707	1/1	0.97	0.07	46,46,46,46	0
58	MG	1A	3998	1/1	0.97	0.09	39,39,39,39	0
58	MG	1A	3804	1/1	0.97	0.15	30,30,30,30	0
58	MG	1A	3303	1/1	0.97	0.15	42,42,42,42	0
58	MG	1A	4001	1/1	0.97	0.10	56,56,56,56	0
58	MG	1B	238	1/1	0.97	0.06	31,31,31,31	0
58	MG	2A	3624	1/1	0.97	0.10	43,43,43,43	0
58	MG	1A	3710	1/1	0.97	0.07	45,45,45,45	0
58	MG	2A	3816	1/1	0.97	0.09	32,32,32,32	0
58	MG	1A	3003	1/1	0.97	0.09	24,24,24,24	0
58	MG	1D	301	1/1	0.97	0.15	22,22,22,22	0
58	MG	2A	3148	1/1	0.97	0.10	55,55,55,55	0
58	MG	1a	1706	1/1	0.97	0.14	39,39,39,39	0
58	MG	1A	3144	1/1	0.97	0.05	39,39,39,39	0
58	MG	2A	3822	1/1	0.97	0.18	47,47,47,47	0
58	MG	1A	3896	1/1	0.97	0.08	41,41,41,41	0
58	MG	2A	3301	1/1	0.97	0.20	51,51,51,51	0
58	MG	2A	3825	1/1	0.97	0.10	49,49,49,49	0
58	MG	2a	3107	1/1	0.97	0.28	48,48,48,48	0
58	MG	1D	304	1/1	0.97	0.09	31,31,31,31	0
58	MG	2A	3303	1/1	0.97	0.15	48,48,48,48	0
58	MG	1D	305	1/1	0.97	0.06	17,17,17,17	0
58	MG	2A	3009	1/1	0.97	0.06	47,47,47,47	0
58	MG	1A	3897	1/1	0.97	0.05	31,31,31,31	0
58	MG	1D	308	1/1	0.97	0.13	29,29,29,29	0
58	MG	2A	3012	1/1	0.97	0.07	46,46,46,46	0
58	MG	2A	3642	1/1	0.97	0.08	34,34,34,34	0
58	MG	1A	3061	1/1	0.97	0.06	32,32,32,32	0
58	MG	1A	4008	1/1	0.97	0.13	36,36,36,36	0
58	MG	1A	3201	1/1	0.97	0.08	19,19,19,19	0
58	MG	1A	3428	1/1	0.97	0.13	41,41,41,41	0
58	MG	2A	3469	1/1	0.97	0.07	29,29,29,29	0
58	MG	1A	4013	1/1	0.97	0.09	42,42,42,42	0
58	MG	2a	3122	1/1	0.97	0.09	44,44,44,44	0
58	MG	1A	3202	1/1	0.97	0.06	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	17	104	1/1	0.97	0.15	34,34,34,34	0
58	MG	1A	3813	1/1	0.97	0.06	37,37,37,37	0
58	MG	1A	3203	1/1	0.97	0.09	40,40,40,40	0
58	MG	2A	3475	1/1	0.97	0.07	36,36,36,36	0
58	MG	1A	3052	1/1	0.97	0.21	39,39,39,39	0
58	MG	2A	3024	1/1	0.97	0.09	50,50,50,50	0
58	MG	1A	3389	1/1	0.97	0.20	29,29,29,29	0
58	MG	1A	3909	1/1	0.97	0.06	29,29,29,29	0
58	MG	1E	309	1/1	0.97	0.08	23,23,23,23	0
58	MG	2D	306	1/1	0.97	0.06	27,27,27,27	0
58	MG	2A	3172	1/1	0.97	0.10	37,37,37,37	0
58	MG	2a	3135	1/1	0.97	0.14	57,57,57,57	0
58	MG	1A	3182	1/1	0.97	0.16	41,41,41,41	0
58	MG	2A	3661	1/1	0.97	0.04	50,50,50,50	0
58	MG	2a	3138	1/1	0.97	0.08	51,51,51,51	0
58	MG	1A	3723	1/1	0.97	0.11	47,47,47,47	0
58	MG	1A	3045	1/1	0.97	0.12	30,30,30,30	0
58	MG	1F	301	1/1	0.97	0.15	27,27,27,27	0
58	MG	2A	3177	1/1	0.97	0.07	43,43,43,43	0
58	MG	2A	3032	1/1	0.97	0.07	40,40,40,40	0
58	MG	1A	3725	1/1	0.97	0.05	46,46,46,46	0
58	MG	1A	3392	1/1	0.97	0.04	26,26,26,26	0
58	MG	1A	3728	1/1	0.97	0.06	46,46,46,46	0
58	MG	1A	3824	1/1	0.97	0.05	47,47,47,47	0
58	MG	1A	3917	1/1	0.97	0.05	17,17,17,17	0
58	MG	1F	310	1/1	0.97	0.04	47,47,47,47	0
58	MG	1a	1737	1/1	0.97	0.08	51,51,51,51	0
58	MG	2a	3151	1/1	0.97	0.21	52,52,52,52	0
58	MG	1A	4028	1/1	0.97	0.06	35,35,35,35	0
58	MG	2a	3153	1/1	0.97	0.07	83,83,83,83	0
58	MG	2A	3676	1/1	0.97	0.06	32,32,32,32	0
58	MG	1A	3584	1/1	0.97	0.06	26,26,26,26	0
58	MG	1A	3730	1/1	0.97	0.17	29,29,29,29	0
58	MG	1A	3585	1/1	0.97	0.05	34,34,34,34	0
58	MG	1A	3586	1/1	0.97	0.16	56,56,56,56	0
58	MG	1A	4034	1/1	0.97	0.11	38,38,38,38	0
58	MG	1A	3924	1/1	0.97	0.05	45,45,45,45	0
58	MG	2A	3507	1/1	0.97	0.06	41,41,41,41	0
58	MG	1A	3654	1/1	0.97	0.07	23,23,23,23	0
58	MG	1A	3734	1/1	0.97	0.05	33,33,33,33	0
58	MG	2U	201	1/1	0.97	0.17	47,47,47,47	0
58	MG	1A	3393	1/1	0.97	0.07	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3511	1/1	0.97	0.06	34,34,34,34	0
58	MG	1A	3009	1/1	0.97	0.04	23,23,23,23	0
58	MG	1a	1618	1/1	0.97	0.10	66,66,66,66	0
58	MG	2A	3198	1/1	0.97	0.22	61,61,61,61	0
58	MG	1A	4042	1/1	0.97	0.12	57,57,57,57	0
58	MG	1A	4044	1/1	0.97	0.06	38,38,38,38	0
58	MG	1a	1621	1/1	0.97	0.25	54,54,54,54	0
58	MG	1O	202	1/1	0.97	0.12	50,50,50,50	0
58	MG	2A	3697	1/1	0.97	0.11	51,51,51,51	0
58	MG	1A	3186	1/1	0.97	0.07	27,27,27,27	0
58	MG	1A	3741	1/1	0.97	0.09	19,19,19,19	0
58	MG	1A	3013	1/1	0.97	0.17	25,25,25,25	0
58	MG	2a	3178	1/1	0.97	0.13	48,48,48,48	0
58	MG	2A	3206	1/1	0.97	0.15	42,42,42,42	0
58	MG	21	104	1/1	0.97	0.07	43,43,43,43	0
58	MG	2A	3523	1/1	0.97	0.17	52,52,52,52	0
58	MG	1P	202	1/1	0.97	0.14	36,36,36,36	0
58	MG	25	101	1/1	0.97	0.30	46,46,46,46	0
58	MG	1A	3591	1/1	0.97	0.07	22,22,22,22	0
58	MG	1P	205	1/1	0.97	0.28	28,28,28,28	0
58	MG	2A	3361	1/1	0.97	0.12	61,61,61,61	0
58	MG	1A	3240	1/1	0.97	0.18	35,35,35,35	0
58	MG	2A	3529	1/1	0.97	0.07	32,32,32,32	0
58	MG	28	101	1/1	0.97	0.10	64,64,64,64	0
58	MG	1A	3355	1/1	0.97	0.07	51,51,51,51	0
58	MG	1a	1763	1/1	0.97	0.08	62,62,62,62	0
58	MG	2A	3214	1/1	0.97	0.21	39,39,39,39	0
58	MG	1A	3538	1/1	0.97	0.19	31,31,31,31	0
58	MG	1A	3841	1/1	0.97	0.04	38,38,38,38	0
58	MG	1A	3166	1/1	0.97	0.06	27,27,27,27	0
58	MG	2A	3369	1/1	0.97	0.13	40,40,40,40	0
58	MG	1A	3843	1/1	0.97	0.12	32,32,32,32	0
58	MG	1Q	203	1/1	0.97	0.18	43,43,43,43	0
58	MG	1A	3667	1/1	0.97	0.06	37,37,37,37	0
58	MG	1A	3668	1/1	0.97	0.05	24,24,24,24	0
58	MG	2A	3545	1/1	0.97	0.09	51,51,51,51	0
58	MG	1A	4062	1/1	0.97	0.10	34,34,34,34	0
58	MG	2A	3722	1/1	0.97	0.08	54,54,54,54	0
58	MG	1A	3243	1/1	0.97	0.18	21,21,21,21	0
58	MG	2A	3075	1/1	0.97	0.11	49,49,49,49	0
58	MG	2A	3725	1/1	0.97	0.06	36,36,36,36	0
58	MG	1A	3490	1/1	0.97	0.04	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	2A	3727	1/1	0.97	0.06	35,35,35,35	0
58	MG	1A	3212	1/1	0.97	0.15	36,36,36,36	0
58	MG	1a	1775	1/1	0.97	0.09	49,49,49,49	0
58	MG	1A	3245	1/1	0.97	0.10	56,56,56,56	0
58	MG	1A	3117	1/1	0.97	0.09	37,37,37,37	0
58	MG	1A	3280	1/1	0.97	0.07	30,30,30,30	0
58	MG	1R	206	1/1	0.97	0.13	34,34,34,34	0
58	MG	1A	3762	1/1	0.97	0.07	24,24,24,24	0
58	MG	1A	4070	1/1	0.97	0.11	40,40,40,40	0
58	MG	1A	3014	1/1	0.97	0.07	27,27,27,27	0
58	MG	1A	3855	1/1	0.97	0.12	36,36,36,36	0
58	MG	1A	3605	1/1	0.97	0.20	11,11,11,11	0
58	MG	1U	203	1/1	0.97	0.17	42,42,42,42	0
58	MG	1A	3049	1/1	0.97	0.10	26,26,26,26	0
58	MG	1A	3549	1/1	0.97	0.13	18,18,18,18	0
58	MG	2A	3564	1/1	0.97	0.20	65,65,65,65	0
58	MG	2A	3565	1/1	0.97	0.04	40,40,40,40	0
58	MG	2A	3746	1/1	0.97	0.05	40,40,40,40	0
58	MG	1A	3770	1/1	0.97	0.11	18,18,18,18	0
58	MG	1A	3285	1/1	0.97	0.06	41,41,41,41	0
58	MG	1A	3773	1/1	0.97	0.07	39,39,39,39	0
58	MG	1A	3960	1/1	0.97	0.06	60,60,60,60	0
58	MG	1a	1659	1/1	0.97	0.28	64,64,64,64	0
58	MG	1A	3499	1/1	0.97	0.29	20,20,20,20	0
58	MG	1A	3612	1/1	0.97	0.14	42,42,42,42	0
58	MG	1A	3216	1/1	0.97	0.16	42,42,42,42	0
58	MG	1A	3218	1/1	0.97	0.07	33,33,33,33	0
58	MG	1A	3965	1/1	0.97	0.10	48,48,48,48	0
59	K	1A	3546	1/1	0.97	0.08	75,75,75,75	0
58	MG	1B	204	1/1	0.97	0.04	26,26,26,26	0
58	MG	1A	3121	1/1	0.97	0.07	39,39,39,39	0
58	MG	1A	3369	1/1	0.97	0.07	39,39,39,39	0
61	ZN	14	102	1/1	0.97	0.07	110,110,110,110	0
61	ZN	2Y	202	1/1	0.97	0.05	100,100,100,100	0
58	MG	2A	3407	1/1	0.97	0.10	40,40,40,40	0
61	ZN	29	501	1/1	0.97	0.05	79,79,79,79	0
61	ZN	2n	501	1/1	0.97	0.05	84,84,84,84	0
62	SF4	2d	303	8/8	0.97	0.05	72,78,84,91	0
58	MG	2A	3766	1/1	0.98	0.04	39,39,39,39	0
58	MG	1A	3799	1/1	0.98	0.04	39,39,39,39	0
58	MG	23	103	1/1	0.98	0.06	49,49,49,49	0
58	MG	1A	3678	1/1	0.98	0.05	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3679	1/1	0.98	0.06	20,20,20,20	0
58	MG	2A	3112	1/1	0.98	0.05	40,40,40,40	0
58	MG	2A	3771	1/1	0.98	0.08	44,44,44,44	0
58	MG	1A	3281	1/1	0.98	0.09	32,32,32,32	0
58	MG	1A	3241	1/1	0.98	0.20	34,34,34,34	0
58	MG	2A	3532	1/1	0.98	0.08	29,29,29,29	0
58	MG	2A	3213	1/1	0.98	0.13	54,54,54,54	0
58	MG	1A	3283	1/1	0.98	0.21	30,30,30,30	0
58	MG	1P	203	1/1	0.98	0.12	26,26,26,26	0
58	MG	2A	3216	1/1	0.98	0.08	33,33,33,33	0
58	MG	2A	3019	1/1	0.98	0.04	38,38,38,38	0
58	MG	1A	3736	1/1	0.98	0.03	23,23,23,23	0
58	MG	1A	3023	1/1	0.98	0.07	37,37,37,37	0
58	MG	1A	3634	1/1	0.98	0.05	26,26,26,26	0
58	MG	17	102	1/1	0.98	0.04	28,28,28,28	0
58	MG	17	103	1/1	0.98	0.09	23,23,23,23	0
58	MG	2A	3787	1/1	0.98	0.07	40,40,40,40	0
58	MG	1A	4011	1/1	0.98	0.05	28,28,28,28	0
58	MG	1A	3869	1/1	0.98	0.12	40,40,40,40	0
58	MG	2A	3790	1/1	0.98	0.12	26,26,26,26	0
58	MG	1A	3484	1/1	0.98	0.12	30,30,30,30	0
58	MG	1A	3939	1/1	0.98	0.10	42,42,42,42	0
58	MG	1A	3742	1/1	0.98	0.06	29,29,29,29	0
58	MG	2A	3794	1/1	0.98	0.04	61,61,61,61	0
58	MG	1A	3743	1/1	0.98	0.10	42,42,42,42	0
58	MG	2A	3796	1/1	0.98	0.10	24,24,24,24	0
58	MG	1A	3942	1/1	0.98	0.04	40,40,40,40	0
58	MG	2A	3437	1/1	0.98	0.05	51,51,51,51	0
58	MG	1A	3262	1/1	0.98	0.05	39,39,39,39	0
58	MG	1A	3068	1/1	0.98	0.10	24,24,24,24	0
58	MG	1A	3523	1/1	0.98	0.10	21,21,21,21	0
58	MG	1A	3012	1/1	0.98	0.04	29,29,29,29	0
58	MG	1a	1781	1/1	0.98	0.08	53,53,53,53	0
58	MG	1B	223	1/1	0.98	0.05	30,30,30,30	0
58	MG	1A	3640	1/1	0.98	0.06	26,26,26,26	0
58	MG	1A	3289	1/1	0.98	0.08	38,38,38,38	0
58	MG	2A	3807	1/1	0.98	0.06	42,42,42,42	0
58	MG	2A	3808	1/1	0.98	0.06	47,47,47,47	0
58	MG	1A	3751	1/1	0.98	0.04	25,25,25,25	0
58	MG	1A	3341	1/1	0.98	0.28	29,29,29,29	0
58	MG	1A	3137	1/1	0.98	0.13	34,34,34,34	0
58	MG	1A	3172	1/1	0.98	0.05	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1a	1789	1/1	0.98	0.05	45,45,45,45	0
58	MG	1B	230	1/1	0.98	0.05	42,42,42,42	0
58	MG	2A	3452	1/1	0.98	0.05	31,31,31,31	0
58	MG	1A	3114	1/1	0.98	0.04	22,22,22,22	0
58	MG	1a	1792	1/1	0.98	0.19	50,50,50,50	0
58	MG	1A	4030	1/1	0.98	0.04	26,26,26,26	0
58	MG	1A	3603	1/1	0.98	0.06	13,13,13,13	0
58	MG	1A	3095	1/1	0.98	0.14	18,18,18,18	0
58	MG	1A	3648	1/1	0.98	0.06	28,28,28,28	0
58	MG	2A	3575	1/1	0.98	0.08	44,44,44,44	0
58	MG	1A	3294	1/1	0.98	0.11	41,41,41,41	0
58	MG	2A	3460	1/1	0.98	0.04	42,42,42,42	0
58	MG	2A	3053	1/1	0.98	0.06	47,47,47,47	0
58	MG	1A	3269	1/1	0.98	0.04	24,24,24,24	0
58	MG	1A	3764	1/1	0.98	0.05	37,37,37,37	0
58	MG	2A	3254	1/1	0.98	0.07	50,50,50,50	0
58	MG	1A	3464	1/1	0.98	0.17	27,27,27,27	0
58	MG	1A	3766	1/1	0.98	0.04	18,18,18,18	0
58	MG	1A	3831	1/1	0.98	0.10	50,50,50,50	0
58	MG	1A	3652	1/1	0.98	0.09	37,37,37,37	0
58	MG	1A	4043	1/1	0.98	0.04	32,32,32,32	0
58	MG	1A	3231	1/1	0.98	0.12	29,29,29,29	0
58	MG	1A	3895	1/1	0.98	0.04	40,40,40,40	0
58	MG	1A	3610	1/1	0.98	0.07	25,25,25,25	0
58	MG	1D	307	1/1	0.98	0.04	28,28,28,28	0
58	MG	1V	208	1/1	0.98	0.04	45,45,45,45	0
58	MG	1A	3706	1/1	0.98	0.15	42,42,42,42	0
58	MG	1A	3969	1/1	0.98	0.06	25,25,25,25	0
58	MG	1A	4050	1/1	0.98	0.04	41,41,41,41	0
58	MG	2A	3595	1/1	0.98	0.06	37,37,37,37	0
58	MG	1A	3655	1/1	0.98	0.07	20,20,20,20	0
58	MG	1A	3772	1/1	0.98	0.06	39,39,39,39	0
58	MG	1l	201	1/1	0.98	0.03	59,59,59,59	0
58	MG	1A	3025	1/1	0.98	0.04	25,25,25,25	0
58	MG	1A	3217	1/1	0.98	0.12	31,31,31,31	0
58	MG	1A	3501	1/1	0.98	0.08	31,31,31,31	0
58	MG	2A	3484	1/1	0.98	0.07	65,65,65,65	0
58	MG	1E	304	1/1	0.98	0.11	22,22,22,22	0
58	MG	1A	3659	1/1	0.98	0.07	21,21,21,21	0
58	MG	2A	3276	1/1	0.98	0.13	45,45,45,45	0
58	MG	1A	4058	1/1	0.98	0.10	37,37,37,37	0
58	MG	2A	3078	1/1	0.98	0.04	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	3379	1/1	0.98	0.14	22,22,22,22	0
58	MG	1A	3977	1/1	0.98	0.04	30,30,30,30	0
58	MG	2A	3610	1/1	0.98	0.07	51,51,51,51	0
58	MG	1A	4061	1/1	0.98	0.05	36,36,36,36	0
58	MG	1A	3615	1/1	0.98	0.07	38,38,38,38	0
58	MG	1A	3907	1/1	0.98	0.05	50,50,50,50	0
58	MG	1A	3908	1/1	0.98	0.04	24,24,24,24	0
58	MG	1A	3844	1/1	0.98	0.18	38,38,38,38	0
58	MG	1A	3071	1/1	0.98	0.08	21,21,21,21	0
58	MG	2F	305	1/1	0.98	0.08	46,46,46,46	0
58	MG	2A	3500	1/1	0.98	0.11	59,59,59,59	0
58	MG	2A	3618	1/1	0.98	0.14	39,39,39,39	0
58	MG	2A	3739	1/1	0.98	0.05	42,42,42,42	0
58	MG	1F	303	1/1	0.98	0.21	28,28,28,28	0
58	MG	2O	202	1/1	0.98	0.04	58,58,58,58	0
58	MG	1A	3080	1/1	0.98	0.11	31,31,31,31	0
58	MG	1F	305	1/1	0.98	0.10	41,41,41,41	0
58	MG	2A	3504	1/1	0.98	0.17	41,41,41,41	0
58	MG	1A	3205	1/1	0.98	0.16	23,23,23,23	0
58	MG	1a	1650	1/1	0.98	0.05	39,39,39,39	0
58	MG	1A	3619	1/1	0.98	0.05	32,32,32,32	0
58	MG	2A	3626	1/1	0.98	0.14	46,46,46,46	0
58	MG	1A	3354	1/1	0.98	0.04	40,40,40,40	0
58	MG	1A	3065	1/1	0.98	0.10	34,34,34,34	0
58	MG	1A	3179	1/1	0.98	0.04	30,30,30,30	0
58	MG	1A	3789	1/1	0.98	0.05	45,45,45,45	0
58	MG	1a	1746	1/1	0.98	0.06	53,53,53,53	0
58	MG	2A	3401	1/1	0.98	0.27	40,40,40,40	0
58	MG	2x	103	1/1	0.98	0.13	53,53,53,53	0
58	MG	1A	3414	1/1	0.98	0.12	28,28,28,28	0
58	MG	2A	3755	1/1	0.98	0.11	42,42,42,42	0
58	MG	1A	3992	1/1	0.98	0.05	13,13,13,13	0
58	MG	1A	3257	1/1	0.98	0.06	33,33,33,33	0
58	MG	1A	3921	1/1	0.98	0.03	22,22,22,22	0
58	MG	2A	3102	1/1	0.98	0.05	38,38,38,38	0
61	ZN	1Y	203	1/1	0.98	0.04	61,61,61,61	0
58	MG	1A	3726	1/1	0.98	0.07	36,36,36,36	0
58	MG	1A	3239	1/1	0.98	0.07	23,23,23,23	0
58	MG	1A	3512	1/1	0.98	0.06	33,33,33,33	0
61	ZN	26	501	1/1	0.98	0.07	66,66,66,66	0
58	MG	1A	3925	1/1	0.98	0.07	53,53,53,53	0
58	MG	1A	3029	1/1	0.98	0.07	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
62	SF4	1d	302	8/8	0.98	0.05	58,60,65,70	0
58	MG	1A	3448	1/1	0.98	0.21	53,53,53,53	0
58	MG	1a	1699	1/1	0.99	0.05	46,46,46,46	0
58	MG	1A	3287	1/1	0.99	0.07	35,35,35,35	0
58	MG	1A	3183	1/1	0.99	0.12	33,33,33,33	0
58	MG	1A	3737	1/1	0.99	0.07	32,32,32,32	0
58	MG	1A	3123	1/1	0.99	0.15	28,28,28,28	0
58	MG	2A	3772	1/1	0.99	0.06	32,32,32,32	0
58	MG	2A	3531	1/1	0.99	0.11	30,30,30,30	0
58	MG	1A	3739	1/1	0.99	0.04	37,37,37,37	0
58	MG	2A	3533	1/1	0.99	0.16	36,36,36,36	0
58	MG	1A	3119	1/1	0.99	0.15	19,19,19,19	0
58	MG	1A	3670	1/1	0.99	0.06	18,18,18,18	0
58	MG	1A	3692	1/1	0.99	0.04	25,25,25,25	0
58	MG	2A	3779	1/1	0.99	0.06	25,25,25,25	0
58	MG	1T	201	1/1	0.99	0.05	30,30,30,30	0
58	MG	2A	3538	1/1	0.99	0.08	30,30,30,30	0
58	MG	1F	307	1/1	0.99	0.04	29,29,29,29	0
58	MG	1A	3983	1/1	0.99	0.05	24,24,24,24	0
58	MG	2A	3379	1/1	0.99	0.06	30,30,30,30	0
58	MG	1A	3583	1/1	0.99	0.07	30,30,30,30	0
58	MG	1A	3774	1/1	0.99	0.03	33,33,33,33	0
58	MG	1A	3672	1/1	0.99	0.03	26,26,26,26	0
58	MG	1A	3719	1/1	0.99	0.04	17,17,17,17	0
58	MG	1A	3101	1/1	0.99	0.03	33,33,33,33	0
58	MG	1l	202	1/1	0.99	0.06	39,39,39,39	0
58	MG	1A	3951	1/1	0.99	0.10	16,16,16,16	0
58	MG	13	101	1/1	0.99	0.05	32,32,32,32	0
58	MG	1A	3126	1/1	0.99	0.03	25,25,25,25	0
58	MG	2A	3494	1/1	0.99	0.07	29,29,29,29	0
58	MG	1A	3779	1/1	0.99	0.04	42,42,42,42	0
58	MG	1A	3814	1/1	0.99	0.06	30,30,30,30	0
58	MG	1A	3601	1/1	0.99	0.10	33,33,33,33	0
58	MG	15	101	1/1	0.99	0.08	35,35,35,35	0
58	MG	2A	3499	1/1	0.99	0.07	42,42,42,42	0
58	MG	1A	3363	1/1	0.99	0.04	36,36,36,36	0
58	MG	2A	3737	1/1	0.99	0.04	43,43,43,43	0
58	MG	1A	3920	1/1	0.99	0.04	22,22,22,22	0
58	MG	1A	4036	1/1	0.99	0.05	34,34,34,34	0
58	MG	1A	3620	1/1	0.99	0.07	24,24,24,24	0
58	MG	1A	3074	1/1	0.99	0.02	11,11,11,11	0
58	MG	1A	3146	1/1	0.99	0.04	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
58	MG	1A	4040	1/1	0.99	0.04	25,25,25,25	0
58	MG	2A	3682	1/1	0.99	0.05	33,33,33,33	0
58	MG	1a	1780	1/1	0.99	0.04	41,41,41,41	0
58	MG	1A	3092	1/1	0.99	0.05	34,34,34,34	0
58	MG	1A	3606	1/1	0.99	0.07	25,25,25,25	0
58	MG	1A	3296	1/1	0.99	0.09	23,23,23,23	0
58	MG	1A	3445	1/1	0.99	0.04	29,29,29,29	0
58	MG	1A	3663	1/1	0.99	0.04	19,19,19,19	0
58	MG	1W	206	1/1	0.99	0.06	17,17,17,17	0
58	MG	2A	3690	1/1	0.99	0.06	41,41,41,41	0
58	MG	1A	3791	1/1	0.99	0.07	19,19,19,19	0
58	MG	2A	3572	1/1	0.99	0.07	35,35,35,35	0
58	MG	1A	4047	1/1	0.99	0.05	20,20,20,20	0
58	MG	1A	3759	1/1	0.99	0.03	38,38,38,38	0
58	MG	1A	3793	1/1	0.99	0.04	19,19,19,19	0
58	MG	1A	3520	1/1	0.99	0.14	37,37,37,37	0
58	MG	2X	102	1/1	0.99	0.04	63,63,63,63	0
58	MG	1A	3761	1/1	0.99	0.07	13,13,13,13	0
61	ZN	19	102	1/1	0.99	0.05	43,43,43,43	0
61	ZN	1n	103	1/1	0.99	0.03	56,56,56,56	0
58	MG	1A	3494	1/1	0.99	0.11	30,30,30,30	0
58	MG	1A	4053	1/1	0.99	0.03	27,27,27,27	0
61	ZN	25	104	1/1	0.99	0.04	70,70,70,70	0
58	MG	1A	3763	1/1	0.99	0.04	58,58,58,58	0
58	MG	1A	4012	1/1	0.99	0.03	16,16,16,16	0
58	MG	2A	3640	1/1	0.99	0.05	59,59,59,59	0
58	MG	1A	3900	1/1	0.99	0.03	24,24,24,24	0
58	MG	1A	3709	1/1	0.99	0.07	22,22,22,22	0
58	MG	1A	3993	1/1	1.00	0.03	27,27,27,27	0
58	MG	1A	3748	1/1	1.00	0.09	34,34,34,34	0
58	MG	1A	3718	1/1	1.00	0.01	20,20,20,20	0
58	MG	1A	3782	1/1	1.00	0.06	15,15,15,15	0
61	ZN	15	109	1/1	1.00	0.01	42,42,42,42	0
61	ZN	16	103	1/1	1.00	0.04	38,38,38,38	0
58	MG	2A	3675	1/1	1.00	0.06	19,19,19,19	0
58	MG	1a	1734	1/1	1.00	0.09	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.