Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2025 – 08:11 PM EDT

PDB ID	:	9O3L / pdb_00009o3l
Title	:	Crystal structure of the wild-type Thermus thermophilus 70S ribosome in complex with macrolide erythromycin, mRNA, deacylated A-site tRNAphe, P-site fMRC-peptidyl-tRNAmet, and deacylated E-site tRNAphe at 2.75A 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	:	2.75 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 (1)) were used in the production of this report:

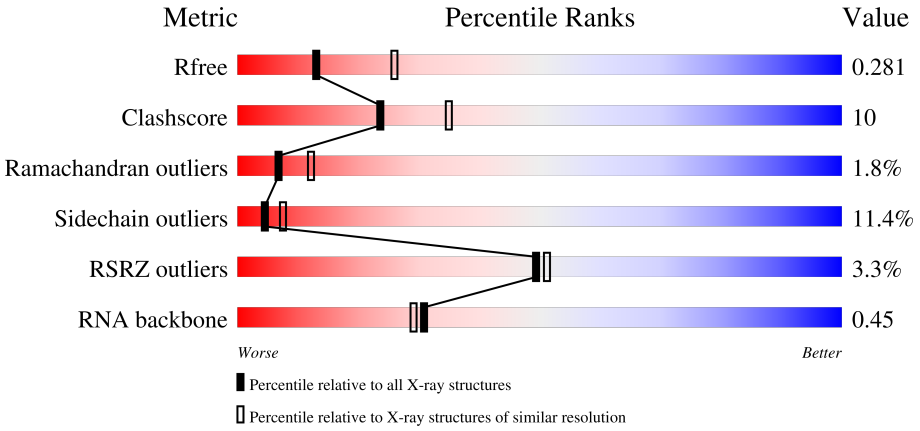
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.75 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	1606 (2.78-2.74)
Clashscore	180529	1689 (2.78-2.74)
Ramachandran outliers	177936	1665 (2.78-2.74)
Sidechain outliers	177891	1665 (2.78-2.74)
RSRZ outliers	164620	1606 (2.78-2.74)
RNA backbone	3690	1094 (3.00-2.52)

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	2% 59% 33% 7%
1	2A	2915	2% 53% 35% 8%
2	1B	121	60% 38%
2	2B	121	2% 43% 47% 9%

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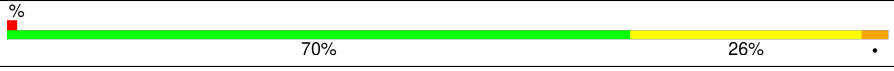
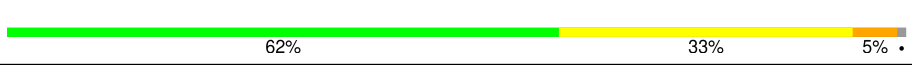
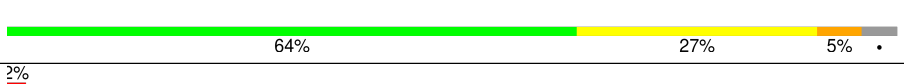
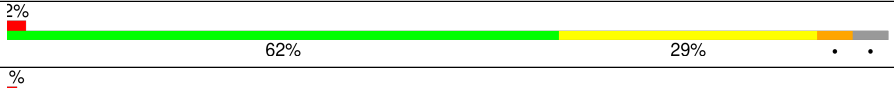
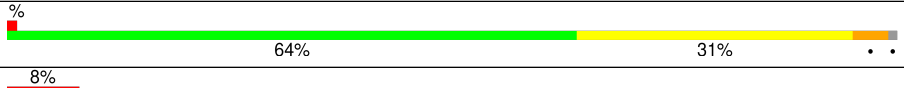
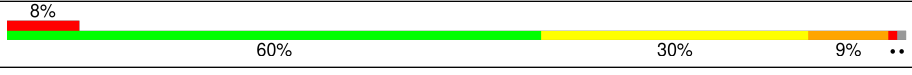
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
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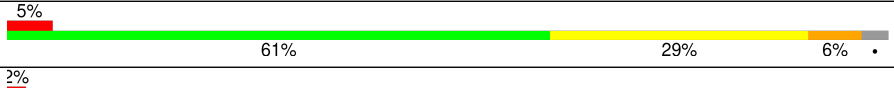
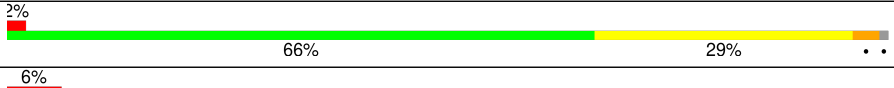
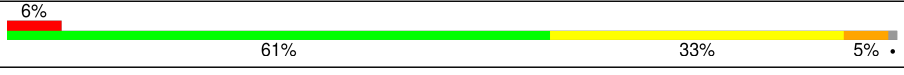
7	2H	180	
8	1I	148	
8	2I	148	
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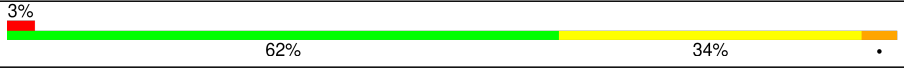
9	2N	140	
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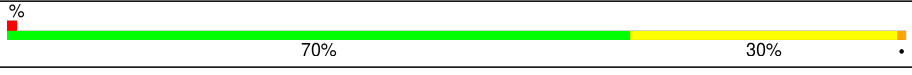
10	2O	122	
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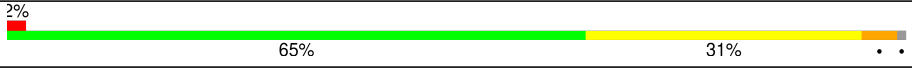
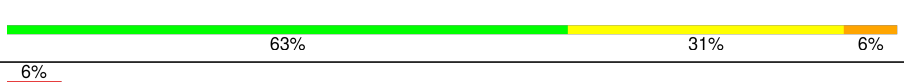
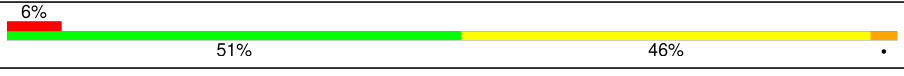
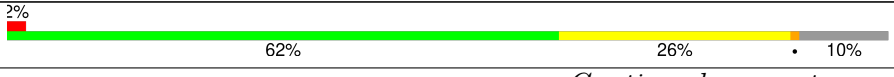
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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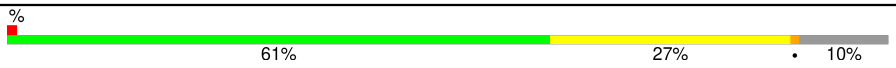
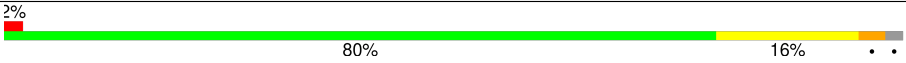
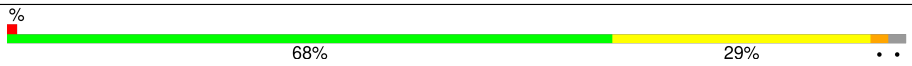
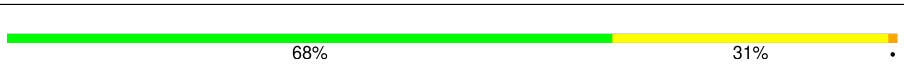
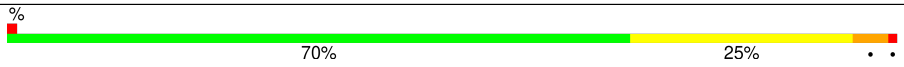
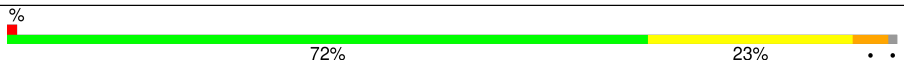
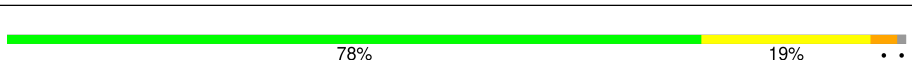
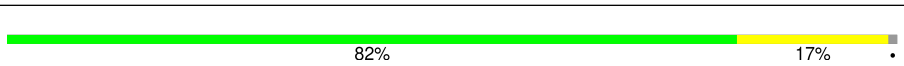
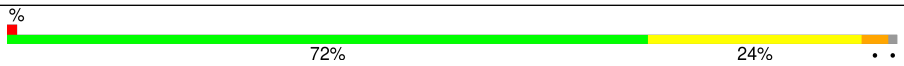
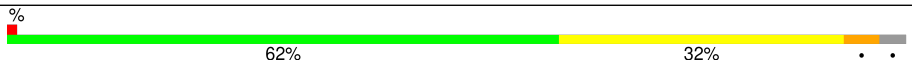
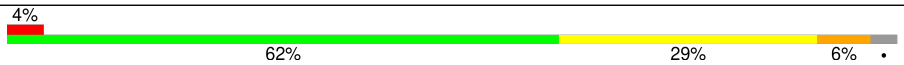
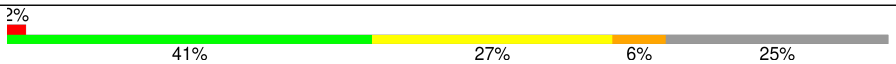
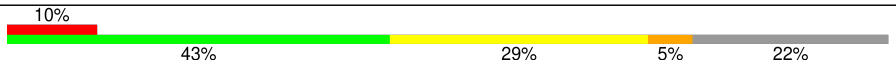
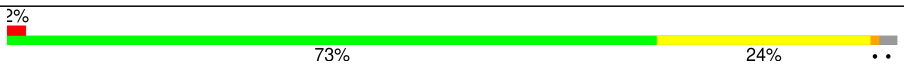
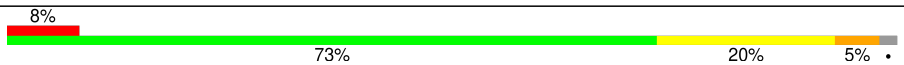
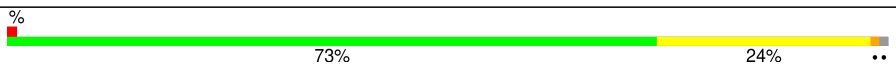
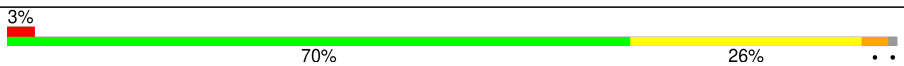
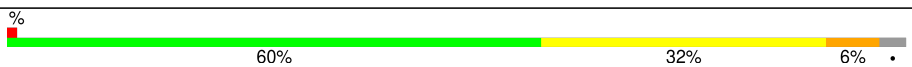
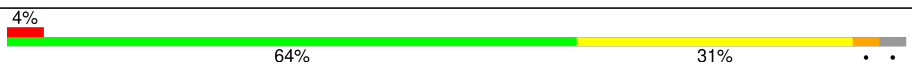
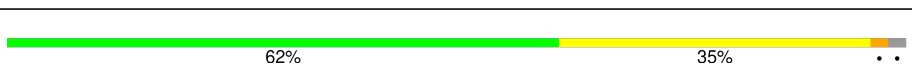
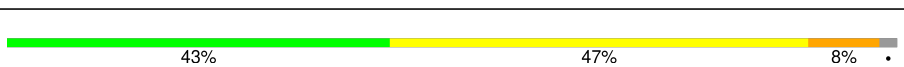
Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
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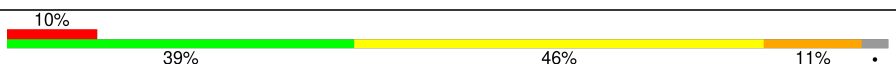
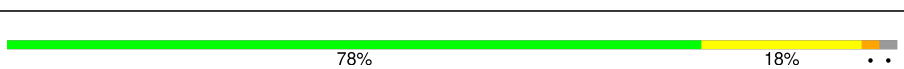
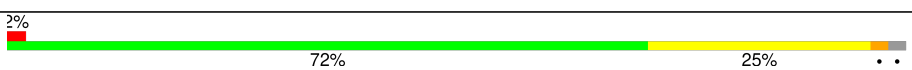
26	24	71	
27	15	60	
27	25	60	

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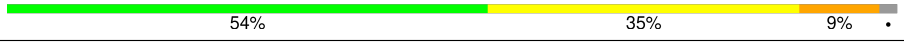
Mol	Chain	Length	Quality of chain
28	16	54	
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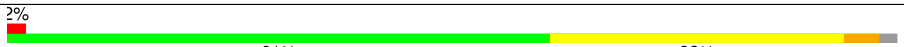
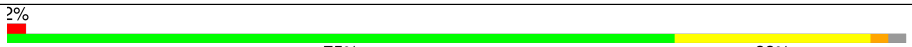
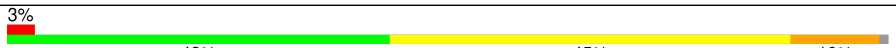
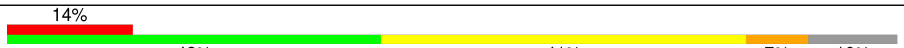
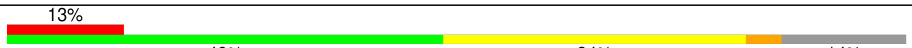
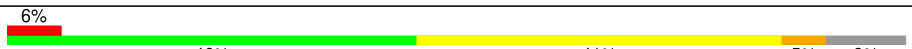
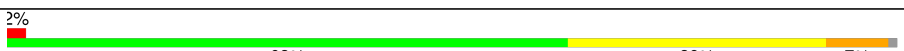
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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Mol	Chain	Length	Quality of chain
40	2i	128	34% 51% 45%
41	1j	105	3% 60% 29% 8%
41	2j	105	18% 49% 37% 6% 9%
42	1k	129	% 70% 15% 12%
42	2k	129	11% 58% 26% 12%
43	1l	132	3% 69% 22% 8%
43	2l	132	2% 66% 22% 5% 8%
44	1m	126	5% 64% 30%
44	2m	126	14% 50% 37% 10%
45	1n	61	2% 62% 36%
45	2n	61	46% 52% 39% 5%
46	1o	89	3% 61% 34%
46	2o	89	2% 67% 31%
47	1p	88	5% 56% 34% 7%
47	2p	88	3% 59% 32% 7%
48	1q	105	4% 54% 37% 6%
48	2q	105	6% 57% 30% 7% 6%
49	1r	88	% 49% 25% 23%
49	2r	88	48% 23% 7% 23%
50	1s	93	59% 28% 11%
50	2s	93	16% 34% 42% 13% 11%
51	1t	106	5% 61% 22% 6% 9%
51	2t	106	2% 58% 28% 5% 9%
52	1u	27	4% 67% 19% 15%
52	2u	27	33% 37% 37% 11% 15%

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Mol	Chain	Length	Quality of chain
53	1v	24	4% 33% 17% 46%
53	2v	24	12% 29% 8% 17% 46%
54	1w	76	7% 34% 46% 14%
54	1y	76	3% 29% 47% 18%
54	2w	76	8% 34% 41% 18% 5%
54	2y	76	4% 38% 41% 17%
55	1x	77	49% 42% 9%
55	2x	77	51% 42% 8%
56	1z	3	67% 33%
56	2z	3	67% 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
57	MG	2a	1695	-	-	-	X
61	SF4	2d	303	-	-	X	-

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 299368 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	202	Total	C	N	O	S	0	0	0
			1583	1009	297	275	2			
5	2F	202	Total	C	N	O	S	0	0	0
			1579	1007	296	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-PHE-mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
53	2v	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			

- Molecule 54 is a RNA chain called A-site and E-site Deacylated tRNAphe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1592	713	285	518	74	2			
54	1y	74	Total	C	N	O	P	S	0	0	0
			1585	707	285	518	74	1			
54	2w	72	Total	C	N	O	P	S	0	0	0
			1544	690	278	502	72	2			
54	2y	73	Total	C	N	O	P	S	0	0	0
			1565	698	283	510	73	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 MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1085	Total	Mg	0	0
			1085	1085		
57	1B	38	Total	Mg	0	0
			38	38		
57	1D	12	Total	Mg	0	0
			12	12		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1E	13	Total Mg 13 13	0	0
57	1F	13	Total Mg 13 13	0	0
57	1G	4	Total Mg 4 4	0	0
57	1H	1	Total Mg 1 1	0	0
57	1I	1	Total Mg 1 1	0	0
57	1N	4	Total Mg 4 4	0	0
57	1O	4	Total Mg 4 4	0	0
57	1P	6	Total Mg 6 6	0	0
57	1Q	7	Total Mg 7 7	0	0
57	1R	6	Total Mg 6 6	0	0
57	1S	2	Total Mg 2 2	0	0
57	1T	3	Total Mg 3 3	0	0
57	1U	11	Total Mg 11 11	0	0
57	1V	7	Total Mg 7 7	0	0
57	1W	7	Total Mg 7 7	0	0
57	1X	7	Total Mg 7 7	0	0
57	1Y	2	Total Mg 2 2	0	0
57	1Z	2	Total Mg 2 2	0	0
57	10	10	Total Mg 10 10	0	0
57	11	3	Total Mg 3 3	0	0
57	12	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	13	5	Total Mg 5 5	0	0
57	14	1	Total Mg 1 1	0	0
57	15	9	Total Mg 9 9	0	0
57	16	2	Total Mg 2 2	0	0
57	17	6	Total Mg 6 6	0	0
57	18	7	Total Mg 7 7	0	0
57	1a	211	Total Mg 211 211	0	0
57	1b	1	Total Mg 1 1	0	0
57	1d	1	Total Mg 1 1	0	0
57	1e	1	Total Mg 1 1	0	0
57	1f	1	Total Mg 1 1	0	0
57	1j	1	Total Mg 1 1	0	0
57	1l	2	Total Mg 2 2	0	0
57	1m	1	Total Mg 1 1	0	0
57	1n	3	Total Mg 3 3	0	0
57	1p	1	Total Mg 1 1	0	0
57	1r	1	Total Mg 1 1	0	0
57	1t	1	Total Mg 1 1	0	0
57	1w	6	Total Mg 6 6	0	0
57	1x	12	Total Mg 12 12	0	0
57	2A	855	Total Mg 855 855	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2B	20	Total Mg 20 20	0	0
57	2D	6	Total Mg 6 6	0	0
57	2E	9	Total Mg 9 9	0	0
57	2F	6	Total Mg 6 6	0	0
57	2N	1	Total Mg 1 1	0	0
57	2O	2	Total Mg 2 2	0	0
57	2P	2	Total Mg 2 2	0	0
57	2Q	1	Total Mg 1 1	0	0
57	2R	4	Total Mg 4 4	0	0
57	2T	3	Total Mg 3 3	0	0
57	2U	2	Total Mg 2 2	0	0
57	2V	1	Total Mg 1 1	0	0
57	2W	2	Total Mg 2 2	0	0
57	2X	1	Total Mg 1 1	0	0
57	2Y	1	Total Mg 1 1	0	0
57	2Z	1	Total Mg 1 1	0	0
57	20	3	Total Mg 3 3	0	0
57	21	1	Total Mg 1 1	0	0
57	23	2	Total Mg 2 2	0	0
57	25	1	Total Mg 1 1	0	0
57	26	1	Total Mg 1 1	0	0

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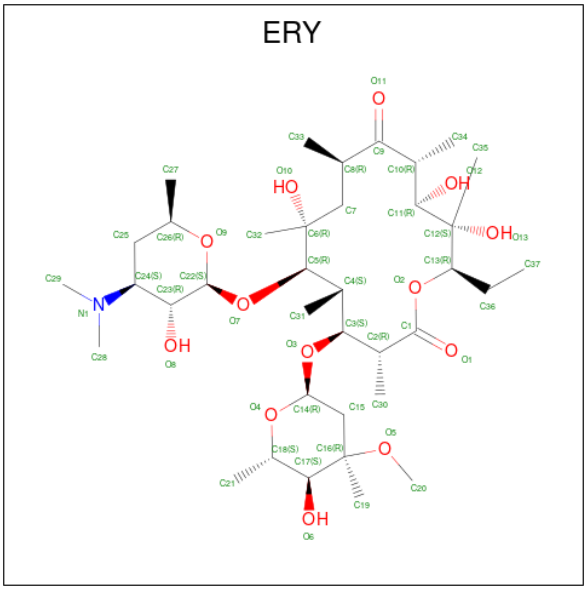
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	27	4	Total Mg 4 4	0	0
57	28	3	Total Mg 3 3	0	0
57	2a	225	Total Mg 225 225	0	0
57	2d	2	Total Mg 2 2	0	0
57	2e	1	Total Mg 1 1	0	0
57	2f	2	Total Mg 2 2	0	0
57	2g	1	Total Mg 1 1	0	0
57	2j	1	Total Mg 1 1	0	0
57	2k	1	Total Mg 1 1	0	0
57	2l	4	Total Mg 4 4	0	0
57	2o	1	Total Mg 1 1	0	0
57	2q	3	Total Mg 3 3	0	0
57	2r	1	Total Mg 1 1	0	0
57	2t	1	Total Mg 1 1	0	0
57	2v	2	Total Mg 2 2	0	0
57	2w	5	Total Mg 5 5	0	0
57	2x	6	Total Mg 6 6	0	0
57	2z	1	Total Mg 1 1	0	0
57	2y	1	Total Mg 1 1	0	0

- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1A	1	Total K 1 1	0	0
58	2A	1	Total K 1 1	0	0

- Molecule 59 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	1	Total C N O 51 37 1 13	0	0
59	2A	1	Total C N O 51 37 1 13	0	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1Y	1	Total Zn 1 1	0	0
60	14	1	Total Zn 1 1	0	0
60	15	1	Total Zn 1 1	0	0
60	16	1	Total Zn 1 1	0	0
60	19	1	Total Zn 1 1	0	0

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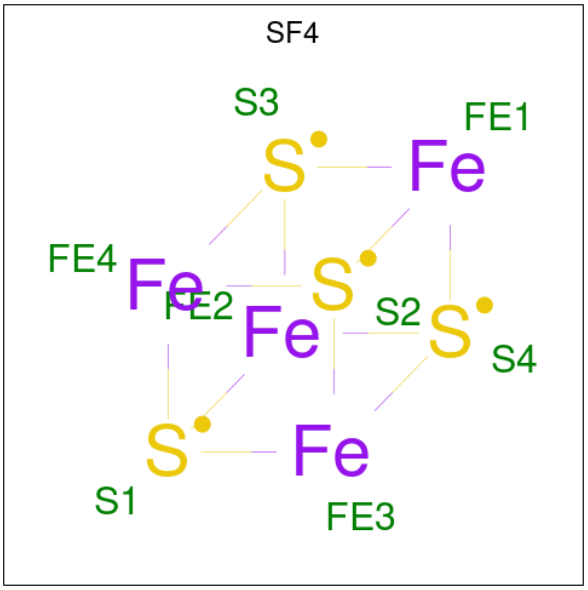
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1n	1	Total Zn 1 1	0	0
60	2Y	1	Total Zn 1 1	0	0
60	24	1	Total Zn 1 1	0	0
60	25	1	Total Zn 1 1	0	0
60	26	1	Total Zn 1 1	0	0
60	29	1	Total Zn 1 1	0	0
60	2n	1	Total Zn 1 1	0	0

- Molecule 61 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1d	1	Total Fe S 8 4 4	0	0
61	2d	1	Total Fe S 8 4 4	0	0

- Molecule 62 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1A	1680	Total O 1680 1680	0	0
62	1B	54	Total O 54 54	0	0
62	1D	32	Total O 32 32	0	0
62	1E	23	Total O 23 23	0	0
62	1F	17	Total O 17 17	0	0
62	1G	1	Total O 1 1	0	0
62	1H	1	Total O 1 1	0	0
62	1N	4	Total O 4 4	0	0
62	1O	3	Total O 3 3	0	0
62	1P	15	Total O 15 15	0	0
62	1Q	8	Total O 8 8	0	0
62	1R	12	Total O 12 12	0	0
62	1S	3	Total O 3 3	0	0
62	1T	6	Total O 6 6	0	0
62	1U	8	Total O 8 8	0	0
62	1V	9	Total O 9 9	0	0
62	1W	9	Total O 9 9	0	0
62	1X	6	Total O 6 6	0	0
62	1Y	1	Total O 1 1	0	0
62	1Z	1	Total O 1 1	0	0
62	10	8	Total O 8 8	0	0
62	11	7	Total O 7 7	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	12	3	Total O 3 3	0	0
62	13	4	Total O 4 4	0	0
62	14	1	Total O 1 1	0	0
62	15	6	Total O 6 6	0	0
62	16	3	Total O 3 3	0	0
62	17	10	Total O 10 10	0	0
62	18	8	Total O 8 8	0	0
62	1a	252	Total O 252 252	0	0
62	1b	1	Total O 1 1	0	0
62	1d	1	Total O 1 1	0	0
62	1f	1	Total O 1 1	0	0
62	1l	3	Total O 3 3	0	0
62	1m	2	Total O 2 2	0	0
62	1o	1	Total O 1 1	0	0
62	1p	1	Total O 1 1	0	0
62	1q	2	Total O 2 2	0	0
62	1u	1	Total O 1 1	0	0
62	1v	3	Total O 3 3	0	0
62	1w	8	Total O 8 8	0	0
62	1x	7	Total O 7 7	0	0
62	1z	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1y	1	Total O 1 1	0	0
62	2A	952	Total O 952 952	0	0
62	2B	21	Total O 21 21	0	0
62	2D	15	Total O 15 15	0	0
62	2E	5	Total O 5 5	0	0
62	2F	13	Total O 13 13	0	0
62	2O	3	Total O 3 3	0	0
62	2P	6	Total O 6 6	0	0
62	2Q	1	Total O 1 1	0	0
62	2R	4	Total O 4 4	0	0
62	2T	2	Total O 2 2	0	0
62	2U	2	Total O 2 2	0	0
62	2V	1	Total O 1 1	0	0
62	2W	1	Total O 1 1	0	0
62	2X	5	Total O 5 5	0	0
62	20	2	Total O 2 2	0	0
62	21	6	Total O 6 6	0	0
62	23	1	Total O 1 1	0	0
62	25	2	Total O 2 2	0	0
62	27	2	Total O 2 2	0	0
62	28	3	Total O 3 3	0	0

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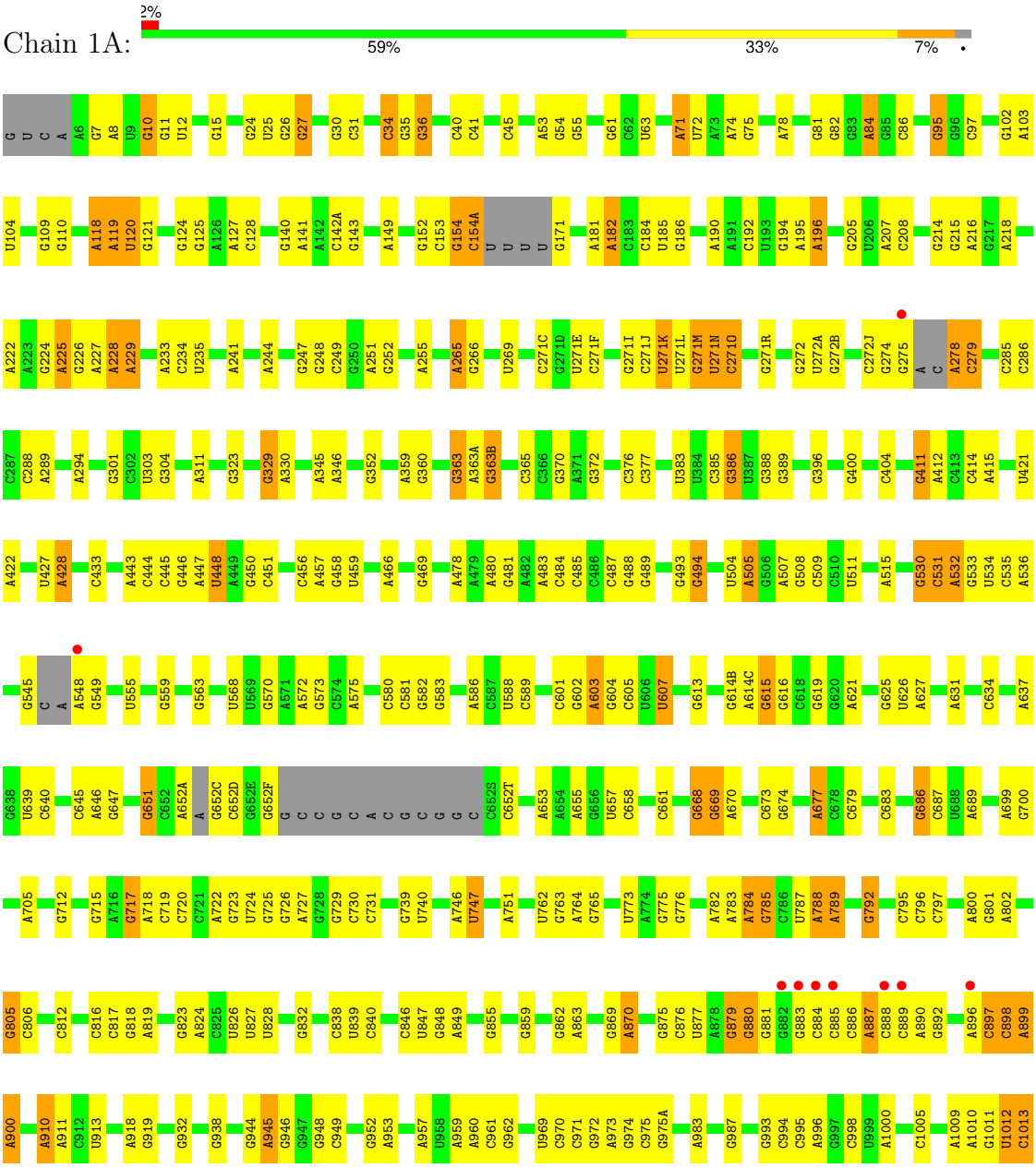
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	29	1	Total O 1 1	0	0
62	2a	150	Total O 150 150	0	0
62	2e	1	Total O 1 1	0	0
62	2j	1	Total O 1 1	0	0
62	2l	4	Total O 4 4	0	0
62	2q	1	Total O 1 1	0	0
62	2v	3	Total O 3 3	0	0
62	2w	3	Total O 3 3	0	0
62	2x	4	Total O 4 4	0	0
62	2z	1	Total O 1 1	0	0

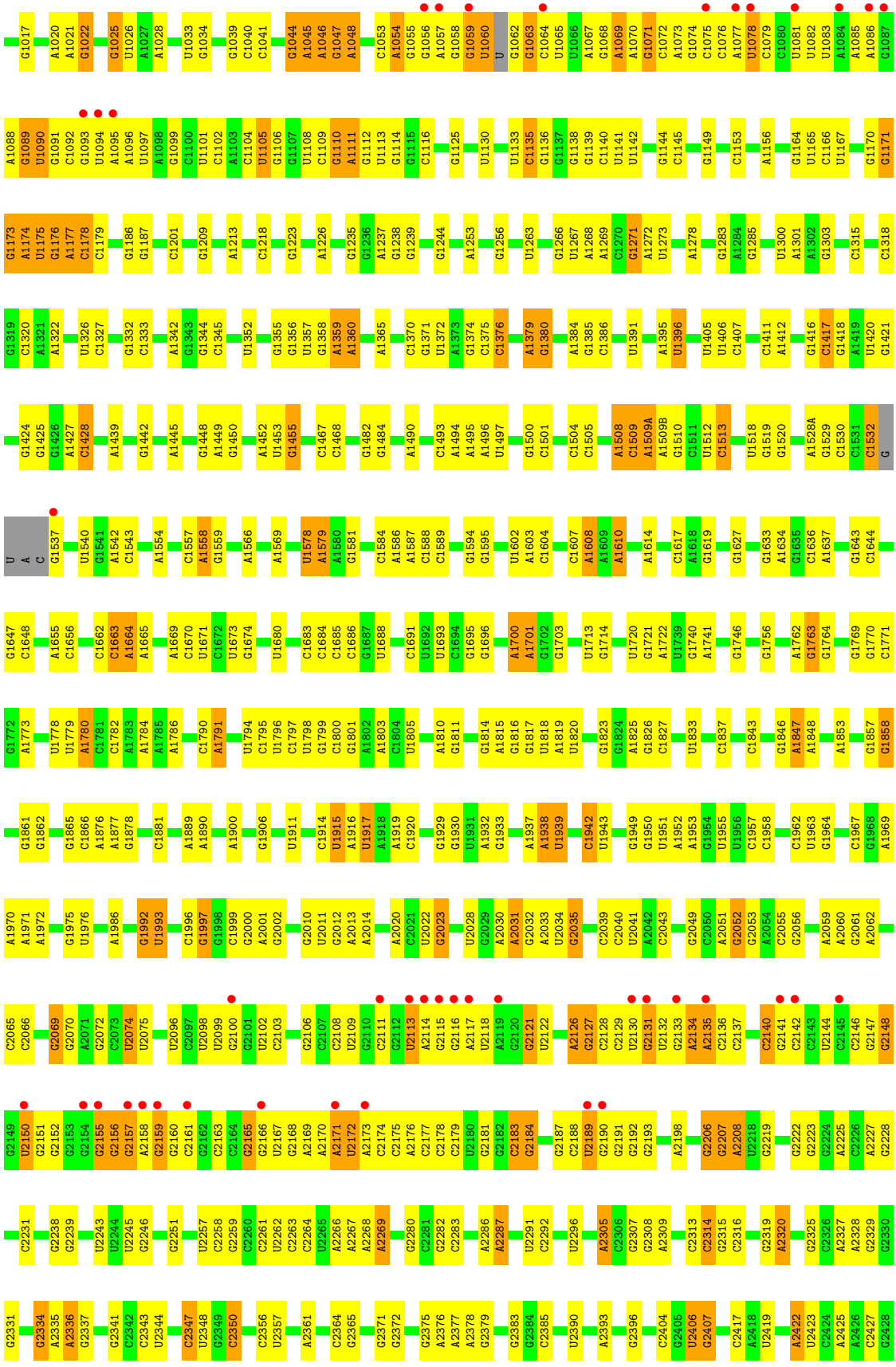
3 Residue-property plots (i)

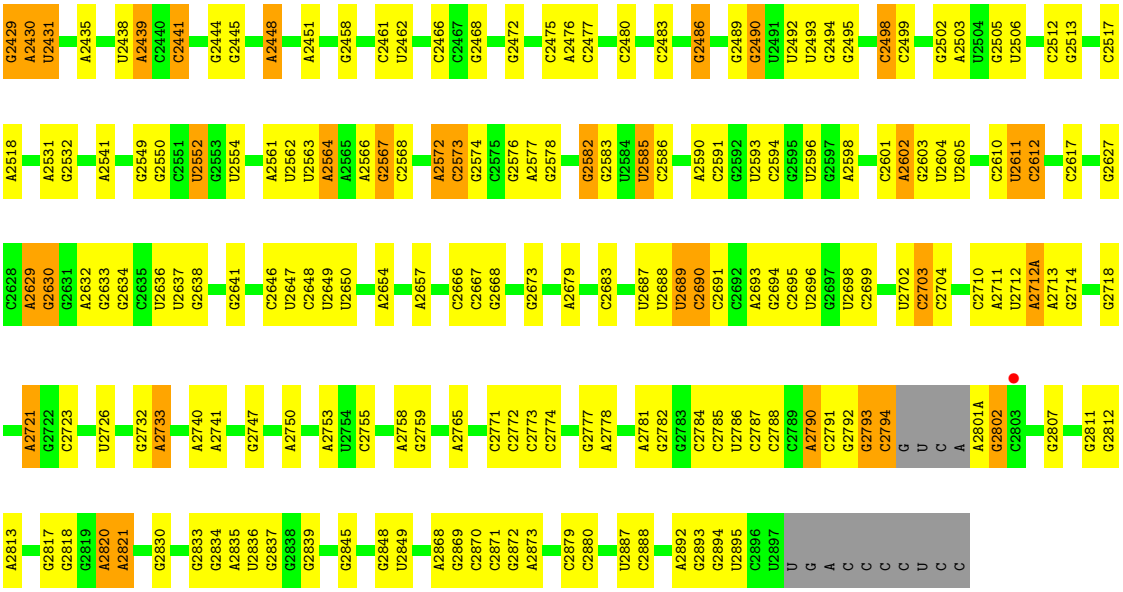
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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:

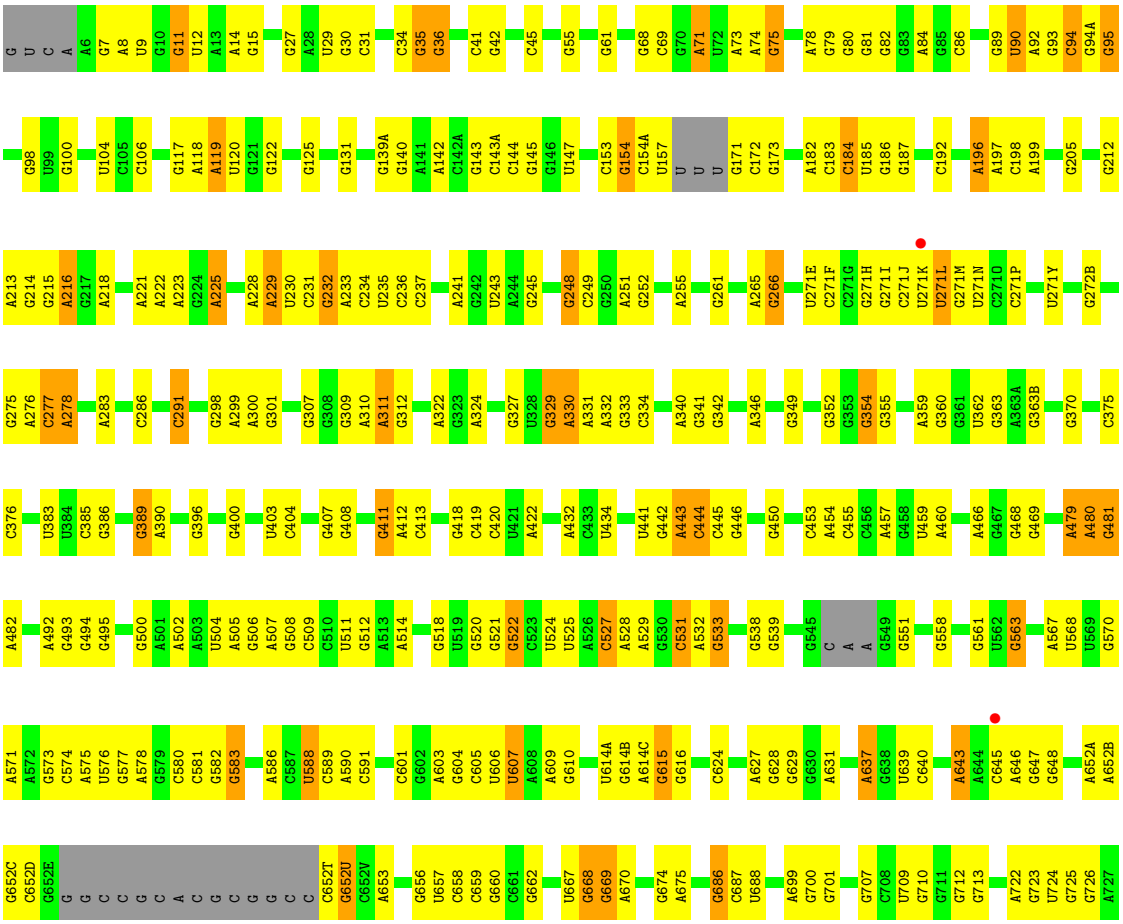


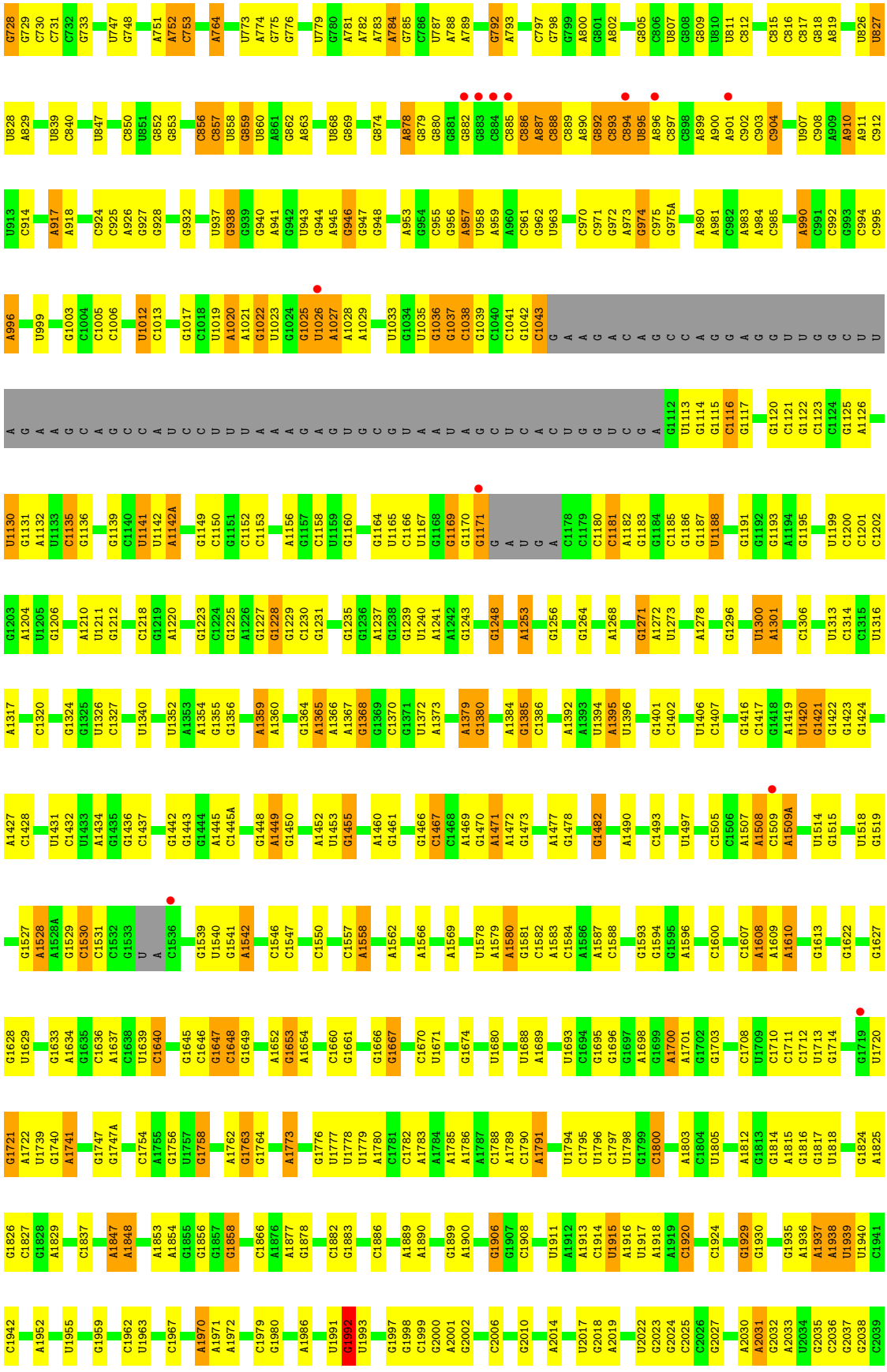


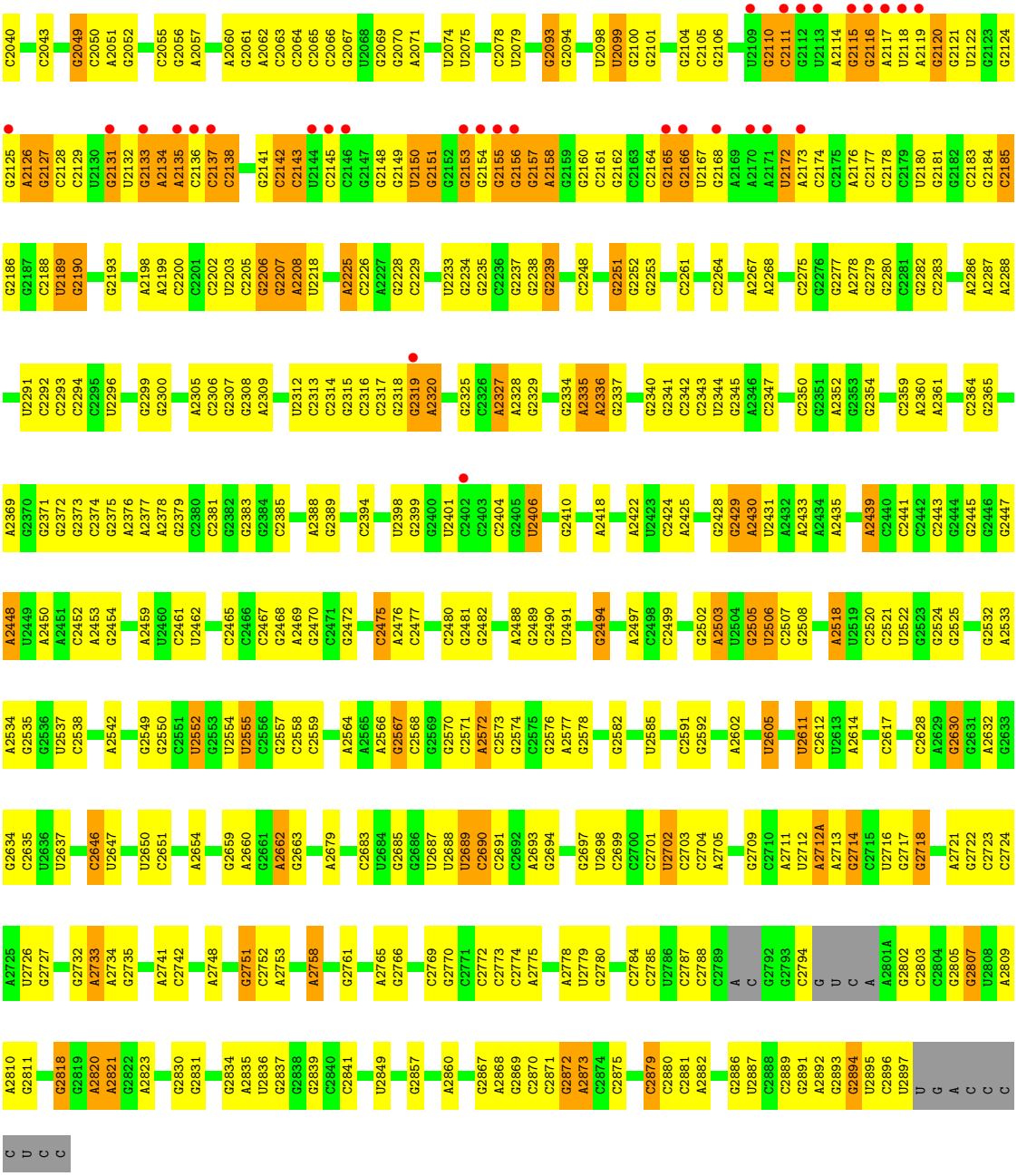


• Molecule 1: 23S Ribosomal RNA

Chain 2A:





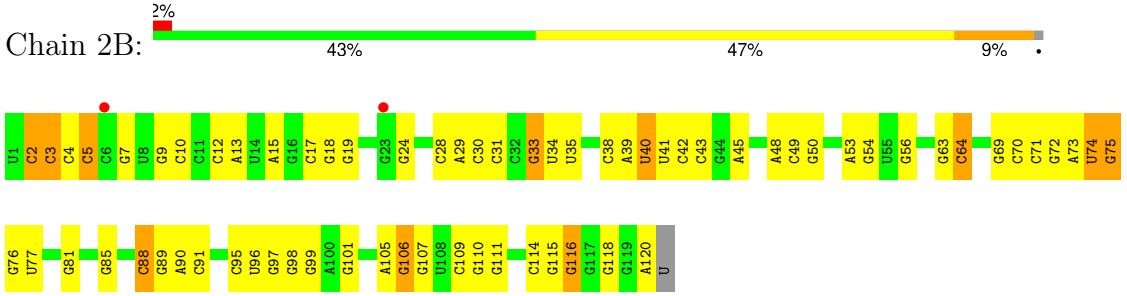


• Molecule 2: 5S Ribosomal RNA

Chain 1B:

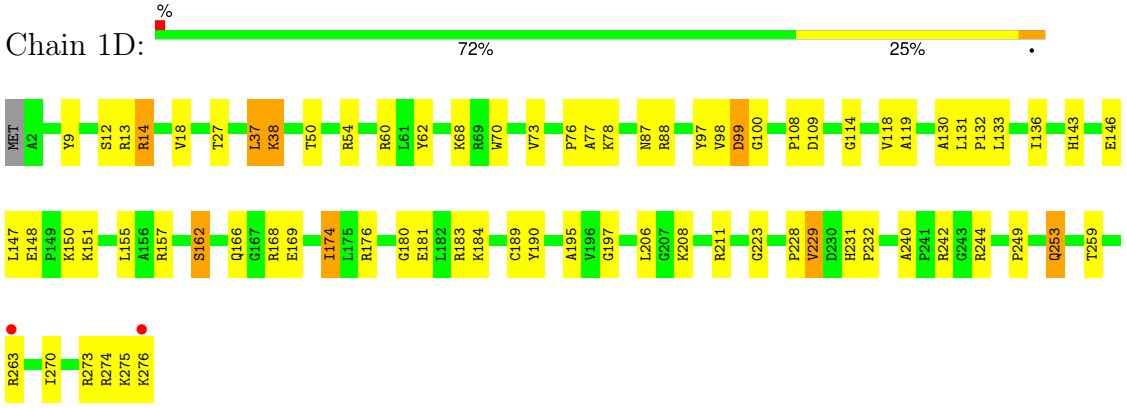
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



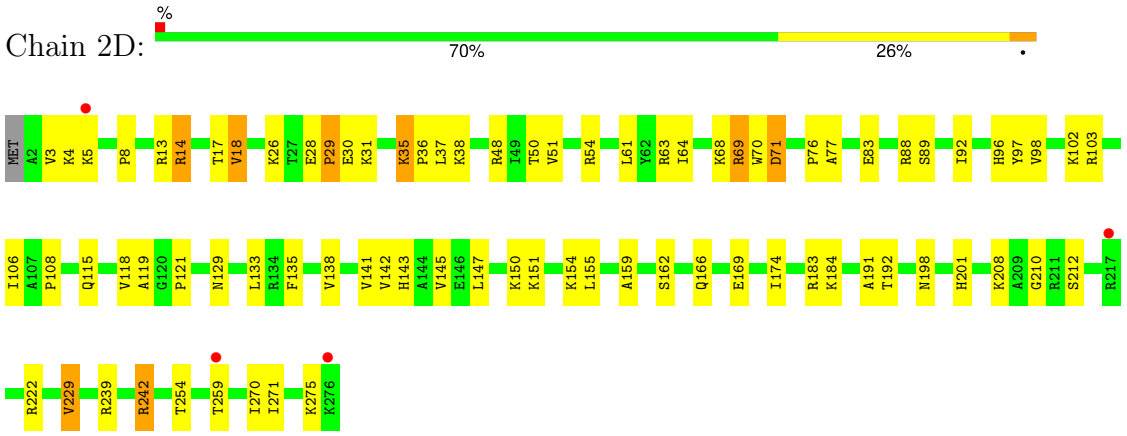
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



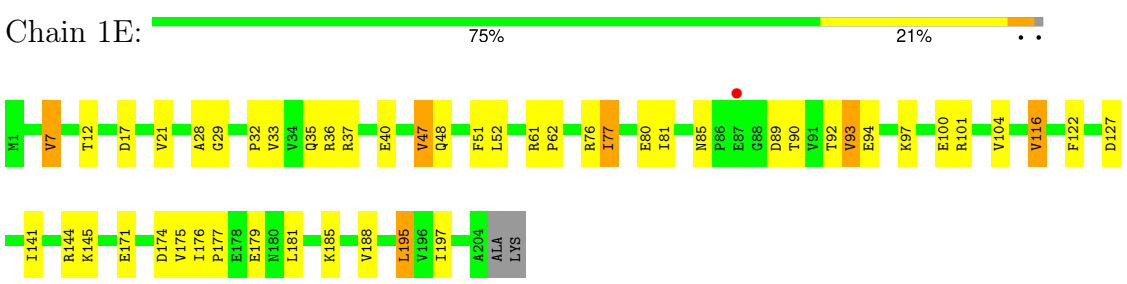
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



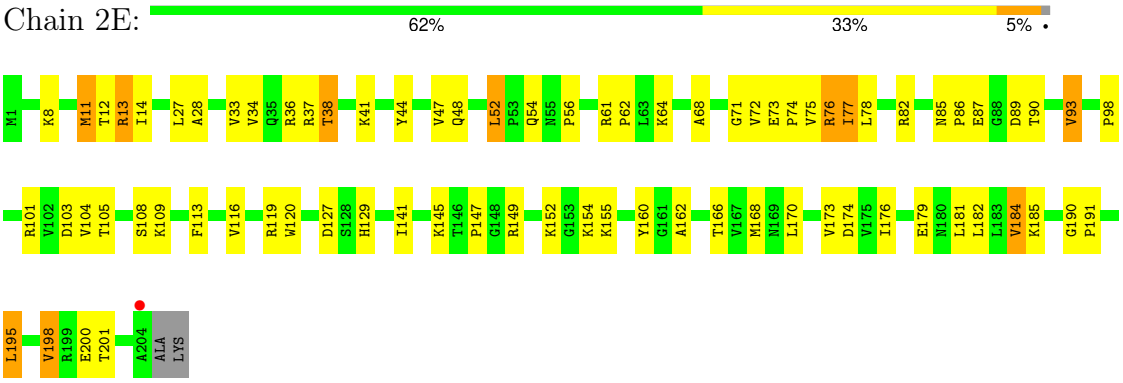
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



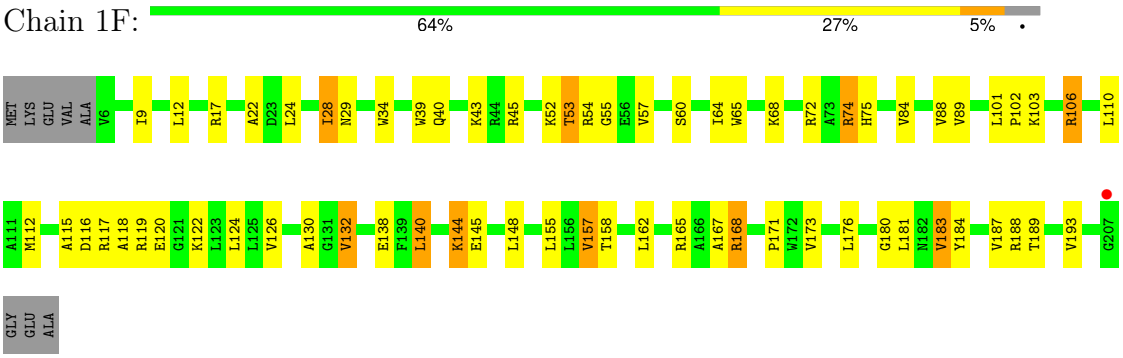
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



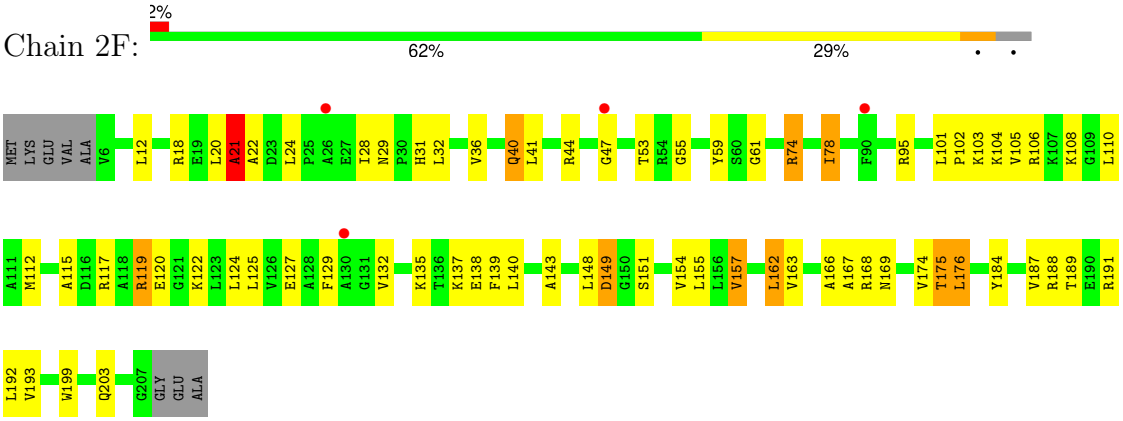
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



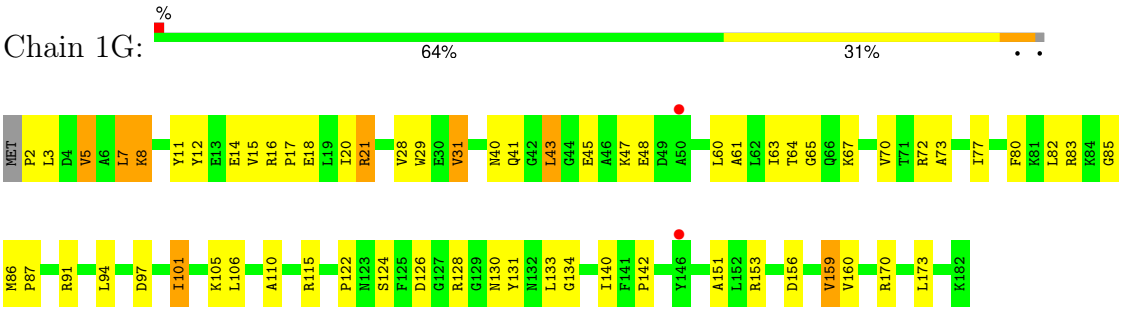
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



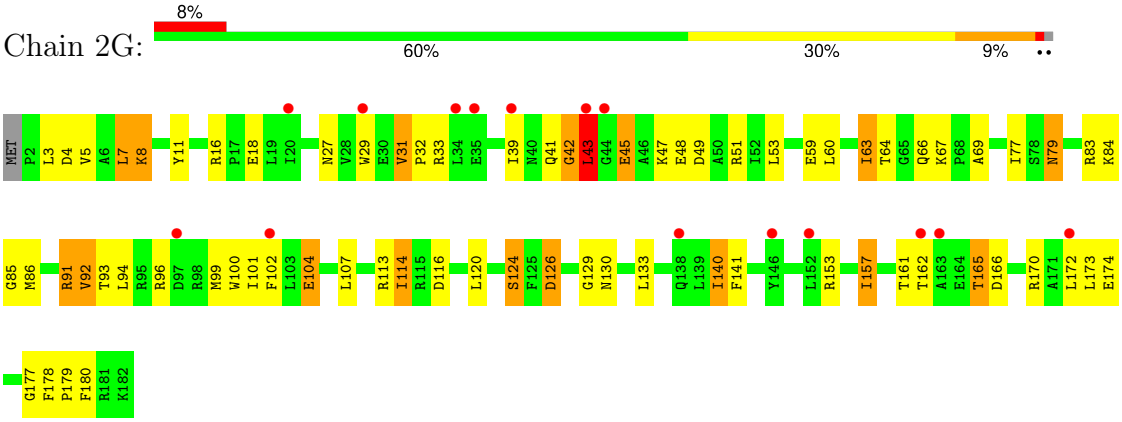
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



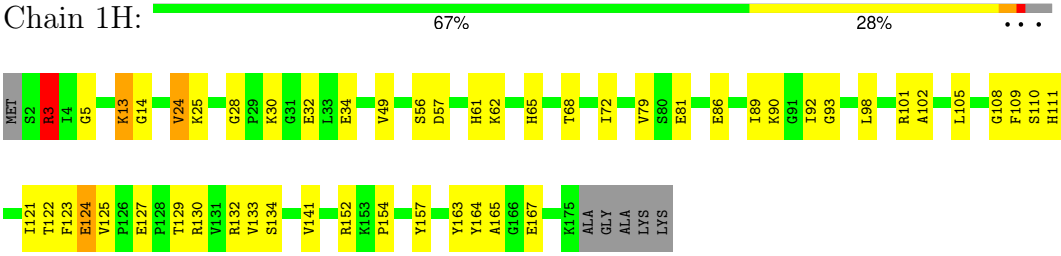
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



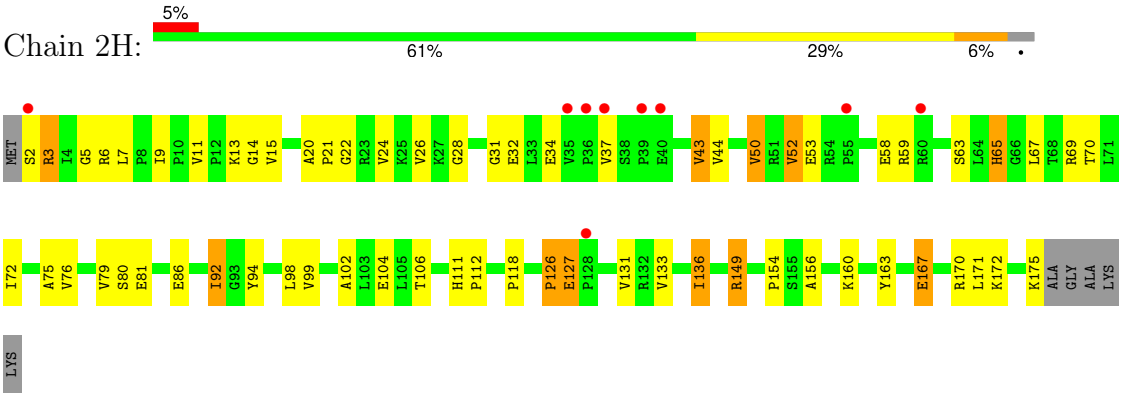
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



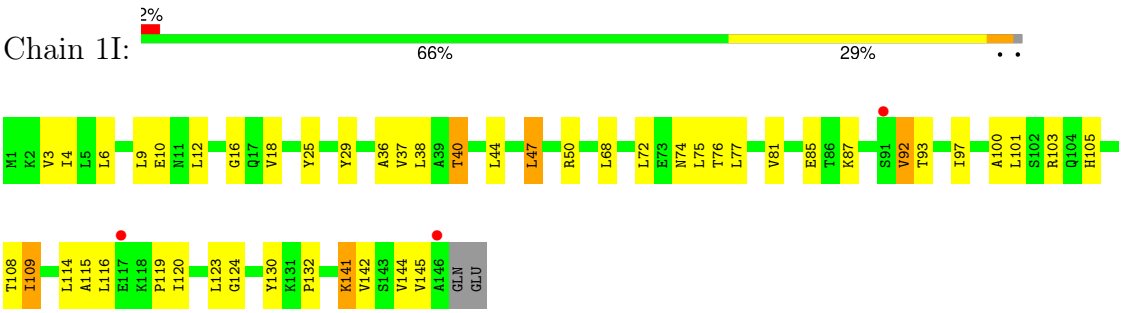
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



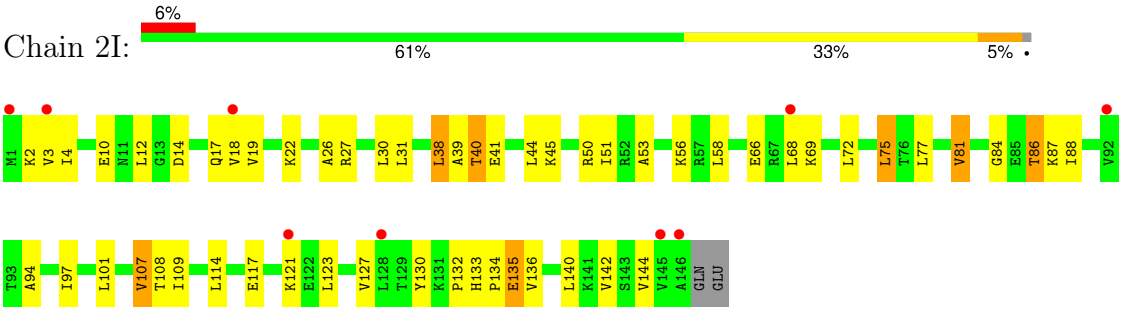
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



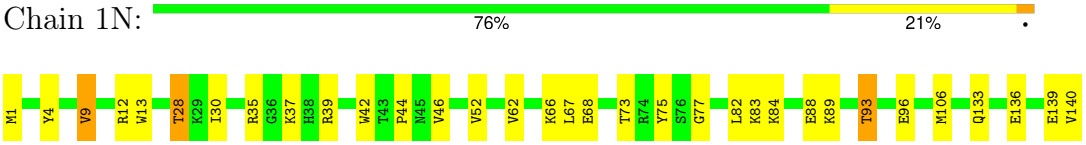
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



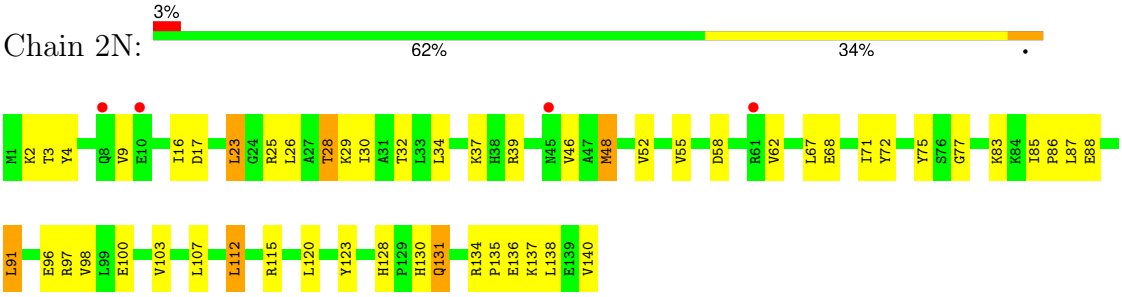
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



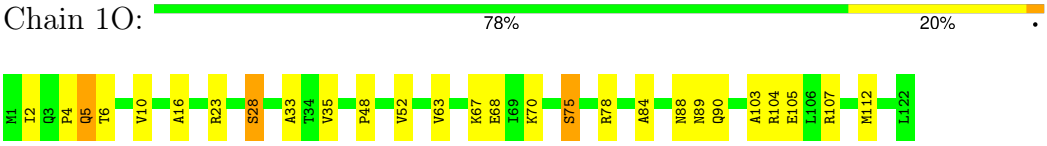
• Molecule 9: 50S ribosomal protein L13

Chain 2N:



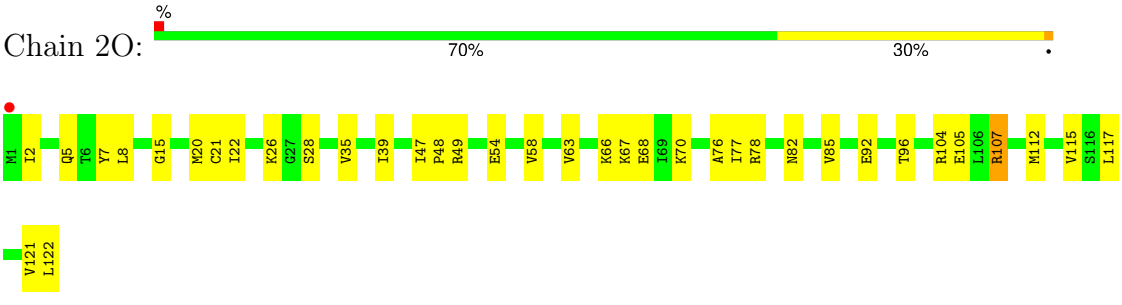
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



• Molecule 10: 50S ribosomal protein L14

Chain 2O:

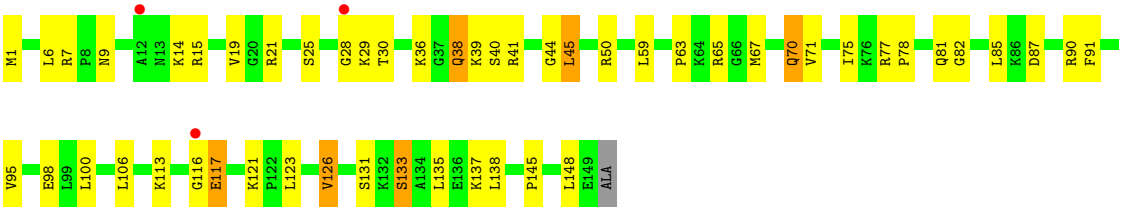


• Molecule 11: 50S ribosomal protein L15

Chain 1P:

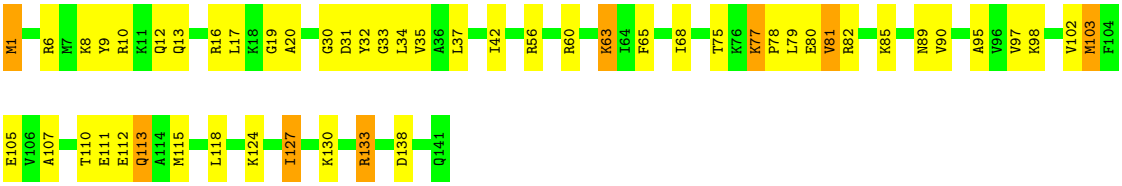
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



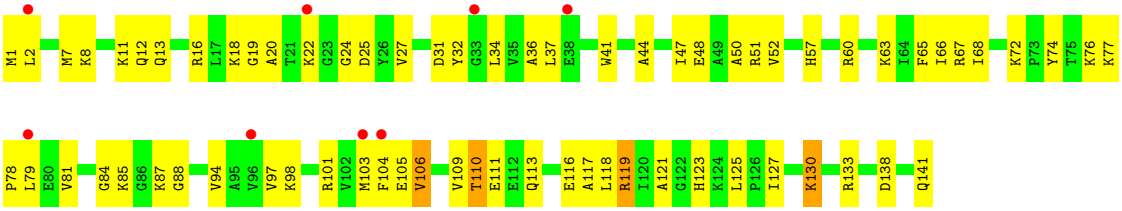
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



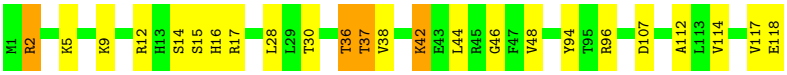
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



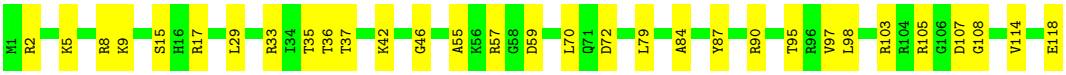
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



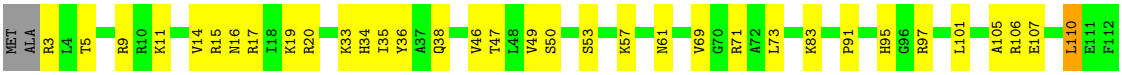
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



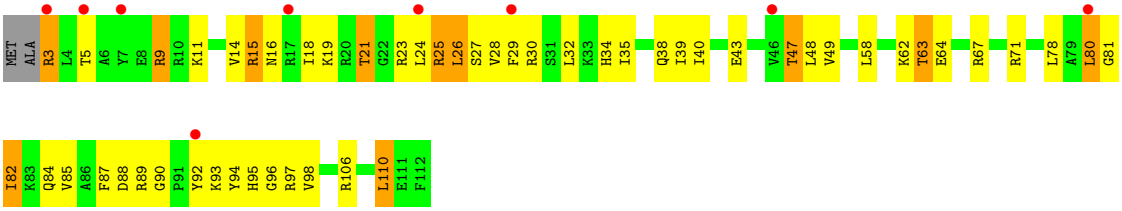
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



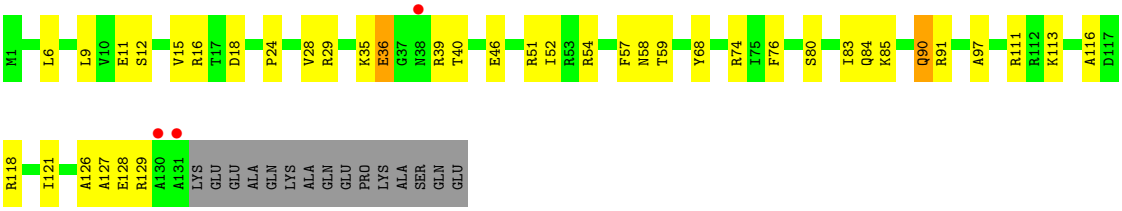
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



• Molecule 15: 50S ribosomal protein L19

Chain 1T:

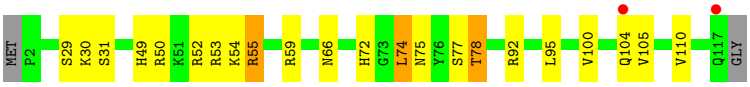


• Molecule 15: 50S ribosomal protein L19

Chain 2T:

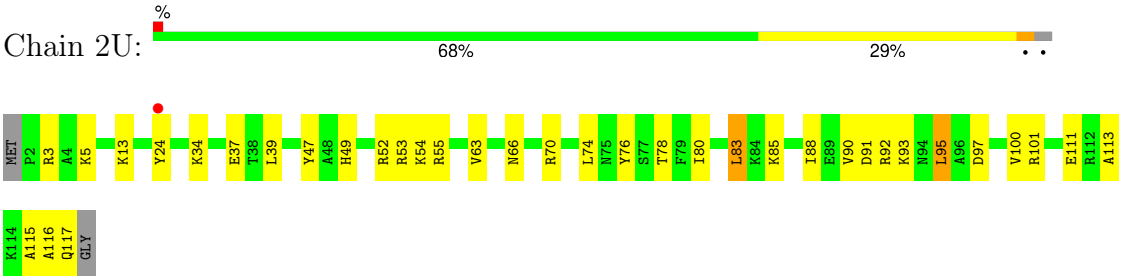
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



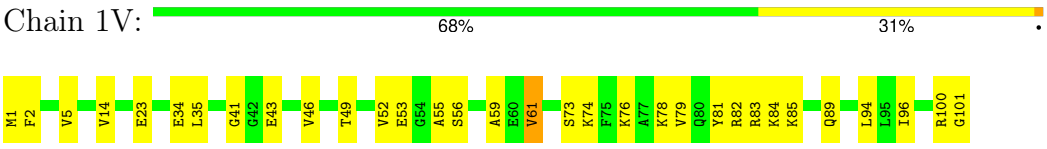
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



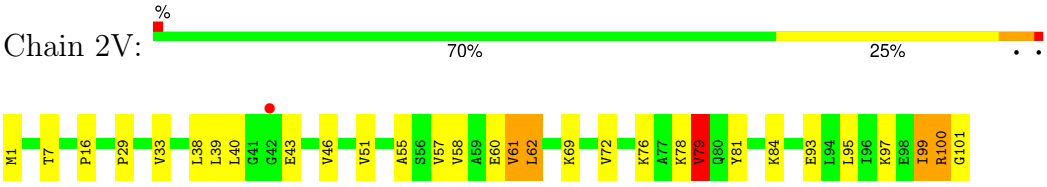
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



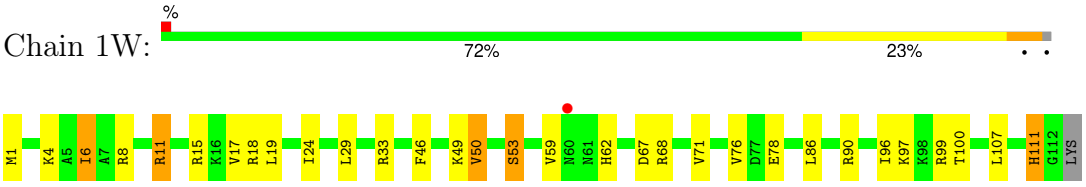
• Molecule 17: 50S ribosomal protein L21

Chain 2V:



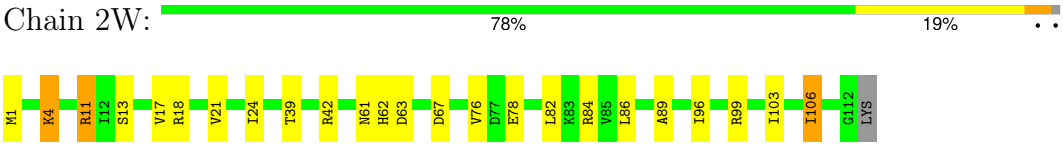
• Molecule 18: 50S ribosomal protein L22

Chain 1W:



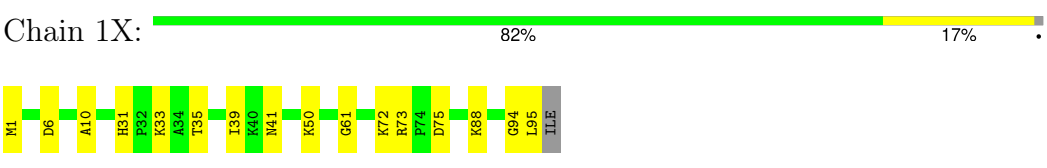
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



• Molecule 19: 50S ribosomal protein L23

Chain 1X:

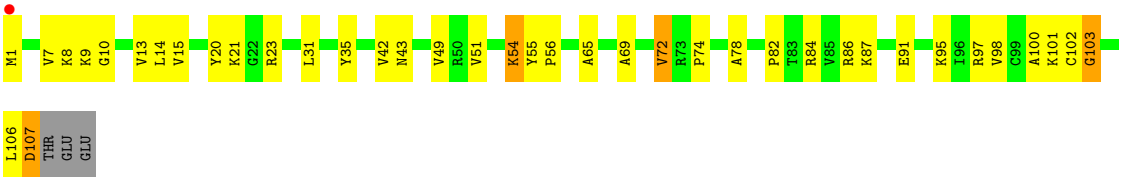


• Molecule 19: 50S ribosomal protein L23

Chain 2X:

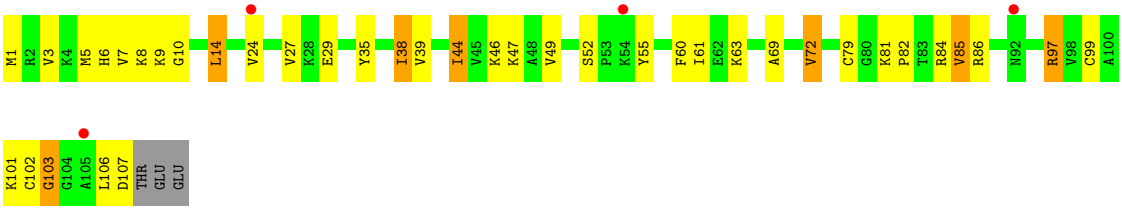
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



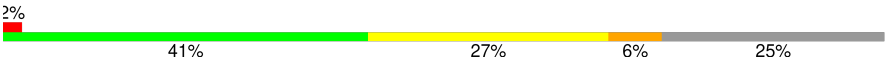
• Molecule 20: 50S ribosomal protein L24

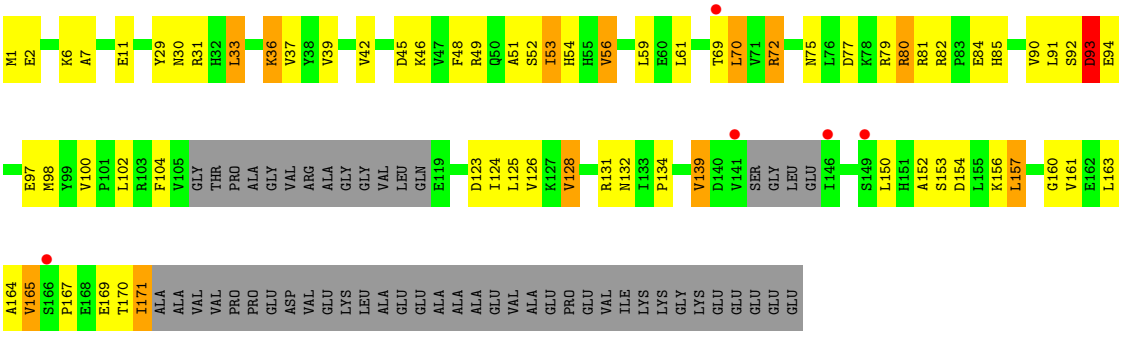
Chain 2Y:



• Molecule 21: 50S ribosomal protein L25

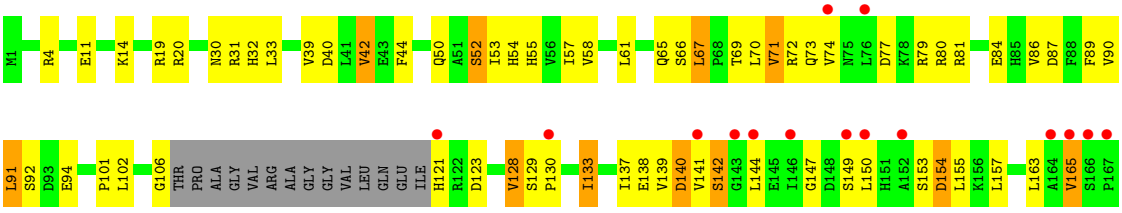
Chain 1Z:

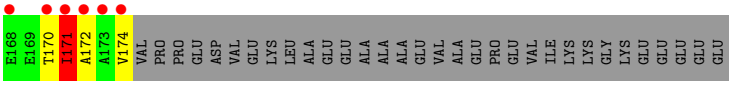




• Molecule 21: 50S ribosomal protein L25

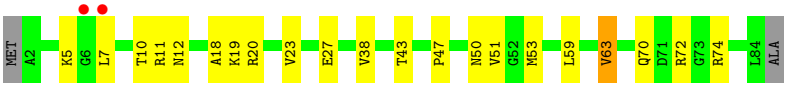
Chain 2Z:





• Molecule 22: 50S ribosomal protein L27

Chain 10:

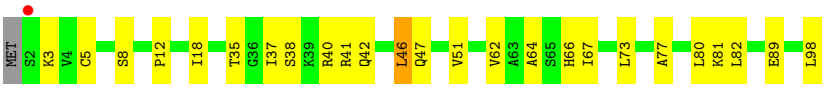


• Molecule 22: 50S ribosomal protein L27

Chain 20:

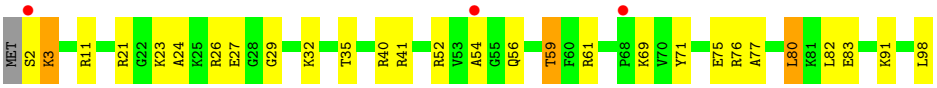
• Molecule 23: 50S ribosomal protein L28

Chain 11:



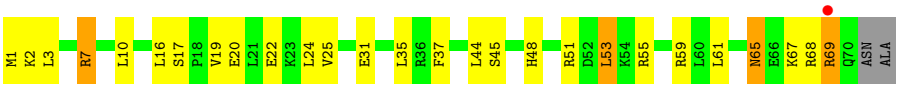
• Molecule 23: 50S ribosomal protein L28

Chain 21:



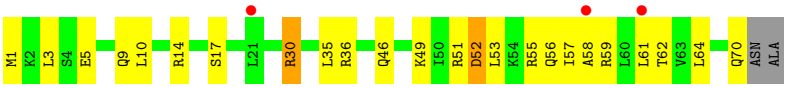
• Molecule 24: 50S ribosomal protein L29

Chain 12:



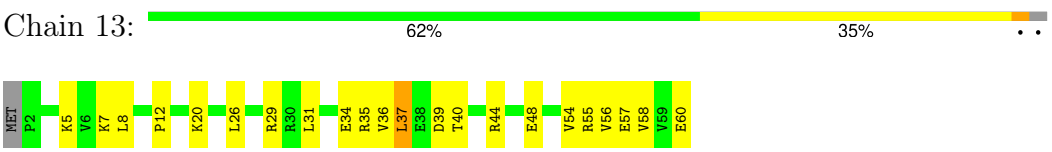
• Molecule 24: 50S ribosomal protein L29

Chain 22:



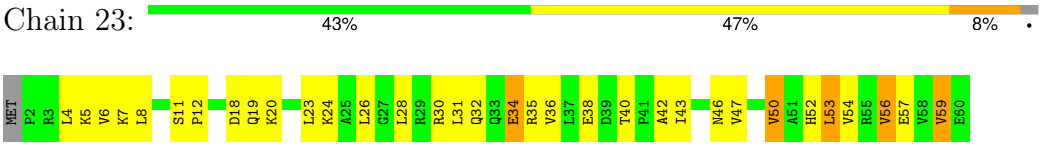
• Molecule 25: 50S ribosomal protein L30

Chain 13:



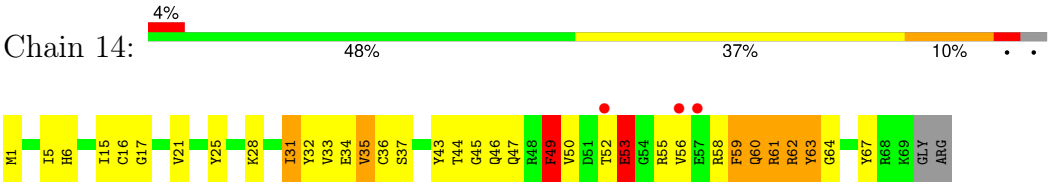
• Molecule 25: 50S ribosomal protein L30

Chain 23:



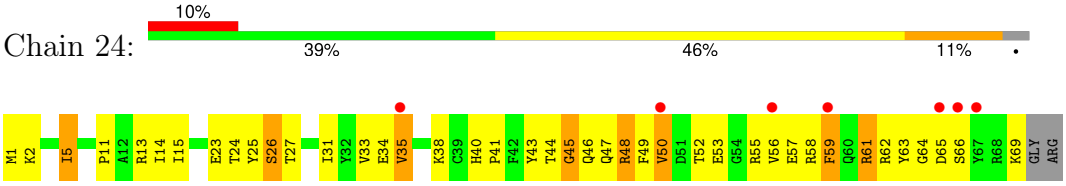
• Molecule 26: 50S ribosomal protein L31

Chain 14:



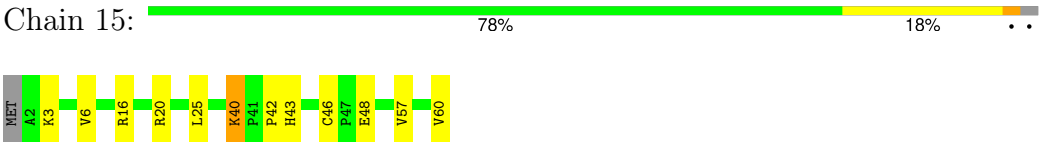
• Molecule 26: 50S ribosomal protein L31

Chain 24:



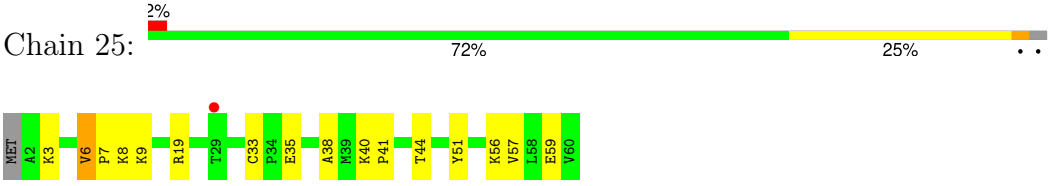
• Molecule 27: 50S ribosomal protein L32

Chain 15:



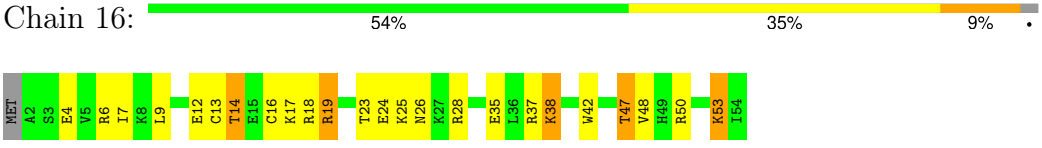
• Molecule 27: 50S ribosomal protein L32

Chain 25:



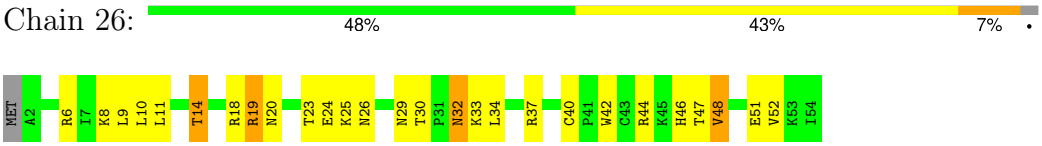
• Molecule 28: 50S ribosomal protein L33

Chain 16:



• Molecule 28: 50S ribosomal protein L33

Chain 26:

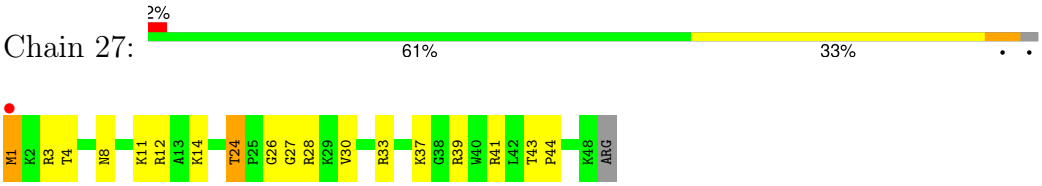


• Molecule 29: 50S ribosomal protein L34

Chain 17:

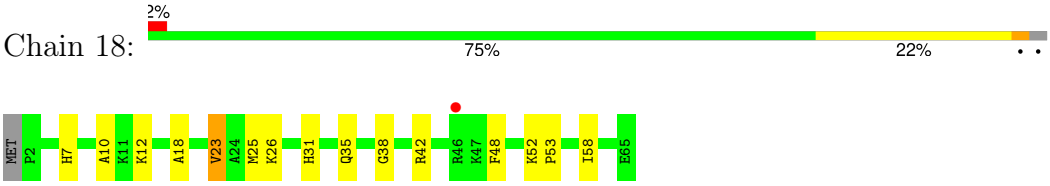
• Molecule 29: 50S ribosomal protein L34

Chain 27:



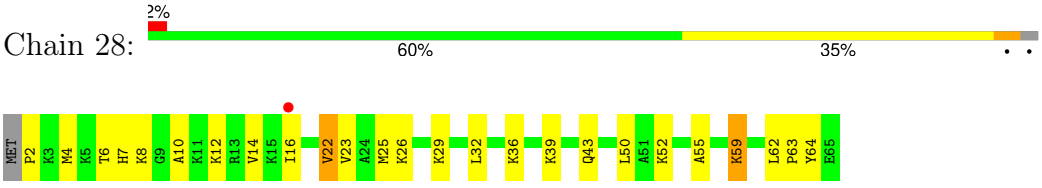
• Molecule 30: 50S ribosomal protein L35

Chain 18:



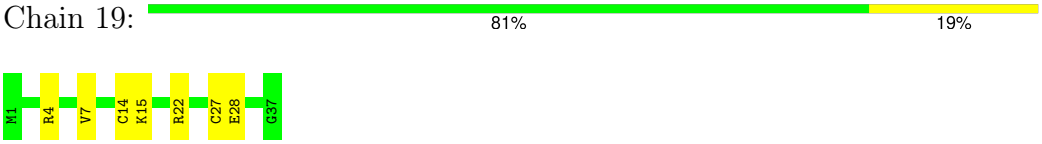
• Molecule 30: 50S ribosomal protein L35

Chain 28:



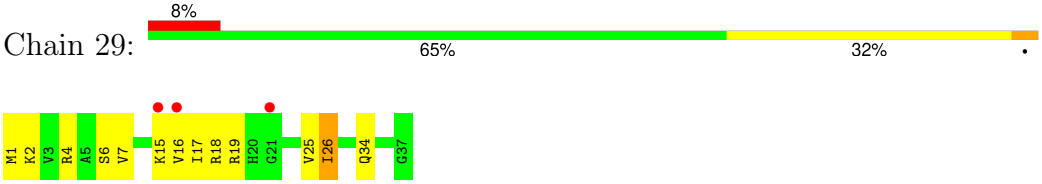
• Molecule 31: 50S ribosomal protein L36

Chain 19:



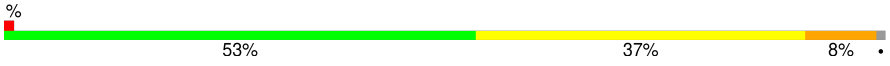
• Molecule 31: 50S ribosomal protein L36

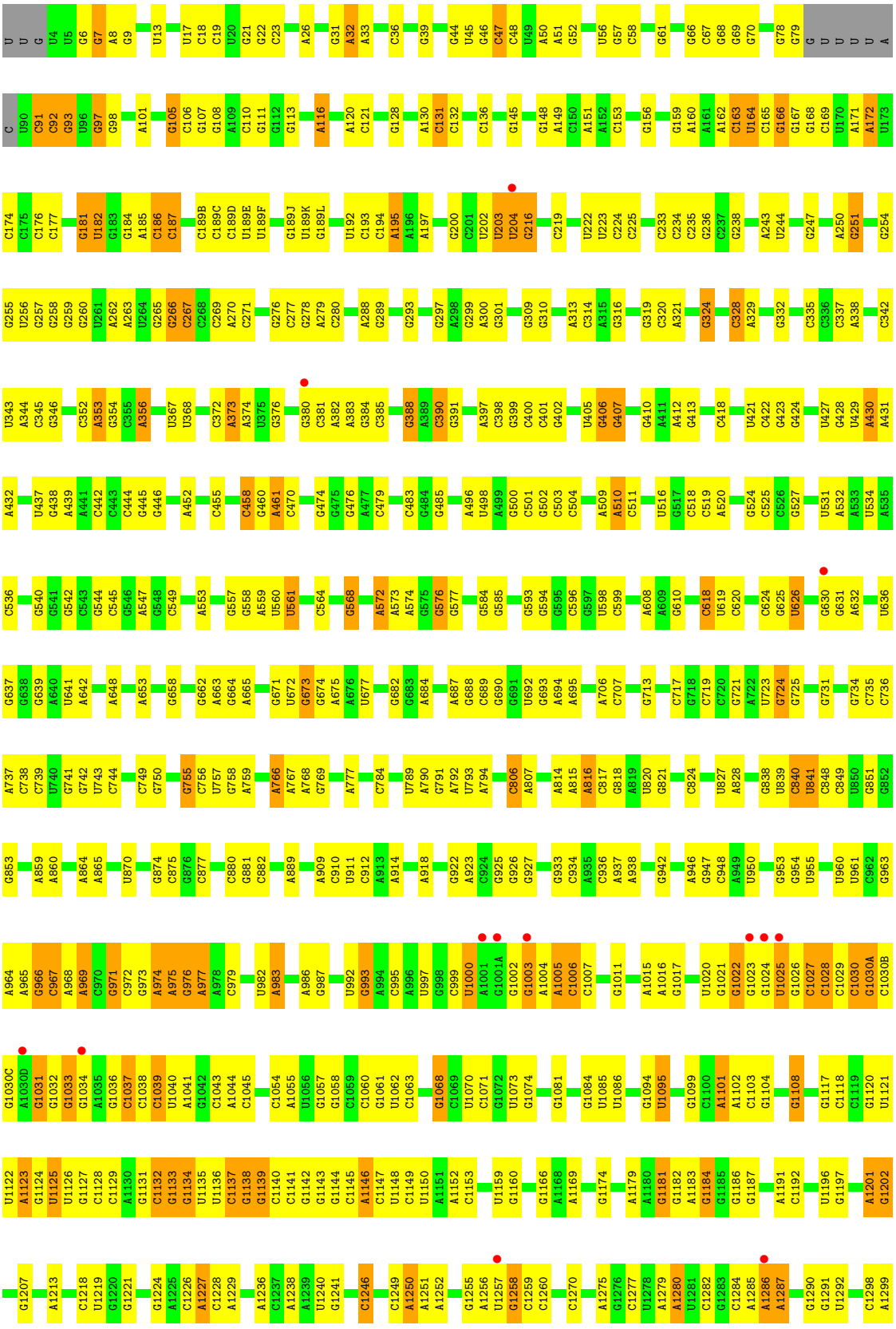
Chain 29:

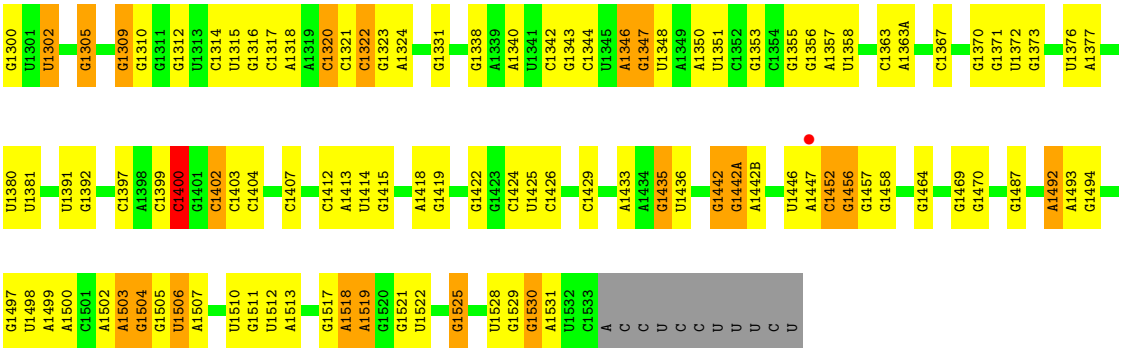


• Molecule 32: 16S Ribosomal RNA

Chain 1a:

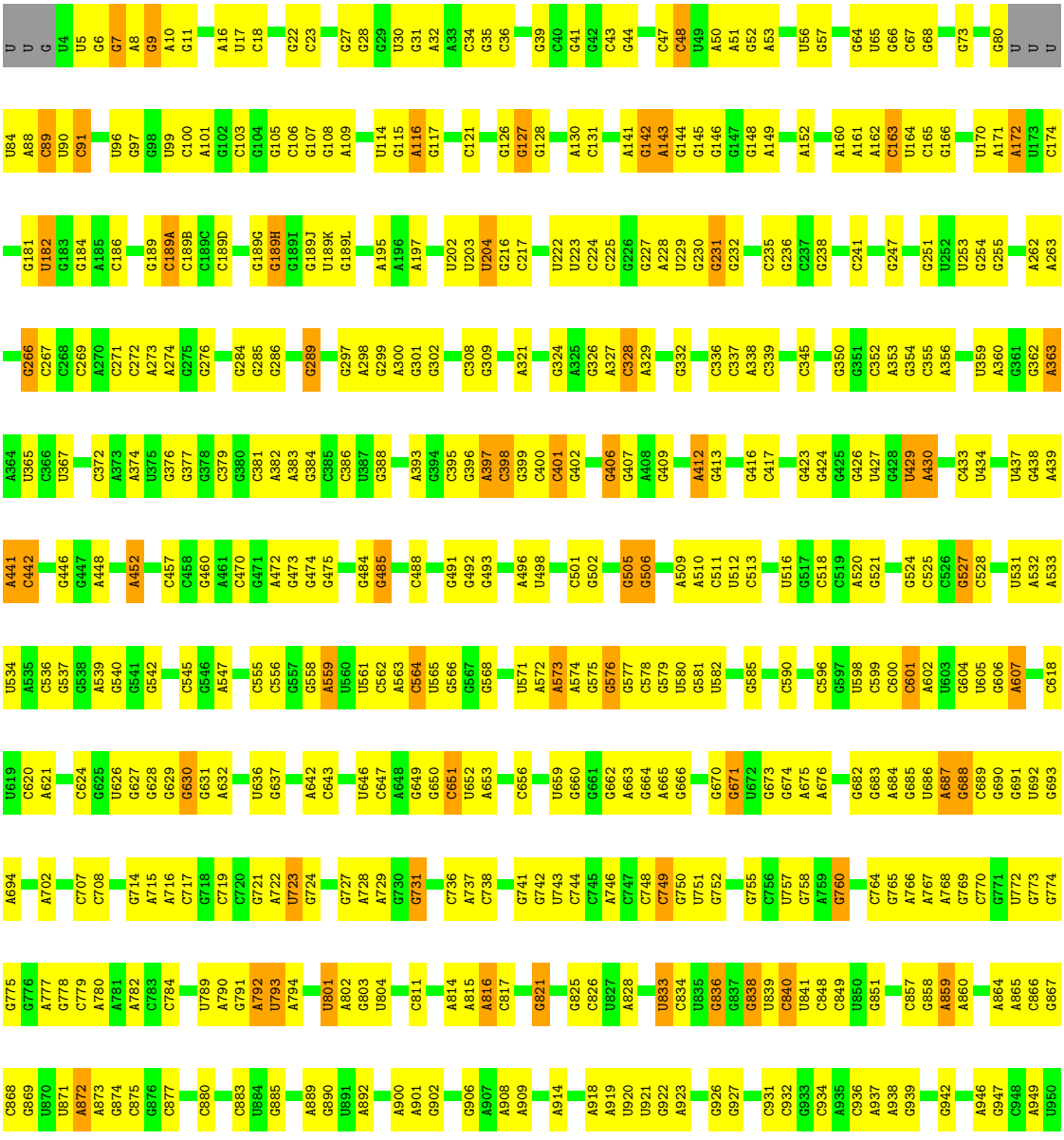


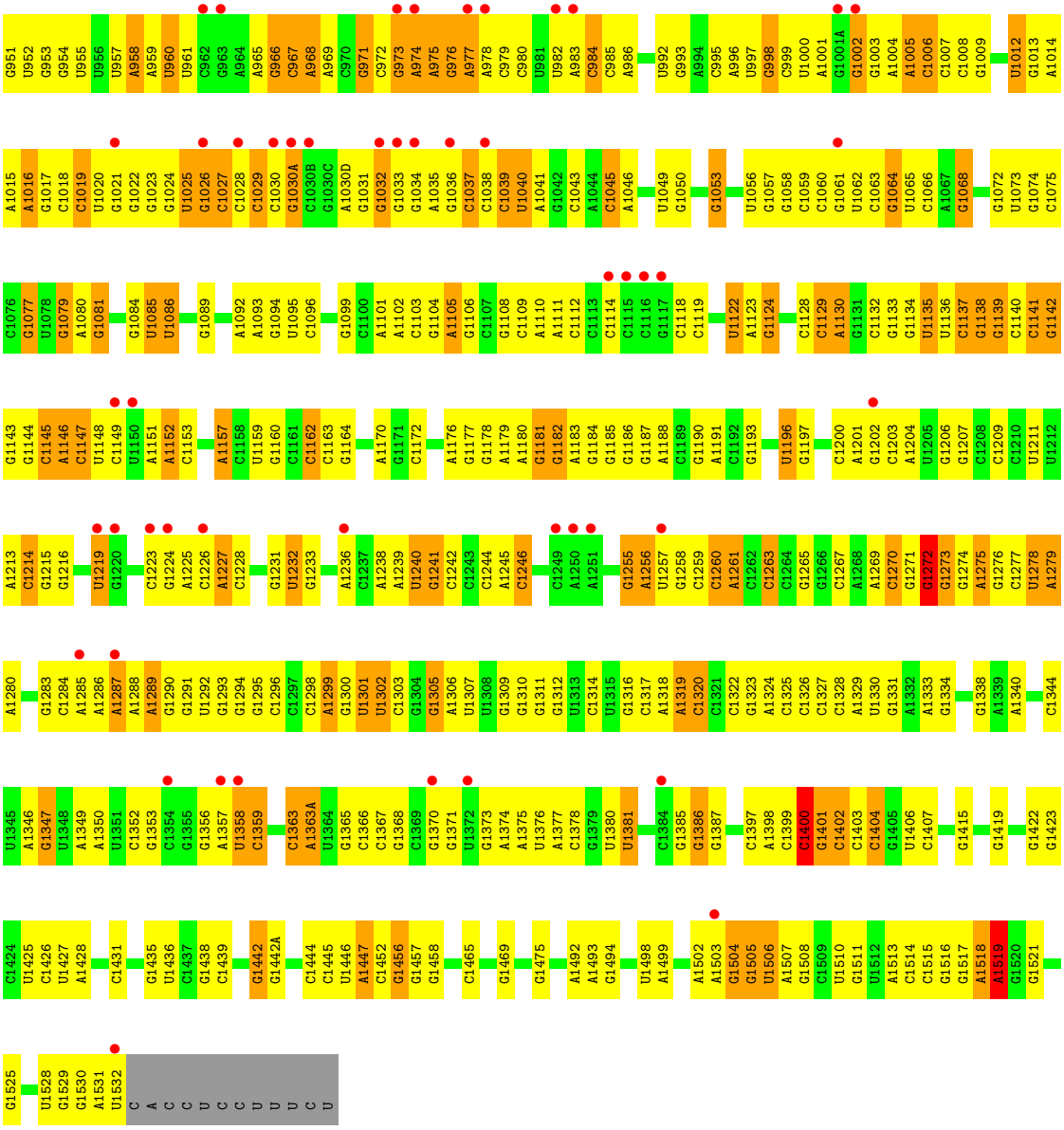




• Molecule 32: 16S Ribosomal RNA

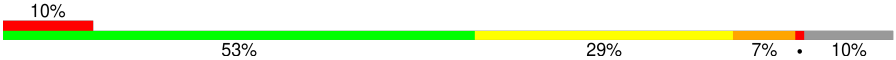
Chain 2a:

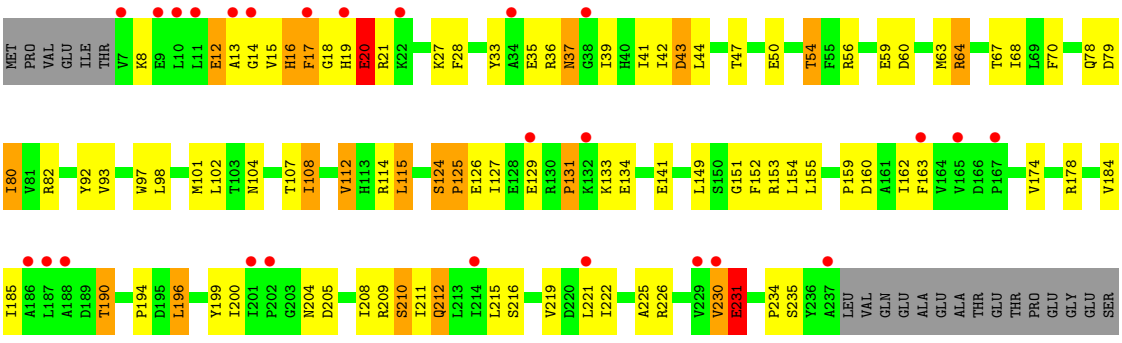




• Molecule 33: 30S ribosomal protein S2

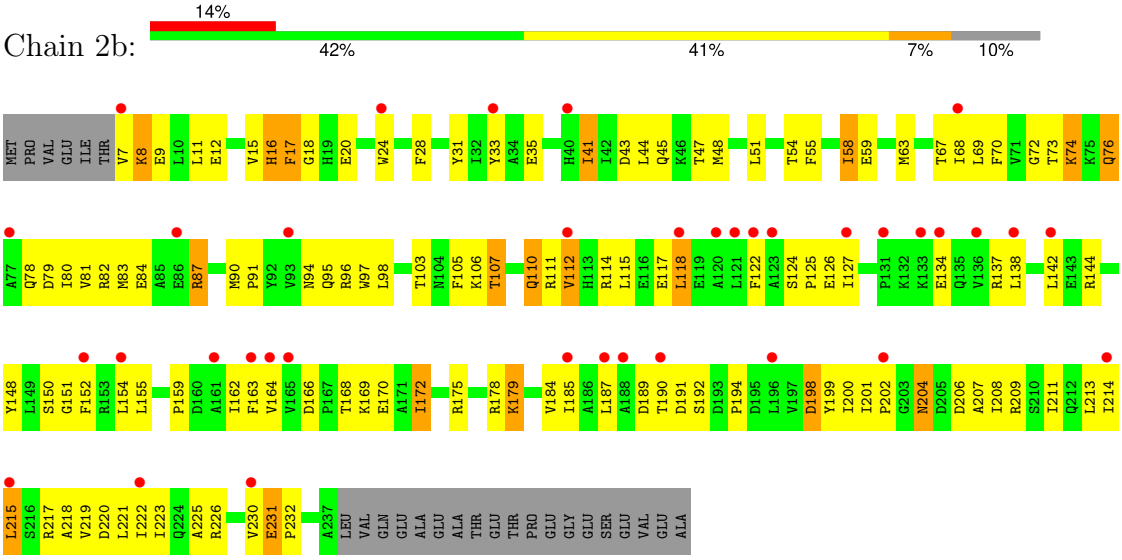
Chain 1b:





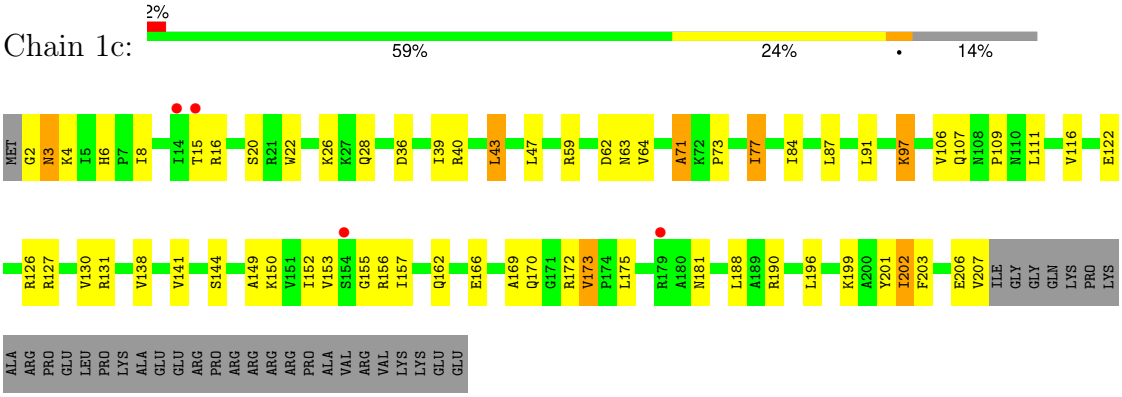
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



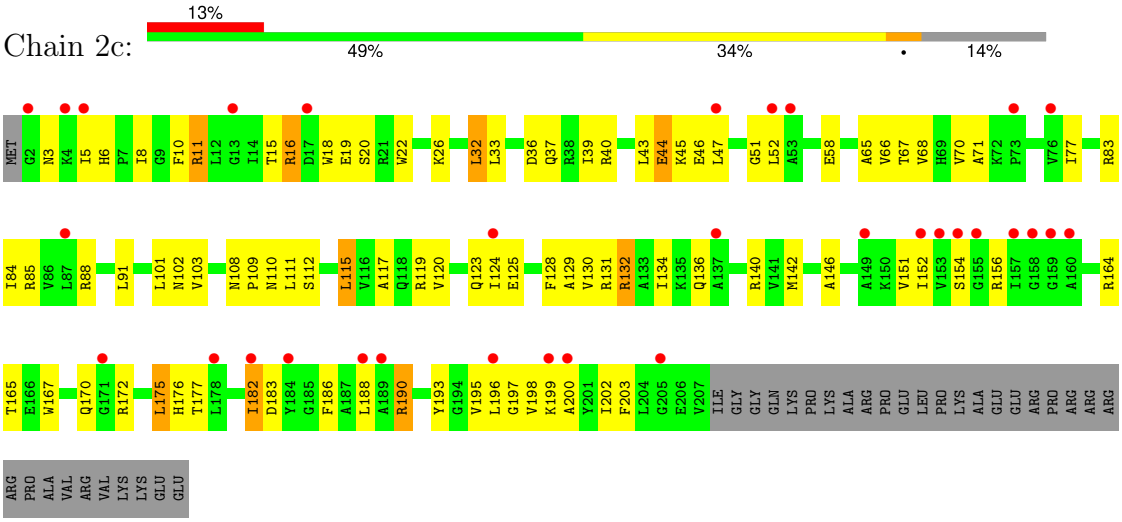
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



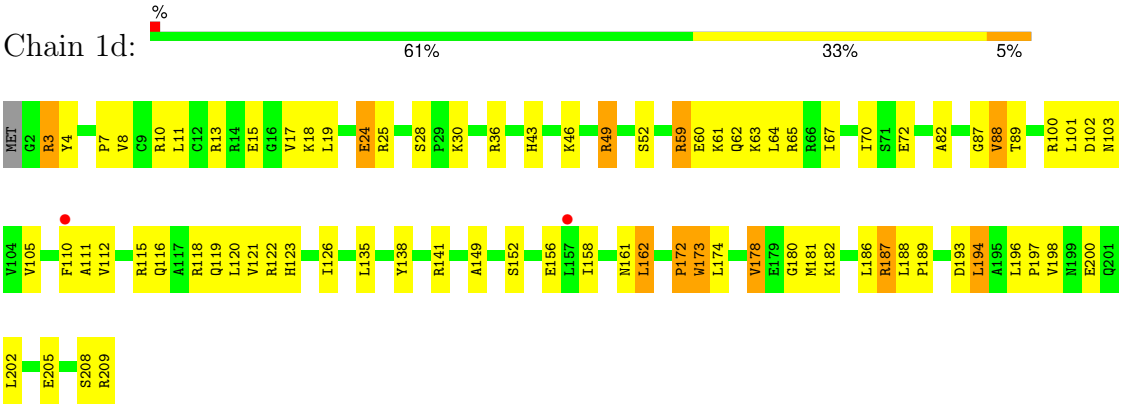
• Molecule 34: 30S ribosomal protein S3

Chain 2c:



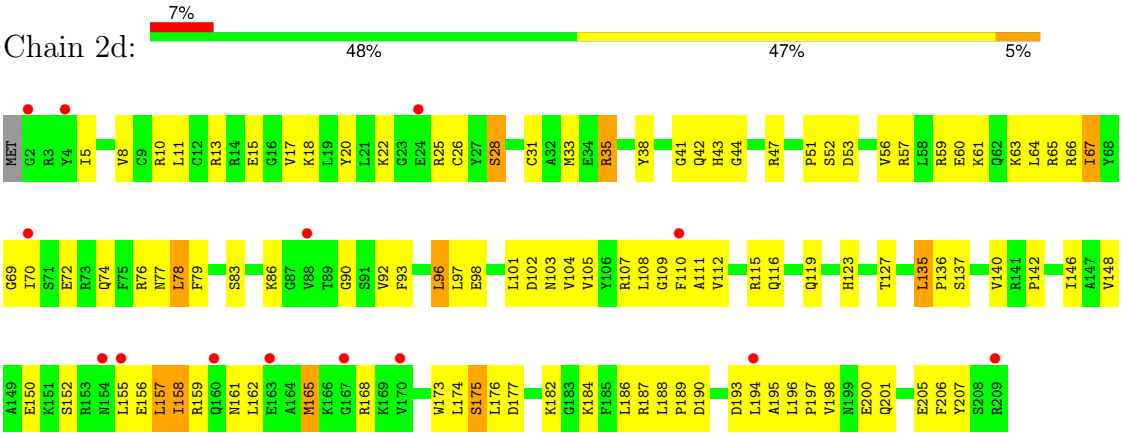
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



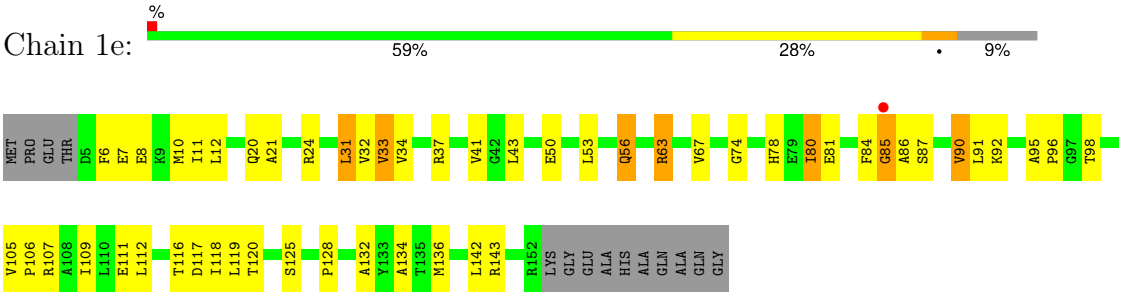
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



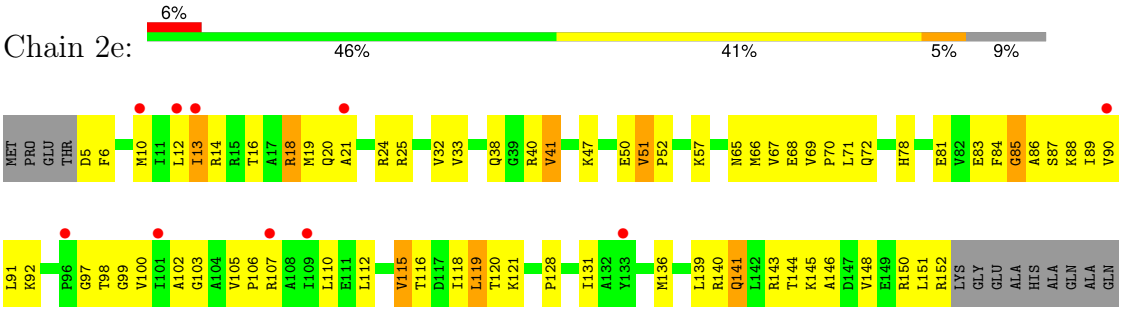
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



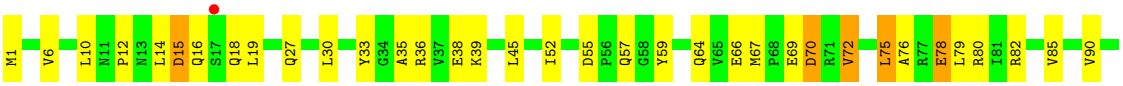
• Molecule 36: 30S ribosomal protein S5

Chain 2e:



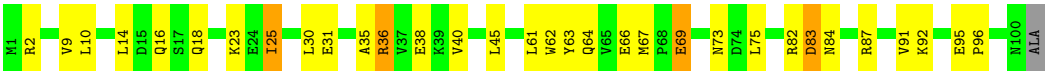
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



• Molecule 37: 30S ribosomal protein S6

Chain 2f:

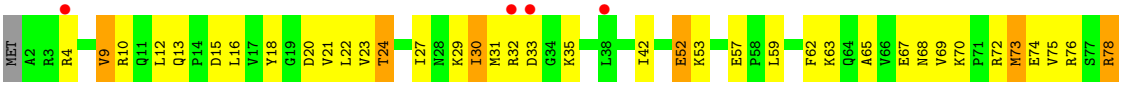


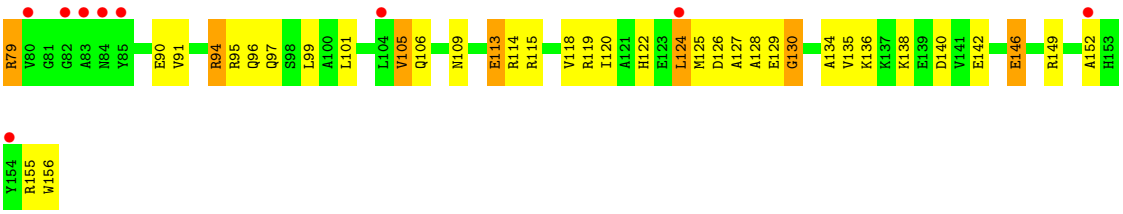
• Molecule 38: 30S ribosomal protein S7

Chain 1g:

• Molecule 38: 30S ribosomal protein S7

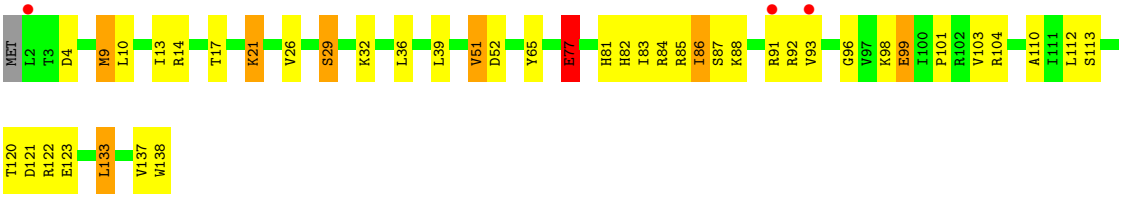
Chain 2g:





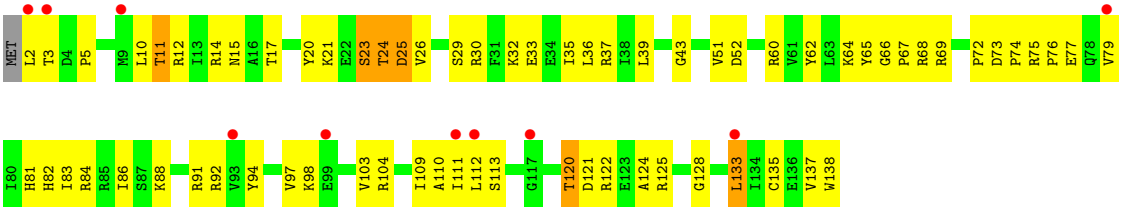
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



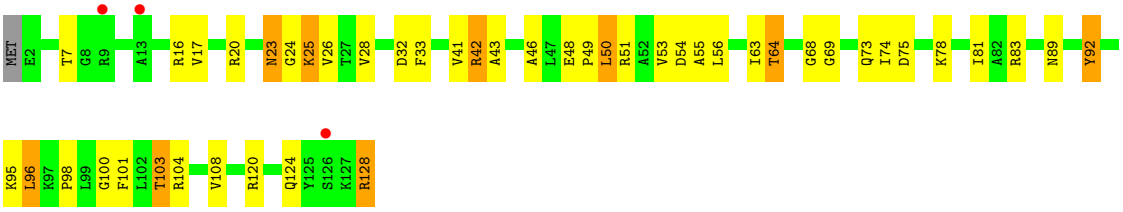
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



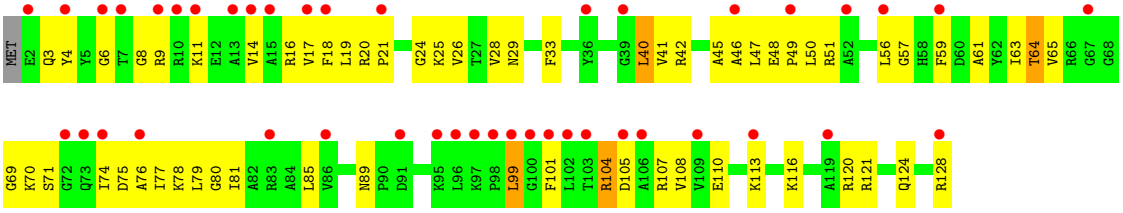
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



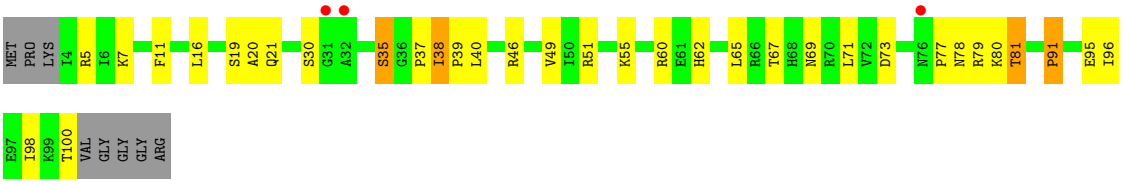
• Molecule 40: 30S ribosomal protein S9

Chain 2i:



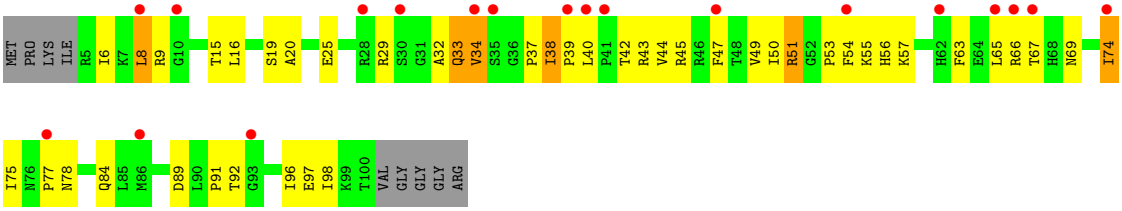
• Molecule 41: 30S ribosomal protein S10

Chain 1j:



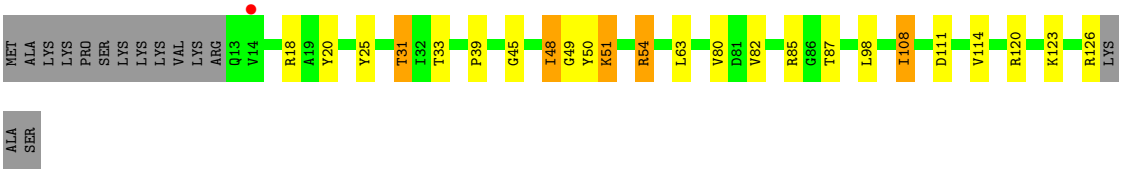
• Molecule 41: 30S ribosomal protein S10

Chain 2j:



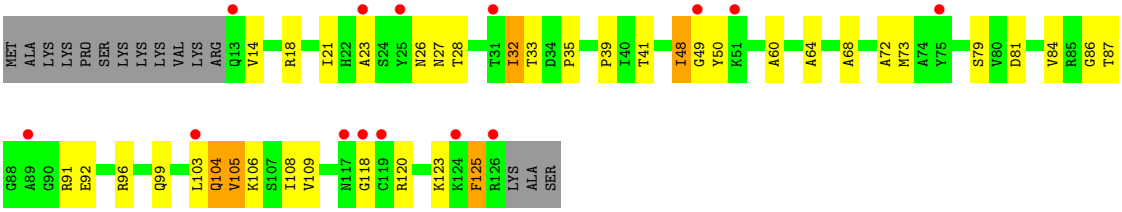
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



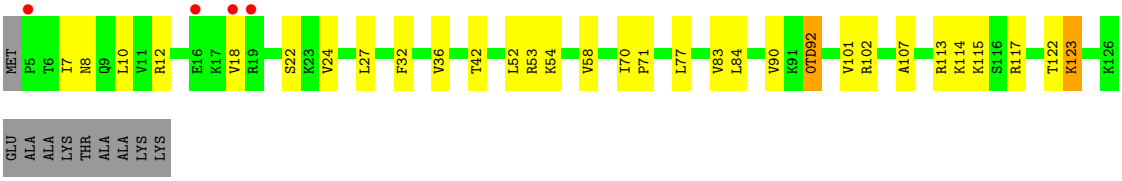
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



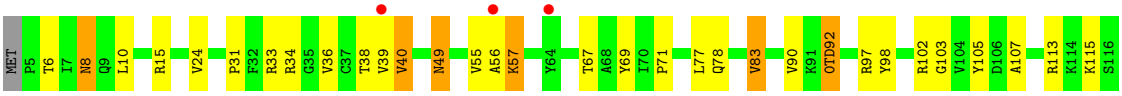
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



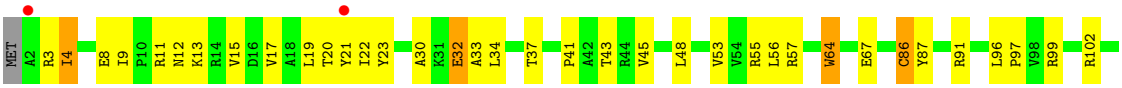
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



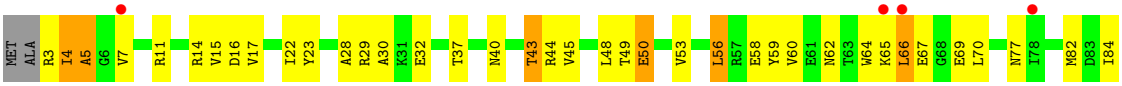
• Molecule 44: 30S ribosomal protein S13

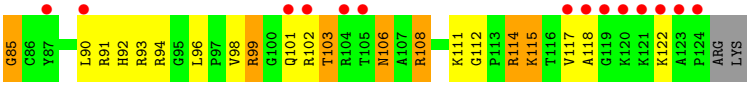
Chain 1m:



• Molecule 44: 30S ribosomal protein S13

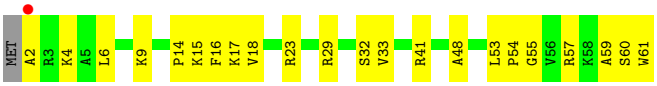
Chain 2m:





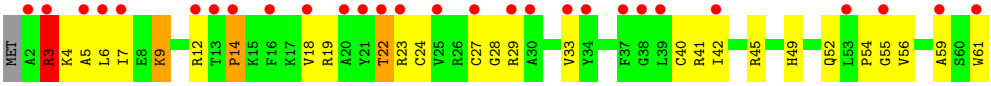
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:

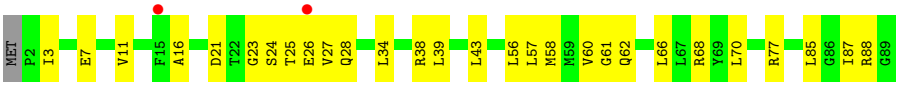


• Molecule 46: 30S ribosomal protein S15

Chain 1o:

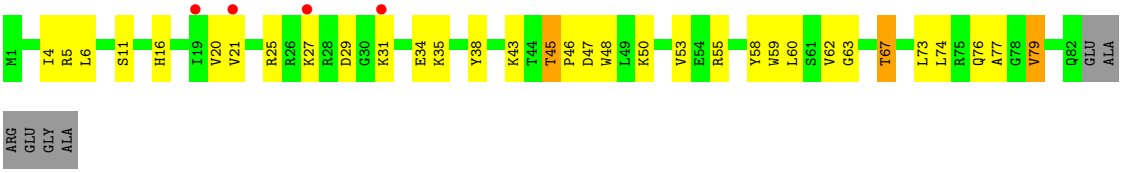
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



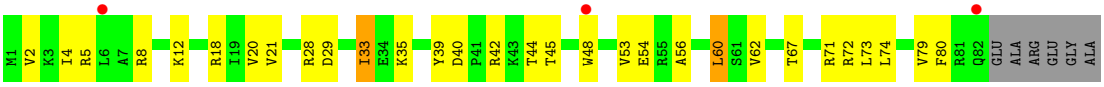
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



• Molecule 47: 30S ribosomal protein S16

Chain 2p:

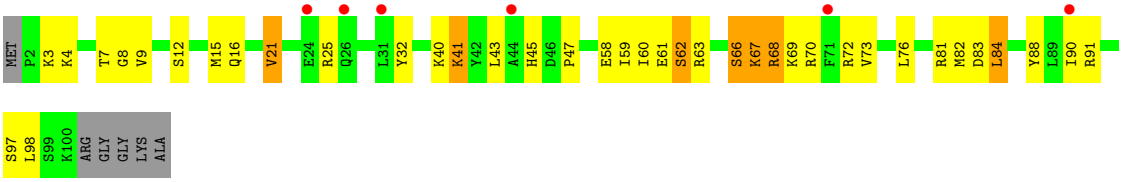


• Molecule 48: 30S ribosomal protein S17

Chain 1q:

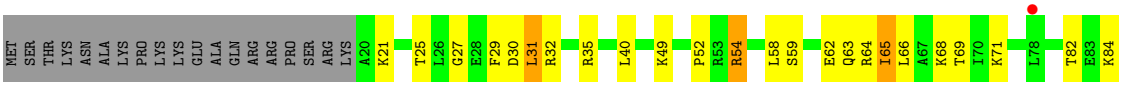
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



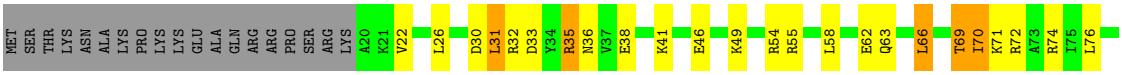
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



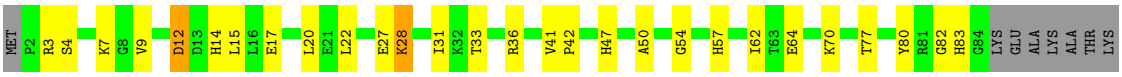
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



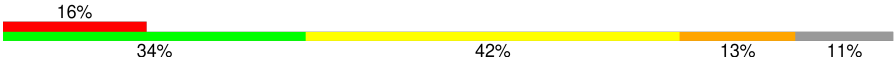
• Molecule 50: 30S ribosomal protein S19

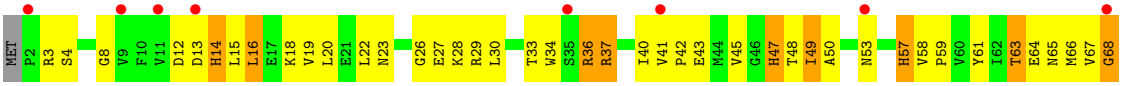
Chain 1s:

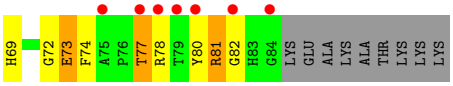


• Molecule 50: 30S ribosomal protein S19

Chain 2s:

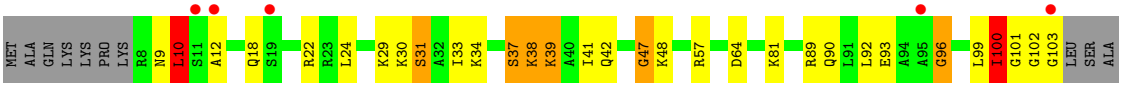






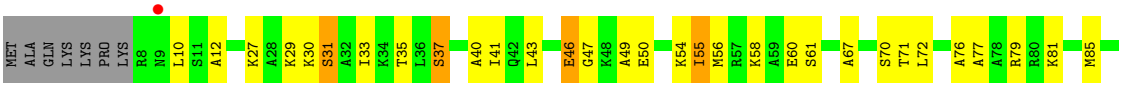
• Molecule 51: 30S ribosomal protein S20

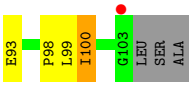
Chain 1t:



• Molecule 51: 30S ribosomal protein S20

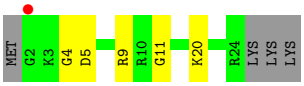
Chain 2t:





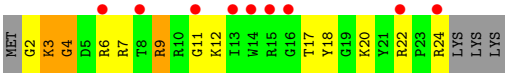
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



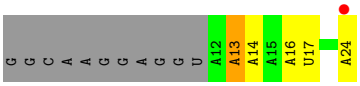
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



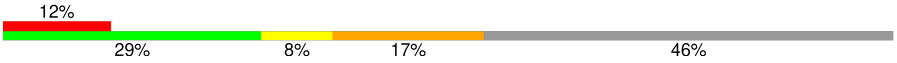
• Molecule 53: MET-PHE-mRNA

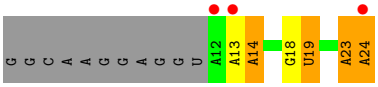
Chain 1v:



• Molecule 53: MET-PHE-mRNA

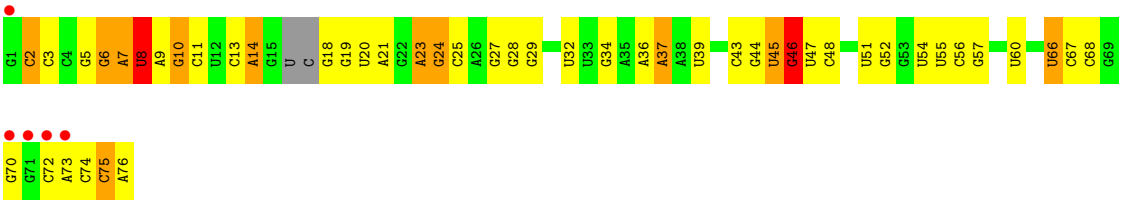
Chain 2v:





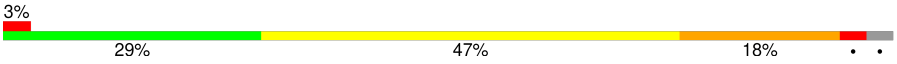
• Molecule 54: A-site and E-site Deacylated tRNAphe

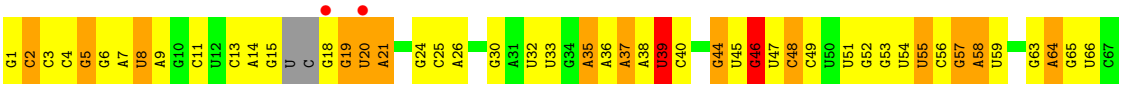
Chain 1w:

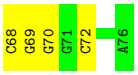


• Molecule 54: A-site and E-site Deacylated tRNAphe

Chain 1y:

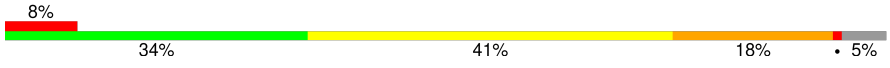


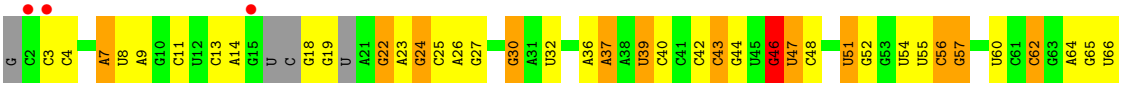


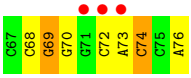


• Molecule 54: A-site and E-site Deacylated tRNAphe

Chain 2w:

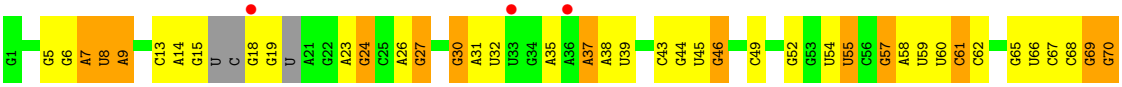






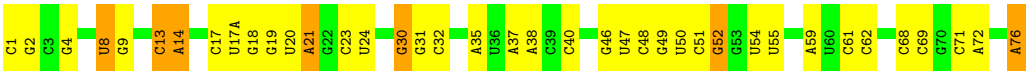
• Molecule 54: A-site and E-site Deacylated tRNAphe

Chain 2y:



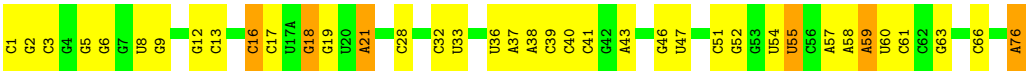
• Molecule 55: P-site Peptidyl-tRNA fMRC-tRNAcys RNA-part

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:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	208.76Å 447.07Å 617.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	122.56 – 2.75 122.56 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (122.56-2.75) 99.8 (122.56-2.75)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.21 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.17.1	Depositor
R, R_{free}	0.228 , 0.282 0.230 , 0.281	Depositor DCC
R_{free} test set	74137 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	58.6	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 49.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.36$, $< L^2 > = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	299368	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.66% 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: M2G, OMC, ZN, 4SU, 4OC, 2MA, MIA, K, G7M, PSU, MA6, MG, 0TD, UR3, 5MU, FME, OMU, SF4, OMG, 2MG, 8AN, ERY, 5MC

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	0.28	1/69011 (0.0%)	0.45	1/107720 (0.0%)
1	2A	0.22	0/67295	0.40	1/105042 (0.0%)
2	1B	0.22	0/2882	0.39	0/4494
2	2B	0.20	0/2879	0.37	0/4487
3	1D	0.28	0/2186	0.50	0/2944
3	2D	0.23	0/2186	0.51	3/2944 (0.1%)
4	1E	0.26	0/1592	0.51	0/2149
4	2E	0.23	0/1592	0.46	0/2149
5	1F	0.27	0/1618	0.50	0/2191
5	2F	0.21	0/1614	0.46	2/2186 (0.1%)
6	1G	0.23	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	0.40	0/1834
8	1I	0.20	0/1112	0.46	0/1514
8	2I	0.22	0/1079	0.45	0/1475
9	1N	0.24	0/1144	0.45	0/1543
9	2N	0.19	0/1144	0.43	0/1543
10	1O	0.27	0/943	0.46	0/1269
10	2O	0.21	0/943	0.45	0/1269
11	1P	0.28	0/1152	0.49	0/1533
11	2P	0.22	0/1152	0.51	0/1533
12	1Q	0.27	0/1143	0.48	0/1527
12	2Q	0.21	0/1143	0.44	0/1527
13	1R	0.25	0/982	0.46	0/1312
13	2R	0.22	0/982	0.45	0/1312
14	1S	0.22	0/883	0.47	0/1176
14	2S	0.23	0/880	0.47	0/1172
15	1T	0.24	0/1105	0.48	0/1477
15	2T	0.23	0/1097	0.45	0/1468
16	1U	0.26	0/977	0.42	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.20	0/977	0.42	0/1301
17	1V	0.23	0/782	0.43	0/1049
17	2V	0.19	0/782	0.41	0/1049
18	1W	0.26	0/897	0.44	0/1205
18	2W	0.22	0/897	0.41	0/1205
19	1X	0.28	0/764	0.51	0/1025
19	2X	0.22	0/764	0.48	0/1025
20	1Y	0.23	0/819	0.48	0/1095
20	2Y	0.20	0/819	0.45	0/1095
21	1Z	0.22	0/1267	0.48	0/1717
21	2Z	0.22	0/1299	0.43	0/1763
22	10	0.24	0/662	0.51	0/881
22	20	0.22	0/662	0.45	0/881
23	11	0.26	0/762	0.42	0/1014
23	21	0.22	0/762	0.43	0/1014
24	12	0.25	0/590	0.46	0/781
24	22	0.22	0/590	0.40	0/781
25	13	0.26	0/474	0.45	0/635
25	23	0.19	0/469	0.42	0/630
26	14	0.24	0/565	0.55	0/761
26	24	0.26	0/545	0.51	0/737
27	15	0.24	0/469	0.47	0/635
27	25	0.26	0/469	0.50	0/635
28	16	0.25	0/460	0.50	0/613
28	26	0.21	0/456	0.41	0/608
29	17	0.31	0/426	0.58	0/561
29	27	0.25	0/426	0.53	0/561
30	18	0.28	0/525	0.50	0/691
30	28	0.22	0/525	0.44	0/691
31	19	0.28	0/310	0.58	0/407
31	29	0.20	0/310	0.43	0/407
32	1a	0.21	0/35795	0.39	2/55864 (0.0%)
32	2a	0.20	1/35886 (0.0%)	0.38	3/56005 (0.0%)
33	1b	0.22	0/1881	0.53	0/2542
33	2b	0.24	0/1860	0.50	0/2518
34	1c	0.20	0/1572	0.41	0/2126
34	2c	0.25	0/1566	0.49	0/2119
35	1d	0.21	0/1685	0.45	0/2262
35	2d	0.21	0/1704	0.47	0/2284
36	1e	0.21	0/1145	0.46	0/1543
36	2e	0.21	0/1149	0.50	0/1548
37	1f	0.20	0/823	0.39	0/1115
37	2f	0.21	0/829	0.41	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.21	0/1250	0.43	0/1679
38	2g	0.20	0/1254	0.46	0/1683
39	1h	0.20	0/1108	0.41	0/1494
39	2h	0.19	0/1108	0.41	0/1494
40	1i	0.22	0/1002	0.47	0/1346
40	2i	0.21	0/997	0.49	0/1343
41	1j	0.20	0/722	0.44	0/982
41	2j	0.21	0/727	0.44	0/988
42	1k	0.20	0/844	0.40	0/1145
42	2k	0.18	0/848	0.40	0/1149
43	1l	0.23	0/937	0.43	0/1260
43	2l	0.21	0/937	0.44	0/1260
44	1m	0.20	0/969	0.45	0/1302
44	2m	0.21	0/961	0.46	0/1291
45	1n	0.22	0/501	0.52	0/664
45	2n	0.21	0/501	0.45	0/664
46	1o	0.20	0/739	0.42	0/985
46	2o	0.19	0/739	0.41	0/985
47	1p	0.22	0/697	0.49	0/939
47	2p	0.19	0/693	0.42	0/935
48	1q	0.19	0/836	0.43	0/1117
48	2q	0.20	0/836	0.48	0/1117
49	1r	0.22	0/560	0.50	0/746
49	2r	0.21	0/560	0.45	0/746
50	1s	0.21	0/667	0.49	0/900
50	2s	0.28	0/661	0.58	0/893
51	1t	0.23	0/730	0.53	0/965
51	2t	0.22	0/729	0.50	0/965
52	1u	0.19	0/203	0.44	0/266
52	2u	0.20	0/203	0.52	0/266
53	1v	0.23	0/310	0.35	0/480
53	2v	0.21	0/310	0.40	0/480
54	1w	0.30	2/1606 (0.1%)	0.42	0/2497
54	1y	0.28	1/1606 (0.1%)	0.43	0/2497
54	2w	0.30	1/1556 (0.1%)	0.43	0/2418
54	2y	0.28	1/1583 (0.1%)	0.39	0/2459
55	1x	0.27	0/1723	0.42	0/2684
55	2x	0.24	0/1723	0.40	0/2684
56	1z	0.34	0/16	0.38	0/19
56	2z	0.34	0/16	0.64	0/19
All	All	0.23	7/316716 (0.0%)	0.43	12/474153 (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
33	1b	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	46	G7M	O3'-P	5.71	1.61	1.56
54	1w	8	4SU	O3'-P	5.36	1.61	1.56
54	1y	8	4SU	O3'-P	5.13	1.61	1.56
1	1A	2552	OMU	O3'-P	5.12	1.61	1.56
32	2a	527	G7M	O3'-P	5.08	1.61	1.56
54	2y	46	G7M	O3'-P	5.07	1.61	1.56
54	1w	46	G7M	O3'-P	5.03	1.61	1.56

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1992	G	C2'-C3'-O3'	5.93	118.40	109.50
5	2F	21	ALA	CA-C-N	5.85	132.22	121.70
5	2F	21	ALA	C-N-CA	5.85	132.22	121.70
1	2A	1992	G	C2'-C3'-O3'	5.64	117.97	109.50
32	1a	266	G	C2'-C3'-O3'	5.61	117.91	109.50
3	2D	275	LYS	CB-CA-C	-5.58	108.33	116.53
3	2D	275	LYS	CA-C-O	5.40	121.73	118.33
32	1a	266	G	P-O3'-C3'	5.38	128.26	120.20
32	2a	1272	G	N1-C2-N2	-5.27	100.40	116.20
32	2a	1272	G	N3-C2-N2	5.11	135.22	119.90
32	2a	1263	C	N1-C2-O2	5.09	134.16	118.90
3	2D	275	LYS	N-CA-C	5.04	113.59	108.75

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	1b	125	PRO	Peptide
33	1b	20	GLU	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	31192	706	0
1	2A	60322	0	30425	775	0
2	1B	2577	0	1305	31	0
2	2B	2575	0	1303	49	0
3	1D	2136	0	2218	54	0
3	2D	2136	0	2218	50	0
4	1E	1559	0	1618	29	0
4	2E	1559	0	1618	46	0
5	1F	1583	0	1625	46	0
5	2F	1579	0	1619	52	0
6	1G	1423	0	1436	47	0
6	2G	1428	0	1438	60	0
7	1H	1330	0	1407	29	0
7	2H	1330	0	1407	35	0
8	1I	1097	0	1140	25	0
8	2I	1064	0	1082	35	0
9	1N	1117	0	1184	19	0
9	2N	1117	0	1184	30	0
10	1O	933	0	996	19	0
10	2O	933	0	996	21	0
11	1P	1135	0	1212	38	0
11	2P	1135	0	1212	38	0
12	1Q	1122	0	1179	44	0
12	2Q	1122	0	1179	47	0
13	1R	968	0	1033	18	0
13	2R	968	0	1033	24	0
14	1S	873	0	927	20	0
14	2S	870	0	923	41	0
15	1T	1091	0	1151	28	0
15	2T	1083	0	1136	26	0
16	1U	959	0	1018	16	0
16	2U	959	0	1019	24	0
17	1V	771	0	828	13	0
17	2V	771	0	830	17	0
18	1W	886	0	940	19	0
18	2W	886	0	940	14	0
19	1X	750	0	814	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	813	14	0
20	1Y	806	0	881	20	0
20	2Y	806	0	881	20	0
21	1Z	1240	0	1240	39	0
21	2Z	1271	0	1273	44	0
22	10	653	0	674	19	0
22	20	653	0	674	12	0
23	11	755	0	826	9	0
23	21	755	0	826	21	0
24	12	588	0	643	16	0
24	22	588	0	643	14	0
25	13	469	0	518	10	0
25	23	464	0	514	20	0
26	14	552	0	533	27	0
26	24	532	0	503	30	0
27	15	455	0	465	9	0
27	25	455	0	465	9	0
28	16	453	0	473	15	0
28	26	449	0	469	16	0
29	17	418	0	467	8	0
29	27	418	0	467	13	0
30	18	517	0	582	14	0
30	28	517	0	582	20	0
31	19	307	0	335	4	0
31	29	307	0	335	8	0
32	1a	32246	0	16293	438	0
32	2a	32327	0	16337	585	0
33	1b	1846	0	1867	61	0
33	2b	1825	0	1828	81	0
34	1c	1548	0	1535	40	0
34	2c	1542	0	1517	68	0
35	1d	1655	0	1672	64	0
35	2d	1674	0	1714	76	0
36	1e	1129	0	1185	38	0
36	2e	1133	0	1191	50	0
37	1f	810	0	804	23	0
37	2f	816	0	808	19	0
38	1g	1231	0	1238	36	0
38	2g	1235	0	1249	48	0
39	1h	1088	0	1126	26	0
39	2h	1088	0	1126	45	0
40	1i	983	0	986	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	978	0	966	45	0
41	1j	709	0	650	23	0
41	2j	714	0	672	30	0
42	1k	829	0	825	18	0
42	2k	833	0	834	23	0
43	1l	932	0	981	18	0
43	2l	932	0	980	23	0
44	1m	958	0	1002	26	0
44	2m	950	0	988	48	0
45	1n	492	0	529	17	0
45	2n	492	0	529	27	0
46	1o	728	0	760	18	0
46	2o	728	0	760	18	0
47	1p	681	0	697	19	0
47	2p	677	0	686	19	0
48	1q	823	0	891	31	0
48	2q	823	0	891	24	0
49	1r	555	0	618	19	0
49	2r	555	0	618	17	0
50	1s	652	0	662	22	0
50	2s	646	0	644	51	0
51	1t	728	0	798	23	0
51	2t	727	0	796	24	0
52	1u	199	0	208	2	0
52	2u	199	0	208	12	0
53	1v	277	0	140	3	0
53	2v	277	0	139	8	0
54	1w	1592	0	818	27	0
54	1y	1585	0	803	29	0
54	2w	1544	0	786	28	0
54	2y	1565	0	793	23	0
55	1x	1646	0	839	22	0
55	2x	1646	0	838	24	0
56	1z	27	0	28	1	0
56	2z	27	0	28	1	0
57	10	10	0	0	0	0
57	11	3	0	0	0	0
57	12	2	0	0	0	0
57	13	5	0	0	0	0
57	14	1	0	0	0	0
57	15	9	0	0	0	0
57	16	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	17	6	0	0	0	0
57	18	7	0	0	0	0
57	1A	1085	0	0	0	0
57	1B	38	0	0	0	0
57	1D	12	0	0	0	0
57	1E	13	0	0	0	0
57	1F	13	0	0	0	0
57	1G	4	0	0	0	0
57	1H	1	0	0	0	0
57	1I	1	0	0	0	0
57	1N	4	0	0	0	0
57	1O	4	0	0	0	0
57	1P	6	0	0	0	0
57	1Q	7	0	0	0	0
57	1R	6	0	0	0	0
57	1S	2	0	0	0	0
57	1T	3	0	0	0	0
57	1U	11	0	0	0	0
57	1V	7	0	0	0	0
57	1W	7	0	0	0	0
57	1X	7	0	0	0	0
57	1Y	2	0	0	0	0
57	1Z	2	0	0	0	0
57	1a	211	0	0	0	0
57	1b	1	0	0	0	0
57	1d	1	0	0	0	0
57	1e	1	0	0	0	0
57	1f	1	0	0	0	0
57	1j	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	3	0	0	0	0
57	1p	1	0	0	0	0
57	1r	1	0	0	0	0
57	1t	1	0	0	0	0
57	1w	6	0	0	0	0
57	1x	12	0	0	0	0
57	20	3	0	0	0	0
57	21	1	0	0	0	0
57	23	2	0	0	0	0
57	25	1	0	0	0	0
57	26	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	27	4	0	0	0	0
57	28	3	0	0	0	0
57	2A	855	0	0	0	0
57	2B	20	0	0	0	0
57	2D	6	0	0	0	0
57	2E	9	0	0	0	0
57	2F	6	0	0	0	0
57	2N	1	0	0	0	0
57	2O	2	0	0	0	0
57	2P	2	0	0	0	0
57	2Q	1	0	0	0	0
57	2R	4	0	0	0	0
57	2T	3	0	0	0	0
57	2U	2	0	0	0	0
57	2V	1	0	0	0	0
57	2W	2	0	0	0	0
57	2X	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2Z	1	0	0	0	0
57	2a	225	0	0	0	0
57	2d	2	0	0	0	0
57	2e	1	0	0	0	0
57	2f	2	0	0	0	0
57	2g	1	0	0	0	0
57	2j	1	0	0	0	0
57	2k	1	0	0	0	0
57	2l	4	0	0	0	0
57	2o	1	0	0	0	0
57	2q	3	0	0	0	0
57	2r	1	0	0	0	0
57	2t	1	0	0	0	0
57	2v	2	0	0	0	0
57	2w	5	0	0	0	0
57	2x	6	0	0	0	0
57	2y	1	0	0	0	0
57	2z	1	0	0	0	0
58	1A	1	0	0	0	0
58	2A	1	0	0	0	0
59	1A	51	0	67	9	0
59	2A	51	0	67	4	0
60	14	1	0	0	0	0
60	15	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	16	1	0	0	0	0
60	19	1	0	0	0	0
60	1Y	1	0	0	0	0
60	1n	1	0	0	0	0
60	24	1	0	0	0	0
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	29	1	0	0	0	0
60	2Y	1	0	0	0	0
60	2n	1	0	0	0	0
61	1d	8	0	0	1	0
61	2d	8	0	0	2	0
62	10	8	0	0	1	0
62	11	7	0	0	0	0
62	12	3	0	0	0	0
62	13	4	0	0	0	0
62	14	1	0	0	0	0
62	15	6	0	0	0	0
62	16	3	0	0	0	0
62	17	10	0	0	1	0
62	18	8	0	0	0	0
62	1A	1680	0	0	117	0
62	1B	54	0	0	3	0
62	1D	32	0	0	3	0
62	1E	23	0	0	1	0
62	1F	17	0	0	2	0
62	1G	1	0	0	0	0
62	1H	1	0	0	0	0
62	1N	4	0	0	0	0
62	1O	3	0	0	0	0
62	1P	15	0	0	3	0
62	1Q	8	0	0	1	0
62	1R	12	0	0	1	0
62	1S	3	0	0	0	0
62	1T	6	0	0	0	0
62	1U	8	0	0	0	0
62	1V	9	0	0	0	0
62	1W	9	0	0	0	0
62	1X	6	0	0	1	0
62	1Y	1	0	0	0	0
62	1Z	1	0	0	0	0
62	1a	252	0	0	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	1b	1	0	0	0	0
62	1d	1	0	0	0	0
62	1f	1	0	0	0	0
62	1l	3	0	0	0	0
62	1m	2	0	0	0	0
62	1o	1	0	0	0	0
62	1p	1	0	0	0	0
62	1q	2	0	0	0	0
62	1u	1	0	0	0	0
62	1v	3	0	0	0	0
62	1w	8	0	0	0	0
62	1x	7	0	0	1	0
62	1y	1	0	0	0	0
62	1z	1	0	0	0	0
62	20	2	0	0	0	0
62	21	6	0	0	1	0
62	23	1	0	0	0	0
62	25	2	0	0	0	0
62	27	2	0	0	0	0
62	28	3	0	0	0	0
62	29	1	0	0	0	0
62	2A	952	0	0	89	0
62	2B	21	0	0	2	0
62	2D	15	0	0	0	0
62	2E	5	0	0	1	0
62	2F	13	0	0	1	0
62	2O	3	0	0	0	0
62	2P	6	0	0	0	0
62	2Q	1	0	0	0	0
62	2R	4	0	0	0	0
62	2T	2	0	0	0	0
62	2U	2	0	0	0	0
62	2V	1	0	0	0	0
62	2W	1	0	0	0	0
62	2X	5	0	0	0	0
62	2a	150	0	0	13	0
62	2e	1	0	0	0	0
62	2j	1	0	0	1	0
62	2l	4	0	0	0	0
62	2q	1	0	0	0	0
62	2v	3	0	0	0	0
62	2w	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	2x	4	0	0	1	0
62	2z	1	0	0	0	0
All	All	299368	0	196882	4775	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 (4775) 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	1.36
22:20:10:THR:HG22	22:20:12:ASN:H	1.28	0.97
1:1A:1082:U:N3	1:1A:1086:A:N6	2.06	0.96
1:1A:1603:A:OP1	62:1A:4102:HOH:O	1.84	0.94
36:1e:78:HIS:HE1	36:1e:143:ARG:H	1.15	0.93
1:1A:1082:U:O4	1:1A:1086:A:N1	2.02	0.93
22:10:10:THR:HG22	22:10:12:ASN:H	1.34	0.92
1:2A:2430:A:OP2	62:2A:3905:HOH:O	1.87	0.91
17:1V:55:ALA:HA	17:1V:101:GLY:HA2	1.52	0.91
1:2A:2137:C:N4	1:2A:2154:G:H1	1.67	0.91
1:1A:2427:C:OP1	62:1A:4103:HOH:O	1.90	0.88
1:2A:81:G:H21	20:2Y:1:MET:HE2	1.39	0.88
3:2D:8:PRO:HB3	3:2D:14:ARG:HB3	1.53	0.88
1:2A:792:G:O6	62:2A:3906:HOH:O	1.91	0.87
7:2H:9:ILE:HB	7:2H:50:VAL:HG13	1.57	0.87
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.07	0.87
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.58	0.86
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.57	0.86
54:2y:18:G:N2	54:2y:55:PSU:N3	2.23	0.86
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.57	0.86
51:1t:57:ARG:NH1	51:1t:101:GLY:O	2.08	0.86
53:2v:23:A:H4'	53:2v:24:A:H5'	1.57	0.85
29:17:24:THR:HG22	29:17:27:GLY:H	1.41	0.85
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.57	0.85
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.59	0.84
1:1A:1395:A:OP1	62:1A:4102:HOH:O	1.96	0.84
1:1A:2499:C:OP1	62:1A:4104:HOH:O	1.95	0.84
32:2a:975:A:H4'	32:2a:976:G:H5"	1.60	0.84
26:14:16:CYS:SG	26:14:17:GLY:N	2.43	0.83
1:2A:2499:C:OP2	62:2A:3907:HOH:O	1.94	0.83
1:1A:826:U:OP1	62:1A:4103:HOH:O	1.96	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.57	0.83
32:1a:664:G:H22	32:1a:741:G:H1	1.27	0.83
1:1A:1670:C:OP2	62:1A:4106:HOH:O	1.96	0.83
26:24:53:GLU:HG2	26:24:55:ARG:H	1.43	0.83
1:2A:1783:A:N7	62:2A:3935:HOH:O	2.12	0.83
1:1A:1664:A:OP1	62:1A:4107:HOH:O	1.97	0.82
1:2A:2138:C:H42	1:2A:2153:G:H1	1.27	0.82
1:1A:2550:G:OP1	62:1A:4106:HOH:O	1.97	0.82
8:2I:40:THR:OG1	8:2I:41:GLU:N	2.05	0.82
1:1A:2096:U:H3	1:1A:2193:G:H1	1.23	0.82
39:1h:9:MET:HG3	39:1h:26:VAL:HG11	1.60	0.82
32:2a:1399:C:H4'	32:2a:1400:5MC:H5'	1.59	0.82
5:2F:135:LYS:HB3	5:2F:138:GLU:HG3	1.61	0.82
1:1A:1166:C:O2'	62:1A:4105:HOH:O	1.96	0.81
54:1y:19:G:N2	54:1y:56:C:N3	2.29	0.81
1:2A:249:C:O2	30:28:12:LYS:NZ	2.12	0.81
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	1.62	0.81
1:2A:1689:A:H62	1:2A:1698:A:H2	1.27	0.81
7:1H:25:LYS:HG3	7:1H:34:GLU:HG3	1.63	0.80
31:29:16:VAL:HG22	31:29:25:VAL:HG22	1.63	0.80
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.45	0.80
1:1A:1604:C:OP2	62:1A:4102:HOH:O	2.00	0.80
12:1Q:110:THR:H	12:1Q:113:GLN:HE21	1.30	0.80
34:2c:125:GLU:HB2	34:2c:190:ARG:HH21	1.46	0.80
1:1A:1779:U:OP2	62:1A:4108:HOH:O	1.98	0.80
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.64	0.80
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.63	0.80
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.15	0.80
11:1P:42:SER:O	62:1P:301:HOH:O	2.00	0.80
1:2A:2150:U:H2'	1:2A:2151:G:H8	1.48	0.79
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.48	0.79
11:1P:38:GLN:O	11:1P:40:SER:N	2.15	0.79
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.65	0.79
1:2A:731:C:OP2	62:2A:3909:HOH:O	2.00	0.79
1:2A:1253:A:N7	62:2A:3940:HOH:O	2.15	0.79
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.46	0.79
1:2A:2518:A:OP2	62:2A:3908:HOH:O	1.99	0.78
32:2a:1075:C:H4'	33:2b:175:ARG:HH22	1.47	0.78
1:2A:827:U:OP1	62:2A:3905:HOH:O	2.01	0.78
1:1A:1865:G:OP1	62:1A:4109:HOH:O	2.00	0.78
32:1a:1458:G:H5"	51:1t:31:SER:HB3	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1434:A:H61	1:2A:1558:A:H62	1.31	0.78
1:1A:1633:G:OP2	62:1A:4111:HOH:O	2.02	0.78
32:1a:7:G:O2'	36:1e:120:THR:O	2.02	0.78
1:2A:198:C:OP2	62:2A:3901:HOH:O	2.01	0.78
32:2a:939:G:H1	32:2a:1344:C:H42	1.28	0.78
32:2a:1316:G:H22	32:2a:1319:A:H5"	1.47	0.78
1:1A:1602:U:O4	62:1A:4112:HOH:O	2.02	0.77
1:2A:1938:A:OP2	62:2A:3911:HOH:O	2.02	0.77
1:2A:2807:G:N1	1:2A:2893:G:O6	2.15	0.77
32:2a:1244:C:H42	32:2a:1293:G:H1	1.32	0.77
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	1.65	0.77
1:2A:563:G:OP2	62:2A:3912:HOH:O	2.03	0.77
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.18	0.77
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.66	0.77
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.67	0.77
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	1.67	0.77
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.03	0.77
1:2A:1986:A:OP1	62:2A:3910:HOH:O	2.02	0.77
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.16	0.77
8:2I:123:LEU:HD12	8:2I:144:VAL:HG12	1.65	0.77
1:1A:249:C:O2	30:18:12:LYS:NZ	2.18	0.76
21:1Z:93:ASP:HB3	21:1Z:131:ARG:HH22	1.48	0.76
1:2A:2319:G:H22	14:2S:3:ARG:HH11	1.33	0.76
1:2A:1647:G:OP1	62:2A:3914:HOH:O	2.03	0.76
40:2i:40:LEU:O	40:2i:42:ARG:N	2.18	0.76
1:1A:674:G:OP2	62:1A:4113:HOH:O	2.03	0.76
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.16	0.76
32:1a:116:A:OP1	62:1a:1902:HOH:O	2.03	0.76
1:2A:962:G:OP1	62:2A:3913:HOH:O	2.03	0.76
21:2Z:39:VAL:HG21	21:2Z:44:PHE:HD1	1.50	0.76
32:2a:1296:C:OP1	44:2m:44:ARG:NH2	2.19	0.76
32:1a:975:A:H4'	32:1a:976:G:H5"	1.66	0.76
1:1A:731:C:OP1	62:1A:4114:HOH:O	2.03	0.76
1:1A:2821:A:OP2	62:1R:301:HOH:O	2.04	0.76
32:2a:1119:C:OP2	40:2i:9:ARG:NH2	2.18	0.76
1:1A:816:C:OP2	62:1A:4116:HOH:O	2.04	0.75
1:1A:1332:G:OP1	62:1A:4110:HOH:O	2.02	0.75
32:1a:677:U:H3	32:1a:713:G:H22	1.32	0.75
12:2Q:97:VAL:HG11	12:2Q:103:MET:HE3	1.69	0.75
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.18	0.75
1:2A:1193:G:OP1	11:2P:14:LYS:NZ	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.67	0.75
41:2j:98:ILE:O	62:2j:301:HOH:O	2.04	0.75
1:1A:2371:G:O6	62:1A:4115:HOH:O	2.04	0.75
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.68	0.75
55:2x:76:8AN:O2P	62:2x:201:HOH:O	2.04	0.75
1:1A:84:A:H5"	20:1Y:8:LYS:HG2	1.69	0.75
1:1A:505:A:OP2	62:1A:4117:HOH:O	2.05	0.74
49:1r:52:PRO:HB2	49:1r:54:ARG:HG3	1.70	0.74
32:2a:1026:G:O6	32:2a:1036:G:N2	2.20	0.74
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.20	0.74
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.20	0.74
51:2t:10:LEU:HG	51:2t:12:ALA:H	1.53	0.74
1:1A:2100:G:H1	1:1A:2189:U:H3	1.33	0.74
1:2A:2126:A:N6	1:2A:2162:G:O2'	2.19	0.74
1:1A:870:A:OP1	12:1Q:6:ARG:NH2	2.21	0.74
1:1A:1156:A:OP2	62:1A:4119:HOH:O	2.05	0.74
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.21	0.74
32:2a:770:C:OP1	62:2a:1901:HOH:O	2.05	0.74
35:1d:7:PRO:HB2	35:1d:10:ARG:HD2	1.68	0.74
5:1F:72:ARG:O	62:1F:401:HOH:O	2.05	0.74
1:2A:2592:G:OP1	62:2A:3915:HOH:O	2.06	0.74
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.22	0.73
1:1A:2448:A:OP1	62:1A:4104:HOH:O	2.06	0.73
32:1a:693:G:OP2	62:1a:1904:HOH:O	2.05	0.73
33:1b:50:GLU:O	33:1b:54:THR:OG1	2.06	0.73
6:2G:120:LEU:N	6:2G:179:PRO:O	2.21	0.73
32:1a:1505:G:OP2	62:1a:1903:HOH:O	2.04	0.73
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.52	0.73
47:2p:53:VAL:HG13	47:2p:79:VAL:HG13	1.69	0.73
23:21:32:LYS:O	62:21:3601:HOH:O	2.04	0.73
27:25:41:PRO:O	27:25:44:THR:OG1	2.06	0.73
1:1A:2070:G:OP2	62:1A:4121:HOH:O	2.06	0.73
32:1a:276:G:O3'	48:1q:68:ARG:NH1	2.21	0.73
1:1A:1013:C:OP2	62:1A:4118:HOH:O	2.05	0.73
34:1c:20:SER:OG	34:1c:40:ARG:NH2	2.20	0.73
10:1O:75:SER:OG	15:1T:74:ARG:NH1	2.22	0.73
1:2A:261:G:HO2'	1:2A:610:G:HO2'	1.30	0.73
1:1A:1938:A:OP2	62:1A:4120:HOH:O	2.06	0.73
37:1f:70:ASP:OD1	37:1f:70:ASP:N	2.19	0.73
1:1A:995:C:OP2	16:1U:54:LYS:NZ	2.22	0.73
1:2A:890:A:H2'	1:2A:892:G:H8	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.54	0.73
1:2A:2468:G:OP1	12:2Q:119:ARG:NH2	2.20	0.73
23:21:23:LYS:NZ	54:2y:73:A:O2'	2.22	0.73
11:2P:39:LYS:HB2	11:2P:45:LEU:HD13	1.70	0.72
1:1A:1669:A:OP2	62:1A:4123:HOH:O	2.07	0.72
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.22	0.72
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.22	0.72
1:1A:2406:U:OP1	62:1A:4122:HOH:O	2.07	0.72
32:2a:1133:G:H1	32:2a:1141:C:H42	1.35	0.72
1:1A:818:G:OP2	62:1A:4125:HOH:O	2.07	0.72
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.53	0.72
1:2A:1452:A:OP2	62:2A:3917:HOH:O	2.07	0.72
6:2G:114:ILE:HA	6:2G:140:ILE:HD11	1.72	0.72
32:2a:1318:A:H1'	50:2s:37:ARG:HH21	1.54	0.72
1:1A:1468:C:OP1	62:1A:4126:HOH:O	2.08	0.72
32:1a:558:G:OP1	62:1a:1905:HOH:O	2.08	0.72
32:1a:642:A:N3	39:1h:113:SER:OG	2.23	0.72
1:2A:1634:A:OP2	62:2A:3920:HOH:O	2.07	0.72
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.23	0.72
1:2A:2062:A:OP1	62:2A:3916:HOH:O	2.06	0.72
52:2u:6:ARG:HA	52:2u:11:GLY:HA3	1.71	0.72
1:1A:2429:G:OP1	62:1A:4103:HOH:O	2.08	0.72
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.72	0.72
1:1A:2106:G:H1	1:1A:2183:C:H42	1.37	0.72
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.22	0.72
32:2a:1456:G:O6	51:2t:54:LYS:NZ	2.18	0.72
1:2A:948:G:OP1	62:2A:3913:HOH:O	2.07	0.72
1:2A:1648:C:OP1	62:2A:3914:HOH:O	2.07	0.72
1:2A:2497:A:O2'	62:2A:3918:HOH:O	2.07	0.72
4:2E:8:LYS:NZ	4:2E:190:GLY:O	2.20	0.72
32:2a:673:G:H2'	32:2a:674:G:C8	2.25	0.72
32:2a:825:G:H21	39:2h:11:THR:HG21	1.55	0.72
34:2c:156:ARG:H	34:2c:196:LEU:HD22	1.54	0.72
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.23	0.71
1:2A:1271:G:OP2	62:2A:3914:HOH:O	2.08	0.71
1:2A:2721:A:OP1	62:2A:3919:HOH:O	2.07	0.71
36:2e:20:GLN:OE1	36:2e:25:ARG:NH1	2.22	0.71
54:2w:18:G:O2'	54:2w:57:G:N2	2.18	0.71
1:1A:1062:G:H1	1:1A:1077:A:H61	1.39	0.71
1:2A:907:U:O2'	12:2Q:101:ARG:NH2	2.23	0.71
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.22	0.71
5:2F:103:LYS:HA	5:2F:106:ARG:HD3	1.72	0.71
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	1.71	0.71
32:1a:181:G:H4'	32:1a:182:U:H5'	1.71	0.71
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.71	0.71
21:1Z:77:ASP:OD2	21:1Z:80:ARG:NH1	2.24	0.71
1:2A:400:G:N7	62:2A:3987:HOH:O	2.23	0.71
1:1A:2759:G:N7	62:1A:4186:HOH:O	2.22	0.71
12:1Q:34:LEU:HB2	12:1Q:118:LEU:HD22	1.72	0.71
32:1a:195:A:HO2'	32:1a:222:U:HO2'	1.36	0.71
32:1a:574:A:OP2	62:1a:1906:HOH:O	2.08	0.71
1:2A:2218:U:O2	23:21:52:ARG:NH1	2.23	0.71
1:2A:1786:A:OP1	62:2A:3926:HOH:O	2.09	0.71
1:1A:2582:G:OP2	62:1A:4130:HOH:O	2.09	0.71
34:1c:36:ASP:OD1	34:1c:59:ARG:NH2	2.23	0.71
1:2A:1123:C:H1'	31:29:18:ARG:HH22	1.56	0.71
21:2Z:121:HIS:N	21:2Z:171:ILE:O	2.24	0.71
22:20:5:LYS:NZ	55:2x:2:G:OP2	2.23	0.71
41:2j:44:VAL:HG22	41:2j:66:ARG:HG2	1.73	0.71
1:1A:1823:G:OP1	3:1D:54:ARG:NH1	2.24	0.70
5:1F:64:ILE:HD11	5:1F:75:HIS:HB2	1.72	0.70
32:2a:953:G:H5'	32:2a:965:A:H61	1.55	0.70
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.73	0.70
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	1.72	0.70
1:2A:1970:A:OP1	62:2A:3925:HOH:O	2.09	0.70
32:2a:148:G:H2'	32:2a:149:A:H8	1.56	0.70
34:2c:88:ARG:HA	34:2c:91:LEU:HD12	1.71	0.70
1:1A:2517:C:OP1	62:1A:4124:HOH:O	2.07	0.70
34:2c:71:ALA:HB1	34:2c:109:PRO:HB3	1.72	0.70
1:1A:422:A:OP2	62:1A:4128:HOH:O	2.09	0.70
1:2A:948:G:O6	62:2A:3921:HOH:O	2.07	0.70
32:1a:1224:G:OP1	62:1a:1907:HOH:O	2.09	0.70
14:2S:62:LYS:HB3	14:2S:97:ARG:HD2	1.73	0.70
1:1A:2099:U:H3	1:1A:2190:G:H1	1.39	0.70
1:2A:2685:G:O6	62:2A:3924:HOH:O	2.09	0.70
1:1A:1770:G:OP1	62:1A:4133:HOH:O	2.10	0.70
3:1D:37:LEU:HD12	3:1D:62:TYR:HB2	1.72	0.70
32:2a:473:G:H2'	32:2a:474:G:H8	1.55	0.70
32:2a:839:U:H3'	32:2a:840:C:H5'	1.73	0.70
1:1A:792:G:O6	62:1A:4127:HOH:O	2.08	0.70
26:14:28:LYS:HG2	26:14:31:ILE:HG13	1.71	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2524:G:O6	62:2A:3928:HOH:O	2.10	0.70
1:1A:1439:A:OP1	62:1A:4126:HOH:O	2.08	0.70
1:1A:1673:U:OP1	62:1A:4129:HOH:O	2.09	0.70
26:14:43:TYR:O	26:14:45:GLY:N	2.25	0.70
32:1a:78:G:N1	32:1a:91:C:C4	2.60	0.70
1:2A:370:G:OP2	62:2A:3930:HOH:O	2.10	0.70
1:1A:2022:U:OP1	62:1A:4137:HOH:O	2.10	0.69
20:1Y:82:PRO:O	20:1Y:101:LYS:NZ	2.25	0.69
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.23	0.69
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.25	0.69
6:2G:69:ALA:HB3	6:2G:91:ARG:HH21	1.56	0.69
32:2a:768:A:OP2	62:2a:1902:HOH:O	2.08	0.69
1:1A:2721:A:OP1	62:1A:4136:HOH:O	2.10	0.69
1:2A:2114:A:H62	1:2A:2115:G:H21	1.40	0.69
4:2E:38:THR:HG23	4:2E:41:LYS:HB3	1.74	0.69
32:1a:78:G:N2	32:1a:91:C:C2	2.60	0.69
35:2d:102:ASP:HB3	35:2d:136:PRO:HB3	1.73	0.69
38:2g:113:GLU:HG3	38:2g:119:ARG:HG2	1.74	0.69
1:1A:1669:A:OP2	62:1A:4106:HOH:O	2.08	0.69
1:1A:2404:C:O3'	11:1P:77:ARG:NH2	2.26	0.69
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.26	0.69
33:2b:12:GLU:HA	33:2b:213:LEU:HD11	1.75	0.69
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.74	0.69
1:2A:1779:U:H2'	62:2A:3935:HOH:O	1.92	0.69
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.74	0.69
1:2A:2239:G:OP2	62:2A:3927:HOH:O	2.09	0.69
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.25	0.69
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.75	0.69
1:2A:570:G:O6	62:2A:3922:HOH:O	2.08	0.69
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.28	0.69
1:1A:365:C:OP2	62:1A:4138:HOH:O	2.11	0.69
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.57	0.69
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.23	0.69
32:1a:766:A:OP2	62:1a:1908:HOH:O	2.11	0.69
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.10	0.69
1:2A:307:G:N1	1:2A:310:A:OP2	2.26	0.69
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.24	0.69
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.40	0.69
32:2a:117:G:OP2	62:2a:1903:HOH:O	2.09	0.69
38:2g:22:LEU:HG	38:2g:62:PHE:HE2	1.58	0.69
47:2p:53:VAL:HG22	47:2p:79:VAL:HG22	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:582:G:N7	62:1A:4212:HOH:O	2.26	0.69
1:1A:2222:G:O6	62:1A:4131:HOH:O	2.09	0.69
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.58	0.69
1:1A:773:U:OP1	62:1A:4134:HOH:O	2.10	0.68
1:1A:1315:C:OP2	62:1A:4110:HOH:O	2.10	0.68
1:1A:1986:A:OP1	62:1A:4135:HOH:O	2.10	0.68
51:2t:33:ILE:O	51:2t:37:SER:OG	2.09	0.68
40:1i:75:ASP:HA	40:1i:78:LYS:HB3	1.76	0.68
1:2A:818:G:OP2	62:2A:3931:HOH:O	2.10	0.68
38:2g:78:ARG:HD3	38:2g:79:ARG:H	1.58	0.68
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.74	0.68
36:1e:43:LEU:HD21	36:1e:132:ALA:HB1	1.76	0.68
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.26	0.68
4:2E:127:ASP:OD2	62:2E:401:HOH:O	2.10	0.68
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.28	0.68
12:1Q:20:ALA:HB2	21:1Z:79:ARG:HG3	1.74	0.68
1:2A:82:G:O6	62:2A:3932:HOH:O	2.11	0.68
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	1.76	0.68
38:2g:16:LEU:HD22	40:2i:42:ARG:HA	1.75	0.68
44:2m:45:VAL:HA	44:2m:48:LEU:HD12	1.73	0.68
1:1A:1418:G:OP2	62:1A:4139:HOH:O	2.11	0.68
1:1A:2243:U:OP1	62:1A:4140:HOH:O	2.12	0.68
32:1a:176:C:OP1	51:1t:29:LYS:NZ	2.26	0.68
41:1j:38:ILE:HG12	41:1j:71:LEU:HB3	1.75	0.68
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.07	0.68
54:1y:19:G:N1	54:1y:56:C:N4	2.41	0.68
2:2B:98:G:H3'	2:2B:99:G:H8	1.58	0.68
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.76	0.68
32:2a:1103:C:H4'	33:2b:98:LEU:HD21	1.74	0.68
4:1E:122:PHE:O	62:1E:401:HOH:O	2.11	0.68
32:1a:510:A:OP2	35:1d:49:ARG:NH1	2.26	0.68
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.75	0.68
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.25	0.68
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.27	0.68
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.76	0.68
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.66	0.68
1:2A:80:G:H1	1:2A:106:C:H42	1.42	0.68
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.75	0.68
12:1Q:68:ILE:HD13	12:1Q:103:MET:HG2	1.75	0.68
36:1e:78:HIS:CE1	36:1e:143:ARG:H	2.07	0.68
21:1Z:80:ARG:HB3	21:1Z:82:ARG:HD3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:120:VAL:HA	34:2c:123:GLN:HB2	1.75	0.68
1:1A:1263:U:OP1	27:15:16:ARG:NH1	2.27	0.67
1:2A:1443:G:N7	62:2A:4015:HOH:O	2.26	0.67
32:2a:664:G:H22	32:2a:741:G:H1	1.41	0.67
32:2a:1029:C:N4	32:2a:1031:G:O6	2.27	0.67
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.13	0.67
2:1B:87:G:N2	2:1B:90:A:OP2	2.20	0.67
36:1e:12:LEU:HB3	36:1e:31:LEU:HB3	1.76	0.67
8:2I:72:LEU:HA	8:2I:75:LEU:HD23	1.75	0.67
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.75	0.67
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.75	0.67
44:2m:37:THR:HG21	44:2m:56:LEU:HD13	1.75	0.67
12:1Q:81:VAL:HB	22:10:7:LEU:HD21	1.77	0.67
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.43	0.67
1:1A:2431:U:OP2	62:1A:4142:HOH:O	2.13	0.67
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.29	0.67
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.60	0.67
35:2d:205:GLU:OE1	36:2e:107:ARG:NH1	2.27	0.67
44:2m:108:ARG:NH1	44:2m:112:GLY:O	2.28	0.67
1:1A:1890:A:OP2	62:1A:4141:HOH:O	2.12	0.67
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.27	0.67
1:2A:2448:A:OP1	62:2A:3922:HOH:O	2.13	0.67
45:2n:23:ARG:NH1	45:2n:28:GLY:O	2.28	0.67
3:1D:228:PRO:O	62:1D:401:HOH:O	2.13	0.67
32:2a:263:A:OP1	51:2t:79:ARG:NH1	2.28	0.67
36:2e:83:GLU:HA	36:2e:88:LYS:HA	1.75	0.67
1:1A:1633:G:O6	62:1A:4132:HOH:O	2.09	0.67
32:1a:299:G:O6	62:1a:1905:HOH:O	2.10	0.67
1:2A:2057:A:OP2	62:2A:3933:HOH:O	2.11	0.67
14:2S:26:LEU:HD12	14:2S:39:ILE:HG12	1.76	0.67
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.76	0.67
1:1A:2296:U:OP2	14:1S:9:ARG:NH2	2.27	0.67
35:1d:60:GLU:OE2	35:1d:63:LYS:NZ	2.28	0.67
1:1A:1671:U:O4	62:1A:4106:HOH:O	2.12	0.66
1:2A:963:U:OP2	62:2A:3913:HOH:O	2.13	0.66
19:1X:6:ASP:OD2	62:1X:201:HOH:O	2.13	0.66
1:2A:574:C:OP1	62:2A:3936:HOH:O	2.13	0.66
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.31	0.66
50:2s:80:TYR:O	50:2s:82:GLY:N	2.28	0.66
5:1F:89:VAL:O	62:1F:402:HOH:O	2.12	0.66
32:2a:289:G:OP2	62:2a:1903:HOH:O	2.12	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1452:A:OP2	62:1A:4143:HOH:O	2.13	0.66
46:1o:18:PHE:O	46:1o:20:GLY:N	2.28	0.66
16:2U:83:LEU:HD13	16:2U:88:ILE:HB	1.76	0.66
38:2g:16:LEU:HD21	40:2i:45:ALA:HB2	1.78	0.66
25:13:35:ARG:HB3	25:13:37:LEU:HD21	1.77	0.66
50:1s:27:GLU:HB2	50:1s:28:LYS:HB3	1.76	0.66
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.13	0.66
1:2A:1670:C:OP1	62:2A:3934:HOH:O	2.12	0.66
1:2A:2401:U:OP1	28:26:18:ARG:NH2	2.25	0.66
12:2Q:110:THR:HB	12:2Q:113:GLN:H	1.61	0.66
32:2a:1219:U:OP1	45:2n:19:ARG:NH1	2.23	0.66
40:2i:110:GLU:OE2	40:2i:113:LYS:NZ	2.28	0.66
1:1A:1041:C:H42	1:1A:1114:G:H1	1.43	0.66
40:1i:23:ASN:OD1	40:1i:23:ASN:N	2.26	0.66
32:2a:473:G:H2'	32:2a:474:G:C8	2.31	0.66
34:2c:120:VAL:HG11	34:2c:134:ILE:HD13	1.77	0.66
1:1A:370:G:OP2	62:1A:4128:HOH:O	2.14	0.66
3:1D:274:ARG:NH1	62:1D:402:HOH:O	2.26	0.66
34:1c:131:ARG:HH21	36:1e:50:GLU:HG3	1.61	0.66
1:2A:1627:G:OP2	62:2A:3937:HOH:O	2.13	0.66
2:2B:118:G:OP2	62:2B:301:HOH:O	2.14	0.66
32:2a:1123:A:H4'	41:2j:37:PRO:HD2	1.75	0.66
8:1I:77:LEU:HD22	8:1I:101:LEU:HG	1.76	0.66
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.77	0.66
9:2N:138:LEU:HB3	9:2N:140:VAL:HG13	1.78	0.66
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.27	0.66
32:2a:501:C:H2'	32:2a:502:G:C8	2.30	0.66
54:2y:18:G:H22	54:2y:55:PSU:HN3	1.39	0.66
1:1A:687:C:H5"	29:17:2:LYS:HE2	1.77	0.66
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.31	0.66
4:1E:77:ILE:HD12	4:1E:195:LEU:HD13	1.78	0.66
5:2F:124:LEU:HB3	5:2F:193:VAL:HG22	1.77	0.66
32:2a:1226:C:O2'	44:2m:111:LYS:NZ	2.24	0.66
38:2g:79:ARG:O	38:2g:79:ARG:NH2	2.27	0.66
22:10:19:LYS:O	62:10:201:HOH:O	2.14	0.66
32:1a:376:G:H5"	47:1p:5:ARG:HG2	1.76	0.66
1:2A:970:C:OP1	25:23:20:LYS:NZ	2.29	0.66
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.30	0.65
15:1T:16:ARG:NH2	15:1T:18:ASP:OD2	2.29	0.65
1:2A:277:C:H4'	1:2A:278:A:OP2	1.95	0.65
14:2S:93:LYS:HD2	14:2S:95:HIS:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:171:ILE:HD12	21:2Z:172:ALA:H	1.61	0.65
26:24:26:SER:OG	26:24:27:THR:N	2.28	0.65
40:2i:63:ILE:HG21	40:2i:77:ILE:HG12	1.78	0.65
1:1A:1113:U:H2'	1:1A:1114:G:H8	1.61	0.65
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.61	0.65
1:1A:2627:G:O2'	1:1A:2781:A:N1	2.26	0.65
6:2G:32:PRO:HB2	6:2G:172:LEU:HD22	1.76	0.65
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.77	0.65
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	1.78	0.65
16:2U:49:HIS:HA	16:2U:52:ARG:HB2	1.78	0.65
1:1A:802:A:OP1	62:1A:4146:HOH:O	2.14	0.65
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.11	0.65
32:1a:373:A:H2'	32:1a:374:A:H8	1.60	0.65
4:1E:176:ILE:HB	4:1E:181:LEU:HB2	1.79	0.65
32:1a:1525:G:OP1	42:1k:120:ARG:NH2	2.28	0.65
32:1a:193:C:H2'	32:1a:194:C:H6	1.62	0.65
33:1b:163:PHE:HD1	33:1b:185:ILE:HG13	1.61	0.65
34:1c:162:GLN:NE2	53:1v:24:A:O2'	2.30	0.65
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.28	0.65
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.32	0.65
32:2a:1329:A:OP2	52:2u:7:ARG:NH1	2.28	0.65
34:2c:110:ASN:OD1	34:2c:140:ARG:NH2	2.22	0.65
16:1U:75:ASN:OD1	16:1U:78:THR:OG1	2.15	0.65
14:2S:16:ASN:HA	14:2S:19:LYS:HG2	1.78	0.65
32:2a:1256:A:H61	32:2a:1278:U:H2'	1.62	0.65
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.29	0.65
9:1N:35:ARG:HD3	9:1N:37:LYS:HD2	1.79	0.65
32:2a:562:C:H1'	43:2l:15:ARG:HD2	1.78	0.65
46:2o:24:SER:HB3	46:2o:27:VAL:HG23	1.78	0.65
2:2B:81:G:OP2	62:2B:302:HOH:O	2.14	0.65
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.77	0.65
32:2a:238:G:OP1	48:2q:25:ARG:NH2	2.29	0.65
32:2a:1401:G:OP1	53:2v:18:G:O2'	2.10	0.65
38:2g:74:GLU:HG2	38:2g:91:VAL:HG22	1.79	0.65
1:1A:1267:U:OP1	62:1A:4145:HOH:O	2.14	0.65
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.78	0.65
32:1a:953:G:H5'	32:1a:965:A:H61	1.61	0.65
10:2O:67:LYS:NZ	10:2O:68:GLU:OE2	2.30	0.65
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.12	0.65
46:2o:7:GLU:OE1	46:2o:38:ARG:NH2	2.29	0.65
50:2s:50:ALA:HA	50:2s:59:PRO:HA	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1235:G:OP1	62:1A:4117:HOH:O	2.13	0.65
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.32	0.65
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.79	0.65
1:2A:89:G:H3'	1:2A:90:U:H5"	1.78	0.65
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.32	0.65
33:2b:231:GLU:H	33:2b:232:PRO:HD2	1.62	0.65
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.78	0.64
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.05	0.64
1:2A:2394:C:N3	54:2y:76:A:O2'	2.30	0.64
32:2a:1004:A:H5"	32:2a:1024:G:H22	1.61	0.64
33:2b:187:LEU:HD11	33:2b:214:ILE:HG21	1.79	0.64
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.32	0.64
7:1H:98:LEU:HD11	7:1H:124:GLU:HA	1.79	0.64
1:2A:2758:A:OP2	62:2A:3938:HOH:O	2.15	0.64
1:1A:832:G:OP1	62:1A:4147:HOH:O	2.15	0.64
1:2A:1379:A:H4'	1:2A:1380:G:OP2	1.97	0.64
1:2A:2818:G:OP2	13:2R:42:LYS:NZ	2.30	0.64
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.32	0.64
32:2a:1274:G:N2	32:2a:1275:A:N7	2.44	0.64
1:2A:1324:G:N7	62:2A:4027:HOH:O	2.29	0.64
1:2A:1890:A:OP2	62:2A:3939:HOH:O	2.15	0.64
26:24:24:THR:OG1	26:24:25:TYR:N	2.31	0.64
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.32	0.64
1:1A:969:U:H2'	1:1A:970:C:C6	2.32	0.64
26:14:55:ARG:N	26:14:56:VAL:HA	2.12	0.64
3:1D:180:GLY:HA3	3:1D:275:LYS:HG2	1.78	0.64
32:1a:8:A:N7	35:1d:208:SER:OG	2.30	0.64
32:1a:244:U:O2	62:1a:1909:HOH:O	2.14	0.64
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.31	0.64
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.31	0.64
25:13:7:LYS:HB2	25:13:34:GLU:HG2	1.79	0.64
32:1a:21:G:H2'	32:1a:22:G:C8	2.33	0.64
32:1a:128:G:O2'	48:1q:3:LYS:NZ	2.31	0.64
11:2P:85:LEU:HG	11:2P:116:GLY:HA2	1.79	0.64
32:2a:128:G:O2'	48:2q:3:LYS:NZ	2.31	0.64
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.30	0.64
35:2d:25:ARG:HA	35:2d:28:SER:HB3	1.80	0.64
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	1.80	0.64
42:2k:21:ILE:HD12	42:2k:84:VAL:HG22	1.80	0.64
45:2n:6:LEU:HA	45:2n:9:LYS:HB2	1.80	0.64
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.30	0.64
39:2h:32:LYS:HA	39:2h:35:ILE:HD12	1.80	0.64
54:2y:52:G:H1	54:2y:62:C:H42	1.44	0.64
1:1A:1355:G:N7	62:1A:4239:HOH:O	2.30	0.64
1:1A:2227:A:OP2	62:1A:4148:HOH:O	2.15	0.64
5:1F:9:ILE:HD13	5:1F:22:ALA:HB3	1.79	0.64
20:1Y:43:ASN:HB3	20:1Y:65:ALA:HB3	1.79	0.64
32:1a:110:C:O2'	47:1p:25:ARG:O	2.15	0.64
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.32	0.64
8:2I:88:ILE:HD11	8:2I:144:VAL:HG11	1.80	0.64
1:1A:1780:A:N7	62:1A:4232:HOH:O	2.29	0.63
1:1A:2102:U:H3	1:1A:2187:G:H1	1.46	0.63
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.43	0.63
1:2A:2632:A:HO2'	1:2A:2811:G:HO2'	1.39	0.63
7:2H:3:ARG:HH22	7:2H:65:HIS:HB3	1.63	0.63
32:2a:1029:C:N3	32:2a:1032:G:N2	2.45	0.63
33:2b:51:LEU:HD23	33:2b:201:ILE:HD12	1.80	0.63
51:2t:40:ALA:HB2	51:2t:55:ILE:HG22	1.80	0.63
32:1a:545:C:OP1	35:1d:61:LYS:NZ	2.31	0.63
1:2A:1296:G:OP1	1:2A:2709:G:O2'	2.15	0.63
32:2a:1381:U:H1'	38:2g:79:ARG:HD3	1.81	0.63
54:2w:52:G:H1	54:2w:62:C:H42	1.45	0.63
1:1A:677:A:OP1	62:1A:4149:HOH:O	2.16	0.63
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.80	0.63
34:2c:67:THR:HA	34:2c:102:ASN:HB2	1.81	0.63
41:2j:8:LEU:HD12	41:2j:16:LEU:HD22	1.81	0.63
32:1a:1377:A:HO2'	38:1g:2:ALA:N	1.96	0.63
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.79	0.63
6:2G:83:ARG:N	6:2G:86:MET:SD	2.70	0.63
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.32	0.63
1:1A:588:U:H2'	1:1A:589:C:C6	2.33	0.63
1:1A:1174:A:H4'	1:1A:1175:U:OP1	1.96	0.63
41:1j:49:VAL:HG13	45:1n:41:ARG:HB2	1.80	0.63
36:1e:143:ARG:NE	39:1h:77:GLU:OE2	2.32	0.63
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.33	0.63
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.63	0.63
5:2F:32:LEU:HD13	5:2F:112:MET:HE1	1.79	0.63
26:24:59:PHE:HE2	50:2s:64:GLU:HB2	1.62	0.63
26:24:64:GLY:C	26:24:66:SER:H	2.07	0.63
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.80	0.63
32:1a:78:G:N1	32:1a:91:C:N4	2.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1639:U:H2'	1:2A:1640:C:H5"	1.79	0.63
5:2F:155:LEU:HB2	5:2F:189:THR:HG21	1.80	0.63
1:1A:880:G:H2'	1:1A:881:G:C8	2.34	0.63
2:1B:104:U:HO2'	21:1Z:29:TYR:HH	1.43	0.63
32:1a:1348:U:H4'	40:1i:120:ARG:HD2	1.81	0.63
1:2A:2375:G:N2	1:2A:2378:A:OP2	2.29	0.63
7:2H:149:ARG:NH1	7:2H:167:GLU:OE2	2.31	0.63
30:28:10:ALA:HB3	30:28:62:LEU:HD21	1.79	0.63
32:2a:1182:G:H4'	32:2a:1183:A:H5"	1.79	0.63
9:1N:96:GLU:OE1	9:1N:96:GLU:N	2.30	0.63
14:1S:11:LYS:HG3	14:1S:91:PRO:HD3	1.81	0.63
24:12:16:LEU:O	24:12:67:LYS:NZ	2.32	0.63
1:2A:974:G:OP1	1:2A:1187:G:O2'	2.15	0.63
1:2A:2137:C:N3	1:2A:2154:G:N2	2.39	0.63
12:2Q:78:PRO:HG2	12:2Q:81:VAL:HG11	1.80	0.63
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.31	0.63
17:2V:55:ALA:HA	17:2V:101:GLY:HA2	1.81	0.63
6:1G:18:GLU:OE2	6:1G:21:ARG:NH1	2.32	0.62
13:1R:117:VAL:HG12	13:1R:118:GLU:H	1.63	0.62
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.29	0.62
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.34	0.62
38:2g:138:LYS:NZ	38:2g:142:GLU:OE2	2.32	0.62
26:14:61:ARG:NE	26:14:61:ARG:O	2.33	0.62
32:1a:235:C:H5'	48:1q:70:ARG:HG3	1.80	0.62
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.34	0.62
1:2A:469:G:O6	29:27:37:LYS:NZ	2.32	0.62
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.33	0.62
32:2a:64:G:H4'	32:2a:65:U:H3'	1.81	0.62
41:2j:8:LEU:HD11	41:2j:20:ALA:HB2	1.81	0.62
7:1H:56:SER:OG	7:1H:57:ASP:N	2.32	0.62
17:1V:23:GLU:OE1	17:1V:89:GLN:NE2	2.32	0.62
32:1a:192:U:H4'	51:1t:57:ARG:HD3	1.82	0.62
32:1a:1186:G:H21	45:1n:61:TRP:C	2.07	0.62
32:1a:1240:U:OP1	38:1g:119:ARG:NH2	2.29	0.62
36:1e:91:LEU:HB3	36:1e:118:ILE:HD11	1.81	0.62
4:2E:54:GLN:HB2	4:2E:76:ARG:HG3	1.80	0.62
17:2V:62:LEU:HD12	17:2V:93:GLU:HG2	1.82	0.62
21:2Z:54:HIS:HB3	21:2Z:101:PRO:HD3	1.81	0.62
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.45	0.62
1:2A:646:A:H2'	1:2A:647:G:O4'	1.99	0.62
6:2G:41:GLN:HE22	6:2G:153:ARG:HB3	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1153:C:OP1	16:1U:92:ARG:NH2	2.32	0.62
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.00	0.62
18:1W:11:ARG:HA	18:1W:100:THR:HG22	1.80	0.62
32:1a:692:U:O2'	32:1a:694:A:N7	2.30	0.62
35:1d:111:ALA:HB1	35:1d:116:GLN:HB3	1.80	0.62
7:2H:5:GLY:HA2	7:2H:69:ARG:HB2	1.80	0.62
32:2a:1137:C:O2	32:2a:1138:G:N2	2.32	0.62
33:2b:28:PHE:CD2	33:2b:190:THR:HA	2.34	0.62
50:2s:33:THR:HG21	50:2s:49:ILE:HD11	1.81	0.62
51:2t:49:ALA:HB3	51:2t:99:LEU:HD22	1.80	0.62
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.33	0.62
21:1Z:52:SER:O	21:1Z:54:HIS:N	2.32	0.62
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.64	0.62
1:2A:2138:C:N4	1:2A:2153:G:H1	1.95	0.62
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.35	0.62
5:1F:155:LEU:HD11	5:1F:176:LEU:HD12	1.82	0.62
15:1T:84:GLN:HG2	15:1T:85:LYS:HG3	1.82	0.62
26:14:45:GLY:O	26:14:47:GLN:N	2.32	0.62
1:2A:212:G:H2'	1:2A:213:A:O4'	1.99	0.62
24:22:9:GLN:HE22	24:22:56:GLN:HG2	1.63	0.62
54:2w:18:G:HO2'	54:2w:57:G:H22	1.47	0.62
34:1c:138:VAL:HG13	34:1c:149:ALA:HB3	1.80	0.62
1:2A:675:A:N3	1:2A:2443:C:O2'	2.30	0.62
14:2S:67:ARG:HG2	14:2S:71:ARG:HD2	1.82	0.62
18:2W:11:ARG:NH1	18:2W:99:ARG:O	2.33	0.62
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.82	0.62
26:14:16:CYS:HB2	26:14:36:CYS:HB3	1.82	0.62
32:1a:176:C:H2'	32:1a:177:C:H6	1.65	0.62
32:2a:715:A:H2'	32:2a:716:A:C8	2.35	0.62
50:2s:63:THR:OG1	50:2s:64:GLU:N	2.30	0.62
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.45	0.61
6:2G:79:ASN:OD1	6:2G:79:ASN:N	2.33	0.61
26:24:44:THR:O	26:24:46:GLN:N	2.32	0.61
32:2a:1058:G:OP1	34:2c:199:LYS:NZ	2.32	0.61
1:2A:852:G:H2'	1:2A:853:G:H8	1.64	0.61
1:2A:1225:G:H4'	17:2V:84:LYS:HG2	1.82	0.61
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.32	0.61
6:2G:59:GLU:OE1	6:2G:153:ARG:NH2	2.29	0.61
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	1.82	0.61
21:1Z:126:VAL:HG12	21:1Z:128:VAL:HB	1.81	0.61
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1025:U:O2	32:1a:1036:G:O6	2.18	0.61
32:2a:142:G:H2'	32:2a:143:A:C8	2.36	0.61
32:2a:939:G:H1	32:2a:1344:C:N4	1.98	0.61
33:2b:166:ASP:OD1	33:2b:168:THR:OG1	2.17	0.61
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.34	0.61
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.36	0.61
21:1Z:92:SER:O	21:1Z:94:GLU:N	2.34	0.61
1:2A:2365:G:O6	30:28:43:GLN:NE2	2.30	0.61
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.33	0.61
34:2c:46:GLU:CD	34:2c:46:GLU:H	2.07	0.61
41:2j:8:LEU:HB3	41:2j:96:ILE:HG12	1.82	0.61
49:2r:58:LEU:HD22	49:2r:62:GLU:HB3	1.82	0.61
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.63	0.61
32:1a:78:G:N2	32:1a:91:C:N3	2.49	0.61
32:1a:572:A:OP1	62:1a:1910:HOH:O	2.16	0.61
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.82	0.61
14:2S:34:HIS:O	14:2S:97:ARG:NH2	2.33	0.61
32:2a:1086:U:H3	32:2a:1099:G:H22	1.48	0.61
33:2b:45:GLN:HG3	33:2b:48:MET:HE3	1.82	0.61
33:2b:200:ILE:HG22	33:2b:202:PRO:HD3	1.82	0.61
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.31	0.61
1:1A:1665:A:OP2	62:1A:4107:HOH:O	2.16	0.61
41:1j:30:SER:OG	41:1j:81:THR:OG1	2.19	0.61
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.81	0.61
32:2a:814:A:H2'	32:2a:816:A:H5"	1.82	0.61
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.33	0.61
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.33	0.61
5:1F:12:LEU:HB2	5:1F:124:LEU:HD11	1.81	0.61
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.18	0.61
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.82	0.61
33:2b:16:HIS:O	33:2b:18:GLY:N	2.30	0.61
34:2c:6:HIS:CD2	34:2c:8:ILE:H	2.18	0.61
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	1.82	0.61
4:1E:7:VAL:HG23	4:1E:51:PHE:HE2	1.66	0.61
39:1h:36:LEU:HD23	39:1h:39:LEU:HD12	1.82	0.61
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.82	0.61
1:2A:29:U:H2'	1:2A:30:G:C8	2.36	0.61
1:2A:453:C:OP1	62:2A:3945:HOH:O	2.16	0.61
1:2A:521:G:H2'	1:2A:522:G:H8	1.65	0.61
5:2F:61:GLY:O	62:2F:401:HOH:O	2.16	0.61
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.19	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.82	0.61
32:2a:429:U:O2'	35:2d:22:LYS:NZ	2.33	0.61
34:2c:190:ARG:NE	34:2c:190:ARG:O	2.34	0.61
1:1A:400:G:N7	62:1A:4249:HOH:O	2.31	0.61
32:1a:56:U:H2'	32:1a:57:G:C8	2.36	0.61
32:1a:789:U:O2'	32:1a:791:G:N7	2.30	0.61
1:1A:568:U:O4	62:1A:4154:HOH:O	2.16	0.61
1:1A:1156:A:OP1	16:1U:55:ARG:NH1	2.34	0.61
1:1A:1239:G:OP1	62:1A:4151:HOH:O	2.16	0.61
6:1G:159:VAL:HG21	6:1G:173:LEU:HD21	1.81	0.61
32:1a:45:U:H2'	32:1a:46:G:C8	2.36	0.61
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.01	0.61
32:2a:308:C:H2'	32:2a:309:G:C8	2.36	0.61
32:2a:1223:C:H5"	32:2a:1224:G:H5"	1.83	0.61
45:2n:3:ARG:HD2	45:2n:7:ILE:HD11	1.82	0.61
1:1A:2419:U:O4	62:1A:4144:HOH:O	2.13	0.60
59:1A:4087:ERY:H11	59:1A:4087:ERY:H71	1.83	0.60
5:1F:148:LEU:HD11	5:1F:193:VAL:HG21	1.82	0.60
9:1N:73:THR:HB	9:1N:82:LEU:HD11	1.83	0.60
32:1a:1255:G:H1	32:1a:1282:C:H42	1.46	0.60
1:2A:1633:G:OP2	62:2A:3944:HOH:O	2.16	0.60
2:2B:18:G:H2'	2:2B:19:G:C8	2.36	0.60
3:2D:26:LYS:HB3	3:2D:83:GLU:HG2	1.82	0.60
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.30	0.60
1:1A:2712:U:O2'	1:1A:2712(A):A:OP2	2.14	0.60
4:1E:29:GLY:H	4:1E:93:VAL:HG12	1.65	0.60
15:1T:16:ARG:NH1	15:1T:83:ILE:O	2.33	0.60
32:1a:148:G:H2'	32:1a:149:A:H8	1.65	0.60
21:2Z:128:VAL:HG22	21:2Z:129:SER:H	1.65	0.60
32:2a:324:G:N7	62:2a:1913:HOH:O	2.31	0.60
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.82	0.60
32:2a:1346:A:H5"	40:2i:120:ARG:HH22	1.66	0.60
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	1.83	0.60
50:2s:22:LEU:O	50:2s:26:GLY:N	2.34	0.60
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.49	0.60
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.37	0.60
8:1I:130:TYR:HE2	8:1I:132:PRO:HB3	1.64	0.60
32:1a:504:C:OP1	62:1a:1912:HOH:O	2.16	0.60
33:1b:16:HIS:HD2	33:1b:204:ASN:H	1.49	0.60
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.19	0.60
1:2A:1022:G:N2	1:2A:1023:U:O4	2.25	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2136:C:N4	1:2A:2155:G:H1	1.99	0.60
5:1F:144:LYS:HD2	5:1F:145:GLU:HG2	1.83	0.60
29:17:33:ARG:NH2	62:17:201:HOH:O	2.27	0.60
32:1a:1179:A:O3'	40:1i:103:THR:HB	2.01	0.60
33:1b:98:LEU:HB2	33:1b:101:MET:HG3	1.84	0.60
1:2A:271(P):C:OP1	8:2I:45:LYS:NZ	2.34	0.60
34:2c:8:ILE:HG23	34:2c:16:ARG:HG2	1.83	0.60
1:1A:739:G:OP1	62:1A:4156:HOH:O	2.17	0.60
5:1F:29:ASN:HB3	5:1F:112:MET:HE1	1.84	0.60
32:1a:1040:U:H2'	32:1a:1041:A:H8	1.67	0.60
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.82	0.60
18:2W:86:LEU:HD13	18:2W:96:ILE:HD11	1.82	0.60
32:2a:1289:A:OP1	52:2u:9:ARG:NH1	2.35	0.60
39:2h:83:ILE:HG13	39:2h:137:VAL:HG22	1.83	0.60
33:1b:178:ARG:NH1	33:1b:196:LEU:O	2.34	0.60
35:1d:59:ARG:HH12	35:1d:62:GLN:HB2	1.65	0.60
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.84	0.60
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.01	0.60
28:26:25:LYS:HD2	28:26:30:THR:HB	1.83	0.60
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	1.83	0.60
51:2t:56:MET:HE3	51:2t:85:MET:HG2	1.84	0.60
1:1A:271(I):G:N7	1:1A:271(J):C:N4	2.49	0.60
1:1A:998:C:OP1	62:1A:4152:HOH:O	2.16	0.60
54:1y:4:C:H2'	54:1y:5:G:O4'	2.01	0.60
1:2A:1169:G:H1	1:2A:1180:C:H42	1.49	0.60
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.18	0.60
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.50	0.60
32:2a:114:U:H2'	32:2a:115:G:C8	2.36	0.60
32:2a:1029:C:N4	32:2a:1032:G:N1	2.49	0.60
1:1A:2632:A:HO2'	1:1A:2811:G:HO2'	1.48	0.60
1:1A:2691:C:OP2	62:1A:4155:HOH:O	2.16	0.60
42:1k:48:ILE:O	42:1k:50:TYR:N	2.34	0.60
1:2A:192:C:O2'	1:2A:802:A:N3	2.32	0.60
1:2A:1773:A:OP2	62:2A:3942:HOH:O	2.16	0.60
6:2G:173:LEU:HB3	6:2G:178:PHE:CD1	2.37	0.60
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.35	0.60
32:2a:1458:G:H5"	51:2t:31:SER:HB3	1.84	0.60
36:2e:143:ARG:NH2	39:2h:77:GLU:OE2	2.31	0.60
1:1A:673:C:OP1	5:1F:54:ARG:NH1	2.34	0.60
11:1P:126:VAL:HG12	11:1P:148:LEU:HD22	1.82	0.60
32:1a:1414:U:H2'	32:1a:1415:G:H8	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1660:C:H2'	1:2A:1661:G:H8	1.67	0.60
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.37	0.60
3:2D:118:VAL:N	3:2D:129:ASN:OD1	2.35	0.60
8:2I:41:GLU:HA	8:2I:44:LEU:HB3	1.84	0.60
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	1.84	0.60
32:2a:222:U:H2'	32:2a:223:U:C6	2.37	0.60
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.35	0.60
1:2A:441:U:H2'	1:2A:442:G:C8	2.37	0.59
1:2A:1026:U:OP1	62:2A:3941:HOH:O	2.15	0.59
1:2A:1636:C:OP2	62:2A:3943:HOH:O	2.16	0.59
4:2E:104:VAL:HG22	4:2E:198:VAL:HG13	1.83	0.59
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.34	0.59
23:21:59:THR:O	23:21:91:LYS:NZ	2.35	0.59
35:2d:157:LEU:O	35:2d:161:ASN:ND2	2.30	0.59
50:2s:33:THR:H	50:2s:57:HIS:HE1	1.50	0.59
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	1.84	0.59
1:2A:1670:C:O2	4:2E:129:HIS:NE2	2.20	0.59
32:2a:181:G:H4'	32:2a:182:U:H5'	1.84	0.59
44:2m:90:LEU:HA	44:2m:93:ARG:HE	1.67	0.59
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.35	0.59
26:14:55:ARG:H	26:14:56:VAL:HA	1.67	0.59
1:2A:894:C:O2'	1:2A:895:U:H5"	2.03	0.59
19:2X:84:ALA:HB3	19:2X:87:GLN:HG3	1.84	0.59
32:2a:1226:C:H2'	44:2m:103:THR:HB	1.85	0.59
39:2h:10:LEU:HD23	39:2h:83:ILE:HG12	1.85	0.59
39:2h:33:GLU:HA	39:2h:36:LEU:HD12	1.84	0.59
50:2s:13:ASP:HA	50:2s:16:LEU:HB3	1.85	0.59
1:1A:2106:G:H1	1:1A:2183:C:N4	2.00	0.59
11:1P:5:ASP:OD1	62:1P:302:HOH:O	2.15	0.59
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	1.83	0.59
33:1b:12:GLU:C	33:1b:14:GLY:H	2.11	0.59
1:2A:36:G:OP1	62:2A:3946:HOH:O	2.17	0.59
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.37	0.59
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.38	0.59
22:20:56:ASP:OD2	22:20:58:THR:OG1	2.20	0.59
35:2d:187:ARG:NH1	35:2d:190:ASP:OD1	2.35	0.59
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.66	0.59
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.84	0.59
1:2A:955:C:OP1	12:2Q:87:LYS:NZ	2.31	0.59
11:2P:138:LEU:HD23	11:2P:145:PRO:HD3	1.84	0.59
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:530:G:N1	1:1A:2023:G:OP1	2.31	0.59
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.28	0.59
32:1a:160:A:H1'	32:1a:344:A:C5	2.38	0.59
47:1p:48:TRP:HH2	47:1p:76:GLN:HE22	1.50	0.59
1:2A:973:A:OP2	62:2A:3947:HOH:O	2.17	0.59
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.37	0.59
2:2B:114:C:H2'	2:2B:115:G:C8	2.37	0.59
4:2E:27:LEU:HD22	15:2T:1:MET:SD	2.43	0.59
32:2a:1124:G:H4'	41:2j:38:ILE:HD11	1.85	0.59
32:2a:1244:C:N4	32:2a:1293:G:H1	1.98	0.59
32:2a:1272:G:N2	32:2a:1273:G:C5	2.71	0.59
33:2b:118:LEU:HD11	33:2b:138:LEU:HB3	1.84	0.59
50:2s:33:THR:H	50:2s:57:HIS:CE1	2.21	0.59
21:1Z:93:ASP:HA	21:1Z:131:ARG:HH12	1.67	0.59
32:1a:300:A:O2'	32:1a:564:C:N3	2.35	0.59
32:1a:1191:A:OP1	34:1c:4:LYS:NZ	2.34	0.59
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.83	0.59
1:2A:615:G:OP1	5:2F:40:GLN:NE2	2.35	0.59
32:2a:1309:G:OP2	44:2m:99:ARG:NH2	2.35	0.59
38:2g:97:GLN:HE21	38:2g:101:LEU:HD11	1.68	0.59
1:1A:272(J):C:H2'	1:1A:274:G:H8	1.67	0.59
32:1a:130:A:N3	32:1a:263:A:O2'	2.29	0.59
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.85	0.59
1:2A:307:G:H21	1:2A:330:A:H62	1.51	0.59
1:2A:1368:G:OP1	29:27:28:ARG:NH2	2.33	0.59
1:2A:1918:A:O2'	1:2A:1920:OMC:N4	2.35	0.59
6:2G:5:VAL:HG23	6:2G:7:LEU:H	1.68	0.59
39:2h:110:ALA:HB1	39:2h:133:LEU:HD21	1.83	0.59
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.85	0.59
41:1j:78:ASN:O	41:1j:80:LYS:N	2.36	0.59
54:1y:33:U:O2'	54:1y:35:A:N7	2.32	0.59
2:2B:76:G:H2'	2:2B:77:U:O4'	2.02	0.59
8:2I:72:LEU:HD23	8:2I:75:LEU:HD21	1.84	0.59
8:2I:84:GLY:O	8:2I:86:THR:N	2.29	0.59
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.85	0.59
32:2a:564:C:O2'	39:2h:91:ARG:NH1	2.32	0.59
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	1.85	0.59
13:1R:38:VAL:HG22	13:1R:112:ALA:HB2	1.85	0.58
35:1d:64:LEU:HA	35:1d:67:ILE:HD12	1.84	0.58
54:1w:2:C:H2'	54:1w:3:C:C6	2.37	0.58
1:2A:958:U:OP1	12:2Q:74:TYR:OH	2.16	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.37	0.58
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.83	0.58
32:2a:145:G:H2'	32:2a:146:G:O4'	2.03	0.58
36:2e:100:VAL:HG22	36:2e:118:ILE:HG22	1.84	0.58
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.83	0.58
1:1A:1326:U:HO2'	1:1A:2010:G:HO2'	1.49	0.58
1:1A:2072:G:N2	62:1A:4288:HOH:O	2.35	0.58
44:1m:4:ILE:HD12	44:1m:57:ARG:HA	1.84	0.58
44:1m:86:CYS:SG	44:1m:87:TYR:N	2.76	0.58
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.38	0.58
5:2F:155:LEU:HD23	5:2F:192:LEU:HD13	1.84	0.58
21:2Z:101:PRO:HA	21:2Z:123:ASP:HA	1.86	0.58
32:2a:573:A:N3	32:2a:883:C:O2'	2.37	0.58
1:1A:796:C:H2'	1:1A:797:C:C6	2.37	0.58
1:1A:1993:U:OP2	62:1A:4157:HOH:O	2.17	0.58
7:1H:86:GLU:HB2	7:1H:165:ALA:HB2	1.85	0.58
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.86	0.58
26:14:58:ARG:O	26:14:61:ARG:N	2.35	0.58
34:1c:71:ALA:HA	34:1c:106:VAL:HG21	1.85	0.58
1:2A:1541:G:H3'	1:2A:1542:A:H2'	1.84	0.58
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.38	0.58
14:2S:26:LEU:HD23	14:2S:87:PHE:HD1	1.67	0.58
55:2x:21:A:H61	55:2x:46:G:H2'	1.68	0.58
2:1B:66:A:H61	2:1B:109:C:H5"	1.69	0.58
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.85	0.58
3:1D:146:GLU:HB2	3:1D:189:CYS:HB3	1.85	0.58
2:2B:3:C:H2'	2:2B:4:C:C6	2.37	0.58
32:2a:1263:C:C4	32:2a:1272:G:O6	2.56	0.58
33:2b:16:HIS:HB2	33:2b:204:ASN:HD22	1.68	0.58
1:1A:2336:A:H61	22:10:43:THR:CG2	2.16	0.58
1:1A:2817:G:OP1	13:1R:42:LYS:NZ	2.36	0.58
14:2S:25:ARG:HB3	14:2S:40:ILE:HB	1.84	0.58
1:1A:2059:A:H61	59:1A:4087:ERY:H283	1.68	0.58
32:1a:975:A:H5'	32:1a:975:A:H8	1.68	0.58
36:1e:12:LEU:HD12	36:1e:128:PRO:HB2	1.86	0.58
7:2H:43:VAL:HG13	7:2H:52:VAL:HG23	1.86	0.58
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.52	0.58
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.52	0.58
1:1A:572:A:OP2	17:1V:78:LYS:NZ	2.36	0.58
1:1A:1614:A:OP1	1:1A:1617:C:N4	2.36	0.58
12:1Q:110:THR:HG22	12:1Q:112:GLU:H	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:8:A:H2'	1:2A:9:U:H6	1.69	0.58
1:2A:271(L):U:H5'	8:2I:50:ARG:HH11	1.68	0.58
1:2A:1937:A:H1'	1:2A:1939:5MU:H72	1.85	0.58
14:2S:80:LEU:O	14:2S:82:ILE:N	2.37	0.58
21:2Z:121:HIS:N	21:2Z:172:ALA:HB2	2.18	0.58
39:2h:20:TYR:HE2	39:2h:75:ARG:HD2	1.68	0.58
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HD3	1.85	0.58
32:1a:560:U:O2'	32:1a:561:U:OP2	2.21	0.58
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.37	0.58
50:1s:31:ILE:O	50:1s:50:ALA:N	2.34	0.58
32:2a:1004:A:N6	32:2a:1037:C:O2	2.27	0.58
32:2a:1040:U:H2'	32:2a:1041:A:H8	1.69	0.58
32:1a:618:C:H5'	32:1a:619:U:H5"	1.84	0.58
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.38	0.58
44:1m:97:PRO:HA	44:1m:110:ARG:HD3	1.85	0.58
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.22	0.58
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.38	0.58
32:2a:359:U:H2'	32:2a:360:A:H8	1.68	0.58
11:1P:89:ALA:O	11:1P:121:LYS:NZ	2.33	0.58
1:2A:154(A):C:H42	1:2A:171:G:H1	1.50	0.58
1:2A:521:G:H2'	1:2A:522:G:C8	2.39	0.58
1:2A:588:U:H2'	1:2A:589:C:C6	2.39	0.58
1:2A:2137:C:H42	1:2A:2154:G:H1	1.49	0.58
4:2E:56:PRO:HG3	4:2E:74:PRO:HG2	1.86	0.58
32:2a:580:U:H5"	46:2o:58:MET:HG2	1.85	0.58
40:2i:9:ARG:HG2	40:2i:14:VAL:HA	1.86	0.58
43:2l:10:LEU:HB3	48:2q:32:TYR:CE2	2.39	0.58
1:1A:1662:C:O2'	1:1A:2687:U:OP1	2.21	0.57
2:1B:25:A:OP2	62:1B:301:HOH:O	2.17	0.57
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	1.86	0.57
32:1a:1005:A:OP2	32:1a:1024:G:N2	2.37	0.57
1:2A:252:G:OP1	11:2P:50:ARG:NH1	2.32	0.57
1:2A:902:C:H2'	1:2A:903:C:C6	2.39	0.57
1:2A:995:C:OP2	16:2U:54:LYS:NZ	2.33	0.57
27:25:6:VAL:HG22	27:25:7:PRO:HD2	1.86	0.57
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.26	0.57
32:2a:714:G:H2'	32:2a:715:A:C8	2.38	0.57
33:2b:84:GLU:HG3	33:2b:215:LEU:HB3	1.86	0.57
1:1A:2517:C:H3'	62:1A:4532:HOH:O	2.04	0.57
8:1I:116:LEU:HD21	8:1I:119:PRO:HA	1.86	0.57
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:114:ARG:NE	33:1b:141:GLU:OE2	2.28	0.57
54:1y:20:U:H1'	54:1y:21:A:H4'	1.85	0.57
1:2A:1356:G:OP1	62:2A:3952:HOH:O	2.18	0.57
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.37	0.57
32:2a:165:C:H2'	32:2a:166:G:C8	2.39	0.57
33:2b:70:PHE:CE2	33:2b:90:MET:HB2	2.39	0.57
35:2d:150:GLU:H	35:2d:150:GLU:CD	2.12	0.57
11:1P:89:ALA:HA	11:1P:121:LYS:HD2	1.86	0.57
44:1m:20:THR:C	44:1m:22:ILE:H	2.13	0.57
44:1m:33:ALA:O	44:1m:37:THR:OG1	2.19	0.57
1:2A:793:A:OP2	1:2A:2071:A:O2'	2.19	0.57
1:2A:1204:A:H2	1:2A:1241:A:H62	1.52	0.57
1:2A:1754:C:N3	1:2A:2716:U:O2'	2.36	0.57
1:2A:2137:C:N4	1:2A:2154:G:N1	2.48	0.57
1:2A:2183:C:H2'	1:2A:2184:G:C8	2.38	0.57
2:2B:74:U:H2'	2:2B:75:G:O4'	2.04	0.57
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.19	0.57
1:1A:488:G:O2'	18:1W:49:LYS:NZ	2.27	0.57
12:1Q:103:MET:HE1	12:1Q:127:ILE:HD11	1.86	0.57
39:1h:96:GLY:N	39:1h:99:GLU:OE1	2.37	0.57
40:1i:53:VAL:O	40:1i:55:ALA:N	2.34	0.57
1:2A:2063:C:OP1	62:2A:3949:HOH:O	2.17	0.57
1:2A:2689:U:H4'	1:2A:2690:C:H5'	1.86	0.57
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.86	0.57
2:2B:48:A:OP1	14:2S:30:ARG:NH2	2.35	0.57
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.21	0.57
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	1.85	0.57
21:2Z:30:ASN:HD22	21:2Z:90:VAL:HB	1.69	0.57
32:2a:601:C:H2'	32:2a:602:A:C8	2.39	0.57
37:2f:83:ASP:N	37:2f:83:ASP:OD1	2.35	0.57
1:1A:1771:C:OP1	62:1A:4153:HOH:O	2.16	0.57
8:1I:6:LEU:HD11	8:1I:37:VAL:HG23	1.86	0.57
25:13:39:ASP:OD1	25:13:44:ARG:NH1	2.37	0.57
37:1f:6:VAL:HG13	37:1f:90:VAL:HG22	1.86	0.57
54:1w:13:C:H2'	54:1w:14:A:H5"	1.86	0.57
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.39	0.57
1:2A:2049:G:OP2	62:2A:3948:HOH:O	2.17	0.57
1:2A:2431:U:O2'	1:2A:2433:A:N7	2.37	0.57
2:2B:72:G:O2'	2:2B:105:A:N6	2.38	0.57
3:2D:77:ALA:HB2	3:2D:97:TYR:CD1	2.39	0.57
32:2a:1102:A:O3'	33:2b:96:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:20:SER:OG	34:2c:40:ARG:NH1	2.31	0.57
44:2m:101:GLN:OE1	44:2m:101:GLN:N	2.38	0.57
50:2s:3:ARG:HE	50:2s:8:GLY:H	1.51	0.57
1:1A:184:C:H2'	1:1A:185:U:C6	2.40	0.57
1:1A:570:G:H2'	1:1A:2030:A:C5	2.39	0.57
1:1A:817:C:OP2	62:1A:4158:HOH:O	2.18	0.57
1:1A:1695:G:N7	3:1D:14:ARG:NH2	2.51	0.57
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.68	0.57
32:1a:1503:A:N3	53:1v:13:A:N6	2.53	0.57
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.04	0.57
32:2a:558:G:OP1	62:2a:1905:HOH:O	2.17	0.57
32:2a:936:C:H2'	32:2a:937:A:O4'	2.05	0.57
33:2b:223:ILE:HD13	33:2b:226:ARG:HD3	1.86	0.57
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.37	0.57
1:2A:1365:A:O2'	23:21:11:ARG:NH1	2.37	0.57
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.40	0.57
32:2a:539:A:H2'	32:2a:540:G:C8	2.40	0.57
32:2a:736:C:OP1	49:2r:72:ARG:NH2	2.25	0.57
32:2a:960:U:H5	50:2s:78:ARG:HD3	1.69	0.57
54:2w:68:C:H2'	54:2w:69:G:C8	2.40	0.57
54:2y:18:G:N1	54:2y:55:PSU:C4	2.73	0.57
1:1A:2155:G:N7	1:1A:2156:G:N2	2.52	0.57
32:1a:159:G:N2	32:1a:162:A:OP2	2.38	0.57
1:2A:2127:G:H21	1:2A:2173:A:H1'	1.69	0.57
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.70	0.57
23:21:80:LEU:HB3	23:21:82:LEU:HG	1.87	0.57
25:23:46:ASN:O	25:23:50:VAL:HG22	2.05	0.57
32:2a:542:G:P	35:2d:10:ARG:HH22	2.27	0.57
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.04	0.57
32:2a:1493:A:O2'	53:2v:19:U:O2'	2.19	0.57
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.40	0.57
12:1Q:78:PRO:HD3	55:1x:1:C:N3	2.20	0.57
43:1l:8:ASN:O	43:1l:12:ARG:HG3	2.05	0.57
1:2A:2136:C:N3	1:2A:2155:G:N2	2.48	0.57
32:2a:1294:G:H2'	32:2a:1295:G:C8	2.40	0.57
34:2c:151:VAL:HG22	34:2c:200:ALA:HA	1.86	0.57
38:2g:120:ILE:O	38:2g:124:LEU:HB2	2.05	0.57
1:1A:34:C:H41	1:1A:447:A:H61	1.52	0.57
13:1R:36:THR:HG22	13:1R:37:THR:H	1.70	0.57
32:1a:923:A:H5'	36:1e:21:ALA:HB2	1.85	0.57
32:1a:1227:A:OP1	50:1s:80:TYR:OH	2.14	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.38	0.57
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.40	0.57
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.40	0.57
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.85	0.57
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.20	0.56
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.70	0.56
15:1T:9:LEU:O	15:1T:12:SER:OG	2.22	0.56
32:1a:381:C:H2'	32:1a:382:A:O4'	2.05	0.56
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.40	0.56
36:1e:107:ARG:HG2	36:1e:111:GLU:HG3	1.87	0.56
1:2A:578:A:OP2	62:2A:3951:HOH:O	2.18	0.56
1:2A:2820:A:OP2	13:2R:2:ARG:NH2	2.38	0.56
5:2F:28:ILE:HD13	11:2P:1:MET:HE1	1.87	0.56
8:2I:81:VAL:HG21	8:2I:88:ILE:HG23	1.87	0.56
26:24:58:ARG:HD2	50:2s:67:VAL:HB	1.87	0.56
27:25:33:CYS:N	27:25:38:ALA:O	2.34	0.56
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.86	0.56
32:1a:36:C:OP1	43:1l:123:LYS:NZ	2.37	0.56
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.05	0.56
55:1x:68:C:H2'	55:1x:69:C:C6	2.39	0.56
54:1y:20:U:O2	54:1y:21:A:O2'	2.17	0.56
1:2A:733:G:OP2	62:2A:3953:HOH:O	2.18	0.56
12:2Q:1:MET:HB2	12:2Q:44:ALA:HB1	1.85	0.56
21:2Z:91:LEU:HD22	21:2Z:91:LEU:H	1.70	0.56
23:21:54:ALA:HB1	23:21:83:GLU:HG3	1.87	0.56
32:2a:148:G:H2'	32:2a:149:A:C8	2.37	0.56
33:2b:15:VAL:HG13	33:2b:209:ARG:HB3	1.86	0.56
1:1A:1683:C:H2'	1:1A:1684:C:C6	2.41	0.56
1:1A:2313:C:H4'	6:1G:91:ARG:HG3	1.87	0.56
8:1I:93:THR:HG22	8:1I:119:PRO:HB3	1.86	0.56
33:1b:97:TRP:HZ2	33:1b:102:LEU:HD13	1.70	0.56
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.38	0.56
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.20	0.56
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.41	0.56
1:2A:2017:U:OP2	62:2A:3950:HOH:O	2.17	0.56
1:2A:2340:G:H2'	1:2A:2341:G:H8	1.70	0.56
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.20	0.56
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.21	0.56
32:2a:35:G:O2'	43:2l:118:SER:O	2.20	0.56
32:2a:276:G:OP1	48:2q:12:SER:OG	2.19	0.56
32:2a:692:U:OP2	42:2k:26:ASN:ND2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1004:A:C6	32:2a:1037:C:H1'	2.40	0.56
32:2a:1129:C:O2'	32:2a:1130:A:N7	2.35	0.56
33:2b:91:PRO:HG2	33:2b:155:LEU:HD13	1.88	0.56
38:2g:9:VAL:HG23	38:2g:94:ARG:HH21	1.69	0.56
39:2h:21:LYS:O	39:2h:65:TYR:OH	2.23	0.56
47:2p:56:ALA:O	47:2p:60:LEU:HB2	2.06	0.56
51:2t:50:GLU:HG3	51:2t:100:ILE:HD13	1.86	0.56
12:1Q:110:THR:H	12:1Q:113:GLN:NE2	2.01	0.56
32:1a:1120:G:H1	32:1a:1153:C:H42	1.54	0.56
1:2A:859:G:N2	1:2A:917:A:OP2	2.34	0.56
1:2A:2104:G:H1	1:2A:2185:C:H42	1.53	0.56
32:2a:53:A:OP2	62:2a:1906:HOH:O	2.17	0.56
32:2a:376:G:H5"	47:2p:5:ARG:HB2	1.87	0.56
32:2a:537:G:H5"	43:2l:113:ARG:NH1	2.20	0.56
34:2c:6:HIS:HB3	45:2n:49:HIS:HD2	1.69	0.56
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.41	0.56
32:1a:148:G:H2'	32:1a:149:A:C8	2.40	0.56
37:1f:27:GLN:HA	37:1f:30:LEU:HD12	1.87	0.56
1:2A:90:U:H1'	1:2A:92:A:C8	2.41	0.56
12:2Q:57:HIS:CE1	12:2Q:116:GLU:HG2	2.40	0.56
12:2Q:81:VAL:HB	22:20:7:LEU:HD22	1.87	0.56
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.40	0.56
34:2c:131:ARG:NH2	36:2e:50:GLU:HG3	2.21	0.56
35:2d:8:VAL:HA	35:2d:11:LEU:HD13	1.88	0.56
39:2h:124:ALA:O	39:2h:128:GLY:N	2.35	0.56
8:1I:76:THR:HG22	8:1I:141:LYS:HE2	1.87	0.56
10:1O:104:ARG:NE	15:1T:36:GLU:OE2	2.38	0.56
32:1a:335:C:O2'	32:1a:1433:A:N3	2.38	0.56
33:1b:16:HIS:CD2	33:1b:204:ASN:H	2.24	0.56
33:1b:115:LEU:HD21	33:1b:153:ARG:HD3	1.88	0.56
1:2A:567:A:OP2	11:2P:29:LYS:NZ	2.39	0.56
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.06	0.56
2:2B:40:U:H1'	2:2B:45:A:H61	1.71	0.56
13:2R:70:LEU:O	13:2R:72:ASP:N	2.34	0.56
32:2a:826:C:O2	39:2h:15:ASN:ND2	2.38	0.56
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.69	0.56
35:2d:112:VAL:H	35:2d:116:GLN:NE2	2.03	0.56
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.87	0.56
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.87	0.56
1:1A:839:U:H2'	1:1A:840:C:C6	2.41	0.56
1:1A:2208:A:N7	62:1A:4255:HOH:O	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.05	0.56
24:12:65:ASN:O	24:12:69:ARG:NH1	2.38	0.56
32:1a:557:G:OP1	62:1a:1913:HOH:O	2.18	0.56
32:1a:1136:U:H5"	32:1a:1137:C:C2	2.41	0.56
32:1a:1249:C:O2'	40:1i:73:GLN:NE2	2.39	0.56
32:2a:107:G:H2'	32:2a:108:G:O4'	2.05	0.56
32:2a:116:A:OP1	62:2a:1903:HOH:O	2.18	0.56
32:2a:716:A:H1'	42:2k:118:GLY:HA2	1.88	0.56
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.21	0.56
54:2w:43:C:H2'	54:2w:44:G:C8	2.40	0.56
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.88	0.56
20:1Y:8:LYS:HD3	20:1Y:97:ARG:NH1	2.20	0.56
49:1r:32:ARG:HE	49:1r:65:ILE:HG21	1.70	0.56
1:2A:890:A:H2'	1:2A:892:G:C8	2.39	0.56
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.17	0.56
10:2O:7:TYR:HE2	10:2O:20:MET:HE3	1.69	0.56
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.06	0.56
23:21:80:LEU:HD23	23:21:82:LEU:HD21	1.88	0.56
32:2a:1002:G:H1	32:2a:1038:C:H42	1.53	0.56
40:2i:78:LYS:HE2	40:2i:101:PHE:CE1	2.41	0.56
42:2k:73:MET:HG3	42:2k:103:LEU:HD11	1.88	0.56
48:2q:67:LYS:HA	48:2q:70:ARG:HH12	1.71	0.56
1:1A:2336:A:H61	22:10:43:THR:HG21	1.71	0.56
6:1G:101:ILE:HG12	26:14:25:TYR:HB2	1.88	0.56
25:13:5:LYS:HG3	25:13:36:VAL:HG22	1.88	0.56
40:1i:28:VAL:HG22	40:1i:63:ILE:HB	1.88	0.56
51:1t:9:ASN:O	51:1t:10:LEU:HB2	2.06	0.56
1:2A:783:A:OP2	62:2A:3955:HOH:O	2.18	0.56
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.06	0.56
3:1D:166:GLN:HB2	3:1D:174:ILE:HG22	1.86	0.56
32:1a:427:U:OP1	35:1d:13:ARG:NH1	2.38	0.56
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.41	0.56
38:1g:86:GLN:HE21	38:1g:144:MET:HE1	1.71	0.56
25:23:7:LYS:NZ	25:23:34:GLU:OE1	2.38	0.56
35:2d:74:GLN:O	35:2d:78:LEU:HB2	2.06	0.56
39:2h:120:THR:OG1	39:2h:121:ASP:N	2.37	0.56
1:1A:601:C:O2'	1:1A:605:C:H5"	2.07	0.55
6:1G:72:ARG:HH12	6:1G:87:PRO:HG3	1.71	0.55
9:1N:12:ARG:NH1	9:1N:136:GLU:OE2	2.38	0.55
32:1a:1302:U:OP1	44:1m:13:LYS:NZ	2.33	0.55
1:2A:1181:C:H2'	1:2A:1182:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2879:C:OP2	62:2A:3956:HOH:O	2.18	0.55
6:2G:64:THR:HG22	6:2G:94:LEU:HD11	1.89	0.55
32:2a:359:U:H2'	32:2a:360:A:C8	2.41	0.55
32:2a:1133:G:H1	32:2a:1141:C:N4	2.03	0.55
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.20	0.55
44:2m:50:GLU:HA	44:2m:53:VAL:HG22	1.87	0.55
50:2s:12:ASP:O	50:2s:14:HIS:N	2.38	0.55
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.41	0.55
1:1A:2156:G:H2'	1:1A:2157:G:C2	2.40	0.55
1:1A:2641:G:H5'	9:1N:83:LYS:HE2	1.88	0.55
23:11:18:ILE:HG12	23:11:37:ILE:HG12	1.89	0.55
32:1a:380:G:N2	32:1a:383:A:OP2	2.35	0.55
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.42	0.55
1:2A:1021:A:H62	1:2A:1141:U:H3	1.53	0.55
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.21	0.55
1:2A:1824:G:N3	3:2D:254:THR:OG1	2.38	0.55
2:2B:39:A:O2'	2:2B:40:U:H5'	2.06	0.55
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.74	0.55
36:2e:98:THR:OG1	36:2e:99:GLY:N	2.36	0.55
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.40	0.55
1:1A:1090:U:C2	1:1A:1102:C:H1'	2.41	0.55
1:1A:2113:U:H5'	1:1A:2114:A:OP2	2.06	0.55
32:1a:97:G:H2'	32:1a:98:G:O4'	2.07	0.55
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.40	0.55
1:2A:375:C:H2'	1:2A:376:C:C6	2.41	0.55
1:2A:643:A:N1	1:2A:2369:A:O2'	2.33	0.55
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.41	0.55
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.42	0.55
5:2F:117:ARG:NH2	5:2F:189:THR:O	2.30	0.55
21:2Z:79:ARG:HB2	21:2Z:80:ARG:NH1	2.21	0.55
25:23:5:LYS:HB3	25:23:57:GLU:HB2	1.88	0.55
32:2a:662:G:O2'	32:2a:836:G:OP1	2.24	0.55
32:2a:864:A:H5'	36:2e:86:ALA:HB2	1.88	0.55
32:2a:1397:C:OP2	36:2e:24:ARG:NH2	2.37	0.55
44:2m:85:GLY:HA2	44:2m:93:ARG:HH22	1.71	0.55
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.37	0.55
24:12:69:ARG:HB3	24:12:69:ARG:HH11	1.71	0.55
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.22	0.55
38:1g:20:ASP:HB3	38:1g:23:VAL:HG23	1.88	0.55
39:1h:91:ARG:HE	48:1q:33:GLY:HA3	1.71	0.55
1:2A:897:C:H5"	54:2w:56:C:OP1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:133:HIS:O	8:2I:135:GLU:N	2.36	0.55
1:1A:1059:G:H3'	1:1A:1060:U:H2'	1.89	0.55
6:1G:73:ALA:HB3	6:1G:85:GLY:H	1.72	0.55
10:1O:2:ILE:HB	10:1O:33:ALA:HB3	1.87	0.55
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.07	0.55
32:1a:1381:U:H1'	38:1g:79:ARG:HG2	1.88	0.55
1:2A:918:A:O2'	2:2B:97:G:N2	2.39	0.55
1:2A:2070:G:H2'	1:2A:2071:A:H8	1.71	0.55
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.72	0.55
7:2H:53:GLU:HA	7:2H:65:HIS:HE2	1.71	0.55
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	1.86	0.55
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.41	0.55
2:1B:43:C:H5"	26:14:1:MET:HG2	1.89	0.55
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.72	0.55
54:1w:28:G:H2'	54:1w:29:G:H8	1.71	0.55
1:2A:243:U:OP1	30:28:6:THR:OG1	2.20	0.55
1:2A:817:C:O2'	1:2A:839:U:OP1	2.23	0.55
1:2A:956:G:H5"	12:2Q:77:LYS:HD2	1.88	0.55
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.06	0.55
32:2a:1053:G:N7	32:2a:1200:C:H5"	2.22	0.55
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.40	0.55
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.89	0.55
33:1b:15:VAL:HB	33:1b:209:ARG:HG3	1.89	0.55
1:2A:197:A:OP1	62:2A:3901:HOH:O	2.18	0.55
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.54	0.55
1:2A:2121:G:H1	1:2A:2177:C:H42	1.54	0.55
1:2A:2141:G:H3'	1:2A:2142:C:H5"	1.89	0.55
31:29:6:SER:O	31:29:6:SER:OG	2.24	0.55
32:2a:254:G:OP1	48:2q:66:SER:OG	2.24	0.55
32:2a:501:C:H2'	32:2a:502:G:H8	1.70	0.55
6:1G:105:LYS:NZ	26:14:25:TYR:O	2.32	0.55
32:1a:1030:C:H42	32:1a:1031:G:H1	1.53	0.55
32:1a:1181:G:O2'	32:1a:1182:G:N7	2.36	0.55
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.89	0.55
1:2A:2422:A:O4'	54:2y:76:A:N6	2.40	0.55
26:24:50:VAL:HG11	44:2m:64:TRP:C	2.32	0.55
26:24:61:ARG:HG2	50:2s:42:PRO:HG2	1.89	0.55
32:2a:952:U:H2'	32:2a:953:G:H8	1.72	0.55
32:2a:1134:G:H1	32:2a:1140:C:H42	1.52	0.55
34:2c:6:HIS:HB3	45:2n:49:HIS:CD2	2.41	0.55
39:2h:97:VAL:HG13	39:2h:98:LYS:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:15:VAL:HB	44:2m:48:LEU:HD11	1.88	0.55
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.41	0.55
24:12:31:GLU:HB3	24:12:53:LEU:HD11	1.89	0.55
32:1a:184:G:H2'	32:1a:185:A:C8	2.41	0.55
33:1b:163:PHE:CD1	33:1b:185:ILE:HG13	2.42	0.55
36:1e:85:GLY:C	36:1e:87:SER:H	2.15	0.55
1:2A:389:G:H8	1:2A:389:G:O5'	1.89	0.55
1:2A:992:C:OP1	16:2U:47:TYR:OH	2.20	0.55
5:2F:157:VAL:HG13	5:2F:176:LEU:HB3	1.88	0.55
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.40	0.55
17:2V:57:VAL:HG22	17:2V:99:ILE:HG23	1.88	0.55
32:2a:949:A:H61	32:2a:1232:U:H3	1.55	0.55
32:2a:973:G:H3'	32:2a:974:A:H5"	1.89	0.55
32:2a:1030(A):G:N1	32:2a:1030(D):A:OP2	2.38	0.55
1:1A:2577:A:H5'	27:15:3:LYS:HD2	1.87	0.55
1:1A:2793:G:H2'	1:1A:2794:C:H5	1.72	0.55
7:1H:30:LYS:NZ	7:1H:81:GLU:O	2.40	0.55
15:1T:127:ALA:C	15:1T:129:ARG:H	2.15	0.55
35:1d:82:ALA:O	35:1d:89:THR:HG22	2.07	0.55
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.89	0.55
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.88	0.55
32:2a:770:C:H5"	62:2a:1956:HOH:O	2.06	0.55
32:2a:866:C:O2'	32:2a:919:A:OP1	2.21	0.55
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.21	0.55
32:2a:1190:G:H5'	34:2c:176:HIS:HE1	1.70	0.55
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	1.89	0.55
1:1A:615:G:OP1	5:1F:40:GLN:NE2	2.40	0.54
19:1X:35:THR:O	19:1X:39:ILE:HG13	2.07	0.54
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.88	0.54
1:2A:520:G:H2'	1:2A:521:G:C8	2.43	0.54
1:2A:582:G:N7	62:2A:4052:HOH:O	2.34	0.54
6:2G:165:THR:OG1	6:2G:166:ASP:N	2.41	0.54
32:2a:396:G:O2'	32:2a:398:C:OP1	2.21	0.54
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.18	0.54
32:2a:1122:U:N3	32:2a:1123:A:N7	2.55	0.54
1:1A:61:G:OP1	24:12:51:ARG:NH2	2.41	0.54
1:1A:2334:G:O6	22:10:74:ARG:NH1	2.37	0.54
2:1B:88:C:H2'	2:1B:89:G:O4'	2.07	0.54
14:1S:15:ARG:HB3	14:1S:19:LYS:HE2	1.88	0.54
32:1a:6:G:H1	36:1e:98:THR:HG21	1.71	0.54
32:1a:864:A:H2'	32:1a:865:A:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1399:C:H4'	32:1a:1400:5MC:H5"	1.89	0.54
35:1d:18:LYS:HG2	61:1d:302:SF4:S1	2.47	0.54
36:1e:85:GLY:O	36:1e:87:SER:N	2.38	0.54
15:2T:91:ARG:HD2	15:2T:120:ARG:NH1	2.22	0.54
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.41	0.54
26:24:59:PHE:CE2	50:2s:64:GLU:HB2	2.42	0.54
32:2a:401:C:H2'	32:2a:402:G:C8	2.42	0.54
32:2a:946:A:OP1	44:2m:114:ARG:NH2	2.39	0.54
33:2b:70:PHE:HE2	33:2b:90:MET:HB2	1.71	0.54
33:2b:144:ARG:NH2	33:2b:148:TYR:OH	2.40	0.54
34:2c:119:ARG:HE	34:2c:140:ARG:NH1	2.05	0.54
46:2o:70:LEU:HD11	46:2o:77:ARG:HB2	1.89	0.54
1:1A:2590:A:H2'	1:1A:2591:C:H6	1.73	0.54
1:1A:2741:A:OP1	31:19:22:ARG:NH2	2.33	0.54
35:1d:8:VAL:HA	35:1d:11:LEU:HD13	1.88	0.54
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.06	0.54
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.42	0.54
32:2a:1004:A:N6	32:2a:1037:C:H1'	2.22	0.54
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.08	0.54
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.43	0.54
33:2b:28:PHE:HD1	33:2b:194:PRO:HG3	1.71	0.54
1:1A:1608:A:H1'	1:1A:1610:A:OP2	2.08	0.54
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.88	0.54
18:1W:4:LYS:HE3	18:1W:6:ILE:HD11	1.89	0.54
32:1a:67:C:H2'	32:1a:68:G:C8	2.43	0.54
32:1a:674:G:H2'	32:1a:675:A:H8	1.72	0.54
38:1g:78:ARG:HH21	38:1g:79:ARG:HH11	1.55	0.54
46:1o:3:ILE:HD13	46:1o:34:LEU:HG	1.90	0.54
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.42	0.54
32:2a:920:U:H2'	32:2a:921:U:C6	2.43	0.54
32:2a:1029:C:N4	32:2a:1032:G:H1	2.04	0.54
33:2b:15:VAL:HG22	33:2b:209:ARG:HD2	1.88	0.54
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.25	0.54
1:1A:1791:A:H5'	3:1D:206:LEU:HD12	1.90	0.54
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.07	0.54
32:1a:1073:U:O2'	33:1b:104:ASN:OD1	2.23	0.54
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.89	0.54
32:2a:1080:A:H5'	36:2e:14:ARG:HH21	1.71	0.54
1:1A:1166:C:H2'	1:1A:1167:U:C6	2.43	0.54
1:1A:2146:C:O2	1:1A:2147:G:N2	2.41	0.54
2:1B:24:G:N7	2:1B:56:G:H2'	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:122:PRO:HB3	6:1G:170:ARG:HH12	1.71	0.54
15:1T:36:GLU:HG2	32:1a:346:G:OP1	2.06	0.54
32:1a:279:A:H4'	32:1a:280:C:H5"	1.88	0.54
33:1b:33:TYR:HB2	33:1b:43:ASP:HB2	1.90	0.54
40:1i:95:LYS:H	40:1i:98:PRO:HG2	1.71	0.54
1:2A:860:U:H1'	1:2A:2268:A:H5'	1.89	0.54
1:2A:2133:G:O2'	1:2A:2157:G:N2	2.40	0.54
6:2G:41:GLN:NE2	6:2G:153:ARG:HB3	2.22	0.54
8:2I:50:ARG:HA	8:2I:53:ALA:HB3	1.88	0.54
18:2W:86:LEU:HB2	18:2W:96:ILE:HG13	1.90	0.54
32:2a:1029:C:C4	32:2a:1032:G:N1	2.74	0.54
37:2f:30:LEU:HD22	37:2f:75:LEU:HD21	1.90	0.54
38:2g:24:THR:HA	38:2g:27:ILE:HD12	1.89	0.54
54:2y:18:G:N2	54:2y:55:PSU:C4	2.73	0.54
54:2y:18:G:N2	54:2y:55:PSU:HN3	2.01	0.54
1:1A:962:G:OP1	62:1A:4161:HOH:O	2.19	0.54
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.43	0.54
1:1A:2417:C:OP1	11:1P:65:ARG:NH2	2.40	0.54
1:1A:2845:G:N2	62:1A:4319:HOH:O	2.40	0.54
12:1Q:35:VAL:HG22	12:1Q:102:VAL:HG22	1.90	0.54
18:1W:18:ARG:HG2	18:1W:76:VAL:HB	1.89	0.54
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.91	0.54
54:1y:25:C:H2'	54:1y:26:A:H8	1.73	0.54
1:2A:586:A:N1	1:2A:809:G:O2'	2.32	0.54
1:2A:817:C:H2'	1:2A:818:G:O4'	2.08	0.54
8:2I:132:PRO:HD2	8:2I:136:VAL:O	2.08	0.54
33:2b:48:MET:HA	33:2b:51:LEU:HB2	1.90	0.54
44:2m:49:THR:O	44:2m:53:VAL:HG13	2.07	0.54
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.22	0.54
1:1A:1082:U:H3	1:1A:1086:A:H61	0.58	0.54
1:1A:2590:A:H2'	1:1A:2591:C:C6	2.42	0.54
10:1O:10:VAL:HG11	10:1O:16:ALA:HB3	1.88	0.54
10:1O:16:ALA:HB2	10:1O:52:VAL:HG21	1.89	0.54
17:1V:2:PHE:CE2	17:1V:41:GLY:HA3	2.43	0.54
1:2A:2701:C:H2'	1:2A:2702:U:H2'	1.89	0.54
14:2S:26:LEU:HD23	14:2S:87:PHE:CD1	2.43	0.54
32:2a:674:G:N2	32:2a:717:C:O2	2.40	0.54
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.08	0.54
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.43	0.54
40:2i:63:ILE:HD13	40:2i:77:ILE:HG23	1.90	0.54
49:2r:70:ILE:O	49:2r:74:ARG:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:458:G:O2'	1:1A:469:G:O6	2.24	0.54
1:1A:887:A:H1'	1:1A:889:C:OP2	2.08	0.54
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.42	0.54
2:1B:11:C:H3'	2:1B:12:C:C6	2.43	0.54
32:1a:973:G:H3'	32:1a:974:A:H5"	1.90	0.54
32:1a:1073:U:H2'	32:1a:1074:G:C8	2.43	0.54
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.74	0.54
54:1y:19:G:H1	54:1y:56:C:N4	2.05	0.54
1:2A:2482:G:HO2'	54:2w:64:A:HO2'	1.55	0.54
32:2a:163:C:H2'	32:2a:164:U:C6	2.42	0.54
1:1A:1619:G:N7	62:1A:4256:HOH:O	2.32	0.54
7:1H:101:ARG:NH2	7:1H:121:ILE:O	2.36	0.54
32:1a:1060:C:H5"	41:1j:51:ARG:HG2	1.89	0.54
35:1d:172:PRO:O	35:1d:174:LEU:N	2.41	0.54
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.90	0.54
40:1i:96:LEU:H	40:1i:98:PRO:HD2	1.73	0.54
50:1s:31:ILE:HD13	50:1s:47:HIS:HB3	1.90	0.54
1:2A:229:A:H2	1:2A:418:G:H4'	1.73	0.54
1:2A:291:C:H42	1:2A:349:G:H1	1.55	0.54
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.24	0.54
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.90	0.54
15:2T:127:ALA:C	15:2T:129:ARG:H	2.15	0.54
32:2a:186:C:O2'	51:2t:85:MET:SD	2.65	0.54
32:2a:662:G:H2'	32:2a:663:A:C8	2.43	0.54
1:1A:1680:U:O2'	1:1A:1763:G:N7	2.34	0.53
32:1a:270:A:H2'	32:1a:271:C:C6	2.42	0.53
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.22	0.53
54:1w:28:G:H2'	54:1w:29:G:C8	2.43	0.53
55:1x:76:8AN:H1'	62:1x:202:HOH:O	2.07	0.53
54:1y:38:A:H2'	54:1y:39:PSU:O4'	2.08	0.53
1:2A:2114:A:H62	1:2A:2115:G:N2	2.06	0.53
16:2U:83:LEU:HD23	16:2U:113:ALA:HB2	1.89	0.53
32:2a:253:U:H2'	32:2a:254:G:H8	1.73	0.53
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.90	0.53
1:1A:880:G:H1	1:1A:898:C:H42	1.56	0.53
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.23	0.53
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.44	0.53
32:1a:1054:C:C4	54:1w:34:G:H1'	2.43	0.53
44:1m:11:ARG:C	44:1m:13:LYS:H	2.16	0.53
54:1w:7:A:H61	54:1w:66:U:H3	1.55	0.53
1:2A:946:G:H2'	1:2A:947:G:C8	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.74	0.53
1:2A:2712(A):A:OP1	62:2A:3957:HOH:O	2.18	0.53
2:2B:42:C:O2'	6:2G:67:LYS:O	2.19	0.53
32:2a:1278:U:H5'	32:2a:1279:A:OP1	2.07	0.53
1:1A:10:G:N2	1:1A:2802:G:OP1	2.34	0.53
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.43	0.53
1:1A:2612:C:OP1	62:1A:4159:HOH:O	2.18	0.53
1:1A:2627:G:N2	1:1A:2777:G:OP2	2.41	0.53
3:1D:109:ASP:HB2	3:1D:197:GLY:HA2	1.91	0.53
7:1H:3:ARG:NE	7:1H:3:ARG:HA	2.23	0.53
54:1w:18:G:H4'	54:1w:60:U:C5	2.44	0.53
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.91	0.53
1:2A:2299:G:H2'	1:2A:2300:G:H8	1.73	0.53
32:2a:324:G:N1	32:2a:327:A:OP2	2.39	0.53
32:2a:338:A:H2'	32:2a:339:C:C6	2.43	0.53
35:2d:63:LYS:O	35:2d:67:ILE:HG13	2.09	0.53
1:1A:1011:G:OP2	16:1U:66:ASN:ND2	2.34	0.53
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.08	0.53
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.74	0.53
33:1b:12:GLU:O	33:1b:15:VAL:HG22	2.08	0.53
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.73	0.53
1:2A:2002:G:OP2	13:2R:9:LYS:NZ	2.39	0.53
6:2G:16:ARG:NE	6:2G:31:VAL:HG11	2.23	0.53
37:2f:45:LEU:HD12	37:2f:45:LEU:H	1.73	0.53
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.44	0.53
26:14:15:ILE:HD12	26:14:32:TYR:CE1	2.44	0.53
42:1k:111:ASP:OD1	49:1r:84:LYS:HE3	2.08	0.53
47:1p:53:VAL:HG13	47:1p:79:VAL:HG22	1.90	0.53
1:2A:407:G:H2'	1:2A:408:G:C8	2.43	0.53
1:2A:878:A:N6	1:2A:899:A:O2'	2.39	0.53
12:2Q:13:GLN:O	12:2Q:72:LYS:NZ	2.42	0.53
33:2b:55:PHE:O	33:2b:59:GLU:N	2.41	0.53
54:2y:70:G:H2'	54:2y:71:G:H8	1.73	0.53
1:1A:1411:C:H2'	1:1A:1412:A:C8	2.43	0.53
1:1A:1779:U:H2'	62:1A:4434:HOH:O	2.09	0.53
32:1a:26:A:O2'	35:1d:209:ARG:NH2	2.42	0.53
32:1a:624:C:H2'	32:1a:625:G:C8	2.44	0.53
36:1e:12:LEU:HB3	36:1e:31:LEU:CB	2.39	0.53
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.89	0.53
1:2A:2712:U:OP1	1:2A:2714:G:H4'	2.08	0.53
5:2F:175:THR:OG1	5:2F:176:LEU:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:2Y:35:TYR:CE2	20:2Y:69:ALA:HB3	2.43	0.53
26:24:58:ARG:HD2	50:2s:68:GLY:H	1.74	0.53
38:2g:67:GLU:HA	38:2g:70:LYS:HE3	1.89	0.53
39:2h:84:ARG:HH11	39:2h:86:ILE:HG12	1.73	0.53
42:2k:86:GLY:O	42:2k:91:ARG:NH1	2.40	0.53
45:2n:59:ALA:HB1	45:2n:61:TRP:HZ3	1.73	0.53
1:1A:580:C:H2'	1:1A:581:C:C6	2.43	0.53
1:1A:2002:G:OP2	13:1R:9:LYS:NZ	2.42	0.53
16:1U:50:ARG:HG2	16:1U:53:ARG:NH2	2.24	0.53
1:2A:8:A:H2'	1:2A:9:U:C6	2.44	0.53
1:2A:893:C:H5'	1:2A:894:C:C5	2.44	0.53
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.42	0.53
1:1A:639:U:H2'	1:1A:640:C:C6	2.44	0.53
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.08	0.53
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.43	0.53
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.24	0.53
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.91	0.53
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	1.91	0.53
46:1o:87:ILE:HG22	46:1o:88:ARG:H	1.74	0.53
48:1q:59:ILE:HG22	48:1q:73:VAL:HA	1.90	0.53
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.44	0.53
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.57	0.53
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.44	0.53
2:2B:42:C:C4	2:2B:43:C:C4	2.97	0.53
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.08	0.53
32:2a:299:G:O6	62:2a:1905:HOH:O	2.15	0.53
1:1A:918:A:H5"	2:1B:98:G:O2'	2.09	0.53
1:1A:2344:U:OP1	28:16:37:ARG:NH1	2.42	0.53
2:1B:21:G:O6	62:1B:302:HOH:O	2.17	0.53
1:2A:7:G:H2'	1:2A:8:A:C8	2.44	0.53
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.44	0.53
32:2a:1148:U:H5'	40:2i:16:ARG:HD2	1.90	0.53
38:2g:20:ASP:HB3	38:2g:23:VAL:HB	1.91	0.53
50:2s:28:LYS:HB3	50:2s:29:ARG:CA	2.39	0.53
1:1A:1762:A:H2'	62:1A:5430:HOH:O	2.09	0.53
3:1D:183:ARG:HG3	3:1D:270:ILE:HD13	1.91	0.53
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.91	0.53
35:1d:178:VAL:C	35:1d:180:GLY:H	2.17	0.53
50:1s:12:ASP:O	50:1s:14:HIS:N	2.42	0.53
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.72	0.53
5:2F:199:TRP:HE1	5:2F:203:GLN:HE21	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	1.90	0.53
19:2X:32:PRO:HA	19:2X:77:LYS:HE3	1.89	0.53
32:2a:636:U:H2'	32:2a:637:G:H8	1.74	0.53
32:2a:901:A:O2'	32:2a:1513:A:OP1	2.23	0.53
32:2a:1294:G:H2'	32:2a:1295:G:H8	1.74	0.53
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.27	0.53
41:2j:6:ILE:HG12	41:2j:98:ILE:HG22	1.91	0.53
1:1A:657:U:H2'	1:1A:658:C:H6	1.74	0.52
32:1a:105:G:H5'	32:1a:106:C:OP2	2.09	0.52
32:1a:1040:U:H2'	32:1a:1041:A:C8	2.44	0.52
48:1q:15:MET:HE1	48:1q:43:LEU:HD22	1.91	0.52
1:2A:75:G:H4'	24:22:55:ARG:CZ	2.39	0.52
1:2A:171:G:H2'	1:2A:172:C:C6	2.44	0.52
1:2A:724:U:H2'	1:2A:725:G:O4'	2.10	0.52
1:2A:1123:C:H1'	31:29:18:ARG:NH2	2.24	0.52
1:2A:2424:C:O2	1:2A:2429:G:O2'	2.22	0.52
11:2P:121:LYS:O	11:2P:123:LEU:N	2.42	0.52
32:2a:1075:C:H4'	33:2b:175:ARG:NH2	2.21	0.52
1:1A:301:G:OP2	20:1Y:84:ARG:NH2	2.42	0.52
1:1A:363:G:H2'	1:1A:363(A):A:H8	1.74	0.52
1:1A:800:A:H8	1:1A:800:A:OP1	1.93	0.52
20:1Y:86:ARG:HH21	20:1Y:100:ALA:HB1	1.74	0.52
27:15:48:GLU:C	27:15:60:VAL:HG11	2.34	0.52
42:1k:82:VAL:HB	42:1k:108:ILE:HG23	1.91	0.52
51:1t:37:SER:O	51:1t:41:ILE:HG13	2.09	0.52
54:1w:27:G:H1	54:1w:43:C:H42	1.57	0.52
54:1y:25:C:H2'	54:1y:26:A:C8	2.45	0.52
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.10	0.52
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.27	0.52
3:2D:77:ALA:HA	3:2D:97:TYR:HA	1.91	0.52
7:2H:22:GLY:C	7:2H:37:VAL:HB	2.35	0.52
14:2S:67:ARG:HD3	14:2S:71:ARG:HH11	1.74	0.52
32:2a:189(D):C:H1'	32:2a:189(H):G:N2	2.25	0.52
32:2a:297:G:N2	32:2a:300:A:OP2	2.40	0.52
32:2a:1081:G:OP1	36:2e:18:ARG:HG2	2.09	0.52
32:2a:1181:G:H4'	32:2a:1182:G:OP1	2.07	0.52
37:2f:2:ARG:HH21	37:2f:69:GLU:HB3	1.74	0.52
1:1A:251:A:C5	1:1A:252:G:H1'	2.45	0.52
1:1A:1055:G:H3'	1:1A:1056:G:H8	1.74	0.52
3:1D:18:VAL:HG12	3:1D:211:ARG:NH2	2.24	0.52
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:4:TYR:CE2	16:1U:100:VAL:HG11	2.44	0.52
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.91	0.52
32:1a:186:C:H2'	32:1a:187:C:C6	2.44	0.52
32:1a:195:A:O2'	32:1a:222:U:O2'	2.15	0.52
32:1a:1118:C:P	40:1i:104:ARG:HH11	2.32	0.52
35:1d:3:ARG:HD3	35:1d:118:ARG:HD3	1.90	0.52
40:1i:32:ASP:OD1	40:1i:33:PHE:N	2.41	0.52
41:1j:20:ALA:HB1	41:1j:37:PRO:HB3	1.91	0.52
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.54	0.52
12:2Q:57:HIS:CD2	12:2Q:117:ALA:HB2	2.44	0.52
21:2Z:70:LEU:HD12	21:2Z:71:VAL:H	1.73	0.52
26:24:61:ARG:HA	26:24:61:ARG:HH11	1.74	0.52
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.40	0.52
1:1A:2812:G:H2'	1:1A:2813:A:C8	2.44	0.52
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.27	0.52
18:1W:71:VAL:HA	18:1W:107:LEU:HD23	1.91	0.52
32:1a:171:A:H2'	32:1a:172:A:C8	2.44	0.52
32:1a:1402:4OC:HM43	32:1a:1500:A:H61	1.75	0.52
39:1h:14:ARG:NH2	39:1h:83:ILE:O	2.30	0.52
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.09	0.52
32:2a:266:G:O3'	48:2q:67:LYS:HB2	2.10	0.52
32:2a:838:G:H1	32:2a:848:C:H42	1.56	0.52
32:2a:1263:C:N3	32:2a:1272:G:O6	2.42	0.52
32:2a:1310:G:H5'	44:2m:77:ASN:ND2	2.25	0.52
42:2k:32:ILE:HD11	42:2k:68:ALA:HB1	1.91	0.52
1:1A:2117:A:O2'	1:1A:2118:U:H5"	2.09	0.52
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.45	0.52
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.25	0.52
5:1F:103:LYS:HA	5:1F:106:ARG:HD3	1.92	0.52
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.90	0.52
32:1a:277:C:P	48:1q:68:ARG:HH12	2.32	0.52
1:2A:2137:C:C2	1:2A:2154:G:N2	2.73	0.52
6:2G:31:VAL:O	6:2G:33:ARG:NH1	2.42	0.52
26:24:13:ARG:HG2	26:24:23:GLU:HG2	1.90	0.52
32:2a:438:G:H4'	35:2d:123:HIS:CE1	2.44	0.52
42:2k:79:SER:HB2	42:2k:104:GLN:HE21	1.75	0.52
1:1A:288:C:H2'	1:1A:289:A:C8	2.45	0.52
1:1A:582:G:H2'	1:1A:583:G:C8	2.44	0.52
1:1A:1833:U:O2'	1:1A:1969:A:N1	2.30	0.52
1:1A:2495:G:H5"	12:1Q:82:ARG:HG2	1.91	0.52
7:1H:68:THR:O	7:1H:72:ILE:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:278:G:OP2	48:1q:92:ARG:NH2	2.43	0.52
1:2A:2006:C:OP2	62:2A:3960:HOH:O	2.19	0.52
1:2A:2153:G:C2	1:2A:2154:G:H1'	2.44	0.52
8:2I:94:ALA:HA	8:2I:97:ILE:HD12	1.92	0.52
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	1.91	0.52
21:2Z:155:LEU:HB2	21:2Z:157:LEU:HD12	1.91	0.52
25:23:40:THR:HG22	25:23:42:ALA:H	1.75	0.52
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.43	0.52
32:2a:1226:C:H6	44:2m:103:THR:HB	1.74	0.52
44:2m:118:ALA:HB2	55:2x:28:C:H4'	1.92	0.52
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.26	0.52
1:1A:2532:G:O2'	1:1A:2657:A:N1	2.42	0.52
1:1A:2552:OMU:OP2	62:1A:4129:HOH:O	2.19	0.52
32:1a:165:C:O2'	32:1a:166:G:H5'	2.10	0.52
32:1a:977:A:O2'	32:1a:979:C:OP2	2.26	0.52
32:1a:1131:G:OP1	40:1i:20:ARG:NH2	2.27	0.52
48:1q:57:VAL:HG12	48:1q:76:LEU:HA	1.92	0.52
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.91	0.52
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.45	0.52
6:2G:5:VAL:HG11	6:2G:101:ILE:HG12	1.91	0.52
36:2e:20:GLN:HG2	36:2e:25:ARG:HD3	1.92	0.52
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.92	0.52
1:1A:603:A:N1	1:1A:625:G:O2'	2.40	0.52
1:1A:880:G:N2	1:1A:898:C:N3	2.56	0.52
1:1A:1144:G:C6	1:1A:1145:C:C4	2.97	0.52
1:1A:1501:C:O4'	3:1D:100:GLY:HA2	2.08	0.52
5:1F:103:LYS:O	5:1F:106:ARG:HG2	2.10	0.52
33:1b:204:ASN:OD1	33:1b:205:ASP:N	2.42	0.52
33:1b:216:SER:O	33:1b:219:VAL:HG12	2.10	0.52
35:1d:4:TYR:HE2	35:1d:11:LEU:HD11	1.75	0.52
36:1e:80:ILE:HG13	36:1e:81:GLU:N	2.24	0.52
1:2A:27:G:N2	1:2A:512:G:H1'	2.24	0.52
1:2A:182:A:H2'	1:2A:183:C:C6	2.45	0.52
1:2A:925:C:H2'	1:2A:926:A:H8	1.75	0.52
1:2A:2552:OMU:H6	1:2A:2552:OMU:O5'	2.09	0.52
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.09	0.52
8:2I:2:LYS:HA	8:2I:19:VAL:O	2.10	0.52
32:2a:266:G:H2'	32:2a:266:G:N3	2.24	0.52
32:2a:1040:U:H2'	32:2a:1041:A:C8	2.45	0.52
34:2c:19:GLU:HB3	34:2c:40:ARG:NH2	2.25	0.52
38:2g:12:LEU:H	38:2g:12:LEU:HD12	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:20:LEU:HA	50:2s:23:ASN:ND2	2.24	0.52
54:2w:22:G:H2'	54:2w:23:A:C8	2.44	0.52
1:1A:194:G:O5'	62:1A:4160:HOH:O	2.19	0.52
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.44	0.52
5:1F:120:GLU:HB3	5:1F:122:LYS:HG2	1.91	0.52
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.10	0.52
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.42	0.52
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.38	0.52
50:1s:28:LYS:HB3	50:1s:47:HIS:HD2	1.75	0.52
1:2A:300:A:P	20:2Y:86:ARG:HH12	2.33	0.52
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.45	0.52
1:2A:2237:G:OP1	62:2A:3959:HOH:O	2.19	0.52
32:2a:22:G:H4'	32:2a:885:G:C8	2.45	0.52
32:2a:328:C:H4'	32:2a:329:A:H5'	1.91	0.52
32:2a:908:A:H2'	32:2a:909:A:H8	1.75	0.52
32:2a:1114:C:H42	32:2a:1186:G:H1	1.58	0.52
35:2d:41:GLY:O	35:2d:44:GLY:N	2.43	0.52
38:2g:65:ALA:O	38:2g:69:VAL:HG23	2.10	0.52
46:2o:87:ILE:HG22	46:2o:88:ARG:H	1.74	0.52
51:2t:37:SER:O	51:2t:41:ILE:HG12	2.10	0.52
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.42	0.52
1:1A:2135:A:N6	1:1A:2156:G:O2'	2.43	0.52
20:1Y:87:LYS:HD2	20:1Y:95:LYS:HD3	1.92	0.52
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.44	0.52
32:2a:96:U:H2'	32:2a:97:G:C8	2.44	0.52
32:2a:971:G:OP1	32:2a:971:G:H3'	2.10	0.52
32:2a:996:A:N1	32:2a:1045:C:O2'	2.34	0.52
39:2h:84:ARG:NH1	39:2h:86:ILE:HG12	2.25	0.52
41:2j:47:PHE:O	41:2j:63:PHE:N	2.37	0.52
1:1A:581:C:H2'	1:1A:582:G:C8	2.45	0.51
1:1A:1495:A:H2'	1:1A:1496:A:C8	2.44	0.51
1:1A:2848:G:C8	15:1T:97:ALA:HB2	2.45	0.51
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.92	0.51
32:1a:407:G:H5"	35:1d:115:ARG:HD3	1.91	0.51
32:1a:431:A:H2'	32:1a:432:A:O4'	2.10	0.51
1:2A:106:C:H1'	20:2Y:1:MET:HE3	1.92	0.51
1:2A:117:G:OP2	1:2A:119:A:O2'	2.23	0.51
1:2A:524:U:H2'	1:2A:525:U:C6	2.45	0.51
14:2S:30:ARG:HE	14:2S:98:VAL:HG23	1.74	0.51
19:2X:5:TYR:OH	24:22:30:ARG:NH1	2.43	0.51
27:25:51:TYR:CE2	27:25:56:LYS:HD3	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:662:G:H2'	32:2a:663:A:H8	1.73	0.51
32:2a:790:A:OP1	55:2x:38:A:O2'	2.25	0.51
32:2a:1000:U:H2'	32:2a:1001:A:O4'	2.10	0.51
33:2b:8:LYS:HD2	33:2b:217:ARG:HB3	1.92	0.51
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.10	0.51
42:2k:108:ILE:HB	49:2r:87:ARG:HD2	1.90	0.51
48:2q:7:THR:OG1	48:2q:58:GLU:HG2	2.10	0.51
1:1A:192:C:O2'	1:1A:802:A:N3	2.42	0.51
11:1P:59:LEU:HD11	30:18:10:ALA:HA	1.91	0.51
11:1P:95:VAL:HB	11:1P:125:VAL:HG12	1.91	0.51
32:1a:1228:C:P	44:1m:108:ARG:HH22	2.33	0.51
39:1h:87:SER:CB	39:1h:93:VAL:H	2.24	0.51
1:2A:225:A:N6	1:2A:419:C:O2'	2.43	0.51
1:2A:1453:U:O2'	1:2A:1455:G:N7	2.43	0.51
1:2A:2712(A):A:OP2	62:2A:3962:HOH:O	2.19	0.51
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.43	0.51
3:2D:121:PRO:HB3	3:2D:135:PHE:CE2	2.45	0.51
10:2O:66:LYS:N	10:2O:82:ASN:OD1	2.37	0.51
28:26:33:LYS:HB3	28:26:51:GLU:HB3	1.92	0.51
32:2a:722:A:C8	32:2a:724:G:H1'	2.45	0.51
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.91	0.51
54:2w:51:U:H2'	54:2w:52:G:C8	2.45	0.51
54:2y:58:A:O2'	54:2y:61:C:N4	2.44	0.51
1:1A:534:U:H2'	1:1A:535:C:C6	2.45	0.51
1:1A:586:A:H5'	5:1F:89:VAL:HG21	1.91	0.51
1:1A:668:G:H5'	1:1A:669:G:OP2	2.09	0.51
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.92	0.51
1:1A:2135:A:N6	1:1A:2155:G:H22	2.09	0.51
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	1.92	0.51
26:14:50:VAL:HG21	44:1m:64:TRP:C	2.35	0.51
32:1a:925:G:H1'	32:1a:1502:A:C4	2.46	0.51
34:1c:172:ARG:HE	34:1c:203:PHE:HE2	1.56	0.51
42:1k:54:ARG:NH1	54:1y:39:PSU:O3'	2.43	0.51
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.91	0.51
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.10	0.51
3:2D:145:VAL:HG13	3:2D:191:ALA:HB2	1.92	0.51
6:2G:41:GLN:O	6:2G:43:LEU:N	2.44	0.51
6:2G:173:LEU:O	6:2G:178:PHE:N	2.42	0.51
8:2I:107:VAL:HG12	8:2I:108:THR:H	1.74	0.51
12:2Q:12:GLN:HE21	12:2Q:72:LYS:HG3	1.75	0.51
20:2Y:6:HIS:HB2	20:2Y:85:VAL:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:56:U:H2'	32:2a:57:G:C8	2.45	0.51
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.43	0.51
1:1A:531:C:H4'	1:1A:532:A:H5"	1.92	0.51
1:1A:1371:G:H2'	1:1A:1372:U:H5	1.75	0.51
1:1A:1374:G:H2'	1:1A:1375:C:C6	2.46	0.51
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.91	0.51
62:1A:4612:HOH:O	13:1R:15:SER:HB3	2.09	0.51
2:1B:91:C:OP2	12:1Q:16:ARG:NH1	2.43	0.51
18:1W:46:PHE:O	18:1W:50:VAL:HG23	2.10	0.51
32:1a:373:A:H2'	32:1a:374:A:C8	2.42	0.51
32:1a:1125:U:H4'	41:1j:5:ARG:HH22	1.75	0.51
32:1a:1179:A:H4'	40:1i:103:THR:HA	1.91	0.51
33:1b:28:PHE:CD1	33:1b:190:THR:HA	2.46	0.51
44:1m:30:ALA:O	44:1m:34:LEU:HG	2.11	0.51
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.93	0.51
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.75	0.51
1:2A:2126:A:H61	1:2A:2162:G:HO2'	1.54	0.51
1:2A:2361:A:OP2	30:28:26:LYS:NZ	2.41	0.51
5:2F:149:ASP:OD1	5:2F:151:SER:OG	2.22	0.51
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.40	0.51
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.26	0.51
32:2a:1352:C:P	52:2u:3:LYS:HZ1	2.33	0.51
50:2s:53:ASN:HB2	50:2s:77:THR:HA	1.92	0.51
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.46	0.51
8:2I:56:LYS:C	8:2I:58:LEU:H	2.17	0.51
17:2V:40:LEU:HB2	17:2V:46:VAL:HG12	1.93	0.51
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.24	0.51
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.26	0.51
34:2c:152:ILE:HD11	34:2c:199:LYS:HZ2	1.75	0.51
55:2x:21:A:N6	55:2x:46:G:H2'	2.24	0.51
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.76	0.51
1:1A:2596:U:OP1	62:1A:4165:HOH:O	2.19	0.51
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.46	0.51
12:1Q:77:LYS:HG2	12:1Q:81:VAL:HG21	1.93	0.51
32:1a:254:G:O2'	48:1q:16:GLN:O	2.29	0.51
32:1a:310:G:H4'	47:1p:31:LYS:HE3	1.92	0.51
32:1a:757:U:H2'	32:1a:758:G:O4'	2.11	0.51
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.45	0.51
1:2A:1856:G:H1	1:2A:1886:C:H42	1.59	0.51
1:2A:2100:G:H1	1:2A:2189:U:H3	1.58	0.51
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.45	0.51
6:2G:29:TRP:O	6:2G:33:ARG:NH1	2.39	0.51
12:2Q:16:ARG:HG2	12:2Q:18:LYS:HE2	1.92	0.51
32:2a:301:G:H2'	32:2a:302:G:C8	2.45	0.51
32:2a:775:G:N2	32:2a:804:U:O4	2.43	0.51
41:2j:47:PHE:HB2	41:2j:63:PHE:HB2	1.92	0.51
1:1A:2773:C:H2'	1:1A:2774:C:H6	1.75	0.51
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.46	0.51
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.35	0.51
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.93	0.51
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.44	0.51
39:1h:86:ILE:HG22	39:1h:93:VAL:HG21	1.92	0.51
44:1m:53:VAL:HG12	44:1m:57:ARG:HH12	1.75	0.51
1:2A:2136:C:N4	1:2A:2155:G:N1	2.59	0.51
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.44	0.51
10:2O:107:ARG:HG2	10:2O:115:VAL:HG11	1.92	0.51
32:2a:109:A:C6	32:2a:326:G:C6	2.99	0.51
32:2a:978:A:H4'	32:2a:1322:C:N3	2.25	0.51
32:2a:1004:A:N1	32:2a:1037:C:H1'	2.25	0.51
33:2b:16:HIS:C	33:2b:18:GLY:H	2.17	0.51
50:2s:20:LEU:HA	50:2s:23:ASN:HD22	1.75	0.51
1:1A:1138:G:N3	9:1N:106:MET:HE2	2.26	0.51
2:1B:2:C:H2'	2:1B:3:C:C6	2.46	0.51
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.74	0.51
8:1I:109:ILE:HD12	8:1I:130:TYR:OH	2.11	0.51
23:11:77:ALA:HB1	23:11:82:LEU:HD11	1.92	0.51
32:1a:1144:G:N2	32:1a:1146:A:H62	2.08	0.51
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.46	0.51
37:1f:45:LEU:HD12	37:1f:59:TYR:CD1	2.45	0.51
43:1l:7:ILE:HD13	43:1l:10:LEU:HD12	1.92	0.51
54:1w:18:G:O2'	54:1w:57:G:N2	2.29	0.51
1:2A:185:U:H2'	1:2A:186:G:C8	2.46	0.51
1:2A:731:C:H5"	62:2A:3992:HOH:O	2.10	0.51
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.32	0.51
15:2T:59:THR:HG23	15:2T:78:LEU:HB3	1.93	0.51
32:2a:427:U:OP1	35:2d:13:ARG:NH1	2.40	0.51
32:2a:921:U:O2'	36:2e:19:MET:O	2.29	0.51
32:2a:1068:G:N2	32:2a:1191:A:N3	2.53	0.51
33:2b:54:THR:HG22	33:2b:199:TYR:HB3	1.92	0.51
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.91	0.51
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:128:ARG:NH2	55:2x:33:U:OP2	2.44	0.51
1:1A:1448:G:O2'	1:1A:1528(A):A:N1	2.44	0.51
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.26	0.51
22:10:50:ASN:HB3	22:10:63:VAL:HG13	1.93	0.51
32:1a:820:U:H4'	32:1a:821:G:OP2	2.10	0.51
9:2N:39:ARG:HE	9:2N:48:MET:HE2	1.76	0.51
21:2Z:40:ASP:OD2	21:2Z:42:VAL:HG13	2.10	0.51
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.44	0.51
23:21:24:ALA:HB3	23:21:27:GLU:HG3	1.93	0.51
26:24:13:ARG:HB3	26:24:15:ILE:HD11	1.93	0.51
30:28:4:MET:HE3	30:28:63:PRO:HG3	1.93	0.51
32:2a:636:U:H2'	32:2a:637:G:C8	2.46	0.51
32:2a:1106:G:H5"	34:2c:172:ARG:HB3	1.91	0.51
32:2a:1386:G:C2	32:2a:1387:G:C8	2.99	0.51
34:2c:83:ARG:C	34:2c:85:ARG:H	2.19	0.51
35:2d:15:GLU:CD	35:2d:59:ARG:HH12	2.18	0.51
40:2i:3:GLN:NE2	40:2i:20:ARG:HD2	2.26	0.51
44:2m:4:ILE:HG23	44:2m:22:ILE:HD11	1.93	0.51
1:1A:26:G:C6	1:1A:27:G:N1	2.79	0.51
1:1A:86:C:H4'	1:1A:104:U:H1'	1.93	0.51
1:1A:1077:A:H2'	1:1A:1078:U:H4'	1.93	0.51
1:1A:1843:C:H5'	3:1D:253:GLN:OE1	2.10	0.51
2:1B:102:A:OP2	62:1B:303:HOH:O	2.18	0.51
28:16:53:LYS:NZ	54:1y:1:G:OP1	2.41	0.51
32:1a:116:A:H61	32:1a:313:A:H1'	1.76	0.51
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.11	0.51
43:1l:77:LEU:HD21	43:1l:107:ALA:HB2	1.92	0.51
1:2A:506:G:O3'	1:2A:507:A:H8	1.94	0.51
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.46	0.51
12:2Q:19:GLY:O	12:2Q:98:LYS:HE2	2.10	0.51
21:2Z:61:LEU:HB2	21:2Z:65:GLN:HB2	1.92	0.51
32:2a:520:A:N1	32:2a:536:C:H1'	2.26	0.51
32:2a:1330:U:H4'	44:2m:23:TYR:CZ	2.46	0.51
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.26	0.51
32:2a:1456:G:N2	51:2t:43:LEU:HD11	2.26	0.51
34:2c:47:LEU:O	34:2c:51:GLY:N	2.44	0.51
35:2d:90:GLY:HA3	35:2d:200:GLU:HG3	1.93	0.51
1:1A:376:C:H2'	1:1A:377:C:C6	2.47	0.50
1:1A:668:G:N7	62:1A:4217:HOH:O	2.35	0.50
1:1A:801:G:OP2	62:1A:4166:HOH:O	2.19	0.50
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2848:G:H8	15:1T:97:ALA:HB2	1.76	0.50
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.46	0.50
18:1W:29:LEU:HG	18:1W:33:ARG:HD2	1.92	0.50
32:1a:568:G:O2'	62:1a:1914:HOH:O	2.19	0.50
37:1f:33:TYR:OH	37:1f:78:GLU:HG3	2.11	0.50
46:1o:26:GLU:HG3	46:1o:81:LEU:HD13	1.92	0.50
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.46	0.50
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.92	0.50
35:2d:112:VAL:HG22	35:2d:116:GLN:HE22	1.76	0.50
39:2h:121:ASP:OD2	39:2h:125:ARG:NH2	2.39	0.50
40:2i:17:VAL:HG11	40:2i:81:ILE:HA	1.94	0.50
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.93	0.50
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.93	0.50
32:1a:663:A:O3'	49:1r:64:ARG:NH2	2.41	0.50
32:1a:674:G:H2'	32:1a:675:A:C8	2.47	0.50
32:1a:839:U:H3'	32:1a:840:C:H5'	1.94	0.50
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.46	0.50
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.46	0.50
32:2a:67:C:H2'	32:2a:68:G:C8	2.46	0.50
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.47	0.50
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.46	0.50
35:2d:22:LYS:HG3	61:2d:303:SF4:S4	2.52	0.50
1:1A:729:G:C8	3:1D:208:LYS:HD2	2.47	0.50
1:1A:1053:C:H42	1:1A:1106:G:H1	1.57	0.50
1:1A:1411:C:H2'	1:1A:1412:A:H8	1.76	0.50
1:1A:2598:A:OP2	62:1A:4164:HOH:O	2.19	0.50
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.93	0.50
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.09	0.50
32:1a:1456:G:O3'	51:1t:39:LYS:NZ	2.38	0.50
43:1l:54:LYS:H	43:1l:54:LYS:HD2	1.75	0.50
1:2A:1327:C:O2'	13:2R:105:ARG:NH1	2.37	0.50
1:2A:2418:A:OP1	30:28:29:LYS:NZ	2.43	0.50
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.25	0.50
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	1.93	0.50
6:2G:133:LEU:HG	6:2G:157:ILE:HG13	1.93	0.50
24:22:10:LEU:O	24:22:14:ARG:HG3	2.12	0.50
32:2a:1139:G:N2	32:2a:1142:G:O6	2.42	0.50
33:2b:73:THR:OG1	33:2b:170:GLU:OE2	2.26	0.50
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.44	0.50
37:2f:14:LEU:HD21	37:2f:84:ASN:ND2	2.27	0.50
51:2t:98:PRO:O	51:2t:99:LEU:HB2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:2:G:H2'	55:2x:3:C:H6	1.77	0.50
1:1A:652(C):G:N2	1:1A:653:A:H1'	2.26	0.50
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.11	0.50
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.93	0.50
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.11	0.50
32:1a:576:G:O6	32:1a:880:C:O2'	2.23	0.50
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.47	0.50
32:1a:1132:C:H2'	32:1a:1133:G:H8	1.75	0.50
1:2A:251:A:C5	1:2A:252:G:H1'	2.47	0.50
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.47	0.50
14:2S:48:LEU:HD23	14:2S:82:ILE:HD11	1.92	0.50
32:2a:399:G:H2'	32:2a:400:C:C6	2.47	0.50
32:2a:590:C:OP1	39:2h:30:ARG:N	2.36	0.50
32:2a:1085:U:H3'	32:2a:1086:U:C5	2.46	0.50
32:2a:1089:G:H1	32:2a:1096:C:H42	1.59	0.50
38:2g:42:ILE:HG22	38:2g:120:ILE:HD12	1.93	0.50
50:2s:14:HIS:O	50:2s:18:LYS:HG3	2.10	0.50
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.10	0.50
7:1H:108:GLY:HA3	7:1H:152:ARG:HH21	1.75	0.50
8:1I:77:LEU:HD23	8:1I:97:ILE:HG23	1.94	0.50
26:14:37:SER:HB2	26:14:43:TYR:CE1	2.47	0.50
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.77	0.50
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.47	0.50
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.11	0.50
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.11	0.50
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.46	0.50
3:2D:5:LYS:HG2	3:2D:17:THR:HG22	1.93	0.50
11:2P:59:LEU:HD21	30:28:10:ALA:HB2	1.94	0.50
11:2P:87:ASP:O	11:2P:90:ARG:NH1	2.42	0.50
12:2Q:68:ILE:HD13	12:2Q:103:MET:HG2	1.93	0.50
30:28:22:VAL:HB	30:28:55:ALA:HB1	1.94	0.50
32:2a:736:C:H2'	32:2a:737:A:C8	2.46	0.50
50:2s:66:MET:HB2	50:2s:74:PHE:CZ	2.47	0.50
55:2x:55:PSU:O2'	55:2x:57:A:N7	2.42	0.50
1:1A:581:C:H2'	1:1A:582:G:H8	1.77	0.50
32:1a:1246:C:H42	32:1a:1291:G:H1	1.60	0.50
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.46	0.50
1:2A:668:G:H5'	1:2A:669:G:OP2	2.11	0.50
1:2A:1959:G:OP2	62:2A:3965:HOH:O	2.20	0.50
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.12	0.50
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.45	0.50
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.47	0.50
7:2H:75:ALA:O	7:2H:79:VAL:HG22	2.12	0.50
12:2Q:85:LYS:HG2	22:20:7:LEU:HB2	1.93	0.50
32:2a:448:A:P	32:2a:485:G:H22	2.34	0.50
37:2f:25:ILE:HD12	37:2f:82:ARG:HD2	1.94	0.50
54:2w:52:G:H1	54:2w:62:C:N4	2.10	0.50
1:1A:271(K):U:O2'	1:1A:271(M):G:N2	2.40	0.50
1:1A:285:C:H2'	1:1A:286:C:C6	2.47	0.50
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.75	0.50
1:1A:2812:G:H2'	1:1A:2813:A:H8	1.76	0.50
6:1G:43:LEU:O	6:1G:45:GLU:N	2.43	0.50
7:1H:56:SER:HB3	7:1H:61:HIS:ND1	2.26	0.50
12:1Q:110:THR:HB	12:1Q:113:GLN:HG3	1.94	0.50
21:1Z:104:PHE:HA	21:1Z:139:VAL:HG23	1.94	0.50
33:1b:230:VAL:HG12	33:1b:231:GLU:H	1.76	0.50
48:1q:64:PRO:HB3	48:1q:70:ARG:HH11	1.75	0.50
48:1q:64:PRO:HB3	48:1q:70:ARG:NH1	2.26	0.50
1:2A:1645:G:H5"	1:2A:1646:C:H5'	1.94	0.50
1:2A:2532:G:N2	1:2A:2663:G:O2'	2.45	0.50
1:2A:2570:G:H2'	1:2A:2571:C:O4'	2.12	0.50
3:2D:36:PRO:HA	3:2D:61:LEU:HD23	1.94	0.50
4:2E:98:PRO:HG3	4:2E:174:ASP:HA	1.93	0.50
12:2Q:32:TYR:OH	12:2Q:111:GLU:OE2	2.22	0.50
32:2a:1289:A:H3'	32:2a:1290:G:H8	1.77	0.50
35:2d:92:VAL:O	35:2d:96:LEU:HD22	2.11	0.50
41:2j:49:VAL:HG22	41:2j:50:ILE:O	2.11	0.50
55:2x:51:C:H2'	55:2x:52:G:H8	1.77	0.50
1:1A:95:G:H4'	24:12:45:SER:O	2.11	0.50
1:1A:2350:C:OP2	62:1A:4167:HOH:O	2.20	0.50
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.46	0.50
32:1a:17:U:H2'	32:1a:18:C:C6	2.47	0.50
54:1y:2:C:H2'	54:1y:3:C:C6	2.47	0.50
1:2A:2286:A:OP1	28:26:29:ASN:ND2	2.45	0.50
5:2F:112:MET:HA	5:2F:115:ALA:HB3	1.94	0.50
28:26:23:THR:OG1	28:26:24:GLU:N	2.45	0.50
32:2a:34:C:H2'	32:2a:35:G:H8	1.77	0.50
32:2a:1261:A:H5'	32:2a:1284:C:OP1	2.12	0.50
1:1A:1062:G:H5"	1:1A:1070:A:H1'	1.93	0.50
1:1A:1665:A:H4'	10:1O:67:LYS:HB2	1.92	0.50
2:1B:14:U:OP2	2:1B:70:C:O2'	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:70:TRP:CE2	3:1D:150:LYS:HD2	2.47	0.50
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.94	0.50
32:1a:982:U:H4'	32:1a:983:A:O5'	2.12	0.50
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.94	0.50
32:1a:1298:C:H2'	38:1g:114:ARG:NH1	2.27	0.50
33:1b:80:ILE:HD12	33:1b:211:ILE:HG22	1.93	0.50
43:1l:117:ARG:HB3	43:1l:122:THR:HB	1.94	0.50
1:2A:946:G:H2'	1:2A:947:G:H8	1.75	0.50
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.27	0.50
32:2a:460:G:OP2	62:2a:1908:HOH:O	2.20	0.50
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.46	0.50
32:2a:1267:C:H1'	52:2u:20:LYS:HE3	1.94	0.50
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.12	0.50
38:2g:62:PHE:HA	38:2g:124:LEU:HD21	1.92	0.50
1:1A:511:U:OP2	62:1A:4169:HOH:O	2.20	0.49
1:1A:1342:A:O2'	1:1A:1344:G:OP2	2.26	0.49
1:1A:1720:U:H2'	1:1A:1721:G:O4'	2.12	0.49
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.11	0.49
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.12	0.49
6:1G:122:PRO:HB3	6:1G:170:ARG:NH1	2.27	0.49
8:1I:6:LEU:HG	8:1I:36:ALA:HA	1.94	0.49
8:1I:100:ALA:HA	8:1I:103:ARG:HH11	1.76	0.49
17:1V:59:ALA:HB2	17:1V:96:ILE:HD13	1.94	0.49
32:1a:78:G:C6	32:1a:91:C:N4	2.79	0.49
32:1a:444:C:H2'	32:1a:445:G:C8	2.47	0.49
32:1a:1006:C:H2'	32:1a:1007:C:C6	2.47	0.49
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.34	0.49
34:1c:130:VAL:HG11	34:1c:157:ILE:HG12	1.94	0.49
38:1g:114:ARG:HB2	38:1g:115:ARG:HE	1.77	0.49
39:1h:83:ILE:HG13	39:1h:137:VAL:HG22	1.94	0.49
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.47	0.49
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.30	0.49
26:24:62:ARG:HA	26:24:62:ARG:HE	1.77	0.49
36:2e:152:ARG:HB3	39:2h:43:GLY:HA3	1.94	0.49
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.77	0.49
54:2w:51:U:H2'	54:2w:52:G:H8	1.77	0.49
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.11	0.49
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.93	0.49
16:1U:74:LEU:HD12	16:1U:74:LEU:H	1.77	0.49
32:1a:1073:U:H2'	32:1a:1074:G:H8	1.77	0.49
32:1a:1142:G:H2'	32:1a:1143:G:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1y:36:A:H2'	54:1y:37:MIA:O4'	2.12	0.49
1:2A:185:U:H2'	1:2A:186:G:H8	1.77	0.49
1:2A:234:C:H2'	1:2A:235:U:C6	2.47	0.49
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.47	0.49
1:2A:1908:C:O2	55:2x:12:G:H4'	2.13	0.49
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.93	0.49
32:2a:141:A:H1'	32:2a:182:U:O2	2.12	0.49
32:2a:792:A:H4'	32:2a:793:U:C5'	2.42	0.49
32:2a:919:A:O2'	32:2a:1080:A:N1	2.45	0.49
32:2a:1033:G:H2'	32:2a:1034:G:H8	1.78	0.49
32:2a:1138:G:O2'	32:2a:1140:C:OP1	2.30	0.49
32:2a:1400:5MC:H6	32:2a:1400:5MC:H5"	1.77	0.49
34:2c:22:TRP:CH2	34:2c:32:LEU:HB3	2.46	0.49
36:2e:102:ALA:HB2	36:2e:120:THR:HG21	1.94	0.49
54:2y:52:G:H1	54:2y:62:C:N4	2.09	0.49
1:1A:763:G:OP1	62:1A:4168:HOH:O	2.20	0.49
1:1A:855:G:O2'	22:10:27:GLU:OE2	2.25	0.49
6:1G:12:TYR:HA	6:1G:16:ARG:HD3	1.94	0.49
32:1a:401:C:H2'	32:1a:402:G:C8	2.47	0.49
43:1l:42:THR:HA	43:1l:53:ARG:O	2.12	0.49
47:1p:45:THR:C	47:1p:47:ASP:H	2.19	0.49
1:2A:774:A:H2'	1:2A:774:A:N3	2.27	0.49
1:2A:1952:A:N3	10:2O:22:ILE:HD12	2.26	0.49
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.47	0.49
1:2A:2452:C:N3	56:2z:2:ARG:NH1	2.60	0.49
4:2E:170:LEU:HD22	4:2E:185:LYS:O	2.11	0.49
20:2Y:29:GLU:HB3	20:2Y:38:ILE:HG13	1.95	0.49
21:2Z:31:ARG:NH1	21:2Z:94:GLU:HG2	2.27	0.49
32:2a:222:U:H2'	32:2a:223:U:H6	1.77	0.49
32:2a:952:U:H2'	32:2a:953:G:C8	2.48	0.49
50:2s:28:LYS:HB3	50:2s:29:ARG:CB	2.42	0.49
1:1A:1740:G:H2'	1:1A:1741:A:C8	2.48	0.49
1:1A:2633:G:H2'	1:1A:2634:G:O4'	2.12	0.49
1:1A:2784:C:H2'	1:1A:2785:C:H6	1.78	0.49
4:1E:32:PRO:HA	4:1E:90:THR:HA	1.94	0.49
22:10:70:GLN:OE1	22:10:72:ARG:HD2	2.12	0.49
32:1a:279:A:C5	48:1q:98:LEU:HD23	2.48	0.49
32:1a:1355:G:H2'	32:1a:1356:G:C8	2.48	0.49
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.47	0.49
1:2A:1539:G:H2'	1:2A:1540:U:O4'	2.12	0.49
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1747:G:H2'	1:2A:1747(A):G:H8	1.77	0.49
8:2I:40:THR:HG1	8:2I:41:GLU:H	1.50	0.49
12:2Q:77:LYS:NZ	12:2Q:84:GLY:O	2.35	0.49
27:25:8:LYS:HG3	27:25:9:LYS:HG2	1.93	0.49
33:2b:16:HIS:ND1	33:2b:204:ASN:HB3	2.28	0.49
33:2b:76:GLN:HG3	33:2b:206:ASP:O	2.13	0.49
38:2g:70:LYS:HG2	38:2g:96:GLN:HG2	1.94	0.49
38:2g:118:VAL:HG13	38:2g:122:HIS:CE1	2.48	0.49
39:2h:64:LYS:HD2	39:2h:79:VAL:HG21	1.94	0.49
41:2j:8:LEU:HB3	41:2j:96:ILE:HG23	1.93	0.49
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.77	0.49
48:2q:62:SER:HB3	48:2q:72:ARG:HE	1.77	0.49
1:1A:1070:A:H5"	1:1A:1072:C:OP1	2.13	0.49
3:1D:169:GLU:OE2	3:1D:184:LYS:NZ	2.38	0.49
12:1Q:81:VAL:HG12	22:10:5:LYS:HD3	1.94	0.49
15:1T:126:ALA:O	15:1T:129:ARG:HB2	2.11	0.49
32:1a:130:A:O2'	32:1a:131:C:O5'	2.28	0.49
32:1a:620:C:C2	35:1d:135:LEU:HD13	2.48	0.49
32:1a:971:G:N2	32:1a:1363(A):A:OP2	2.41	0.49
43:1l:70:ILE:HD13	43:1l:77:LEU:HD12	1.94	0.49
54:1w:7:A:N6	54:1w:66:U:H3	2.11	0.49
32:2a:165:C:H2'	32:2a:166:G:H8	1.76	0.49
32:2a:1103:C:H2'	32:2a:1104:G:C8	2.47	0.49
36:2e:136:MET:HA	36:2e:139:LEU:HD12	1.94	0.49
41:2j:42:THR:HG22	41:2j:66:ARG:HB3	1.95	0.49
43:2l:55:VAL:HG12	43:2l:56:ALA:H	1.77	0.49
55:2x:51:C:H2'	55:2x:52:G:C8	2.48	0.49
1:1A:657:U:H2'	1:1A:658:C:C6	2.47	0.49
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.47	0.49
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.42	0.49
32:1a:256:U:P	48:1q:17:LYS:HZ2	2.36	0.49
32:1a:384:G:H2'	32:1a:385:C:C6	2.47	0.49
32:1a:865:A:H2	32:1a:918:A:H4'	1.78	0.49
32:1a:946:A:H2'	32:1a:947:G:C8	2.48	0.49
36:1e:87:SER:OG	36:1e:125:SER:O	2.30	0.49
51:1t:33:ILE:O	51:1t:37:SER:OG	2.21	0.49
1:2A:531:C:OP1	1:2A:561:G:N1	2.44	0.49
1:2A:2470:G:O6	1:2A:2481:G:N2	2.45	0.49
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.13	0.49
2:2B:17:C:H2'	2:2B:18:G:O4'	2.12	0.49
12:2Q:2:LEU:HD12	12:2Q:47:ILE:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:1:MET:SD	24:22:56:GLN:NE2	2.86	0.49
32:2a:224:C:H2'	32:2a:225:C:C6	2.48	0.49
32:2a:1005:A:H5"	32:2a:1006:C:C5	2.47	0.49
32:2a:1239:A:H62	32:2a:1299:A:N6	2.11	0.49
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.13	0.49
47:2p:4:ILE:HG12	47:2p:21:VAL:HG12	1.95	0.49
54:2w:68:C:H2'	54:2w:69:G:H8	1.76	0.49
1:1A:919:G:N2	1:1A:2269:A:OP2	2.46	0.49
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.12	0.49
14:1S:35:ILE:HG12	14:1S:101:LEU:HD12	1.94	0.49
14:1S:71:ARG:NH1	14:1S:107:GLU:OE2	2.46	0.49
42:1k:45:GLY:O	42:1k:50:TYR:HB2	2.13	0.49
1:2A:11:G:H8	1:2A:11:G:OP2	1.95	0.49
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.43	0.49
8:2I:26:ALA:HB1	8:2I:31:LEU:HD13	1.95	0.49
13:2R:33:ARG:HA	13:2R:114:VAL:O	2.13	0.49
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.95	0.49
32:2a:1073:U:H3	32:2a:1102:A:H61	1.60	0.49
33:2b:223:ILE:O	33:2b:226:ARG:HG2	2.11	0.49
34:2c:129:ALA:HB3	34:2c:132:ARG:HD2	1.94	0.49
35:2d:176:LEU:HD12	35:2d:177:ASP:H	1.78	0.49
38:2g:149:ARG:HG3	38:2g:152:ALA:HB2	1.94	0.49
44:2m:4:ILE:HG13	44:2m:5:ALA:N	2.27	0.49
1:1A:7:G:H2'	1:1A:8:A:H8	1.77	0.49
1:1A:234:C:H2'	1:1A:235:U:H6	1.78	0.49
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.47	0.49
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.48	0.49
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.30	0.49
26:14:58:ARG:O	26:14:60:GLN:N	2.46	0.49
27:15:42:PRO:HB2	27:15:43:HIS:ND1	2.28	0.49
32:1a:297:G:H4'	32:1a:557:G:H4'	1.94	0.49
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.13	0.49
34:1c:172:ARG:NH2	34:1c:206:GLU:OE2	2.46	0.49
39:1h:82:HIS:CE1	39:1h:84:ARG:HB2	2.47	0.49
47:1p:55:ARG:HH21	47:1p:59:TRP:NE1	2.10	0.49
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.45	0.49
55:1x:23:C:H2'	55:1x:24:U:C6	2.48	0.49
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.12	0.49
1:2A:868:U:C4	1:2A:869:G:N7	2.81	0.49
1:2A:1120:G:O6	62:2A:3954:HOH:O	2.18	0.49
1:2A:1653:G:H8	1:2A:1653:G:OP2	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.13	0.49
21:2Z:4:ARG:HG2	21:2Z:58:VAL:HB	1.95	0.49
32:2a:142:G:H2'	32:2a:143:A:H8	1.77	0.49
32:2a:707:C:H2'	32:2a:708:C:C6	2.48	0.49
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.46	0.49
33:2b:16:HIS:CE1	33:2b:204:ASN:H	2.31	0.49
35:2d:101:LEU:HA	35:2d:104:VAL:HG22	1.95	0.49
37:2f:16:GLN:CD	37:2f:16:GLN:H	2.20	0.49
1:1A:1512:U:H2'	1:1A:1513:C:H6	1.78	0.49
1:1A:2376:A:N3	14:1S:106:ARG:NH2	2.57	0.49
30:18:26:LYS:HD2	30:18:48:PHE:CD2	2.48	0.49
32:1a:1036:G:H3'	32:1a:1037:C:C6	2.48	0.49
1:2A:35:G:H1'	1:2A:454:A:C4	2.48	0.49
1:2A:971:C:H2'	1:2A:972:G:O4'	2.13	0.49
1:2A:1814:G:O6	62:2A:3966:HOH:O	2.20	0.49
1:2A:2131:G:C8	1:2A:2133:G:C2	3.00	0.49
1:2A:2506:U:O2'	54:2w:76:A:H4'	2.13	0.49
32:2a:90:U:H2'	32:2a:91:C:C6	2.48	0.49
32:2a:505:G:H2'	32:2a:506:G:C8	2.48	0.49
32:2a:524:G:H2'	32:2a:525:C:C6	2.48	0.49
32:2a:1206:G:O2'	34:2c:193:TYR:HA	2.12	0.49
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.77	0.49
1:1A:651:G:H4'	30:18:18:ALA:HB3	1.95	0.49
1:1A:2319:G:H22	14:1S:3:ARG:NE	2.11	0.49
4:1E:97:LYS:N	4:1E:100:GLU:OE2	2.29	0.49
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.48	0.49
31:19:27:CYS:SG	31:19:28:GLU:N	2.86	0.49
32:1a:176:C:H2'	32:1a:177:C:C6	2.45	0.49
32:1a:520:A:N1	32:1a:536:C:H1'	2.27	0.49
32:1a:662:G:H2'	32:1a:663:A:C8	2.48	0.49
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.12	0.49
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.47	0.49
1:2A:839:U:H2'	1:2A:840:C:C6	2.48	0.49
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.45	0.49
1:2A:2697:G:H2'	1:2A:2698:U:O4'	2.13	0.49
9:2N:68:GLU:HG3	9:2N:88:GLU:OE1	2.13	0.49
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.20	0.49
32:2a:376:G:OP2	47:2p:67:THR:HG21	2.13	0.49
32:2a:401:C:H2'	32:2a:402:G:H8	1.78	0.49
32:2a:1128:C:H1'	32:2a:1147:C:N4	2.21	0.49
32:2a:1132:C:H2'	32:2a:1133:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:108:LEU:HD21	35:2d:174:LEU:HB3	1.95	0.49
48:2q:68:ARG:H	48:2q:70:ARG:NH1	2.10	0.49
1:1A:2183:C:O2'	1:1A:2184:G:OP1	2.31	0.48
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.13	0.48
21:1Z:11:GLU:HA	21:1Z:36:LYS:HE2	1.95	0.48
32:1a:189(D):C:H2'	32:1a:189(E):U:O4'	2.13	0.48
32:1a:461:A:O2'	32:1a:470:C:H5'	2.13	0.48
32:1a:626:U:H5'	47:1p:38:TYR:CD2	2.48	0.48
35:1d:172:PRO:C	35:1d:174:LEU:H	2.21	0.48
48:1q:41:LYS:HD3	48:1q:88:TYR:CE1	2.48	0.48
1:2A:140:G:N3	1:2A:142:A:N6	2.57	0.48
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.13	0.48
1:2A:576:U:H2'	1:2A:577:G:C8	2.48	0.48
1:2A:699:A:H2'	1:2A:700:G:O4'	2.13	0.48
1:2A:903:C:H2'	1:2A:904:C:C6	2.48	0.48
1:2A:1183:G:H5"	25:23:30:ARG:NH2	2.27	0.48
1:2A:1639:U:C2'	1:2A:1640:C:H5"	2.43	0.48
1:2A:2313:C:H2'	1:2A:2314:C:H6	1.79	0.48
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.78	0.48
12:2Q:48:GLU:O	12:2Q:52:VAL:HG23	2.13	0.48
32:2a:441:A:H3'	32:2a:442:C:H6	1.78	0.48
35:2d:51:PRO:HB2	35:2d:56:VAL:HG22	1.95	0.48
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.95	0.48
37:2f:35:ALA:HB2	37:2f:67:MET:HE2	1.94	0.48
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.77	0.48
47:2p:67:THR:O	47:2p:71:ARG:N	2.41	0.48
1:1A:1047:G:O2'	1:1A:1048:A:H8	1.96	0.48
1:1A:1057:A:H61	1:1A:1081:U:H3	1.61	0.48
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.13	0.48
1:1A:2393:A:H5"	11:1P:63:PRO:HB3	1.96	0.48
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.95	0.48
32:1a:999:C:H2'	32:1a:1000:U:O4'	2.12	0.48
35:1d:149:ALA:HB3	35:1d:152:SER:HB2	1.95	0.48
1:2A:479:A:H4'	1:2A:480:A:H5'	1.94	0.48
1:2A:1042:G:H3'	1:2A:1043:C:C6	2.48	0.48
1:2A:2831:G:OP1	1:2A:2834:G:H4'	2.14	0.48
4:2E:34:VAL:HB	4:2E:48:GLN:HE21	1.77	0.48
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.95	0.48
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.94	0.48
7:2H:92:ILE:H	7:2H:92:ILE:HD12	1.77	0.48
9:2N:17:ASP:HB2	9:2N:137:LYS:HE3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.93	0.48
32:2a:9:G:H2'	32:2a:10:A:H8	1.77	0.48
32:2a:17:U:H2'	32:2a:18:C:C6	2.48	0.48
32:2a:578:C:H2'	32:2a:579:G:H8	1.77	0.48
32:2a:789:U:O2'	32:2a:791:G:N7	2.41	0.48
32:2a:1059:C:O2'	45:2n:45:ARG:NH1	2.46	0.48
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.49	0.48
32:2a:1359:C:OP1	45:2n:22:THR:OG1	2.22	0.48
34:2c:47:LEU:HD22	34:2c:70:VAL:HG11	1.95	0.48
36:2e:139:LEU:C	36:2e:141:GLN:H	2.22	0.48
53:2v:23:A:C4'	53:2v:24:A:H5'	2.35	0.48
1:1A:876:C:H2'	1:1A:877:U:O4'	2.13	0.48
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.49	0.48
8:1I:72:LEU:C	8:1I:74:ASN:H	2.20	0.48
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	1.95	0.48
15:1T:39:ARG:NH2	32:1a:345:C:H5"	2.28	0.48
28:16:14:THR:HB	28:16:48:VAL:O	2.13	0.48
32:1a:19:C:OP1	36:1e:125:SER:OG	2.24	0.48
32:1a:390:C:H2'	32:1a:391:G:C8	2.47	0.48
32:1a:790:A:OP1	55:1x:38:A:O2'	2.32	0.48
32:1a:975:A:N6	41:1j:60:ARG:HH12	2.11	0.48
34:1c:150:LYS:HG3	34:1c:169:ALA:HB2	1.96	0.48
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.78	0.48
49:1r:58:LEU:HB2	49:1r:63:GLN:NE2	2.28	0.48
55:1x:71:C:H2'	55:1x:72:A:O4'	2.14	0.48
1:2A:996:A:OP2	16:2U:93:LYS:NZ	2.43	0.48
1:2A:1199:U:O2'	62:2A:3923:HOH:O	2.09	0.48
1:2A:2549:G:H2'	1:2A:2550:G:H8	1.77	0.48
2:2B:105:A:H5'	2:2B:106:G:OP2	2.13	0.48
32:2a:272:C:H2'	32:2a:273:A:H8	1.78	0.48
32:2a:407:G:H5"	35:2d:115:ARG:HB3	1.95	0.48
36:2e:51:VAL:HG13	36:2e:52:PRO:HD3	1.94	0.48
44:2m:91:ARG:HA	44:2m:96:LEU:HB2	1.95	0.48
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.78	0.48
54:2y:55:PSU:HN1	54:2y:57:G:C5'	2.26	0.48
1:1A:127:A:H5"	1:1A:128:C:C6	2.48	0.48
1:1A:603:A:H3'	11:1P:90:ARG:HH22	1.77	0.48
11:1P:39:LYS:HB2	11:1P:45:LEU:HD13	1.96	0.48
32:1a:625:G:H2'	32:1a:626:U:C6	2.48	0.48
32:1a:1136:U:H5"	32:1a:1137:C:N3	2.28	0.48
33:1b:174:VAL:HG13	33:1b:184:VAL:HG11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.94	0.48
48:1q:10:VAL:HA	48:1q:20:THR:O	2.13	0.48
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.48	0.48
1:2A:2306:C:N4	6:2G:42:GLY:O	2.46	0.48
4:2E:120:TRP:CD1	4:2E:155:LYS:HB3	2.48	0.48
9:2N:103:VAL:HG11	9:2N:120:LEU:HD22	1.95	0.48
10:2O:7:TYR:CE2	10:2O:20:MET:HB2	2.49	0.48
29:27:1:MET:N	29:27:1:MET:HE2	2.27	0.48
32:2a:757:U:H2'	32:2a:758:G:O4'	2.13	0.48
32:2a:971:G:N2	32:2a:1363(A):A:OP2	2.40	0.48
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.48	0.48
32:2a:1255:G:O3'	32:2a:1258:G:H1'	2.13	0.48
35:2d:155:LEU:HD22	35:2d:157:LEU:H	1.79	0.48
1:1A:762:U:OP1	62:1A:4170:HOH:O	2.20	0.48
1:1A:787:U:OP2	62:1A:4173:HOH:O	2.20	0.48
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.13	0.48
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.46	0.48
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.28	0.48
32:1a:682:G:N7	62:1a:1936:HOH:O	2.35	0.48
32:1a:1054:C:C5	54:1w:34:G:H1'	2.49	0.48
32:1a:1260:C:O5'	32:1a:1284:C:H4'	2.14	0.48
33:1b:97:TRP:CZ2	33:1b:102:LEU:HD13	2.47	0.48
51:1t:47:GLY:N	51:1t:48:LYS:HB2	2.27	0.48
1:2A:450:G:O6	62:2A:3945:HOH:O	2.19	0.48
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.11	0.48
2:2B:89:G:H2'	2:2B:90:A:C8	2.49	0.48
12:2Q:1:MET:SD	12:2Q:1:MET:N	2.63	0.48
32:2a:600:C:H2'	32:2a:601:C:C6	2.48	0.48
32:2a:792:A:H4'	32:2a:793:U:H5"	1.95	0.48
32:2a:1039:C:C2	32:2a:1040:U:H1'	2.49	0.48
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.46	0.48
42:2k:99:GLN:HG2	42:2k:105:VAL:HG11	1.95	0.48
54:2w:46:G7M:O2'	54:2w:47:U:H5'	2.14	0.48
1:1A:226:G:H21	1:1A:228:A:H62	1.61	0.48
1:1A:1090:U:H2'	1:1A:1091:G:O4'	2.14	0.48
1:1A:2069:G:OP2	62:1A:4172:HOH:O	2.20	0.48
1:1A:2695:C:H2'	1:1A:2696:U:H6	1.78	0.48
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.94	0.48
7:1H:127:GLU:HG2	7:1H:130:ARG:HB2	1.95	0.48
21:1Z:156:LYS:O	21:1Z:157:LEU:HB2	2.13	0.48
32:1a:673:G:H2'	32:1a:674:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:111:ARG:HD2	38:1g:123:GLU:HB2	1.96	0.48
1:2A:709:U:H2'	1:2A:710:G:C8	2.48	0.48
4:2E:147:PRO:HG2	4:2E:149:ARG:HG2	1.95	0.48
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.95	0.48
25:23:18:ASP:OD1	25:23:19:GLN:N	2.47	0.48
32:2a:254:G:N2	48:2q:16:GLN:OE1	2.34	0.48
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.49	0.48
32:2a:1080:A:H5'	36:2e:14:ARG:NH2	2.28	0.48
39:2h:60:ARG:HG2	39:2h:62:TYR:CZ	2.49	0.48
40:2i:47:LEU:HB3	40:2i:50:LEU:HD21	1.96	0.48
1:1A:747:U:O2	1:1A:2014:A:H1'	2.14	0.48
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.95	0.48
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.96	0.48
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.13	0.48
45:1n:2:ALA:HB1	45:1n:6:LEU:HG	1.95	0.48
1:2A:518:G:H4'	18:2W:18:ARG:NE	2.28	0.48
1:2A:1777:U:H2'	1:2A:1778:U:H6	1.77	0.48
7:2H:26:VAL:HG12	7:2H:79:VAL:HG21	1.94	0.48
11:2P:81:GLN:OE1	11:2P:106:LEU:HD12	2.14	0.48
17:2V:29:PRO:HA	17:2V:61:VAL:HG22	1.96	0.48
33:2b:20:GLU:HG3	33:2b:189:ASP:HB3	1.96	0.48
40:2i:11:LYS:H	40:2i:104:ARG:HH21	1.61	0.48
50:2s:3:ARG:HH11	50:2s:8:GLY:N	2.12	0.48
50:2s:67:VAL:O	50:2s:69:HIS:N	2.46	0.48
50:2s:80:TYR:O	50:2s:81:ARG:HG2	2.12	0.48
1:1A:81:G:H21	20:1Y:1:MET:HE2	1.79	0.48
1:1A:2206:G:H5"	1:1A:2207:G:N7	2.28	0.48
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.14	0.48
28:16:16:CYS:O	28:16:17:LYS:HB2	2.14	0.48
32:1a:405:U:P	35:1d:3:ARG:HH22	2.35	0.48
32:1a:848:C:H2'	32:1a:849:C:C6	2.49	0.48
32:1a:1025:U:O2	32:1a:1036:G:C6	2.67	0.48
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.95	0.48
54:1y:18:G:C2	54:1y:58:A:C5	3.02	0.48
1:2A:582:G:H2'	1:2A:583:G:C8	2.49	0.48
1:2A:787:U:OP2	62:2A:3961:HOH:O	2.19	0.48
1:2A:940:G:N3	1:2A:1191:G:H4'	2.29	0.48
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.13	0.48
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.14	0.48
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.48	0.48
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:14:ASP:N	8:2I:17:GLN:OE1	2.27	0.48
22:20:63:VAL:HG21	22:20:83:PRO:HG3	1.96	0.48
24:22:53:LEU:O	24:22:57:ILE:HG13	2.13	0.48
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.49	0.48
34:2c:112:SER:HB3	34:2c:115:LEU:HD22	1.96	0.48
42:2k:33:THR:HG22	42:2k:39:PRO:HA	1.95	0.48
44:2m:82:MET:HE2	44:2m:92:HIS:HB3	1.94	0.48
1:1A:1173:G:OP2	1:1A:1173:G:H2'	2.14	0.48
1:1A:1614:A:P	1:1A:1614:A:H8	2.37	0.48
1:1A:2711:A:N3	62:1A:4289:HOH:O	2.35	0.48
2:1B:11:C:H3'	2:1B:12:C:H6	1.77	0.48
3:1D:176:ARG:NH2	32:1a:713:G:OP1	2.37	0.48
6:1G:14:GLU:O	6:1G:17:PRO:HD2	2.13	0.48
21:1Z:52:SER:C	21:1Z:54:HIS:N	2.71	0.48
23:11:46:LEU:O	23:11:47:GLN:NE2	2.47	0.48
32:1a:1025:U:C2	32:1a:1036:G:O6	2.67	0.48
33:1b:19:HIS:CE1	33:1b:20:GLU:HG3	2.48	0.48
38:1g:78:ARG:HH21	38:1g:79:ARG:NH1	2.12	0.48
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.46	0.48
2:2B:56:G:H5'	6:2G:27:ASN:ND2	2.28	0.48
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.28	0.48
8:2I:26:ALA:HA	8:2I:30:LEU:HB2	1.96	0.48
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	1.96	0.48
21:2Z:31:ARG:HG3	21:2Z:32:HIS:CD2	2.49	0.48
21:2Z:130:PRO:HA	21:2Z:133:ILE:HG13	1.95	0.48
32:2a:576:G:O6	32:2a:880:C:O2'	2.26	0.48
32:2a:1026:G:H5'	32:2a:1027:C:O5'	2.14	0.48
33:2b:24:TRP:H	33:2b:24:TRP:HD1	1.60	0.48
50:2s:12:ASP:OD2	50:2s:37:ARG:HD2	2.14	0.48
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.14	0.48
1:1A:1504:C:H2'	1:1A:1505:C:C6	2.49	0.48
1:1A:1805:U:O2	3:1D:50:THR:HB	2.14	0.48
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.46	0.48
16:1U:49:HIS:HA	16:1U:52:ARG:HB2	1.95	0.48
32:1a:376:G:OP2	47:1p:67:THR:HG21	2.14	0.48
32:1a:524:G:H2'	32:1a:525:C:C6	2.48	0.48
32:1a:584:G:H2'	32:1a:585:G:C8	2.49	0.48
33:1b:37:ASN:C	33:1b:39:ILE:H	2.22	0.48
37:1f:69:GLU:O	37:1f:72:VAL:HG12	2.14	0.48
50:1s:22:LEU:HB3	50:1s:27:GLU:HB3	1.96	0.48
54:1w:45:U:H5'	54:1w:46:G7M:OP2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:908:C:OP1	12:2Q:22:LYS:HB3	2.14	0.48
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.13	0.48
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.14	0.48
8:2I:27:ARG:HG2	23:21:71:TYR:CZ	2.49	0.48
32:2a:9:G:H2'	32:2a:10:A:C8	2.49	0.48
32:2a:628:G:H2'	32:2a:629:G:C8	2.49	0.48
32:2a:1134:G:C2	32:2a:1135:U:H1'	2.49	0.48
33:2b:118:LEU:HD13	33:2b:122:PHE:HB2	1.95	0.48
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.96	0.48
34:2c:18:TRP:NE1	45:2n:55:GLY:H	2.12	0.48
54:2w:11:C:H42	54:2w:24:G:H1	1.62	0.48
38:1g:76:ARG:HD3	38:1g:156:TRP:CZ2	2.49	0.47
1:2A:98:G:H5'	24:22:3:LEU:HD13	1.96	0.47
1:2A:231:C:C2'	1:2A:232:G:H5'	2.44	0.47
1:2A:797:C:H2'	1:2A:798:G:O4'	2.12	0.47
1:2A:798:G:O6	62:2A:3958:HOH:O	2.18	0.47
1:2A:943:U:OP2	62:2A:3967:HOH:O	2.20	0.47
1:2A:2098:U:H2'	1:2A:2099:U:O4'	2.14	0.47
6:2G:4:ASP:HA	6:2G:8:LYS:NZ	2.29	0.47
11:2P:95:VAL:HG13	11:2P:100:LEU:HD21	1.96	0.47
12:2Q:78:PRO:HD3	55:2x:1:C:C2	2.48	0.47
32:2a:363:A:OP2	43:2l:34:ARG:NH2	2.40	0.47
32:2a:630:G:H2'	32:2a:631:G:C8	2.50	0.47
32:2a:890:G:O2'	32:2a:906:G:O6	2.22	0.47
34:2c:182:ILE:HG22	34:2c:203:PHE:HA	1.96	0.47
35:2d:158:ILE:H	35:2d:158:ILE:HG12	1.43	0.47
38:2g:126:ASP:O	38:2g:130:GLY:N	2.45	0.47
39:2h:66:GLY:H	39:2h:76:PRO:HB2	1.79	0.47
1:1A:1176:G:N2	1:1A:1178:C:O5'	2.41	0.47
1:1A:1359:A:H2	1:1A:1372:U:O4	1.96	0.47
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.49	0.47
1:1A:2629:A:HO2'	1:1A:2630:G:P	2.33	0.47
15:1T:80:SER:HB3	15:1T:83:ILE:HG13	1.95	0.47
21:1Z:128:VAL:HG23	21:1Z:161:VAL:HG12	1.95	0.47
25:13:55:ARG:HH22	25:13:57:GLU:HB2	1.78	0.47
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.28	0.47
32:1a:545:C:O2'	32:1a:549:C:OP1	2.29	0.47
35:1d:189:PRO:HB3	35:1d:193:ASP:HB2	1.96	0.47
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.78	0.47
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.48	0.47
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:39:ILE:HB	6:2G:92:VAL:HG13	1.96	0.47
8:2I:84:GLY:C	8:2I:86:THR:H	2.21	0.47
21:2Z:154:ASP:OD1	21:2Z:154:ASP:N	2.34	0.47
26:24:41:PRO:HG3	26:24:49:PHE:CE1	2.49	0.47
32:2a:545:C:OP2	35:2d:65:ARG:NH2	2.47	0.47
32:2a:1269:A:N1	32:2a:1312:G:O2'	2.46	0.47
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.29	0.47
45:2n:4:LYS:HA	45:2n:7:ILE:HD12	1.96	0.47
52:2u:2:GLY:C	52:2u:4:GLY:H	2.22	0.47
1:1A:1064:C:H2'	1:1A:1065:U:H5'	1.95	0.47
1:1A:1186:G:OP1	62:1A:4171:HOH:O	2.20	0.47
1:1A:1371:G:H2'	1:1A:1372:U:C5	2.49	0.47
1:1A:2266:A:H4'	1:1A:2267:A:C4	2.49	0.47
1:1A:2375:G:N2	1:1A:2378:A:OP2	2.42	0.47
14:1S:105:ALA:O	14:1S:110:LEU:HB2	2.14	0.47
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.80	0.47
22:10:38:VAL:HB	22:10:59:LEU:HB2	1.96	0.47
32:1a:111:G:H5"	47:1p:27:LYS:HB3	1.95	0.47
32:1a:1342:C:H2'	32:1a:1343:G:C8	2.50	0.47
1:2A:800:A:H8	1:2A:800:A:OP1	1.97	0.47
1:2A:912:C:OP1	12:2Q:8:LYS:NZ	2.41	0.47
1:2A:937:U:H2'	1:2A:938:G:C8	2.48	0.47
1:2A:1882:C:H2'	1:2A:1883:G:O4'	2.14	0.47
7:2H:86:GLU:HA	7:2H:131:VAL:O	2.14	0.47
32:2a:585:G:O2'	43:2l:8:ASN:OD1	2.19	0.47
32:2a:689:C:H2'	32:2a:690:G:O4'	2.13	0.47
32:2a:1236:A:OP1	52:2u:2:GLY:HA3	2.13	0.47
35:2d:65:ARG:HG3	35:2d:70:ILE:HG23	1.96	0.47
39:2h:23:SER:OG	39:2h:24:THR:N	2.47	0.47
1:1A:185:U:H4'	1:1A:218:A:H4'	1.97	0.47
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.96	0.47
32:1a:92:C:H2'	32:1a:93:G:C8	2.49	0.47
32:1a:1318:A:H5"	50:1s:3:ARG:NH1	2.30	0.47
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.13	0.47
33:1b:212:GLN:NE2	33:1b:235:SER:HA	2.29	0.47
1:2A:223:A:N1	1:2A:407:G:O2'	2.43	0.47
1:2A:728:G:H5"	3:2D:13:ARG:NH2	2.29	0.47
1:2A:892:G:H3'	1:2A:893:C:C5'	2.44	0.47
1:2A:1805:U:O2	3:2D:50:THR:HB	2.14	0.47
14:2S:92:TYR:HB3	14:2S:98:VAL:HG21	1.94	0.47
32:2a:542:G:OP1	35:2d:10:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:998:G:H1	32:2a:1043:C:H42	1.62	0.47
34:2c:125:GLU:O	34:2c:190:ARG:NH2	2.47	0.47
39:2h:51:VAL:HG21	39:2h:60:ARG:HH21	1.78	0.47
1:1A:185:U:H2'	1:1A:186:G:H8	1.78	0.47
1:1A:411:G:C5	11:1P:72:PRO:HB3	2.49	0.47
1:1A:715:G:OP1	46:1o:64:ARG:NH2	2.47	0.47
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.49	0.47
32:1a:1133:G:H2'	32:1a:1134:G:C8	2.50	0.47
32:1a:1305:G:H5"	52:1u:4:GLY:HA3	1.95	0.47
42:1k:108:ILE:HB	49:1r:87:ARG:HD3	1.96	0.47
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.15	0.47
1:2A:184:C:H2'	1:2A:185:U:C6	2.50	0.47
1:2A:479:A:N3	1:2A:481:G:H5"	2.30	0.47
1:2A:784:A:C5	3:2D:229:VAL:HG21	2.50	0.47
1:2A:1223:G:O6	17:2V:69:LYS:NZ	2.47	0.47
1:2A:2052:G:OP1	4:2E:141:ILE:HG12	2.15	0.47
1:2A:2359:C:H2'	1:2A:2360:A:O4'	2.14	0.47
5:2F:139:PHE:CG	5:2F:167:ALA:HB2	2.49	0.47
32:2a:446:G:O6	62:2a:1907:HOH:O	2.19	0.47
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.29	0.47
48:2q:81:ARG:NH2	48:2q:84:LEU:HD21	2.29	0.47
1:1A:1713:U:H2'	1:1A:1714:G:H8	1.79	0.47
1:1A:2461:C:H2'	1:1A:2462:U:H6	1.79	0.47
1:1A:2820:A:OP1	13:1R:2:ARG:NH2	2.47	0.47
2:1B:40:U:H1'	2:1B:45:A:H61	1.79	0.47
18:1W:68:ARG:NH1	18:1W:111:HIS:HA	2.29	0.47
32:1a:428:G:O2'	35:1d:36:ARG:NH2	2.48	0.47
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.95	0.47
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	1.96	0.47
38:1g:85:TYR:N	38:1g:85:TYR:CD2	2.82	0.47
1:2A:514:A:N3	1:2A:581:C:O2'	2.43	0.47
1:2A:601:C:O2'	1:2A:605:C:H5"	2.15	0.47
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.38	0.47
1:2A:2156:G:H2'	1:2A:2157:G:C6	2.50	0.47
4:2E:52:LEU:O	4:2E:76:ARG:N	2.45	0.47
7:2H:24:VAL:HG21	7:2H:72:ILE:HD12	1.96	0.47
10:2O:112:MET:HA	10:2O:115:VAL:HB	1.97	0.47
11:2P:39:LYS:HG3	11:2P:45:LEU:HD22	1.96	0.47
32:2a:738:C:H5"	37:2f:2:ARG:NH2	2.29	0.47
32:2a:1265:G:C4	32:2a:1271:G:N2	2.83	0.47
33:2b:126:GLU:N	33:2b:126:GLU:OE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:32:ALA:HA	41:2j:33:GLN:HA	1.73	0.47
44:2m:3:ARG:N	44:2m:7:VAL:O	2.48	0.47
51:2t:67:ALA:HA	51:2t:72:LEU:O	2.14	0.47
1:1A:24:G:O2'	18:1W:78:GLU:O	2.30	0.47
1:1A:152:G:H2'	1:1A:153:C:C6	2.50	0.47
1:1A:234:C:H2'	1:1A:235:U:C6	2.49	0.47
1:1A:602:G:O2'	1:1A:655:A:N6	2.46	0.47
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.50	0.47
1:1A:1022:G:C5	1:1A:1140:C:C4	3.03	0.47
1:1A:1028:A:N3	1:1A:2486:G:O2'	2.45	0.47
1:1A:1174:A:H1'	1:1A:1175:U:H5"	1.97	0.47
1:1A:1356:G:OP2	62:1A:4174:HOH:O	2.20	0.47
1:1A:1500:G:O2'	3:1D:100:GLY:O	2.24	0.47
1:1A:2636:U:H2'	1:1A:2637:U:H6	1.80	0.47
1:1A:2732:G:H3'	1:1A:2733:A:O4'	2.14	0.47
5:1F:34:TRP:HA	11:1P:6:LEU:HD13	1.96	0.47
5:1F:110:LEU:HD11	5:1F:181:LEU:HG	1.97	0.47
7:1H:102:ALA:HA	7:1H:117:PRO:HD3	1.97	0.47
17:1V:61:VAL:HA	17:1V:94:LEU:HD23	1.96	0.47
18:1W:19:LEU:HB3	27:15:25:LEU:HD11	1.97	0.47
32:1a:254:G:H21	48:1q:16:GLN:NE2	2.13	0.47
32:1a:719:C:H1'	49:1r:49:LYS:HG2	1.97	0.47
32:1a:1371:G:O3'	40:1i:69:GLY:HA3	2.15	0.47
35:1d:63:LYS:O	35:1d:67:ILE:HG13	2.15	0.47
38:1g:15:ASP:HB3	38:1g:24:THR:HG23	1.96	0.47
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.96	0.47
55:1x:8:4SU:O2	55:1x:21:A:H2	1.98	0.47
1:2A:862:G:H2'	1:2A:863:A:O4'	2.14	0.47
1:2A:1037:G:H2'	1:2A:1038:C:O4'	2.15	0.47
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.15	0.47
1:2A:2340:G:H2'	1:2A:2341:G:C8	2.47	0.47
2:2B:18:G:H2'	2:2B:19:G:H8	1.79	0.47
4:2E:179:GLU:HG3	15:2T:9:LEU:HD21	1.96	0.47
6:2G:11:TYR:O	6:2G:16:ARG:HG2	2.15	0.47
8:2I:66:GLU:OE1	8:2I:69:LYS:HD3	2.14	0.47
14:2S:11:LYS:O	14:2S:15:ARG:HB2	2.14	0.47
15:2T:108:ARG:NH2	32:2a:1465:C:OP2	2.48	0.47
25:23:11:SER:HA	25:23:31:LEU:HD21	1.97	0.47
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.29	0.47
32:2a:34:C:H2'	32:2a:35:G:C8	2.50	0.47
32:2a:235:C:H2'	32:2a:236:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:646:U:H2'	32:2a:647:C:C6	2.50	0.47
32:2a:866:C:H4'	32:2a:919:A:H5'	1.96	0.47
32:2a:908:A:H2'	32:2a:909:A:C8	2.50	0.47
32:2a:1111:A:H61	34:2c:176:HIS:HB2	1.79	0.47
32:2a:1228:C:OP1	44:2m:115:LYS:NZ	2.48	0.47
36:2e:65:ASN:HD21	36:2e:140:ARG:HH21	1.62	0.47
38:2g:115:ARG:HG2	38:2g:118:VAL:HB	1.97	0.47
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.15	0.47
49:2r:66:LEU:HG	49:2r:70:ILE:HG13	1.96	0.47
54:2y:26:A:C2'	54:2y:27:G:H5'	2.45	0.47
1:1A:487:C:O2	18:1W:53:SER:OG	2.33	0.47
1:1A:588:U:O4	1:1A:670:A:H1'	2.14	0.47
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.13	0.47
1:1A:1065:U:H1'	1:1A:1074:G:N1	2.30	0.47
1:1A:1070:A:N6	1:1A:1096:A:H2	2.13	0.47
1:1A:1357:U:H2'	1:1A:1358:G:O4'	2.15	0.47
1:1A:1509(B):A:H3'	1:1A:1510:G:H8	1.79	0.47
1:1A:2541:A:N7	62:1A:4285:HOH:O	2.35	0.47
10:1O:107:ARG:NH2	32:1a:346:G:OP2	2.47	0.47
11:1P:126:VAL:HA	11:1P:146:VAL:HB	1.97	0.47
12:1Q:1:MET:HE2	12:1Q:1:MET:HB2	1.77	0.47
12:1Q:10:ARG:HH12	12:1Q:90:VAL:H	1.63	0.47
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.61	0.47
20:1Y:15:VAL:O	20:1Y:21:LYS:HA	2.15	0.47
53:1v:16:A:H2'	53:1v:17:U:O4'	2.15	0.47
1:2A:1324:G:O2'	1:2A:1326:U:OP2	2.33	0.47
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.45	0.47
6:2G:4:ASP:HA	6:2G:8:LYS:HZ1	1.80	0.47
32:2a:376:G:H5"	47:2p:5:ARG:HD2	1.96	0.47
32:2a:1005:A:H5"	32:2a:1006:C:H5	1.80	0.47
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.48	0.47
43:2l:103:GLY:N	43:2l:107:ALA:O	2.34	0.47
1:1A:359:A:H2'	1:1A:360:G:O4'	2.15	0.47
1:1A:897:C:H2'	1:1A:898:C:C6	2.49	0.47
1:1A:1837:C:OP1	32:1a:784:C:H4'	2.15	0.47
1:1A:2576:G:H1'	62:1A:4562:HOH:O	2.15	0.47
1:1A:2679:A:N3	62:1A:4286:HOH:O	2.35	0.47
1:1A:2753:A:N3	31:19:15:LYS:NZ	2.54	0.47
11:1P:106:LEU:HD22	11:1P:112:LEU:HD13	1.97	0.47
15:1T:118:ARG:HA	15:1T:121:ILE:HD12	1.96	0.47
22:10:47:PRO:HG3	22:10:53:MET:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:328:C:H4'	32:1a:329:A:H5'	1.96	0.47
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.45	0.47
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	1.97	0.47
38:1g:16:LEU:HD11	40:1i:42:ARG:HA	1.96	0.47
54:1w:18:G:HO2'	54:1w:57:G:H22	1.56	0.47
1:2A:143:G:H2'	1:2A:143(A):C:H6	1.78	0.47
1:2A:944:G:O3'	62:2A:3964:HOH:O	2.19	0.47
1:2A:1423:G:H2'	1:2A:1424:G:H8	1.79	0.47
1:2A:2261:C:H1'	1:2A:2388:A:N3	2.30	0.47
3:2D:147:LEU:HD13	3:2D:155:LEU:HD11	1.97	0.47
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	1.95	0.47
12:2Q:24:GLY:HA2	12:2Q:67:ARG:NH2	2.30	0.47
21:2Z:171:ILE:H	21:2Z:171:ILE:HG13	1.44	0.47
25:23:8:LEU:HB2	25:23:28:LEU:HD13	1.97	0.47
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.50	0.47
32:2a:1016:A:H3'	32:2a:1017:G:H8	1.79	0.47
38:2g:57:GLU:HG3	38:2g:59:LEU:H	1.80	0.47
54:2y:7:A:H61	54:2y:66:U:H3	1.63	0.47
1:1A:34:C:H5"	1:1A:35:G:OP2	2.14	0.47
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.12	0.47
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.50	0.47
1:1A:1095:A:H2'	1:1A:1096:A:H8	1.80	0.47
1:1A:2059:A:C2	59:1A:4087:ERY:H322	2.50	0.47
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.28	0.47
5:1F:165:ARG:HA	5:1F:168:ARG:HD2	1.95	0.47
8:1I:16:GLY:O	8:1I:47:LEU:HD11	2.15	0.47
32:1a:31:G:N2	32:1a:47:C:O5'	2.48	0.47
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.15	0.47
37:1f:36:ARG:HB2	37:1f:66:GLU:O	2.15	0.47
1:2A:657:U:H2'	1:2A:658:C:C6	2.50	0.47
1:2A:815:C:H2'	1:2A:816:C:C6	2.49	0.47
1:2A:910:A:N1	1:2A:2277:G:H1'	2.30	0.47
1:2A:1300:U:H4'	1:2A:1301:A:H5"	1.97	0.47
1:2A:1777:U:H2'	1:2A:1778:U:C6	2.50	0.47
1:2A:2398:U:H2'	1:2A:2399:G:C8	2.50	0.47
1:2A:2751:G:H8	7:2H:2:SER:HA	1.80	0.47
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.95	0.47
32:2a:412:A:C6	35:2d:35:ARG:HG2	2.50	0.47
36:2e:145:LYS:HD2	36:2e:148:VAL:HB	1.96	0.47
39:2h:103:VAL:HG21	39:2h:109:ILE:C	2.40	0.47
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:972:G:H3'	1:1A:973:A:H2'	1.96	0.46
1:1A:1062:G:C8	1:1A:1070:A:H4'	2.49	0.46
1:1A:1213:A:N3	1:1A:1238:G:O2'	2.46	0.46
1:1A:1791:A:H4'	3:1D:206:LEU:HB2	1.98	0.46
27:15:16:ARG:O	27:15:20:ARG:HG3	2.15	0.46
32:1a:189(B):C:H2'	32:1a:189(C):C:C6	2.50	0.46
32:1a:337:C:H2'	32:1a:338:A:C8	2.50	0.46
32:1a:724:G:H2'	32:1a:725:G:H8	1.80	0.46
32:1a:1322:C:N4	62:1a:1962:HOH:O	2.48	0.46
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.78	0.46
41:1j:30:SER:HG	41:1j:81:THR:HG1	1.51	0.46
42:1k:33:THR:HA	42:1k:39:PRO:HA	1.97	0.46
54:1y:44:G:H8	54:1y:44:G:OP2	1.97	0.46
1:2A:460:A:OP1	29:27:41:ARG:NH2	2.48	0.46
1:2A:2252:G:H2'	1:2A:2253:G:O4'	2.15	0.46
1:2A:2439:A:N6	55:2x:76:8AN:O1P	2.48	0.46
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.34	0.46
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.50	0.46
6:2G:59:GLU:O	6:2G:63:ILE:HG12	2.16	0.46
6:2G:113:ARG:HD2	26:24:33:VAL:HG23	1.97	0.46
28:26:19:ARG:HH12	28:26:52:VAL:HG21	1.79	0.46
32:2a:284:G:H2'	32:2a:285:G:C8	2.50	0.46
32:2a:382:A:H2'	32:2a:383:A:C8	2.50	0.46
32:2a:452:A:H4'	47:2p:72:ARG:HE	1.80	0.46
32:2a:958:A:N6	50:2s:77:THR:O	2.48	0.46
32:2a:1263:C:H3'	32:2a:1263:C:H6	1.80	0.46
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.15	0.46
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.80	0.46
34:2c:130:VAL:O	34:2c:134:ILE:HG12	2.15	0.46
36:2e:105:VAL:HB	36:2e:106:PRO:HD3	1.97	0.46
42:2k:18:ARG:NH2	42:2k:35:PRO:O	2.47	0.46
1:1A:383:U:H2'	1:1A:385:C:H5	1.80	0.46
1:1A:1359:A:C2	1:1A:1372:U:O4	2.68	0.46
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.15	0.46
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.15	0.46
1:1A:2667:C:N3	7:1H:110:SER:OG	2.46	0.46
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.50	0.46
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.96	0.46
21:1Z:30:ASN:OD1	21:1Z:33:LEU:HD23	2.14	0.46
32:1a:356:A:N3	32:1a:368:U:O2'	2.47	0.46
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:664:G:N2	32:1a:741:G:H1	2.05	0.46
32:1a:1350:A:C6	32:1a:1351:U:C4	3.03	0.46
33:1b:67:THR:N	33:1b:160:ASP:OD1	2.40	0.46
37:1f:38:GLU:HB2	37:1f:64:GLN:HG3	1.96	0.46
1:2A:580:C:H2'	1:2A:581:C:H6	1.79	0.46
1:2A:606:U:OP1	5:2F:104:LYS:HG3	2.15	0.46
1:2A:722:A:H2'	1:2A:723:G:C8	2.50	0.46
1:2A:887:A:H4'	1:2A:888:C:C5	2.50	0.46
1:2A:1710:C:H2'	1:2A:1711:C:C6	2.51	0.46
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.50	0.46
1:2A:2748:A:C2	7:2H:63:SER:HB3	2.51	0.46
3:2D:68:LYS:C	3:2D:70:TRP:H	2.22	0.46
3:2D:71:ASP:CG	3:2D:103:ARG:HH12	2.22	0.46
4:2E:101:ARG:HB2	4:2E:201:THR:HG21	1.97	0.46
21:2Z:44:PHE:CE1	21:2Z:86:VAL:HG21	2.51	0.46
32:2a:670:G:H2'	32:2a:671:G:O4'	2.15	0.46
32:2a:954:G:H2'	32:2a:955:U:O4'	2.16	0.46
32:2a:977:A:O2'	32:2a:980:C:N4	2.44	0.46
32:2a:1227:A:O2'	44:2m:115:LYS:HD2	2.14	0.46
32:2a:1298:C:H1'	32:2a:1299:A:C2	2.49	0.46
32:2a:1320:C:H1'	50:2s:73:GLU:HG3	1.97	0.46
35:2d:112:VAL:H	35:2d:116:GLN:HE21	1.62	0.46
37:2f:36:ARG:NH2	37:2f:38:GLU:HG2	2.31	0.46
51:2t:72:LEU:HG	51:2t:76:ALA:HB3	1.97	0.46
54:2w:4:C:H42	54:2w:69:G:H1	1.63	0.46
1:1A:1268:A:C2	1:1A:2013:A:C4	3.04	0.46
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.16	0.46
1:1A:2552:OMU:O5'	1:1A:2552:OMU:H6	2.15	0.46
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.51	0.46
3:1D:132:PRO:HG3	3:1D:190:TYR:CE2	2.49	0.46
3:1D:223:GLY:HA3	3:1D:231:HIS:CE1	2.50	0.46
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.96	0.46
12:1Q:1:MET:HB3	62:1Q:302:HOH:O	2.15	0.46
14:1S:16:ASN:HA	14:1S:19:LYS:HD2	1.97	0.46
21:1Z:45:ASP:OD1	21:1Z:49:ARG:NH2	2.29	0.46
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.50	0.46
32:1a:737:A:H2'	32:1a:738:C:C6	2.50	0.46
33:1b:155:LEU:HD21	33:1b:159:PRO:HD3	1.97	0.46
35:1d:187:ARG:HH11	35:1d:187:ARG:HB2	1.80	0.46
41:1j:40:LEU:HB2	41:1j:69:ASN:HB3	1.97	0.46
48:1q:3:LYS:HD3	48:1q:61:GLU:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:89:ARG:O	51:1t:93:GLU:HG2	2.15	0.46
54:1w:23:A:H3'	54:1w:24:G:H8	1.81	0.46
1:2A:154(A):C:N4	1:2A:171:G:H1	2.13	0.46
1:2A:2100:G:C6	1:2A:2190:G:C6	3.03	0.46
5:2F:18:ARG:NH1	5:2F:127:GLU:OE2	2.49	0.46
32:2a:253:U:H2'	32:2a:254:G:C8	2.50	0.46
32:2a:416:G:H1	32:2a:427:U:H3	1.63	0.46
32:2a:520:A:C2	32:2a:536:C:H1'	2.50	0.46
32:2a:1014:A:H1'	50:2s:34:TRP:HB2	1.96	0.46
32:2a:1109:C:H2'	32:2a:1110:A:O4'	2.15	0.46
34:2c:152:ILE:HD11	34:2c:199:LYS:NZ	2.31	0.46
36:2e:84:PHE:O	36:2e:86:ALA:N	2.49	0.46
44:2m:28:ALA:C	44:2m:30:ALA:H	2.24	0.46
1:1A:271(N):U:O2'	1:1A:271(O):C:H5'	2.15	0.46
1:1A:414:C:H2'	1:1A:415:A:C8	2.50	0.46
1:1A:1045:A:OP1	1:1A:1046:A:H3'	2.15	0.46
1:1A:1685:C:H2'	1:1A:1686:C:H6	1.79	0.46
1:1A:1862:G:C2	1:1A:1881:C:C2	3.03	0.46
1:1A:2314:C:H2'	1:1A:2315:G:H8	1.79	0.46
1:1A:2648:C:H2'	1:1A:2649:U:C6	2.50	0.46
1:1A:2879:C:OP2	62:1A:4175:HOH:O	2.20	0.46
7:1H:109:PHE:C	7:1H:111:HIS:H	2.23	0.46
32:1a:1355:G:H2'	32:1a:1356:G:H8	1.81	0.46
41:1j:19:SER:OG	41:1j:91:PRO:HD2	2.15	0.46
54:1w:66:U:C4	54:1w:67:C:C4	3.03	0.46
1:2A:752:A:H4'	1:2A:753:C:H5'	1.98	0.46
1:2A:852:G:H2'	1:2A:853:G:C8	2.47	0.46
1:2A:1394:U:C4	1:2A:1395:A:C5	3.03	0.46
1:2A:1628:G:H2'	1:2A:1629:U:C6	2.51	0.46
32:2a:441:A:H3'	32:2a:442:C:C6	2.50	0.46
32:2a:604:G:H2'	32:2a:605:U:O4'	2.15	0.46
32:2a:1196:U:H5	53:2v:24:A:C4	2.33	0.46
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.80	0.46
38:2g:13:GLN:O	38:2g:24:THR:HG21	2.16	0.46
39:2h:92:ARG:HB3	39:2h:94:TYR:CE2	2.51	0.46
42:2k:23:ALA:HA	42:2k:28:THR:HA	1.97	0.46
1:1A:1683:C:H2'	1:1A:1684:C:H6	1.78	0.46
1:1A:1815:A:H8	1:1A:1815:A:OP1	1.99	0.46
1:1A:1825:A:OP1	3:1D:249:PRO:HD3	2.15	0.46
1:1A:1975:G:OP2	62:1A:4176:HOH:O	2.21	0.46
12:1Q:32:TYR:CZ	12:1Q:111:GLU:HG3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:48:PHE:CE1	21:1Z:52:SER:HA	2.50	0.46
54:1w:36:A:H2'	54:1w:37:MIA:H8	1.98	0.46
1:2A:829:A:N7	1:2A:2248:C:H5'	2.31	0.46
4:2E:68:ALA:O	4:2E:71:GLY:N	2.46	0.46
21:2Z:39:VAL:HG21	21:2Z:44:PHE:CD1	2.39	0.46
25:23:50:VAL:HB	25:23:53:LEU:HD12	1.98	0.46
32:2a:1085:U:H3'	32:2a:1086:U:H5	1.80	0.46
34:2c:40:ARG:HA	34:2c:43:LEU:HB2	1.97	0.46
36:2e:24:ARG:NH1	53:2v:23:A:O2'	2.39	0.46
46:2o:56:LEU:O	46:2o:60:VAL:HG13	2.16	0.46
48:2q:43:LEU:HD23	48:2q:43:LEU:HA	1.66	0.46
1:1A:2140:C:H2'	1:1A:2141:G:H8	1.80	0.46
1:1A:2647:U:H2'	1:1A:2648:C:C6	2.50	0.46
23:11:5:CYS:SG	23:11:62:VAL:HG23	2.55	0.46
26:14:63:TYR:N	26:14:64:GLY:HA2	2.30	0.46
32:1a:542:G:P	35:1d:10:ARG:HH22	2.38	0.46
32:1a:1033:G:H3'	32:1a:1034:G:H8	1.81	0.46
40:1i:100:GLY:O	40:1i:103:THR:HG23	2.15	0.46
44:1m:19:LEU:HD11	44:1m:56:LEU:HD21	1.98	0.46
46:1o:5:LYS:O	46:1o:9:GLN:HG2	2.14	0.46
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.51	0.46
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.15	0.46
1:2A:2533:A:H2'	1:2A:2534:A:O4'	2.16	0.46
2:2B:105:A:OP1	21:2Z:72:ARG:NH2	2.44	0.46
3:2D:35:LYS:HG2	3:2D:64:ILE:HD11	1.98	0.46
6:2G:120:LEU:HD12	6:2G:178:PHE:HB3	1.97	0.46
31:29:17:ILE:HG12	31:29:26:ILE:HD12	1.98	0.46
32:2a:872:A:O2'	32:2a:873:A:H3'	2.15	0.46
32:2a:1014:A:H4'	50:2s:14:HIS:CD2	2.50	0.46
32:2a:1130:A:H5"	40:2i:18:PHE:CE2	2.51	0.46
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	1.98	0.46
35:2d:175:SER:OG	35:2d:176:LEU:N	2.49	0.46
37:2f:14:LEU:HD22	37:2f:18:GLN:HB3	1.96	0.46
37:2f:69:GLU:H	37:2f:69:GLU:HG3	1.53	0.46
39:2h:12:ARG:HD2	39:2h:26:VAL:HG22	1.98	0.46
40:2i:49:PRO:HB2	40:2i:85:LEU:HD11	1.97	0.46
44:2m:29:ARG:HB3	44:2m:64:TRP:CH2	2.50	0.46
51:2t:58:LYS:HA	51:2t:58:LYS:HD2	1.76	0.46
54:2y:9:A:H4'	54:2y:46:G7M:H5'	1.98	0.46
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.50	0.46
1:1A:725:G:C6	1:1A:726:G:N1	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:751:A:H5'	18:1W:90:ARG:HA	1.98	0.46
1:1A:2781:A:H5"	1:1A:2782:G:H5'	1.98	0.46
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.16	0.46
6:1G:70:VAL:HG11	6:1G:87:PRO:HB3	1.97	0.46
6:1G:83:ARG:O	6:1G:86:MET:HG3	2.16	0.46
26:14:33:VAL:HG12	26:14:35:VAL:H	1.81	0.46
32:1a:767:A:H2'	32:1a:768:A:O4'	2.15	0.46
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.31	0.46
40:1i:41:VAL:C	40:1i:43:ALA:H	2.24	0.46
1:2A:196:A:N3	1:2A:196:A:H2'	2.31	0.46
1:2A:1713:U:H2'	1:2A:1714:G:H8	1.81	0.46
1:2A:1825:A:O4'	3:2D:254:THR:HG21	2.16	0.46
1:2A:2099:U:H3	1:2A:2190:G:H1	1.63	0.46
1:2A:2576:G:OP1	62:2A:3969:HOH:O	2.20	0.46
32:2a:90:U:H2'	32:2a:91:C:H6	1.81	0.46
34:2c:108:ASN:HB3	34:2c:111:LEU:HB2	1.98	0.46
43:2l:57:LYS:HA	43:2l:67:THR:HA	1.97	0.46
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.55	0.46
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.31	0.46
1:1A:1012:U:C5	9:1N:28:THR:HG21	2.51	0.46
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.49	0.46
1:1A:2489:G:C6	1:1A:2490:G:N1	2.84	0.46
1:1A:2790:A:H3'	1:1A:2790:A:N3	2.30	0.46
26:14:59:PHE:CD1	26:14:60:GLN:HG2	2.50	0.46
34:1c:87:LEU:O	34:1c:91:LEU:N	2.44	0.46
37:1f:97:PHE:N	49:1r:30:ASP:OD1	2.46	0.46
39:1h:4:ASP:OD2	39:1h:85:ARG:NE	2.37	0.46
46:1o:3:ILE:HG12	46:1o:38:ARG:HD3	1.98	0.46
49:1r:58:LEU:HB2	49:1r:63:GLN:HE21	1.81	0.46
49:1r:65:ILE:H	49:1r:65:ILE:HG13	1.49	0.46
51:1t:100:ILE:HB	51:1t:101:GLY:H	1.60	0.46
55:1x:52:G:H1	55:1x:62:C:H42	1.64	0.46
1:2A:147:U:O4	62:2A:3963:HOH:O	2.19	0.46
1:2A:533:G:H5'	16:2U:24:TYR:CD1	2.51	0.46
1:2A:656:G:H2'	1:2A:657:U:O4'	2.14	0.46
1:2A:1028:A:H2'	1:2A:1029:A:C8	2.51	0.46
13:2R:29:LEU:HD22	13:2R:79:LEU:HD13	1.98	0.46
32:2a:433:C:H2'	32:2a:434:U:C6	2.51	0.46
32:2a:642:A:N3	39:2h:113:SER:OG	2.44	0.46
32:2a:868:C:H2'	32:2a:869:G:O4'	2.15	0.46
32:2a:1005:A:H3'	32:2a:1006:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.80	0.46
32:2a:1270:C:OP2	52:2u:24:ARG:NH2	2.47	0.46
33:2b:91:PRO:HG3	33:2b:154:LEU:O	2.15	0.46
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.26	0.46
35:2d:76:ARG:HA	35:2d:79:PHE:HB3	1.98	0.46
38:2g:63:LYS:HB2	38:2g:63:LYS:HE3	1.73	0.46
1:1A:82:G:N1	1:1A:103:A:OP2	2.37	0.46
1:1A:879:G:H8	1:1A:879:G:O5'	1.98	0.46
1:1A:2577:A:O4'	27:15:3:LYS:HB2	2.15	0.46
4:1E:181:LEU:HD21	15:1T:6:LEU:HD22	1.98	0.46
6:1G:3:LEU:HD13	26:14:25:TYR:CZ	2.51	0.46
24:12:17:SER:N	24:12:20:GLU:OE1	2.49	0.46
32:1a:262:A:C6	32:1a:263:A:C6	3.03	0.46
32:1a:1004:A:H5"	32:1a:1025:U:H5	1.79	0.46
32:1a:1027:C:H5"	32:1a:1028:C:OP2	2.16	0.46
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.81	0.46
32:1a:1317:C:OP1	45:1n:17:LYS:HG2	2.14	0.46
36:1e:142:LEU:O	36:1e:143:ARG:NH1	2.49	0.46
40:1i:7:THR:O	40:1i:83:ARG:HD2	2.15	0.46
40:1i:48:GLU:CD	40:1i:51:ARG:HE	2.24	0.46
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.97	0.46
1:2A:11:G:H22	1:2A:2628:C:P	2.39	0.46
1:2A:298:G:H5"	1:2A:299:A:OP1	2.16	0.46
1:2A:938:G:OP2	30:28:52:LYS:NZ	2.43	0.46
1:2A:984:A:H5"	1:2A:985:C:H5	1.81	0.46
1:2A:1164:G:H1	1:2A:1185:C:H42	1.64	0.46
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.34	0.46
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.51	0.46
7:2H:156:ALA:O	7:2H:172:LYS:HG2	2.16	0.46
11:2P:77:ARG:HB2	11:2P:78:PRO:HD2	1.97	0.46
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.50	0.46
20:2Y:99:CYS:SG	20:2Y:101:LYS:HB2	2.56	0.46
22:20:52:GLY:O	22:20:59:LEU:HA	2.16	0.46
30:28:32:LEU:O	30:28:36:LYS:NZ	2.47	0.46
32:2a:164:U:H2'	32:2a:165:C:C6	2.51	0.46
32:2a:1080:A:OP1	36:2e:47:LYS:HD3	2.15	0.46
32:2a:1263:C:O2	32:2a:1273:G:C2	2.69	0.46
34:2c:183:ASP:N	34:2c:202:ILE:O	2.42	0.46
46:2o:43:LEU:HD12	46:2o:56:LEU:HD13	1.97	0.46
50:2s:36:ARG:NH1	50:2s:72:GLY:HA2	2.31	0.46
54:2y:26:A:H2'	54:2y:27:G:H5'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:7:G:H2'	1:1A:8:A:C8	2.51	0.46
1:1A:971:C:H2'	1:1A:972:G:O4'	2.16	0.46
5:1F:64:ILE:HD12	5:1F:65:TRP:CZ3	2.50	0.46
11:1P:86:LYS:C	11:1P:88:LEU:H	2.24	0.46
28:16:17:LYS:HE3	28:16:17:LYS:HB3	1.83	0.46
32:1a:238:G:OP1	48:1q:25:ARG:NH2	2.49	0.46
32:1a:1004:A:H5"	32:1a:1025:U:C5	2.51	0.46
32:1a:1120:G:H2'	32:1a:1121:U:C6	2.51	0.46
33:1b:101:MET:HA	33:1b:108:ILE:HD12	1.97	0.46
42:1k:85:ARG:NH2	42:1k:111:ASP:OD2	2.48	0.46
54:1y:6:G:O6	54:1y:7:A:N6	2.49	0.46
1:2A:248:G:OP1	62:2A:3972:HOH:O	2.21	0.46
1:2A:383:U:H2'	1:2A:385:C:H5	1.81	0.46
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.80	0.46
15:2T:67:SER:N	15:2T:70:VAL:O	2.47	0.46
21:2Z:44:PHE:C	21:2Z:44:PHE:CD2	2.94	0.46
32:2a:1003:G:H2'	32:2a:1004:A:O4'	2.16	0.46
32:2a:1152:A:H2'	32:2a:1153:C:C6	2.51	0.46
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.49	0.46
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.15	0.46
40:2i:116:LYS:HE3	40:2i:120:ARG:HA	1.98	0.46
54:2w:42:C:O2'	54:2w:43:C:H5'	2.16	0.46
1:1A:1060:U:C2	1:1A:1062:G:H1'	2.51	0.45
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.99	0.45
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.49	0.45
32:1a:113:G:N3	32:1a:353:A:O2'	2.45	0.45
32:1a:1255:G:H1	32:1a:1282:C:N4	2.13	0.45
1:2A:1660:C:H2'	1:2A:1661:G:C8	2.50	0.45
1:2A:2875:C:O2'	15:2T:2:ASN:OD1	2.22	0.45
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.16	0.45
32:2a:779:C:H2'	32:2a:780:A:O4'	2.15	0.45
33:2b:134:GLU:HA	33:2b:137:ARG:HB3	1.99	0.45
34:2c:19:GLU:HB3	34:2c:40:ARG:HH22	1.81	0.45
34:2c:44:GLU:HA	34:2c:52:LEU:HD23	1.98	0.45
41:2j:34:VAL:HG12	41:2j:74:ILE:HA	1.98	0.45
44:2m:92:HIS:NE2	44:2m:98:VAL:HG21	2.31	0.45
1:1A:388:G:O2'	1:1A:389:G:N7	2.47	0.45
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.49	0.45
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.17	0.45
1:1A:2126:A:H4'	1:1A:2127:G:OP1	2.17	0.45
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:68:G:H5'	32:1a:171:A:O2'	2.16	0.45
32:1a:1192:C:OP2	34:1c:4:LYS:NZ	2.48	0.45
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.51	0.45
39:1h:81:HIS:HB2	39:1h:138:TRP:CD1	2.50	0.45
43:1l:52:LEU:O	43:1l:54:LYS:NZ	2.21	0.45
1:2A:245:G:O6	30:28:8:LYS:HE3	2.17	0.45
1:2A:422:A:OP2	62:2A:3930:HOH:O	2.21	0.45
1:2A:686:G:N2	1:2A:788:A:H61	2.13	0.45
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.17	0.45
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.15	0.45
1:2A:1785:A:N6	62:2A:4142:HOH:O	2.48	0.45
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.50	0.45
2:2B:42:C:O2	6:2G:93:THR:N	2.40	0.45
5:2F:40:GLN:HE21	5:2F:40:GLN:HB3	1.66	0.45
8:2I:140:LEU:O	8:2I:142:VAL:HG23	2.16	0.45
18:2W:1:MET:HE3	18:2W:62:HIS:HB3	1.97	0.45
32:2a:8:A:N6	35:2d:205:GLU:O	2.47	0.45
32:2a:576:G:N2	32:2a:760:G:OP2	2.49	0.45
32:2a:1033:G:H2'	32:2a:1034:G:C8	2.50	0.45
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.31	0.45
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.51	0.45
35:2d:150:GLU:C	35:2d:152:SER:H	2.24	0.45
39:2h:98:LYS:HE2	39:2h:98:LYS:HB2	1.79	0.45
12:1Q:78:PRO:HG2	12:1Q:81:VAL:HG11	1.98	0.45
15:1T:54:ARG:HA	15:1T:59:THR:HB	1.98	0.45
21:1Z:69:THR:HG22	21:1Z:90:VAL:HG22	1.99	0.45
21:1Z:132:ASN:HD22	21:1Z:160:GLY:HA3	1.80	0.45
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.52	0.45
32:1a:1086:U:H3	32:1a:1099:G:H22	1.65	0.45
33:1b:131:PRO:HB2	33:1b:134:GLU:CB	2.46	0.45
34:1c:131:ARG:NH1	34:1c:166:GLU:HG3	2.31	0.45
46:1o:40:SER:O	46:1o:44:LYS:HG3	2.17	0.45
54:1y:51:U:H2'	54:1y:52:G:C8	2.51	0.45
1:2A:309:G:N3	1:2A:329:G:O2'	2.47	0.45
1:2A:1938:A:N3	1:2A:2605:PSU:O2'	2.48	0.45
1:2A:2024:G:H2'	1:2A:2025:C:C6	2.51	0.45
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.31	0.45
9:2N:131:GLN:H	9:2N:131:GLN:HG2	1.59	0.45
16:2U:111:GLU:O	16:2U:115:ALA:N	2.46	0.45
21:2Z:54:HIS:HB2	21:2Z:55:HIS:CD2	2.52	0.45
32:2a:363:A:C5	43:2l:31:PRO:HD2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:972:C:OP2	41:2j:57:LYS:NZ	2.40	0.45
33:2b:112:VAL:C	33:2b:114:ARG:H	2.24	0.45
35:2d:31:CYS:HB2	61:2d:303:SF4:S3	2.56	0.45
39:2h:25:ASP:OD1	39:2h:25:ASP:N	2.49	0.45
39:2h:82:HIS:HB3	39:2h:138:TRP:CE2	2.52	0.45
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.98	0.45
50:2s:19:VAL:O	50:2s:23:ASN:ND2	2.49	0.45
51:2t:27:LYS:HA	51:2t:30:LYS:HE3	1.97	0.45
1:1A:910:A:C5	12:1Q:13:GLN:HG3	2.51	0.45
32:1a:78:G:C2	32:1a:91:C:N3	2.85	0.45
32:1a:203:U:O2	32:1a:216:G:N1	2.49	0.45
32:1a:299:G:H2'	32:1a:300:A:C8	2.51	0.45
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.98	0.45
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.49	0.45
35:1d:3:ARG:H	35:1d:3:ARG:HG3	1.47	0.45
54:1y:68:C:H2'	54:1y:69:G:H8	1.82	0.45
1:2A:479:A:H4'	1:2A:480:A:OP1	2.16	0.45
1:2A:674:G:H1'	5:2F:74:ARG:HD3	1.98	0.45
1:2A:1227:G:OP1	16:2U:13:LYS:HG2	2.16	0.45
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.51	0.45
1:2A:2769:C:H2'	1:2A:2770:G:O4'	2.16	0.45
4:2E:11:MET:HE2	4:2E:11:MET:HB3	1.85	0.45
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.51	0.45
18:2W:21:VAL:O	18:2W:24:ILE:HG12	2.17	0.45
19:2X:2:LYS:HD2	19:2X:2:LYS:HA	1.71	0.45
32:2a:1108:G:OP1	34:2c:175:LEU:HD12	2.16	0.45
33:2b:73:THR:HB	33:2b:95:GLN:O	2.16	0.45
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.30	0.45
1:1A:1104:C:H2'	1:1A:1105:U:O4'	2.17	0.45
1:1A:1952:A:C6	1:1A:1953:A:N1	2.85	0.45
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.16	0.45
6:1G:130:ASN:OD1	6:1G:160:VAL:HG13	2.17	0.45
10:1O:63:VAL:HG22	10:1O:84:ALA:HA	1.98	0.45
21:1Z:132:ASN:O	21:1Z:134:PRO:HD3	2.17	0.45
32:1a:69:G:H2'	32:1a:70:G:C8	2.51	0.45
32:1a:250:A:H4'	32:1a:251:G:O5'	2.16	0.45
32:1a:736:C:H2'	32:1a:737:A:C8	2.51	0.45
32:1a:865:A:C2	32:1a:918:A:H4'	2.51	0.45
43:1l:113:ARG:HG3	43:1l:114:LYS:N	2.32	0.45
50:1s:28:LYS:HB3	50:1s:47:HIS:CD2	2.51	0.45
54:1y:56:C:C4	54:1y:57:G:C8	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:520:G:H2'	1:2A:521:G:H8	1.78	0.45
1:2A:590:A:H2'	1:2A:591:C:C6	2.51	0.45
1:2A:2030:A:H4'	1:2A:2031:A:C8	2.52	0.45
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.32	0.45
1:2A:2577:A:H2'	1:2A:2614:A:N6	2.32	0.45
1:2A:2820:A:P	13:2R:2:ARG:HH22	2.39	0.45
6:2G:41:GLN:HB3	6:2G:43:LEU:HD22	1.99	0.45
8:2I:130:TYR:HE2	8:2I:132:PRO:HB3	1.81	0.45
13:2R:118:GLU:OE1	13:2R:118:GLU:N	2.36	0.45
14:2S:18:ILE:O	14:2S:21:THR:HG23	2.15	0.45
19:2X:2:LYS:NZ	19:2X:38:GLU:OE2	2.43	0.45
32:2a:675:A:H2'	32:2a:676:A:O4'	2.16	0.45
32:2a:889:A:H8	32:2a:889:A:OP1	2.00	0.45
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.16	0.45
33:2b:118:LEU:HD21	33:2b:138:LEU:HD23	1.98	0.45
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.16	0.45
55:2x:59:A:H2'	55:2x:60:U:H5'	1.97	0.45
12:1Q:78:PRO:HD3	55:1x:1:C:C4	2.51	0.45
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.98	0.45
32:1a:950:U:O4	44:1m:105:THR:HG21	2.16	0.45
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.51	0.45
34:1c:141:VAL:HG11	34:1c:149:ALA:HB2	1.99	0.45
1:2A:571:A:N6	1:2A:2499:C:O3'	2.47	0.45
1:2A:2180:U:H2'	1:2A:2181:G:O4'	2.16	0.45
1:2A:2637:U:H5'	4:2E:44:TYR:CE2	2.52	0.45
1:2A:2711:A:OP1	62:2A:3957:HOH:O	2.21	0.45
1:2A:2872:G:O2'	1:2A:2873:A:H5'	2.17	0.45
5:2F:78:ILE:HD13	5:2F:78:ILE:H	1.82	0.45
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	1.98	0.45
7:2H:99:VAL:HB	7:2H:102:ALA:HB3	1.98	0.45
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.17	0.45
20:2Y:14:LEU:HB2	20:2Y:24:VAL:HG22	1.98	0.45
32:2a:23:C:OP2	32:2a:561:U:N3	2.49	0.45
32:2a:1072:G:O6	32:2a:1102:A:N6	2.49	0.45
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.16	0.45
32:2a:1310:G:H5'	44:2m:77:ASN:HD21	1.82	0.45
35:2d:18:LYS:HD3	35:2d:20:TYR:CZ	2.52	0.45
37:2f:62:TRP:CH2	37:2f:64:GLN:HB2	2.52	0.45
40:2i:16:ARG:CZ	40:2i:64:THR:HG21	2.47	0.45
1:1A:153:C:N4	62:1A:4215:HOH:O	2.26	0.45
1:1A:1069:A:H1'	1:1A:1096:A:H4'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2171:A:O2'	1:1A:2172:U:H5"	2.17	0.45
1:1A:2188:C:H2'	1:1A:2189:U:O4'	2.17	0.45
1:1A:2695:C:H2'	1:1A:2696:U:C6	2.51	0.45
9:1N:89:LYS:O	9:1N:93:THR:OG1	2.32	0.45
13:1R:117:VAL:HG12	13:1R:118:GLU:N	2.31	0.45
32:1a:421:U:O4	34:1c:127:ARG:NH2	2.47	0.45
32:1a:500:G:H2'	32:1a:501:C:C6	2.51	0.45
32:1a:743:U:H2'	32:1a:744:C:C6	2.51	0.45
32:1a:1229:A:O2'	55:1x:30:G:OP1	2.35	0.45
36:1e:84:PHE:HB3	36:1e:134:ALA:HB2	1.99	0.45
41:1j:5:ARG:O	41:1j:98:ILE:HA	2.17	0.45
41:1j:65:LEU:HD12	45:1n:55:GLY:O	2.17	0.45
41:1j:78:ASN:C	41:1j:80:LYS:H	2.23	0.45
1:2A:580:C:H2'	1:2A:581:C:C6	2.50	0.45
1:2A:1790:C:H5"	1:2A:1791:A:OP1	2.17	0.45
1:2A:2154:G:H2'	1:2A:2155:G:C8	2.51	0.45
1:2A:2280:G:O2'	1:2A:2388:A:N1	2.38	0.45
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.76	0.45
28:26:14:THR:OG1	28:26:48:VAL:O	2.35	0.45
32:2a:6:G:H1	36:2e:98:THR:HG21	1.82	0.45
32:2a:1502:A:C8	32:2a:1505:G:N2	2.85	0.45
1:1A:570:G:H2'	1:1A:2030:A:N7	2.31	0.45
1:1A:1374:G:H2'	1:1A:1375:C:H6	1.81	0.45
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.17	0.45
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.50	0.45
4:1E:175:VAL:O	4:1E:177:PRO:HD3	2.17	0.45
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.98	0.45
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.31	0.45
1:2A:413:C:OP2	62:2A:3971:HOH:O	2.21	0.45
1:2A:1003:G:N2	1:2A:1153:C:C2	2.85	0.45
1:2A:1202:C:H42	1:2A:1243:G:H1	1.65	0.45
1:2A:2228:G:C6	1:2A:2229:C:C4	3.05	0.45
1:2A:2809:A:C6	1:2A:2810:A:C6	3.05	0.45
4:2E:109:LYS:HE2	4:2E:191:PRO:HB3	1.99	0.45
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.99	0.45
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.32	0.45
32:2a:377:G:H1	32:2a:386:C:H42	1.65	0.45
32:2a:743:U:H2'	32:2a:744:C:C6	2.52	0.45
32:2a:1077:G:H2'	32:2a:1079:G:N7	2.32	0.45
44:2m:16:ASP:OD1	44:2m:17:VAL:N	2.47	0.45
1:1A:1846:G:H5"	1:1A:1847:A:OP2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.98	0.45
3:1D:162:SER:HB3	3:1D:195:ALA:HB2	1.97	0.45
8:1I:114:LEU:HD12	8:1I:115:ALA:H	1.81	0.45
12:1Q:79:LEU:O	12:1Q:80:GLU:HB2	2.16	0.45
32:1a:6:G:O2'	32:1a:7:G:H5"	2.17	0.45
32:1a:309:G:H1'	32:1a:608:A:C2	2.52	0.45
32:1a:313:A:H2'	32:1a:314:C:C6	2.52	0.45
32:1a:418:C:H1'	32:1a:540:G:O2'	2.17	0.45
32:1a:859:A:H2'	32:1a:860:A:C8	2.52	0.45
32:1a:954:G:C6	32:1a:955:U:C4	3.05	0.45
37:1f:99:ALA:HB3	49:1r:29:PHE:CE1	2.52	0.45
40:1i:42:ARG:O	40:1i:74:ILE:HD13	2.17	0.45
45:1n:14:PRO:HG2	45:1n:16:PHE:O	2.16	0.45
49:1r:59:SER:H	49:1r:62:GLU:HB2	1.82	0.45
1:2A:927:G:H2'	1:2A:928:G:O4'	2.16	0.45
1:2A:1365:A:O5'	23:21:41:ARG:NH2	2.46	0.45
8:2I:3:VAL:HA	8:2I:39:ALA:H	1.81	0.45
16:2U:85:LYS:HB2	16:2U:116:ALA:HB1	1.97	0.45
19:2X:9:LEU:HB2	19:2X:29:TRP:O	2.16	0.45
29:27:24:THR:HG23	29:27:27:GLY:HA3	1.98	0.45
32:2a:670:G:H21	37:2f:73:ASN:ND2	2.15	0.45
32:2a:985:C:H2'	32:2a:986:A:C8	2.51	0.45
32:2a:1060:C:H2'	32:2a:1061:G:H8	1.81	0.45
32:2a:1103:C:P	33:2b:96:ARG:HH22	2.40	0.45
32:2a:1145:C:H4'	32:2a:1146:A:H8	1.81	0.45
32:2a:1241:G:H2'	32:2a:1242:C:H6	1.82	0.45
32:2a:1445:C:O2'	32:2a:1447:A:N6	2.40	0.45
35:2d:63:LYS:HD2	35:2d:198:VAL:HG22	1.99	0.45
39:2h:2:LEU:HD21	39:2h:5:PRO:HA	1.99	0.45
40:2i:70:LYS:O	40:2i:74:ILE:N	2.44	0.45
41:2j:54:PHE:O	41:2j:56:HIS:N	2.42	0.45
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.57	0.45
1:1A:580:C:H2'	1:1A:581:C:H6	1.82	0.45
1:1A:1062:G:H22	1:1A:1077:A:H61	1.65	0.45
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	2.17	0.45
1:1A:1663:C:O2'	1:1A:1664:A:O5'	2.34	0.45
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.16	0.45
59:1A:4087:ERY:H203	59:1A:4087:ERY:H151	1.64	0.45
3:1D:130:ALA:C	3:1D:131:LEU:HD12	2.41	0.45
9:1N:67:LEU:O	9:1N:88:GLU:HB2	2.17	0.45
11:1P:121:LYS:HG2	11:1P:122:PRO:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:16:13:CYS:SG	28:16:47:THR:HG21	2.56	0.45
32:1a:553:A:H5"	43:1l:24:VAL:HG21	1.99	0.45
32:1a:986:A:H2'	32:1a:987:G:O4'	2.17	0.45
33:1b:27:LYS:HB3	33:1b:194:PRO:HD2	1.99	0.45
33:1b:70:PHE:O	33:1b:92:TYR:HA	2.17	0.45
36:1e:116:THR:HG23	36:1e:117:ASP:OD2	2.16	0.45
54:1y:11:C:H42	54:1y:24:G:H1	1.65	0.45
1:2A:94(A):G:H2'	1:2A:95:G:O4'	2.17	0.45
1:2A:1582:C:H2'	1:2A:1583:A:H8	1.82	0.45
1:2A:2251:OMG:H1'	1:2A:2251:OMG:HM23	1.71	0.45
1:2A:2371:G:O2'	28:26:46:HIS:ND1	2.47	0.45
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.52	0.45
5:2F:139:PHE:CD2	5:2F:167:ALA:HB2	2.52	0.45
6:2G:179:PRO:HG3	26:24:43:TYR:HE2	1.82	0.45
9:2N:128:HIS:C	9:2N:130:HIS:H	2.25	0.45
12:2Q:27:VAL:O	12:2Q:138:ASP:HB3	2.17	0.45
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.16	0.45
24:22:58:ALA:O	24:22:62:THR:OG1	2.34	0.45
26:24:57:GLU:HA	26:24:58:ARG:HA	1.79	0.45
32:2a:36:C:O2'	43:2l:117:ARG:NH2	2.50	0.45
32:2a:301:G:H2'	32:2a:302:G:H8	1.81	0.45
34:2c:193:TYR:HE1	34:2c:196:LEU:HD11	1.82	0.45
38:2g:130:GLY:O	38:2g:135:VAL:HG11	2.16	0.45
40:2i:71:SER:HA	40:2i:74:ILE:HB	1.97	0.45
47:2p:60:LEU:HD21	47:2p:80:PHE:HE1	1.81	0.45
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.98	0.45
1:1A:2348:U:OP2	30:18:42:ARG:NH2	2.50	0.44
3:1D:9:TYR:CE1	3:1D:13:ARG:HG3	2.52	0.44
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.99	0.44
32:1a:78:G:H8	32:1a:78:G:OP2	1.99	0.44
32:1a:1117:G:H5"	40:1i:104:ARG:CZ	2.47	0.44
32:1a:1350:A:O2'	38:1g:33:ASP:OD1	2.34	0.44
32:1a:1506:U:O2'	32:1a:1507:A:H5'	2.17	0.44
34:1c:138:VAL:HG12	34:1c:170:GLN:HB2	1.99	0.44
51:1t:64:ASP:OD2	51:1t:81:LYS:NZ	2.43	0.44
1:2A:312:G:H4'	1:2A:331:A:N3	2.32	0.44
1:2A:403:U:H4'	1:2A:404:C:H5'	1.99	0.44
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.52	0.44
1:2A:1639:U:H4'	1:2A:2699:C:H4'	1.99	0.44
2:2B:115:G:H2'	2:2B:116:G:O4'	2.17	0.44
4:2E:77:ILE:HD13	4:2E:195:LEU:HD13	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.98	0.44
10:2O:2:ILE:HG21	10:2O:8:LEU:HD11	2.00	0.44
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.57	0.44
14:2S:85:VAL:HG11	14:2S:110:LEU:HG	1.99	0.44
15:2T:127:ALA:C	15:2T:129:ARG:N	2.74	0.44
32:2a:731:G:OP1	32:2a:766:A:H1'	2.17	0.44
32:2a:782:A:OP1	32:2a:1521:G:N2	2.50	0.44
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.56	0.44
54:2w:36:A:H61	54:2w:37:MIA:H112	1.82	0.44
1:1A:1949:G:H1	1:1A:1957:C:H42	1.65	0.44
1:1A:2228:G:P	3:1D:263:ARG:HH12	2.40	0.44
1:1A:2356:C:H2'	1:1A:2357:U:O4'	2.16	0.44
1:1A:2451:A:C2	56:1z:2:ARG:HG2	2.52	0.44
11:1P:6:LEU:HD23	11:1P:6:LEU:HA	1.82	0.44
12:1Q:89:ASN:HB2	55:1x:1:C:C4	2.52	0.44
28:16:38:LYS:HE2	28:16:38:LYS:HB3	1.87	0.44
32:1a:45:U:H2'	32:1a:46:G:H8	1.82	0.44
32:1a:976:G:OP1	45:1n:32:SER:N	2.40	0.44
38:1g:78:ARG:HG3	38:1g:80:VAL:HG23	2.00	0.44
1:2A:892:G:H3'	1:2A:893:C:H5"	2.00	0.44
1:2A:1364:G:P	23:21:3:LYS:HG3	2.57	0.44
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.30	0.44
1:2A:1582:C:H2'	1:2A:1583:A:C8	2.52	0.44
1:2A:1587:A:H2'	1:2A:1588:C:C6	2.51	0.44
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.17	0.44
1:2A:2135:A:C8	1:2A:2136:C:H5	2.35	0.44
6:2G:39:ILE:HD11	6:2G:102:PHE:CZ	2.52	0.44
16:2U:66:ASN:O	16:2U:70:ARG:HG3	2.18	0.44
20:2Y:6:HIS:CE1	20:2Y:7:VAL:HG23	2.51	0.44
32:2a:581:G:OP1	46:2o:61:GLY:HA3	2.17	0.44
32:2a:683:G:H2'	32:2a:684:A:C8	2.52	0.44
32:2a:1144:G:C2'	32:2a:1145:C:H5'	2.46	0.44
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.53	0.44
32:2a:1402:4OC:H2'	32:2a:1403:C:O4'	2.17	0.44
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.17	0.44
35:2d:17:VAL:HG11	35:2d:197:PRO:HG3	1.99	0.44
38:2g:76:ARG:HB3	38:2g:156:TRP:HH2	1.82	0.44
44:2m:84:ILE:HB	50:2s:66:MET:HE2	1.99	0.44
1:1A:448:U:H1'	5:1F:84:VAL:HG11	1.99	0.44
1:1A:2593:U:H2'	1:1A:2594:C:C6	2.52	0.44
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:5:VAL:HG22	6:1G:8:LYS:H	1.82	0.44
11:1P:29:LYS:HG2	11:1P:30:THR:HG23	1.99	0.44
24:12:25:VAL:HG21	24:12:61:LEU:HD21	1.99	0.44
32:1a:222:U:H2'	32:1a:223:U:C6	2.52	0.44
32:1a:684:A:H1'	42:1k:39:PRO:HD2	2.00	0.44
32:1a:1003:G:H2'	32:1a:1004:A:N3	2.31	0.44
32:1a:1292:U:OP2	38:1g:41:ARG:NH1	2.50	0.44
32:1a:1492:A:H2'	32:1a:1493:A:C8	2.51	0.44
38:1g:9:VAL:HG21	38:1g:94:ARG:HD3	1.99	0.44
38:1g:78:ARG:HD3	38:1g:156:TRP:CZ3	2.53	0.44
38:1g:90:GLU:H	38:1g:90:GLU:HG2	1.58	0.44
49:1r:21:LYS:O	49:1r:25:THR:HG23	2.17	0.44
54:1w:37:MIA:H163	54:1w:37:MIA:H121	1.82	0.44
1:2A:1471:A:OP2	1:2A:1519:G:N1	2.46	0.44
1:2A:2202:C:O2'	3:2D:151:LYS:NZ	2.38	0.44
1:2A:2307:G:H8	1:2A:2307:G:OP1	1.99	0.44
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.50	0.44
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.48	0.44
3:2D:69:ARG:HH21	3:2D:119:ALA:HB2	1.82	0.44
5:2F:47:GLY:HA3	5:2F:95:ARG:O	2.18	0.44
6:2G:5:VAL:HG23	6:2G:8:LYS:H	1.82	0.44
10:2O:77:ILE:HB	15:2T:74:ARG:HH11	1.82	0.44
28:26:40:CYS:O	28:26:44:ARG:N	2.48	0.44
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.00	0.44
32:2a:1224:G:H1	32:2a:1363:C:H42	1.65	0.44
32:2a:1271:G:C2	32:2a:1272:G:C8	3.06	0.44
33:2b:41:ILE:HA	33:2b:41:ILE:HD13	1.71	0.44
35:2d:189:PRO:HB2	35:2d:194:LEU:HD11	1.98	0.44
36:2e:78:HIS:HD2	39:2h:104:ARG:HD2	1.82	0.44
36:2e:143:ARG:HD3	36:2e:143:ARG:HA	1.76	0.44
48:2q:59:ILE:HG22	48:2q:73:VAL:HA	2.00	0.44
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.99	0.44
1:1A:185:U:H2'	1:1A:186:G:C8	2.52	0.44
1:1A:484:C:OP1	20:1Y:51:VAL:HG22	2.17	0.44
1:1A:723:G:H2'	1:1A:724:U:O4'	2.17	0.44
1:1A:1532:C:N4	1:1A:1537:G:O6	2.51	0.44
1:1A:1685:C:H2'	1:1A:1686:C:C6	2.52	0.44
1:1A:2347:C:OP1	28:16:38:LYS:NZ	2.49	0.44
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.17	0.44
33:1b:28:PHE:CE1	33:1b:190:THR:HA	2.53	0.44
33:1b:196:LEU:HD12	33:1b:196:LEU:HA	1.87	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:63:LYS:HE3	35:1d:63:LYS:HB2	1.79	0.44
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	1.99	0.44
38:1g:50:ILE:HD13	38:1g:50:ILE:HA	1.71	0.44
55:1x:23:C:H2'	55:1x:24:U:H6	1.82	0.44
1:2A:286:C:H42	1:2A:355:G:H1	1.65	0.44
1:2A:443:A:H5"	1:2A:444:C:OP1	2.17	0.44
1:2A:764:A:H5"	3:2D:210:GLY:HA2	1.98	0.44
1:2A:2032:G:H22	1:2A:2572:A:H5'	1.82	0.44
1:2A:2482:G:O2'	54:2w:64:A:O2'	2.28	0.44
2:2B:2:C:H2'	2:2B:3:C:H6	1.82	0.44
10:2O:21:CYS:HB2	10:2O:39:ILE:HD12	1.99	0.44
13:2R:55:ALA:HB1	13:2R:84:ALA:HB2	1.99	0.44
20:2Y:5:MET:HE1	20:2Y:35:TYR:HA	1.99	0.44
32:2a:631:G:H2'	32:2a:632:A:H8	1.83	0.44
35:2d:119:GLN:HE21	35:2d:119:GLN:HB2	1.68	0.44
49:2r:58:LEU:HB2	49:2r:63:GLN:NE2	2.33	0.44
1:1A:493:G:H2'	1:1A:494:G:O4'	2.18	0.44
1:1A:2466:C:OP1	31:19:4:ARG:HB2	2.18	0.44
1:1A:2492:U:H2'	1:1A:2493:U:C6	2.53	0.44
1:1A:2689:U:O2	1:1A:2689:U:H2'	2.17	0.44
3:1D:136:ILE:O	3:1D:168:ARG:NH2	2.50	0.44
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	2.00	0.44
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.48	0.44
6:1G:61:ALA:O	6:1G:65:GLY:N	2.49	0.44
10:1O:88:ASN:C	10:1O:90:GLN:H	2.25	0.44
32:1a:1226:C:H4'	50:1s:80:TYR:OH	2.17	0.44
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	1.98	0.44
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	2.00	0.44
47:1p:50:LYS:HA	47:1p:50:LYS:HD2	1.77	0.44
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.42	0.44
1:2A:558:G:H5'	9:2N:112:LEU:HD23	1.98	0.44
1:2A:781:A:N1	1:2A:1776:G:O2'	2.49	0.44
1:2A:990:A:C6	1:2A:1186:G:H1'	2.53	0.44
1:2A:1607:C:H5"	1:2A:1608:A:H5'	2.00	0.44
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.39	0.44
1:2A:2555:U:O2	54:2w:74:C:C2	2.71	0.44
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.33	0.44
5:2F:29:ASN:N	5:2F:112:MET:SD	2.81	0.44
12:2Q:41:TRP:HB3	12:2Q:94:VAL:HB	1.98	0.44
12:2Q:66:ILE:HG12	12:2Q:104:PHE:CD1	2.51	0.44
24:22:1:MET:HE3	24:22:5:GLU:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:64:GLY:C	26:24:66:SER:N	2.74	0.44
32:2a:127:G:N2	48:2q:61:GLU:OE2	2.46	0.44
32:2a:401:C:O2'	32:2a:621:A:N3	2.46	0.44
32:2a:865:A:H2	32:2a:918:A:H4'	1.82	0.44
32:2a:1320:C:N3	50:2s:36:ARG:NH2	2.65	0.44
36:2e:103:GLY:O	36:2e:106:PRO:HD2	2.17	0.44
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.33	0.44
38:2g:33:ASP:HB2	38:2g:35:LYS:HD3	2.00	0.44
42:2k:92:GLU:O	42:2k:96:ARG:HG2	2.18	0.44
43:2l:49:ASN:N	43:2l:49:ASN:OD1	2.50	0.44
48:2q:45:HIS:NE2	48:2q:47:PRO:HG3	2.33	0.44
1:1A:226:G:N2	1:1A:228:A:H62	2.16	0.44
1:1A:2134:A:H2'	1:1A:2159:G:O2'	2.18	0.44
1:1A:2147:G:H2'	1:1A:2148:G:H4'	1.99	0.44
1:1A:2316:C:O2'	6:1G:128:ARG:NH2	2.51	0.44
3:1D:60:ARG:HD3	3:1D:87:ASN:ND2	2.33	0.44
32:1a:194:C:H2'	32:1a:195:A:H5"	1.99	0.44
32:1a:288:A:H3'	62:1a:2002:HOH:O	2.17	0.44
32:1a:909:A:H2'	32:1a:910:C:O4'	2.17	0.44
32:1a:1381:U:O2	38:1g:79:ARG:HG2	2.17	0.44
33:1b:82:ARG:HD2	33:1b:92:TYR:CZ	2.52	0.44
33:1b:163:PHE:HA	33:1b:185:ILE:O	2.18	0.44
54:1y:46:G7M:O2'	54:1y:48:C:OP2	2.35	0.44
1:2A:784:A:N6	3:2D:229:VAL:HG11	2.33	0.44
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.17	0.44
1:2A:1359:A:H2	1:2A:1372:U:O4	2.01	0.44
1:2A:1472:A:H2'	1:2A:1473:G:O4'	2.18	0.44
1:2A:1747:G:H2'	1:2A:1747(A):G:C8	2.52	0.44
1:2A:2494:G:N7	62:2A:4070:HOH:O	2.36	0.44
1:2A:2722:G:H2'	1:2A:2723:C:C6	2.53	0.44
2:2B:98:G:H3'	2:2B:99:G:C8	2.47	0.44
3:2D:159:ALA:HB1	3:2D:198:ASN:O	2.18	0.44
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.53	0.44
6:2G:83:ARG:O	6:2G:85:GLY:N	2.51	0.44
7:2H:104:GLU:HG3	7:2H:112:PRO:HB2	1.99	0.44
15:2T:8:LYS:HZ3	15:2T:57:PHE:H	1.65	0.44
22:20:28:GLY:HA2	22:20:66:VAL:HG13	2.00	0.44
30:28:16:ILE:HD11	30:28:59:LYS:HG2	2.00	0.44
32:2a:558:G:H2'	32:2a:559:A:H2	1.83	0.44
32:2a:778:G:H2'	32:2a:779:C:O4'	2.17	0.44
32:2a:780:A:H1'	32:2a:803:G:N2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:218:ALA:O	33:2b:222:ILE:HG23	2.16	0.44
44:2m:40:ASN:ND2	44:2m:43:THR:HG23	2.32	0.44
1:1A:224:G:H2'	1:1A:225:A:O4'	2.18	0.44
1:1A:303:U:H2'	1:1A:304:G:H8	1.82	0.44
1:1A:1322:A:N1	1:1A:1333:C:O2'	2.43	0.44
1:1A:1396:U:H6	1:1A:1396:U:H2'	1.68	0.44
1:1A:1578:U:C2'	1:1A:1579:A:H5'	2.48	0.44
1:1A:2028:U:O4	62:1A:4177:HOH:O	2.21	0.44
1:1A:2040:C:H2'	1:1A:2041:U:O4'	2.18	0.44
2:1B:92:C:OP1	12:1Q:19:GLY:N	2.45	0.44
3:1D:78:LYS:HE2	3:1D:114:GLY:HA2	1.99	0.44
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.18	0.44
11:1P:42:SER:OG	62:1P:303:HOH:O	2.21	0.44
16:1U:104:GLN:NE2	16:1U:105:VAL:HG23	2.32	0.44
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.52	0.44
30:18:52:LYS:N	30:18:53:PRO:HD2	2.33	0.44
32:1a:1347:G:O2'	32:1a:1373:G:O6	2.25	0.44
32:1a:1414:U:H2'	32:1a:1415:G:C8	2.50	0.44
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.17	0.44
35:1d:65:ARG:NH1	35:1d:72:GLU:OE1	2.50	0.44
35:1d:111:ALA:HA	35:1d:161:ASN:HD22	1.83	0.44
35:1d:112:VAL:H	35:1d:116:GLN:NE2	2.15	0.44
36:1e:90:VAL:O	36:1e:120:THR:HA	2.18	0.44
51:1t:30:LYS:O	51:1t:34:LYS:HG3	2.17	0.44
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.17	0.44
1:2A:1401:G:H2'	1:2A:1402:C:O4'	2.18	0.44
1:2A:1858:G:H8	1:2A:1858:G:OP2	1.99	0.44
1:2A:2010:G:H5"	18:2W:42:ARG:HB2	2.00	0.44
1:2A:2886:G:H2'	1:2A:2887:U:C6	2.53	0.44
2:2B:77:U:H4'	21:2Z:84:GLU:OE1	2.17	0.44
9:2N:28:THR:HG22	9:2N:29:LYS:N	2.31	0.44
21:2Z:106:GLY:HA3	21:2Z:141:VAL:HB	1.99	0.44
32:2a:84:U:H4'	32:2a:89:C:C4	2.52	0.44
32:2a:284:G:H2'	32:2a:285:G:H8	1.82	0.44
32:2a:877:C:H5"	39:2h:88:LYS:HD3	2.00	0.44
32:2a:984:C:H2'	32:2a:985:C:C6	2.52	0.44
32:2a:1003:G:N2	32:2a:1025:U:O4	2.51	0.44
32:2a:1209:C:O2'	32:2a:1214:C:N4	2.44	0.44
32:2a:1259:C:C4	32:2a:1260:C:H1'	2.53	0.44
33:2b:163:PHE:HA	33:2b:185:ILE:HG13	1.99	0.44
34:2c:136:GLN:O	34:2c:140:ARG:N	2.30	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:68:GLU:HG2	36:2e:70:PRO:HD3	2.00	0.44
40:2i:78:LYS:HE2	40:2i:101:PHE:HE1	1.81	0.44
42:2k:32:ILE:HD12	42:2k:72:ALA:HB2	2.00	0.44
1:1A:207:A:H2'	1:1A:208:C:O4'	2.17	0.44
1:1A:1108:U:H2'	1:1A:1109:C:O4'	2.17	0.44
1:1A:1417:C:H2'	1:1A:1418:G:O4'	2.17	0.44
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.52	0.44
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.17	0.44
6:1G:17:PRO:HA	6:1G:20:ILE:HD12	1.99	0.44
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.52	0.44
24:12:3:LEU:O	24:12:7:ARG:HG3	2.18	0.44
32:1a:444:C:H2'	32:1a:445:G:H8	1.83	0.44
32:1a:458:C:H2'	32:1a:460:G:O4'	2.17	0.44
32:1a:502:G:C2	32:1a:503:C:C2	3.06	0.44
32:1a:1318:A:H5"	50:1s:3:ARG:HH12	1.83	0.44
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	2.00	0.44
33:1b:210:SER:OG	33:1b:211:ILE:N	2.51	0.44
34:1c:63:ASN:N	34:1c:63:ASN:OD1	2.50	0.44
47:1p:55:ARG:NH2	47:1p:58:TYR:HD2	2.14	0.44
1:2A:492:A:H2'	1:2A:493:G:O4'	2.18	0.44
1:2A:2156:G:H2'	1:2A:2157:G:C5	2.53	0.44
1:2A:2207:G:H2'	1:2A:2208:A:C2	2.53	0.44
1:2A:2342:C:O2'	1:2A:2374:C:H5"	2.18	0.44
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.50	0.44
1:2A:2591:C:P	3:2D:239:ARG:HG3	2.57	0.44
32:2a:236:G:OP1	48:2q:40:LYS:NZ	2.45	0.44
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.85	0.44
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.82	0.44
34:2c:33:LEU:HA	34:2c:36:ASP:HB2	1.98	0.44
39:2h:36:LEU:HA	39:2h:39:LEU:HD12	1.99	0.44
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.83	0.44
40:2i:57:GLY:C	40:2i:59:PHE:H	2.26	0.44
1:1A:118:A:H3'	1:1A:119:A:C5'	2.48	0.44
1:1A:154(A):C:N4	1:1A:171:G:H1	2.15	0.44
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.53	0.44
1:1A:1636:C:H2'	1:1A:1637:A:C8	2.53	0.44
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.53	0.44
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.82	0.44
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	2.00	0.44
15:1T:35:LYS:HG3	15:1T:40:THR:HG22	1.99	0.44
22:10:18:ALA:HB3	22:10:20:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:62:ARG:C	26:14:63:TYR:CG	2.96	0.44
32:1a:256:U:H2'	32:1a:257:G:O4'	2.17	0.44
32:1a:1127:G:H5'	32:1a:1280:A:O2'	2.18	0.44
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.99	0.44
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.52	0.44
35:1d:182:LYS:HB2	35:1d:182:LYS:HE3	1.83	0.44
39:1h:29:SER:OG	39:1h:32:LYS:HG3	2.18	0.44
42:1k:48:ILE:HD12	42:1k:63:LEU:HB3	1.99	0.44
43:1l:90:VAL:O	43:1l:92:0TD:N	2.50	0.44
1:2A:729:G:O5'	3:2D:208:LYS:NZ	2.48	0.44
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.99	0.44
1:2A:910:A:C5	12:2Q:13:GLN:HG3	2.52	0.44
1:2A:1449:A:C2	1:2A:1529:G:H1'	2.53	0.44
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.53	0.44
1:2A:1508:A:H5'	1:2A:1509(A):A:N7	2.33	0.44
1:2A:1666:G:C2'	1:2A:1667:G:H5'	2.48	0.44
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.18	0.44
1:2A:2114:A:N6	1:2A:2115:G:H21	2.12	0.44
1:2A:2335:A:O2'	1:2A:2336:A:OP2	2.35	0.44
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.18	0.44
13:2R:57:ARG:NE	13:2R:59:ASP:OD1	2.44	0.44
19:2X:25:LYS:HA	19:2X:81:VAL:O	2.18	0.44
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.18	0.44
32:2a:1128:C:O2'	32:2a:1129:C:OP1	2.27	0.44
32:2a:1164:G:H1	32:2a:1172:C:H42	1.64	0.44
32:2a:1306:A:H2'	32:2a:1307:U:O4'	2.18	0.44
36:2e:83:GLU:O	36:2e:85:GLY:N	2.49	0.44
41:2j:15:THR:O	41:2j:19:SER:N	2.48	0.44
44:2m:23:TYR:CD2	44:2m:70:LEU:HD23	2.53	0.44
55:2x:16:C:H4'	55:2x:60:U:H1'	2.00	0.44
55:2x:55:PSU:N3	55:2x:58:A:OP2	2.41	0.44
1:1A:2190:G:C2	1:1A:2191:G:C8	3.06	0.43
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.18	0.43
1:1A:2422:A:N7	30:18:31:HIS:HE1	2.16	0.43
4:1E:35:GLN:H	4:1E:48:GLN:HB3	1.83	0.43
5:1F:28:ILE:HG21	11:1P:1:MET:HE1	1.99	0.43
5:1F:117:ARG:NH2	11:1P:1:MET:O	2.35	0.43
9:1N:9:VAL:HG21	9:1N:39:ARG:NH1	2.33	0.43
15:1T:113:LYS:HA	15:1T:113:LYS:HD3	1.80	0.43
18:1W:67:ASP:N	18:1W:67:ASP:OD1	2.49	0.43
20:1Y:86:ARG:HB3	20:1Y:98:VAL:HG23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:167:G:H2'	32:1a:168:G:C8	2.53	0.43
32:1a:399:G:H2'	32:1a:400:C:C6	2.52	0.43
55:1x:17:C:OP2	55:1x:17(A):U:O2'	2.28	0.43
54:1y:8:4SU:H4'	54:1y:48:C:H4'	1.99	0.43
1:2A:390:A:C6	11:2P:71:VAL:HG11	2.53	0.43
1:2A:527:C:N4	1:2A:2779:U:OP2	2.44	0.43
1:2A:1671:U:H1'	4:2E:129:HIS:CE1	2.53	0.43
1:2A:1817:G:C6	1:2A:1818:U:C4	3.06	0.43
1:2A:2200:C:O2	1:2A:2226:C:N4	2.51	0.43
1:2A:2282:G:H4'	1:2A:2389:G:O2'	2.18	0.43
1:2A:2335:A:C8	1:2A:2337:G:C5	3.05	0.43
1:2A:2503:2MA:C8	59:2A:3857:ERY:H282	2.48	0.43
2:2B:105:A:P	21:2Z:72:ARG:HE	2.41	0.43
5:2F:59:TYR:HB3	5:2F:78:ILE:HD11	2.00	0.43
9:2N:32:THR:HG23	9:2N:37:LYS:HB2	1.99	0.43
16:2U:88:ILE:HG22	16:2U:90:VAL:HG23	1.99	0.43
32:2a:631:G:H2'	32:2a:632:A:C8	2.52	0.43
32:2a:767:A:H2'	32:2a:768:A:O4'	2.18	0.43
32:2a:1240:U:N3	38:2g:30:ILE:O	2.46	0.43
32:2a:1255:G:OP2	41:2j:45:ARG:NH2	2.51	0.43
33:2b:44:LEU:H	33:2b:44:LEU:HD12	1.82	0.43
34:2c:88:ARG:O	34:2c:91:LEU:HB2	2.18	0.43
35:2d:162:LEU:HA	35:2d:165:MET:HB2	2.00	0.43
50:2s:49:ILE:HG12	50:2s:50:ALA:N	2.33	0.43
54:2w:36:A:H2'	54:2w:37:MIA:H8	2.00	0.43
1:1A:661:C:H4'	11:1P:13:ASN:OD1	2.17	0.43
1:1A:862:G:H2'	1:1A:863:A:O4'	2.18	0.43
1:1A:1826:G:H2'	1:1A:1827:C:O4'	2.18	0.43
6:1G:151:ALA:HB3	6:1G:153:ARG:NH1	2.33	0.43
8:1I:130:TYR:CE2	8:1I:132:PRO:HB3	2.48	0.43
13:1R:2:ARG:HA	13:1R:5:LYS:HD2	2.00	0.43
13:1R:9:LYS:O	13:1R:17:ARG:HD3	2.18	0.43
25:13:26:LEU:O	25:13:35:ARG:HD3	2.19	0.43
32:1a:438:G:H4'	35:1d:123:HIS:CE1	2.53	0.43
32:1a:636:U:H2'	32:1a:637:G:C8	2.53	0.43
32:1a:658:G:OP1	46:1o:8:LYS:NZ	2.44	0.43
32:1a:995:C:O2	45:1n:4:LYS:NZ	2.33	0.43
32:1a:1128:C:H4'	32:1a:1148:U:O2	2.18	0.43
32:1a:1372:U:H2'	32:1a:1373:G:O4'	2.17	0.43
33:1b:125:PRO:O	33:1b:127:ILE:N	2.51	0.43
36:1e:81:GLU:HG2	36:1e:90:VAL:HG13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:75:LEU:O	37:1f:79:LEU:HG	2.18	0.43
40:1i:96:LEU:HD13	40:1i:101:PHE:HB2	1.99	0.43
46:1o:33:THR:HG23	46:1o:63:ARG:NH1	2.33	0.43
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.18	0.43
51:1t:89:ARG:HH12	51:1t:103:GLY:HA3	1.81	0.43
54:1y:52:G:H2'	54:1y:53:G:C8	2.52	0.43
1:2A:2018:G:H2'	1:2A:2019:A:O4'	2.17	0.43
1:2A:2650:U:H2'	1:2A:2651:C:H6	1.83	0.43
2:2B:48:A:P	14:2S:30:ARG:HH22	2.39	0.43
4:2E:176:ILE:HB	4:2E:181:LEU:HB2	2.00	0.43
21:2Z:77:ASP:OD2	21:2Z:80:ARG:NH1	2.51	0.43
26:24:11:PRO:HA	26:24:24:THR:O	2.18	0.43
29:27:26:GLY:O	29:27:30:VAL:HG23	2.17	0.43
32:2a:1320:C:C2	50:2s:72:GLY:HA3	2.53	0.43
41:2j:55:LYS:O	41:2j:57:LYS:N	2.51	0.43
47:2p:39:TYR:CD1	47:2p:73:LEU:HD21	2.53	0.43
55:2x:17:C:OP2	55:2x:18:G:H5"	2.19	0.43
1:1A:783:A:O2'	1:1A:785:G:OP1	2.31	0.43
1:1A:1355:G:P	3:1D:38:LYS:HE2	2.58	0.43
1:1A:1951:U:O2	1:1A:1953:A:H8	2.01	0.43
1:1A:2335:A:C8	1:1A:2337:G:C5	3.06	0.43
1:1A:2492:U:H2'	1:1A:2493:U:H6	1.83	0.43
1:1A:2610:C:O2	59:1A:4087:ERY:H201	2.18	0.43
1:1A:2690:C:OP2	13:1R:14:SER:HB2	2.17	0.43
22:10:23:VAL:HG22	22:10:38:VAL:HG22	2.01	0.43
27:15:40:LYS:HD3	27:15:46:CYS:HB2	2.00	0.43
32:1a:911:U:H2'	32:1a:912:C:C6	2.54	0.43
32:1a:977:A:H1'	32:1a:982:U:O4	2.18	0.43
35:1d:101:LEU:HD22	35:1d:121:VAL:HG21	1.99	0.43
36:1e:37:ARG:HH12	36:1e:111:GLU:HB3	1.83	0.43
37:1f:45:LEU:HD23	37:1f:57:GLN:NE2	2.34	0.43
1:2A:153:C:H2'	1:2A:154:G:O4'	2.17	0.43
1:2A:1130:U:O2	1:2A:2025:C:H5"	2.17	0.43
1:2A:2317:C:H2'	1:2A:2318:G:H5'	2.00	0.43
1:2A:2688:U:O2'	1:2A:2721:A:N6	2.51	0.43
3:2D:29:PRO:HB2	3:2D:30:GLU:H	1.69	0.43
10:2O:105:GLU:OE1	10:2O:105:GLU:N	2.49	0.43
11:2P:121:LYS:HE2	11:2P:121:LYS:HB3	1.66	0.43
20:2Y:46:LYS:HG3	20:2Y:60:PHE:HB3	2.00	0.43
32:2a:56:U:H2'	32:2a:57:G:H8	1.82	0.43
32:2a:164:U:H2'	32:2a:165:C:H6	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:224:C:H2'	32:2a:225:C:H6	1.82	0.43
32:2a:227:G:H2'	32:2a:228:A:C8	2.53	0.43
32:2a:575:G:O2'	32:2a:821:G:H5'	2.17	0.43
32:2a:875:C:O2'	39:2h:14:ARG:HD2	2.19	0.43
32:2a:1347:G:H8	40:2i:107:ARG:HB3	1.82	0.43
32:2a:1425:U:H2'	32:2a:1426:C:C6	2.52	0.43
43:2l:113:ARG:HB3	43:2l:122:THR:HG21	2.00	0.43
52:2u:2:GLY:O	52:2u:4:GLY:N	2.46	0.43
1:1A:227:A:C2	1:1A:2407:G:H1'	2.53	0.43
1:1A:329:G:H8	1:1A:329:G:OP1	2.02	0.43
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.52	0.43
1:1A:1063:G:H2'	1:1A:1064:C:H5	1.83	0.43
4:1E:179:GLU:HG3	15:1T:9:LEU:HD21	1.99	0.43
15:1T:11:GLU:OE2	15:1T:57:PHE:HB3	2.18	0.43
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.53	0.43
32:1a:519:C:H2'	32:1a:520:A:C8	2.52	0.43
32:1a:1132:C:H2'	32:1a:1133:G:C8	2.53	0.43
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.53	0.43
32:1a:1499:A:H3'	62:1a:1920:HOH:O	2.18	0.43
34:1c:43:LEU:O	34:1c:47:LEU:HB2	2.18	0.43
35:1d:173:TRP:N	35:1d:173:TRP:CD1	2.86	0.43
48:1q:14:LYS:HD3	48:1q:14:LYS:HA	1.72	0.43
54:1w:43:C:H2'	54:1w:44:G:C8	2.54	0.43
1:2A:30:G:H2'	1:2A:31:C:C6	2.53	0.43
1:2A:924:C:H2'	1:2A:925:C:C6	2.53	0.43
1:2A:1199:U:H2'	1:2A:1200:C:C6	2.52	0.43
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.33	0.43
2:2B:4:C:H2'	2:2B:5:C:C6	2.53	0.43
2:2B:48:A:H5'	14:2S:93:LYS:HE2	2.00	0.43
3:2D:169:GLU:OE2	3:2D:184:LYS:NZ	2.41	0.43
7:2H:31:GLY:HA3	7:2H:136:ILE:HG21	1.99	0.43
7:2H:76:VAL:O	7:2H:80:SER:OG	2.31	0.43
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.18	0.43
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.49	0.43
12:2Q:103:MET:HE1	12:2Q:127:ILE:HD11	1.99	0.43
25:23:38:GLU:HB2	25:23:43:ILE:HD12	2.00	0.43
32:2a:309:G:O2'	32:2a:607:A:N1	2.51	0.43
32:2a:362:G:N2	32:2a:365:U:OP2	2.50	0.43
32:2a:848:C:H2'	32:2a:849:C:C6	2.54	0.43
32:2a:860:A:H61	32:2a:872:A:H62	1.65	0.43
32:2a:865:A:C2	32:2a:918:A:H4'	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:866:C:C4	32:2a:867:G:H1'	2.53	0.43
33:2b:118:LEU:HD11	33:2b:138:LEU:HD23	2.01	0.43
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	2.00	0.43
38:2g:97:GLN:O	38:2g:101:LEU:N	2.38	0.43
40:2i:24:GLY:O	40:2i:25:LYS:HD3	2.19	0.43
54:2y:68:C:H2'	54:2y:69:G:O4'	2.19	0.43
1:1A:30:G:H2'	1:1A:31:C:C6	2.54	0.43
1:1A:196:A:H2'	1:1A:196:A:N3	2.33	0.43
1:1A:196:A:O2'	1:1A:805:G:O6	2.29	0.43
1:1A:806:C:O2	1:1A:2444:G:O2'	2.32	0.43
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.53	0.43
1:1A:2053:G:OP1	4:1E:144:ARG:HG3	2.18	0.43
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.33	0.43
5:1F:64:ILE:HG13	5:1F:65:TRP:H	1.82	0.43
7:1H:24:VAL:HG21	7:1H:72:ILE:HD12	2.00	0.43
12:1Q:138:ASP:OD2	21:1Z:81:ARG:NH1	2.51	0.43
23:11:12:PRO:HB2	23:11:41:ARG:HH21	1.83	0.43
32:1a:107:G:H2'	32:1a:108:G:O4'	2.18	0.43
32:1a:136:C:O2'	47:1p:63:GLY:O	2.37	0.43
32:1a:966:M2G:HM13	32:1a:967:5MC:H1'	1.99	0.43
32:1a:1038:C:H2'	32:1a:1039:C:C6	2.54	0.43
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.18	0.43
33:1b:12:GLU:C	33:1b:14:GLY:N	2.76	0.43
35:1d:173:TRP:O	35:1d:186:LEU:HB2	2.19	0.43
36:1e:56:GLN:O	36:1e:56:GLN:HG2	2.16	0.43
40:1i:128:ARG:NH1	55:1x:35:A:OP2	2.51	0.43
41:1j:11:PHE:HB3	45:1n:55:GLY:HA3	2.00	0.43
54:1w:10:G:H2'	54:1w:11:C:H6	1.83	0.43
55:1x:14:A:N1	55:1x:21:A:O2'	2.44	0.43
1:2A:407:G:H2'	1:2A:408:G:H8	1.83	0.43
1:2A:947:G:H2'	1:2A:948:G:C8	2.54	0.43
1:2A:1229:G:C2	1:2A:1230:C:C2	3.06	0.43
1:2A:2774:C:H2'	1:2A:2775:A:O4'	2.17	0.43
7:2H:126:PRO:HB2	7:2H:127:GLU:H	1.65	0.43
8:2I:66:GLU:HA	8:2I:69:LYS:HB3	2.00	0.43
19:2X:92:LEU:HA	19:2X:92:LEU:HD23	1.76	0.43
20:2Y:82:PRO:O	20:2Y:101:LYS:NZ	2.51	0.43
21:2Z:150:LEU:HD23	21:2Z:150:LEU:HA	1.86	0.43
32:2a:189(A):C:H2'	32:2a:189(B):C:H6	1.83	0.43
32:2a:555:C:H2'	32:2a:556:C:C6	2.54	0.43
32:2a:598:U:H2'	32:2a:599:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.48	0.43
32:2a:1183:A:O2'	32:2a:1185:G:OP2	2.36	0.43
32:2a:1271:G:C2	32:2a:1272:G:N7	2.87	0.43
33:2b:198:ASP:OD1	33:2b:198:ASP:N	2.52	0.43
33:2b:207:ALA:O	33:2b:211:ILE:HG13	2.18	0.43
35:2d:155:LEU:O	35:2d:159:ARG:HG3	2.18	0.43
51:2t:29:LYS:HB2	51:2t:71:THR:HG21	1.99	0.43
1:1A:218:A:C2	1:1A:235:U:H4'	2.53	0.43
1:1A:428:A:H8	1:1A:428:A:OP2	2.01	0.43
1:1A:751:A:C6	1:1A:789:A:C5	3.07	0.43
1:1A:2472:G:H2'	1:1A:2475:C:H42	1.83	0.43
2:1B:78:A:H2'	2:1B:79:C:O4'	2.18	0.43
3:1D:118:VAL:HG22	3:1D:119:ALA:H	1.82	0.43
28:16:12:GLU:HB2	28:16:19:ARG:HG3	2.01	0.43
32:1a:430:A:OP2	35:1d:8:VAL:HG12	2.18	0.43
32:1a:964:A:N3	32:1a:969:A:O2'	2.44	0.43
32:1a:1227:A:O3'	44:1m:115:LYS:HE2	2.18	0.43
32:1a:1309:G:H2'	32:1a:1310:G:O4'	2.18	0.43
32:1a:1530:G:OP1	32:1a:1530:G:H4'	2.17	0.43
54:1y:55:PSU:N3	54:1y:57:G:H5'	2.33	0.43
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.54	0.43
3:2D:76:PRO:O	3:2D:98:VAL:HG22	2.18	0.43
4:2E:12:THR:HG22	4:2E:13:ARG:N	2.34	0.43
6:2G:45:GLU:H	6:2G:45:GLU:HG2	1.38	0.43
15:2T:92:GLY:O	15:2T:120:ARG:NH2	2.52	0.43
15:2T:105:LEU:HB2	15:2T:110:ILE:HG13	2.00	0.43
32:2a:491:G:H2'	32:2a:492:G:O4'	2.18	0.43
32:2a:723:U:O2'	32:2a:724:G:H5'	2.19	0.43
32:2a:748:C:H4'	32:2a:749:C:O5'	2.18	0.43
35:2d:43:HIS:CD2	35:2d:43:HIS:H	2.36	0.43
36:2e:145:LYS:HA	36:2e:148:VAL:HB	2.00	0.43
39:2h:81:HIS:ND1	39:2h:138:TRP:OXT	2.38	0.43
42:2k:125:PHE:HD1	42:2k:125:PHE:HA	1.67	0.43
51:2t:77:ALA:O	51:2t:81:LYS:HG3	2.18	0.43
54:2w:11:C:N4	54:2w:24:G:H1	2.17	0.43
1:1A:124:G:OP1	1:1A:1376:C:O2'	2.35	0.43
1:1A:536:A:H5'	16:1U:53:ARG:HD3	2.00	0.43
1:1A:603:A:H3'	11:1P:90:ARG:NH2	2.33	0.43
1:1A:944:G:H5"	1:1A:945:A:O5'	2.19	0.43
1:1A:2512:C:H4'	4:1E:122:PHE:CE2	2.54	0.43
2:1B:41:U:P	2:1B:43:C:H41	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:76:PRO:O	3:1D:98:VAL:HG22	2.19	0.43
4:1E:104:VAL:HA	4:1E:197:ILE:O	2.19	0.43
15:1T:90:GLN:HG3	15:1T:91:ARG:N	2.32	0.43
19:1X:41:ASN:OD1	19:1X:41:ASN:N	2.51	0.43
21:1Z:152:ALA:HB3	21:1Z:167:PRO:HA	2.01	0.43
32:1a:193:C:H2'	32:1a:194:C:C6	2.48	0.43
32:1a:841:U:OP2	32:1a:841:U:H6	2.01	0.43
32:1a:942:G:C2	32:1a:1342:C:C2	3.06	0.43
32:1a:1122:U:C4	32:1a:1123:A:N7	2.87	0.43
35:1d:43:HIS:HB3	35:1d:46:LYS:HG3	2.01	0.43
35:1d:122:ARG:HD2	35:1d:122:ARG:HA	1.79	0.43
39:1h:87:SER:OG	39:1h:92:ARG:HA	2.19	0.43
41:1j:16:LEU:HD12	41:1j:16:LEU:HA	1.88	0.43
42:1k:51:LYS:HA	42:1k:51:LYS:HD3	1.72	0.43
48:1q:81:ARG:HD2	48:1q:83:ASP:OD1	2.18	0.43
54:1w:5:G:H2'	54:1w:6:G:C8	2.53	0.43
1:2A:1121:C:H2'	1:2A:1122:G:O4'	2.18	0.43
1:2A:1529:G:C6	1:2A:1530:C:N4	2.86	0.43
1:2A:2521:C:C4	1:2A:2522:U:C4	3.07	0.43
2:2B:7:G:H4'	14:2S:29:PHE:CG	2.54	0.43
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.65	0.43
21:2Z:73:GLN:HB3	21:2Z:87:ASP:CG	2.43	0.43
32:2a:5:U:H5'	32:2a:6:G:C5	2.53	0.43
32:2a:512:U:H2'	32:2a:513:C:C6	2.53	0.43
32:2a:578:C:H2'	32:2a:579:G:C8	2.53	0.43
32:2a:741:G:H2'	32:2a:742:G:O4'	2.18	0.43
32:2a:833:U:H2'	32:2a:834:C:H6	1.84	0.43
32:2a:1225:A:OP1	44:2m:103:THR:OG1	2.36	0.43
32:2a:1402:4OC:H6	32:2a:1402:4OC:O5'	2.19	0.43
34:2c:20:SER:HB3	34:2c:22:TRP:HE1	1.83	0.43
35:2d:98:GLU:HG3	35:2d:194:LEU:HD21	2.01	0.43
35:2d:177:ASP:HB3	35:2d:182:LYS:HB2	2.01	0.43
38:2g:94:ARG:HG3	38:2g:95:ARG:N	2.34	0.43
54:2y:37:MIA:H2'	54:2y:38:A:O4'	2.18	0.43
1:1A:121:G:H4'	1:1A:149:A:H5'	2.01	0.43
1:1A:182:A:N3	1:1A:433:C:O2'	2.45	0.43
1:1A:687:C:H1'	29:17:4:THR:HG22	2.01	0.43
1:1A:805:G:C4'	11:1P:38:GLN:HG3	2.48	0.43
1:1A:1010:A:H1'	1:1A:1153:C:H1'	2.00	0.43
1:1A:1814:G:O3'	3:1D:54:ARG:NH2	2.52	0.43
1:1A:1949:G:C6	1:1A:1950:G:C6	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2314:C:H2'	1:1A:2315:G:C8	2.54	0.43
7:1H:28:GLY:HA3	7:1H:79:VAL:HB	2.01	0.43
14:1S:38:GLN:HB2	14:1S:47:THR:CG2	2.48	0.43
32:1a:975:A:H5'	32:1a:975:A:C8	2.51	0.43
35:1d:196:LEU:HD23	35:1d:197:PRO:HD2	1.99	0.43
35:1d:196:LEU:C	35:1d:198:VAL:H	2.27	0.43
42:1k:33:THR:HG22	42:1k:39:PRO:HA	2.00	0.43
47:1p:43:LYS:HG2	47:1p:48:TRP:CE2	2.54	0.43
54:1y:68:C:H2'	54:1y:69:G:C8	2.53	0.43
1:2A:359:A:H2'	1:2A:360:G:O4'	2.19	0.43
1:2A:624:C:O2'	1:2A:657:U:OP1	2.37	0.43
1:2A:817:C:O2'	1:2A:839:U:H5"	2.18	0.43
1:2A:1218:C:H42	1:2A:1231:G:H1	1.65	0.43
1:2A:1421:G:C2	1:2A:1422:G:C8	3.07	0.43
3:2D:63:ARG:HG2	3:2D:92:ILE:HD13	1.99	0.43
25:23:26:LEU:O	25:23:35:ARG:NE	2.51	0.43
32:2a:6:G:H4'	32:2a:298:A:H4'	2.01	0.43
32:2a:130:A:H1'	32:2a:263:A:O2'	2.19	0.43
32:2a:229:U:H5"	47:2p:33:ILE:HD13	2.00	0.43
32:2a:241:C:C2	32:2a:286:G:C2	3.07	0.43
32:2a:801:U:H2'	32:2a:802:A:C8	2.54	0.43
32:2a:1227:A:OP2	44:2m:111:LYS:HD3	2.19	0.43
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.54	0.43
32:2a:1371:G:O3'	40:2i:69:GLY:HA3	2.19	0.43
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.32	0.43
32:2a:1427:U:H2'	32:2a:1428:A:H8	1.84	0.43
33:2b:105:PHE:C	33:2b:107:THR:H	2.26	0.43
34:2c:22:TRP:CZ2	45:2n:54:PRO:HG2	2.54	0.43
35:2d:79:PHE:HA	35:2d:93:PHE:CD1	2.54	0.43
38:2g:73:MET:SD	38:2g:90:GLU:HG3	2.59	0.43
43:2l:92:0TD:H4	43:2l:92:0TD:H8	1.79	0.43
1:1A:478:A:C6	1:1A:480:A:C6	3.07	0.43
1:1A:1209:G:OP2	62:1A:4178:HOH:O	2.21	0.43
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.53	0.43
3:1D:68:LYS:C	3:1D:70:TRP:H	2.27	0.43
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.59	0.43
17:1V:34:GLU:HB3	17:1V:56:SER:HB2	2.01	0.43
17:1V:49:THR:O	17:1V:49:THR:OG1	2.34	0.43
25:13:35:ARG:HE	25:13:37:LEU:HD21	1.83	0.43
32:1a:936:C:H2'	32:1a:937:A:O4'	2.19	0.43
33:1b:64:ARG:HB2	33:1b:64:ARG:HH11	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:441:U:H2'	1:2A:442:G:H8	1.83	0.43
1:2A:631:A:OP1	11:2P:65:ARG:HD3	2.19	0.43
1:2A:667:U:O2	30:28:2:PRO:HD2	2.18	0.43
1:2A:687:C:H2'	1:2A:688:U:O4'	2.19	0.43
1:2A:856:C:H2'	1:2A:857:C:C6	2.54	0.43
1:2A:975(A):G:H1'	1:2A:990:A:C2	2.54	0.43
1:2A:1667:G:H8	1:2A:1667:G:OP2	2.02	0.43
1:2A:1788:C:H2'	1:2A:1789:A:O4'	2.19	0.43
1:2A:2064:C:H2'	1:2A:2065:C:C6	2.54	0.43
1:2A:2630:G:H1	1:2A:2788:C:H42	1.66	0.43
1:2A:2869:G:H2'	1:2A:2870:C:O4'	2.18	0.43
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.49	0.43
13:2R:36:THR:HG22	13:2R:37:THR:N	2.34	0.43
17:2V:40:LEU:HB2	17:2V:46:VAL:CG1	2.49	0.43
24:22:1:MET:N	24:22:52:ASP:OD1	2.50	0.43
32:2a:651:C:H2'	32:2a:652:U:C6	2.54	0.43
32:2a:751:U:H2'	32:2a:752:G:O4'	2.19	0.43
32:2a:764:C:H2'	32:2a:765:G:O4'	2.19	0.43
32:2a:1145:C:H4'	32:2a:1146:A:C8	2.53	0.43
32:2a:1162:C:H2'	32:2a:1163:C:C6	2.54	0.43
32:2a:1273:G:C6	32:2a:1274:G:C4	3.07	0.43
40:2i:46:ALA:HA	40:2i:78:LYS:HB2	2.00	0.43
43:2l:69:TYR:CD1	43:2l:90:VAL:HG21	2.53	0.43
50:2s:63:THR:HG23	50:2s:66:MET:HE3	2.00	0.43
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.33	0.43
1:1A:1594:G:H2'	1:1A:1595:G:O4'	2.18	0.43
1:1A:2710:C:H2'	1:1A:2711:A:C8	2.54	0.43
5:1F:39:TRP:O	5:1F:43:LYS:HG2	2.19	0.43
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	2.01	0.43
8:1I:109:ILE:HD13	8:1I:109:ILE:HA	1.68	0.43
11:1P:8:PRO:HB2	11:1P:12:ALA:HB3	2.01	0.43
11:1P:63:PRO:HG2	30:18:25:MET:HB2	2.01	0.43
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.80	0.43
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	2.01	0.43
26:14:16:CYS:SG	26:14:36:CYS:N	2.90	0.43
26:14:49:PHE:HB3	26:14:50:VAL:H	1.47	0.43
32:1a:184:G:H2'	32:1a:185:A:H8	1.83	0.43
32:1a:1309:G:OP2	44:1m:99:ARG:NH2	2.52	0.43
33:1b:60:ASP:HA	33:1b:63:MET:HE3	2.00	0.43
35:1d:102:ASP:OD1	35:1d:103:ASN:N	2.52	0.43
35:1d:194:LEU:HA	35:1d:194:LEU:HD13	1.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:94:ASN:O	48:1q:98:LEU:HD13	2.19	0.43
1:2A:236:C:H2'	1:2A:237:C:C6	2.54	0.43
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.54	0.43
1:2A:751:A:C6	1:2A:789:A:C5	3.07	0.43
1:2A:885:C:H2'	1:2A:886:C:O4'	2.19	0.43
1:2A:975(A):G:O2'	1:2A:1156:A:N1	2.40	0.43
1:2A:2078:C:C4	1:2A:2079:U:C4	3.07	0.43
1:2A:2505:G:C2	59:2A:3857:ERY:H203	2.54	0.43
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.51	0.43
4:2E:14:ILE:HD11	4:2E:173:VAL:HG11	2.01	0.43
7:2H:7:LEU:HD23	7:2H:69:ARG:NH2	2.33	0.43
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.84	0.43
21:2Z:57:ILE:O	21:2Z:69:THR:OG1	2.36	0.43
22:20:29:GLN:H	22:20:67:VAL:HG23	1.83	0.43
25:23:6:VAL:HG22	25:23:56:VAL:HG12	2.00	0.43
30:28:29:LYS:HE3	30:28:29:LYS:HB2	1.80	0.43
32:2a:437:U:H5"	35:2d:155:LEU:HD11	2.00	0.43
32:2a:772:U:H2'	32:2a:773:G:O4'	2.19	0.43
32:2a:1326:C:OP1	52:2u:17:THR:OG1	2.34	0.43
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	2.01	0.43
35:2d:158:ILE:O	35:2d:162:LEU:N	2.43	0.43
51:2t:54:LYS:HB3	51:2t:54:LYS:HE2	1.65	0.43
55:2x:37:A:H2'	55:2x:38:A:O4'	2.19	0.43
55:2x:39:C:H2'	55:2x:40:C:C6	2.54	0.43
1:1A:451:C:OP1	5:1F:52:LYS:NZ	2.52	0.42
1:1A:484:C:H2'	1:1A:485:C:C6	2.54	0.42
1:1A:1171:G:OP2	1:1A:1174:A:N6	2.52	0.42
1:1A:1424:G:H2'	1:1A:1425:G:O4'	2.19	0.42
1:1A:1688:U:H1'	1:1A:1701:A:C6	2.54	0.42
1:1A:1914:C:H2'	1:1A:1915:5MU:O4'	2.19	0.42
1:1A:2563:U:O2'	10:1O:28:SER:HB2	2.19	0.42
7:1H:56:SER:HB3	7:1H:61:HIS:CE1	2.54	0.42
7:1H:92:ILE:HG22	7:1H:93:GLY:N	2.34	0.42
11:1P:68:GLN:OE1	30:18:12:LYS:HG2	2.19	0.42
12:1Q:10:ARG:NH1	12:1Q:90:VAL:H	2.17	0.42
12:1Q:85:LYS:N	12:1Q:85:LYS:HD2	2.34	0.42
21:1Z:98:MET:HE2	21:1Z:100:VAL:HG22	2.01	0.42
32:1a:963:G:H5'	62:1a:1949:HOH:O	2.18	0.42
33:1b:28:PHE:HD2	33:1b:28:PHE:O	2.01	0.42
34:1c:39:ILE:HG23	34:1c:91:LEU:HD11	2.01	0.42
34:1c:73:PRO:O	34:1c:77:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:24:ARG:H	36:1e:24:ARG:HG2	1.60	0.42
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.60	0.42
1:2A:332:A:O2'	1:2A:334:C:OP2	2.28	0.42
1:2A:1527:G:H5"	1:2A:1528:A:OP1	2.19	0.42
6:2G:102:PHE:HE1	6:2G:141:PHE:CE1	2.37	0.42
7:2H:28:GLY:N	7:2H:31:GLY:O	2.47	0.42
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.54	0.42
8:2I:114:LEU:HD12	8:2I:114:LEU:HA	1.95	0.42
9:2N:34:LEU:HD13	9:2N:107:LEU:HD21	2.01	0.42
10:2O:49:ARG:HH12	32:2a:1423:G:P	2.41	0.42
21:2Z:30:ASN:ND2	21:2Z:90:VAL:HB	2.33	0.42
25:23:4:LEU:O	25:23:36:VAL:HA	2.19	0.42
31:29:7:VAL:HG12	31:29:34:GLN:HB3	2.01	0.42
32:2a:626:U:H2'	32:2a:627:G:C8	2.54	0.42
33:2b:172:ILE:H	33:2b:172:ILE:HG13	1.40	0.42
34:2c:111:LEU:HD21	34:2c:146:ALA:H	1.84	0.42
34:2c:117:ALA:O	34:2c:198:VAL:HG11	2.19	0.42
37:2f:62:TRP:CD1	49:2r:35:ARG:HE	2.37	0.42
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.52	0.42
50:2s:15:LEU:HA	50:2s:15:LEU:HD12	1.85	0.42
50:2s:40:ILE:HB	50:2s:67:VAL:O	2.19	0.42
53:2v:19:U:O5'	53:2v:19:U:H6	2.02	0.42
55:2x:36:U:H2'	55:2x:37:A:C8	2.54	0.42
1:1A:24:G:H2'	1:1A:25:U:O4'	2.19	0.42
1:1A:265:A:N1	1:1A:427:U:O2'	2.39	0.42
1:1A:303:U:H2'	1:1A:304:G:C8	2.53	0.42
1:1A:705:A:C2	1:1A:727:A:H1'	2.55	0.42
1:1A:717:G:H2'	1:1A:718:A:O4'	2.19	0.42
1:1A:1012:U:H5	9:1N:28:THR:HG21	1.83	0.42
1:1A:1021:A:H3'	1:1A:1021:A:N3	2.35	0.42
1:1A:1055:G:H2'	1:1A:1056:G:O4'	2.18	0.42
2:1B:75:G:H21	21:1Z:85:HIS:CE1	2.37	0.42
2:1B:87:G:N2	2:1B:89:G:H3'	2.33	0.42
5:1F:28:ILE:HD11	5:1F:115:ALA:HB3	2.01	0.42
5:1F:181:LEU:HD12	5:1F:181:LEU:HA	1.88	0.42
14:1S:15:ARG:HB3	14:1S:19:LYS:CE	2.49	0.42
21:1Z:6:LYS:HB3	21:1Z:6:LYS:HE2	1.75	0.42
32:1a:1030(A):G:H1'	32:1a:1031:G:H22	1.83	0.42
32:1a:1128:C:O2'	32:1a:1147:C:N3	2.47	0.42
40:1i:33:PHE:HE2	40:1i:43:ALA:HB1	1.83	0.42
41:1j:46:ARG:HB2	41:1j:46:ARG:HH11	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:74:LEU:HA	47:1p:77:ALA:HB3	2.00	0.42
1:2A:236:C:H2'	1:2A:237:C:H6	1.84	0.42
1:2A:411:G:OP2	1:2A:2406:U:O2'	2.35	0.42
1:2A:511:U:H4'	1:2A:1235:G:H4'	2.00	0.42
1:2A:707:G:H1	1:2A:724:U:H3	1.66	0.42
1:2A:1419:A:C8	1:2A:1421:G:C6	3.07	0.42
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.18	0.42
1:2A:2292:C:H2'	1:2A:2293:C:C6	2.54	0.42
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.19	0.42
2:2B:28:C:H2'	2:2B:29:A:O4'	2.19	0.42
2:2B:49:C:OP1	14:2S:97:ARG:HB2	2.19	0.42
5:2F:137:LYS:HB3	5:2F:137:LYS:HE2	1.79	0.42
14:2S:88:ASP:C	14:2S:90:GLY:H	2.27	0.42
21:2Z:139:VAL:HG12	21:2Z:140:ASP:O	2.19	0.42
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.19	0.42
32:2a:966:M2G:H2'	32:2a:967:5MC:C6	2.54	0.42
32:2a:1060:C:O2'	41:2j:56:HIS:ND1	2.31	0.42
32:2a:1458:G:OP1	51:2t:35:THR:OG1	2.28	0.42
33:2b:28:PHE:CD1	33:2b:194:PRO:HG3	2.54	0.42
39:2h:67:PRO:O	39:2h:69:ARG:HG3	2.19	0.42
54:2w:18:G:H4'	54:2w:60:U:C5	2.54	0.42
1:1A:40:C:H2'	1:1A:41:C:C6	2.54	0.42
1:1A:869:G:H2'	1:1A:870:A:O4'	2.20	0.42
1:1A:2583:G:O2'	54:1w:76:A:N1	2.49	0.42
6:1G:5:VAL:HG13	6:1G:8:LYS:HZ2	1.84	0.42
32:1a:256:U:OP1	48:1q:17:LYS:NZ	2.48	0.42
32:1a:324:G:OP1	51:1t:22:ARG:NE	2.46	0.42
32:1a:1095:U:OP2	62:1a:1911:HOH:O	2.22	0.42
32:1a:1221:G:OP1	50:1s:36:ARG:HD3	2.19	0.42
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.54	0.42
41:1j:5:ARG:HH21	41:1j:73:ASP:CG	2.27	0.42
42:1k:54:ARG:H	42:1k:54:ARG:HG3	1.61	0.42
1:2A:71:A:H5"	1:2A:73:A:C8	2.54	0.42
1:2A:86:C:H4'	1:2A:104:U:H1'	2.00	0.42
1:2A:586:A:OP2	62:2A:3973:HOH:O	2.21	0.42
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.53	0.42
1:2A:1420:U:H3'	1:2A:1420:U:H6	1.85	0.42
1:2A:1721:G:H8	1:2A:1741:A:H62	1.68	0.42
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.52	0.42
1:2A:2094:G:OP1	8:2I:22:LYS:HG3	2.19	0.42
1:2A:2126:A:H4'	1:2A:2127:G:OP1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:41:LEU:O	5:2F:44:ARG:HG2	2.19	0.42
6:2G:166:ASP:O	6:2G:170:ARG:N	2.48	0.42
12:2Q:31:ASP:N	12:2Q:106:VAL:O	2.44	0.42
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.52	0.42
17:2V:58:VAL:HG12	17:2V:97:LYS:HB2	2.01	0.42
18:2W:13:SER:O	18:2W:17:VAL:HG23	2.19	0.42
21:2Z:150:LEU:O	21:2Z:171:ILE:HG13	2.19	0.42
26:24:35:VAL:HG11	26:24:40:HIS:CD2	2.54	0.42
26:24:40:HIS:CD2	26:24:41:PRO:HD2	2.55	0.42
26:24:45:GLY:C	26:24:47:GLN:H	2.27	0.42
28:26:10:LEU:O	28:26:11:LEU:HD23	2.18	0.42
32:2a:35:G:H2'	32:2a:36:C:C6	2.54	0.42
32:2a:231:G:C2	32:2a:232:G:C8	3.07	0.42
32:2a:235:C:H2'	32:2a:236:G:H8	1.84	0.42
32:2a:336:C:H2'	32:2a:337:C:C6	2.54	0.42
32:2a:605:U:H2'	32:2a:606:G:O4'	2.19	0.42
32:2a:1431:C:H42	32:2a:1469:G:H1	1.68	0.42
32:2a:1505:G:H4'	32:2a:1506:U:H5"	2.00	0.42
33:2b:54:THR:O	33:2b:58:ILE:HG13	2.19	0.42
33:2b:107:THR:O	33:2b:110:GLN:NE2	2.52	0.42
37:2f:96:PRO:HB3	49:2r:30:ASP:OD2	2.19	0.42
1:1A:674:G:O2'	5:1F:74:ARG:HD3	2.19	0.42
1:1A:686:G:H21	1:1A:788:A:H61	1.68	0.42
1:1A:1009:A:OP2	9:1N:37:LYS:NZ	2.27	0.42
1:1A:1557:C:H5"	1:1A:1558:A:OP2	2.20	0.42
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.34	0.42
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.33	0.42
1:1A:2601:C:H2'	1:1A:2603:G:C8	2.53	0.42
1:1A:2836:U:H2'	1:1A:2837:G:C8	2.55	0.42
2:1B:18:G:H1	2:1B:65:C:H42	1.67	0.42
6:1G:97:ASP:O	6:1G:101:ILE:HD12	2.18	0.42
22:10:43:THR:O	22:10:43:THR:HG23	2.19	0.42
26:14:34:GLU:HG2	26:14:35:VAL:HG12	2.01	0.42
32:1a:593:G:H2'	32:1a:594:G:O4'	2.20	0.42
32:1a:1134:G:H5'	32:1a:1135:U:OP2	2.19	0.42
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.54	0.42
34:1c:188:LEU:HD12	34:1c:188:LEU:HA	1.90	0.42
37:1f:10:LEU:HB2	37:1f:59:TYR:HB3	2.01	0.42
38:1g:87:VAL:HG11	38:1g:156:TRP:CZ3	2.54	0.42
47:1p:48:TRP:HH2	47:1p:76:GLN:NE2	2.17	0.42
50:1s:27:GLU:HB2	50:1s:28:LYS:CB	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:186:G:H2'	1:2A:187:G:H8	1.83	0.42
1:2A:275:G:H2'	1:2A:276:A:O4'	2.19	0.42
1:2A:500:G:N2	1:2A:502:A:H3'	2.35	0.42
1:2A:629:G:H1'	1:2A:639:U:H1'	2.02	0.42
1:2A:747:U:O2	1:2A:2014:A:H1'	2.19	0.42
1:2A:752:A:H3'	29:27:1:MET:HE1	2.01	0.42
1:2A:2104:G:H1	1:2A:2185:C:N4	2.16	0.42
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.51	0.42
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.55	0.42
1:2A:2378:A:O5'	1:2A:2378:A:H8	2.02	0.42
1:2A:2751:G:H8	7:2H:2:SER:CA	2.33	0.42
2:2B:2:C:H2'	2:2B:3:C:C6	2.54	0.42
4:2E:103:ASP:CG	4:2E:168:MET:HE2	2.45	0.42
14:2S:93:LYS:HG2	14:2S:94:TYR:N	2.34	0.42
15:2T:18:ASP:OD1	15:2T:19:LEU:HG	2.19	0.42
32:2a:1128:C:HO2'	32:2a:1129:C:P	2.38	0.42
32:2a:1347:G:O2'	32:2a:1373:G:N1	2.39	0.42
33:2b:51:LEU:O	33:2b:55:PHE:HB2	2.19	0.42
35:2d:104:VAL:HG21	35:2d:146:ILE:HD13	2.01	0.42
36:2e:110:LEU:HD13	36:2e:118:ILE:HD13	2.00	0.42
43:2l:83:VAL:HG23	43:2l:107:ALA:HB2	2.01	0.42
48:2q:8:GLY:C	48:2q:21:VAL:HG12	2.44	0.42
50:2s:22:LEU:HD21	50:2s:29:ARG:N	2.34	0.42
50:2s:28:LYS:NZ	50:2s:47:HIS:HA	2.34	0.42
1:1A:34:C:H41	1:1A:447:A:N6	2.16	0.42
1:1A:271(E):U:H2'	1:1A:271(F):C:H6	1.82	0.42
1:1A:1082:U:O4	1:1A:1086:A:C6	2.71	0.42
1:1A:2171:A:H1'	1:1A:2172:U:O4'	2.20	0.42
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	2.02	0.42
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.54	0.42
10:1O:23:ARG:NH2	10:1O:28:SER:O	2.52	0.42
32:1a:224:C:H2'	32:1a:225:C:C6	2.54	0.42
32:1a:383:A:C5	32:1a:384:G:H1'	2.54	0.42
32:1a:1103:C:H2'	32:1a:1104:G:O4'	2.20	0.42
32:1a:1350:A:C5	32:1a:1351:U:C4	3.07	0.42
33:1b:44:LEU:HA	33:1b:47:THR:OG1	2.19	0.42
36:1e:33:VAL:HG22	36:1e:112:LEU:HD12	2.02	0.42
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.44	0.42
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	2.02	0.42
55:1x:21:A:N6	55:1x:46:G:H2'	2.34	0.42
1:2A:29:U:H2'	1:2A:30:G:H8	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:445:C:N4	1:2A:446:G:O6	2.53	0.42
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.19	0.42
1:2A:2165:G:H5"	1:2A:2166:G:OP2	2.20	0.42
6:2G:101:ILE:O	6:2G:104:GLU:HB3	2.19	0.42
6:2G:107:LEU:HD13	6:2G:177:GLY:O	2.19	0.42
6:2G:140:ILE:HG22	6:2G:141:PHE:CD2	2.55	0.42
7:2H:11:VAL:HG23	7:2H:50:VAL:HG12	2.02	0.42
9:2N:25:ARG:O	9:2N:28:THR:HB	2.20	0.42
9:2N:75:TYR:CE2	9:2N:77:GLY:HA2	2.54	0.42
23:21:52:ARG:HA	23:21:56:GLN:O	2.20	0.42
32:2a:1134:G:C4	32:2a:1135:U:H1'	2.55	0.42
35:2d:41:GLY:O	35:2d:43:HIS:N	2.51	0.42
49:2r:38:GLU:HA	49:2r:41:LYS:HD3	2.02	0.42
1:1A:724:U:H2'	1:1A:725:G:O4'	2.19	0.42
1:1A:897:C:H5'	54:1w:56:C:OP1	2.20	0.42
1:1A:1047:G:H1'	1:1A:1111:A:N6	2.35	0.42
1:1A:1769:G:O2'	1:1A:1958:C:OP1	2.28	0.42
1:1A:2121:G:H1	1:1A:2177:C:H42	1.68	0.42
1:1A:2156:G:H2'	1:1A:2157:G:N2	2.34	0.42
1:1A:2231:C:OP1	23:11:42:GLN:HA	2.20	0.42
1:1A:2561:A:H2'	1:1A:2562:U:O4'	2.19	0.42
4:1E:21:VAL:HG13	4:1E:185:LYS:HD2	2.01	0.42
4:1E:47:VAL:HG23	4:1E:81:ILE:HB	2.01	0.42
6:1G:40:ASN:HD22	6:1G:156:ASP:HB2	1.83	0.42
6:1G:77:ILE:HD12	6:1G:82:LEU:HD23	2.01	0.42
11:1P:138:LEU:C	11:1P:140:ALA:H	2.28	0.42
21:1Z:7:ALA:HB2	21:1Z:59:LEU:HB3	2.01	0.42
32:1a:741:G:H2'	32:1a:742:G:O4'	2.18	0.42
32:1a:756:C:H2'	32:1a:757:U:O4'	2.20	0.42
32:1a:975:A:H62	41:1j:60:ARG:HH12	1.67	0.42
32:1a:1201:A:H4'	32:1a:1202:G:O5'	2.19	0.42
33:1b:151:GLY:O	33:1b:154:LEU:N	2.47	0.42
34:1c:109:PRO:C	34:1c:111:LEU:H	2.26	0.42
38:1g:78:ARG:HD2	38:1g:78:ARG:HA	1.90	0.42
38:1g:79:ARG:HD2	38:1g:80:VAL:N	2.34	0.42
1:2A:310:A:H1'	1:2A:311:A:H2'	2.02	0.42
1:2A:850:C:H5"	25:23:18:ASP:HB2	2.02	0.42
1:2A:1541:G:C8	1:2A:1542:A:C8	3.08	0.42
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.83	0.42
2:2B:30:C:OP2	14:2S:32:LEU:HD11	2.19	0.42
2:2B:50:G:P	14:2S:62:LYS:HB2	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:95:C:H2'	2:2B:96:U:C6	2.55	0.42
5:2F:28:ILE:H	5:2F:28:ILE:HG13	1.69	0.42
9:2N:91:LEU:HG	9:2N:98:VAL:HG21	2.01	0.42
12:2Q:48:GLU:OE2	12:2Q:51:ARG:NH2	2.52	0.42
17:2V:1:MET:HE3	17:2V:43:GLU:H	1.84	0.42
32:2a:152:A:N6	32:2a:170:U:C2	2.88	0.42
32:2a:951:G:N7	44:2m:102:ARG:NH2	2.68	0.42
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.54	0.42
33:2b:150:SER:OG	33:2b:151:GLY:N	2.53	0.42
36:2e:41:VAL:O	36:2e:66:MET:HA	2.19	0.42
1:1A:848:G:H2'	1:1A:849:A:C8	2.55	0.42
1:1A:1054:A:C6	1:1A:1055:G:C6	3.08	0.42
1:1A:2052:G:C8	4:1E:141:ILE:HD11	2.55	0.42
1:1A:2750:A:OP2	7:1H:62:LYS:NZ	2.52	0.42
59:1A:4087:ERY:H312	59:1A:4087:ERY:H2	1.74	0.42
6:1G:43:LEU:C	6:1G:45:GLU:H	2.27	0.42
15:1T:29:ARG:HA	15:1T:46:GLU:HA	2.00	0.42
19:1X:88:LYS:HB2	19:1X:88:LYS:HE3	1.65	0.42
21:1Z:104:PHE:HE1	21:1Z:171:ILE:HD11	1.84	0.42
32:1a:319:G:H2'	32:1a:320:C:O4'	2.20	0.42
32:1a:986:A:H1'	50:1s:54:GLY:O	2.19	0.42
34:1c:150:LYS:HB2	34:1c:173:VAL:HG21	2.02	0.42
35:1d:187:ARG:NH1	35:1d:188:LEU:O	2.52	0.42
37:1f:15:ASP:OD1	37:1f:18:GLN:N	2.33	0.42
38:1g:57:GLU:OE1	38:1g:59:LEU:N	2.53	0.42
39:1h:36:LEU:HA	39:1h:39:LEU:HD12	2.02	0.42
54:1y:1:G:H1	54:1y:72:C:H42	1.66	0.42
1:2A:570:G:H2'	1:2A:2030:A:C5	2.55	0.42
1:2A:571:A:O2'	17:2V:78:LYS:HE2	2.20	0.42
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.20	0.42
1:2A:1248:G:C4	16:2U:3:ARG:HD2	2.55	0.42
1:2A:1340:U:H4'	1:2A:1394:U:O2'	2.19	0.42
1:2A:2125:G:N2	1:2A:2172:U:OP1	2.40	0.42
1:2A:2572:A:OP1	1:2A:2574:G:O2'	2.29	0.42
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.19	0.42
1:2A:2823:A:OP1	4:2E:113:PHE:HB2	2.20	0.42
4:2E:33:VAL:HG12	4:2E:89:ASP:O	2.20	0.42
6:2G:126:ASP:OD2	6:2G:130:ASN:HB2	2.20	0.42
12:2Q:138:ASP:OD1	21:2Z:81:ARG:NH1	2.52	0.42
16:2U:52:ARG:HA	16:2U:55:ARG:HD3	2.01	0.42
26:24:62:ARG:HA	26:24:62:ARG:NE	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:6:G:O2'	32:2a:7:G:H5'	2.20	0.42
32:2a:162:A:H8	32:2a:162:A:O5'	2.02	0.42
32:2a:505:G:H2'	32:2a:506:G:H8	1.85	0.42
32:2a:833:U:H2'	32:2a:834:C:C6	2.55	0.42
33:2b:105:PHE:O	33:2b:107:THR:N	2.52	0.42
33:2b:179:LYS:HE2	39:2h:72:PRO:HG3	2.01	0.42
36:2e:12:LEU:HD22	36:2e:128:PRO:HB2	2.02	0.42
38:2g:146:GLU:OE2	38:2g:149:ARG:NE	2.52	0.42
42:2k:87:THR:HA	42:2k:91:ARG:CZ	2.50	0.42
53:2v:14:A:H2'	53:2v:14:A:N3	2.35	0.42
54:2w:39:PSU:H2'	54:2w:40:C:C6	2.55	0.42
54:2y:23:A:H2'	54:2y:24:G:C8	2.54	0.42
1:1A:244:A:C2	1:1A:255:A:C4	3.08	0.42
1:1A:795:C:H2'	1:1A:796:C:H6	1.85	0.42
1:1A:846:C:O2'	62:1A:4180:HOH:O	2.22	0.42
1:1A:847:U:H5'	62:1A:4240:HOH:O	2.19	0.42
1:1A:899:A:O2'	1:1A:900:A:O4'	2.37	0.42
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.19	0.42
1:1A:2259:G:C2	1:1A:2282:G:C6	3.08	0.42
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.54	0.42
6:1G:126:ASP:HB2	6:1G:130:ASN:O	2.19	0.42
12:1Q:85:LYS:HD3	22:10:7:LEU:HD13	2.02	0.42
13:1R:96:ARG:NH2	13:1R:117:VAL:HG13	2.35	0.42
21:1Z:46:LYS:HB3	21:1Z:46:LYS:HE2	1.84	0.42
21:1Z:150:LEU:O	21:1Z:171:ILE:HG23	2.19	0.42
32:1a:204:U:H3'	32:1a:204:U:OP2	2.20	0.42
32:1a:1095:U:P	32:1a:1108:G:H1	2.42	0.42
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.35	0.42
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.54	0.42
32:1a:1241:G:OP1	38:1g:35:LYS:NZ	2.38	0.42
46:1o:85:LEU:HB3	46:1o:87:ILE:HD11	2.02	0.42
50:1s:41:VAL:HG13	50:1s:42:PRO:HD2	2.02	0.42
1:2A:712:G:H2'	1:2A:713:G:O4'	2.19	0.42
1:2A:2717:G:H2'	1:2A:2718:G:O4'	2.19	0.42
6:2G:33:ARG:O	6:2G:161:THR:HG23	2.20	0.42
18:2W:82:LEU:HD22	18:2W:84:ARG:NH2	2.34	0.42
28:26:10:LEU:HB2	28:26:52:VAL:HG13	2.02	0.42
32:2a:189(A):C:H2'	32:2a:189(B):C:C6	2.54	0.42
32:2a:626:U:H2'	32:2a:627:G:H8	1.85	0.42
32:2a:628:G:H2'	32:2a:629:G:H8	1.84	0.42
32:2a:736:C:H2'	32:2a:737:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.20	0.42
32:2a:1227:A:OP1	50:2s:80:TYR:OH	2.19	0.42
32:2a:1324:A:H2'	32:2a:1325:C:C6	2.54	0.42
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.34	0.42
32:2a:1445:C:C2	32:2a:1458:G:C2	3.08	0.42
33:2b:47:THR:HA	33:2b:202:PRO:HG2	2.02	0.42
34:2c:129:ALA:HB3	34:2c:132:ARG:HB3	2.00	0.42
36:2e:19:MET:SD	36:2e:24:ARG:HG3	2.60	0.42
38:2g:70:LYS:O	38:2g:138:LYS:HD2	2.20	0.42
41:2j:65:LEU:HD13	45:2n:55:GLY:O	2.19	0.42
47:2p:40:ASP:HB3	47:2p:48:TRP:HB2	2.01	0.42
54:2y:30:G:C6	54:2y:31:A:N7	2.88	0.42
1:1A:7:G:H2'	1:1A:8:A:O4'	2.20	0.42
1:1A:228:A:H3'	1:1A:229:A:C5'	2.50	0.42
1:1A:897:C:N3	1:1A:898:C:N4	2.68	0.42
1:1A:1283:G:N2	1:1A:1285:G:H3'	2.35	0.42
1:1A:1529:G:H2'	1:1A:1530:C:O4'	2.20	0.42
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.27	0.42
1:1A:2611:U:C5	59:1A:4087:ERY:H312	2.54	0.42
2:1B:7:G:H1	2:1B:114:C:H42	1.66	0.42
6:1G:16:ARG:NH2	6:1G:31:VAL:HG11	2.35	0.42
7:1H:123:PHE:CD1	7:1H:133:VAL:HG12	2.55	0.42
8:1I:124:GLY:H	8:1I:144:VAL:HG23	1.84	0.42
10:1O:70:LYS:HE2	10:1O:70:LYS:HB3	1.78	0.42
16:1U:29:SER:O	16:1U:30:LYS:HD3	2.20	0.42
25:13:12:PRO:O	25:13:20:LYS:NZ	2.46	0.42
32:1a:598:U:H2'	32:1a:599:C:H6	1.85	0.42
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	2.02	0.42
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.35	0.42
54:1y:7:A:H5"	54:1y:8:4SU:H5	2.02	0.42
54:1y:63:G:H2'	54:1y:64:A:O4'	2.20	0.42
1:2A:140:G:N2	1:2A:1596:A:H4'	2.35	0.42
1:2A:946:G:O6	1:2A:972:G:N2	2.52	0.42
1:2A:1680:U:O2'	1:2A:1763:G:N7	2.52	0.42
1:2A:1827:C:OP2	3:2D:222:ARG:NH1	2.45	0.42
1:2A:2110:G:C2	1:2A:2120:G:H1'	2.55	0.42
1:2A:2134:A:H1'	1:2A:2158:A:C2	2.54	0.42
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.85	0.42
1:2A:2558:C:H2'	1:2A:2559:C:O4'	2.20	0.42
2:2B:54:G:H21	6:2G:29:TRP:HZ2	1.68	0.42
12:2Q:130:LYS:HB3	12:2Q:130:LYS:HE2	1.64	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2U:97:ASP:O	16:2U:101:ARG:HG3	2.20	0.42
32:2a:43:C:H2'	32:2a:44:G:O4'	2.20	0.42
32:2a:642:A:H2'	32:2a:643:C:C6	2.55	0.42
32:2a:737:A:H2'	32:2a:738:C:C6	2.55	0.42
32:2a:1157:A:H61	32:2a:1178:G:H21	1.68	0.42
32:2a:1375:A:H4'	38:2g:29:LYS:NZ	2.35	0.42
33:2b:144:ARG:HA	33:2b:144:ARG:HD2	1.91	0.42
50:2s:64:GLU:HG2	50:2s:65:ASN:N	2.34	0.42
55:2x:2:G:H2'	55:2x:3:C:C6	2.54	0.42
1:1A:142(A):C:H2'	1:1A:143:G:O4'	2.20	0.42
1:1A:1020:A:N1	1:1A:1141:U:O2'	2.46	0.42
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.50	0.42
1:1A:2011:U:H2'	1:1A:2012:G:O4'	2.20	0.42
8:1I:77:LEU:HD21	8:1I:100:ALA:HB3	2.01	0.42
12:1Q:95:ALA:O	12:1Q:97:VAL:HG23	2.19	0.42
17:1V:5:VAL:HG21	17:1V:35:LEU:HD13	2.01	0.42
28:16:18:ARG:HD2	28:16:42:TRP:CG	2.55	0.42
32:1a:236:G:H5"	48:1q:42:TYR:OH	2.20	0.42
32:1a:401:C:H2'	32:1a:402:G:H8	1.85	0.42
32:1a:455:C:H42	32:1a:476:G:H1	1.68	0.42
32:1a:1318:A:OP1	50:1s:7:LYS:NZ	2.32	0.42
35:1d:202:LEU:HA	35:1d:205:GLU:HB2	2.01	0.42
47:1p:45:THR:O	47:1p:47:ASP:N	2.53	0.42
51:1t:100:ILE:H	51:1t:100:ILE:HG12	1.36	0.42
55:1x:31:G:C2	55:1x:40:C:C2	3.08	0.42
1:2A:237:C:O2	1:2A:609:A:O2'	2.38	0.42
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.51	0.42
1:2A:1152:C:H2'	1:2A:1153:C:C6	2.54	0.42
1:2A:1423:G:H2'	1:2A:1424:G:C8	2.55	0.42
1:2A:2141:G:C6	1:2A:2151:G:C6	3.08	0.42
1:2A:2893:G:H4'	1:2A:2894:G:OP2	2.19	0.42
6:2G:43:LEU:HD12	6:2G:45:GLU:HG3	2.01	0.42
9:2N:71:ILE:HA	9:2N:86:PRO:HA	2.01	0.42
9:2N:134:ARG:N	9:2N:135:PRO:HD3	2.35	0.42
12:2Q:20:ALA:HB2	21:2Z:79:ARG:HG3	2.02	0.42
12:2Q:36:ALA:O	12:2Q:37:LEU:HD23	2.20	0.42
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.84	0.42
15:2T:56:GLY:O	15:2T:59:THR:HG22	2.19	0.42
18:2W:76:VAL:HG22	18:2W:103:ILE:HG23	2.02	0.42
23:21:75:GLU:C	23:21:77:ALA:H	2.27	0.42
25:23:40:THR:HB	25:23:43:ILE:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:28:50:LEU:HA	30:28:50:LEU:HD23	1.60	0.42
32:2a:11:G:H8	32:2a:11:G:O5'	2.03	0.42
32:2a:811:C:H4'	32:2a:900:A:N6	2.34	0.42
32:2a:826:C:H42	32:2a:874:G:H1	1.68	0.42
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.20	0.42
43:2l:117:ARG:HB3	43:2l:122:THR:O	2.20	0.42
1:1A:466:A:N3	1:1A:683:C:H1'	2.35	0.41
1:1A:762:U:H5"	62:1A:4168:HOH:O	2.20	0.41
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.20	0.41
1:1A:2649:U:H2'	1:1A:2650:U:H6	1.85	0.41
1:1A:2790:A:H5'	1:1A:2893:G:H21	1.84	0.41
5:1F:118:ALA:C	5:1F:120:GLU:H	2.27	0.41
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.84	0.41
8:1I:81:VAL:HG22	8:1I:145:VAL:O	2.21	0.41
11:1P:45:LEU:HD12	11:1P:45:LEU:HA	1.87	0.41
19:1X:72:LYS:NZ	19:1X:75:ASP:OD2	2.53	0.41
21:1Z:125:LEU:C	21:1Z:164:ALA:HB3	2.45	0.41
24:12:35:LEU:HD23	24:12:35:LEU:HA	1.85	0.41
28:16:35:GLU:OE1	28:16:50:ARG:NH2	2.52	0.41
32:1a:874:G:C6	32:1a:875:C:C4	3.08	0.41
32:1a:1057:G:H2'	32:1a:1058:G:O4'	2.20	0.41
35:1d:87:GLY:O	35:1d:89:THR:HG23	2.20	0.41
35:1d:101:LEU:HB2	35:1d:138:TYR:HB3	2.02	0.41
49:1r:31:LEU:HD23	49:1r:31:LEU:H	1.85	0.41
1:2A:301:G:H5'	1:2A:334:C:H2'	2.00	0.41
1:2A:518:G:H4'	18:2W:18:ARG:HE	1.84	0.41
1:2A:897:C:H5'	54:2w:56:C:H5'	2.02	0.41
1:2A:2841:C:N4	62:2A:4167:HOH:O	2.53	0.41
7:2H:106:THR:HG23	7:2H:112:PRO:HB3	2.00	0.41
10:2O:68:GLU:CD	10:2O:68:GLU:H	2.28	0.41
15:2T:8:LYS:HD3	15:2T:8:LYS:HA	1.94	0.41
32:2a:229:U:H2'	32:2a:230:G:C8	2.55	0.41
32:2a:620:C:C2	35:2d:135:LEU:HG	2.55	0.41
32:2a:1002:G:H1	32:2a:1038:C:N4	2.17	0.41
32:2a:1074:G:H4'	33:2b:103:THR:O	2.19	0.41
32:2a:1228:C:OP1	44:2m:114:ARG:HA	2.20	0.41
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.20	0.41
34:2c:152:ILE:HA	34:2c:167:TRP:HB3	2.02	0.41
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.19	0.41
35:2d:109:GLY:HA3	35:2d:165:MET:HE2	2.02	0.41
38:2g:32:ARG:O	38:2g:33:ASP:HB2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:109:G:H2'	1:1A:110:G:O4'	2.20	0.41
1:1A:960:A:C8	1:1A:962:G:C8	3.07	0.41
1:1A:1056:G:H5"	1:1A:1057:A:O4'	2.20	0.41
1:1A:1643:G:H2'	1:1A:1644:C:O4'	2.20	0.41
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.55	0.41
1:1A:2506:U:C2	1:1A:2585:U:O4	2.73	0.41
1:1A:2666:C:H3'	1:1A:2667:C:H6	1.85	0.41
20:1Y:54:LYS:C	20:1Y:56:PRO:HD3	2.45	0.41
32:1a:1418:A:H8	32:1a:1418:A:O5'	2.02	0.41
33:1b:82:ARG:HD2	33:1b:92:TYR:OH	2.21	0.41
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.56	0.41
36:1e:10:MET:HA	36:1e:32:VAL:HG22	2.03	0.41
38:1g:87:VAL:HG11	38:1g:156:TRP:HZ3	1.84	0.41
44:1m:20:THR:C	44:1m:22:ILE:N	2.78	0.41
48:1q:74:LEU:HG	48:1q:75:ARG:HG2	2.01	0.41
1:2A:1142:U:H5"	1:2A:1142(A):A:C8	2.55	0.41
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.21	0.41
1:2A:2065:C:H2'	1:2A:2066:C:H6	1.84	0.41
3:2D:141:VAL:HG13	3:2D:162:SER:HB2	2.02	0.41
8:2I:77:LEU:HD13	8:2I:101:LEU:HB3	2.02	0.41
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HG23	2.03	0.41
25:23:24:LYS:HE3	25:23:24:LYS:HB2	1.91	0.41
26:24:2:LYS:HD2	26:24:5:ILE:HD13	2.01	0.41
32:2a:27:G:H2'	32:2a:28:G:C8	2.55	0.41
32:2a:395:C:N4	62:2a:1928:HOH:O	2.52	0.41
32:2a:659:U:H2'	32:2a:660:G:O4'	2.20	0.41
32:2a:923:A:O2'	32:2a:1398:A:H2'	2.20	0.41
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.29	0.41
33:2b:152:PHE:O	33:2b:154:LEU:N	2.53	0.41
35:2d:57:ARG:NH1	35:2d:205:GLU:HB3	2.36	0.41
1:1A:247:G:H4'	1:1A:386:G:C5	2.56	0.41
1:1A:559:G:H22	16:1U:49:HIS:CE1	2.38	0.41
1:1A:614(C):A:C4	5:1F:180:GLY:HA2	2.56	0.41
1:1A:1062:G:H1	1:1A:1077:A:N6	2.12	0.41
1:1A:1857:G:C6	1:1A:1858:G:C6	3.08	0.41
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.83	0.41
1:1A:2531:A:H5'	7:1H:157:TYR:CE1	2.56	0.41
1:1A:2567:G:H2'	1:1A:2568:C:H6	1.82	0.41
59:1A:4087:ERY:H71	59:1A:4087:ERY:H4	1.67	0.41
15:1T:118:ARG:HG2	32:1a:1442(A):G:C8	2.55	0.41
22:10:10:THR:HG22	22:10:12:ASN:N	2.16	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:58:C:O2'	32:1a:388:G:N7	2.38	0.41
32:1a:706:A:N3	42:1k:31:THR:HG21	2.34	0.41
32:1a:814:A:H2'	32:1a:816:A:H5"	2.01	0.41
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	2.03	0.41
54:1w:75:C:H2'	54:1w:76:A:C8	2.55	0.41
1:2A:538:G:H2'	1:2A:539:G:H8	1.84	0.41
1:2A:1005:C:O2'	9:2N:28:THR:HG23	2.20	0.41
1:2A:1115:G:C2	1:2A:1116:C:C2	3.08	0.41
1:2A:1999:C:H5"	1:2A:2723:C:O2'	2.20	0.41
1:2A:2116:G:N1	1:2A:2162:G:OP1	2.53	0.41
1:2A:2134:A:H62	1:2A:2157:G:H4'	1.85	0.41
1:2A:2279:G:H2'	1:2A:2280:G:O4'	2.20	0.41
1:2A:2453:A:H2'	1:2A:2454:G:C8	2.55	0.41
1:2A:2572:A:N7	4:2E:145:LYS:HB2	2.35	0.41
59:2A:3857:ERY:H332	59:2A:3857:ERY:H10	1.81	0.41
2:2B:19:G:H1	2:2B:64:C:H42	1.69	0.41
6:2G:174:GLU:HB2	6:2G:180:PHE:HE2	1.86	0.41
19:2X:1:MET:HB2	24:22:61:LEU:HD21	2.01	0.41
27:25:40:LYS:NZ	27:25:44:THR:O	2.38	0.41
32:2a:99:U:H2'	32:2a:100:C:C6	2.55	0.41
32:2a:966:M2G:HM23	32:2a:967:5MC:H1'	2.02	0.41
32:2a:979:C:OP1	32:2a:1223:C:N4	2.54	0.41
32:2a:1298:C:OP2	38:2g:114:ARG:NH1	2.44	0.41
35:2d:195:ALA:C	35:2d:196:LEU:HD12	2.45	0.41
38:2g:74:GLU:OE2	38:2g:76:ARG:NH2	2.53	0.41
40:2i:9:ARG:HD3	40:2i:14:VAL:HG12	2.02	0.41
42:2k:50:TYR:CD2	42:2k:60:ALA:HB2	2.56	0.41
43:2l:102:ARG:HE	43:2l:102:ARG:HB3	1.65	0.41
50:2s:67:VAL:C	50:2s:69:HIS:H	2.27	0.41
1:1A:2168:G:H3'	1:1A:2170:A:OP2	2.20	0.41
2:1B:78:A:C2	2:1B:100:A:C4	3.07	0.41
7:1H:105:LEU:HD23	7:1H:105:LEU:HA	1.94	0.41
13:1R:44:LEU:HD12	13:1R:44:LEU:HA	1.86	0.41
32:1a:22:G:C5	32:1a:23:C:C5	3.08	0.41
32:1a:163:C:H2'	32:1a:164:U:C6	2.56	0.41
32:1a:1424:C:H2'	32:1a:1425:U:O4'	2.20	0.41
40:1i:41:VAL:O	40:1i:43:ALA:N	2.48	0.41
42:1k:123:LYS:HE3	42:1k:123:LYS:HB2	1.87	0.41
55:1x:37:A:H2'	55:1x:38:A:O4'	2.21	0.41
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.55	0.41
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.50	0.41
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.37	0.41
1:2A:2203:U:H2'	1:2A:2205:C:H6	1.84	0.41
6:2G:53:LEU:HD13	6:2G:53:LEU:HA	1.82	0.41
7:2H:94:TYR:N	7:2H:94:TYR:CD1	2.88	0.41
16:2U:34:LYS:NZ	16:2U:37:GLU:OE1	2.46	0.41
22:20:46:LYS:HG2	22:20:77:ARG:O	2.20	0.41
24:22:35:LEU:HD12	24:22:53:LEU:HD12	2.02	0.41
29:27:8:ASN:HB3	29:27:11:LYS:HB3	2.01	0.41
32:2a:31:G:O2'	32:2a:48:C:N4	2.53	0.41
32:2a:272:C:H2'	32:2a:273:A:C8	2.55	0.41
32:2a:429:U:H1'	32:2a:430:A:H5"	2.02	0.41
32:2a:719:C:N4	49:2r:71:LYS:HE2	2.35	0.41
32:2a:1317:C:O2	50:2s:37:ARG:NH2	2.53	0.41
45:2n:12:ARG:HH21	45:2n:14:PRO:HB3	1.84	0.41
50:2s:61:TYR:CD2	50:2s:63:THR:HG22	2.55	0.41
54:2w:30:G:H1	54:2w:40:C:H42	1.66	0.41
1:1A:119:A:H4'	1:1A:120:U:OP1	2.21	0.41
1:1A:190:A:N3	1:1A:679:C:O2'	2.44	0.41
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.20	0.41
1:1A:2261:C:O2'	1:1A:2262:U:H5'	2.20	0.41
2:1B:19:G:H2'	2:1B:20:C:O4'	2.21	0.41
11:1P:50:ARG:HD3	30:18:7:HIS:NE2	2.34	0.41
12:1Q:63:LYS:HG2	12:1Q:65:PHE:CZ	2.55	0.41
12:1Q:75:THR:HA	12:1Q:89:ASN:O	2.20	0.41
21:1Z:7:ALA:HA	21:1Z:39:VAL:HG12	2.02	0.41
24:12:10:LEU:HD21	24:12:59:ARG:HD3	2.01	0.41
25:13:44:ARG:O	25:13:48:GLU:HG3	2.21	0.41
32:1a:742:G:H2'	32:1a:743:U:O4'	2.19	0.41
32:1a:993:G:H1	32:1a:1045:C:H42	1.68	0.41
32:1a:1258:G:O2'	32:1a:1259:C:H5'	2.20	0.41
33:1b:19:HIS:NE2	33:1b:20:GLU:HG3	2.35	0.41
33:1b:56:ARG:O	33:1b:60:ASP:HB2	2.20	0.41
33:1b:59:GLU:HG3	33:1b:225:ALA:HB2	2.02	0.41
35:1d:24:GLU:H	35:1d:24:GLU:HG2	1.45	0.41
55:1x:50:U:H2'	55:1x:51:C:C6	2.54	0.41
1:2A:68:G:H2'	1:2A:69:C:O4'	2.20	0.41
1:2A:93:G:H2'	1:2A:94:C:C6	2.56	0.41
1:2A:624:C:OP1	62:2A:3970:HOH:O	2.21	0.41
1:2A:659:C:H2'	1:2A:660:G:H8	1.85	0.41
1:2A:1689:A:H4'	32:2a:1475:G:H4'	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.19	0.41
1:2A:2000:G:OP1	13:2R:5:LYS:NZ	2.40	0.41
1:2A:2344:U:OP1	28:26:37:ARG:HD3	2.20	0.41
1:2A:2549:G:H2'	1:2A:2550:G:C8	2.55	0.41
1:2A:2772:C:H2'	1:2A:2773:C:C6	2.56	0.41
3:2D:129:ASN:O	3:2D:192:THR:HA	2.20	0.41
11:2P:67:MET:HE3	11:2P:67:MET:HB2	1.95	0.41
11:2P:133:SER:O	11:2P:137:LYS:HG3	2.20	0.41
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.56	0.41
32:2a:141:A:O2'	32:2a:182:U:H1'	2.21	0.41
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.55	0.41
32:2a:685:G:C2	32:2a:686:U:C4	3.09	0.41
32:2a:1013:G:N2	32:2a:1015:A:H3'	2.35	0.41
32:2a:1187:G:C6	32:2a:1188:A:C6	3.09	0.41
32:2a:1265:G:C2	32:2a:1271:G:C2	3.08	0.41
32:2a:1275:A:H5'	32:2a:1276:G:OP2	2.21	0.41
32:2a:1329:A:H5'	44:2m:29:ARG:NE	2.35	0.41
34:2c:37:GLN:NE2	45:2n:52:GLN:OE1	2.42	0.41
34:2c:111:LEU:HD23	34:2c:111:LEU:HA	1.86	0.41
36:2e:78:HIS:CD2	39:2h:104:ARG:HD2	2.56	0.41
38:2g:105:VAL:O	38:2g:109:ASN:ND2	2.43	0.41
40:2i:11:LYS:N	40:2i:104:ARG:HH21	2.19	0.41
40:2i:48:GLU:O	40:2i:51:ARG:N	2.46	0.41
49:2r:22:VAL:HG23	49:2r:55:ARG:O	2.19	0.41
1:1A:154(A):C:H42	1:1A:171:G:H1	1.68	0.41
1:1A:459:U:H4'	29:17:40:TRP:CZ3	2.55	0.41
1:1A:823:G:O6	1:1A:824:A:N6	2.54	0.41
1:1A:1327:C:O2'	62:1A:4183:HOH:O	2.22	0.41
1:1A:1740:G:H2'	1:1A:1741:A:H8	1.86	0.41
1:1A:2034:U:C2'	1:1A:2035:G:H5'	2.51	0.41
1:1A:2051:A:H5'	1:1A:2578:G:O4'	2.20	0.41
13:1R:12:ARG:HG2	13:1R:16:HIS:ND1	2.36	0.41
22:10:70:GLN:HG2	22:10:72:ARG:HG3	2.02	0.41
32:1a:131:C:H2'	32:1a:132:C:C6	2.56	0.41
32:1a:841:U:H6	32:1a:841:U:P	2.44	0.41
32:1a:955:U:O2'	50:1s:83:HIS:HD2	2.03	0.41
32:1a:1055:A:H2'	34:1c:156:ARG:HD2	2.03	0.41
32:1a:1452:C:H4'	32:1a:1457:G:C8	2.56	0.41
39:1h:9:MET:HE3	39:1h:9:MET:HB3	1.87	0.41
41:1j:49:VAL:HG11	45:1n:41:ARG:O	2.20	0.41
49:1r:68:LYS:HE2	49:1r:68:LYS:HB2	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:15:LEU:HD13	50:1s:33:THR:HB	2.03	0.41
54:1w:8:4SU:O5'	54:1w:8:4SU:H6	2.20	0.41
1:2A:628:G:H2'	1:2A:629:G:C8	2.56	0.41
1:2A:910:A:C6	1:2A:911:A:C6	3.09	0.41
1:2A:1227:G:C2	1:2A:1228:G:C4	3.08	0.41
1:2A:2127:G:H22	1:2A:2160:G:H22	1.69	0.41
1:2A:2557:G:H2'	1:2A:2558:C:H6	1.86	0.41
1:2A:2741:A:H2'	1:2A:2742:C:O4'	2.20	0.41
6:2G:8:LYS:HD3	6:2G:100:TRP:CD1	2.55	0.41
6:2G:161:THR:HG22	6:2G:162:THR:N	2.36	0.41
24:22:46:GLN:HB2	24:22:49:LYS:HD3	2.02	0.41
32:2a:397:A:O2'	32:2a:399:G:OP2	2.34	0.41
32:2a:565:U:OP2	32:2a:566:G:O2'	2.35	0.41
32:2a:664:G:N2	32:2a:741:G:H1	2.14	0.41
32:2a:971:G:H1'	32:2a:1365:G:O2'	2.20	0.41
32:2a:1239:A:H4'	32:2a:1240:U:H5'	2.01	0.41
32:2a:1338:G:N3	55:2x:41:C:O2'	2.54	0.41
32:2a:1346:A:N1	38:2g:10:ARG:NH2	2.69	0.41
41:2j:53:PRO:HB3	45:2n:42:ILE:HD13	2.02	0.41
42:2k:48:ILE:O	42:2k:50:TYR:N	2.53	0.41
48:2q:41:LYS:NZ	48:2q:88:TYR:OH	2.45	0.41
54:2y:18:G:N2	54:2y:58:A:C5	2.88	0.41
1:1A:36:G:N3	1:1A:450:G:O2'	2.49	0.41
1:1A:95:G:O2'	24:12:48:HIS:ND1	2.50	0.41
1:1A:241:A:H5"	62:1A:5568:HOH:O	2.20	0.41
1:1A:272:G:N7	1:1A:421:U:H2'	2.36	0.41
1:1A:278:A:H2'	1:1A:279:C:C6	2.56	0.41
1:1A:686:G:N2	1:1A:788:A:H61	2.18	0.41
1:1A:1044:G:H5'	1:1A:1045:A:OP2	2.21	0.41
1:1A:1271:G:C2	1:1A:1617:C:H4'	2.55	0.41
1:1A:1508:A:O2'	1:1A:1509:C:H5"	2.20	0.41
1:1A:1942:5MC:OP2	1:1A:1943:U:O2'	2.31	0.41
1:1A:2156:G:C8	1:1A:2157:G:N1	2.89	0.41
1:1A:2257:U:H2'	1:1A:2258:C:C6	2.56	0.41
6:1G:77:ILE:HD13	6:1G:80:PHE:CD2	2.55	0.41
8:1I:25:TYR:O	8:1I:29:TYR:HB3	2.21	0.41
9:1N:30:ILE:HG23	9:1N:52:VAL:HG11	2.03	0.41
11:1P:100:LEU:HA	11:1P:100:LEU:HD23	1.79	0.41
12:1Q:42:ILE:O	12:1Q:95:ALA:N	2.44	0.41
29:17:30:VAL:O	29:17:34:ARG:HG3	2.21	0.41
32:1a:259:G:H2'	32:1a:260:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:153:VAL:HG12	34:1c:196:LEU:HD23	2.03	0.41
34:1c:155:GLY:HA3	34:1c:196:LEU:HG	2.03	0.41
35:1d:49:ARG:H	35:1d:49:ARG:HG3	1.63	0.41
35:1d:87:GLY:O	35:1d:89:THR:N	2.53	0.41
35:1d:172:PRO:C	35:1d:174:LEU:N	2.79	0.41
38:1g:15:ASP:OD1	38:1g:19:GLY:N	2.54	0.41
43:1l:24:VAL:HB	43:1l:27:LEU:HD12	2.02	0.41
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.21	0.41
54:1w:11:C:H42	54:1w:24:G:H1	1.67	0.41
1:2A:216:A:C8	1:2A:432:A:C6	3.09	0.41
1:2A:218:A:C2	1:2A:235:U:H4'	2.55	0.41
1:2A:652(A):A:H2'	1:2A:652(A):A:N3	2.35	0.41
1:2A:1253:A:OP1	62:2A:3974:HOH:O	2.22	0.41
1:2A:1998:G:H4'	1:2A:2724:C:O2'	2.20	0.41
59:2A:3857:ERY:H10	59:2A:3857:ERY:H353	1.72	0.41
2:2B:88:C:H2'	2:2B:89:G:O4'	2.21	0.41
5:2F:102:PRO:HB2	5:2F:105:VAL:HG23	2.02	0.41
6:2G:129:GLY:O	6:2G:161:THR:HB	2.20	0.41
32:2a:204:U:H6	32:2a:204:U:H2'	1.68	0.41
32:2a:417:C:H42	32:2a:426:G:H1	1.69	0.41
32:2a:971:G:OP2	32:2a:1231:G:N2	2.33	0.41
32:2a:1001:A:N1	32:2a:1040:U:O4	2.53	0.41
32:2a:1004:A:N3	32:2a:1038:C:C2	2.89	0.41
32:2a:1438:G:H2'	32:2a:1439:C:C6	2.55	0.41
36:2e:71:LEU:HD23	36:2e:115:VAL:HG23	2.03	0.41
36:2e:90:VAL:O	36:2e:91:LEU:HD13	2.21	0.41
49:2r:31:LEU:H	49:2r:31:LEU:HD23	1.85	0.41
52:2u:12:LYS:HB3	52:2u:17:THR:O	2.21	0.41
1:1A:26:G:H1'	1:1A:515:A:H61	1.86	0.41
1:1A:288:C:H2'	1:1A:289:A:H8	1.84	0.41
1:1A:987:G:O2'	1:1A:1000:A:N3	2.48	0.41
1:1A:1449:A:N3	1:1A:1529:G:H1'	2.36	0.41
1:1A:1818:U:OP2	3:1D:157:ARG:NH2	2.44	0.41
1:1A:2141:G:O6	1:1A:2150:U:O2	2.38	0.41
1:1A:2286:A:N6	28:16:23:THR:OG1	2.53	0.41
1:1A:2439:A:N6	55:1x:76:8AN:O1P	2.53	0.41
1:1A:2801(A):A:H1'	1:1A:2895:U:C1'	2.50	0.41
2:1B:66:A:N6	2:1B:109:C:H5"	2.35	0.41
6:1G:41:GLN:O	6:1G:43:LEU:HD22	2.21	0.41
12:1Q:30:GLY:HA2	12:1Q:107:ALA:HB2	2.03	0.41
19:1X:94:GLY:H	19:1X:95:LEU:C	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:52:SER:O	21:1Z:52:SER:OG	2.26	0.41
32:1a:342:C:C4	32:1a:343:U:C4	3.09	0.41
32:1a:437:U:O2'	35:1d:123:HIS:CD2	2.73	0.41
32:1a:738:C:H2'	32:1a:739:C:C6	2.56	0.41
32:1a:806:C:H2'	32:1a:807:A:C8	2.55	0.41
32:1a:947:G:H2'	32:1a:948:C:C6	2.56	0.41
37:1f:33:TYR:CD2	37:1f:75:LEU:HD23	2.56	0.41
38:1g:74:GLU:CD	38:1g:95:ARG:HE	2.28	0.41
40:1i:89:ASN:OD1	40:1i:92:TYR:N	2.54	0.41
41:1j:35:SER:HB2	41:1j:73:ASP:HB2	2.03	0.41
44:1m:32:GLU:C	44:1m:34:LEU:H	2.29	0.41
50:1s:17:GLU:O	50:1s:20:LEU:N	2.51	0.41
1:2A:265:A:H1'	1:2A:266:G:O4'	2.20	0.41
1:2A:354:G:H2'	1:2A:355:G:C8	2.56	0.41
1:2A:637:A:OP1	11:2P:133:SER:OG	2.33	0.41
1:2A:995:C:O2	9:2N:3:THR:OG1	2.38	0.41
1:2A:1600:C:OP1	19:2X:58:HIS:NE2	2.34	0.41
1:2A:1906:G:OP2	1:2A:1929:G:O2'	2.39	0.41
1:2A:2489:G:C6	1:2A:2490:G:N1	2.89	0.41
2:2B:38:C:O4'	14:2S:95:HIS:NE2	2.53	0.41
2:2B:106:G:H2'	2:2B:107:G:H5'	2.03	0.41
3:2D:133:LEU:HD23	3:2D:133:LEU:HA	1.94	0.41
7:2H:3:ARG:HG2	7:2H:6:ARG:HE	1.86	0.41
9:2N:26:LEU:O	9:2N:30:ILE:HG13	2.21	0.41
15:2T:58:ASN:HD22	15:2T:58:ASN:HA	1.67	0.41
16:2U:39:LEU:HD23	16:2U:39:LEU:HA	1.91	0.41
16:2U:76:TYR:O	16:2U:80:ILE:HG12	2.21	0.41
28:26:32:ASN:OD1	28:26:32:ASN:N	2.50	0.41
32:2a:106:C:O2'	32:2a:379:C:OP1	2.38	0.41
32:2a:355:C:H1'	32:2a:388:G:H1'	2.01	0.41
32:2a:1190:G:OP1	34:2c:5:ILE:HG22	2.21	0.41
32:2a:1347:G:H22	32:2a:1374:A:P	2.43	0.41
35:2d:98:GLU:CD	35:2d:103:ASN:HD21	2.29	0.41
45:2n:3:ARG:HA	45:2n:3:ARG:HD3	1.42	0.41
46:2o:39:LEU:HD12	46:2o:39:LEU:HA	1.89	0.41
46:2o:57:LEU:O	46:2o:60:VAL:HG22	2.20	0.41
46:2o:87:ILE:HG22	46:2o:88:ARG:N	2.35	0.41
47:2p:39:TYR:CG	47:2p:73:LEU:HD21	2.56	0.41
51:2t:30:LYS:HE3	51:2t:30:LYS:HB2	1.77	0.41
54:2y:70:G:H2'	54:2y:71:G:C8	2.54	0.41
1:1A:483:A:H3'	1:1A:484:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:875:G:H2'	1:1A:876:C:C6	2.56	0.41
1:1A:948:G:H2'	1:1A:949:C:O4'	2.20	0.41
1:1A:952:G:OP1	12:1Q:16:ARG:NH2	2.53	0.41
1:1A:1177:A:H8	1:1A:1177:A:O5'	2.04	0.41
1:1A:1587:A:H2'	1:1A:1588:C:H6	1.79	0.41
1:1A:1999:C:H4'	1:1A:2723:C:O2	2.20	0.41
1:1A:2178:C:H2'	1:1A:2179:C:C6	2.55	0.41
1:1A:2773:C:H2'	1:1A:2774:C:C6	2.55	0.41
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.37	0.41
10:1O:10:VAL:HG21	10:1O:16:ALA:HB1	2.01	0.41
15:1T:116:ALA:HB1	15:1T:121:ILE:HD11	2.02	0.41
16:1U:72:HIS:ND1	16:1U:110:VAL:HG21	2.36	0.41
19:1X:10:ALA:HA	24:12:37:PHE:CE1	2.56	0.41
28:16:6:ARG:HD3	28:16:24:GLU:OE2	2.21	0.41
32:1a:269:C:H2'	32:1a:270:A:C8	2.56	0.41
32:1a:674:G:H8	32:1a:674:G:O5'	2.03	0.41
32:1a:827:U:C2	32:1a:874:G:N2	2.89	0.41
32:1a:979:C:H42	45:1n:18:VAL:HG22	1.86	0.41
32:1a:1061:G:H2'	32:1a:1062:U:O4'	2.21	0.41
32:1a:1117:G:H5"	40:1i:104:ARG:NH1	2.36	0.41
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.37	0.41
32:1a:1285:A:H4'	32:1a:1286:A:O5'	2.20	0.41
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.89	0.41
37:1f:35:ALA:HA	37:1f:67:MET:HB3	2.02	0.41
39:1h:87:SER:HB2	39:1h:93:VAL:H	1.85	0.41
43:1l:113:ARG:NE	43:1l:115:LYS:O	2.54	0.41
45:1n:6:LEU:HD13	45:1n:23:ARG:HH22	1.86	0.41
48:1q:21:VAL:HG21	48:1q:59:ILE:HG21	2.01	0.41
48:1q:45:HIS:O	48:1q:47:PRO:HD3	2.20	0.41
48:1q:81:ARG:HD2	48:1q:81:ARG:HA	1.88	0.41
54:1w:51:U:H2'	54:1w:52:G:C8	2.55	0.41
55:1x:13:C:H2'	55:1x:14:A:H5"	2.03	0.41
1:2A:241:A:N1	1:2A:255:A:H5"	2.36	0.41
1:2A:815:C:H2'	1:2A:816:C:H6	1.85	0.41
1:2A:910:A:N3	1:2A:2264:C:O2'	2.49	0.41
1:2A:1036:G:OP2	7:2H:59:ARG:HD2	2.21	0.41
1:2A:1186:G:H2'	1:2A:1187:G:O4'	2.21	0.41
1:2A:1223:G:N2	1:2A:1225:G:H3'	2.36	0.41
1:2A:1227:G:OP1	16:2U:13:LYS:HE3	2.20	0.41
1:2A:1364:G:OP1	23:21:2:SER:HA	2.20	0.41
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1482:G:O6	1:2A:1507:A:N6	2.54	0.41
1:2A:1711:C:H2'	1:2A:1712:C:H6	1.85	0.41
1:2A:1712:C:N3	1:2A:1747(A):G:N1	2.69	0.41
1:2A:1853:A:H2'	1:2A:1854:A:C8	2.56	0.41
1:2A:1882:C:H5"	23:21:26:ARG:NH1	2.36	0.41
1:2A:2093:G:C6	1:2A:2225:A:C8	3.09	0.41
1:2A:2162:G:H5"	1:2A:2172:U:H2'	2.02	0.41
1:2A:2378:A:O3'	14:2S:23:ARG:NH2	2.54	0.41
1:2A:2691:C:O2'	1:2A:2871:C:O2'	2.35	0.41
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.21	0.41
4:2E:61:ARG:HA	4:2E:64:LYS:HB2	2.01	0.41
5:2F:120:GLU:HG3	5:2F:122:LYS:HG2	2.03	0.41
7:2H:53:GLU:CA	7:2H:65:HIS:HE2	2.34	0.41
7:2H:170:ARG:O	7:2H:171:LEU:HD23	2.21	0.41
9:2N:72:TYR:N	9:2N:85:ILE:O	2.48	0.41
11:2P:29:LYS:HG3	11:2P:30:THR:H	1.85	0.41
14:2S:80:LEU:HD22	14:2S:80:LEU:HA	1.93	0.41
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH1	2.35	0.41
20:2Y:79:CYS:O	20:2Y:81:LYS:HG3	2.21	0.41
26:24:47:GLN:O	26:24:48:ARG:C	2.63	0.41
28:26:40:CYS:SG	28:26:42:TRP:HB2	2.61	0.41
32:2a:528:C:H41	43:2l:49:ASN:ND2	2.19	0.41
32:2a:687:A:H4'	32:2a:688:G:O5'	2.20	0.41
32:2a:728:A:H2'	32:2a:729:A:C8	2.56	0.41
32:2a:977:A:H2'	32:2a:978:A:H5"	2.02	0.41
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.21	0.41
32:2a:1232:U:C4	32:2a:1233:G:N7	2.89	0.41
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.84	0.41
33:2b:63:MET:HG2	33:2b:225:ALA:HB1	2.02	0.41
34:2c:124:ILE:HG22	34:2c:130:VAL:HA	2.02	0.41
36:2e:40:ARG:CZ	36:2e:68:GLU:HA	2.50	0.41
36:2e:84:PHE:N	36:2e:87:SER:O	2.54	0.41
36:2e:136:MET:O	36:2e:140:ARG:HG3	2.21	0.41
38:2g:68:ASN:HD22	38:2g:128:ALA:HA	1.85	0.41
38:2g:115:ARG:O	38:2g:119:ARG:HG3	2.21	0.41
39:2h:111:ILE:HD12	39:2h:135:CYS:SG	2.61	0.41
41:2j:89:ASP:O	41:2j:91:PRO:HD3	2.21	0.41
43:2l:24:VAL:HG12	43:2l:98:TYR:CE1	2.56	0.41
44:2m:65:LYS:C	44:2m:66:LEU:HG	2.45	0.41
48:2q:81:ARG:C	48:2q:83:ASP:H	2.29	0.41
1:1A:53:A:H2'	1:1A:54:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:97:C:O3'	24:12:2:LYS:HA	2.21	0.41
1:1A:483:A:H3'	1:1A:484:C:H6	1.86	0.41
1:1A:1071:G:H4'	1:1A:1089:G:OP2	2.21	0.41
1:1A:2245:U:H5"	1:1A:2246:G:H5'	2.02	0.41
1:1A:2703:C:H2'	1:1A:2704:C:H6	1.86	0.41
1:1A:2740:A:C6	1:1A:2741:A:C6	3.09	0.41
7:1H:5:GLY:HA3	7:1H:65:HIS:CD2	2.56	0.41
8:1I:4:ILE:HG12	8:1I:18:VAL:HG22	2.02	0.41
9:1N:13:TRP:CE2	9:1N:133:GLN:HG2	2.55	0.41
11:1P:81:GLN:HE22	11:1P:106:LEU:HA	1.86	0.41
12:1Q:42:ILE:HG13	12:1Q:103:MET:CE	2.51	0.41
14:1S:38:GLN:HB2	14:1S:47:THR:HG23	2.03	0.41
15:1T:127:ALA:C	15:1T:129:ARG:N	2.78	0.41
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.67	0.41
23:11:73:LEU:HA	23:11:73:LEU:HD23	1.75	0.41
30:18:38:GLY:O	30:18:42:ARG:HB2	2.20	0.41
32:1a:6:G:C4	36:1e:119:LEU:HD11	2.56	0.41
32:1a:44:G:C2	32:1a:45:U:H1'	2.56	0.41
32:1a:156:G:C4	32:1a:166:G:C2	3.09	0.41
32:1a:345:C:H5'	32:1a:346:G:C5	2.56	0.41
32:1a:735:C:H5'	49:1r:71:LYS:HD3	2.03	0.41
32:1a:1138:G:H3'	32:1a:1138:G:N3	2.36	0.41
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.86	0.41
34:1c:97:LYS:H	34:1c:97:LYS:HD2	1.85	0.41
35:1d:25:ARG:O	35:1d:28:SER:OG	2.37	0.41
35:1d:120:LEU:HD23	35:1d:120:LEU:HA	1.89	0.41
40:1i:23:ASN:HB2	40:1i:25:LYS:HE2	2.01	0.41
43:1l:42:THR:HG22	43:1l:54:LYS:HE3	2.02	0.41
47:1p:55:ARG:HH21	47:1p:59:TRP:HE1	1.68	0.41
49:1r:40:LEU:HD23	49:1r:40:LEU:HA	1.95	0.41
54:1w:51:U:H2'	54:1w:52:G:H8	1.86	0.41
1:2A:389:G:N1	11:2P:70:GLN:HG3	2.36	0.41
1:2A:773:U:O2'	3:2D:48:ARG:HD3	2.21	0.41
1:2A:1021:A:H2'	1:2A:1022:G:H4'	2.03	0.41
1:2A:1171:G:O5'	1:2A:1171:G:H8	2.04	0.41
1:2A:2660:A:N7	7:2H:175:LYS:NZ	2.51	0.41
4:2E:108:SER:OG	4:2E:162:ALA:N	2.54	0.41
5:2F:20:LEU:HD12	5:2F:20:LEU:HA	1.73	0.41
5:2F:132:VAL:HG22	5:2F:138:GLU:O	2.21	0.41
5:2F:155:LEU:HD12	5:2F:174:VAL:O	2.21	0.41
12:2Q:63:LYS:HE2	12:2Q:65:PHE:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:18:ASP:OD1	15:2T:19:LEU:N	2.54	0.41
20:2Y:52:SER:OG	20:2Y:55:TYR:HB2	2.21	0.41
32:2a:103:C:O2'	32:2a:172:A:N1	2.42	0.41
32:2a:160:A:H2'	32:2a:161:A:C8	2.56	0.41
32:2a:1385:G:H2'	32:2a:1386:G:H8	1.86	0.41
33:2b:91:PRO:CG	33:2b:155:LEU:HB2	2.50	0.41
35:2d:52:SER:O	35:2d:56:VAL:HG23	2.21	0.41
35:2d:64:LEU:HD11	35:2d:97:LEU:HD13	2.01	0.41
36:2e:87:SER:HB3	36:2e:131:ILE:HD13	2.03	0.41
52:2u:18:TYR:CG	52:2u:24:ARG:HD3	2.56	0.41
54:2w:25:C:H2'	54:2w:26:A:C8	2.56	0.41
1:1A:507:A:H5"	1:1A:508:G:H3'	2.04	0.40
1:1A:1490:A:O2'	3:1D:99:ASP:OD1	2.38	0.40
1:1A:2065:C:H2'	1:1A:2066:C:C6	2.56	0.40
1:1A:2390:U:P	30:18:35:GLN:HE22	2.43	0.40
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.57	0.40
1:1A:2512:C:H2'	1:1A:2513:G:O4'	2.22	0.40
3:1D:240:ALA:HB1	62:1D:411:HOH:O	2.21	0.40
5:1F:140:LEU:HD13	5:1F:140:LEU:HA	1.84	0.40
6:1G:77:ILE:HG21	6:1G:80:PHE:CD2	2.56	0.40
24:12:44:LEU:HD12	24:12:44:LEU:HA	1.85	0.40
32:1a:160:A:H1'	32:1a:344:A:C4	2.56	0.40
32:1a:233:C:H2'	32:1a:234:C:H6	1.87	0.40
32:1a:343:U:O2'	32:1a:344:A:H2'	2.21	0.40
32:1a:1187:G:N2	45:1n:60:SER:OG	2.49	0.40
32:1a:1521:G:H2'	32:1a:1522:U:C6	2.56	0.40
37:1f:12:PRO:O	37:1f:14:LEU:N	2.50	0.40
40:1i:49:PRO:HB2	40:1i:81:ILE:HG22	2.03	0.40
1:2A:41:C:H2'	1:2A:42:G:C8	2.56	0.40
1:2A:700:G:H2'	1:2A:701:G:O4'	2.21	0.40
1:2A:2050:C:N4	1:2A:2051:A:C6	2.89	0.40
1:2A:2143:C:H42	1:2A:2148:G:H1	1.68	0.40
1:2A:2635:C:H5"	4:2E:78:LEU:O	2.21	0.40
3:2D:96:HIS:HD2	3:2D:102:LYS:HG2	1.86	0.40
4:2E:105:THR:HG23	4:2E:166:THR:OG1	2.21	0.40
5:2F:137:LYS:HA	5:2F:140:LEU:HD12	2.03	0.40
7:2H:160:LYS:N	7:2H:163:TYR:OH	2.54	0.40
10:2O:96:THR:O	10:2O:117:LEU:HD13	2.21	0.40
12:2Q:50:ALA:HB1	12:2Q:121:ALA:HB1	2.02	0.40
15:2T:51:ARG:HB3	15:2T:62:THR:HB	2.02	0.40
32:2a:73:G:C6	32:2a:97:G:C6	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:691:G:H2'	32:2a:692:U:C6	2.56	0.40
32:2a:918:A:H2'	32:2a:919:A:O4'	2.21	0.40
32:2a:1118:C:P	40:2i:104:ARG:HH11	2.44	0.40
32:2a:1291:G:C6	32:2a:1292:U:C4	3.09	0.40
33:2b:31:TYR:CE2	33:2b:200:ILE:HG21	2.55	0.40
35:2d:47:ARG:NH1	35:2d:47:ARG:HB2	2.36	0.40
36:2e:41:VAL:O	36:2e:67:VAL:HG12	2.21	0.40
41:2j:9:ARG:HH12	41:2j:69:ASN:CG	2.29	0.40
42:2k:123:LYS:C	42:2k:125:PHE:H	2.29	0.40
1:1A:719:C:H2'	1:1A:720:C:H6	1.86	0.40
1:1A:722:A:H2'	1:1A:723:G:C8	2.56	0.40
1:1A:818:G:H4'	1:1A:838:C:O3'	2.21	0.40
1:1A:2059:A:N1	59:1A:4087:ERY:H283	2.36	0.40
1:1A:2602:A:N6	62:1A:4483:HOH:O	2.52	0.40
6:1G:63:ILE:HG22	6:1G:64:THR:HG23	2.03	0.40
7:1H:124:GLU:HG2	7:1H:132:ARG:HB3	2.04	0.40
13:1R:94:TYR:C	13:1R:117:VAL:HG23	2.46	0.40
32:1a:189(B):C:H2'	32:1a:189(C):C:H6	1.86	0.40
32:1a:631:G:C2	32:1a:632:A:C4	3.09	0.40
32:1a:881:G:H2'	32:1a:882:C:O4'	2.20	0.40
32:1a:1518:MA6:H93	32:1a:1519:MA6:C9	2.52	0.40
34:1c:8:ILE:HD12	34:1c:16:ARG:NE	2.36	0.40
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.54	0.40
39:1h:110:ALA:HB3	39:1h:121:ASP:HB3	2.02	0.40
47:1p:6:LEU:HD11	47:1p:73:LEU:HD12	2.02	0.40
51:1t:38:LYS:HA	51:1t:41:ILE:HD12	2.03	0.40
51:1t:99:LEU:HA	51:1t:100:ILE:O	2.22	0.40
1:2A:643:A:C8	28:26:44:ARG:NH1	2.89	0.40
1:2A:662:G:H5'	11:2P:14:LYS:O	2.22	0.40
1:2A:1448:G:H5"	1:2A:1542:A:OP1	2.21	0.40
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.21	0.40
1:2A:2155:G:C5	1:2A:2156:G:H1'	2.56	0.40
1:2A:2199:A:O3'	62:2A:3977:HOH:O	2.22	0.40
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.57	0.40
1:2A:2893:G:H5"	1:2A:2894:G:O4'	2.20	0.40
3:2D:4:LYS:HB3	3:2D:18:VAL:HG23	2.03	0.40
5:2F:119:ARG:HB3	5:2F:119:ARG:NH1	2.36	0.40
5:2F:125:LEU:HD21	5:2F:199:TRP:CE3	2.56	0.40
6:2G:66:GLN:HG3	26:24:1:MET:HE2	2.03	0.40
6:2G:124:SER:O	6:2G:124:SER:OG	2.33	0.40
13:2R:87:TYR:CD1	13:2R:90:ARG:HD2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:98:LEU:HD12	27:25:57:VAL:HG11	2.03	0.40
32:2a:682:G:H2'	32:2a:683:G:H8	1.84	0.40
32:2a:1049:U:O4	45:2n:3:ARG:NH1	2.54	0.40
32:2a:1064:G:OP1	32:2a:1386:G:H4'	2.20	0.40
32:2a:1134:G:H1	32:2a:1140:C:N4	2.17	0.40
38:2g:69:VAL:HG13	38:2g:134:ALA:O	2.20	0.40
38:2g:125:MET:O	38:2g:129:GLU:HG3	2.21	0.40
48:2q:88:TYR:O	48:2q:91:ARG:HB2	2.21	0.40
1:1A:153:C:H2'	1:1A:154:G:C8	2.57	0.40
1:1A:469:G:O6	29:17:37:LYS:HE2	2.22	0.40
1:1A:530:G:H4'	1:1A:531:C:OP1	2.21	0.40
1:1A:2130:U:O2'	1:1A:2131:G:N2	2.55	0.40
1:1A:2305:A:H5"	6:1G:134:GLY:HA3	2.02	0.40
1:1A:2573:C:H3'	62:1A:4233:HOH:O	2.21	0.40
1:1A:2667:C:H2'	1:1A:2668:G:O4'	2.21	0.40
1:1A:2785:C:H2'	1:1A:2786:U:O4'	2.22	0.40
2:1B:30:C:H2'	2:1B:31:C:H5'	2.03	0.40
7:1H:89:ILE:HB	7:1H:129:THR:HA	2.04	0.40
12:1Q:33:GLY:HA2	12:1Q:105:GLU:HA	2.04	0.40
32:1a:32:A:C2	32:1a:33:A:C4	3.09	0.40
32:1a:265:G:H2'	32:1a:267:C:H5	1.86	0.40
32:1a:684:A:O2'	42:1k:39:PRO:O	2.38	0.40
40:1i:50:LEU:H	40:1i:50:LEU:HG	1.76	0.40
51:1t:64:ASP:CG	51:1t:81:LYS:HZ3	2.24	0.40
1:2A:144:C:H2'	1:2A:145:G:H8	1.86	0.40
1:2A:658:C:H2'	1:2A:659:C:C6	2.55	0.40
1:2A:956:G:H2'	1:2A:957:A:H2'	2.04	0.40
1:2A:981:A:N1	1:2A:2027:G:O2'	2.43	0.40
1:2A:996:A:N6	1:2A:1160:G:C6	2.89	0.40
1:2A:1019:U:OP1	1:2A:1035:U:O2'	2.30	0.40
1:2A:1028:A:H61	1:2A:1125:G:H2'	1.84	0.40
1:2A:1158:C:H4'	25:23:32:GLN:HB2	2.04	0.40
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	2.04	0.40
1:2A:2343:C:O2'	1:2A:2373:G:O2'	2.38	0.40
3:2D:89:SER:HB2	3:2D:201:HIS:CD2	2.56	0.40
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	2.04	0.40
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.21	0.40
19:2X:26:TYR:CD2	19:2X:89:ILE:HD12	2.56	0.40
32:2a:27:G:H2'	32:2a:28:G:H8	1.86	0.40
32:2a:170:U:O2'	32:2a:171:A:H5'	2.22	0.40
32:2a:232:G:H1'	32:2a:262:A:N1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:393:A:OP2	47:2p:12:LYS:HD3	2.22	0.40
32:2a:859:A:H2'	32:2a:860:A:O4'	2.21	0.40
32:2a:1349:A:C4	32:2a:1350:A:C8	3.10	0.40
35:2d:61:LYS:HD3	35:2d:206:PHE:CD2	2.56	0.40
36:2e:144:THR:OG1	36:2e:146:ALA:HB3	2.22	0.40
38:2g:18:TYR:CD1	38:2g:59:LEU:HD22	2.56	0.40
39:2h:29:SER:HB3	39:2h:32:LYS:CG	2.51	0.40
43:2l:77:LEU:HD21	43:2l:107:ALA:HA	2.03	0.40
44:2m:66:LEU:O	44:2m:69:GLU:HB2	2.21	0.40
50:2s:28:LYS:HB3	50:2s:29:ARG:HA	2.01	0.40
54:2w:7:A:H61	54:2w:66:U:H3	1.69	0.40
1:1A:699:A:H2'	1:1A:700:G:O4'	2.22	0.40
1:1A:910:A:N3	1:1A:2264:C:O2'	2.47	0.40
1:1A:957:A:N1	1:1A:2458:G:H4'	2.36	0.40
1:1A:1637:A:H4'	1:1A:2711:A:O2'	2.21	0.40
1:1A:2263:C:OP2	62:1A:4182:HOH:O	2.22	0.40
1:1A:2830:G:OP1	4:1E:76:ARG:NH1	2.38	0.40
62:1A:4371:HOH:O	5:1F:68:LYS:HE2	2.21	0.40
6:1G:7:LEU:HD23	6:1G:7:LEU:HA	1.90	0.40
12:1Q:31:ASP:HB2	12:1Q:32:TYR:CD2	2.57	0.40
21:1Z:56:VAL:HA	21:1Z:70:LEU:HD23	2.03	0.40
23:11:8:SER:HB3	23:11:66:HIS:CD2	2.57	0.40
26:14:53:GLU:HB2	26:14:55:ARG:O	2.22	0.40
28:16:26:ASN:HD21	28:16:28:ARG:NH2	2.19	0.40
30:18:23:VAL:HA	30:18:48:PHE:O	2.22	0.40
32:1a:13:U:OP1	62:1a:1916:HOH:O	2.22	0.40
32:1a:222:U:H2'	32:1a:223:U:H6	1.85	0.40
32:1a:255:G:H2'	32:1a:256:U:C6	2.56	0.40
32:1a:707:C:H4'	42:1k:20:TYR:CD2	2.56	0.40
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	2.04	0.40
32:1a:1250:A:H4'	40:1i:68:GLY:N	2.37	0.40
32:1a:1528:U:C2	32:1a:1530:G:C8	3.10	0.40
34:1c:62:ASP:O	34:1c:97:LYS:HB3	2.22	0.40
40:1i:56:LEU:HD23	40:1i:56:LEU:H	1.85	0.40
1:2A:41:C:H2'	1:2A:42:G:H8	1.86	0.40
1:2A:459:U:OP2	29:27:39:ARG:NH1	2.54	0.40
1:2A:468:G:N7	29:27:39:ARG:NH2	2.66	0.40
1:2A:639:U:H2'	1:2A:640:C:C6	2.56	0.40
1:2A:1445(A):C:H42	1:2A:1466:G:H1	1.69	0.40
1:2A:1756:G:H4'	1:2A:1758:G:O4'	2.21	0.40
1:2A:2867:G:OP2	15:2T:119:LYS:NZ	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:90:A:C5	2:2B:91:C:H1'	2.57	0.40
5:2F:199:TRP:NE1	5:2F:203:GLN:HE21	2.20	0.40
11:2P:38:GLN:C	11:2P:40:SER:H	2.30	0.40
11:2P:45:LEU:HA	11:2P:45:LEU:HD12	1.82	0.40
14:2S:25:ARG:NE	14:2S:88:ASP:OD2	2.52	0.40
21:2Z:67:LEU:HD12	21:2Z:67:LEU:HA	1.77	0.40
22:20:27:GLU:HB2	22:20:69:PHE:HD1	1.85	0.40
32:2a:406:G:N2	35:2d:119:GLN:OE1	2.53	0.40
32:2a:472:A:H4'	47:2p:80:PHE:O	2.22	0.40
32:2a:1018:C:H2'	32:2a:1019:C:O4'	2.22	0.40
33:2b:33:TYR:HB2	33:2b:43:ASP:HA	2.03	0.40
44:2m:29:ARG:HD3	44:2m:64:TRP:CD2	2.57	0.40
46:2o:62:GLN:O	46:2o:66:LEU:HG	2.21	0.40
1:1A:445:C:O2'	1:1A:446:G:H5'	2.22	0.40
1:1A:494:G:OP1	18:1W:8:ARG:HD3	2.21	0.40
1:1A:647:G:H8	1:1A:647:G:O5'	2.04	0.40
1:1A:875:G:H2'	1:1A:876:C:O4'	2.22	0.40
1:1A:1047:G:O2'	1:1A:1048:A:C8	2.74	0.40
1:1A:1092:C:H2'	1:1A:1093:G:O4'	2.22	0.40
1:1A:1223:G:N2	1:1A:1226:A:OP2	2.42	0.40
1:1A:1655:A:H3'	1:1A:1656:C:C6	2.56	0.40
1:1A:2000:G:C2	1:1A:2001:A:C8	3.09	0.40
1:1A:2130:U:H1'	1:1A:2159:G:N2	2.36	0.40
1:1A:2541:A:OP2	62:1A:4181:HOH:O	2.22	0.40
5:1F:155:LEU:HG	5:1F:157:VAL:HG22	2.04	0.40
7:1H:98:LEU:HG	7:1H:125:VAL:HG23	2.01	0.40
12:1Q:16:ARG:HG3	12:1Q:17:LEU:H	1.86	0.40
14:1S:83:LYS:HB2	14:1S:83:LYS:HE3	1.88	0.40
18:1W:97:LYS:HD3	18:1W:99:ARG:NH2	2.36	0.40
32:1a:293:G:H5'	32:1a:610:G:N2	2.35	0.40
32:1a:501:C:H2'	32:1a:502:G:C8	2.56	0.40
32:1a:689:C:H2'	32:1a:690:G:O4'	2.21	0.40
32:1a:1134:G:C2	32:1a:1141:C:C2	3.10	0.40
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.21	0.40
33:1b:82:ARG:HD2	33:1b:92:TYR:CE1	2.56	0.40
34:1c:122:GLU:O	34:1c:126:ARG:HD2	2.20	0.40
35:1d:126:ILE:HD13	35:1d:126:ILE:HA	1.85	0.40
36:1e:43:LEU:HB2	36:1e:136:MET:HG3	2.03	0.40
37:1f:19:LEU:HD11	37:1f:59:TYR:CE1	2.57	0.40
38:1g:74:GLU:OE2	38:1g:95:ARG:NE	2.45	0.40
43:1l:32:PHE:HB3	43:1l:84:LEU:HD11	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:92:LEU:O	51:1t:96:GLY:HA2	2.22	0.40
1:2A:340:A:H2'	1:2A:341:G:O4'	2.22	0.40
1:2A:466:A:O3'	29:27:33:ARG:NH1	2.55	0.40
1:2A:637:A:H5"	11:2P:117:GLU:HB2	2.03	0.40
1:2A:723:G:H2'	1:2A:724:U:O4'	2.21	0.40
1:2A:1431:U:H2'	1:2A:1432:C:O4'	2.21	0.40
1:2A:1649:G:O2'	13:2R:107:ASP:OD2	2.22	0.40
1:2A:1979:C:N4	1:2A:1980:G:O6	2.55	0.40
2:2B:33:G:H1'	2:2B:50:G:H22	1.87	0.40
2:2B:70:C:H2'	2:2B:71:C:H6	1.87	0.40
3:2D:118:VAL:HG22	3:2D:119:ALA:H	1.86	0.40
3:2D:166:GLN:HB2	3:2D:174:ILE:HG22	2.02	0.40
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.22	0.40
9:2N:23:LEU:HD13	9:2N:98:VAL:HG12	2.03	0.40
15:2T:25:GLY:C	15:2T:92:GLY:HA3	2.47	0.40
15:2T:46:GLU:OE2	15:2T:89:VAL:HG11	2.22	0.40
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.56	0.40
26:24:64:GLY:O	26:24:66:SER:N	2.52	0.40
29:27:1:MET:HE3	29:27:3:ARG:CZ	2.52	0.40
32:2a:814:A:N7	32:2a:816:A:C4	2.90	0.40
32:2a:979:C:H42	45:2n:18:VAL:HG22	1.87	0.40
34:2c:10:PHE:HD2	34:2c:11:ARG:HH12	1.69	0.40
34:2c:154:SER:O	34:2c:197:GLY:N	2.36	0.40
35:2d:107:ARG:HH11	35:2d:173:TRP:HZ2	1.68	0.40
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	2.03	0.40
44:2m:59:TYR:HD2	44:2m:60:VAL:HG23	1.86	0.40
48:2q:97:SER:O	48:2q:98:LEU:HD12	2.20	0.40
49:2r:76:LEU:HD23	49:2r:76:LEU:HA	1.98	0.40
51:2t:46:GLU:H	51:2t:46:GLU:HG3	1.52	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%)	250 (92%)	22 (8%)	1 (0%)	30 47
3	2D	273/276 (99%)	245 (90%)	25 (9%)	3 (1%)	12 21
4	1E	202/206 (98%)	182 (90%)	19 (9%)	1 (0%)	25 41
4	2E	202/206 (98%)	181 (90%)	20 (10%)	1 (0%)	25 41
5	1F	200/210 (95%)	187 (94%)	11 (6%)	2 (1%)	13 23
5	2F	200/210 (95%)	179 (90%)	18 (9%)	3 (2%)	8 14
6	1G	179/182 (98%)	154 (86%)	25 (14%)	0	100 100
6	2G	179/182 (98%)	141 (79%)	28 (16%)	10 (6%)	1 1
7	1H	172/180 (96%)	162 (94%)	9 (5%)	1 (1%)	22 36
7	2H	172/180 (96%)	142 (83%)	27 (16%)	3 (2%)	7 13
8	1I	144/148 (97%)	125 (87%)	19 (13%)	0	100 100
8	2I	144/148 (97%)	107 (74%)	32 (22%)	5 (4%)	3 4
9	1N	138/140 (99%)	131 (95%)	7 (5%)	0	100 100
9	2N	138/140 (99%)	126 (91%)	10 (7%)	2 (1%)	9 16
10	1O	120/122 (98%)	112 (93%)	6 (5%)	2 (2%)	7 13
10	2O	120/122 (98%)	109 (91%)	8 (7%)	3 (2%)	4 7
11	1P	147/150 (98%)	130 (88%)	11 (8%)	6 (4%)	2 2
11	2P	147/150 (98%)	129 (88%)	14 (10%)	4 (3%)	4 6
12	1Q	139/141 (99%)	129 (93%)	10 (7%)	0	100 100
12	2Q	139/141 (99%)	121 (87%)	17 (12%)	1 (1%)	19 32
13	1R	116/118 (98%)	110 (95%)	4 (3%)	2 (2%)	7 13
13	2R	116/118 (98%)	108 (93%)	8 (7%)	0	100 100
14	1S	108/112 (96%)	101 (94%)	7 (6%)	0	100 100
14	2S	108/112 (96%)	96 (89%)	9 (8%)	3 (3%)	4 6
15	1T	129/146 (88%)	114 (88%)	14 (11%)	1 (1%)	16 29
15	2T	129/146 (88%)	122 (95%)	6 (5%)	1 (1%)	16 29
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
16	2U	114/118 (97%)	109 (96%)	5 (4%)	0	100 100
17	1V	99/101 (98%)	92 (93%)	4 (4%)	3 (3%)	3 5
17	2V	99/101 (98%)	88 (89%)	9 (9%)	2 (2%)	6 11
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100 100
18	2W	110/113 (97%)	102 (93%)	8 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
19	1X	93/96 (97%)	87 (94%)	6 (6%)	0	100 100
19	2X	93/96 (97%)	81 (87%)	11 (12%)	1 (1%)	12 21
20	1Y	105/110 (96%)	94 (90%)	8 (8%)	3 (3%)	3 5
20	2Y	105/110 (96%)	95 (90%)	8 (8%)	2 (2%)	6 11
21	1Z	148/206 (72%)	126 (85%)	18 (12%)	4 (3%)	4 6
21	2Z	156/206 (76%)	123 (79%)	24 (15%)	9 (6%)	1 1
22	10	81/85 (95%)	77 (95%)	4 (5%)	0	100 100
22	20	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	11 19
23	11	95/98 (97%)	91 (96%)	3 (3%)	1 (1%)	12 21
23	21	95/98 (97%)	90 (95%)	4 (4%)	1 (1%)	12 21
24	12	68/72 (94%)	66 (97%)	2 (3%)	0	100 100
24	22	68/72 (94%)	63 (93%)	5 (7%)	0	100 100
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
25	23	57/60 (95%)	52 (91%)	3 (5%)	2 (4%)	3 4
26	14	67/71 (94%)	46 (69%)	15 (22%)	6 (9%)	0 0
26	24	67/71 (94%)	47 (70%)	15 (22%)	5 (8%)	1 1
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
27	25	57/60 (95%)	52 (91%)	5 (9%)	0	100 100
28	16	51/54 (94%)	46 (90%)	5 (10%)	0	100 100
28	26	51/54 (94%)	44 (86%)	7 (14%)	0	100 100
29	17	46/49 (94%)	46 (100%)	0	0	100 100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
30	18	62/65 (95%)	62 (100%)	0	0	100 100
30	28	62/65 (95%)	58 (94%)	4 (6%)	0	100 100
31	19	35/37 (95%)	33 (94%)	2 (6%)	0	100 100
31	29	35/37 (95%)	31 (89%)	4 (11%)	0	100 100
33	1b	229/256 (90%)	184 (80%)	31 (14%)	14 (6%)	1 1
33	2b	229/256 (90%)	170 (74%)	51 (22%)	8 (4%)	3 4
34	1c	204/239 (85%)	185 (91%)	16 (8%)	3 (2%)	8 14
34	2c	204/239 (85%)	153 (75%)	48 (24%)	3 (2%)	8 14
35	1d	206/209 (99%)	191 (93%)	12 (6%)	3 (2%)	8 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
35	2d	206/209 (99%)	173 (84%)	27 (13%)	6 (3%)	3 5
36	1e	146/162 (90%)	134 (92%)	10 (7%)	2 (1%)	9 16
36	2e	146/162 (90%)	116 (80%)	23 (16%)	7 (5%)	2 2
37	1f	98/101 (97%)	91 (93%)	7 (7%)	0	100 100
37	2f	98/101 (97%)	87 (89%)	11 (11%)	0	100 100
38	1g	153/156 (98%)	137 (90%)	13 (8%)	3 (2%)	6 11
38	2g	153/156 (98%)	129 (84%)	21 (14%)	3 (2%)	6 11
39	1h	135/138 (98%)	120 (89%)	13 (10%)	2 (2%)	8 14
39	2h	135/138 (98%)	122 (90%)	11 (8%)	2 (2%)	8 14
40	1i	125/128 (98%)	105 (84%)	17 (14%)	3 (2%)	5 8
40	2i	125/128 (98%)	105 (84%)	16 (13%)	4 (3%)	3 5
41	1j	95/105 (90%)	80 (84%)	11 (12%)	4 (4%)	2 2
41	2j	94/105 (90%)	72 (77%)	17 (18%)	5 (5%)	1 1
42	1k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	14 26
42	2k	112/129 (87%)	96 (86%)	13 (12%)	3 (3%)	4 6
43	1l	119/132 (90%)	108 (91%)	10 (8%)	1 (1%)	16 29
43	2l	119/132 (90%)	108 (91%)	9 (8%)	2 (2%)	7 13
44	1m	121/126 (96%)	102 (84%)	16 (13%)	3 (2%)	4 7
44	2m	120/126 (95%)	99 (82%)	17 (14%)	4 (3%)	3 4
45	1n	58/61 (95%)	54 (93%)	4 (7%)	0	100 100
45	2n	58/61 (95%)	50 (86%)	6 (10%)	2 (3%)	3 4
46	1o	86/89 (97%)	74 (86%)	8 (9%)	4 (5%)	2 2
46	2o	86/89 (97%)	79 (92%)	7 (8%)	0	100 100
47	1p	80/88 (91%)	69 (86%)	10 (12%)	1 (1%)	10 17
47	2p	80/88 (91%)	72 (90%)	7 (9%)	1 (1%)	10 17
48	1q	97/105 (92%)	87 (90%)	10 (10%)	0	100 100
48	2q	97/105 (92%)	78 (80%)	16 (16%)	3 (3%)	3 5
49	1r	66/88 (75%)	57 (86%)	8 (12%)	1 (2%)	8 14
49	2r	66/88 (75%)	59 (89%)	7 (11%)	0	100 100
50	1s	81/93 (87%)	66 (82%)	15 (18%)	0	100 100
50	2s	81/93 (87%)	65 (80%)	14 (17%)	2 (2%)	4 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	1t	94/106 (89%)	81 (86%)	8 (8%)	5 (5%)	1 1
51	2t	94/106 (89%)	82 (87%)	11 (12%)	1 (1%)	12 21
52	1u	21/27 (78%)	18 (86%)	3 (14%)	0	100 100
52	2u	21/27 (78%)	13 (62%)	6 (29%)	2 (10%)	0 0
56	1z	1/3 (33%)	0	1 (100%)	0	100 100
56	2z	1/3 (33%)	1 (100%)	0	0	100 100
All	All	11370/12134 (94%)	10019 (88%)	1148 (10%)	203 (2%)	7 12

All (203) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
11	1P	38	GLN
21	1Z	53	ILE
21	1Z	93	ASP
26	14	46	GLN
26	14	49	PHE
26	14	59	PHE
33	1b	17	PHE
33	1b	126	GLU
35	1d	173	TRP
41	1j	79	ARG
6	2G	47	LYS
6	2G	48	GLU
6	2G	84	LYS
7	2H	126	PRO
8	2I	10	GLU
8	2I	127	VAL
8	2I	135	GLU
11	2P	36	LYS
11	2P	44	GLY
14	2S	81	GLY
21	2Z	52	SER
23	21	3	LYS
26	24	45	GLY
33	2b	17	PHE
35	2d	42	GLN
38	2g	4	ARG
40	2i	33	PHE
40	2i	41	VAL

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Mol	Chain	Res	Type
40	2i	56	LEU
41	2j	29	ARG
42	2k	49	GLY
44	2m	106	ASN
50	2s	81	ARG
3	1D	133	LEU
10	1O	89	ASN
17	1V	43	GLU
21	1Z	165	VAL
26	14	44	THR
26	14	53	GLU
33	1b	8	LYS
33	1b	13	ALA
33	1b	36	ARG
33	1b	129	GLU
33	1b	152	PHE
35	1d	88	VAL
36	1e	85	GLY
38	1g	79	ARG
39	1h	77	GLU
46	1o	19	PRO
49	1r	27	GLY
51	1t	10	LEU
5	2F	21	ALA
6	2G	42	GLY
6	2G	43	LEU
6	2G	126	ASP
7	2H	92	ILE
7	2H	118	PRO
10	2O	54	GLU
11	2P	38	GLN
14	2S	84	GLN
14	2S	96	GLY
17	2V	100	ARG
21	2Z	128	VAL
21	2Z	149	SER
21	2Z	165	VAL
21	2Z	171	ILE
26	24	48	ARG
33	2b	125	PRO
36	2e	21	ALA
36	2e	85	GLY

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Mol	Chain	Res	Type
38	2g	52	GLU
40	2i	121	ARG
41	2j	77	PRO
44	2m	4	ILE
45	2n	3	ARG
45	2n	14	PRO
48	2q	68	ARG
11	1P	29	LYS
13	1R	107	ASP
23	11	81	LYS
26	14	62	ARG
33	1b	16	HIS
33	1b	20	GLU
33	1b	131	PRO
36	1e	86	ALA
42	1k	49	GLY
44	1m	21	TYR
44	1m	106	ASN
51	1t	100	ILE
51	1t	102	GLY
3	2D	29	PRO
5	2F	162	LEU
6	2G	104	GLU
11	2P	28	GLY
20	2Y	103	GLY
26	24	65	ASP
33	2b	74	LYS
33	2b	106	LYS
36	2e	13	ILE
36	2e	141	GLN
39	2h	68	ARG
41	2j	51	ARG
42	2k	104	GLN
42	2k	106	LYS
48	2q	67	LYS
48	2q	82	MET
51	2t	47	GLY
52	2u	3	LYS
4	1E	52	LEU
5	1F	17	ARG
7	1H	3	ARG
11	1P	39	LYS

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Mol	Chain	Res	Type
11	1P	139	LYS
13	1R	2	ARG
17	1V	100	ARG
20	1Y	54	LYS
21	1Z	51	ALA
33	1b	124	SER
33	1b	190	THR
33	1b	231	GLU
40	1i	42	ARG
46	1o	23	GLY
51	1t	96	GLY
4	2E	52	LEU
6	2G	49	ASP
8	2I	134	PRO
9	2N	2	LYS
9	2N	28	THR
10	2O	26	LYS
17	2V	79	VAL
19	2X	94	GLY
21	2Z	142	SER
26	24	26	SER
26	24	38	LYS
33	2b	231	GLU
34	2c	84	ILE
35	2d	35	ARG
41	2j	78	ASN
50	2s	68	GLY
10	1O	5	GLN
11	1P	45	LEU
20	1Y	78	ALA
34	1c	71	ALA
34	1c	84	ILE
40	1i	54	ASP
44	1m	12	ASN
46	1o	88	ARG
51	1t	47	GLY
3	2D	69	ARG
5	2F	166	ALA
6	2G	124	SER
10	2O	5	GLN
12	2Q	130	LYS
15	2T	128	GLU

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Mol	Chain	Res	Type
21	2Z	11	GLU
21	2Z	66	SER
33	2b	230	VAL
34	2c	66	VAL
34	2c	115	LEU
35	2d	5	ILE
36	2e	121	LYS
39	2h	73	ASP
43	2l	105	TYR
44	2m	5	ALA
15	1T	68	TYR
17	1V	53	GLU
20	1Y	103	GLY
34	1c	107	GLN
35	1d	172	PRO
38	1g	55	GLY
43	1l	123	LYS
3	2D	28	GLU
21	2Z	147	GLY
33	2b	97	TRP
38	2g	130	GLY
44	2m	85	GLY
47	2p	62	VAL
33	1b	234	PRO
40	1i	24	GLY
41	1j	39	PRO
25	23	59	VAL
35	2d	142	PRO
38	1g	130	GLY
41	1j	91	PRO
46	1o	20	GLY
20	2Y	27	VAL
25	23	50	VAL
33	2b	72	GLY
35	2d	67	ILE
41	2j	75	ILE
11	1P	23	PRO
36	2e	69	VAL
52	2u	4	GLY
47	1p	46	PRO
6	2G	63	ILE
8	2I	109	ILE

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Mol	Chain	Res	Type
22	20	30	VAL
35	2d	69	GLY
39	1h	101	PRO
41	1j	77	PRO
36	2e	97	GLY
43	2l	40	VAL

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%)	202 (94%)	13 (6%)	16 29
3	2D	215/218 (99%)	197 (92%)	18 (8%)	9 16
4	1E	164/166 (99%)	149 (91%)	15 (9%)	7 13
4	2E	164/166 (99%)	145 (88%)	19 (12%)	4 7
5	1F	160/166 (96%)	142 (89%)	18 (11%)	4 8
5	2F	159/166 (96%)	145 (91%)	14 (9%)	8 15
6	1G	143/156 (92%)	129 (90%)	14 (10%)	6 11
6	2G	143/156 (92%)	125 (87%)	18 (13%)	3 5
7	1H	144/148 (97%)	133 (92%)	11 (8%)	11 19
7	2H	144/148 (97%)	124 (86%)	20 (14%)	3 4
8	1I	113/124 (91%)	99 (88%)	14 (12%)	4 6
8	2I	105/124 (85%)	93 (89%)	12 (11%)	4 7
9	1N	118/119 (99%)	109 (92%)	9 (8%)	11 19
9	2N	118/119 (99%)	104 (88%)	14 (12%)	4 7
10	1O	100/100 (100%)	96 (96%)	4 (4%)	27 47
10	2O	100/100 (100%)	92 (92%)	8 (8%)	10 18
11	1P	115/116 (99%)	99 (86%)	16 (14%)	3 4
11	2P	115/116 (99%)	102 (89%)	13 (11%)	4 8
12	1Q	111/111 (100%)	97 (87%)	14 (13%)	3 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	2Q	111/111 (100%)	100 (90%)	11 (10%)	6 11
13	1R	101/101 (100%)	96 (95%)	5 (5%)	20 37
13	2R	101/101 (100%)	98 (97%)	3 (3%)	36 58
14	1S	86/88 (98%)	73 (85%)	13 (15%)	2 3
14	2S	85/88 (97%)	65 (76%)	20 (24%)	0 0
15	1T	115/127 (91%)	108 (94%)	7 (6%)	15 28
15	2T	113/127 (89%)	104 (92%)	9 (8%)	10 18
16	1U	93/94 (99%)	86 (92%)	7 (8%)	11 20
16	2U	93/94 (99%)	86 (92%)	7 (8%)	11 20
17	1V	80/82 (98%)	71 (89%)	9 (11%)	4 8
17	2V	80/82 (98%)	69 (86%)	11 (14%)	3 4
18	1W	90/92 (98%)	82 (91%)	8 (9%)	8 14
18	2W	90/92 (98%)	83 (92%)	7 (8%)	10 19
19	1X	77/78 (99%)	75 (97%)	2 (3%)	41 63
19	2X	77/78 (99%)	69 (90%)	8 (10%)	5 10
20	1Y	85/91 (93%)	76 (89%)	9 (11%)	5 9
20	2Y	85/91 (93%)	72 (85%)	13 (15%)	2 3
21	1Z	135/179 (75%)	109 (81%)	26 (19%)	1 1
21	2Z	137/179 (76%)	114 (83%)	23 (17%)	1 2
22	10	65/67 (97%)	63 (97%)	2 (3%)	35 56
22	20	65/67 (97%)	60 (92%)	5 (8%)	10 19
23	11	80/83 (96%)	71 (89%)	9 (11%)	4 8
23	21	80/83 (96%)	74 (92%)	6 (8%)	11 20
24	12	65/67 (97%)	57 (88%)	8 (12%)	4 6
24	22	65/67 (97%)	58 (89%)	7 (11%)	5 9
25	13	51/52 (98%)	44 (86%)	7 (14%)	3 4
25	23	50/52 (96%)	43 (86%)	7 (14%)	3 4
26	14	59/63 (94%)	48 (81%)	11 (19%)	1 2
26	24	53/63 (84%)	41 (77%)	12 (23%)	1 0
27	15	50/52 (96%)	47 (94%)	3 (6%)	16 29
27	25	50/52 (96%)	47 (94%)	3 (6%)	16 29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
28	16	51/52 (98%)	42 (82%)	9 (18%)	1 2
28	26	50/52 (96%)	41 (82%)	9 (18%)	1 2
29	17	41/42 (98%)	38 (93%)	3 (7%)	11 21
29	27	41/42 (98%)	36 (88%)	5 (12%)	4 6
30	18	54/55 (98%)	52 (96%)	2 (4%)	29 50
30	28	54/55 (98%)	50 (93%)	4 (7%)	11 20
31	19	34/34 (100%)	32 (94%)	2 (6%)	16 30
31	29	34/34 (100%)	29 (85%)	5 (15%)	2 3
33	1b	192/220 (87%)	164 (85%)	28 (15%)	2 3
33	2b	187/220 (85%)	148 (79%)	39 (21%)	1 1
34	1c	142/188 (76%)	128 (90%)	14 (10%)	6 11
34	2c	140/188 (74%)	121 (86%)	19 (14%)	3 4
35	1d	169/181 (93%)	151 (89%)	18 (11%)	5 9
35	2d	173/181 (96%)	151 (87%)	22 (13%)	3 5
36	1e	113/123 (92%)	100 (88%)	13 (12%)	4 7
36	2e	114/123 (93%)	95 (83%)	19 (17%)	2 2
37	1f	84/90 (93%)	74 (88%)	10 (12%)	4 7
37	2f	85/90 (94%)	74 (87%)	11 (13%)	3 5
38	1g	119/127 (94%)	103 (87%)	16 (13%)	3 4
38	2g	120/127 (94%)	97 (81%)	23 (19%)	1 1
39	1h	114/119 (96%)	100 (88%)	14 (12%)	4 6
39	2h	114/119 (96%)	102 (90%)	12 (10%)	5 9
40	1i	90/99 (91%)	79 (88%)	11 (12%)	4 6
40	2i	89/99 (90%)	79 (89%)	10 (11%)	5 8
41	1j	66/92 (72%)	56 (85%)	10 (15%)	2 3
41	2j	69/92 (75%)	59 (86%)	10 (14%)	2 3
42	1k	82/99 (83%)	70 (85%)	12 (15%)	2 3
42	2k	83/99 (84%)	75 (90%)	8 (10%)	7 12
43	1l	96/108 (89%)	90 (94%)	6 (6%)	15 27
43	2l	96/108 (89%)	84 (88%)	12 (12%)	3 6
44	1m	93/101 (92%)	84 (90%)	9 (10%)	6 12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
44	2m	92/101 (91%)	77 (84%)	15 (16%)	2 2
45	1n	49/50 (98%)	45 (92%)	4 (8%)	9 17
45	2n	49/50 (98%)	44 (90%)	5 (10%)	6 10
46	1o	78/80 (98%)	73 (94%)	5 (6%)	14 27
46	2o	78/80 (98%)	75 (96%)	3 (4%)	28 49
47	1p	69/74 (93%)	56 (81%)	13 (19%)	1 1
47	2p	68/74 (92%)	59 (87%)	9 (13%)	3 5
48	1q	94/97 (97%)	84 (89%)	10 (11%)	5 9
48	2q	94/97 (97%)	82 (87%)	12 (13%)	3 5
49	1r	59/77 (77%)	53 (90%)	6 (10%)	6 10
49	2r	59/77 (77%)	49 (83%)	10 (17%)	1 2
50	1s	69/80 (86%)	62 (90%)	7 (10%)	6 10
50	2s	67/80 (84%)	51 (76%)	16 (24%)	0 0
51	1t	70/82 (85%)	61 (87%)	9 (13%)	3 5
51	2t	70/82 (85%)	62 (89%)	8 (11%)	4 7
52	1u	18/22 (82%)	16 (89%)	2 (11%)	5 8
52	2u	18/22 (82%)	16 (89%)	2 (11%)	5 8
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%)	8242 (89%)	1065 (11%)	4 7

All (1065) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	14	ARG
3	1D	27	THR
3	1D	37	LEU
3	1D	38	LYS
3	1D	73	VAL
3	1D	99	ASP
3	1D	162	SER
3	1D	174	ILE
3	1D	229	VAL
3	1D	242	ARG
3	1D	253	GLN

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Mol	Chain	Res	Type
3	1D	273	ARG
3	1D	276	LYS
4	1E	7	VAL
4	1E	12	THR
4	1E	17	ASP
4	1E	33	VAL
4	1E	40	GLU
4	1E	47	VAL
4	1E	77	ILE
4	1E	89	ASP
4	1E	92	THR
4	1E	93	VAL
4	1E	94	GLU
4	1E	116	VAL
4	1E	127	ASP
4	1E	188	VAL
4	1E	195	LEU
5	1F	24	LEU
5	1F	28	ILE
5	1F	53	THR
5	1F	57	VAL
5	1F	60	SER
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	126	VAL
5	1F	132	VAL
5	1F	140	LEU
5	1F	144	LYS
5	1F	157	VAL
5	1F	158	THR
5	1F	162	LEU
5	1F	168	ARG
5	1F	183	VAL
5	1F	189	THR
6	1G	5	VAL
6	1G	7	LEU
6	1G	8	LYS
6	1G	21	ARG
6	1G	28	VAL
6	1G	31	VAL
6	1G	43	LEU

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Mol	Chain	Res	Type
6	1G	60	LEU
6	1G	101	ILE
6	1G	115	ARG
6	1G	124	SER
6	1G	133	LEU
6	1G	140	ILE
6	1G	159	VAL
7	1H	3	ARG
7	1H	13	LYS
7	1H	24	VAL
7	1H	32	GLU
7	1H	49	VAL
7	1H	90	LYS
7	1H	116	GLU
7	1H	122	THR
7	1H	124	GLU
7	1H	134	SER
7	1H	141	VAL
8	1I	9	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	40	THR
8	1I	47	LEU
8	1I	50	ARG
8	1I	68	LEU
8	1I	85	GLU
8	1I	87	LYS
8	1I	92	VAL
8	1I	108	THR
8	1I	109	ILE
8	1I	123	LEU
8	1I	141	LYS
9	1N	1	MET
9	1N	9	VAL
9	1N	28	THR
9	1N	46	VAL
9	1N	68	GLU
9	1N	84	LYS
9	1N	93	THR
9	1N	139	GLU
9	1N	140	VAL
10	1O	28	SER

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Mol	Chain	Res	Type
10	1O	75	SER
10	1O	105	GLU
10	1O	112	MET
11	1P	3	LEU
11	1P	7	ARG
11	1P	27	HIS
11	1P	42	SER
11	1P	45	LEU
11	1P	50	ARG
11	1P	79	ARG
11	1P	92	GLU
11	1P	96	THR
11	1P	98	GLU
11	1P	101	VAL
11	1P	125	VAL
11	1P	133	SER
11	1P	147	LEU
11	1P	148	LEU
11	1P	149	GLU
12	1Q	1	MET
12	1Q	8	LYS
12	1Q	12	GLN
12	1Q	56	ARG
12	1Q	60	ARG
12	1Q	63	LYS
12	1Q	77	LYS
12	1Q	81	VAL
12	1Q	98	LYS
12	1Q	103	MET
12	1Q	113	GLN
12	1Q	115	MET
12	1Q	127	ILE
12	1Q	133	ARG
13	1R	30	THR
13	1R	36	THR
13	1R	37	THR
13	1R	42	LYS
13	1R	114	VAL
14	1S	5	THR
14	1S	14	VAL
14	1S	17	ARG
14	1S	33	LYS

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Mol	Chain	Res	Type
14	1S	36	TYR
14	1S	46	VAL
14	1S	49	VAL
14	1S	50	SER
14	1S	57	LYS
14	1S	61	ASN
14	1S	69	VAL
14	1S	73	LEU
14	1S	110	LEU
15	1T	15	VAL
15	1T	28	VAL
15	1T	36	GLU
15	1T	51	ARG
15	1T	58	ASN
15	1T	90	GLN
15	1T	128	GLU
16	1U	31	SER
16	1U	55	ARG
16	1U	59	ARG
16	1U	74	LEU
16	1U	77	SER
16	1U	78	THR
16	1U	95	LEU
17	1V	1	MET
17	1V	46	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	73	SER
17	1V	79	VAL
17	1V	82	ARG
17	1V	84	LYS
17	1V	85	LYS
18	1W	6	ILE
18	1W	11	ARG
18	1W	17	VAL
18	1W	24	ILE
18	1W	50	VAL
18	1W	53	SER
18	1W	59	VAL
18	1W	111	HIS
19	1X	1	MET
19	1X	50	LYS

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Mol	Chain	Res	Type
20	1Y	14	LEU
20	1Y	23	ARG
20	1Y	31	LEU
20	1Y	49	VAL
20	1Y	55	TYR
20	1Y	72	VAL
20	1Y	91	GLU
20	1Y	106	LEU
20	1Y	107	ASP
21	1Z	31	ARG
21	1Z	33	LEU
21	1Z	36	LYS
21	1Z	37	VAL
21	1Z	42	VAL
21	1Z	53	ILE
21	1Z	56	VAL
21	1Z	61	LEU
21	1Z	70	LEU
21	1Z	72	ARG
21	1Z	80	ARG
21	1Z	91	LEU
21	1Z	93	ASP
21	1Z	102	LEU
21	1Z	123	ASP
21	1Z	124	ILE
21	1Z	128	VAL
21	1Z	139	VAL
21	1Z	153	SER
21	1Z	154	ASP
21	1Z	157	LEU
21	1Z	163	LEU
21	1Z	165	VAL
21	1Z	169	GLU
21	1Z	170	THR
21	1Z	171	ILE
22	10	11	ARG
22	10	63	VAL
23	11	3	LYS
23	11	35	THR
23	11	38	SER
23	11	40	ARG
23	11	46	LEU

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Mol	Chain	Res	Type
23	11	51	VAL
23	11	80	LEU
23	11	89	GLU
23	11	98	LEU
24	12	1	MET
24	12	7	ARG
24	12	19	VAL
24	12	24	LEU
24	12	53	LEU
24	12	55	ARG
24	12	65	ASN
24	12	69	ARG
25	13	29	ARG
25	13	37	LEU
25	13	40	THR
25	13	54	VAL
25	13	56	VAL
25	13	58	VAL
25	13	60	GLU
26	14	5	ILE
26	14	21	VAL
26	14	31	ILE
26	14	35	VAL
26	14	49	PHE
26	14	52	THR
26	14	53	GLU
26	14	60	GLN
26	14	61	ARG
26	14	63	TYR
26	14	67	TYR
27	15	6	VAL
27	15	40	LYS
27	15	57	VAL
28	16	4	GLU
28	16	7	ILE
28	16	9	LEU
28	16	14	THR
28	16	19	ARG
28	16	25	LYS
28	16	38	LYS
28	16	47	THR
28	16	53	LYS

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Mol	Chain	Res	Type
29	17	24	THR
29	17	29	LYS
29	17	43	THR
30	18	23	VAL
30	18	58	ILE
31	19	7	VAL
31	19	14	CYS
33	1b	12	GLU
33	1b	21	ARG
33	1b	35	GLU
33	1b	37	ASN
33	1b	41	ILE
33	1b	43	ASP
33	1b	54	THR
33	1b	64	ARG
33	1b	68	ILE
33	1b	78	GLN
33	1b	79	ASP
33	1b	80	ILE
33	1b	93	VAL
33	1b	107	THR
33	1b	108	ILE
33	1b	112	VAL
33	1b	115	LEU
33	1b	133	LYS
33	1b	196	LEU
33	1b	200	ILE
33	1b	208	ILE
33	1b	210	SER
33	1b	212	GLN
33	1b	215	LEU
33	1b	222	ILE
33	1b	226	ARG
33	1b	230	VAL
33	1b	231	GLU
34	1c	3	ASN
34	1c	26	LYS
34	1c	28	GLN
34	1c	43	LEU
34	1c	64	VAL
34	1c	77	ILE
34	1c	97	LYS

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Mol	Chain	Res	Type
34	1c	144	SER
34	1c	173	VAL
34	1c	175	LEU
34	1c	190	ARG
34	1c	201	TYR
34	1c	202	ILE
34	1c	207	VAL
35	1d	3	ARG
35	1d	17	VAL
35	1d	19	LEU
35	1d	24	GLU
35	1d	49	ARG
35	1d	52	SER
35	1d	59	ARG
35	1d	70	ILE
35	1d	88	VAL
35	1d	100	ARG
35	1d	141	ARG
35	1d	156	GLU
35	1d	158	ILE
35	1d	162	LEU
35	1d	178	VAL
35	1d	187	ARG
35	1d	194	LEU
35	1d	200	GLU
36	1e	7	GLU
36	1e	11	ILE
36	1e	31	LEU
36	1e	33	VAL
36	1e	41	VAL
36	1e	53	LEU
36	1e	56	GLN
36	1e	63	ARG
36	1e	67	VAL
36	1e	80	ILE
36	1e	90	VAL
36	1e	92	LYS
36	1e	109	ILE
37	1f	15	ASP
37	1f	16	GLN
37	1f	39	LYS
37	1f	52	ILE

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Mol	Chain	Res	Type
37	1f	55	ASP
37	1f	70	ASP
37	1f	72	VAL
37	1f	75	LEU
37	1f	78	GLU
37	1f	94	GLN
38	1g	10	ARG
38	1g	15	ASP
38	1g	17	VAL
38	1g	21	VAL
38	1g	50	ILE
38	1g	61	VAL
38	1g	64	GLN
38	1g	76	ARG
38	1g	85	TYR
38	1g	90	GLU
38	1g	104	LEU
38	1g	114	ARG
38	1g	115	ARG
38	1g	135	VAL
38	1g	144	MET
38	1g	155	ARG
39	1h	9	MET
39	1h	13	ILE
39	1h	17	THR
39	1h	21	LYS
39	1h	29	SER
39	1h	51	VAL
39	1h	77	GLU
39	1h	86	ILE
39	1h	98	LYS
39	1h	99	GLU
39	1h	103	VAL
39	1h	112	LEU
39	1h	122	ARG
39	1h	133	LEU
40	1i	17	VAL
40	1i	23	ASN
40	1i	25	LYS
40	1i	26	VAL
40	1i	50	LEU
40	1i	64	THR

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Mol	Chain	Res	Type
40	1i	92	TYR
40	1i	96	LEU
40	1i	103	THR
40	1i	108	VAL
40	1i	128	ARG
41	1j	7	LYS
41	1j	21	GLN
41	1j	35	SER
41	1j	38	ILE
41	1j	55	LYS
41	1j	67	THR
41	1j	81	THR
41	1j	95	GLU
41	1j	96	ILE
41	1j	100	THR
42	1k	18	ARG
42	1k	25	TYR
42	1k	31	THR
42	1k	48	ILE
42	1k	51	LYS
42	1k	54	ARG
42	1k	80	VAL
42	1k	87	THR
42	1k	98	LEU
42	1k	108	ILE
42	1k	114	VAL
42	1k	126	ARG
43	1l	18	VAL
43	1l	22	SER
43	1l	36	VAL
43	1l	58	VAL
43	1l	83	VAL
43	1l	101	VAL
44	1m	4	ILE
44	1m	17	VAL
44	1m	32	GLU
44	1m	43	THR
44	1m	64	TRP
44	1m	86	CYS
44	1m	96	LEU
44	1m	102	ARG
44	1m	117	VAL

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Mol	Chain	Res	Type
45	1n	9	LYS
45	1n	15	LYS
45	1n	33	VAL
45	1n	57	ARG
46	1o	11	VAL
46	1o	17	ARG
46	1o	83	GLU
46	1o	84	LYS
46	1o	87	ILE
47	1p	4	ILE
47	1p	11	SER
47	1p	16	HIS
47	1p	20	VAL
47	1p	21	VAL
47	1p	29	ASP
47	1p	34	GLU
47	1p	35	LYS
47	1p	45	THR
47	1p	60	LEU
47	1p	62	VAL
47	1p	67	THR
47	1p	79	VAL
48	1q	9	VAL
48	1q	21	VAL
48	1q	24	GLU
48	1q	34	LYS
48	1q	36	ILE
48	1q	60	ILE
48	1q	67	LYS
48	1q	81	ARG
48	1q	90	ILE
48	1q	96	GLU
49	1r	31	LEU
49	1r	35	ARG
49	1r	54	ARG
49	1r	65	ILE
49	1r	66	LEU
49	1r	82	THR
50	1s	9	VAL
50	1s	12	ASP
50	1s	28	LYS
50	1s	62	ILE

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Mol	Chain	Res	Type
50	1s	64	GLU
50	1s	70	LYS
50	1s	77	THR
51	1t	10	LEU
51	1t	24	LEU
51	1t	31	SER
51	1t	37	SER
51	1t	38	LYS
51	1t	39	LYS
51	1t	42	GLN
51	1t	90	GLN
51	1t	100	ILE
52	1u	9	ARG
52	1u	20	LYS
56	1z	2	ARG
3	2D	3	VAL
3	2D	14	ARG
3	2D	18	VAL
3	2D	31	LYS
3	2D	35	LYS
3	2D	37	LEU
3	2D	38	LYS
3	2D	71	ASP
3	2D	106	ILE
3	2D	115	GLN
3	2D	138	VAL
3	2D	142	VAL
3	2D	154	LYS
3	2D	212	SER
3	2D	229	VAL
3	2D	242	ARG
3	2D	270	ILE
3	2D	271	ILE
4	2E	11	MET
4	2E	13	ARG
4	2E	38	THR
4	2E	72	VAL
4	2E	73	GLU
4	2E	75	VAL
4	2E	76	ARG
4	2E	77	ILE
4	2E	87	GLU

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Mol	Chain	Res	Type
4	2E	90	THR
4	2E	93	VAL
4	2E	116	VAL
4	2E	152	LYS
4	2E	154	LYS
4	2E	182	LEU
4	2E	184	VAL
4	2E	195	LEU
4	2E	198	VAL
4	2E	200	GLU
5	2F	12	LEU
5	2F	24	LEU
5	2F	40	GLN
5	2F	74	ARG
5	2F	78	ILE
5	2F	108	LYS
5	2F	110	LEU
5	2F	119	ARG
5	2F	149	ASP
5	2F	157	VAL
5	2F	162	LEU
5	2F	175	THR
5	2F	176	LEU
5	2F	187	VAL
6	2G	3	LEU
6	2G	7	LEU
6	2G	8	LYS
6	2G	18	GLU
6	2G	31	VAL
6	2G	43	LEU
6	2G	45	GLU
6	2G	51	ARG
6	2G	60	LEU
6	2G	77	ILE
6	2G	79	ASN
6	2G	91	ARG
6	2G	92	VAL
6	2G	114	ILE
6	2G	116	ASP
6	2G	140	ILE
6	2G	157	ILE
6	2G	165	THR

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Mol	Chain	Res	Type
7	2H	3	ARG
7	2H	15	VAL
7	2H	32	GLU
7	2H	34	GLU
7	2H	43	VAL
7	2H	44	VAL
7	2H	50	VAL
7	2H	52	VAL
7	2H	58	GLU
7	2H	65	HIS
7	2H	67	LEU
7	2H	70	THR
7	2H	81	GLU
7	2H	98	LEU
7	2H	111	HIS
7	2H	127	GLU
7	2H	133	VAL
7	2H	136	ILE
7	2H	149	ARG
7	2H	167	GLU
8	2I	12	LEU
8	2I	38	LEU
8	2I	40	THR
8	2I	51	ILE
8	2I	68	LEU
8	2I	75	LEU
8	2I	81	VAL
8	2I	86	THR
8	2I	87	LYS
8	2I	107	VAL
8	2I	117	GLU
8	2I	121	LYS
9	2N	9	VAL
9	2N	16	ILE
9	2N	23	LEU
9	2N	46	VAL
9	2N	48	MET
9	2N	55	VAL
9	2N	62	VAL
9	2N	83	LYS
9	2N	87	LEU
9	2N	91	LEU

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Mol	Chain	Res	Type
9	2N	112	LEU
9	2N	115	ARG
9	2N	131	GLN
9	2N	136	GLU
10	2O	28	SER
10	2O	35	VAL
10	2O	58	VAL
10	2O	78	ARG
10	2O	92	GLU
10	2O	104	ARG
10	2O	107	ARG
10	2O	122	LEU
11	2P	7	ARG
11	2P	15	ARG
11	2P	19	VAL
11	2P	25	SER
11	2P	45	LEU
11	2P	70	GLN
11	2P	75	ILE
11	2P	98	GLU
11	2P	117	GLU
11	2P	126	VAL
11	2P	131	SER
11	2P	133	SER
11	2P	135	LEU
12	2Q	7	MET
12	2Q	25	ASP
12	2Q	60	ARG
12	2Q	76	LYS
12	2Q	79	LEU
12	2Q	105	GLU
12	2Q	106	VAL
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	119	ARG
12	2Q	125	LEU
13	2R	15	SER
13	2R	35	THR
13	2R	95	THR
14	2S	3	ARG
14	2S	5	THR
14	2S	9	ARG

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Mol	Chain	Res	Type
14	2S	15	ARG
14	2S	21	THR
14	2S	24	LEU
14	2S	25	ARG
14	2S	26	LEU
14	2S	28	VAL
14	2S	35	ILE
14	2S	43	GLU
14	2S	47	THR
14	2S	49	VAL
14	2S	58	LEU
14	2S	63	THR
14	2S	64	GLU
14	2S	78	LEU
14	2S	80	LEU
14	2S	82	ILE
14	2S	110	LEU
15	2T	9	LEU
15	2T	21	GLU
15	2T	28	VAL
15	2T	40	THR
15	2T	89	VAL
15	2T	93	ARG
15	2T	95	ARG
15	2T	96	ARG
15	2T	111	ARG
16	2U	5	LYS
16	2U	63	VAL
16	2U	74	LEU
16	2U	78	THR
16	2U	83	LEU
16	2U	95	LEU
16	2U	117	GLN
17	2V	7	THR
17	2V	33	VAL
17	2V	38	LEU
17	2V	39	LEU
17	2V	51	VAL
17	2V	61	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL

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Mol	Chain	Res	Type
17	2V	99	ILE
17	2V	100	ARG
18	2W	4	LYS
18	2W	11	ARG
18	2W	39	THR
18	2W	63	ASP
18	2W	67	ASP
18	2W	78	GLU
18	2W	106	ILE
19	2X	1	MET
19	2X	49	VAL
19	2X	72	LYS
19	2X	75	ASP
19	2X	81	VAL
19	2X	83	VAL
19	2X	87	GLN
19	2X	95	LEU
20	2Y	3	VAL
20	2Y	14	LEU
20	2Y	38	ILE
20	2Y	39	VAL
20	2Y	44	ILE
20	2Y	47	LYS
20	2Y	49	VAL
20	2Y	61	ILE
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	97	ARG
20	2Y	106	LEU
20	2Y	107	ASP
21	2Z	14	LYS
21	2Z	20	ARG
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	50	GLN
21	2Z	67	LEU
21	2Z	71	VAL
21	2Z	91	LEU
21	2Z	92	SER
21	2Z	102	LEU
21	2Z	133	ILE
21	2Z	137	ILE

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Mol	Chain	Res	Type
21	2Z	138	GLU
21	2Z	140	ASP
21	2Z	142	SER
21	2Z	144	LEU
21	2Z	153	SER
21	2Z	154	ASP
21	2Z	163	LEU
21	2Z	165	VAL
21	2Z	170	THR
21	2Z	171	ILE
21	2Z	174	VAL
22	20	7	LEU
22	20	46	LYS
22	20	63	VAL
22	20	67	VAL
22	20	68	GLU
23	21	40	ARG
23	21	59	THR
23	21	69	LYS
23	21	76	ARG
23	21	80	LEU
23	21	98	LEU
24	22	17	SER
24	22	30	ARG
24	22	51	ARG
24	22	52	ASP
24	22	59	ARG
24	22	64	LEU
24	22	70	GLN
25	23	23	LEU
25	23	34	GLU
25	23	47	VAL
25	23	53	LEU
25	23	54	VAL
25	23	56	VAL
25	23	59	VAL
26	24	5	ILE
26	24	14	ILE
26	24	31	ILE
26	24	34	GLU
26	24	35	VAL
26	24	50	VAL

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Mol	Chain	Res	Type
26	24	52	THR
26	24	56	VAL
26	24	59	PHE
26	24	61	ARG
26	24	63	TYR
26	24	69	LYS
27	25	6	VAL
27	25	35	GLU
27	25	59	GLU
28	26	8	LYS
28	26	9	LEU
28	26	14	THR
28	26	19	ARG
28	26	20	ASN
28	26	32	ASN
28	26	34	LEU
28	26	47	THR
28	26	48	VAL
29	27	1	MET
29	27	4	THR
29	27	14	LYS
29	27	24	THR
29	27	43	THR
30	28	14	VAL
30	28	22	VAL
30	28	23	VAL
30	28	59	LYS
31	29	1	MET
31	29	2	LYS
31	29	4	ARG
31	29	19	ARG
31	29	26	ILE
33	2b	7	VAL
33	2b	8	LYS
33	2b	9	GLU
33	2b	11	LEU
33	2b	16	HIS
33	2b	35	GLU
33	2b	41	ILE
33	2b	58	ILE
33	2b	67	THR
33	2b	68	ILE

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Mol	Chain	Res	Type
33	2b	76	GLN
33	2b	79	ASP
33	2b	80	ILE
33	2b	81	VAL
33	2b	82	ARG
33	2b	83	MET
33	2b	87	ARG
33	2b	94	ASN
33	2b	107	THR
33	2b	110	GLN
33	2b	111	ARG
33	2b	112	VAL
33	2b	115	LEU
33	2b	117	GLU
33	2b	118	LEU
33	2b	124	SER
33	2b	127	ILE
33	2b	142	LEU
33	2b	164	VAL
33	2b	169	LYS
33	2b	172	ILE
33	2b	179	LYS
33	2b	191	ASP
33	2b	192	SER
33	2b	198	ASP
33	2b	204	ASN
33	2b	208	ILE
33	2b	215	LEU
33	2b	221	LEU
34	2c	11	ARG
34	2c	15	THR
34	2c	16	ARG
34	2c	26	LYS
34	2c	32	LEU
34	2c	39	ILE
34	2c	44	GLU
34	2c	45	LYS
34	2c	68	VAL
34	2c	77	ILE
34	2c	101	LEU
34	2c	103	VAL
34	2c	132	ARG

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Mol	Chain	Res	Type
34	2c	175	LEU
34	2c	182	ILE
34	2c	186	PHE
34	2c	188	LEU
34	2c	190	ARG
34	2c	195	VAL
35	2d	28	SER
35	2d	33	MET
35	2d	53	ASP
35	2d	60	GLU
35	2d	77	ASN
35	2d	78	LEU
35	2d	83	SER
35	2d	86	LYS
35	2d	96	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	137	SER
35	2d	148	VAL
35	2d	156	GLU
35	2d	157	LEU
35	2d	158	ILE
35	2d	165	MET
35	2d	168	ARG
35	2d	175	SER
35	2d	186	LEU
35	2d	188	LEU
35	2d	201	GLN
36	2e	5	ASP
36	2e	6	PHE
36	2e	10	MET
36	2e	13	ILE
36	2e	16	THR
36	2e	18	ARG
36	2e	32	VAL
36	2e	38	GLN
36	2e	41	VAL
36	2e	51	VAL
36	2e	57	LYS
36	2e	72	GLN
36	2e	81	GLU
36	2e	89	ILE

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Mol	Chain	Res	Type
36	2e	115	VAL
36	2e	116	THR
36	2e	119	LEU
36	2e	150	ARG
36	2e	151	LEU
37	2f	10	LEU
37	2f	23	LYS
37	2f	25	ILE
37	2f	31	GLU
37	2f	36	ARG
37	2f	40	VAL
37	2f	66	GLU
37	2f	69	GLU
37	2f	83	ASP
37	2f	92	LYS
37	2f	95	GLU
38	2g	9	VAL
38	2g	15	ASP
38	2g	21	VAL
38	2g	24	THR
38	2g	30	ILE
38	2g	31	MET
38	2g	52	GLU
38	2g	53	LYS
38	2g	72	ARG
38	2g	73	MET
38	2g	75	VAL
38	2g	78	ARG
38	2g	79	ARG
38	2g	94	ARG
38	2g	99	LEU
38	2g	105	VAL
38	2g	106	GLN
38	2g	113	GLU
38	2g	124	LEU
38	2g	136	LYS
38	2g	140	ASP
38	2g	146	GLU
38	2g	155	ARG
39	2h	3	THR
39	2h	11	THR
39	2h	17	THR

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Mol	Chain	Res	Type
39	2h	23	SER
39	2h	24	THR
39	2h	25	ASP
39	2h	37	ARG
39	2h	52	ASP
39	2h	112	LEU
39	2h	120	THR
39	2h	122	ARG
39	2h	133	LEU
40	2i	29	ASN
40	2i	40	LEU
40	2i	64	THR
40	2i	65	VAL
40	2i	75	ASP
40	2i	89	ASN
40	2i	99	LEU
40	2i	104	ARG
40	2i	105	ASP
40	2i	108	VAL
41	2j	8	LEU
41	2j	25	GLU
41	2j	33	GLN
41	2j	34	VAL
41	2j	38	ILE
41	2j	43	ARG
41	2j	67	THR
41	2j	74	ILE
41	2j	84	GLN
41	2j	97	GLU
42	2k	14	VAL
42	2k	32	ILE
42	2k	41	THR
42	2k	48	ILE
42	2k	81	ASP
42	2k	105	VAL
42	2k	109	VAL
42	2k	125	PHE
43	2l	6	THR
43	2l	8	ASN
43	2l	33	ARG
43	2l	36	VAL
43	2l	38	THR

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Mol	Chain	Res	Type
43	2l	39	VAL
43	2l	40	VAL
43	2l	49	ASN
43	2l	57	LYS
43	2l	78	GLN
43	2l	83	VAL
43	2l	97	ARG
44	2m	11	ARG
44	2m	32	GLU
44	2m	43	THR
44	2m	50	GLU
44	2m	56	LEU
44	2m	66	LEU
44	2m	94	ARG
44	2m	99	ARG
44	2m	103	THR
44	2m	106	ASN
44	2m	108	ARG
44	2m	114	ARG
44	2m	115	LYS
44	2m	117	VAL
44	2m	122	LYS
45	2n	3	ARG
45	2n	9	LYS
45	2n	22	THR
45	2n	33	VAL
45	2n	56	VAL
46	2o	3	ILE
46	2o	26	GLU
46	2o	85	LEU
47	2p	2	VAL
47	2p	20	VAL
47	2p	33	ILE
47	2p	42	ARG
47	2p	44	THR
47	2p	45	THR
47	2p	54	GLU
47	2p	60	LEU
47	2p	74	LEU
48	2q	4	LYS
48	2q	9	VAL
48	2q	15	MET

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Mol	Chain	Res	Type
48	2q	21	VAL
48	2q	41	LYS
48	2q	60	ILE
48	2q	62	SER
48	2q	63	ARG
48	2q	66	SER
48	2q	76	LEU
48	2q	84	LEU
48	2q	90	ILE
49	2r	26	LEU
49	2r	31	LEU
49	2r	35	ARG
49	2r	46	GLU
49	2r	54	ARG
49	2r	66	LEU
49	2r	69	THR
49	2r	70	ILE
49	2r	84	LYS
49	2r	87	ARG
50	2s	14	HIS
50	2s	16	LEU
50	2s	27	GLU
50	2s	36	ARG
50	2s	37	ARG
50	2s	41	VAL
50	2s	43	GLU
50	2s	45	VAL
50	2s	47	HIS
50	2s	48	THR
50	2s	49	ILE
50	2s	57	HIS
50	2s	58	VAL
50	2s	63	THR
50	2s	73	GLU
50	2s	77	THR
51	2t	31	SER
51	2t	37	SER
51	2t	46	GLU
51	2t	55	ILE
51	2t	61	SER
51	2t	70	SER
51	2t	93	GLU

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Mol	Chain	Res	Type
51	2t	100	ILE
52	2u	9	ARG
52	2u	22	ARG
56	2z	2	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (141) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	166	GLN
4	1E	48	GLN
5	1F	8	GLN
5	1F	67	GLN
5	1F	69	HIS
6	1G	132	ASN
8	1I	105	HIS
8	1I	139	GLN
9	1N	94	HIS
12	1Q	113	GLN
13	1R	13	HIS
13	1R	71	GLN
14	1S	95	HIS
16	1U	94	ASN
17	1V	87	HIS
18	1W	60	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
21	1Z	34	ASN
21	1Z	55	HIS
21	1Z	151	HIS
24	12	38	GLN
24	12	46	GLN
24	12	65	ASN
26	14	60	GLN
28	16	20	ASN
33	1b	16	HIS
33	1b	40	HIS
33	1b	95	GLN
33	1b	140	HIS
33	1b	212	GLN
34	1c	6	HIS

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Mol	Chain	Res	Type
34	1c	98	ASN
34	1c	162	GLN
34	1c	170	GLN
35	1d	77	ASN
35	1d	116	GLN
35	1d	119	GLN
35	1d	123	HIS
35	1d	201	GLN
36	1e	38	GLN
36	1e	78	HIS
37	1f	18	GLN
37	1f	57	GLN
37	1f	64	GLN
38	1g	28	ASN
38	1g	86	GLN
38	1g	97	GLN
40	1i	31	GLN
40	1i	34	ASN
40	1i	38	GLN
40	1i	73	GLN
40	1i	124	GLN
41	1j	56	HIS
41	1j	62	HIS
42	1k	104	GLN
44	1m	77	ASN
47	1p	13	HIS
48	1q	16	GLN
48	1q	45	HIS
48	1q	93	GLN
49	1r	63	GLN
50	1s	47	HIS
50	1s	57	HIS
50	1s	83	HIS
51	1t	75	ASN
4	2E	48	GLN
5	2F	69	HIS
5	2F	182	ASN
5	2F	203	GLN
6	2G	26	GLN
6	2G	27	ASN
6	2G	66	GLN
7	2H	111	HIS

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Mol	Chain	Res	Type
9	2N	8	GLN
9	2N	94	HIS
11	2P	27	HIS
11	2P	128	HIS
12	2Q	12	GLN
12	2Q	57	HIS
13	2R	13	HIS
13	2R	50	HIS
13	2R	61	HIS
13	2R	71	GLN
14	2S	38	GLN
15	2T	90	GLN
17	2V	64	HIS
19	2X	31	HIS
21	2Z	32	HIS
21	2Z	50	GLN
21	2Z	55	HIS
21	2Z	73	GLN
24	22	9	GLN
24	22	38	GLN
24	22	56	GLN
24	22	65	ASN
25	23	32	GLN
26	24	40	HIS
28	26	20	ASN
30	28	7	HIS
33	2b	76	GLN
33	2b	94	ASN
33	2b	110	GLN
34	2c	118	GLN
34	2c	123	GLN
34	2c	162	GLN
35	2d	45	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	123	HIS
36	2e	38	GLN
36	2e	65	ASN
36	2e	78	HIS
36	2e	127	ASN
37	2f	73	ASN
37	2f	84	ASN

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Mol	Chain	Res	Type
37	2f	100	ASN
38	2g	97	GLN
38	2g	148	ASN
40	2i	3	GLN
40	2i	31	GLN
41	2j	13	HIS
42	2k	104	GLN
42	2k	117	ASN
43	2l	9	GLN
43	2l	99	HIS
44	2m	77	ASN
44	2m	106	ASN
46	2o	13	GLN
46	2o	62	GLN
47	2p	13	HIS
47	2p	14	ASN
47	2p	16	HIS
49	2r	63	GLN
50	2s	23	ASN
50	2s	47	HIS
50	2s	57	HIS
51	2t	16	HIS
51	2t	75	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	505 (17%)	24 (0%)
1	2A	2791/2915 (95%)	520 (18%)	23 (0%)
2	1B	119/121 (98%)	7 (5%)	0
2	2B	118/121 (97%)	30 (25%)	0
32	1a	1497/1521 (98%)	277 (18%)	0
32	2a	1501/1521 (98%)	347 (23%)	0
53	1v	12/24 (50%)	2 (16%)	0
53	2v	12/24 (50%)	5 (41%)	0
54	1w	72/76 (94%)	24 (33%)	0
54	1y	72/76 (94%)	26 (36%)	0
54	2w	69/76 (90%)	24 (34%)	0
54	2y	70/76 (92%)	25 (35%)	0
55	1x	75/77 (97%)	16 (21%)	0
55	2x	75/77 (97%)	13 (17%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	9347/9620 (97%)	1821 (19%)	47 (0%)

All (1821) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	10	G
1	1A	11	G
1	1A	12	U
1	1A	15	G
1	1A	27	G
1	1A	34	C
1	1A	36	G
1	1A	45	C
1	1A	55	G
1	1A	63	U
1	1A	71	A
1	1A	72	U
1	1A	74	A
1	1A	75	G
1	1A	78	A
1	1A	84	A
1	1A	95	G
1	1A	102	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	140	G
1	1A	141	A
1	1A	154	G
1	1A	154(A)	C
1	1A	181	A
1	1A	182	A
1	1A	196	A
1	1A	205	G
1	1A	214	G
1	1A	215	G
1	1A	216	A
1	1A	222	A
1	1A	225	A
1	1A	228	A
1	1A	229	A

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Mol	Chain	Res	Type
1	1A	233	A
1	1A	248	G
1	1A	265	A
1	1A	266	G
1	1A	269	U
1	1A	271(C)	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(R)	G
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	294	A
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	345	A
1	1A	346	A
1	1A	352	G
1	1A	363	G
1	1A	363(B)	G
1	1A	372	G
1	1A	386	G
1	1A	396	G
1	1A	404	C
1	1A	411	G
1	1A	412	A
1	1A	428	A
1	1A	444	C
1	1A	448	U
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	509	C
1	1A	530	G

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Mol	Chain	Res	Type
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	555	U
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	616	G
1	1A	619	G
1	1A	626	U
1	1A	627	A
1	1A	634	C
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	651	G
1	1A	652(A)	A
1	1A	652(D)	C
1	1A	652(F)	G
1	1A	652(T)	C
1	1A	668	G
1	1A	669	G
1	1A	677	A
1	1A	686	G
1	1A	689	A
1	1A	712	G
1	1A	717	G
1	1A	730	C
1	1A	740	U
1	1A	746	A
1	1A	747	U
1	1A	764	A
1	1A	765	G
1	1A	775	G
1	1A	776	G

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Mol	Chain	Res	Type
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	788	A
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	859	G
1	1A	870	A
1	1A	879	G
1	1A	880	G
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	890	A
1	1A	892	G
1	1A	896	A
1	1A	897	C
1	1A	898	C
1	1A	899	A
1	1A	900	A
1	1A	910	A
1	1A	913	U
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	974	G
1	1A	975	C
1	1A	975(A)	G
1	1A	983	A
1	1A	996	A

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Mol	Chain	Res	Type
1	1A	1005	C
1	1A	1012	U
1	1A	1013	C
1	1A	1017	G
1	1A	1022	G
1	1A	1025	G
1	1A	1026	U
1	1A	1033	U
1	1A	1034	G
1	1A	1039	G
1	1A	1040	C
1	1A	1044	G
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1058	G
1	1A	1059	G
1	1A	1060	U
1	1A	1063	G
1	1A	1068	G
1	1A	1069	A
1	1A	1071	G
1	1A	1073	A
1	1A	1075	C
1	1A	1076	C
1	1A	1078	U
1	1A	1079	C
1	1A	1083	U
1	1A	1085	A
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1094	U
1	1A	1097	U
1	1A	1099	G
1	1A	1101	U
1	1A	1105	U
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G

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Mol	Chain	Res	Type
1	1A	1116	C
1	1A	1130	U
1	1A	1133	U
1	1A	1135	C
1	1A	1136	G
1	1A	1139	G
1	1A	1142	U
1	1A	1149	G
1	1A	1170	G
1	1A	1171	G
1	1A	1173	G
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	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	1303	G
1	1A	1318	C
1	1A	1320	C
1	1A	1345	C
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1376	C
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1386	C
1	1A	1391	U
1	1A	1396	U

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Mol	Chain	Res	Type
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1450	G
1	1A	1455	G
1	1A	1467	C
1	1A	1482	G
1	1A	1484	G
1	1A	1493	C
1	1A	1494	A
1	1A	1497	U
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1513	C
1	1A	1520	G
1	1A	1532	C
1	1A	1540	U
1	1A	1543	C
1	1A	1554	A
1	1A	1558	A
1	1A	1559	G
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1579	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1610	A
1	1A	1627	G
1	1A	1634	A
1	1A	1647	G
1	1A	1648	C
1	1A	1664	A
1	1A	1674	G
1	1A	1691	C
1	1A	1696	G

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Mol	Chain	Res	Type
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1746	G
1	1A	1756	G
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1816	G
1	1A	1819	A
1	1A	1820	U
1	1A	1847	A
1	1A	1848	A
1	1A	1853	A
1	1A	1858	G
1	1A	1861	G
1	1A	1877	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1919	A
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1964	G
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1976	U
1	1A	1992	G
1	1A	1993	U

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Mol	Chain	Res	Type
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	2035	G
1	1A	2039	C
1	1A	2043	C
1	1A	2049	G
1	1A	2052	G
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A
1	1A	2069	G
1	1A	2074	U
1	1A	2098	U
1	1A	2103	C
1	1A	2108	C
1	1A	2109	U
1	1A	2111	C
1	1A	2113	U
1	1A	2115	G
1	1A	2116	G
1	1A	2121	G
1	1A	2122	U
1	1A	2126	A
1	1A	2127	G
1	1A	2128	C
1	1A	2129	C
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

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Mol	Chain	Res	Type
1	1A	2148	G
1	1A	2150	U
1	1A	2151	G
1	1A	2152	G
1	1A	2155	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G
1	1A	2160	G
1	1A	2161	C
1	1A	2165	G
1	1A	2166	G
1	1A	2167	U
1	1A	2169	A
1	1A	2171	A
1	1A	2172	U
1	1A	2173	A
1	1A	2174	C
1	1A	2175	C
1	1A	2181	G
1	1A	2183	C
1	1A	2184	G
1	1A	2189	U
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2219	G
1	1A	2223	G
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2305	A
1	1A	2307	G
1	1A	2308	G

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Mol	Chain	Res	Type
1	1A	2309	A
1	1A	2314	C
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2341	G
1	1A	2343	C
1	1A	2347	C
1	1A	2350	C
1	1A	2361	A
1	1A	2372	G
1	1A	2379	G
1	1A	2383	G
1	1A	2385	C
1	1A	2396	G
1	1A	2406	U
1	1A	2407	G
1	1A	2422	A
1	1A	2423	U
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2435	A
1	1A	2438	U
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2476	A
1	1A	2477	C
1	1A	2480	C
1	1A	2486	G
1	1A	2490	G
1	1A	2494	G
1	1A	2498	C
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2549	G
1	1A	2554	U

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Mol	Chain	Res	Type
1	1A	2564	A
1	1A	2566	A
1	1A	2567	G
1	1A	2572	A
1	1A	2573	C
1	1A	2574	G
1	1A	2582	G
1	1A	2585	U
1	1A	2602	A
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2638	G
1	1A	2654	A
1	1A	2673	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	2733	A
1	1A	2758	A
1	1A	2765	A
1	1A	2778	A
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	2807	G
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2834	G

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Mol	Chain	Res	Type
1	1A	2835	A
1	1A	2872	G
1	1A	2873	A
1	1A	2880	C
1	1A	2892	A
1	1A	2894	G
2	1B	13	A
2	1B	17	C
2	1B	29	A
2	1B	35	U
2	1B	56	G
2	1B	73	A
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	52	G
32	1a	61	G
32	1a	66	G
32	1a	79	G
32	1a	91	C
32	1a	92	C
32	1a	93	G
32	1a	97	G
32	1a	101	A
32	1a	105	G
32	1a	116	A
32	1a	120	A
32	1a	121	C
32	1a	131	C
32	1a	145	G
32	1a	151	A
32	1a	153	C
32	1a	163	C
32	1a	164	U
32	1a	166	G
32	1a	169	C

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Mol	Chain	Res	Type
32	1a	172	A
32	1a	174	C
32	1a	181	G
32	1a	182	U
32	1a	186	C
32	1a	187	C
32	1a	189(F)	U
32	1a	189(J)	G
32	1a	195	A
32	1a	197	A
32	1a	200	G
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	219	C
32	1a	243	A
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	316	G
32	1a	321	A
32	1a	324	G
32	1a	328	C
32	1a	332	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	388	G
32	1a	390	C
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	407	G

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Mol	Chain	Res	Type
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	430	A
32	1a	439	A
32	1a	442	C
32	1a	446	G
32	1a	452	A
32	1a	458	C
32	1a	461	A
32	1a	474	G
32	1a	479	C
32	1a	483	C
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	531	U
32	1a	532	A
32	1a	534	U
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	618	C
32	1a	626	U
32	1a	630	G
32	1a	639	G
32	1a	641	U
32	1a	648	A
32	1a	653	A

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Mol	Chain	Res	Type
32	1a	665	A
32	1a	671	G
32	1a	672	U
32	1a	673	G
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	717	C
32	1a	721	G
32	1a	723	U
32	1a	724	G
32	1a	731	G
32	1a	734	G
32	1a	749	C
32	1a	755	G
32	1a	759	A
32	1a	766	A
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	816	A
32	1a	817	C
32	1a	818	G
32	1a	824	C
32	1a	828	A
32	1a	838	G
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	853	G
32	1a	870	U
32	1a	889	A
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	938	A
32	1a	960	U
32	1a	961	U

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Mol	Chain	Res	Type
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	972	C
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	983	A
32	1a	992	U
32	1a	993	G
32	1a	997	U
32	1a	1000	U
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1011	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(B)	C
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1037	C
32	1a	1039	C
32	1a	1043	C
32	1a	1044	A
32	1a	1063	C
32	1a	1068	G
32	1a	1081	G
32	1a	1084	G
32	1a	1085	U
32	1a	1094	G
32	1a	1095	U

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Mol	Chain	Res	Type
32	1a	1101	A
32	1a	1108	G
32	1a	1123	A
32	1a	1124	G
32	1a	1125	U
32	1a	1126	U
32	1a	1132	C
32	1a	1133	G
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1160	G
32	1a	1166	G
32	1a	1169	A
32	1a	1174	G
32	1a	1181	G
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1213	A
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1246	C
32	1a	1250	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1270	C
32	1a	1275	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1290	G
32	1a	1299	A
32	1a	1300	G

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Mol	Chain	Res	Type
32	1a	1302	U
32	1a	1305	G
32	1a	1309	G
32	1a	1312	G
32	1a	1320	C
32	1a	1322	C
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1367	C
32	1a	1370	G
32	1a	1380	U
32	1a	1397	C
32	1a	1400	5MC
32	1a	1419	G
32	1a	1429	C
32	1a	1435	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1442(B)	A
32	1a	1446	U
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1487	G
32	1a	1492	A
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	1525	G
32	1a	1529	G
32	1a	1530	G
53	1v	13	A
53	1v	14	A
54	1w	2	C
54	1w	6	G

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Mol	Chain	Res	Type
54	1w	7	A
54	1w	8	4SU
54	1w	9	A
54	1w	10	G
54	1w	14	A
54	1w	19	G
54	1w	20	U
54	1w	21	A
54	1w	23	A
54	1w	24	G
54	1w	25	C
54	1w	45	U
54	1w	46	G7M
54	1w	47	U
54	1w	48	C
54	1w	66	U
54	1w	68	C
54	1w	70	G
54	1w	72	C
54	1w	73	A
54	1w	74	C
54	1w	75	C
55	1x	2	G
55	1x	4	G
55	1x	9	G
55	1x	13	C
55	1x	14	A
55	1x	18	G
55	1x	19	G
55	1x	20	U
55	1x	21	A
55	1x	30	G
55	1x	47	U
55	1x	48	C
55	1x	49	G
55	1x	52	G
55	1x	59	A
55	1x	61	C
54	1y	2	C
54	1y	5	G
54	1y	9	A
54	1y	13	C

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Mol	Chain	Res	Type
54	1y	14	A
54	1y	15	G
54	1y	19	G
54	1y	20	U
54	1y	21	A
54	1y	30	G
54	1y	35	A
54	1y	39	PSU
54	1y	40	C
54	1y	44	G
54	1y	45	U
54	1y	46	G7M
54	1y	47	U
54	1y	48	C
54	1y	49	C
54	1y	57	G
54	1y	58	A
54	1y	59	U
54	1y	64	A
54	1y	65	G
54	1y	66	U
54	1y	70	G
1	2A	11	G
1	2A	12	U
1	2A	14	A
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	36	G
1	2A	45	C
1	2A	55	G
1	2A	61	G
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	100	G

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Mol	Chain	Res	Type
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	122	G
1	2A	125	G
1	2A	131	G
1	2A	139(A)	G
1	2A	154	G
1	2A	157	U
1	2A	173	G
1	2A	184	C
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	230	U
1	2A	232	G
1	2A	233	A
1	2A	248	G
1	2A	266	G
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(Y)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	283	A
1	2A	291	C
1	2A	311	A
1	2A	324	A
1	2A	327	G
1	2A	329	G

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Mol	Chain	Res	Type
1	2A	330	A
1	2A	333	G
1	2A	342	G
1	2A	346	A
1	2A	352	G
1	2A	354	G
1	2A	362	U
1	2A	363	G
1	2A	363(B)	G
1	2A	386	G
1	2A	389	G
1	2A	396	G
1	2A	411	G
1	2A	412	A
1	2A	420	C
1	2A	434	U
1	2A	443	A
1	2A	444	C
1	2A	455	C
1	2A	457	A
1	2A	480	A
1	2A	481	G
1	2A	482	A
1	2A	494	G
1	2A	504	U
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	522	G
1	2A	527	C
1	2A	528	A
1	2A	529	A
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	551	G
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	583	G
1	2A	588	U

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Mol	Chain	Res	Type
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(A)	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	643	A
1	2A	645	C
1	2A	648	G
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(D)	C
1	2A	652(U)	G
1	2A	653	A
1	2A	668	G
1	2A	669	G
1	2A	670	A
1	2A	686	G
1	2A	726	G
1	2A	728	G
1	2A	730	C
1	2A	753	C
1	2A	764	A
1	2A	775	G
1	2A	776	G
1	2A	779	U
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	826	U
1	2A	827	U
1	2A	828	U
1	2A	847	U
1	2A	857	C

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Mol	Chain	Res	Type
1	2A	858	U
1	2A	859	G
1	2A	874	G
1	2A	878	A
1	2A	879	G
1	2A	880	G
1	2A	882	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	892	G
1	2A	893	C
1	2A	894	C
1	2A	895	U
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	904	C
1	2A	910	A
1	2A	914	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	953	A
1	2A	957	A
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	990	A
1	2A	996	A
1	2A	999	U
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1020	A

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Mol	Chain	Res	Type
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1027	A
1	2A	1033	U
1	2A	1036	G
1	2A	1037	G
1	2A	1038	C
1	2A	1039	G
1	2A	1041	C
1	2A	1043	C
1	2A	1113	U
1	2A	1114	G
1	2A	1116	C
1	2A	1117	G
1	2A	1126	A
1	2A	1130	U
1	2A	1132	A
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1141	U
1	2A	1142(A)	A
1	2A	1167	U
1	2A	1169	G
1	2A	1170	G
1	2A	1171	G
1	2A	1181	C
1	2A	1188	U
1	2A	1195	G
1	2A	1206	G
1	2A	1210	A
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1228	G
1	2A	1237	A
1	2A	1248	G
1	2A	1253	A
1	2A	1256	G
1	2A	1268	A
1	2A	1271	G

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Mol	Chain	Res	Type
1	2A	1272	A
1	2A	1273	U
1	2A	1300	U
1	2A	1301	A
1	2A	1306	C
1	2A	1313	U
1	2A	1314	C
1	2A	1320	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	1373	A
1	2A	1379	A
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1392	A
1	2A	1395	A
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1436	G
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1461	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1497	U

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Mol	Chain	Res	Type
1	2A	1505	C
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1528	A
1	2A	1531	C
1	2A	1542	A
1	2A	1547	C
1	2A	1558	A
1	2A	1562	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1584	C
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1613	G
1	2A	1640	C
1	2A	1647	G
1	2A	1648	C
1	2A	1653	G
1	2A	1654	A
1	2A	1667	G
1	2A	1674	G
1	2A	1695	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1703	G
1	2A	1708	C
1	2A	1721	G
1	2A	1722	A
1	2A	1739	U
1	2A	1740	G
1	2A	1741	A
1	2A	1758	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A

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Mol	Chain	Res	Type
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1812	A
1	2A	1816	G
1	2A	1829	A
1	2A	1847	A
1	2A	1848	A
1	2A	1858	G
1	2A	1866	C
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1937	A
1	2A	1938	A
1	2A	1940	U
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1993	U
1	2A	1997	G
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2035	G
1	2A	2036	C
1	2A	2043	C
1	2A	2049	G
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G

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Mol	Chain	Res	Type
1	2A	2067	G
1	2A	2069	G
1	2A	2093	G
1	2A	2099	U
1	2A	2101	G
1	2A	2110	G
1	2A	2111	C
1	2A	2115	G
1	2A	2116	G
1	2A	2117	A
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U
1	2A	2124	G
1	2A	2126	A
1	2A	2127	G
1	2A	2128	C
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	2153	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2161	C
1	2A	2164	C
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G

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Mol	Chain	Res	Type
1	2A	2172	U
1	2A	2174	C
1	2A	2176	A
1	2A	2178	C
1	2A	2185	C
1	2A	2188	C
1	2A	2189	U
1	2A	2190	G
1	2A	2193	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2225	A
1	2A	2235	G
1	2A	2238	G
1	2A	2239	G
1	2A	2267	A
1	2A	2275	C
1	2A	2278	A
1	2A	2283	C
1	2A	2287	A
1	2A	2288	A
1	2A	2305	A
1	2A	2308	G
1	2A	2309	A
1	2A	2312	U
1	2A	2319	G
1	2A	2320	A
1	2A	2325	G
1	2A	2327	A
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2372	G
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U

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Mol	Chain	Res	Type
1	2A	2410	G
1	2A	2425	A
1	2A	2428	G
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2445	G
1	2A	2448	A
1	2A	2459	A
1	2A	2465	C
1	2A	2469	A
1	2A	2475	C
1	2A	2476	A
1	2A	2477	C
1	2A	2480	C
1	2A	2491	U
1	2A	2494	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2535	G
1	2A	2542	A
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2572	A
1	2A	2573	C
1	2A	2582	G
1	2A	2585	U
1	2A	2602	A
1	2A	2611	U
1	2A	2612	C
1	2A	2630	G
1	2A	2634	G
1	2A	2646	C
1	2A	2654	A

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Mol	Chain	Res	Type
1	2A	2662	A
1	2A	2679	A
1	2A	2689	U
1	2A	2690	C
1	2A	2702	U
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2718	G
1	2A	2726	U
1	2A	2733	A
1	2A	2751	G
1	2A	2752	C
1	2A	2758	A
1	2A	2761	G
1	2A	2765	A
1	2A	2766	G
1	2A	2778	A
1	2A	2780	G
1	2A	2794	C
1	2A	2802	G
1	2A	2803	C
1	2A	2807	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2830	G
1	2A	2835	A
1	2A	2872	G
1	2A	2873	A
1	2A	2879	C
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2895	U
1	2A	2896	C
1	2A	2897	U
2	2B	2	C
2	2B	3	C
2	2B	5	C
2	2B	9	G

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Mol	Chain	Res	Type
2	2B	10	C
2	2B	12	C
2	2B	13	A
2	2B	15	A
2	2B	24	G
2	2B	33	G
2	2B	34	U
2	2B	35	U
2	2B	40	U
2	2B	41	U
2	2B	53	A
2	2B	63	G
2	2B	64	C
2	2B	69	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G
2	2B	88	C
2	2B	101	G
2	2B	106	G
2	2B	109	C
2	2B	110	G
2	2B	111	G
2	2B	116	G
2	2B	120	A
32	2a	7	G
32	2a	9	G
32	2a	16	A
32	2a	30	U
32	2a	32	A
32	2a	39	G
32	2a	41	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	52	G
32	2a	66	G
32	2a	80	G
32	2a	88	A
32	2a	89	C

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Mol	Chain	Res	Type
32	2a	91	C
32	2a	101	A
32	2a	105	G
32	2a	116	A
32	2a	121	C
32	2a	126	G
32	2a	127	G
32	2a	131	C
32	2a	142	G
32	2a	143	A
32	2a	144	G
32	2a	163	C
32	2a	172	A
32	2a	174	C
32	2a	182	U
32	2a	184	G
32	2a	189	G
32	2a	189(A)	C
32	2a	189(G)	G
32	2a	189(H)	G
32	2a	189(J)	G
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	217	C
32	2a	231	G
32	2a	247	G
32	2a	251	G
32	2a	266	G
32	2a	267	C
32	2a	269	C
32	2a	271	C
32	2a	274	A
32	2a	289	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	345	C
32	2a	350	G

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Mol	Chain	Res	Type
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	356	A
32	2a	363	A
32	2a	367	U
32	2a	372	C
32	2a	374	A
32	2a	381	C
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	401	C
32	2a	406	G
32	2a	409	G
32	2a	412	A
32	2a	413	G
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	441	A
32	2a	442	C
32	2a	452	A
32	2a	457	C
32	2a	470	C
32	2a	475	G
32	2a	484	G
32	2a	485	G
32	2a	488	C
32	2a	493	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	506	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G
32	2a	527	G7M

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Mol	Chain	Res	Type
32	2a	531	U
32	2a	532	A
32	2a	533	A
32	2a	534	U
32	2a	547	A
32	2a	559	A
32	2a	563	A
32	2a	564	C
32	2a	568	G
32	2a	571	U
32	2a	572	A
32	2a	573	A
32	2a	574	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	601	C
32	2a	607	A
32	2a	618	C
32	2a	624	C
32	2a	630	G
32	2a	649	G
32	2a	650	G
32	2a	651	C
32	2a	653	A
32	2a	665	A
32	2a	666	G
32	2a	671	G
32	2a	687	A
32	2a	688	G
32	2a	693	G
32	2a	694	A
32	2a	702	A
32	2a	721	G
32	2a	723	U
32	2a	727	G
32	2a	731	G
32	2a	746	A
32	2a	749	C
32	2a	755	G
32	2a	760	G
32	2a	774	G

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Mol	Chain	Res	Type
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	801	U
32	2a	815	A
32	2a	816	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	833	U
32	2a	836	G
32	2a	838	G
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	871	U
32	2a	872	A
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	932	C
32	2a	934	C
32	2a	938	A
32	2a	947	G
32	2a	957	U
32	2a	958	A
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	973	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A

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Mol	Chain	Res	Type
32	2a	982	U
32	2a	983	A
32	2a	984	C
32	2a	992	U
32	2a	993	G
32	2a	995	C
32	2a	997	U
32	2a	998	G
32	2a	999	C
32	2a	1002	G
32	2a	1005	A
32	2a	1006	C
32	2a	1007	C
32	2a	1008	C
32	2a	1009	G
32	2a	1012	U
32	2a	1016	A
32	2a	1019	C
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	1032	G
32	2a	1035	A
32	2a	1037	C
32	2a	1039	C
32	2a	1040	U
32	2a	1045	C
32	2a	1046	A
32	2a	1050	G
32	2a	1053	G
32	2a	1056	U
32	2a	1057	G
32	2a	1064	G
32	2a	1065	U

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Mol	Chain	Res	Type
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1079	G
32	2a	1081	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	1112	C
32	2a	1122	U
32	2a	1124	G
32	2a	1129	C
32	2a	1130	A
32	2a	1135	U
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1141	C
32	2a	1142	G
32	2a	1145	C
32	2a	1146	A
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1160	G
32	2a	1162	C
32	2a	1170	A
32	2a	1181	G
32	2a	1182	G
32	2a	1184	G
32	2a	1193	G
32	2a	1196	U
32	2a	1197	G
32	2a	1201	A
32	2a	1202	G

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Mol	Chain	Res	Type
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	1232	U
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1246	C
32	2a	1255	G
32	2a	1256	A
32	2a	1257	U
32	2a	1260	C
32	2a	1261	A
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1275	A
32	2a	1277	C
32	2a	1278	U
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
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1311	G
32	2a	1319	A
32	2a	1320	C
32	2a	1323	G
32	2a	1340	A
32	2a	1347	G
32	2a	1353	G
32	2a	1358	U

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Mol	Chain	Res	Type
32	2a	1359	C
32	2a	1363	C
32	2a	1363(A)	A
32	2a	1368	G
32	2a	1370	G
32	2a	1378	C
32	2a	1380	U
32	2a	1381	U
32	2a	1386	G
32	2a	1400	5MC
32	2a	1401	G
32	2a	1406	U
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1444	C
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G
32	2a	1492	A
32	2a	1494	G
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1505	G
32	2a	1506	U
32	2a	1507	A
32	2a	1508	G
32	2a	1517	G
32	2a	1519	MA6
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	19	U
53	2v	23	A
53	2v	24	A

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Mol	Chain	Res	Type
54	2w	3	C
54	2w	7	A
54	2w	9	A
54	2w	13	C
54	2w	14	A
54	2w	19	G
54	2w	22	G
54	2w	24	G
54	2w	27	G
54	2w	30	G
54	2w	43	C
54	2w	46	G7M
54	2w	47	U
54	2w	48	C
54	2w	51	U
54	2w	56	C
54	2w	57	G
54	2w	62	C
54	2w	65	G
54	2w	69	G
54	2w	70	G
54	2w	72	C
54	2w	73	A
54	2w	74	C
55	2x	5	G
55	2x	6	G
55	2x	9	G
55	2x	16	C
55	2x	18	G
55	2x	19	G
55	2x	21	A
55	2x	43	A
55	2x	47	U
55	2x	59	A
55	2x	61	C
55	2x	63	G
55	2x	66	C
54	2y	5	G
54	2y	6	G
54	2y	7	A
54	2y	8	4SU
54	2y	9	A

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Mol	Chain	Res	Type
54	2y	13	C
54	2y	14	A
54	2y	15	G
54	2y	19	G
54	2y	24	G
54	2y	27	G
54	2y	30	G
54	2y	35	A
54	2y	43	C
54	2y	44	G
54	2y	45	U
54	2y	49	C
54	2y	57	G
54	2y	59	U
54	2y	60	U
54	2y	61	C
54	2y	65	G
54	2y	67	C
54	2y	69	G
54	2y	70	G

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	195	A
1	1A	266	G
1	1A	278	A
1	1A	548	A
1	1A	746	A
1	1A	827	U
1	1A	859	G
1	1A	1033	U
1	1A	1047	G
1	1A	1067	A
1	1A	1174	A
1	1A	1379	A
1	1A	1442	G
1	1A	1508	A
1	1A	1663	C
1	1A	1992	G
1	1A	2126	A
1	1A	2134	A

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Mol	Chain	Res	Type
1	1A	2183	C
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2629	A
1	1A	2689	U
1	2A	229	A
1	2A	266	G
1	2A	271(K)	U
1	2A	271(M)	G
1	2A	277	C
1	2A	479	A
1	2A	528	A
1	2A	614(B)	G
1	2A	752	A
1	2A	856	C
1	2A	1026	U
1	2A	1210	A
1	2A	1379	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1653	G
1	2A	1913	A
1	2A	1935	G
1	2A	1992	G
1	2A	2119	A
1	2A	2126	A
1	2A	2689	U

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

88 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	$\#\|Z\|>2$
1	5MU	2A	1915	1,57	19,22,23	1.45	5 (26%)	27,32,35	2.05	5 (18%)
32	PSU	2a	516	32,57	18,21,22	1.35	2 (11%)	21,30,33	2.01	5 (23%)
55	PSU	2x	55	55	18,21,22	1.38	3 (16%)	21,30,33	1.94	3 (14%)
54	PSU	2w	55	54	18,21,22	1.41	2 (11%)	21,30,33	2.05	4 (19%)
32	5MC	2a	1407	32	19,22,23	1.64	3 (15%)	26,32,35	1.20	3 (11%)
54	G7M	1w	46	54	20,26,27	1.19	1 (5%)	16,39,42	0.91	0
32	PSU	1a	516	32,57	18,21,22	1.34	2 (11%)	21,30,33	2.12	4 (19%)
1	OMU	2A	2552	1,57	19,22,23	1.20	3 (15%)	25,31,34	1.74	5 (20%)
54	4SU	2y	8	54	18,21,22	1.61	3 (16%)	25,30,33	2.26	5 (20%)
32	4OC	2a	1402	32,57	20,23,24	0.78	0	25,32,35	1.00	1 (4%)
54	5MU	2w	54	54	19,22,23	1.46	4 (21%)	27,32,35	1.62	5 (18%)
1	PSU	2A	1911	1	18,21,22	1.39	3 (16%)	21,30,33	1.94	3 (14%)
32	4OC	1a	1402	32	20,23,24	0.75	0	25,32,35	0.92	1 (4%)
32	MA6	2a	1518	32	19,26,27	1.03	2 (10%)	18,38,41	1.93	3 (16%)
54	PSU	2w	32	54	18,21,22	1.37	2 (11%)	21,30,33	1.88	3 (14%)
32	5MC	2a	967	32	19,22,23	1.72	3 (15%)	26,32,35	1.14	3 (11%)
56	FME	1z	1	56	8,9,10	0.99	0	8,9,11	0.70	0
32	2MG	2a	1207	32,57	18,26,27	0.94	1 (5%)	16,38,41	1.52	4 (25%)
54	5MU	1w	54	54	19,22,23	1.40	4 (21%)	27,32,35	1.95	7 (25%)
1	2MA	1A	2503	1,57	18,25,26	0.69	0	20,37,40	2.10	6 (30%)
54	G7M	2w	46	54	20,26,27	1.16	1 (5%)	16,39,42	1.00	1 (6%)
54	PSU	2y	55	54	18,21,22	1.38	2 (11%)	21,30,33	1.91	4 (19%)
1	5MC	1A	1942	1	19,22,23	1.67	3 (15%)	26,32,35	1.14	3 (11%)
54	G7M	2y	46	54	20,26,27	1.37	2 (10%)	16,39,42	0.58	0
54	4SU	2w	8	54	18,21,22	1.81	5 (27%)	25,30,33	2.11	5 (20%)
32	MA6	1a	1518	32	19,26,27	1.02	2 (10%)	18,38,41	1.83	3 (16%)
32	5MC	2a	1400	32	19,22,23	1.68	3 (15%)	26,32,35	1.18	2 (7%)
1	5MU	1A	1939	1,57	19,22,23	1.56	6 (31%)	27,32,35	2.24	5 (18%)
1	OMG	2A	2251	55,1,57	19,26,27	0.94	1 (5%)	21,38,41	1.24	4 (19%)
1	2MA	2A	2503	1,57	18,25,26	0.71	0	20,37,40	1.90	4 (20%)
32	5MC	1a	1400	32	19,22,23	1.54	3 (15%)	26,32,35	1.15	3 (11%)
32	G7M	1a	527	32,57	20,26,27	1.22	2 (10%)	16,39,42	0.62	0
54	MIA	1w	37	54	24,31,32	2.12	4 (16%)	22,44,47	2.16	6 (27%)
55	5MC	2x	32	55	19,22,23	1.55	3 (15%)	26,32,35	1.14	3 (11%)
1	5MC	2A	1962	1,57	19,22,23	1.56	3 (15%)	26,32,35	1.21	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MC	1A	1962	1,57	19,22,23	1.69	3 (15%)	26,32,35	0.99	2 (7%)
1	PSU	2A	2605	1	18,21,22	1.43	3 (16%)	21,30,33	2.11	5 (23%)
32	5MC	1a	1404	32	19,22,23	1.67	3 (15%)	26,32,35	1.10	2 (7%)
55	PSU	1x	55	55	18,21,22	1.35	2 (11%)	21,30,33	2.05	3 (14%)
1	OMC	2A	1920	1	19,22,23	0.79	0	25,31,34	0.98	1 (4%)
32	UR3	1a	1498	32	19,22,23	1.07	1 (5%)	26,32,35	1.76	4 (15%)
54	PSU	1y	39	54	18,21,22	1.38	2 (11%)	21,30,33	1.85	4 (19%)
32	M2G	2a	966	32	20,27,28	1.42	3 (15%)	19,40,43	0.95	1 (5%)
55	5MU	2x	54	55	19,22,23	1.43	5 (26%)	27,32,35	2.08	6 (22%)
43	0TD	1l	92	43	8,9,10	4.46	1 (12%)	6,11,13	4.45	2 (33%)
55	8AN	1x	76	55,57	17,24,25	1.19	2 (11%)	13,35,38	3.18	3 (23%)
32	MA6	1a	1519	32	19,26,27	1.02	1 (5%)	18,38,41	2.10	3 (16%)
32	5MC	2a	1404	32	19,22,23	1.74	3 (15%)	26,32,35	1.19	3 (11%)
1	OMU	1A	2552	1,57	19,22,23	1.18	3 (15%)	25,31,34	1.85	5 (20%)
54	PSU	1w	39	54	18,21,22	1.26	2 (11%)	21,30,33	2.06	4 (19%)
54	G7M	1y	46	54	20,26,27	1.28	2 (10%)	16,39,42	0.55	0
54	5MU	1y	54	54	19,22,23	1.45	4 (21%)	27,32,35	1.94	6 (22%)
32	G7M	2a	527	32	20,26,27	1.18	2 (10%)	16,39,42	0.57	0
43	0TD	2l	92	43	8,9,10	4.51	1 (12%)	6,11,13	4.08	1 (16%)
32	M2G	1a	966	32	20,27,28	1.38	3 (15%)	19,40,43	1.04	2 (10%)
55	8AN	2x	76	58,55,57	17,24,25	1.09	2 (11%)	13,35,38	4.07	3 (23%)
54	MIA	1y	37	54	17,24,32	1.00	1 (5%)	16,35,47	1.28	2 (12%)
1	PSU	1A	1911	1	18,21,22	1.44	4 (22%)	21,30,33	2.15	3 (14%)
1	5MU	1A	1915	1	19,22,23	1.41	6 (31%)	27,32,35	2.08	6 (22%)
55	5MU	1x	54	55	19,22,23	1.38	5 (26%)	27,32,35	1.91	7 (25%)
54	4SU	1w	8	54	18,21,22	1.90	5 (27%)	25,30,33	1.74	5 (20%)
1	5MU	2A	1939	1	19,22,23	1.46	6 (31%)	27,32,35	2.25	6 (22%)
1	PSU	1A	2605	1,57	18,21,22	1.35	3 (16%)	21,30,33	2.02	3 (14%)
32	UR3	2a	1498	32,57	19,22,23	1.11	2 (10%)	26,32,35	1.76	4 (15%)
1	OMC	1A	1920	1	19,22,23	0.82	0	25,31,34	1.12	2 (8%)
54	PSU	1w	55	54	18,21,22	1.36	2 (11%)	21,30,33	1.97	3 (14%)
1	OMG	1A	2251	55,1,57	19,26,27	0.97	1 (5%)	21,38,41	1.01	2 (9%)
56	FME	2z	1	56	8,9,10	0.98	0	8,9,11	1.05	0
54	PSU	1y	55	54	18,21,22	1.35	2 (11%)	21,30,33	2.06	3 (14%)
54	PSU	2y	39	54	18,21,22	1.36	2 (11%)	21,30,33	1.73	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
55	4SU	1x	8	55	18,21,22	2.19	5 (27%)	25,30,33	1.78	6 (24%)
55	4SU	2x	8	55	18,21,22	2.23	6 (33%)	25,30,33	1.77	5 (20%)
54	MIA	2y	37	54	17,24,32	1.00	1 (5%)	16,35,47	1.29	2 (12%)
54	PSU	2y	32	54	18,21,22	1.38	2 (11%)	21,30,33	1.97	4 (19%)
1	PSU	1A	1917	1	18,21,22	1.46	3 (16%)	21,30,33	2.12	5 (23%)
32	MA6	2a	1519	32	19,26,27	1.03	2 (10%)	18,38,41	1.93	3 (16%)
32	5MC	1a	1407	32	19,22,23	1.56	2 (10%)	26,32,35	1.17	3 (11%)
54	5MU	2y	54	54	19,22,23	1.51	5 (26%)	27,32,35	1.77	7 (25%)
1	5MC	2A	1942	1	19,22,23	1.70	2 (10%)	26,32,35	1.14	2 (7%)
1	PSU	2A	1917	1	18,21,22	1.42	3 (16%)	21,30,33	2.09	4 (19%)
54	PSU	2w	39	54	18,21,22	1.38	2 (11%)	21,30,33	1.57	3 (14%)
54	MIA	2w	37	53,54	19,27,32	2.05	2 (10%)	18,39,47	2.72	4 (22%)
32	5MC	1a	967	32	19,22,23	1.66	3 (15%)	26,32,35	1.12	2 (7%)
54	4SU	1y	8	54	18,21,22	1.77	6 (33%)	25,30,33	2.08	4 (16%)
54	PSU	1w	32	54	18,21,22	1.32	2 (11%)	21,30,33	1.93	3 (14%)
55	5MC	1x	32	55	19,22,23	1.63	3 (15%)	26,32,35	1.17	2 (7%)
32	2MG	1a	1207	32	18,26,27	0.99	1 (5%)	16,38,41	1.54	5 (31%)
54	PSU	1y	32	54	18,21,22	1.34	2 (11%)	21,30,33	2.00	4 (19%)

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
1	5MU	2A	1915	1,57	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32,57	-	0/7/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
54	PSU	2w	55	54	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
54	G7M	1w	46	54	-	2/3/25/26	0/3/3/3
32	PSU	1a	516	32,57	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	1,57	-	0/9/27/28	0/2/2/2
54	4SU	2y	8	54	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32,57	-	1/9/29/30	0/2/2/2
54	5MU	2w	54	54	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	1/9/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	MA6	2a	1518	32	-	0/7/29/30	0/3/3/3
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
56	FME	1z	1	56	-	4/7/9/11	-
32	2MG	2a	1207	32,57	-	0/5/27/28	0/3/3/3
54	5MU	1w	54	54	-	0/7/25/26	0/2/2/2
1	2MA	1A	2503	1,57	-	1/3/25/26	0/3/3/3
54	G7M	2w	46	54	-	1/3/25/26	0/3/3/3
54	PSU	2y	55	54	-	5/7/25/26	0/2/2/2
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
54	G7M	2y	46	54	-	0/3/25/26	0/3/3/3
54	4SU	2w	8	54	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/7/29/30	0/3/3/3
32	5MC	2a	1400	32	-	2/7/25/26	0/2/2/2
1	5MU	1A	1939	1,57	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	55,1,57	-	0/5/27/28	0/3/3/3
1	2MA	2A	2503	1,57	-	1/3/25/26	0/3/3/3
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
32	G7M	1a	527	32,57	-	2/3/25/26	0/3/3/3
54	MIA	1w	37	54	-	1/11/33/34	0/3/3/3
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1,57	-	0/7/25/26	0/2/2/2
1	5MC	1A	1962	1,57	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
54	PSU	1y	39	54	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/7/29/30	0/3/3/3
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	2/7/12/14	-
55	8AN	1x	76	55,57	-	3/3/25/26	0/3/3/3
32	MA6	1a	1519	32	-	2/7/29/30	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	1,57	-	0/9/27/28	0/2/2/2
54	PSU	1w	39	54	-	0/7/25/26	0/2/2/2
54	G7M	1y	46	54	-	2/3/25/26	0/3/3/3
54	5MU	1y	54	54	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	32	-	3/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
43	0TD	2l	92	43	-	2/7/12/14	-
32	M2G	1a	966	32	-	0/7/29/30	0/3/3/3
55	8AN	2x	76	58,55,57	-	3/3/25/26	0/3/3/3
54	MIA	1y	37	54	-	0/3/25/34	0/3/3/3
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	0/7/25/26	0/2/2/2
55	5MU	1x	54	55	-	0/7/25/26	0/2/2/2
54	4SU	1w	8	54	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	1,57	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32,57	-	0/7/25/26	0/2/2/2
1	OMC	1A	1920	1	-	2/9/27/28	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	55,1,57	-	0/5/27/28	0/3/3/3
56	FME	2z	1	56	-	1/7/9/11	-
54	PSU	1y	55	54	-	0/7/25/26	0/2/2/2
54	PSU	2y	39	54	-	0/7/25/26	0/2/2/2
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
54	MIA	2y	37	54	-	0/3/25/34	0/3/3/3
54	PSU	2y	32	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	3/7/29/30	0/3/3/3
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
54	5MU	2y	54	54	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	1/7/25/26	0/2/2/2
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
54	MIA	2w	37	53,54	-	4/7/29/34	0/3/3/3
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
54	4SU	1y	8	54	-	0/7/25/26	0/2/2/2
54	PSU	1w	32	54	-	0/7/25/26	0/2/2/2
55	5MC	1x	32	55	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/5/27/28	0/3/3/3
54	PSU	1y	32	54	-	0/7/25/26	0/2/2/2

All (222) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.35	1.69	1.82
43	1l	92	0TD	CB-SB	-12.14	1.70	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	37	MIA	C2-S10	-7.90	1.69	1.75
54	1w	37	MIA	C13-C14	7.07	1.53	1.32
32	2a	1404	5MC	C5-C4	6.38	1.48	1.44
1	1A	1942	5MC	C5-C4	6.22	1.48	1.44
32	2a	967	5MC	C5-C4	6.20	1.48	1.44
1	2A	1942	5MC	C5-C4	6.14	1.48	1.44
1	1A	1962	5MC	C5-C4	6.13	1.48	1.44
32	2a	1400	5MC	C5-C4	6.08	1.48	1.44
32	1a	1404	5MC	C5-C4	5.96	1.48	1.44
32	1a	967	5MC	C5-C4	5.92	1.48	1.44
32	2a	1407	5MC	C5-C4	5.85	1.48	1.44
55	1x	32	5MC	C5-C4	5.69	1.48	1.44
32	1a	1407	5MC	C5-C4	5.63	1.48	1.44
54	1w	37	MIA	C2-S10	-5.59	1.71	1.75
1	2A	1962	5MC	C5-C4	5.42	1.48	1.44
55	2x	32	5MC	C5-C4	5.40	1.48	1.44
32	1a	1400	5MC	C5-C4	5.33	1.48	1.44
55	2x	8	4SU	C4-S4	-5.05	1.59	1.68
55	2x	8	4SU	C4-N3	-4.99	1.32	1.37
55	1x	8	4SU	C4-N3	-4.94	1.32	1.37
54	1w	8	4SU	C4-S4	-4.85	1.60	1.68
54	2w	8	4SU	C4-S4	-4.76	1.60	1.68
54	1y	8	4SU	C4-S4	-4.54	1.60	1.68
54	2y	8	4SU	C4-S4	-4.49	1.60	1.68
32	2a	966	M2G	C2-N3	4.46	1.36	1.30
55	1x	8	4SU	C4-S4	-4.42	1.60	1.68
54	2y	46	G7M	C5-C4	4.08	1.47	1.39
54	2w	55	PSU	C6-C5	4.04	1.39	1.35
32	1a	966	M2G	C2-N3	3.95	1.36	1.30
55	1x	8	4SU	C2-N3	-3.89	1.31	1.38
54	1y	46	G7M	C5-C4	3.89	1.46	1.39
54	1y	39	PSU	C6-C5	3.82	1.39	1.35
54	2y	39	PSU	C6-C5	3.82	1.39	1.35
54	2w	32	PSU	C6-C5	3.79	1.39	1.35
54	2y	32	PSU	C6-C5	3.78	1.39	1.35
54	2w	39	PSU	C6-C5	3.75	1.39	1.35
54	1w	55	PSU	C6-C5	3.74	1.39	1.35
32	2a	516	PSU	C6-C5	3.71	1.39	1.35
55	1x	55	PSU	C6-C5	3.71	1.39	1.35
55	1x	8	4SU	C5-C4	-3.71	1.38	1.42
54	1w	46	G7M	C5-C4	3.70	1.46	1.39
54	1w	8	4SU	C4-N3	-3.67	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	527	G7M	C5-C4	3.67	1.46	1.39
32	2a	527	G7M	C5-C4	3.66	1.46	1.39
1	1A	1917	PSU	C6-C5	3.66	1.39	1.35
54	1y	55	PSU	C6-C5	3.64	1.39	1.35
55	2x	8	4SU	C5-C4	-3.64	1.38	1.42
55	2x	55	PSU	C6-C5	3.62	1.39	1.35
54	2w	46	G7M	C5-C4	3.60	1.46	1.39
1	1A	1911	PSU	C6-C5	3.56	1.39	1.35
54	1y	32	PSU	C6-C5	3.44	1.39	1.35
54	1y	8	4SU	C4-N3	-3.42	1.34	1.37
1	2A	1911	PSU	C6-C5	3.41	1.39	1.35
54	2w	8	4SU	C4-N3	-3.31	1.34	1.37
54	1y	54	5MU	C6-C5	3.30	1.40	1.34
54	1w	32	PSU	C6-C5	3.27	1.38	1.35
1	1A	1939	5MU	C4-N3	-3.24	1.32	1.38
54	1w	39	PSU	C6-C5	3.22	1.38	1.35
54	2y	55	PSU	C6-C5	3.22	1.38	1.35
1	2A	1917	PSU	C6-C5	3.19	1.38	1.35
32	1a	516	PSU	C6-C5	3.18	1.38	1.35
55	1x	32	5MC	C6-C5	3.18	1.39	1.34
54	2w	54	5MU	C6-C5	3.17	1.39	1.34
1	2A	1942	5MC	C6-C5	3.11	1.39	1.34
32	1a	967	5MC	C6-C5	3.06	1.39	1.34
32	1a	966	M2G	C2-N2	2.97	1.40	1.35
55	2x	32	5MC	C6-C5	2.96	1.39	1.34
1	1A	1962	5MC	C6-C5	2.95	1.39	1.34
54	2y	54	5MU	C2-N1	2.94	1.43	1.38
1	2A	1915	5MU	C6-C5	2.92	1.39	1.34
1	2A	1939	5MU	C6-C5	2.91	1.39	1.34
55	2x	8	4SU	C2-N3	-2.91	1.32	1.38
1	2A	1917	PSU	C4-N3	-2.90	1.33	1.38
54	1y	37	MIA	C2-N3	2.88	1.36	1.32
55	2x	54	5MU	C6-C5	2.87	1.39	1.34
32	2a	966	M2G	C2-N2	2.87	1.40	1.35
54	2y	54	5MU	C6-C5	2.86	1.39	1.34
55	2x	54	5MU	C4-N3	-2.85	1.33	1.38
32	1a	1404	5MC	C6-C5	2.84	1.39	1.34
1	2A	2605	PSU	C4-N3	-2.83	1.33	1.38
1	2A	1915	5MU	C2-N1	2.82	1.42	1.38
1	1A	2605	PSU	C6-C5	2.82	1.38	1.35
54	1w	54	5MU	C6-C5	2.81	1.39	1.34
1	1A	1939	5MU	C2-N3	-2.81	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	1915	5MU	C6-C5	2.80	1.39	1.34
1	2A	2552	OMU	C4-N3	-2.79	1.33	1.38
1	1A	2552	OMU	C4-N3	-2.78	1.33	1.38
55	2x	76	8AN	C6-C5	-2.78	1.33	1.43
54	2y	37	MIA	C2-N3	2.78	1.36	1.32
54	1w	8	4SU	C5-C4	-2.78	1.39	1.42
1	2A	2605	PSU	C6-C5	2.78	1.38	1.35
1	2A	1939	5MU	C4-N3	-2.77	1.33	1.38
1	2A	1962	5MC	C6-C5	2.77	1.39	1.34
1	2A	2251	OMG	C6-N1	-2.77	1.33	1.37
1	1A	1917	PSU	C4-N3	-2.76	1.33	1.38
32	2a	1498	UR3	C2-N1	2.76	1.42	1.38
32	2a	967	5MC	C6-C5	2.75	1.39	1.34
1	1A	1939	5MU	C6-C5	2.75	1.39	1.34
1	2A	1911	PSU	C4-N3	-2.74	1.33	1.38
1	1A	1911	PSU	C4-N3	-2.74	1.33	1.38
55	1x	54	5MU	C4-N3	-2.74	1.33	1.38
54	2y	54	5MU	C4-N3	-2.71	1.33	1.38
32	2a	1400	5MC	C6-C5	2.67	1.39	1.34
32	2a	1404	5MC	C6-C5	2.67	1.39	1.34
55	1x	76	8AN	C6-C5	-2.66	1.33	1.43
32	1a	1207	2MG	C6-N1	-2.63	1.33	1.37
1	1A	1915	5MU	C4-N3	-2.63	1.33	1.38
32	1a	1400	5MC	C6-C5	2.62	1.38	1.34
32	1a	516	PSU	C4-N3	-2.61	1.34	1.38
55	1x	54	5MU	C6-C5	2.61	1.38	1.34
54	2w	8	4SU	C5-C4	-2.61	1.39	1.42
1	1A	1939	5MU	C6-N1	-2.60	1.33	1.38
32	1a	1407	5MC	C6-C5	2.59	1.38	1.34
1	2A	2605	PSU	C2-N3	-2.59	1.33	1.37
54	1y	54	5MU	C4-N3	-2.59	1.34	1.38
54	2w	39	PSU	C4-N3	-2.58	1.34	1.38
54	1y	54	5MU	C4-C5	2.58	1.49	1.44
32	1a	1498	UR3	C2-N1	2.57	1.42	1.38
54	1w	55	PSU	C4-N3	-2.57	1.34	1.38
1	1A	2605	PSU	C4-N3	-2.56	1.34	1.38
54	1w	37	MIA	C6-C5	2.56	1.48	1.44
1	2A	1939	5MU	C4-C5	2.56	1.49	1.44
32	1a	966	M2G	C6-N1	-2.55	1.33	1.37
54	2w	54	5MU	C4-N3	-2.54	1.34	1.38
32	1a	1518	MA6	C6-C5	-2.53	1.41	1.44
54	1y	39	PSU	C4-N3	-2.52	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2y	46	G7M	C6-N1	-2.51	1.34	1.37
54	2y	8	4SU	C4-N3	-2.50	1.35	1.37
55	2x	8	4SU	O2-C2	2.50	1.27	1.23
55	2x	8	4SU	C2-N1	2.50	1.42	1.38
54	2y	55	PSU	C4-N3	-2.49	1.34	1.38
54	1y	32	PSU	C4-N3	-2.48	1.34	1.38
54	2w	37	MIA	C6-C5	2.48	1.48	1.44
1	1A	1942	5MC	C6-C5	2.48	1.38	1.34
32	2a	1407	5MC	C6-C5	2.48	1.38	1.34
54	2w	54	5MU	C4-C5	2.47	1.48	1.44
54	1w	54	5MU	C4-C5	2.46	1.48	1.44
32	2a	516	PSU	C4-N3	-2.46	1.34	1.38
1	1A	2605	PSU	C2-N1	-2.46	1.33	1.36
54	1w	54	5MU	C2-N1	2.44	1.42	1.38
32	2a	1518	MA6	C6-C5	-2.43	1.41	1.44
54	2w	54	5MU	C2-N1	2.43	1.42	1.38
32	1a	1519	MA6	C6-C5	-2.42	1.41	1.44
54	2w	32	PSU	C4-N3	-2.41	1.34	1.38
54	1w	32	PSU	C4-N3	-2.41	1.34	1.38
1	1A	1915	5MU	C2-N1	2.41	1.42	1.38
55	2x	55	PSU	C4-N3	-2.41	1.34	1.38
1	1A	1962	5MC	C6-N1	-2.40	1.33	1.38
54	1w	54	5MU	C4-N3	-2.39	1.34	1.38
1	2A	1915	5MU	C4-C5	2.39	1.48	1.44
54	2w	55	PSU	C4-N3	-2.39	1.34	1.38
55	2x	54	5MU	C2-N3	-2.39	1.33	1.38
54	2y	39	PSU	C4-N3	-2.39	1.34	1.38
54	2y	54	5MU	C4-C5	2.39	1.48	1.44
1	2A	2552	OMU	C2-N3	-2.38	1.33	1.38
1	1A	1939	5MU	C4-C5	2.38	1.48	1.44
1	1A	1942	5MC	C6-N1	-2.38	1.34	1.38
55	2x	54	5MU	C4-C5	2.36	1.48	1.44
1	2A	1915	5MU	C4-N3	-2.36	1.34	1.38
32	2a	967	5MC	C6-N1	-2.36	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.36	1.34	1.37
55	1x	54	5MU	C4-C5	2.35	1.48	1.44
32	2a	1519	MA6	C6-C5	-2.35	1.41	1.44
54	1y	8	4SU	C5-C4	-2.35	1.39	1.42
55	1x	8	4SU	O2-C2	2.34	1.27	1.23
1	2A	1939	5MU	C6-N1	-2.33	1.34	1.38
54	1w	37	MIA	C6-N1	2.32	1.36	1.33
54	1y	55	PSU	C4-N3	-2.32	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2y	32	PSU	C4-N3	-2.32	1.34	1.38
54	1w	39	PSU	C4-N3	-2.32	1.34	1.38
54	2w	8	4SU	C2-N3	-2.31	1.33	1.38
32	2a	1404	5MC	C6-N1	-2.31	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.30	1.34	1.38
54	1w	8	4SU	C2-N3	-2.30	1.34	1.38
55	1x	76	8AN	C5-N7	-2.30	1.31	1.39
1	1A	2552	OMU	C5-C4	-2.28	1.38	1.43
54	1w	8	4SU	C2-N1	2.27	1.42	1.38
55	1x	55	PSU	C4-N3	-2.27	1.34	1.38
1	1A	2552	OMU	C2-N3	-2.25	1.34	1.38
54	2y	8	4SU	C5-C4	-2.25	1.39	1.42
55	2x	76	8AN	C5-N7	-2.25	1.31	1.39
54	2w	8	4SU	C2-N1	2.25	1.42	1.38
32	2a	1400	5MC	C6-N1	-2.24	1.34	1.38
54	2y	54	5MU	C2-N3	-2.21	1.34	1.38
1	1A	1939	5MU	C2-N1	2.21	1.41	1.38
1	2A	1962	5MC	C6-N1	-2.21	1.34	1.38
32	2a	527	G7M	C6-N1	-2.21	1.34	1.37
55	2x	54	5MU	C6-N1	-2.20	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.19	1.34	1.38
54	1y	8	4SU	C2-N3	-2.19	1.34	1.38
32	1a	1404	5MC	C6-N1	-2.18	1.34	1.38
1	2A	1917	PSU	C2-N3	-2.16	1.33	1.37
55	1x	32	5MC	C6-N1	-2.15	1.34	1.38
1	1A	1915	5MU	C4-C5	2.14	1.48	1.44
32	2a	1207	2MG	C6-N1	-2.14	1.34	1.37
1	2A	1915	5MU	C6-N1	-2.14	1.34	1.38
54	1y	54	5MU	C2-N1	2.14	1.41	1.38
55	1x	54	5MU	C2-N3	-2.12	1.34	1.38
32	1a	967	5MC	C6-N1	-2.12	1.34	1.38
54	1y	46	G7M	C6-N1	-2.11	1.34	1.37
32	2a	1498	UR3	C6-C5	2.10	1.40	1.35
1	2A	2552	OMU	C5-C4	-2.10	1.39	1.43
32	1a	1400	5MC	C6-N1	-2.10	1.34	1.38
1	1A	1917	PSU	C2-N3	-2.10	1.34	1.37
54	1y	8	4SU	C2-N1	2.09	1.41	1.38
55	1x	54	5MU	C6-N1	-2.09	1.34	1.38
32	1a	527	G7M	C6-N1	-2.09	1.34	1.37
32	2a	1519	MA6	C6-N1	2.08	1.35	1.32
1	1A	1911	PSU	C2-N1	-2.07	1.34	1.36
55	2x	55	PSU	C4-C5	2.06	1.50	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1518	MA6	C6-N1	2.06	1.35	1.32
32	2a	966	M2G	C6-N1	-2.05	1.34	1.37
1	1A	1915	5MU	C6-N1	-2.05	1.34	1.38
1	2A	1939	5MU	C2-N1	2.03	1.41	1.38
55	2x	32	5MC	C6-N1	-2.03	1.34	1.38
1	1A	1911	PSU	C2-N3	-2.02	1.34	1.37
32	1a	1518	MA6	C6-N1	2.01	1.35	1.32
1	1A	1915	5MU	C2-N3	-2.01	1.34	1.38
54	1y	8	4SU	C6-C5	2.01	1.39	1.35
1	2A	1911	PSU	C2-N3	-2.00	1.34	1.37

All (293) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2w	37	MIA	C11-S10-C2	-10.36	94.48	102.25
55	2x	76	8AN	O4'-C1'-N9	-10.28	95.12	108.75
43	1l	92	0TD	CSB-SB-CB	10.24	120.77	102.36
43	2l	92	0TD	CSB-SB-CB	-9.64	85.04	102.36
55	1x	76	8AN	C4'-O4'-C1'	-8.79	101.88	109.92
55	2x	76	8AN	C4'-O4'-C1'	-7.60	102.96	109.92
1	1A	2503	2MA	C2-N3-C4	7.03	121.14	115.46
54	2y	8	4SU	C4-N3-C2	-6.97	120.63	127.31
1	1A	1917	PSU	N1-C2-N3	6.81	122.36	115.17
32	1a	1498	UR3	C4-N3-C2	-6.81	119.10	124.58
54	1w	37	MIA	C12-C13-C14	-6.78	114.84	127.01
1	2A	1917	PSU	N1-C2-N3	6.77	122.31	115.17
1	1A	1911	PSU	N1-C2-N3	6.72	122.25	115.17
1	2A	2605	PSU	N1-C2-N3	6.68	122.21	115.17
55	2x	76	8AN	N3-C2-N1	-6.67	119.62	128.67
32	2a	1498	UR3	C4-N3-C2	-6.62	119.25	124.58
32	1a	516	PSU	N1-C2-N3	6.53	122.05	115.17
55	1x	76	8AN	N3-C2-N1	-6.49	119.86	128.67
54	1y	55	PSU	N1-C2-N3	6.31	121.83	115.17
54	1y	8	4SU	C4-N3-C2	-6.29	121.29	127.31
55	1x	55	PSU	N1-C2-N3	6.25	121.76	115.17
32	2a	516	PSU	N1-C2-N3	6.22	121.73	115.17
54	2w	8	4SU	C4-N3-C2	-6.15	121.42	127.31
54	1w	39	PSU	N1-C2-N3	6.08	121.58	115.17
54	1w	55	PSU	N1-C2-N3	6.06	121.56	115.17
54	2w	55	PSU	N1-C2-N3	6.05	121.55	115.17
55	2x	55	PSU	N1-C2-N3	6.04	121.54	115.17
54	1y	32	PSU	N1-C2-N3	6.04	121.54	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1911	PSU	N1-C2-N3	5.96	121.46	115.17
1	2A	2503	2MA	C2-N3-C4	5.91	120.23	115.46
54	2y	32	PSU	N1-C2-N3	5.87	121.36	115.17
32	1a	1519	MA6	N3-C2-N1	-5.87	120.71	128.67
54	2w	32	PSU	N1-C2-N3	5.82	121.31	115.17
54	1y	39	PSU	N1-C2-N3	5.75	121.23	115.17
54	1w	32	PSU	N1-C2-N3	5.69	121.17	115.17
1	1A	2605	PSU	N1-C2-N3	5.66	121.14	115.17
32	2a	1518	MA6	N3-C2-N1	-5.59	121.08	128.67
54	2y	55	PSU	N1-C2-N3	5.59	121.07	115.17
1	2A	1939	5MU	C4-N3-C2	-5.57	120.04	127.34
54	2w	8	4SU	C5-C4-N3	5.55	119.91	114.75
32	2a	1519	MA6	N3-C2-N1	-5.54	121.16	128.67
1	1A	1939	5MU	C4-N3-C2	-5.53	120.08	127.34
54	2y	8	4SU	C5-C4-N3	5.42	119.79	114.75
1	1A	1939	5MU	N3-C2-N1	5.34	121.84	114.89
55	2x	54	5MU	N3-C2-N1	5.33	121.82	114.89
32	1a	1519	MA6	C2-N1-C6	5.24	121.98	116.84
54	1y	54	5MU	N3-C2-N1	5.21	121.68	114.89
1	2A	1939	5MU	N3-C2-N1	5.16	121.61	114.89
54	2y	39	PSU	N1-C2-N3	5.14	120.59	115.17
32	1a	1518	MA6	N3-C2-N1	-5.10	121.75	128.67
1	2A	1915	5MU	N3-C2-N1	5.07	121.49	114.89
1	1A	1915	5MU	N3-C2-N1	5.06	121.47	114.89
55	2x	54	5MU	C4-N3-C2	-5.04	120.73	127.34
1	1A	1915	5MU	C4-N3-C2	-4.93	120.87	127.34
54	1w	8	4SU	C5-C4-N3	4.90	119.31	114.75
1	1A	2605	PSU	O2-C2-N1	-4.89	117.75	122.79
1	1A	1939	5MU	C5-C4-N3	4.85	119.53	115.32
54	1y	8	4SU	C5-C4-N3	4.81	119.22	114.75
1	2A	1915	5MU	C4-N3-C2	-4.79	121.06	127.34
32	2a	1518	MA6	C2-N1-C6	4.73	121.48	116.84
1	1A	1939	5MU	C5-C6-N1	-4.72	118.19	123.31
1	2A	1939	5MU	C5-C4-N3	4.71	119.42	115.32
1	2A	1939	5MU	C5-C6-N1	-4.71	118.20	123.31
1	1A	2552	OMU	C4-N3-C2	-4.63	120.87	126.61
1	2A	2552	OMU	N3-C2-N1	4.61	120.90	114.89
54	1w	39	PSU	C4-N3-C2	-4.61	120.02	126.37
54	2w	39	PSU	N1-C2-N3	4.60	120.02	115.17
32	1a	1518	MA6	C2-N1-C6	4.59	121.34	116.84
54	1y	54	5MU	C4-N3-C2	-4.59	121.32	127.34
55	1x	54	5MU	N3-C2-N1	4.55	120.81	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2x	8	4SU	C5-C4-N3	4.52	118.96	114.75
1	1A	2552	OMU	N3-C2-N1	4.51	120.76	114.89
54	1w	54	5MU	C4-N3-C2	-4.49	121.46	127.34
54	1w	54	5MU	N3-C2-N1	4.49	120.73	114.89
54	1y	8	4SU	N3-C2-N1	4.47	120.71	114.89
1	2A	2552	OMU	C4-N3-C2	-4.45	121.09	126.61
1	1A	1915	5MU	C5-C4-N3	4.43	119.18	115.32
55	1x	8	4SU	C6-C5-C4	-4.42	116.12	119.95
1	1A	1911	PSU	O2-C2-N1	-4.41	118.24	122.79
32	2a	1519	MA6	C2-N1-C6	4.39	121.14	116.84
1	2A	2605	PSU	C4-N3-C2	-4.35	120.38	126.37
55	1x	54	5MU	C4-N3-C2	-4.34	121.65	127.34
55	1x	8	4SU	O2-C2-N1	4.32	128.42	122.80
1	1A	1915	5MU	O4-C4-C5	-4.29	120.01	124.92
1	2A	1915	5MU	O4-C4-C5	-4.23	120.08	124.92
54	1w	54	5MU	C5-C4-N3	4.22	118.99	115.32
55	2x	8	4SU	C1'-N1-C2	4.22	125.17	117.59
54	2y	8	4SU	N3-C2-N1	4.22	120.38	114.89
54	1w	8	4SU	C4-N3-C2	-4.16	123.33	127.31
32	1a	516	PSU	C4-N3-C2	-4.15	120.65	126.37
54	1y	32	PSU	C4-N3-C2	-4.12	120.70	126.37
1	1A	1917	PSU	C4-N3-C2	-4.12	120.70	126.37
1	2A	1917	PSU	C4-N3-C2	-4.09	120.74	126.37
54	1y	55	PSU	O2-C2-N1	-4.06	118.60	122.79
55	1x	55	PSU	C4-N3-C2	-4.05	120.79	126.37
54	2w	55	PSU	C4-N3-C2	-4.04	120.81	126.37
54	2y	54	5MU	N3-C2-N1	4.03	120.14	114.89
1	2A	1939	5MU	O4-C4-C5	-4.03	120.31	124.92
54	2y	8	4SU	C5-C4-S4	-4.02	119.72	124.31
55	2x	54	5MU	C5-C6-N1	-4.02	118.95	123.31
32	2a	516	PSU	C4-N3-C2	-4.02	120.84	126.37
55	2x	54	5MU	C5-C4-N3	3.99	118.79	115.32
32	1a	516	PSU	O2-C2-N1	-3.98	118.68	122.79
1	1A	1911	PSU	C4-N3-C2	-3.97	120.90	126.37
54	1y	55	PSU	C4-N3-C2	-3.97	120.90	126.37
1	2A	1911	PSU	C4-N3-C2	-3.97	120.90	126.37
54	1w	32	PSU	O2-C2-N1	-3.97	118.69	122.79
54	2w	54	5MU	N3-C2-N1	3.95	120.03	114.89
1	2A	1915	5MU	C5-C4-N3	3.94	118.75	115.32
54	1w	37	MIA	C15-C14-C13	-3.90	110.94	122.66
54	1w	55	PSU	C4-N3-C2	-3.90	120.99	126.37
55	2x	55	PSU	C4-N3-C2	-3.89	121.01	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2y	55	PSU	C4-N3-C2	-3.88	121.02	126.37
55	1x	55	PSU	O2-C2-N1	-3.85	118.82	122.79
54	2y	32	PSU	C4-N3-C2	-3.80	121.14	126.37
54	2w	32	PSU	C4-N3-C2	-3.79	121.15	126.37
54	2y	54	5MU	C5-C4-N3	3.78	118.61	115.32
54	1w	32	PSU	C4-N3-C2	-3.78	121.16	126.37
54	1w	54	5MU	O4-C4-C5	-3.78	120.59	124.92
54	2w	8	4SU	N3-C2-N1	3.75	119.78	114.89
54	2y	37	MIA	N3-C2-N1	-3.74	123.60	128.67
55	1x	54	5MU	C5-C4-N3	3.70	118.54	115.32
54	2y	54	5MU	C4-N3-C2	-3.64	122.57	127.34
54	1y	32	PSU	O2-C2-N1	-3.64	119.04	122.79
1	1A	2605	PSU	C4-N3-C2	-3.63	121.37	126.37
1	1A	2552	OMU	C5-C4-N3	3.62	119.87	114.80
54	1y	37	MIA	N3-C2-N1	-3.59	123.80	128.67
1	2A	1942	5MC	C5-C6-N1	-3.59	119.41	123.31
54	1y	54	5MU	O4-C4-C5	-3.59	120.81	124.92
55	1x	54	5MU	O4-C4-C5	-3.56	120.85	124.92
54	1y	54	5MU	C5-C4-N3	3.55	118.41	115.32
54	1y	39	PSU	C4-N3-C2	-3.55	121.48	126.37
54	2w	8	4SU	C5-C4-S4	-3.55	120.26	124.31
32	1a	1498	UR3	C5-C4-N3	3.54	119.70	115.04
54	2w	54	5MU	C4-N3-C2	-3.51	122.74	127.34
1	1A	1939	5MU	O4-C4-C5	-3.49	120.92	124.92
55	2x	54	5MU	O4-C4-C5	-3.48	120.94	124.92
54	2y	32	PSU	O2-C2-N1	-3.47	119.21	122.79
1	2A	1917	PSU	O2-C2-N1	-3.47	119.21	122.79
32	1a	1404	5MC	C5-C6-N1	-3.46	119.55	123.31
55	2x	8	4SU	C6-C5-C4	-3.45	116.97	119.95
32	2a	1407	5MC	C5-C6-N1	-3.44	119.57	123.31
54	2w	54	5MU	C5-C4-N3	3.41	118.29	115.32
54	2y	39	PSU	C4-N3-C2	-3.41	121.67	126.37
32	1a	1407	5MC	C5-C4-N3	-3.39	118.28	121.75
32	2a	1404	5MC	C5-C6-N1	-3.38	119.64	123.31
1	1A	2552	OMU	O2-C2-N1	-3.33	118.47	122.80
32	1a	967	5MC	C5-C6-N1	-3.33	119.70	123.31
1	1A	1917	PSU	O2-C2-N1	-3.32	119.36	122.79
32	2a	967	5MC	C5-C6-N1	-3.32	119.70	123.31
54	2w	54	5MU	O4-C4-C5	-3.31	121.12	124.92
54	1w	55	PSU	O2-C2-N1	-3.29	119.39	122.79
54	1y	54	5MU	C5-C6-N1	-3.29	119.74	123.31
54	2w	55	PSU	O2-C2-N1	-3.27	119.41	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1x	32	5MC	C5-C6-N1	-3.27	119.77	123.31
32	1a	1207	2MG	C8-N7-C5	3.25	108.09	102.55
55	1x	8	4SU	C1'-N1-C2	3.24	123.42	117.59
1	1A	1942	5MC	C5-C4-N3	-3.24	118.43	121.75
55	1x	54	5MU	C5-C6-N1	-3.23	119.80	123.31
32	2a	516	PSU	O2-C2-N1	-3.23	119.46	122.79
1	2A	2552	OMU	C5-C4-N3	3.22	119.31	114.80
1	2A	2605	PSU	O2-C2-N1	-3.20	119.49	122.79
54	1w	39	PSU	O2-C2-N1	-3.16	119.53	122.79
55	2x	32	5MC	C5-C6-N1	-3.15	119.89	123.31
32	1a	967	5MC	C5-C4-N3	-3.15	118.53	121.75
32	2a	1207	2MG	N1-C2-N2	3.15	119.77	116.56
54	2y	54	5MU	O4-C4-C5	-3.14	121.32	124.92
1	2A	1962	5MC	C5-C4-N3	-3.14	118.53	121.75
55	1x	32	5MC	C5-C4-N3	-3.11	118.57	121.75
54	1w	37	MIA	C16-C14-C13	-3.11	113.33	122.66
54	2y	8	4SU	O2-C2-N1	-3.11	118.75	122.80
32	2a	1519	MA6	C4-C5-N7	-3.09	106.07	109.34
1	1A	2503	2MA	C2-N1-C6	3.09	122.84	118.10
32	1a	966	M2G	C8-N7-C5	3.07	107.78	102.55
32	2a	1207	2MG	C8-N7-C5	3.05	107.74	102.55
1	2A	1939	5MU	O2-C2-N1	-3.05	118.83	122.80
55	2x	55	PSU	O2-C2-N1	-3.04	119.65	122.79
1	2A	1911	PSU	O2-C2-N1	-3.03	119.66	122.79
1	2A	2503	2MA	C2-N1-C6	3.03	122.76	118.10
1	2A	1962	5MC	C5-C6-N1	-3.03	120.03	123.31
32	2a	1400	5MC	C5-C6-N1	-3.03	120.03	123.31
54	1y	8	4SU	C5-C4-S4	-3.01	120.86	124.31
1	1A	1942	5MC	C5-C6-N1	-2.99	120.07	123.31
32	1a	1519	MA6	C4-C5-N7	-2.98	106.18	109.34
32	2a	1498	UR3	C5-C4-N3	2.97	118.95	115.04
54	1w	37	MIA	C2-N1-C6	2.96	122.68	117.42
1	1A	1962	5MC	C5-C4-N3	-2.95	118.73	121.75
54	2y	55	PSU	C6-C5-C4	-2.93	116.19	118.17
54	2w	39	PSU	C4-N3-C2	-2.93	122.34	126.37
54	2y	55	PSU	O2-C2-N1	-2.92	119.78	122.79
55	2x	32	5MC	C5-C4-N3	-2.89	118.80	121.75
1	1A	1915	5MU	C5-C6-N1	-2.88	120.18	123.31
54	1w	8	4SU	C5-C4-S4	-2.87	121.02	124.31
32	1a	1404	5MC	C5-C4-N3	-2.87	118.81	121.75
1	2A	2251	OMG	C8-N7-C5	2.85	107.40	102.55
54	2w	32	PSU	O2-C2-N1	-2.85	119.85	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	2251	OMG	C8-N7-C5	2.85	107.39	102.55
1	1A	1920	OMC	O2-C2-N3	-2.85	117.84	122.33
54	1w	37	MIA	N3-C2-N1	-2.83	121.85	127.03
55	2x	54	5MU	O2-C2-N1	-2.83	119.12	122.80
54	1y	54	5MU	O2-C2-N1	-2.82	119.13	122.80
54	2w	55	PSU	C6-C5-C4	-2.81	116.28	118.17
54	2y	37	MIA	C4-C5-N7	-2.81	106.37	109.34
32	2a	1207	2MG	N2-C2-N3	-2.81	116.93	120.51
55	1x	76	8AN	O4'-C1'-N9	2.80	112.46	108.75
54	1w	8	4SU	N3-C2-N1	2.80	118.54	114.89
55	2x	8	4SU	O2-C2-N1	2.80	126.44	122.80
55	1x	8	4SU	C4-N3-C2	2.79	129.99	127.31
1	2A	1915	5MU	C5-C6-N1	-2.78	120.29	123.31
32	2a	966	M2G	C8-N7-C5	2.77	107.27	102.55
54	1w	54	5MU	C5-C6-N1	-2.77	120.31	123.31
1	1A	2552	OMU	O4-C4-C5	-2.76	120.40	125.16
54	1y	37	MIA	C4-C5-N7	-2.76	106.42	109.34
1	2A	1942	5MC	C5-C4-N3	-2.76	118.93	121.75
32	2a	1404	5MC	C5-C4-N3	-2.73	118.96	121.75
32	2a	1407	5MC	C5-C4-N3	-2.73	118.96	121.75
32	2a	1400	5MC	C5-C4-N3	-2.73	118.96	121.75
32	2a	1518	MA6	C4-C5-N7	-2.72	106.46	109.34
32	1a	1207	2MG	N1-C2-N2	2.71	119.33	116.56
32	1a	1518	MA6	C4-C5-N7	-2.70	106.48	109.34
54	1w	37	MIA	C4-C5-N7	-2.69	106.49	109.34
55	1x	8	4SU	C5-C4-N3	2.68	117.25	114.75
32	2a	967	5MC	C5-C4-N3	-2.67	119.02	121.75
1	2A	2552	OMU	O2-C2-N1	-2.67	119.33	122.80
54	2y	32	PSU	C6-C5-C4	-2.65	116.39	118.17
54	1w	8	4SU	C1'-N1-C2	2.65	122.34	117.59
55	1x	54	5MU	O2-C2-N1	-2.63	119.37	122.80
32	1a	1400	5MC	C5-C4-N3	-2.62	119.07	121.75
1	2A	2503	2MA	C5-C6-N1	-2.61	117.75	120.84
54	2w	37	MIA	C12-N6-C6	-2.61	120.43	122.85
54	1y	39	PSU	O2-C2-N1	-2.61	120.10	122.79
1	1A	1962	5MC	C5-C6-N1	-2.57	120.53	123.31
32	1a	1400	5MC	O2-C2-N3	-2.55	118.31	122.33
43	1l	92	0TD	OD2-CG-CB	2.55	118.65	113.15
1	2A	2552	OMU	O4-C4-C5	-2.54	120.78	125.16
54	2y	54	5MU	C5-C6-N1	-2.54	120.56	123.31
54	2w	54	5MU	C5-C6-N1	-2.53	120.56	123.31
32	1a	1400	5MC	C5-C6-N1	-2.52	120.57	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2w	8	4SU	C1'-N1-C2	2.52	122.12	117.59
1	1A	1942	5MC	CM5-C5-C6	-2.50	119.47	122.85
1	2A	2605	PSU	C5-C6-N1	-2.49	118.69	122.14
32	2a	1402	4OC	C6-C5-C4	2.47	119.97	117.00
32	2a	1407	5MC	O2-C2-N3	-2.47	118.44	122.33
32	2a	1498	UR3	C1'-N1-C2	2.44	121.04	117.04
32	2a	1498	UR3	C6-N1-C2	-2.44	119.81	121.80
1	2A	2503	2MA	C4-C5-N7	-2.41	106.79	109.34
32	1a	1407	5MC	C5-C6-N1	-2.40	120.70	123.31
32	2a	1404	5MC	CM5-C5-C6	-2.39	119.61	122.85
1	2A	1920	OMC	O2-C2-N3	-2.39	118.56	122.33
1	1A	1915	5MU	O2-C2-N1	-2.38	119.69	122.80
54	1w	54	5MU	C5M-C5-C4	2.38	121.32	118.78
1	2A	2251	OMG	CM2-O2'-C2'	-2.38	108.36	114.47
1	1A	2503	2MA	C4-C5-N7	-2.34	106.86	109.34
54	2y	54	5MU	O2-C2-N3	-2.34	117.18	121.49
1	2A	2251	OMG	O6-C6-C5	-2.33	119.71	124.32
55	2x	8	4SU	C1'-N1-C6	-2.33	115.81	120.78
54	2y	54	5MU	C5M-C5-C4	2.31	121.25	118.78
32	1a	1207	2MG	N2-C2-N3	-2.30	117.58	120.51
1	2A	1917	PSU	C5-C6-N1	-2.27	118.98	122.14
54	2w	37	MIA	C4-C5-N7	-2.26	106.95	109.34
1	1A	2503	2MA	C5-C6-N1	-2.25	118.18	120.84
32	2a	516	PSU	O4'-C1'-C2'	2.23	108.24	105.15
1	2A	2251	OMG	C5-C6-N1	2.22	118.31	114.07
1	1A	2503	2MA	N3-C2-N1	-2.22	121.89	125.77
32	1a	1207	2MG	CM2-N2-C2	-2.22	118.89	123.65
54	2y	39	PSU	O2-C2-N1	-2.21	120.50	122.79
54	2w	37	MIA	C2-N1-C6	2.21	121.35	117.42
54	2y	39	PSU	C6-C5-C4	-2.21	116.69	118.17
54	1y	32	PSU	C5-C6-N1	-2.21	119.08	122.14
32	1a	516	PSU	O4'-C1'-C2'	2.20	108.20	105.15
32	1a	1207	2MG	C5-C6-N1	2.18	118.22	114.07
55	2x	32	5MC	O2-C2-N3	-2.17	118.90	122.33
1	1A	1920	OMC	C1'-N1-C2	2.17	123.24	118.44
54	1w	39	PSU	C5-C6-N1	-2.17	119.12	122.14
54	1w	54	5MU	O2-C2-N1	-2.17	119.97	122.80
55	1x	54	5MU	C5M-C5-C4	2.16	121.08	118.78
32	2a	967	5MC	O2-C2-N3	-2.14	118.96	122.33
32	1a	1498	UR3	C1'-N1-C2	2.13	120.52	117.04
54	1y	39	PSU	C6-C5-C4	-2.12	116.75	118.17
32	1a	1407	5MC	CM5-C5-C6	-2.12	119.99	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1402	4OC	C6-C5-C4	2.11	119.55	117.00
54	2w	46	G7M	N2-C2-N3	-2.11	115.55	119.67
32	1a	1498	UR3	C3U-N3-C2	2.08	120.96	117.33
54	2w	39	PSU	C6-C5-C4	-2.07	116.77	118.17
32	1a	966	M2G	C5-C6-N1	2.06	118.01	114.07
1	1A	2503	2MA	CM2-C2-N1	2.06	120.21	117.13
32	2a	516	PSU	C5-C6-N1	-2.05	119.29	122.14
55	1x	8	4SU	O2-C2-N3	-2.05	117.72	121.49
1	1A	1917	PSU	C5-C6-N1	-2.04	119.31	122.14
1	1A	2251	OMG	C5-C6-N1	2.03	117.94	114.07
32	2a	1207	2MG	CM2-N2-C2	-2.03	119.29	123.65
1	1A	1917	PSU	O2-C2-N3	-2.02	118.28	121.86
1	2A	2605	PSU	O2-C2-N3	-2.00	118.30	121.86

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1400	5MC	O4'-C4'-C5'-O5'
54	1w	37	MIA	C12-C13-C14-C15
54	1y	46	G7M	C4'-C5'-O5'-P
32	2a	1519	MA6	O4'-C4'-C5'-O5'
54	2w	37	MIA	C5-C6-N6-C12
54	2w	37	MIA	N1-C6-N6-C12
54	2w	37	MIA	N1-C2-S10-C11
54	2w	37	MIA	N3-C2-S10-C11
54	2y	55	PSU	C2'-C1'-C5-C4
54	2y	55	PSU	C2'-C1'-C5-C6
56	1z	1	FME	O1-CN-N-CA
56	1z	1	FME	C-CA-CB-CG
56	2z	1	FME	O-C-CA-CB
55	1x	76	8AN	C3'-C4'-C5'-O5'
55	2x	76	8AN	C3'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
55	2x	76	8AN	O4'-C4'-C5'-O5'
56	1z	1	FME	CA-CB-CG-SD
32	1a	527	G7M	C3'-C4'-C5'-O5'
55	1x	76	8AN	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	1400	5MC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
54	1y	46	G7M	C3'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
54	1w	46	G7M	O4'-C4'-C5'-O5'
56	1z	1	FME	N-CA-CB-CG
32	1a	967	5MC	O4'-C4'-C5'-O5'
54	2y	55	PSU	C3'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
55	2x	76	8AN	C4'-C5'-O5'-P
43	2l	92	0TD	SB-CB-CG-OD1
55	1x	76	8AN	C4'-C5'-O5'-P
54	2w	46	G7M	C4'-C5'-O5'-P
54	2y	55	PSU	O4'-C1'-C5-C4
54	1w	46	G7M	C3'-C4'-C5'-O5'
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C4'-C5'-O5'-P
32	2a	527	G7M	C4'-C5'-O5'-P
1	2A	1917	PSU	O4'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD2
32	1a	1402	4OC	O4'-C4'-C5'-O5'
54	2y	55	PSU	O4'-C1'-C5-C6
32	2a	1402	4OC	O4'-C4'-C5'-O5'
1	1A	1920	OMC	C2'-C1'-N1-C6
1	1A	2503	2MA	C4'-C5'-O5'-P
1	1A	1920	OMC	C2'-C1'-N1-C2
1	2A	1920	OMC	C2'-C1'-N1-C2

There are no ring outliers.

45 monomers are involved in 64 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1915	5MU	1	0
55	2x	55	PSU	2	0
54	1w	46	G7M	1	0
1	2A	2552	OMU	1	0
32	2a	1402	4OC	4	0
32	1a	1402	4OC	2	0
32	2a	1518	MA6	1	0
32	2a	967	5MC	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	2w	46	G7M	1	0
54	2y	55	PSU	6	0
1	1A	1942	5MC	1	0
54	2y	46	G7M	1	0
32	1a	1518	MA6	2	0
32	2a	1400	5MC	2	0
1	1A	1939	5MU	1	0
1	2A	2251	OMG	1	0
1	2A	2503	2MA	1	0
32	1a	1400	5MC	1	0
54	1w	37	MIA	2	0
1	2A	2605	PSU	1	0
1	2A	1920	OMC	1	0
54	1y	39	PSU	2	0
32	2a	966	M2G	2	0
43	1l	92	0TD	1	0
55	1x	76	8AN	2	0
32	1a	1519	MA6	2	0
32	2a	1404	5MC	1	0
1	1A	2552	OMU	2	0
54	1y	46	G7M	1	0
43	2l	92	0TD	1	0
32	1a	966	M2G	1	0
55	2x	76	8AN	2	0
54	1y	37	MIA	1	0
1	1A	1915	5MU	1	0
54	1w	8	4SU	1	0
1	2A	1939	5MU	1	0
54	1y	55	PSU	1	0
55	1x	8	4SU	2	0
54	2y	37	MIA	1	0
1	1A	1917	PSU	1	0
32	2a	1519	MA6	3	0
54	2w	39	PSU	1	0
54	2w	37	MIA	2	0
32	1a	967	5MC	1	0
54	1y	8	4SU	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2731 ligands modelled in this entry, 2727 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	$\#\|Z\| > 2$
61	SF4	2d	303	35	0,12,12	-	-	-		
59	ERY	2A	3857	-	53,53,53	0.93	1 (1%)	82,82,82	1.49	15 (18%)
59	ERY	1A	4087	-	53,53,53	0.95	1 (1%)	82,82,82	1.72	17 (20%)
61	SF4	1d	302	35	0,12,12	-	-	-		

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
61	SF4	2d	303	35	-	-	0/6/5/5
59	ERY	2A	3857	-	-	19/72/107/107	0/3/3/3
59	ERY	1A	4087	-	-	15/72/107/107	0/3/3/3
61	SF4	1d	302	35	-	-	0/6/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1A	4087	ERY	O2-C1	5.17	1.46	1.34
59	2A	3857	ERY	O2-C1	4.97	1.45	1.34

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	1A	4087	ERY	C15-C16-C17	4.64	115.58	107.64
59	1A	4087	ERY	O5-C16-C15	-4.23	106.44	112.95
59	1A	4087	ERY	O7-C5-C4	-4.20	105.50	111.58
59	1A	4087	ERY	C6-C5-C4	-4.19	107.81	113.89
59	2A	3857	ERY	O5-C16-C15	-3.98	106.83	112.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	1A	4087	ERY	O4-C18-C17	3.73	116.46	110.04
59	1A	4087	ERY	O5-C16-C17	3.53	108.98	103.86
59	2A	3857	ERY	C13-O2-C1	-3.41	112.25	118.20
59	1A	4087	ERY	O7-C5-C6	3.36	110.41	106.40
59	1A	4087	ERY	O2-C1-C2	3.36	118.70	111.53
59	1A	4087	ERY	C13-O2-C1	-3.34	112.37	118.20
59	2A	3857	ERY	O5-C16-C17	3.26	108.58	103.86
59	2A	3857	ERY	C7-C8-C9	-3.08	108.17	113.32
59	2A	3857	ERY	C20-O5-C16	3.03	123.67	117.51
59	2A	3857	ERY	O2-C1-C2	2.97	117.88	111.53
59	2A	3857	ERY	C16-C15-C14	-2.87	110.15	114.99
59	1A	4087	ERY	C16-C17-C18	2.82	115.23	111.12
59	1A	4087	ERY	C14-O4-C18	2.56	120.84	113.82
59	2A	3857	ERY	C6-C5-C4	-2.56	110.17	113.89
59	1A	4087	ERY	C2-C3-C4	-2.53	105.63	112.91
59	2A	3857	ERY	C12-C11-C10	-2.42	113.57	116.40
59	1A	4087	ERY	C32-C6-C5	2.28	114.03	110.13
59	1A	4087	ERY	C36-C13-C12	-2.26	111.07	115.20
59	2A	3857	ERY	O4-C18-C21	2.20	111.63	106.74
59	2A	3857	ERY	C15-C16-C17	2.14	111.30	107.64
59	2A	3857	ERY	C16-C17-C18	2.13	114.22	111.12
59	1A	4087	ERY	O2-C1-O1	-2.12	120.12	123.95
59	2A	3857	ERY	O3-C3-C4	2.11	110.72	108.23
59	2A	3857	ERY	C25-C24-N1	-2.10	109.70	115.59
59	2A	3857	ERY	C6-C7-C8	-2.08	111.45	115.61
59	1A	4087	ERY	C20-O5-C16	2.04	121.66	117.51
59	1A	4087	ERY	O4-C18-C21	2.02	111.22	106.74

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	1A	4087	ERY	C17-C16-O5-C20
59	1A	4087	ERY	C19-C16-O5-C20
59	2A	3857	ERY	C9-C10-C11-C12
59	2A	3857	ERY	C9-C10-C11-O12
59	2A	3857	ERY	C34-C10-C11-C12
59	2A	3857	ERY	C34-C10-C11-O12
59	2A	3857	ERY	C33-C8-C9-C10
59	2A	3857	ERY	C33-C8-C9-O11
59	2A	3857	ERY	C15-C16-O5-C20
59	2A	3857	ERY	C19-C16-O5-C20

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Mol	Chain	Res	Type	Atoms
59	2A	3857	ERY	C17-C16-O5-C20
59	2A	3857	ERY	C35-C12-C13-C36
59	2A	3857	ERY	O13-C12-C13-C36
59	2A	3857	ERY	C11-C12-C13-C36
59	1A	4087	ERY	C32-C6-C7-C8
59	1A	4087	ERY	O10-C6-C7-C8
59	2A	3857	ERY	C32-C6-C7-C8
59	1A	4087	ERY	C4-C5-C6-O10
59	2A	3857	ERY	C4-C5-C6-O10
59	1A	4087	ERY	C15-C16-O5-C20
59	1A	4087	ERY	O7-C5-C6-C7
59	2A	3857	ERY	O7-C5-C6-C7
59	1A	4087	ERY	C34-C10-C9-C8
59	2A	3857	ERY	C7-C8-C9-C10
59	1A	4087	ERY	C11-C10-C9-C8
59	1A	4087	ERY	O9-C22-O7-C5
59	2A	3857	ERY	C35-C12-C13-O2
59	2A	3857	ERY	O13-C12-C13-O2
59	1A	4087	ERY	C11-C10-C9-O11
59	1A	4087	ERY	C23-C22-O7-C5
59	1A	4087	ERY	O2-C13-C36-C37
59	1A	4087	ERY	C34-C10-C9-O11
59	1A	4087	ERY	C30-C2-C3-C4
59	2A	3857	ERY	C7-C8-C9-O11

There are no ring outliers.

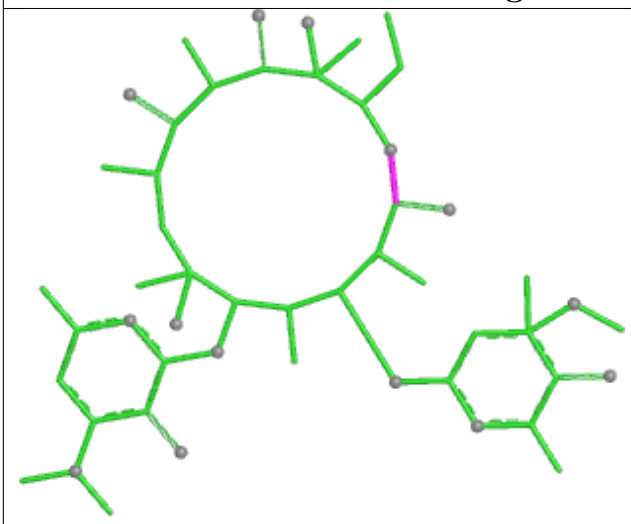
4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	2d	303	SF4	2	0
59	2A	3857	ERY	4	0
59	1A	4087	ERY	9	0
61	1d	302	SF4	1	0

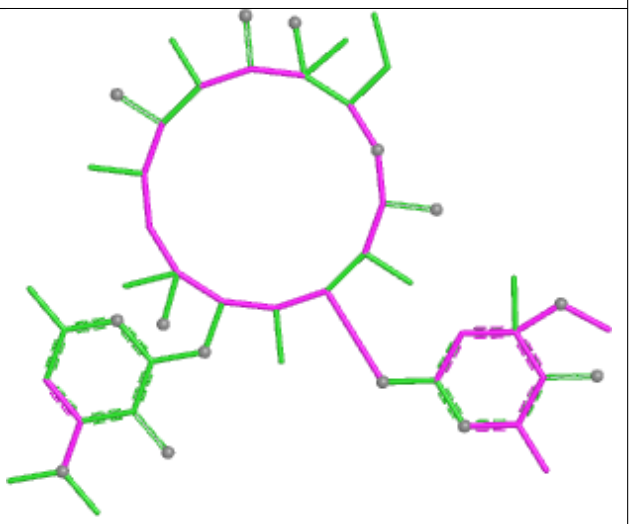
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

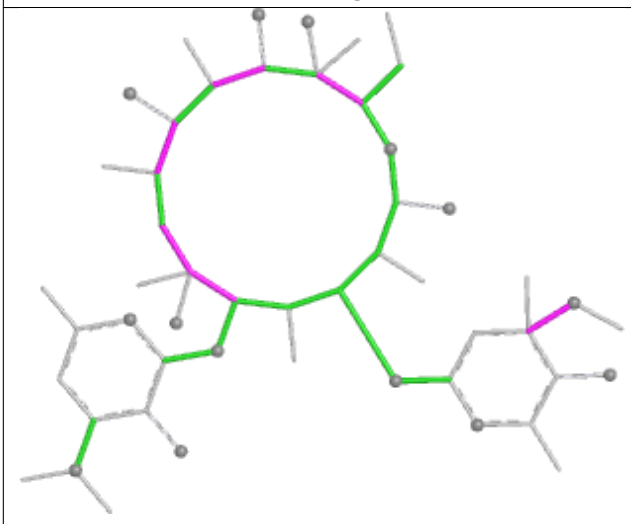
Ligand ERY 2A 3857



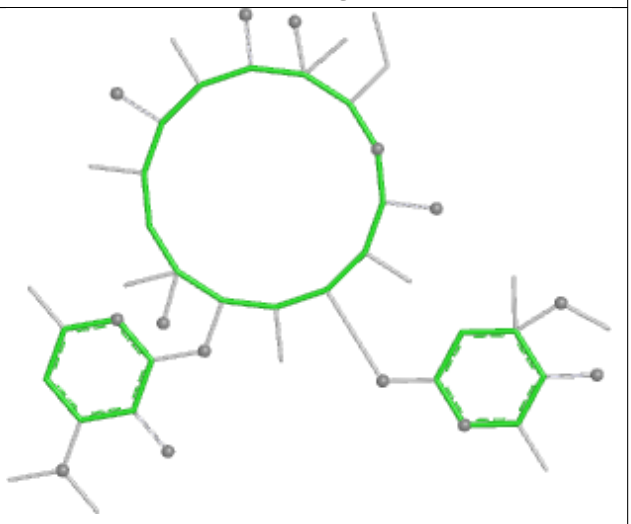
Bond lengths



Bond angles

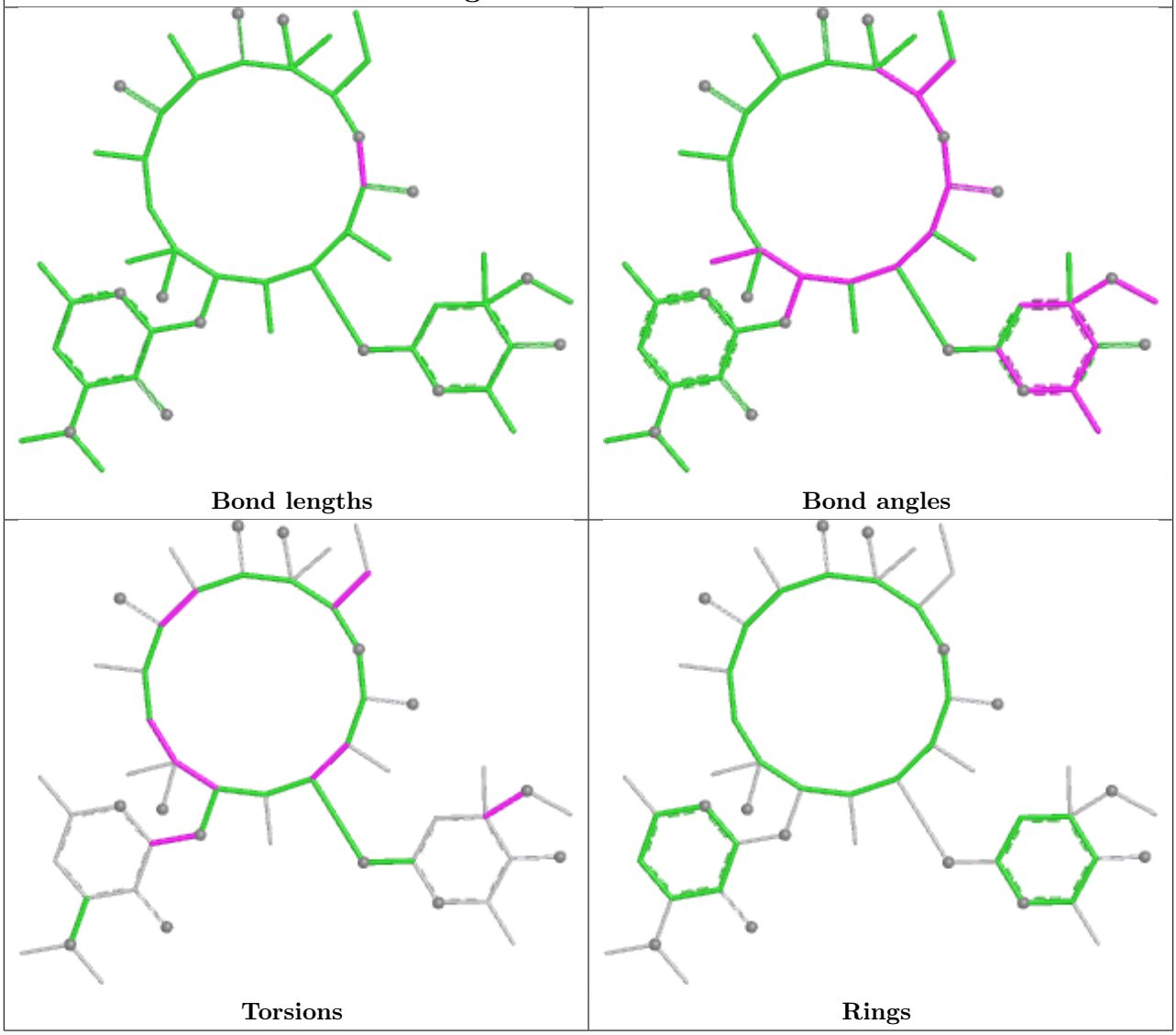


Torsions



Rings

Ligand ERY 1A 4087



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%)	-0.60	52 (1%) 67 68	19, 37, 92, 108	0
1	2A	2789/2915 (95%)	-0.19	44 (1%) 70 71	32, 56, 91, 105	0
2	1B	120/121 (99%)	-0.54	0 100 100	31, 50, 64, 83	0
2	2B	120/121 (99%)	0.50	2 (1%) 69 70	57, 77, 86, 91	0
3	1D	275/276 (99%)	-0.28	2 (0%) 84 85	19, 36, 51, 71	0
3	2D	275/276 (99%)	0.14	4 (1%) 71 73	29, 50, 62, 75	0
4	1E	204/206 (99%)	-0.14	1 (0%) 87 89	20, 44, 63, 79	0
4	2E	204/206 (99%)	0.08	1 (0%) 87 89	29, 56, 69, 81	0
5	1F	202/210 (96%)	-0.26	1 (0%) 87 89	19, 43, 65, 84	0
5	2F	202/210 (96%)	0.22	4 (1%) 64 65	34, 67, 80, 85	0
6	1G	181/182 (99%)	0.21	2 (1%) 77 80	39, 57, 74, 88	0
6	2G	181/182 (99%)	0.93	15 (8%) 19 22	66, 78, 86, 89	0
7	1H	174/180 (96%)	0.04	0 100 100	39, 54, 67, 75	0
7	2H	174/180 (96%)	0.80	9 (5%) 34 35	62, 80, 87, 95	0
8	1I	146/148 (98%)	0.35	3 (2%) 63 64	39, 70, 80, 84	0
8	2I	146/148 (98%)	0.81	9 (6%) 28 30	57, 74, 84, 87	0
9	1N	140/140 (100%)	-0.12	0 100 100	28, 45, 61, 79	0
9	2N	140/140 (100%)	0.51	4 (2%) 54 55	44, 63, 75, 83	0
10	1O	122/122 (100%)	-0.25	0 100 100	28, 42, 60, 67	0
10	2O	122/122 (100%)	0.23	1 (0%) 82 84	37, 55, 68, 72	0
11	1P	149/150 (99%)	-0.05	0 100 100	21, 43, 67, 75	0
11	2P	149/150 (99%)	0.29	3 (2%) 64 65	36, 66, 82, 87	0
12	1Q	141/141 (100%)	-0.19	0 100 100	27, 42, 55, 73	0
12	2Q	141/141 (100%)	0.67	8 (5%) 30 33	46, 64, 74, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.24	0 100 100	29, 38, 51, 60	0
13	2R	118/118 (100%)	-0.02	0 100 100	37, 50, 60, 69	0
14	1S	110/112 (98%)	0.00	0 100 100	38, 49, 60, 65	0
14	2S	110/112 (98%)	0.87	9 (8%) 19 22	60, 70, 78, 82	0
15	1T	131/146 (89%)	0.03	3 (2%) 61 61	35, 49, 71, 80	0
15	2T	131/146 (89%)	0.28	1 (0%) 82 84	45, 57, 73, 83	0
16	1U	116/118 (98%)	-0.20	2 (1%) 69 70	24, 37, 55, 73	0
16	2U	116/118 (98%)	0.19	1 (0%) 81 83	43, 58, 73, 78	0
17	1V	101/101 (100%)	-0.12	0 100 100	23, 48, 62, 72	0
17	2V	101/101 (100%)	0.46	1 (0%) 79 82	46, 70, 78, 82	0
18	1W	112/113 (99%)	-0.35	1 (0%) 81 83	27, 38, 56, 76	0
18	2W	112/113 (99%)	0.21	0 100 100	38, 50, 67, 93	0
19	1X	95/96 (98%)	-0.28	0 100 100	28, 38, 55, 71	0
19	2X	95/96 (98%)	0.38	1 (1%) 77 80	41, 58, 71, 76	0
20	1Y	107/110 (97%)	0.14	1 (0%) 81 83	35, 50, 68, 75	0
20	2Y	107/110 (97%)	0.79	4 (3%) 45 47	60, 72, 80, 86	0
21	1Z	154/206 (74%)	0.16	5 (3%) 50 52	42, 63, 82, 90	0
21	2Z	160/206 (77%)	0.97	21 (13%) 8 11	67, 79, 89, 99	0
22	10	83/85 (97%)	-0.13	2 (2%) 59 60	28, 37, 56, 64	0
22	20	83/85 (97%)	0.85	7 (8%) 18 21	47, 61, 70, 81	0
23	11	97/98 (98%)	0.01	1 (1%) 79 82	23, 43, 65, 70	0
23	21	97/98 (98%)	0.48	3 (3%) 51 53	38, 56, 73, 76	0
24	12	70/72 (97%)	0.02	1 (1%) 73 75	34, 47, 57, 71	0
24	22	70/72 (97%)	0.66	3 (4%) 40 42	58, 68, 75, 77	0
25	13	59/60 (98%)	-0.23	0 100 100	29, 41, 65, 78	0
25	23	59/60 (98%)	0.26	0 100 100	52, 65, 78, 83	0
26	14	69/71 (97%)	0.42	3 (4%) 40 42	50, 73, 87, 93	0
26	24	69/71 (97%)	0.81	7 (10%) 14 16	75, 85, 93, 96	0
27	15	59/60 (98%)	-0.35	0 100 100	21, 42, 64, 74	0
27	25	59/60 (98%)	0.04	1 (1%) 69 70	34, 51, 70, 80	0
28	16	53/54 (98%)	-0.15	0 100 100	31, 40, 53, 59	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.49	0 100 100	49, 59, 66, 73	0
29	17	48/49 (97%)	-0.55	0 100 100	21, 27, 46, 54	0
29	27	48/49 (97%)	-0.07	1 (2%) 63 64	32, 41, 60, 67	0
30	18	64/65 (98%)	-0.22	1 (1%) 70 71	28, 33, 42, 55	0
30	28	64/65 (98%)	0.38	1 (1%) 70 71	42, 54, 64, 71	0
31	19	37/37 (100%)	0.02	0 100 100	34, 42, 55, 64	0
31	29	37/37 (100%)	0.92	3 (8%) 19 22	57, 66, 76, 78	0
32	1a	1488/1521 (97%)	-0.05	14 (0%) 81 83	34, 63, 90, 107	0
32	2a	1491/1521 (98%)	0.36	49 (3%) 49 51	51, 76, 94, 109	0
33	1b	231/256 (90%)	0.83	26 (11%) 11 13	61, 76, 84, 94	0
33	2b	231/256 (90%)	1.18	37 (16%) 6 7	72, 84, 90, 93	0
34	1c	206/239 (86%)	0.42	4 (1%) 66 67	54, 66, 77, 87	0
34	2c	206/239 (86%)	1.12	32 (15%) 6 7	68, 83, 88, 93	0
35	1d	208/209 (99%)	0.33	2 (0%) 79 82	51, 64, 75, 81	0
35	2d	208/209 (99%)	0.81	14 (6%) 25 28	63, 72, 81, 86	0
36	1e	148/162 (91%)	0.24	1 (0%) 84 85	47, 61, 73, 86	0
36	2e	148/162 (91%)	0.83	10 (6%) 25 28	64, 77, 83, 87	0
37	1f	100/101 (99%)	0.31	1 (1%) 79 82	47, 60, 75, 77	0
37	2f	100/101 (99%)	0.32	0 100 100	60, 69, 78, 86	0
38	1g	155/156 (99%)	0.46	10 (6%) 26 29	54, 67, 79, 86	0
38	2g	155/156 (99%)	0.76	13 (8%) 18 21	69, 79, 87, 94	0
39	1h	137/138 (99%)	0.33	3 (2%) 62 62	56, 65, 73, 78	0
39	2h	137/138 (99%)	0.94	10 (7%) 22 26	67, 77, 84, 89	0
40	1i	127/128 (99%)	0.68	3 (2%) 59 60	52, 72, 81, 87	0
40	2i	127/128 (99%)	1.68	43 (33%) 1 1	70, 83, 90, 93	0
41	1j	97/105 (92%)	0.70	3 (3%) 51 53	51, 73, 84, 91	0
41	2j	96/105 (91%)	1.32	19 (19%) 3 4	72, 83, 89, 93	0
42	1k	114/129 (88%)	0.16	1 (0%) 81 83	40, 63, 74, 82	0
42	2k	114/129 (88%)	0.97	14 (12%) 9 12	63, 74, 80, 85	0
43	1l	121/132 (91%)	0.03	4 (3%) 49 51	40, 51, 64, 71	0
43	2l	121/132 (91%)	0.43	3 (2%) 58 59	46, 65, 74, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	123/126 (97%)	0.41	6 (4%) 36 38	49, 65, 76, 93	0
44	2m	122/126 (96%)	1.11	18 (14%) 7 8	72, 81, 88, 91	0
45	1n	60/61 (98%)	0.54	1 (1%) 69 70	52, 61, 68, 69	0
45	2n	60/61 (98%)	1.97	28 (46%) 0 0	74, 82, 88, 89	0
46	1o	88/89 (98%)	0.46	3 (3%) 48 50	47, 60, 71, 76	0
46	2o	88/89 (98%)	0.67	2 (2%) 61 61	60, 72, 80, 83	0
47	1p	82/88 (93%)	0.81	4 (4%) 36 38	57, 66, 74, 79	0
47	2p	82/88 (93%)	0.74	3 (3%) 45 47	56, 65, 75, 77	0
48	1q	99/105 (94%)	0.87	4 (4%) 43 44	53, 66, 76, 81	0
48	2q	99/105 (94%)	0.82	6 (6%) 28 31	64, 72, 80, 86	0
49	1r	68/88 (77%)	0.25	1 (1%) 71 73	49, 63, 75, 77	0
49	2r	68/88 (77%)	0.39	0 100 100	63, 74, 83, 85	0
50	1s	83/93 (89%)	0.19	0 100 100	54, 66, 76, 81	0
50	2s	83/93 (89%)	1.29	15 (18%) 4 5	75, 83, 90, 93	0
51	1t	96/106 (90%)	0.62	5 (5%) 34 35	55, 66, 78, 89	0
51	2t	96/106 (90%)	0.61	2 (2%) 63 64	54, 65, 82, 85	0
52	1u	23/27 (85%)	0.73	1 (4%) 40 42	57, 64, 71, 72	0
52	2u	23/27 (85%)	1.72	9 (39%) 1 1	75, 78, 83, 87	0
53	1v	13/24 (54%)	0.19	1 (7%) 21 24	42, 57, 82, 91	0
53	2v	13/24 (54%)	1.47	3 (23%) 2 3	72, 79, 92, 94	0
54	1w	67/76 (88%)	0.65	5 (7%) 22 24	34, 90, 98, 109	0
54	1y	67/76 (88%)	0.40	2 (2%) 52 54	38, 90, 98, 102	0
54	2w	65/76 (85%)	0.76	6 (9%) 16 18	52, 92, 100, 103	0
54	2y	66/76 (86%)	0.71	3 (4%) 39 40	50, 96, 101, 104	0
55	1x	72/77 (93%)	-0.02	0 100 100	29, 61, 79, 84	0
55	2x	72/77 (93%)	0.36	0 100 100	44, 78, 88, 91	0
56	1z	2/3 (66%)	0.01	0 100 100	35, 35, 35, 38	0
56	2z	2/3 (66%)	0.46	0 100 100	48, 48, 48, 52	0
All	All	20877/21754 (95%)	0.15	693 (3%) 49 51	19, 62, 88, 109	0

All (693) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	1m	124	PRO	7.4
44	2m	124	PRO	7.2
44	2m	123	ALA	6.7
23	21	2	SER	6.7
44	2m	122	LYS	6.6
23	11	2	SER	5.2
40	2i	7	THR	5.0
40	2i	14	VAL	4.9
40	2i	102	LEU	4.8
40	2i	10	ARG	4.7
45	1n	2	ALA	4.6
38	1g	81	GLY	4.5
22	10	6	GLY	4.3
40	2i	101	PHE	4.2
32	2a	1224	G	4.2
21	2Z	174	VAL	4.2
38	2g	80	VAL	4.2
42	2k	118	GLY	4.2
33	2b	165	VAL	4.1
21	2Z	149	SER	4.1
32	2a	1251	A	4.0
1	1A	2141	G	4.0
7	2H	35	VAL	4.0
45	2n	39	LEU	4.0
44	1m	121	LYS	3.9
51	2t	103	GLY	3.9
53	2v	24	A	3.9
54	1w	73	A	3.9
21	2Z	166	SER	3.9
44	2m	102	ARG	3.9
33	1b	17	PHE	3.9
1	2A	2112	G	3.8
33	1b	7	VAL	3.8
45	2n	21	TYR	3.8
52	2u	14	TRP	3.8
45	2n	29	ARG	3.8
1	1A	888	C	3.8
42	2k	117	ASN	3.8
40	2i	15	ALA	3.7
40	2i	9	ARG	3.7
33	1b	237	ALA	3.7
40	2i	13	ALA	3.7
50	2s	9	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
51	1t	103	GLY	3.7
39	1h	2	LEU	3.7
54	2w	73	A	3.7
40	2i	96	LEU	3.6
45	2n	2	ALA	3.6
6	2G	20	ILE	3.6
54	2w	72	C	3.6
1	1A	2115	G	3.6
33	2b	214	ILE	3.6
32	2a	1030(B)	C	3.6
45	2n	20	ALA	3.5
21	1Z	141	VAL	3.5
34	2c	199	LYS	3.5
41	2j	47	PHE	3.5
39	2h	112	LEU	3.5
33	1b	186	ALA	3.5
1	1A	885	C	3.5
36	2e	90	VAL	3.5
40	2i	109	VAL	3.5
45	2n	34	TYR	3.5
8	1I	117	GLU	3.5
45	2n	3	ARG	3.5
45	2n	30	ALA	3.5
21	2Z	146	ILE	3.5
1	1A	1078	U	3.5
29	27	1	MET	3.5
33	1b	22	LYS	3.4
34	2c	160	ALA	3.4
26	14	52	THR	3.4
34	2c	188	LEU	3.4
45	2n	42	ILE	3.4
1	2A	884	C	3.4
36	2e	12	LEU	3.4
45	2n	14	PRO	3.3
6	2G	39	ILE	3.3
33	2b	77	ALA	3.3
32	2a	1219	U	3.3
38	1g	80	VAL	3.3
38	1g	79	ARG	3.3
32	2a	1030(A)	G	3.3
1	2A	896	A	3.2
32	2a	1503	A	3.2

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Mol	Chain	Res	Type	RSRZ
53	2v	13	A	3.2
21	2Z	172	ALA	3.2
32	1a	1257	U	3.2
1	1A	2142	C	3.2
50	2s	77	THR	3.2
34	2c	200	ALA	3.2
44	1m	123	ALA	3.2
32	1a	1030(D)	A	3.2
33	2b	163	PHE	3.2
1	2A	2115	G	3.2
48	1q	68	ARG	3.2
8	2I	146	ALA	3.2
33	1b	221	LEU	3.2
33	2b	188	ALA	3.2
42	2k	126	ARG	3.2
21	2Z	168	GLU	3.1
38	2g	84	ASN	3.1
1	1A	1094	U	3.1
8	1I	146	ALA	3.1
26	24	66	SER	3.1
33	1b	188	ALA	3.1
1	2A	2155	G	3.1
32	2a	1149	C	3.1
54	1w	72	C	3.1
34	2c	152	ILE	3.1
41	2j	65	LEU	3.1
38	1g	156	TRP	3.1
32	2a	1117	G	3.1
40	2i	36	TYR	3.1
33	1b	9	GLU	3.1
34	2c	157	ILE	3.1
33	1b	229	VAL	3.1
44	2m	7	VAL	3.1
22	20	69	PHE	3.1
34	2c	158	GLY	3.1
1	1A	896	A	3.0
40	2i	99	LEU	3.0
45	2n	22	THR	3.0
1	1A	883	G	3.0
54	1w	1	G	3.0
14	2S	3	ARG	3.0
38	2g	83	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
10	2O	1	MET	3.0
1	1A	884	C	3.0
1	1A	2145	C	3.0
1	2A	1536	C	3.0
22	10	7	LEU	3.0
40	2i	103	THR	3.0
42	2k	31	THR	3.0
1	2A	2173	A	3.0
41	1j	32	ALA	3.0
54	2w	71	G	3.0
42	2k	49	GLY	3.0
6	1G	146	TYR	3.0
48	2q	24	GLU	3.0
21	2Z	144	LEU	3.0
1	1A	2114	A	3.0
31	29	21	GLY	3.0
32	1a	1447	A	3.0
34	2c	155	GLY	3.0
52	1u	2	GLY	3.0
33	1b	187	LEU	3.0
33	2b	123	ALA	3.0
45	2n	18	VAL	3.0
3	2D	5	LYS	3.0
41	1j	76	ASN	3.0
33	2b	131	PRO	3.0
1	1A	2117	A	2.9
3	2D	276	LYS	2.9
1	1A	2190	G	2.9
8	2I	3	VAL	2.9
32	1a	630	G	2.9
32	1a	1024	G	2.9
32	2a	1033	G	2.9
43	1l	18	VAL	2.9
51	2t	9	ASN	2.9
2	2B	6	C	2.9
32	2a	1114	C	2.9
34	2c	13	GLY	2.9
50	2s	2	PRO	2.9
52	2u	22	ARG	2.9
26	14	56	VAL	2.9
45	2n	59	ALA	2.9
6	2G	152	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
44	2m	90	LEU	2.9
38	2g	32	ARG	2.9
32	2a	1002	G	2.9
54	1w	71	G	2.9
7	2H	36	PRO	2.9
38	2g	82	GLY	2.9
1	1A	1057	A	2.9
40	2i	74	ILE	2.8
38	2g	154	TYR	2.8
47	2p	82	GLN	2.8
40	2i	59	PHE	2.8
32	2a	1032	G	2.8
1	2A	1509	C	2.8
1	2A	2146	C	2.8
35	2d	2	GLY	2.8
38	1g	78	ARG	2.8
48	1q	100	LYS	2.8
46	2o	26	GLU	2.8
52	2u	15	ARG	2.8
44	2m	117	VAL	2.8
45	2n	33	VAL	2.8
14	2S	29	PHE	2.8
33	1b	11	LEU	2.8
36	2e	10	MET	2.8
45	2n	6	LEU	2.8
35	2d	154	ASN	2.8
1	1A	2154	G	2.8
32	2a	1202	G	2.8
40	2i	76	ALA	2.8
42	2k	75	TYR	2.8
44	1m	122	LYS	2.8
37	1f	17	SER	2.8
32	2a	1249	C	2.8
54	2w	2	C	2.8
24	22	58	ALA	2.8
40	2i	119	ALA	2.8
41	2j	77	PRO	2.8
17	2V	42	GLY	2.8
41	2j	93	GLY	2.8
44	2m	65	LYS	2.8
44	2m	119	GLY	2.8
40	2i	83	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
47	1p	21	VAL	2.7
50	2s	11	VAL	2.7
21	2Z	152	ALA	2.7
6	2G	172	LEU	2.7
20	2Y	54	LYS	2.7
24	22	61	LEU	2.7
1	2A	2136	C	2.7
6	2G	146	TYR	2.7
1	2A	1171	G	2.7
1	2A	2166	G	2.7
7	2H	60	ARG	2.7
21	2Z	121	HIS	2.7
1	1A	2119	A	2.7
39	2h	9	MET	2.7
23	21	54	ALA	2.7
33	1b	34	ALA	2.7
45	2n	13	THR	2.7
14	2S	24	LEU	2.7
33	2b	154	LEU	2.7
50	2s	82	GLY	2.7
26	24	67	TYR	2.7
36	2e	133	TYR	2.7
54	1w	70	G	2.7
33	2b	112	VAL	2.7
40	2i	46	ALA	2.7
39	2h	133	LEU	2.7
34	2c	205	GLY	2.7
1	1A	2189	U	2.7
43	2l	64	TYR	2.7
32	2a	1116	C	2.7
39	2h	3	THR	2.7
1	1A	2158	A	2.7
1	2A	2117	A	2.7
32	2a	1287	A	2.7
50	2s	78	ARG	2.7
50	2s	13	ASP	2.6
35	2d	170	VAL	2.6
33	2b	120	ALA	2.6
1	1A	2173	A	2.6
1	1A	882	G	2.6
1	1A	2131	G	2.6
39	2h	99	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
44	1m	21	TYR	2.6
41	2j	41	PRO	2.6
44	2m	66	LEU	2.6
5	2F	90	PHE	2.6
6	1G	50	ALA	2.6
15	2T	131	ALA	2.6
3	2D	259	THR	2.6
33	2b	40	HIS	2.6
40	2i	6	GLY	2.6
45	2n	55	GLY	2.6
35	2d	70	ILE	2.6
1	1A	1064	C	2.6
40	2i	11	LYS	2.6
44	2m	121	LYS	2.6
32	2a	974	A	2.6
38	1g	84	ASN	2.6
32	2a	1220	G	2.6
34	2c	196	LEU	2.6
54	1y	18	G	2.6
51	1t	95	ALA	2.6
41	2j	67	THR	2.6
44	2m	105	THR	2.6
33	1b	201	ILE	2.6
33	2b	187	LEU	2.6
34	2c	52	LEU	2.6
33	1b	202	PRO	2.6
34	2c	189	ALA	2.6
42	2k	89	ALA	2.6
11	2P	28	GLY	2.6
34	2c	182	ILE	2.6
41	1j	31	GLY	2.6
41	2j	10	GLY	2.6
1	2A	2133	G	2.6
32	2a	1370	G	2.6
20	1Y	1	MET	2.5
3	1D	276	LYS	2.5
33	2b	24	TRP	2.5
35	2d	4	TYR	2.5
33	1b	10	LEU	2.5
34	2c	87	LEU	2.5
41	2j	8	LEU	2.5
16	1U	117	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	53	ALA	2.5
40	2i	52	ALA	2.5
50	2s	75	ALA	2.5
22	20	76	GLY	2.5
41	2j	35	SER	2.5
47	2p	6	LEU	2.5
14	2S	46	VAL	2.5
35	2d	160	GLN	2.5
52	2u	24	ARG	2.5
34	2c	4	LYS	2.5
50	2s	79	THR	2.5
50	2s	35	SER	2.5
1	2A	2144	U	2.5
24	22	21	LEU	2.5
34	1c	179	ARG	2.5
34	2c	76	VAL	2.5
42	1k	14	VAL	2.5
21	2Z	164	ALA	2.5
1	2A	1719	G	2.5
1	2A	2154	G	2.5
32	1a	1003	G	2.5
32	2a	973	G	2.5
32	2a	1001(A)	G	2.5
52	2u	16	GLY	2.5
35	2d	163	GLU	2.5
47	2p	48	TRP	2.5
22	20	75	LEU	2.5
33	2b	215	LEU	2.5
41	2j	40	LEU	2.5
7	2H	39	PRO	2.5
1	1A	889	C	2.5
1	2A	2119	A	2.5
9	2N	8	GLN	2.5
32	2a	1532	U	2.5
33	1b	132	LYS	2.5
52	2u	13	ILE	2.5
1	1A	1537	G	2.4
33	2b	118	LEU	2.4
40	2i	56	LEU	2.4
40	2i	49	PRO	2.4
35	2d	88	VAL	2.4
21	2Z	173	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
33	2b	161	ALA	2.4
32	2a	982	U	2.4
34	2c	171	GLY	2.4
36	2e	107	ARG	2.4
12	2Q	22	LYS	2.4
21	2Z	165	VAL	2.4
33	2b	133	LYS	2.4
40	2i	86	VAL	2.4
44	2m	120	LYS	2.4
5	2F	26	ALA	2.4
14	2S	92	TYR	2.4
42	2k	25	TYR	2.4
43	2l	56	ALA	2.4
50	2s	80	TYR	2.4
34	2c	17	ASP	2.4
52	2u	11	GLY	2.4
1	2A	2109	U	2.4
21	2Z	150	LEU	2.4
32	2a	977	A	2.4
53	2v	12	A	2.4
1	2A	2111	C	2.4
32	2a	1115	C	2.4
41	2j	28	ARG	2.4
21	2Z	130	PRO	2.4
47	1p	27	LYS	2.4
26	24	35	VAL	2.4
46	2o	15	PHE	2.4
36	2e	13	ILE	2.4
36	2e	21	ALA	2.4
40	1i	13	ALA	2.4
1	1A	1056	G	2.4
1	2A	882	G	2.4
1	2A	883	G	2.4
32	1a	204	U	2.4
32	2a	1150	U	2.4
41	2j	86	MET	2.4
26	24	56	VAL	2.4
1	2A	885	C	2.4
21	1Z	149	SER	2.4
21	1Z	166	SER	2.4
35	1d	110	PHE	2.4
21	2Z	171	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
34	2c	124	ILE	2.4
41	2j	74	ILE	2.4
33	1b	14	GLY	2.4
40	2i	4	TYR	2.4
9	2N	45	ASN	2.4
33	2b	190	THR	2.3
32	2a	1021	G	2.3
32	2a	1034	G	2.3
46	1o	19	PRO	2.3
1	2A	1026	U	2.3
32	1a	1025	U	2.3
33	2b	93	VAL	2.3
38	1g	86	GLN	2.3
33	2b	222	ILE	2.3
34	1c	14	ILE	2.3
34	2c	137	ALA	2.3
40	1i	126	SER	2.3
51	1t	19	SER	2.3
32	2a	1030	C	2.3
32	2a	1038	C	2.3
8	2I	128	LEU	2.3
33	2b	196	LEU	2.3
48	2q	31	LEU	2.3
9	2N	61	ARG	2.3
30	18	46	ARG	2.3
40	2i	113	LYS	2.3
43	1l	19	ARG	2.3
7	2H	128	PRO	2.3
6	2G	138	GLN	2.3
8	2I	145	VAL	2.3
21	1Z	146	ILE	2.3
1	1A	2159	G	2.3
1	2A	2116	G	2.3
1	2A	2165	G	2.3
44	1m	2	ALA	2.3
32	2a	1372	U	2.3
6	2G	34	LEU	2.3
38	2g	38	LEU	2.3
42	2k	103	LEU	2.3
45	2n	53	LEU	2.3
1	1A	1084	A	2.3
21	2Z	170	THR	2.3

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Mol	Chain	Res	Type	RSRZ
35	2d	24	GLU	2.3
40	2i	95	LYS	2.3
1	1A	2803	C	2.3
23	21	68	PRO	2.3
32	2a	962	C	2.3
8	2I	18	VAL	2.3
12	2Q	96	VAL	2.3
45	2n	61	TRP	2.3
7	2H	2	SER	2.3
12	2Q	33	GLY	2.3
1	1A	1081	U	2.3
1	1A	1093	G	2.3
1	2A	2156	G	2.3
1	2A	2168	G	2.3
21	1Z	69	THR	2.3
40	1i	9	ARG	2.3
41	2j	66	ARG	2.3
44	2m	87	TYR	2.3
32	1a	1001(A)	G	2.3
32	2a	1061	G	2.3
45	2n	12	ARG	2.3
45	2n	23	ARG	2.3
45	2n	27	CYS	2.3
48	1q	28	PRO	2.3
32	2a	978	A	2.3
39	2h	79	VAL	2.3
1	2A	2137	C	2.3
45	2n	38	GLY	2.3
38	1g	3	ARG	2.2
36	2e	96	PRO	2.2
1	2A	2125	G	2.2
16	1U	104	GLN	2.2
33	2b	136	VAL	2.2
35	2d	110	PHE	2.2
1	1A	1077	A	2.2
15	1T	131	ALA	2.2
8	2I	68	LEU	2.2
21	2Z	143	GLY	2.2
42	2k	124	LYS	2.2
1	1A	2111	C	2.2
1	2A	645	C	2.2
3	2D	217	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
48	1q	99	SER	2.2
34	2c	184	TYR	2.2
6	2G	97	ASP	2.2
8	2I	92	VAL	2.2
36	2e	101	ILE	2.2
39	2h	111	ILE	2.2
45	2n	7	ILE	2.2
5	2F	47	GLY	2.2
12	2Q	2	LEU	2.2
21	2Z	76	LEU	2.2
35	2d	194	LEU	2.2
46	1o	61	GLY	2.2
1	1A	2157	G	2.2
1	2A	2170	A	2.2
14	2S	17	ARG	2.2
32	1a	1023	G	2.2
52	2u	6	ARG	2.2
54	2w	15	G	2.2
32	2a	1357	A	2.2
40	2i	2	GLU	2.2
14	2S	5	THR	2.2
41	2j	39	PRO	2.2
14	2S	7	TYR	2.2
50	2s	53	ASN	2.2
54	2w	3	C	2.2
39	2h	93	VAL	2.2
50	2s	41	VAL	2.2
1	2A	2113	U	2.2
54	1y	20	U	2.2
54	2y	33	U	2.2
33	2b	138	LEU	2.2
38	2g	104	LEU	2.2
9	2N	10	GLU	2.2
26	14	57	GLU	2.2
33	2b	202	PRO	2.2
40	2i	21	PRO	2.2
40	2i	98	PRO	2.2
41	2j	30	SER	2.2
43	1l	16	GLU	2.2
51	1t	11	SER	2.2
52	2u	8	THR	2.2
1	1A	2100	G	2.2

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Mol	Chain	Res	Type	RSRZ
1	1A	2133	G	2.2
1	2A	2319	G	2.2
18	1W	60	ASN	2.2
32	2a	1036	G	2.2
26	24	50	VAL	2.2
30	28	16	ILE	2.2
33	1b	165	VAL	2.2
33	2b	7	VAL	2.2
39	1h	93	VAL	2.2
43	2l	39	VAL	2.2
45	2n	25	VAL	2.2
8	2I	1	MET	2.2
32	2a	1223	C	2.2
32	2a	1384	C	2.2
6	2G	43	LEU	2.2
14	2S	80	LEU	2.2
15	1T	130	ALA	2.2
35	2d	155	LEU	2.2
38	2g	152	ALA	2.2
44	2m	118	ALA	2.2
22	20	42	GLY	2.2
33	1b	38	GLY	2.2
21	2Z	167	PRO	2.1
33	2b	86	GLU	2.1
40	2i	91	ASP	2.1
33	2b	152	PHE	2.1
47	1p	19	ILE	2.1
1	1A	2135	A	2.1
1	1A	2171	A	2.1
1	1A	275	G	2.1
32	1a	380	G	2.1
32	1a	1034	G	2.1
34	2c	178	LEU	2.1
35	1d	157	LEU	2.1
38	2g	124	LEU	2.1
5	2F	130	ALA	2.1
11	2P	12	ALA	2.1
33	1b	13	ALA	2.1
42	2k	119	CYS	2.1
45	2n	5	ALA	2.1
3	1D	263	ARG	2.1
6	2G	44	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
11	2P	116	GLY	2.1
36	1e	85	GLY	2.1
38	1g	82	GLY	2.1
32	2a	1226	C	2.1
4	1E	87	GLU	2.1
34	2c	73	PRO	2.1
43	1l	5	PRO	2.1
1	1A	2113	U	2.1
32	2a	1257	U	2.1
34	1c	15	THR	2.1
34	2c	154	SER	2.1
20	2Y	92	ASN	2.1
26	24	59	PHE	2.1
36	2e	109	ILE	2.1
38	2g	33	ASP	2.1
40	2i	17	VAL	2.1
45	2n	16	PHE	2.1
34	2c	47	LEU	2.1
49	1r	78	LEU	2.1
38	2g	4	ARG	2.1
46	1o	65	ARG	2.1
1	2A	2135	A	2.1
32	2a	1285	A	2.1
54	2y	36	A	2.1
1	1A	1059	G	2.1
32	2a	1026	G	2.1
33	1b	129	GLU	2.1
1	1A	2161	C	2.1
1	2A	894	C	2.1
1	2A	2145	C	2.1
31	29	15	LYS	2.1
42	2k	51	LYS	2.1
1	2A	2118	U	2.1
20	2Y	24	VAL	2.1
31	29	16	VAL	2.1
33	1b	214	ILE	2.1
33	1b	230	VAL	2.1
33	2b	68	ILE	2.1
33	2b	185	ILE	2.1
12	2Q	104	PHE	2.1
33	2b	122	PHE	2.1
40	2i	73	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
41	2j	34	VAL	2.1
42	2k	13	GLN	2.1
45	2n	37	PHE	2.1
48	2q	26	GLN	2.1
38	2g	85	TYR	2.1
22	20	7	LEU	2.1
39	2h	2	LEU	2.1
6	2G	163	ALA	2.1
20	2Y	105	ALA	2.1
39	1h	91	ARG	2.1
40	2i	128	ARG	2.1
42	2k	23	ALA	2.1
5	1F	207	GLY	2.1
34	2c	159	GLY	2.1
40	2i	67	GLY	2.1
40	2i	72	GLY	2.1
50	2s	68	GLY	2.1
7	2H	40	GLU	2.1
12	2Q	38	GLU	2.1
1	2A	2171	A	2.1
6	2G	29	TRP	2.1
32	1a	1001	A	2.1
32	1a	1286	A	2.1
40	2i	97	LYS	2.1
47	1p	31	LYS	2.1
12	2Q	103	MET	2.1
33	2b	127	ILE	2.1
34	2c	5	ILE	2.1
44	2m	78	ILE	2.1
48	2q	90	ILE	2.1
1	2A	2153	G	2.1
2	2B	23	G	2.1
6	2G	102	PHE	2.1
21	2Z	74	VAL	2.1
21	2Z	141	VAL	2.1
32	2a	963	G	2.1
33	1b	163	PHE	2.1
33	2b	164	VAL	2.1
33	2b	230	VAL	2.1
34	2c	153	VAL	2.1
40	2i	18	PHE	2.1
41	2j	54	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
44	2m	101	GLN	2.1
48	2q	71	PHE	2.1
15	1T	38	ASN	2.1
1	1A	1075	C	2.1
1	1A	2130	U	2.1
1	1A	2150	U	2.1
16	2U	24	TYR	2.1
22	20	72	ARG	2.1
34	2c	2	GLY	2.1
39	2h	117	GLY	2.1
40	2i	100	GLY	2.1
7	2H	55	PRO	2.0
6	2G	35	GLU	2.0
33	2b	134	GLU	2.0
27	25	29	THR	2.0
1	1A	548	A	2.0
1	2A	901	A	2.0
8	1I	91	SER	2.0
32	2a	983	A	2.0
32	2a	1236	A	2.0
34	1c	154	SER	2.0
53	1v	24	A	2.0
12	2Q	79	LEU	2.0
19	2X	92	LEU	2.0
22	20	84	LEU	2.0
33	2b	142	LEU	2.0
44	2m	104	ARG	2.0
26	24	65	ASP	2.0
38	1g	85	TYR	2.0
40	2i	106	ALA	2.0
48	2q	44	ALA	2.0
1	1A	1087	G	2.0
1	1A	2116	G	2.0
1	1A	2155	G	2.0
1	1A	2166	G	2.0
1	2A	271(K)	U	2.0
1	2A	2131	G	2.0
32	2a	1358	U	2.0
35	2d	167	GLY	2.0
40	2i	39	GLY	2.0
50	2s	84	GLY	2.0
54	2y	18	G	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2402	C	2.0
32	2a	1028	C	2.0
32	2a	1354	C	2.0
33	1b	167	PRO	2.0
8	2I	121	LYS	2.0
33	1b	19	HIS	2.0
41	2j	62	HIS	2.0
6	2G	162	THR	2.0
7	2H	37	VAL	2.0
33	2b	121	LEU	2.0
24	12	69	ARG	2.0
35	2d	209	ARG	2.0
1	1A	1086	A	2.0
1	1A	1095	A	2.0
4	2E	204	ALA	2.0
32	2a	1250	A	2.0
33	2b	33	TYR	2.0
34	2c	149	ALA	2.0
40	2i	105	ASP	2.0
51	1t	12	ALA	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	G7M	2y	46	24/25	0.57	0.15	90,98,107,119	0
54	G7M	1w	46	24/25	0.63	0.12	83,92,104,119	0
54	PSU	1y	55	20/21	0.66	0.13	87,97,107,116	0
54	PSU	2y	55	20/21	0.66	0.14	84,95,107,111	0
54	G7M	1y	46	24/25	0.67	0.12	87,93,102,111	0
54	G7M	2w	46	24/25	0.69	0.12	83,93,106,120	0
54	PSU	2w	55	20/21	0.72	0.11	79,89,96,103	0
54	4SU	2y	8	20/21	0.73	0.13	90,99,108,111	0
54	MIA	2y	37	22/30	0.75	0.15	87,92,98,108	0
54	4SU	2w	8	20/21	0.75	0.11	89,95,108,109	0
54	5MU	2y	54	21/22	0.75	0.15	85,90,102,117	0
54	5MU	1y	54	21/22	0.75	0.14	82,93,102,114	0
54	4SU	1w	8	20/21	0.76	0.10	87,93,101,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	5MU	2w	54	21/22	0.76	0.12	73,81,85,96	0
54	MIA	1y	37	22/30	0.78	0.11	69,83,100,110	0
54	PSU	2y	32	20/21	0.79	0.14	86,90,97,103	0
54	PSU	2y	39	20/21	0.81	0.14	84,90,98,102	0
54	4SU	1y	8	20/21	0.81	0.09	88,94,103,104	0
32	2MG	2a	1207	24/25	0.83	0.13	81,89,99,109	0
54	PSU	1w	55	20/21	0.83	0.10	76,85,92,94	0
55	4SU	2x	8	20/21	0.86	0.10	74,78,81,86	0
55	PSU	2x	55	20/21	0.87	0.10	70,77,88,94	0
54	PSU	1w	32	20/21	0.87	0.13	61,74,77,78	0
54	PSU	1y	32	20/21	0.88	0.09	74,80,91,97	0
32	M2G	2a	966	25/26	0.88	0.16	63,74,87,94	0
54	PSU	2w	39	20/21	0.88	0.12	73,83,91,93	0
32	PSU	2a	516	20/21	0.89	0.09	63,73,85,88	0
54	PSU	1y	39	20/21	0.89	0.08	74,81,85,87	0
54	PSU	2w	32	20/21	0.89	0.12	73,83,89,90	0
32	5MC	2a	967	21/22	0.89	0.13	70,77,82,88	0
55	5MU	2x	54	21/22	0.90	0.10	79,82,86,93	0
54	5MU	1w	54	21/22	0.90	0.09	63,74,83,85	0
55	5MU	1x	54	21/22	0.90	0.10	59,67,72,75	0
54	MIA	1w	37	29/30	0.91	0.15	49,63,78,88	0
1	5MU	2A	1915	21/22	0.91	0.09	66,71,76,82	0
55	5MC	2x	32	21/22	0.92	0.12	69,74,79,80	0
32	G7M	2a	527	24/25	0.92	0.11	58,63,69,74	0
32	5MC	2a	1400	21/22	0.92	0.15	68,74,79,81	0
54	MIA	2w	37	25/30	0.92	0.10	64,76,84,92	0
43	0TD	2l	92	10/11	0.92	0.12	61,63,71,79	0
1	PSU	2A	1917	20/21	0.93	0.08	58,64,72,74	0
55	PSU	1x	55	20/21	0.93	0.08	56,59,70,71	0
32	5MC	2a	1407	21/22	0.94	0.10	50,62,65,68	0
32	UR3	2a	1498	21/22	0.94	0.11	51,59,66,71	0
32	MA6	2a	1519	24/25	0.94	0.13	60,67,74,77	0
55	4SU	1x	8	20/21	0.94	0.09	51,57,64,77	0
32	PSU	1a	516	20/21	0.94	0.10	52,57,61,63	0
1	PSU	2A	1911	20/21	0.94	0.09	42,59,66,66	0
1	5MU	1A	1915	21/22	0.94	0.08	43,51,55,59	0
54	PSU	1w	39	20/21	0.94	0.08	67,71,74,87	0
1	5MC	2A	1962	21/22	0.94	0.11	44,54,58,73	0
32	4OC	2a	1402	22/23	0.94	0.10	59,70,73,73	0
32	5MC	2a	1404	21/22	0.94	0.10	52,64,70,74	0
56	FME	1z	1	10/11	0.94	0.15	37,49,52,63	0
1	OMC	2A	1920	21/22	0.95	0.08	54,60,62,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	2MG	1a	1207	24/25	0.95	0.09	57,65,68,77	0
55	5MC	1x	32	21/22	0.95	0.09	38,45,52,57	0
56	FME	2z	1	10/11	0.95	0.14	52,55,58,58	0
32	4OC	1a	1402	22/23	0.96	0.09	43,48,52,58	0
43	0TD	1l	92	10/11	0.96	0.08	34,44,50,51	0
1	PSU	1A	1917	20/21	0.96	0.08	36,47,51,52	0
1	5MC	2A	1942	21/22	0.96	0.09	42,58,62,69	0
32	M2G	1a	966	25/26	0.96	0.10	46,51,56,57	0
1	OMU	2A	2552	21/22	0.96	0.09	35,39,48,49	0
32	5MC	1a	967	21/22	0.96	0.09	44,55,61,68	0
32	MA6	2a	1518	24/25	0.96	0.09	57,65,70,73	0
1	5MC	1A	1942	21/22	0.96	0.08	33,39,43,54	0
32	5MC	1a	1400	21/22	0.96	0.10	37,42,49,56	0
32	5MC	1a	1407	21/22	0.97	0.08	26,40,45,48	0
55	8AN	1x	76	22/23	0.97	0.08	25,33,41,43	0
55	8AN	2x	76	22/23	0.97	0.09	40,44,49,53	0
32	MA6	1a	1518	24/25	0.97	0.09	32,41,45,48	0
32	MA6	1a	1519	24/25	0.97	0.08	36,43,48,56	0
32	G7M	1a	527	24/25	0.97	0.07	38,44,50,56	0
1	5MU	2A	1939	21/22	0.97	0.07	34,38,44,45	0
1	5MC	1A	1962	21/22	0.97	0.07	27,34,40,46	0
1	OMC	1A	1920	21/22	0.97	0.07	34,40,46,50	0
1	OMG	2A	2251	24/25	0.97	0.07	33,39,44,46	0
32	5MC	1a	1404	21/22	0.97	0.09	28,40,43,51	0
1	PSU	2A	2605	20/21	0.97	0.07	30,38,46,47	0
1	PSU	1A	1911	20/21	0.98	0.06	38,42,46,50	0
1	5MU	1A	1939	21/22	0.98	0.06	23,26,32,35	0
1	OMG	1A	2251	24/25	0.98	0.07	17,26,28,30	0
1	2MA	1A	2503	23/24	0.98	0.05	20,22,26,26	0
32	UR3	1a	1498	21/22	0.98	0.07	36,41,46,51	0
1	2MA	2A	2503	23/24	0.98	0.06	28,34,36,39	0
1	OMU	1A	2552	21/22	0.98	0.06	24,28,32,40	0
1	PSU	1A	2605	20/21	0.99	0.06	18,27,31,34	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
57	MG	1a	1720	1/1	0.51	0.38	82,82,82,82	0
57	MG	1B	232	1/1	0.55	0.16	76,76,76,76	0
57	MG	2A	3772	1/1	0.56	0.15	71,71,71,71	0
57	MG	2A	3710	1/1	0.58	0.17	79,79,79,79	0
57	MG	2A	3434	1/1	0.58	0.21	78,78,78,78	0
57	MG	2A	3576	1/1	0.64	0.18	67,67,67,67	0
57	MG	1A	3589	1/1	0.66	0.27	71,71,71,71	0
57	MG	2A	3273	1/1	0.66	0.22	78,78,78,78	0
57	MG	2a	1738	1/1	0.66	0.25	79,79,79,79	0
57	MG	2a	1800	1/1	0.67	0.25	79,79,79,79	0
57	MG	2A	3678	1/1	0.68	0.23	79,79,79,79	0
57	MG	2A	3203	1/1	0.69	0.27	68,68,68,68	0
57	MG	2a	1647	1/1	0.70	0.21	64,64,64,64	0
57	MG	1w	104	1/1	0.70	0.23	81,81,81,81	0
57	MG	2A	3236	1/1	0.70	0.18	67,67,67,67	0
57	MG	18	105	1/1	0.71	0.20	65,65,65,65	0
57	MG	2A	3643	1/1	0.71	0.34	83,83,83,83	0
57	MG	2A	3655	1/1	0.71	0.18	70,70,70,70	0
57	MG	2A	3569	1/1	0.72	0.19	79,79,79,79	0
57	MG	2A	3107	1/1	0.72	0.17	70,70,70,70	0
57	MG	2A	3199	1/1	0.72	0.24	71,71,71,71	0
57	MG	2A	3340	1/1	0.72	0.18	70,70,70,70	0
57	MG	1A	3749	1/1	0.72	0.21	60,60,60,60	0
57	MG	2A	3200	1/1	0.73	0.25	68,68,68,68	0
57	MG	1A	4070	1/1	0.73	0.36	89,89,89,89	0
57	MG	2y	101	1/1	0.73	0.29	79,79,79,79	0
57	MG	2A	3321	1/1	0.74	0.16	84,84,84,84	0
57	MG	2A	3326	1/1	0.74	0.25	77,77,77,77	0
57	MG	2A	3305	1/1	0.74	0.18	62,62,62,62	0
57	MG	2A	3103	1/1	0.75	0.17	76,76,76,76	0
57	MG	2a	1695	1/1	0.75	0.48	81,81,81,81	0
57	MG	2A	3276	1/1	0.75	0.13	70,70,70,70	0
57	MG	2B	204	1/1	0.75	0.15	77,77,77,77	0
57	MG	2w	101	1/1	0.75	0.28	83,83,83,83	0
57	MG	2B	215	1/1	0.75	0.23	69,69,69,69	0
57	MG	2A	3278	1/1	0.76	0.17	72,72,72,72	0
57	MG	1A	4001	1/1	0.76	0.11	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3212	1/1	0.76	0.15	58,58,58,58	0
57	MG	1A	3894	1/1	0.76	0.16	62,62,62,62	0
57	MG	1A	3939	1/1	0.76	0.18	79,79,79,79	0
57	MG	2a	1784	1/1	0.76	0.21	73,73,73,73	0
57	MG	2A	3097	1/1	0.76	0.32	80,80,80,80	0
57	MG	2A	3741	1/1	0.76	0.12	50,50,50,50	0
57	MG	2A	3469	1/1	0.76	0.19	65,65,65,65	0
57	MG	2a	1605	1/1	0.77	0.36	73,73,73,73	0
57	MG	1a	1804	1/1	0.77	0.25	74,74,74,74	0
57	MG	2a	1671	1/1	0.77	0.25	69,69,69,69	0
57	MG	1A	3256	1/1	0.77	0.26	63,63,63,63	0
57	MG	2a	1721	1/1	0.77	0.15	50,50,50,50	0
57	MG	2A	3734	1/1	0.77	0.17	80,80,80,80	0
57	MG	2A	3089	1/1	0.77	0.10	64,64,64,64	0
57	MG	1A	3873	1/1	0.77	0.15	67,67,67,67	0
57	MG	2v	102	1/1	0.77	0.30	80,80,80,80	0
57	MG	1A	3955	1/1	0.77	0.22	39,39,39,39	0
57	MG	1A	3877	1/1	0.77	0.12	22,22,22,22	0
57	MG	1A	3543	1/1	0.78	0.14	40,40,40,40	0
57	MG	2A	3649	1/1	0.78	0.20	74,74,74,74	0
57	MG	1A	3505	1/1	0.78	0.12	61,61,61,61	0
57	MG	2A	3671	1/1	0.78	0.18	63,63,63,63	0
57	MG	2a	1713	1/1	0.78	0.12	64,64,64,64	0
57	MG	2A	3253	1/1	0.78	0.16	74,74,74,74	0
57	MG	2a	1728	1/1	0.78	0.35	80,80,80,80	0
57	MG	1A	3725	1/1	0.78	0.20	73,73,73,73	0
57	MG	2A	3384	1/1	0.78	0.13	73,73,73,73	0
57	MG	2a	1785	1/1	0.78	0.17	85,85,85,85	0
57	MG	1A	3968	1/1	0.78	0.13	61,61,61,61	0
57	MG	2a	1809	1/1	0.78	0.29	65,65,65,65	0
57	MG	1a	1607	1/1	0.78	0.31	73,73,73,73	0
57	MG	2A	3294	1/1	0.78	0.12	66,66,66,66	0
57	MG	2A	3302	1/1	0.78	0.15	66,66,66,66	0
57	MG	2A	3184	1/1	0.79	0.29	66,66,66,66	0
57	MG	2A	3785	1/1	0.79	0.13	55,55,55,55	0
57	MG	2A	3065	1/1	0.79	0.12	57,57,57,57	0
57	MG	2A	3383	1/1	0.79	0.09	63,63,63,63	0
57	MG	1B	236	1/1	0.79	0.18	76,76,76,76	0
57	MG	2a	1786	1/1	0.79	0.15	66,66,66,66	0
57	MG	1A	3833	1/1	0.79	0.17	70,70,70,70	0
57	MG	1A	3228	1/1	0.79	0.20	66,66,66,66	0
57	MG	2A	3052	1/1	0.79	0.16	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3168	1/1	0.79	0.26	77,77,77,77	0
57	MG	2a	1720	1/1	0.79	0.26	55,55,55,55	0
57	MG	2a	1639	1/1	0.80	0.21	76,76,76,76	0
57	MG	2A	3600	1/1	0.80	0.10	74,74,74,74	0
57	MG	1a	1736	1/1	0.80	0.20	65,65,65,65	0
57	MG	1a	1738	1/1	0.80	0.14	74,74,74,74	0
57	MG	2a	1705	1/1	0.80	0.26	78,78,78,78	0
57	MG	1a	1765	1/1	0.80	0.11	58,58,58,58	0
57	MG	1A	3809	1/1	0.80	0.14	48,48,48,48	0
57	MG	1w	101	1/1	0.80	0.17	66,66,66,66	0
57	MG	1A	4074	1/1	0.80	0.18	49,49,49,49	0
57	MG	2A	3382	1/1	0.80	0.12	74,74,74,74	0
57	MG	2a	1783	1/1	0.80	0.15	71,71,71,71	0
57	MG	1A	3347	1/1	0.80	0.19	43,43,43,43	0
57	MG	2A	3754	1/1	0.80	0.12	59,59,59,59	0
57	MG	1A	3947	1/1	0.80	0.19	58,58,58,58	0
57	MG	2a	1788	1/1	0.80	0.21	72,72,72,72	0
57	MG	1A	3687	1/1	0.80	0.12	57,57,57,57	0
57	MG	2A	3827	1/1	0.80	0.13	45,45,45,45	0
57	MG	2A	3093	1/1	0.80	0.15	58,58,58,58	0
57	MG	1A	3874	1/1	0.80	0.13	46,46,46,46	0
57	MG	1A	3774	1/1	0.80	0.10	20,20,20,20	0
57	MG	2A	3242	1/1	0.81	0.14	57,57,57,57	0
57	MG	2a	1736	1/1	0.81	0.20	69,69,69,69	0
57	MG	1a	1713	1/1	0.81	0.16	50,50,50,50	0
57	MG	2a	1771	1/1	0.81	0.32	77,77,77,77	0
57	MG	1A	3206	1/1	0.81	0.13	67,67,67,67	0
57	MG	2a	1618	1/1	0.81	0.14	61,61,61,61	0
57	MG	2A	3690	1/1	0.81	0.23	77,77,77,77	0
57	MG	2A	3021	1/1	0.81	0.24	72,72,72,72	0
57	MG	2A	3531	1/1	0.81	0.29	65,65,65,65	0
57	MG	1A	3555	1/1	0.81	0.14	46,46,46,46	0
57	MG	2a	1808	1/1	0.81	0.14	64,64,64,64	0
57	MG	2A	3355	1/1	0.81	0.24	73,73,73,73	0
57	MG	2A	3366	1/1	0.81	0.16	74,74,74,74	0
57	MG	2A	3375	1/1	0.81	0.38	66,66,66,66	0
57	MG	2x	102	1/1	0.81	0.10	71,71,71,71	0
57	MG	2A	3188	1/1	0.81	0.11	62,62,62,62	0
57	MG	1A	3860	1/1	0.82	0.09	45,45,45,45	0
57	MG	2a	1744	1/1	0.82	0.29	69,69,69,69	0
57	MG	2B	219	1/1	0.82	0.22	67,67,67,67	0
57	MG	2A	3252	1/1	0.82	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
57	MG	1w	102	1/1	0.82	0.09	69,69,69,69	0
57	MG	1a	1678	1/1	0.82	0.16	59,59,59,59	0
57	MG	2A	3737	1/1	0.82	0.17	49,49,49,49	0
57	MG	1A	3322	1/1	0.82	0.14	53,53,53,53	0
57	MG	1a	1795	1/1	0.82	0.09	75,75,75,75	0
57	MG	2A	3159	1/1	0.82	0.15	70,70,70,70	0
57	MG	2A	3301	1/1	0.82	0.16	71,71,71,71	0
57	MG	1A	4080	1/1	0.82	0.27	57,57,57,57	0
57	MG	2A	3837	1/1	0.82	0.12	74,74,74,74	0
57	MG	2A	3842	1/1	0.82	0.13	54,54,54,54	0
57	MG	2A	3303	1/1	0.82	0.23	60,60,60,60	0
57	MG	2a	1637	1/1	0.83	0.19	65,65,65,65	0
57	MG	2a	1638	1/1	0.83	0.28	70,70,70,70	0
57	MG	2A	3654	1/1	0.83	0.11	82,82,82,82	0
57	MG	1w	103	1/1	0.83	0.18	72,72,72,72	0
57	MG	2a	1654	1/1	0.83	0.20	83,83,83,83	0
57	MG	2a	1663	1/1	0.83	0.27	63,63,63,63	0
57	MG	1a	1656	1/1	0.83	0.12	64,64,64,64	0
57	MG	1A	3865	1/1	0.83	0.23	45,45,45,45	0
57	MG	1a	1694	1/1	0.83	0.20	78,78,78,78	0
57	MG	2A	3692	1/1	0.83	0.11	69,69,69,69	0
57	MG	2a	1715	1/1	0.83	0.23	61,61,61,61	0
57	MG	1A	3944	1/1	0.83	0.13	60,60,60,60	0
57	MG	2A	3718	1/1	0.83	0.28	63,63,63,63	0
57	MG	2a	1727	1/1	0.83	0.08	60,60,60,60	0
57	MG	1A	3101	1/1	0.83	0.08	50,50,50,50	0
57	MG	1A	3717	1/1	0.83	0.08	62,62,62,62	0
57	MG	1A	3579	1/1	0.83	0.25	65,65,65,65	0
57	MG	2A	3257	1/1	0.83	0.22	63,63,63,63	0
57	MG	2a	1745	1/1	0.83	0.24	73,73,73,73	0
57	MG	2A	3389	1/1	0.83	0.13	46,46,46,46	0
57	MG	2A	3101	1/1	0.83	0.26	58,58,58,58	0
57	MG	2A	3444	1/1	0.83	0.17	68,68,68,68	0
57	MG	1D	311	1/1	0.83	0.15	33,33,33,33	0
57	MG	1a	1778	1/1	0.83	0.17	53,53,53,53	0
57	MG	2A	3850	1/1	0.83	0.23	58,58,58,58	0
57	MG	2A	3134	1/1	0.83	0.25	65,65,65,65	0
57	MG	2a	1803	1/1	0.83	0.21	72,72,72,72	0
57	MG	2B	214	1/1	0.83	0.17	75,75,75,75	0
57	MG	1G	203	1/1	0.83	0.10	54,54,54,54	0
57	MG	2a	1818	1/1	0.83	0.21	74,74,74,74	0
57	MG	2d	302	1/1	0.83	0.20	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1Q	204	1/1	0.83	0.10	52,52,52,52	0
57	MG	1A	3987	1/1	0.83	0.24	62,62,62,62	0
57	MG	1A	3027	1/1	0.83	0.21	54,54,54,54	0
57	MG	2x	103	1/1	0.83	0.24	74,74,74,74	0
57	MG	2a	1635	1/1	0.83	0.25	63,63,63,63	0
57	MG	2A	3255	1/1	0.84	0.20	58,58,58,58	0
57	MG	1a	1660	1/1	0.84	0.19	63,63,63,63	0
57	MG	1A	3830	1/1	0.84	0.13	67,67,67,67	0
57	MG	2A	3789	1/1	0.84	0.11	55,55,55,55	0
57	MG	2A	3137	1/1	0.84	0.20	63,63,63,63	0
57	MG	1F	301	1/1	0.84	0.22	36,36,36,36	0
57	MG	2A	3289	1/1	0.84	0.15	51,51,51,51	0
57	MG	1A	3161	1/1	0.84	0.21	51,51,51,51	0
57	MG	2B	203	1/1	0.84	0.17	54,54,54,54	0
57	MG	2A	3173	1/1	0.84	0.17	49,49,49,49	0
57	MG	2a	1750	1/1	0.84	0.17	68,68,68,68	0
57	MG	2a	1764	1/1	0.84	0.16	73,73,73,73	0
57	MG	2A	3174	1/1	0.84	0.12	66,66,66,66	0
57	MG	1x	109	1/1	0.84	0.13	70,70,70,70	0
57	MG	1B	216	1/1	0.84	0.11	61,61,61,61	0
57	MG	1A	3250	1/1	0.84	0.21	74,74,74,74	0
57	MG	1B	233	1/1	0.84	0.15	61,61,61,61	0
57	MG	2a	1633	1/1	0.84	0.32	73,73,73,73	0
57	MG	2A	3676	1/1	0.84	0.15	66,66,66,66	0
57	MG	2A	3086	1/1	0.84	0.18	50,50,50,50	0
57	MG	2A	3684	1/1	0.84	0.09	69,69,69,69	0
57	MG	1a	1622	1/1	0.84	0.19	62,62,62,62	0
57	MG	2a	1812	1/1	0.84	0.28	69,69,69,69	0
57	MG	1a	1768	1/1	0.84	0.12	71,71,71,71	0
57	MG	2A	3367	1/1	0.84	0.16	75,75,75,75	0
57	MG	2j	201	1/1	0.84	0.20	63,63,63,63	0
57	MG	2q	202	1/1	0.84	0.13	77,77,77,77	0
57	MG	2a	1659	1/1	0.84	0.12	73,73,73,73	0
57	MG	2A	3237	1/1	0.84	0.13	60,60,60,60	0
57	MG	2x	101	1/1	0.84	0.20	72,72,72,72	0
57	MG	1a	1655	1/1	0.84	0.19	63,63,63,63	0
57	MG	1A	3642	1/1	0.84	0.11	43,43,43,43	0
57	MG	1a	1659	1/1	0.84	0.28	74,74,74,74	0
57	MG	2A	3339	1/1	0.85	0.08	56,56,56,56	0
57	MG	1a	1709	1/1	0.85	0.28	46,46,46,46	0
57	MG	2a	1677	1/1	0.85	0.13	61,61,61,61	0
57	MG	2A	3343	1/1	0.85	0.13	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1703	1/1	0.85	0.18	66,66,66,66	0
57	MG	2A	3099	1/1	0.85	0.16	52,52,52,52	0
57	MG	1a	1806	1/1	0.85	0.21	74,74,74,74	0
57	MG	1A	3647	1/1	0.85	0.14	65,65,65,65	0
57	MG	1a	1719	1/1	0.85	0.16	64,64,64,64	0
57	MG	1a	1630	1/1	0.85	0.23	73,73,73,73	0
57	MG	1A	3935	1/1	0.85	0.24	64,64,64,64	0
57	MG	1A	3128	1/1	0.85	0.13	59,59,59,59	0
57	MG	2a	1732	1/1	0.85	0.14	58,58,58,58	0
57	MG	2A	3258	1/1	0.85	0.11	82,82,82,82	0
57	MG	2A	3410	1/1	0.85	0.13	51,51,51,51	0
57	MG	2A	3260	1/1	0.85	0.10	65,65,65,65	0
57	MG	2A	3261	1/1	0.85	0.12	63,63,63,63	0
57	MG	2A	3457	1/1	0.85	0.12	50,50,50,50	0
57	MG	2A	3852	1/1	0.85	0.14	45,45,45,45	0
57	MG	2A	3264	1/1	0.85	0.17	53,53,53,53	0
57	MG	2A	3165	1/1	0.85	0.08	60,60,60,60	0
57	MG	1A	4082	1/1	0.85	0.18	69,69,69,69	0
57	MG	1A	4007	1/1	0.85	0.17	53,53,53,53	0
57	MG	2A	3057	1/1	0.85	0.21	62,62,62,62	0
57	MG	2W	202	1/1	0.85	0.14	57,57,57,57	0
57	MG	2a	1797	1/1	0.85	0.14	79,79,79,79	0
57	MG	2a	1604	1/1	0.85	0.09	54,54,54,54	0
57	MG	2A	3637	1/1	0.85	0.13	40,40,40,40	0
57	MG	2a	1614	1/1	0.85	0.26	68,68,68,68	0
57	MG	2A	3064	1/1	0.85	0.20	41,41,41,41	0
57	MG	2a	1624	1/1	0.85	0.15	65,65,65,65	0
57	MG	1A	4021	1/1	0.85	0.10	35,35,35,35	0
57	MG	2a	1822	1/1	0.85	0.18	67,67,67,67	0
57	MG	2A	3195	1/1	0.85	0.10	61,61,61,61	0
57	MG	1a	1789	1/1	0.85	0.16	77,77,77,77	0
57	MG	2A	3664	1/1	0.85	0.14	48,48,48,48	0
57	MG	2v	101	1/1	0.85	0.21	68,68,68,68	0
57	MG	1A	4025	1/1	0.85	0.12	35,35,35,35	0
57	MG	2a	1642	1/1	0.85	0.13	78,78,78,78	0
57	MG	2w	105	1/1	0.85	0.13	64,64,64,64	0
57	MG	1a	1798	1/1	0.85	0.22	63,63,63,63	0
57	MG	2A	3206	1/1	0.85	0.13	53,53,53,53	0
57	MG	2A	3334	1/1	0.85	0.22	53,53,53,53	0
57	MG	2a	1661	1/1	0.85	0.22	60,60,60,60	0
57	MG	1A	3423	1/1	0.86	0.13	42,42,42,42	0
57	MG	2A	3784	1/1	0.86	0.08	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3458	1/1	0.86	0.15	70,70,70,70	0
57	MG	1a	1799	1/1	0.86	0.23	62,62,62,62	0
57	MG	2A	3826	1/1	0.86	0.15	54,54,54,54	0
57	MG	2a	1719	1/1	0.86	0.18	60,60,60,60	0
57	MG	2A	3495	1/1	0.86	0.12	61,61,61,61	0
57	MG	1A	4023	1/1	0.86	0.12	57,57,57,57	0
57	MG	2A	3315	1/1	0.86	0.15	62,62,62,62	0
57	MG	2A	3575	1/1	0.86	0.17	62,62,62,62	0
57	MG	1A	3471	1/1	0.86	0.10	64,64,64,64	0
57	MG	2a	1733	1/1	0.86	0.10	67,67,67,67	0
57	MG	2A	3584	1/1	0.86	0.10	68,68,68,68	0
57	MG	2a	1737	1/1	0.86	0.18	64,64,64,64	0
57	MG	2A	3599	1/1	0.86	0.18	50,50,50,50	0
57	MG	1A	4069	1/1	0.86	0.11	75,75,75,75	0
57	MG	2A	3614	1/1	0.86	0.22	59,59,59,59	0
57	MG	2A	3327	1/1	0.86	0.14	80,80,80,80	0
57	MG	2a	1760	1/1	0.86	0.20	70,70,70,70	0
57	MG	2B	220	1/1	0.86	0.16	65,65,65,65	0
57	MG	2E	309	1/1	0.86	0.08	41,41,41,41	0
57	MG	1A	3301	1/1	0.86	0.11	51,51,51,51	0
57	MG	1A	3254	1/1	0.86	0.17	52,52,52,52	0
57	MG	2A	3155	1/1	0.86	0.10	58,58,58,58	0
57	MG	1A	3959	1/1	0.86	0.10	66,66,66,66	0
57	MG	2a	1787	1/1	0.86	0.28	72,72,72,72	0
57	MG	1a	1723	1/1	0.86	0.24	59,59,59,59	0
57	MG	2a	1621	1/1	0.86	0.17	60,60,60,60	0
57	MG	2A	3356	1/1	0.86	0.21	68,68,68,68	0
57	MG	2a	1801	1/1	0.86	0.22	64,64,64,64	0
57	MG	2a	1626	1/1	0.86	0.08	88,88,88,88	0
57	MG	2a	1805	1/1	0.86	0.21	66,66,66,66	0
57	MG	2A	3358	1/1	0.86	0.18	64,64,64,64	0
57	MG	2a	1634	1/1	0.86	0.35	68,68,68,68	0
57	MG	1A	3050	1/1	0.86	0.13	33,33,33,33	0
57	MG	1B	214	1/1	0.86	0.10	40,40,40,40	0
57	MG	1a	1763	1/1	0.86	0.12	60,60,60,60	0
57	MG	2A	3691	1/1	0.86	0.12	70,70,70,70	0
57	MG	1a	1647	1/1	0.86	0.15	63,63,63,63	0
57	MG	2A	3699	1/1	0.86	0.23	64,64,64,64	0
57	MG	1a	1652	1/1	0.86	0.18	51,51,51,51	0
57	MG	2A	3071	1/1	0.86	0.11	57,57,57,57	0
57	MG	1A	3910	1/1	0.86	0.18	49,49,49,49	0
57	MG	1A	3916	1/1	0.86	0.10	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3424	1/1	0.86	0.10	56,56,56,56	0
57	MG	2A	3299	1/1	0.86	0.18	72,72,72,72	0
57	MG	2a	1678	1/1	0.86	0.15	70,70,70,70	0
57	MG	2a	1682	1/1	0.86	0.28	56,56,56,56	0
57	MG	1B	210	1/1	0.87	0.09	51,51,51,51	0
57	MG	1A	3812	1/1	0.87	0.14	50,50,50,50	0
57	MG	1A	3566	1/1	0.87	0.21	56,56,56,56	0
57	MG	1a	1676	1/1	0.87	0.17	62,62,62,62	0
57	MG	2a	1676	1/1	0.87	0.19	64,64,64,64	0
57	MG	1B	226	1/1	0.87	0.13	41,41,41,41	0
57	MG	2A	3717	1/1	0.87	0.21	70,70,70,70	0
57	MG	2A	3232	1/1	0.87	0.17	57,57,57,57	0
57	MG	1a	1688	1/1	0.87	0.27	50,50,50,50	0
57	MG	1A	3065	1/1	0.87	0.13	53,53,53,53	0
57	MG	2A	3239	1/1	0.87	0.15	64,64,64,64	0
57	MG	2a	1707	1/1	0.87	0.16	55,55,55,55	0
57	MG	2a	1709	1/1	0.87	0.18	75,75,75,75	0
57	MG	2A	3747	1/1	0.87	0.12	56,56,56,56	0
57	MG	1A	3845	1/1	0.87	0.10	51,51,51,51	0
57	MG	2a	1717	1/1	0.87	0.16	62,62,62,62	0
57	MG	2A	3755	1/1	0.87	0.12	65,65,65,65	0
57	MG	2A	3767	1/1	0.87	0.10	66,66,66,66	0
57	MG	2A	3386	1/1	0.87	0.10	52,52,52,52	0
57	MG	2a	1726	1/1	0.87	0.30	75,75,75,75	0
57	MG	1A	3371	1/1	0.87	0.09	62,62,62,62	0
57	MG	1a	1716	1/1	0.87	0.15	49,49,49,49	0
57	MG	2A	3423	1/1	0.87	0.18	62,62,62,62	0
57	MG	2A	3794	1/1	0.87	0.07	72,72,72,72	0
57	MG	1A	3989	1/1	0.87	0.13	51,51,51,51	0
57	MG	1A	3130	1/1	0.87	0.06	70,70,70,70	0
57	MG	1F	311	1/1	0.87	0.14	56,56,56,56	0
57	MG	2A	3838	1/1	0.87	0.11	62,62,62,62	0
57	MG	2A	3094	1/1	0.87	0.21	68,68,68,68	0
57	MG	2A	3466	1/1	0.87	0.08	70,70,70,70	0
57	MG	2a	1756	1/1	0.87	0.06	87,87,87,87	0
57	MG	1A	3066	1/1	0.87	0.13	44,44,44,44	0
57	MG	2A	3487	1/1	0.87	0.20	75,75,75,75	0
57	MG	1a	1737	1/1	0.87	0.12	54,54,54,54	0
57	MG	2B	208	1/1	0.87	0.19	62,62,62,62	0
57	MG	1A	3654	1/1	0.87	0.12	58,58,58,58	0
57	MG	1Q	207	1/1	0.87	0.10	37,37,37,37	0
57	MG	1R	203	1/1	0.87	0.16	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3112	1/1	0.87	0.24	63,63,63,63	0
57	MG	1T	201	1/1	0.87	0.12	50,50,50,50	0
57	MG	2P	202	1/1	0.87	0.26	51,51,51,51	0
57	MG	2A	3597	1/1	0.87	0.14	50,50,50,50	0
57	MG	2Z	301	1/1	0.87	0.20	72,72,72,72	0
57	MG	1A	3180	1/1	0.87	0.16	51,51,51,51	0
57	MG	1A	3704	1/1	0.87	0.07	34,34,34,34	0
57	MG	2a	1606	1/1	0.87	0.16	70,70,70,70	0
57	MG	2a	1613	1/1	0.87	0.18	57,57,57,57	0
57	MG	2A	3601	1/1	0.87	0.16	53,53,53,53	0
57	MG	2a	1814	1/1	0.87	0.16	75,75,75,75	0
57	MG	1a	1621	1/1	0.87	0.38	73,73,73,73	0
57	MG	2A	3620	1/1	0.87	0.17	64,64,64,64	0
57	MG	1A	3492	1/1	0.87	0.08	29,29,29,29	0
57	MG	1A	3200	1/1	0.87	0.11	47,47,47,47	0
57	MG	2k	201	1/1	0.87	0.16	65,65,65,65	0
57	MG	2A	3170	1/1	0.87	0.12	55,55,55,55	0
57	MG	2A	3318	1/1	0.87	0.16	54,54,54,54	0
57	MG	1a	1800	1/1	0.87	0.10	41,41,41,41	0
57	MG	1A	3513	1/1	0.87	0.09	55,55,55,55	0
57	MG	2A	3180	1/1	0.87	0.15	62,62,62,62	0
57	MG	2A	3672	1/1	0.87	0.11	53,53,53,53	0
57	MG	1A	3302	1/1	0.87	0.17	53,53,53,53	0
57	MG	1a	1807	1/1	0.87	0.13	52,52,52,52	0
57	MG	1A	3053	1/1	0.87	0.18	55,55,55,55	0
57	MG	2a	1646	1/1	0.88	0.18	57,57,57,57	0
57	MG	2A	3329	1/1	0.88	0.22	68,68,68,68	0
57	MG	2a	1648	1/1	0.88	0.13	73,73,73,73	0
57	MG	2A	3194	1/1	0.88	0.11	54,54,54,54	0
57	MG	2a	1656	1/1	0.88	0.16	65,65,65,65	0
57	MG	1a	1708	1/1	0.88	0.17	46,46,46,46	0
57	MG	2A	3018	1/1	0.88	0.09	59,59,59,59	0
57	MG	1A	3246	1/1	0.88	0.07	47,47,47,47	0
57	MG	2A	3044	1/1	0.88	0.08	78,78,78,78	0
57	MG	1A	3718	1/1	0.88	0.10	48,48,48,48	0
57	MG	1O	201	1/1	0.88	0.08	61,61,61,61	0
57	MG	2A	3365	1/1	0.88	0.34	66,66,66,66	0
57	MG	2A	3215	1/1	0.88	0.19	64,64,64,64	0
57	MG	2A	3222	1/1	0.88	0.19	43,43,43,43	0
57	MG	2a	1697	1/1	0.88	0.11	68,68,68,68	0
57	MG	2A	3372	1/1	0.88	0.09	40,40,40,40	0
57	MG	1a	1717	1/1	0.88	0.13	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3376	1/1	0.88	0.10	56,56,56,56	0
57	MG	2A	3378	1/1	0.88	0.10	49,49,49,49	0
57	MG	2A	3379	1/1	0.88	0.25	66,66,66,66	0
57	MG	1A	3875	1/1	0.88	0.13	67,67,67,67	0
57	MG	1A	3414	1/1	0.88	0.12	47,47,47,47	0
57	MG	1A	3884	1/1	0.88	0.13	25,25,25,25	0
57	MG	2A	3241	1/1	0.88	0.44	76,76,76,76	0
57	MG	1A	3494	1/1	0.88	0.13	57,57,57,57	0
57	MG	2A	3786	1/1	0.88	0.13	59,59,59,59	0
57	MG	2A	3246	1/1	0.88	0.14	57,57,57,57	0
57	MG	2A	3419	1/1	0.88	0.18	58,58,58,58	0
57	MG	2A	3821	1/1	0.88	0.10	58,58,58,58	0
57	MG	1A	3900	1/1	0.88	0.10	45,45,45,45	0
57	MG	1A	3599	1/1	0.88	0.35	60,60,60,60	0
57	MG	1A	3641	1/1	0.88	0.13	27,27,27,27	0
57	MG	1A	4081	1/1	0.88	0.12	51,51,51,51	0
57	MG	2a	1743	1/1	0.88	0.21	66,66,66,66	0
57	MG	2A	3454	1/1	0.88	0.15	51,51,51,51	0
57	MG	1a	1628	1/1	0.88	0.17	52,52,52,52	0
57	MG	1A	3917	1/1	0.88	0.09	27,27,27,27	0
57	MG	2A	3468	1/1	0.88	0.23	64,64,64,64	0
57	MG	2a	1758	1/1	0.88	0.19	67,67,67,67	0
57	MG	2a	1759	1/1	0.88	0.18	72,72,72,72	0
57	MG	1a	1780	1/1	0.88	0.14	64,64,64,64	0
57	MG	2A	3262	1/1	0.88	0.17	61,61,61,61	0
57	MG	2A	3493	1/1	0.88	0.18	48,48,48,48	0
57	MG	2a	1777	1/1	0.88	0.22	59,59,59,59	0
57	MG	1B	203	1/1	0.88	0.11	56,56,56,56	0
57	MG	2A	3499	1/1	0.88	0.16	64,64,64,64	0
57	MG	2A	3119	1/1	0.88	0.13	69,69,69,69	0
57	MG	2A	3544	1/1	0.88	0.10	41,41,41,41	0
57	MG	2F	302	1/1	0.88	0.10	48,48,48,48	0
57	MG	1a	1648	1/1	0.88	0.21	55,55,55,55	0
57	MG	2A	3571	1/1	0.88	0.17	51,51,51,51	0
57	MG	1A	3340	1/1	0.88	0.09	57,57,57,57	0
57	MG	20	101	1/1	0.88	0.20	66,66,66,66	0
57	MG	2A	3279	1/1	0.88	0.24	69,69,69,69	0
57	MG	2A	3149	1/1	0.88	0.27	64,64,64,64	0
57	MG	1A	3427	1/1	0.88	0.19	65,65,65,65	0
57	MG	2A	3158	1/1	0.88	0.13	50,50,50,50	0
57	MG	1A	3526	1/1	0.88	0.23	62,62,62,62	0
57	MG	1A	3841	1/1	0.88	0.15	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3441	1/1	0.88	0.10	56,56,56,56	0
57	MG	2a	1821	1/1	0.88	0.16	65,65,65,65	0
57	MG	1a	1665	1/1	0.88	0.15	57,57,57,57	0
57	MG	2A	3309	1/1	0.88	0.18	63,63,63,63	0
57	MG	2a	1627	1/1	0.88	0.21	67,67,67,67	0
57	MG	2a	1628	1/1	0.88	0.30	69,69,69,69	0
57	MG	2A	3641	1/1	0.88	0.13	59,59,59,59	0
57	MG	1A	3846	1/1	0.88	0.15	43,43,43,43	0
57	MG	1A	3694	1/1	0.88	0.09	25,25,25,25	0
57	MG	2a	1636	1/1	0.88	0.37	71,71,71,71	0
57	MG	1A	3096	1/1	0.88	0.12	61,61,61,61	0
57	MG	2A	3324	1/1	0.88	0.11	63,63,63,63	0
57	MG	1A	3870	1/1	0.88	0.17	50,50,50,50	0
57	MG	1x	105	1/1	0.88	0.24	58,58,58,58	0
57	MG	2a	1645	1/1	0.88	0.23	58,58,58,58	0
57	MG	2a	1625	1/1	0.89	0.28	59,59,59,59	0
57	MG	1B	231	1/1	0.89	0.08	46,46,46,46	0
57	MG	1a	1700	1/1	0.89	0.20	63,63,63,63	0
57	MG	1A	3837	1/1	0.89	0.09	51,51,51,51	0
57	MG	2A	3292	1/1	0.89	0.10	53,53,53,53	0
57	MG	1A	3403	1/1	0.89	0.08	52,52,52,52	0
57	MG	2A	3602	1/1	0.89	0.12	58,58,58,58	0
57	MG	2A	3612	1/1	0.89	0.13	43,43,43,43	0
57	MG	1B	234	1/1	0.89	0.15	65,65,65,65	0
57	MG	1A	3949	1/1	0.89	0.09	48,48,48,48	0
57	MG	1A	3844	1/1	0.89	0.19	50,50,50,50	0
57	MG	2A	3110	1/1	0.89	0.17	58,58,58,58	0
57	MG	1A	3502	1/1	0.89	0.14	46,46,46,46	0
57	MG	2A	3306	1/1	0.89	0.15	56,56,56,56	0
57	MG	1A	3967	1/1	0.89	0.12	54,54,54,54	0
57	MG	1a	1721	1/1	0.89	0.22	65,65,65,65	0
57	MG	1A	3325	1/1	0.89	0.21	61,61,61,61	0
57	MG	1A	3657	1/1	0.89	0.09	44,44,44,44	0
57	MG	1A	3669	1/1	0.89	0.10	44,44,44,44	0
57	MG	2a	1660	1/1	0.89	0.08	56,56,56,56	0
57	MG	2A	3673	1/1	0.89	0.12	48,48,48,48	0
57	MG	2A	3325	1/1	0.89	0.25	64,64,64,64	0
57	MG	2a	1666	1/1	0.89	0.12	68,68,68,68	0
57	MG	1A	3992	1/1	0.89	0.09	26,26,26,26	0
57	MG	2a	1673	1/1	0.89	0.15	55,55,55,55	0
57	MG	2A	3680	1/1	0.89	0.11	60,60,60,60	0
57	MG	2A	3682	1/1	0.89	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
57	MG	1A	3507	1/1	0.89	0.09	52,52,52,52	0
57	MG	1A	3332	1/1	0.89	0.21	59,59,59,59	0
57	MG	2a	1684	1/1	0.89	0.28	64,64,64,64	0
57	MG	2a	1688	1/1	0.89	0.12	65,65,65,65	0
57	MG	2A	3333	1/1	0.89	0.08	49,49,49,49	0
57	MG	2a	1696	1/1	0.89	0.18	62,62,62,62	0
57	MG	1Y	202	1/1	0.89	0.10	57,57,57,57	0
57	MG	1a	1769	1/1	0.89	0.12	64,64,64,64	0
57	MG	1a	1772	1/1	0.89	0.14	63,63,63,63	0
57	MG	2a	1706	1/1	0.89	0.18	68,68,68,68	0
57	MG	2A	3713	1/1	0.89	0.14	56,56,56,56	0
57	MG	13	105	1/1	0.89	0.10	51,51,51,51	0
57	MG	2a	1711	1/1	0.89	0.27	55,55,55,55	0
57	MG	2A	3346	1/1	0.89	0.14	61,61,61,61	0
57	MG	2A	3720	1/1	0.89	0.21	55,55,55,55	0
57	MG	2A	3722	1/1	0.89	0.14	59,59,59,59	0
57	MG	14	101	1/1	0.89	0.19	75,75,75,75	0
57	MG	2A	3735	1/1	0.89	0.19	69,69,69,69	0
57	MG	2A	3181	1/1	0.89	0.14	55,55,55,55	0
57	MG	2a	1723	1/1	0.89	0.25	51,51,51,51	0
57	MG	1a	1784	1/1	0.89	0.15	61,61,61,61	0
57	MG	2A	3187	1/1	0.89	0.32	63,63,63,63	0
57	MG	16	101	1/1	0.89	0.11	44,44,44,44	0
57	MG	2A	3189	1/1	0.89	0.13	63,63,63,63	0
57	MG	1A	3333	1/1	0.89	0.08	55,55,55,55	0
57	MG	2A	3770	1/1	0.89	0.09	72,72,72,72	0
57	MG	1A	3533	1/1	0.89	0.23	47,47,47,47	0
57	MG	2A	3775	1/1	0.89	0.15	50,50,50,50	0
57	MG	1a	1617	1/1	0.89	0.16	56,56,56,56	0
57	MG	1A	3088	1/1	0.89	0.27	42,42,42,42	0
57	MG	2A	3201	1/1	0.89	0.09	48,48,48,48	0
57	MG	1A	4027	1/1	0.89	0.07	29,29,29,29	0
57	MG	2a	1754	1/1	0.89	0.12	71,71,71,71	0
57	MG	1a	1623	1/1	0.89	0.23	59,59,59,59	0
57	MG	1a	1627	1/1	0.89	0.17	54,54,54,54	0
57	MG	1p	101	1/1	0.89	0.10	51,51,51,51	0
57	MG	1A	3722	1/1	0.89	0.12	54,54,54,54	0
57	MG	2A	3830	1/1	0.89	0.13	61,61,61,61	0
57	MG	2a	1767	1/1	0.89	0.14	52,52,52,52	0
57	MG	2A	3836	1/1	0.89	0.13	67,67,67,67	0
57	MG	1A	3885	1/1	0.89	0.11	36,36,36,36	0
57	MG	2A	3417	1/1	0.89	0.18	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3840	1/1	0.89	0.09	56,56,56,56	0
57	MG	2A	3233	1/1	0.89	0.08	45,45,45,45	0
57	MG	2A	3848	1/1	0.89	0.16	50,50,50,50	0
57	MG	1a	1638	1/1	0.89	0.14	51,51,51,51	0
57	MG	1A	3454	1/1	0.89	0.21	58,58,58,58	0
57	MG	2a	1795	1/1	0.89	0.21	72,72,72,72	0
57	MG	2a	1796	1/1	0.89	0.15	65,65,65,65	0
57	MG	2A	3430	1/1	0.89	0.21	53,53,53,53	0
57	MG	2A	3238	1/1	0.89	0.25	60,60,60,60	0
57	MG	1A	3257	1/1	0.89	0.10	63,63,63,63	0
57	MG	2A	3240	1/1	0.89	0.19	61,61,61,61	0
57	MG	1A	3467	1/1	0.89	0.07	56,56,56,56	0
57	MG	2B	217	1/1	0.89	0.12	66,66,66,66	0
57	MG	1A	3585	1/1	0.89	0.08	49,49,49,49	0
57	MG	1A	3300	1/1	0.89	0.17	47,47,47,47	0
57	MG	2A	3041	1/1	0.89	0.28	48,48,48,48	0
57	MG	2A	3486	1/1	0.89	0.18	55,55,55,55	0
57	MG	1B	209	1/1	0.89	0.13	48,48,48,48	0
57	MG	2Q	201	1/1	0.89	0.12	68,68,68,68	0
57	MG	2T	202	1/1	0.89	0.19	55,55,55,55	0
57	MG	1A	3933	1/1	0.89	0.10	31,31,31,31	0
57	MG	2A	3054	1/1	0.89	0.17	66,66,66,66	0
57	MG	1B	211	1/1	0.89	0.12	50,50,50,50	0
57	MG	2A	3511	1/1	0.89	0.10	24,24,24,24	0
57	MG	2A	3062	1/1	0.89	0.19	66,66,66,66	0
57	MG	1a	1672	1/1	0.89	0.12	64,64,64,64	0
57	MG	2A	3566	1/1	0.89	0.20	51,51,51,51	0
57	MG	1A	3489	1/1	0.89	0.12	45,45,45,45	0
57	MG	1A	3391	1/1	0.89	0.20	45,45,45,45	0
57	MG	1a	1682	1/1	0.89	0.18	63,63,63,63	0
57	MG	1A	3941	1/1	0.89	0.11	46,46,46,46	0
57	MG	2A	3438	1/1	0.90	0.18	51,51,51,51	0
57	MG	1A	3243	1/1	0.90	0.14	57,57,57,57	0
57	MG	1A	3193	1/1	0.90	0.17	32,32,32,32	0
57	MG	1a	1775	1/1	0.90	0.09	56,56,56,56	0
57	MG	2A	3460	1/1	0.90	0.26	45,45,45,45	0
57	MG	1a	1777	1/1	0.90	0.10	46,46,46,46	0
57	MG	1A	3195	1/1	0.90	0.16	40,40,40,40	0
57	MG	1A	3730	1/1	0.90	0.13	71,71,71,71	0
57	MG	2a	1610	1/1	0.90	0.12	48,48,48,48	0
57	MG	2a	1612	1/1	0.90	0.12	68,68,68,68	0
57	MG	2A	3470	1/1	0.90	0.16	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3472	1/1	0.90	0.06	63,63,63,63	0
57	MG	2A	3483	1/1	0.90	0.14	42,42,42,42	0
57	MG	1A	3739	1/1	0.90	0.10	57,57,57,57	0
57	MG	2a	1622	1/1	0.90	0.11	48,48,48,48	0
57	MG	1A	3957	1/1	0.90	0.15	61,61,61,61	0
57	MG	1A	3199	1/1	0.90	0.39	47,47,47,47	0
57	MG	2A	3226	1/1	0.90	0.21	71,71,71,71	0
57	MG	2A	3227	1/1	0.90	0.15	66,66,66,66	0
57	MG	2A	3231	1/1	0.90	0.10	34,34,34,34	0
57	MG	2a	1632	1/1	0.90	0.05	78,78,78,78	0
57	MG	2A	3527	1/1	0.90	0.08	40,40,40,40	0
57	MG	1a	1796	1/1	0.90	0.19	57,57,57,57	0
57	MG	2A	3543	1/1	0.90	0.09	44,44,44,44	0
57	MG	1a	1797	1/1	0.90	0.07	66,66,66,66	0
57	MG	2A	3556	1/1	0.90	0.13	50,50,50,50	0
57	MG	15	106	1/1	0.90	0.21	44,44,44,44	0
57	MG	15	109	1/1	0.90	0.10	62,62,62,62	0
57	MG	1A	3962	1/1	0.90	0.10	32,32,32,32	0
57	MG	1A	3255	1/1	0.90	0.28	72,72,72,72	0
57	MG	1a	1602	1/1	0.90	0.15	57,57,57,57	0
57	MG	1A	3793	1/1	0.90	0.18	70,70,70,70	0
57	MG	2A	3586	1/1	0.90	0.16	58,58,58,58	0
57	MG	1f	201	1/1	0.90	0.12	54,54,54,54	0
57	MG	1l	201	1/1	0.90	0.07	57,57,57,57	0
57	MG	1A	3058	1/1	0.90	0.13	41,41,41,41	0
57	MG	1t	201	1/1	0.90	0.17	59,59,59,59	0
57	MG	1A	3988	1/1	0.90	0.15	65,65,65,65	0
57	MG	1A	3810	1/1	0.90	0.14	47,47,47,47	0
57	MG	1A	3379	1/1	0.90	0.23	56,56,56,56	0
57	MG	1A	3814	1/1	0.90	0.13	47,47,47,47	0
57	MG	1A	3519	1/1	0.90	0.17	40,40,40,40	0
57	MG	2a	1674	1/1	0.90	0.27	69,69,69,69	0
57	MG	2a	1675	1/1	0.90	0.21	61,61,61,61	0
57	MG	1a	1629	1/1	0.90	0.14	50,50,50,50	0
57	MG	2A	3001	1/1	0.90	0.19	37,37,37,37	0
57	MG	2A	3646	1/1	0.90	0.16	59,59,59,59	0
57	MG	1A	3171	1/1	0.90	0.13	45,45,45,45	0
57	MG	1A	3400	1/1	0.90	0.09	49,49,49,49	0
57	MG	2A	3028	1/1	0.90	0.15	54,54,54,54	0
57	MG	2a	1690	1/1	0.90	0.18	63,63,63,63	0
57	MG	2A	3658	1/1	0.90	0.08	37,37,37,37	0
57	MG	2A	3031	1/1	0.90	0.14	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3670	1/1	0.90	0.20	55,55,55,55	0
57	MG	2A	3035	1/1	0.90	0.11	53,53,53,53	0
57	MG	1A	3264	1/1	0.90	0.16	44,44,44,44	0
57	MG	1A	3404	1/1	0.90	0.16	47,47,47,47	0
57	MG	2A	3296	1/1	0.90	0.13	62,62,62,62	0
57	MG	2a	1708	1/1	0.90	0.33	69,69,69,69	0
57	MG	2A	3045	1/1	0.90	0.15	58,58,58,58	0
57	MG	1A	4067	1/1	0.90	0.14	63,63,63,63	0
57	MG	1A	3277	1/1	0.90	0.17	46,46,46,46	0
57	MG	1A	3422	1/1	0.90	0.20	37,37,37,37	0
57	MG	1A	4072	1/1	0.90	0.09	49,49,49,49	0
57	MG	1A	3582	1/1	0.90	0.30	55,55,55,55	0
57	MG	1A	3584	1/1	0.90	0.14	61,61,61,61	0
57	MG	1a	1668	1/1	0.90	0.07	58,58,58,58	0
57	MG	2A	3083	1/1	0.90	0.10	52,52,52,52	0
57	MG	1a	1670	1/1	0.90	0.31	74,74,74,74	0
57	MG	2A	3087	1/1	0.90	0.08	45,45,45,45	0
57	MG	1A	3286	1/1	0.90	0.17	53,53,53,53	0
57	MG	1A	3223	1/1	0.90	0.11	48,48,48,48	0
57	MG	1a	1677	1/1	0.90	0.19	51,51,51,51	0
57	MG	2A	3726	1/1	0.90	0.11	43,43,43,43	0
57	MG	2A	3095	1/1	0.90	0.09	51,51,51,51	0
57	MG	1B	201	1/1	0.90	0.07	44,44,44,44	0
57	MG	2A	3098	1/1	0.90	0.26	67,67,67,67	0
57	MG	2A	3335	1/1	0.90	0.11	52,52,52,52	0
57	MG	1A	3598	1/1	0.90	0.12	41,41,41,41	0
57	MG	1a	1684	1/1	0.90	0.07	50,50,50,50	0
57	MG	1B	208	1/1	0.90	0.08	57,57,57,57	0
57	MG	1A	3435	1/1	0.90	0.11	48,48,48,48	0
57	MG	1a	1698	1/1	0.90	0.10	52,52,52,52	0
57	MG	1A	3876	1/1	0.90	0.17	47,47,47,47	0
57	MG	2A	3357	1/1	0.90	0.26	63,63,63,63	0
57	MG	2A	3776	1/1	0.90	0.20	65,65,65,65	0
57	MG	2A	3116	1/1	0.90	0.16	49,49,49,49	0
57	MG	1A	3600	1/1	0.90	0.21	43,43,43,43	0
57	MG	2a	1775	1/1	0.90	0.18	58,58,58,58	0
57	MG	1A	3438	1/1	0.90	0.13	63,63,63,63	0
57	MG	1A	3149	1/1	0.90	0.13	43,43,43,43	0
57	MG	2A	3791	1/1	0.90	0.08	39,39,39,39	0
57	MG	1A	3446	1/1	0.90	0.08	41,41,41,41	0
57	MG	2A	3801	1/1	0.90	0.11	40,40,40,40	0
57	MG	2A	3373	1/1	0.90	0.12	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3232	1/1	0.90	0.36	34,34,34,34	0
57	MG	1A	3304	1/1	0.90	0.22	51,51,51,51	0
57	MG	1A	3459	1/1	0.90	0.20	55,55,55,55	0
57	MG	2A	3833	1/1	0.90	0.08	47,47,47,47	0
57	MG	2A	3164	1/1	0.90	0.18	60,60,60,60	0
57	MG	1A	3463	1/1	0.90	0.32	45,45,45,45	0
57	MG	1A	3927	1/1	0.90	0.21	48,48,48,48	0
57	MG	1a	1725	1/1	0.90	0.17	61,61,61,61	0
57	MG	1A	3932	1/1	0.90	0.10	23,23,23,23	0
57	MG	2A	3846	1/1	0.90	0.07	60,60,60,60	0
57	MG	2a	1811	1/1	0.90	0.21	73,73,73,73	0
57	MG	2A	3388	1/1	0.90	0.14	55,55,55,55	0
57	MG	1A	3241	1/1	0.90	0.14	57,57,57,57	0
57	MG	2A	3396	1/1	0.90	0.17	47,47,47,47	0
57	MG	2A	3403	1/1	0.90	0.24	53,53,53,53	0
57	MG	1A	3934	1/1	0.90	0.15	58,58,58,58	0
57	MG	1a	1742	1/1	0.90	0.23	68,68,68,68	0
57	MG	2g	201	1/1	0.90	0.10	67,67,67,67	0
57	MG	2B	211	1/1	0.90	0.22	64,64,64,64	0
57	MG	2B	212	1/1	0.90	0.24	61,61,61,61	0
57	MG	2l	204	1/1	0.90	0.05	51,51,51,51	0
57	MG	2B	213	1/1	0.90	0.14	56,56,56,56	0
57	MG	1a	1747	1/1	0.90	0.09	59,59,59,59	0
57	MG	1a	1757	1/1	0.90	0.15	54,54,54,54	0
57	MG	1F	312	1/1	0.90	0.08	53,53,53,53	0
57	MG	2w	102	1/1	0.90	0.23	52,52,52,52	0
57	MG	2A	3429	1/1	0.90	0.23	51,51,51,51	0
57	MG	1A	3324	1/1	0.90	0.07	42,42,42,42	0
57	MG	1A	3479	1/1	0.90	0.23	56,56,56,56	0
57	MG	2A	3435	1/1	0.90	0.25	46,46,46,46	0
57	MG	2A	3436	1/1	0.90	0.11	49,49,49,49	0
57	MG	1A	3940	1/1	0.91	0.10	55,55,55,55	0
57	MG	1a	1735	1/1	0.91	0.11	56,56,56,56	0
57	MG	1A	3303	1/1	0.91	0.21	52,52,52,52	0
57	MG	1A	3202	1/1	0.91	0.08	26,26,26,26	0
57	MG	1O	202	1/1	0.91	0.20	52,52,52,52	0
57	MG	2A	3854	1/1	0.91	0.10	58,58,58,58	0
57	MG	2A	3166	1/1	0.91	0.15	67,67,67,67	0
57	MG	1A	3406	1/1	0.91	0.16	55,55,55,55	0
57	MG	2B	205	1/1	0.91	0.06	55,55,55,55	0
57	MG	2B	206	1/1	0.91	0.19	63,63,63,63	0
57	MG	1A	3319	1/1	0.91	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
57	MG	2A	3421	1/1	0.91	0.20	43,43,43,43	0
57	MG	1A	3520	1/1	0.91	0.26	57,57,57,57	0
57	MG	1S	201	1/1	0.91	0.08	44,44,44,44	0
57	MG	2A	3177	1/1	0.91	0.22	53,53,53,53	0
57	MG	1A	3762	1/1	0.91	0.08	24,24,24,24	0
57	MG	1A	3770	1/1	0.91	0.12	31,31,31,31	0
57	MG	10	107	1/1	0.91	0.09	50,50,50,50	0
57	MG	10	108	1/1	0.91	0.13	53,53,53,53	0
57	MG	1a	1774	1/1	0.91	0.10	36,36,36,36	0
57	MG	2A	3442	1/1	0.91	0.07	60,60,60,60	0
57	MG	2N	201	1/1	0.91	0.23	65,65,65,65	0
57	MG	10	110	1/1	0.91	0.21	66,66,66,66	0
57	MG	2A	3449	1/1	0.91	0.14	50,50,50,50	0
57	MG	2A	3452	1/1	0.91	0.44	57,57,57,57	0
57	MG	11	103	1/1	0.91	0.12	45,45,45,45	0
57	MG	2A	3455	1/1	0.91	0.11	60,60,60,60	0
57	MG	1A	3415	1/1	0.91	0.12	56,56,56,56	0
57	MG	23	101	1/1	0.91	0.15	56,56,56,56	0
57	MG	28	101	1/1	0.91	0.12	62,62,62,62	0
57	MG	2a	1602	1/1	0.91	0.17	55,55,55,55	0
57	MG	2a	1603	1/1	0.91	0.15	57,57,57,57	0
57	MG	2A	3459	1/1	0.91	0.13	58,58,58,58	0
57	MG	1A	3964	1/1	0.91	0.08	54,54,54,54	0
57	MG	1A	3531	1/1	0.91	0.09	68,68,68,68	0
57	MG	1A	3801	1/1	0.91	0.13	44,44,44,44	0
57	MG	1a	1794	1/1	0.91	0.08	77,77,77,77	0
57	MG	1A	3532	1/1	0.91	0.09	54,54,54,54	0
57	MG	2A	3208	1/1	0.91	0.17	52,52,52,52	0
57	MG	2A	3479	1/1	0.91	0.24	48,48,48,48	0
57	MG	2a	1619	1/1	0.91	0.19	64,64,64,64	0
57	MG	1A	3114	1/1	0.91	0.09	41,41,41,41	0
57	MG	18	106	1/1	0.91	0.26	47,47,47,47	0
57	MG	2A	3216	1/1	0.91	0.12	51,51,51,51	0
57	MG	2A	3488	1/1	0.91	0.09	49,49,49,49	0
57	MG	1A	3115	1/1	0.91	0.09	45,45,45,45	0
57	MG	2A	3223	1/1	0.91	0.29	52,52,52,52	0
57	MG	1A	3424	1/1	0.91	0.09	52,52,52,52	0
57	MG	2a	1630	1/1	0.91	0.20	64,64,64,64	0
57	MG	2a	1631	1/1	0.91	0.10	46,46,46,46	0
57	MG	2A	3504	1/1	0.91	0.17	61,61,61,61	0
57	MG	2A	3505	1/1	0.91	0.18	53,53,53,53	0
57	MG	1A	3996	1/1	0.91	0.08	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3516	1/1	0.91	0.20	65,65,65,65	0
57	MG	2A	3520	1/1	0.91	0.11	62,62,62,62	0
57	MG	1a	1802	1/1	0.91	0.10	54,54,54,54	0
57	MG	2A	3529	1/1	0.91	0.11	62,62,62,62	0
57	MG	1A	3999	1/1	0.91	0.10	44,44,44,44	0
57	MG	2a	1640	1/1	0.91	0.16	58,58,58,58	0
57	MG	2a	1641	1/1	0.91	0.08	59,59,59,59	0
57	MG	2A	3534	1/1	0.91	0.10	41,41,41,41	0
57	MG	2A	3536	1/1	0.91	0.08	44,44,44,44	0
57	MG	1A	3004	1/1	0.91	0.08	31,31,31,31	0
57	MG	2A	3234	1/1	0.91	0.16	57,57,57,57	0
57	MG	1A	3575	1/1	0.91	0.10	37,37,37,37	0
57	MG	2a	1651	1/1	0.91	0.20	67,67,67,67	0
57	MG	2a	1652	1/1	0.91	0.06	70,70,70,70	0
57	MG	2A	3563	1/1	0.91	0.09	38,38,38,38	0
57	MG	2a	1655	1/1	0.91	0.07	46,46,46,46	0
57	MG	2A	3565	1/1	0.91	0.08	37,37,37,37	0
57	MG	2a	1658	1/1	0.91	0.17	50,50,50,50	0
57	MG	1a	1809	1/1	0.91	0.08	65,65,65,65	0
57	MG	1A	4016	1/1	0.91	0.12	51,51,51,51	0
57	MG	1A	3329	1/1	0.91	0.12	56,56,56,56	0
57	MG	1n	102	1/1	0.91	0.17	46,46,46,46	0
57	MG	1A	3261	1/1	0.91	0.15	57,57,57,57	0
57	MG	2A	3578	1/1	0.91	0.09	49,49,49,49	0
57	MG	1A	3030	1/1	0.91	0.30	64,64,64,64	0
57	MG	1a	1633	1/1	0.91	0.13	35,35,35,35	0
57	MG	2A	3595	1/1	0.91	0.13	57,57,57,57	0
57	MG	2A	3247	1/1	0.91	0.12	48,48,48,48	0
57	MG	1a	1636	1/1	0.91	0.10	40,40,40,40	0
57	MG	1a	1637	1/1	0.91	0.22	55,55,55,55	0
57	MG	2a	1680	1/1	0.91	0.24	70,70,70,70	0
57	MG	1A	3267	1/1	0.91	0.06	53,53,53,53	0
57	MG	1x	102	1/1	0.91	0.15	58,58,58,58	0
57	MG	2A	3609	1/1	0.91	0.11	50,50,50,50	0
57	MG	1a	1644	1/1	0.91	0.12	43,43,43,43	0
57	MG	2a	1694	1/1	0.91	0.12	66,66,66,66	0
57	MG	1A	4039	1/1	0.91	0.11	63,63,63,63	0
57	MG	1A	4044	1/1	0.91	0.11	58,58,58,58	0
57	MG	2A	3623	1/1	0.91	0.10	36,36,36,36	0
57	MG	2a	1702	1/1	0.91	0.20	68,68,68,68	0
57	MG	1A	4058	1/1	0.91	0.12	42,42,42,42	0
57	MG	1A	3448	1/1	0.91	0.10	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3147	1/1	0.91	0.14	46,46,46,46	0
57	MG	2A	3029	1/1	0.91	0.10	37,37,37,37	0
57	MG	2A	3030	1/1	0.91	0.09	47,47,47,47	0
57	MG	1A	3353	1/1	0.91	0.22	35,35,35,35	0
57	MG	2a	1710	1/1	0.91	0.14	59,59,59,59	0
57	MG	1A	3361	1/1	0.91	0.18	52,52,52,52	0
57	MG	2A	3290	1/1	0.91	0.08	51,51,51,51	0
57	MG	2A	3038	1/1	0.91	0.24	66,66,66,66	0
57	MG	1A	3631	1/1	0.91	0.15	54,54,54,54	0
57	MG	1a	1666	1/1	0.91	0.22	63,63,63,63	0
57	MG	1a	1667	1/1	0.91	0.18	59,59,59,59	0
57	MG	2A	3300	1/1	0.91	0.21	64,64,64,64	0
57	MG	2A	3675	1/1	0.91	0.20	52,52,52,52	0
57	MG	2A	3047	1/1	0.91	0.10	49,49,49,49	0
57	MG	2A	3050	1/1	0.91	0.21	58,58,58,58	0
57	MG	1A	3634	1/1	0.91	0.07	39,39,39,39	0
57	MG	2A	3681	1/1	0.91	0.20	59,59,59,59	0
57	MG	2A	3304	1/1	0.91	0.17	60,60,60,60	0
57	MG	2a	1734	1/1	0.91	0.34	72,72,72,72	0
57	MG	1A	3639	1/1	0.91	0.18	56,56,56,56	0
57	MG	1A	3461	1/1	0.91	0.14	40,40,40,40	0
57	MG	2A	3059	1/1	0.91	0.16	56,56,56,56	0
57	MG	2a	1741	1/1	0.91	0.32	60,60,60,60	0
57	MG	2a	1742	1/1	0.91	0.14	57,57,57,57	0
57	MG	2A	3314	1/1	0.91	0.14	41,41,41,41	0
57	MG	2A	3693	1/1	0.91	0.07	58,58,58,58	0
57	MG	1A	3370	1/1	0.91	0.15	43,43,43,43	0
57	MG	2a	1748	1/1	0.91	0.26	68,68,68,68	0
57	MG	2A	3700	1/1	0.91	0.11	61,61,61,61	0
57	MG	2A	3316	1/1	0.91	0.09	40,40,40,40	0
57	MG	1A	3148	1/1	0.91	0.33	37,37,37,37	0
57	MG	1A	3470	1/1	0.91	0.10	45,45,45,45	0
57	MG	2A	3070	1/1	0.91	0.10	43,43,43,43	0
57	MG	1A	3890	1/1	0.91	0.12	43,43,43,43	0
57	MG	2A	3079	1/1	0.91	0.10	49,49,49,49	0
57	MG	2a	1765	1/1	0.91	0.14	58,58,58,58	0
57	MG	2a	1766	1/1	0.91	0.13	60,60,60,60	0
57	MG	1A	3055	1/1	0.91	0.09	38,38,38,38	0
57	MG	2a	1769	1/1	0.91	0.24	71,71,71,71	0
57	MG	2A	3727	1/1	0.91	0.22	51,51,51,51	0
57	MG	2A	3730	1/1	0.91	0.16	68,68,68,68	0
57	MG	1a	1686	1/1	0.91	0.18	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1782	1/1	0.91	0.13	51,51,51,51	0
57	MG	1A	3898	1/1	0.91	0.14	62,62,62,62	0
57	MG	2A	3088	1/1	0.91	0.23	63,63,63,63	0
57	MG	1a	1689	1/1	0.91	0.20	47,47,47,47	0
57	MG	1A	3665	1/1	0.91	0.09	35,35,35,35	0
57	MG	2A	3749	1/1	0.91	0.11	53,53,53,53	0
57	MG	1a	1695	1/1	0.91	0.23	59,59,59,59	0
57	MG	2a	1791	1/1	0.91	0.22	60,60,60,60	0
57	MG	2a	1794	1/1	0.91	0.24	69,69,69,69	0
57	MG	1A	3380	1/1	0.91	0.23	38,38,38,38	0
57	MG	1B	218	1/1	0.91	0.12	49,49,49,49	0
57	MG	2A	3351	1/1	0.91	0.18	55,55,55,55	0
57	MG	2a	1798	1/1	0.91	0.16	58,58,58,58	0
57	MG	2A	3353	1/1	0.91	0.07	63,63,63,63	0
57	MG	1a	1705	1/1	0.91	0.14	50,50,50,50	0
57	MG	1A	3480	1/1	0.91	0.08	37,37,37,37	0
57	MG	2a	1804	1/1	0.91	0.09	64,64,64,64	0
57	MG	2A	3779	1/1	0.91	0.11	56,56,56,56	0
57	MG	2A	3782	1/1	0.91	0.20	54,54,54,54	0
57	MG	1A	3690	1/1	0.91	0.06	45,45,45,45	0
57	MG	1a	1710	1/1	0.91	0.23	41,41,41,41	0
57	MG	2A	3361	1/1	0.91	0.16	52,52,52,52	0
57	MG	2A	3364	1/1	0.91	0.20	51,51,51,51	0
57	MG	2a	1817	1/1	0.91	0.12	55,55,55,55	0
57	MG	1A	3923	1/1	0.91	0.09	42,42,42,42	0
57	MG	2A	3793	1/1	0.91	0.10	54,54,54,54	0
57	MG	2A	3108	1/1	0.91	0.11	52,52,52,52	0
57	MG	2A	3798	1/1	0.91	0.17	43,43,43,43	0
57	MG	2e	201	1/1	0.91	0.07	82,82,82,82	0
57	MG	2A	3800	1/1	0.91	0.11	63,63,63,63	0
57	MG	1a	1714	1/1	0.91	0.12	48,48,48,48	0
57	MG	2A	3802	1/1	0.91	0.07	28,28,28,28	0
57	MG	2l	201	1/1	0.91	0.11	58,58,58,58	0
57	MG	2A	3817	1/1	0.91	0.10	46,46,46,46	0
57	MG	1A	3383	1/1	0.91	0.22	66,66,66,66	0
57	MG	2A	3113	1/1	0.91	0.16	47,47,47,47	0
57	MG	2A	3115	1/1	0.91	0.11	49,49,49,49	0
57	MG	1A	3388	1/1	0.91	0.20	42,42,42,42	0
57	MG	1A	3706	1/1	0.91	0.15	25,25,25,25	0
57	MG	2w	104	1/1	0.91	0.09	89,89,89,89	0
57	MG	2A	3122	1/1	0.91	0.25	46,46,46,46	0
57	MG	1A	3708	1/1	0.91	0.08	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3248	1/1	0.91	0.14	47,47,47,47	0
57	MG	1A	3201	1/1	0.91	0.07	32,32,32,32	0
57	MG	2x	104	1/1	0.91	0.28	65,65,65,65	0
57	MG	2x	105	1/1	0.91	0.17	60,60,60,60	0
57	MG	2A	3841	1/1	0.91	0.13	65,65,65,65	0
58	K	1A	3546	1/1	0.91	0.20	73,73,73,73	0
58	K	2A	3445	1/1	0.91	0.08	64,64,64,64	0
57	MG	2B	202	1/1	0.92	0.08	55,55,55,55	0
57	MG	2A	3399	1/1	0.92	0.15	45,45,45,45	0
57	MG	1B	206	1/1	0.92	0.07	56,56,56,56	0
57	MG	1A	3565	1/1	0.92	0.14	42,42,42,42	0
57	MG	2A	3414	1/1	0.92	0.25	53,53,53,53	0
57	MG	2B	207	1/1	0.92	0.15	68,68,68,68	0
57	MG	1A	3338	1/1	0.92	0.10	42,42,42,42	0
57	MG	1A	3339	1/1	0.92	0.08	40,40,40,40	0
57	MG	2A	3139	1/1	0.92	0.10	56,56,56,56	0
57	MG	2A	3147	1/1	0.92	0.19	53,53,53,53	0
57	MG	2A	3148	1/1	0.92	0.16	46,46,46,46	0
57	MG	2A	3428	1/1	0.92	0.29	62,62,62,62	0
57	MG	1A	3124	1/1	0.92	0.10	41,41,41,41	0
57	MG	2B	218	1/1	0.92	0.16	67,67,67,67	0
57	MG	1A	3854	1/1	0.92	0.10	47,47,47,47	0
57	MG	1A	3581	1/1	0.92	0.16	57,57,57,57	0
57	MG	2D	306	1/1	0.92	0.09	63,63,63,63	0
57	MG	2E	304	1/1	0.92	0.20	43,43,43,43	0
57	MG	2E	305	1/1	0.92	0.08	44,44,44,44	0
57	MG	1A	3341	1/1	0.92	0.14	40,40,40,40	0
57	MG	2F	301	1/1	0.92	0.07	54,54,54,54	0
57	MG	2A	3160	1/1	0.92	0.14	53,53,53,53	0
57	MG	1A	3436	1/1	0.92	0.11	41,41,41,41	0
57	MG	2O	201	1/1	0.92	0.16	64,64,64,64	0
57	MG	2O	202	1/1	0.92	0.14	58,58,58,58	0
57	MG	2A	3441	1/1	0.92	0.16	61,61,61,61	0
57	MG	1B	228	1/1	0.92	0.09	55,55,55,55	0
57	MG	1A	3299	1/1	0.92	0.26	64,64,64,64	0
57	MG	2W	201	1/1	0.92	0.14	48,48,48,48	0
57	MG	1a	1730	1/1	0.92	0.08	46,46,46,46	0
57	MG	1A	3586	1/1	0.92	0.21	50,50,50,50	0
57	MG	2A	3171	1/1	0.92	0.11	54,54,54,54	0
57	MG	1A	3587	1/1	0.92	0.17	50,50,50,50	0
57	MG	27	102	1/1	0.92	0.10	53,53,53,53	0
57	MG	27	103	1/1	0.92	0.42	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3588	1/1	0.92	0.19	45,45,45,45	0
57	MG	1A	3074	1/1	0.92	0.22	57,57,57,57	0
57	MG	2A	3178	1/1	0.92	0.13	50,50,50,50	0
57	MG	2A	3465	1/1	0.92	0.10	40,40,40,40	0
57	MG	1A	3354	1/1	0.92	0.17	39,39,39,39	0
57	MG	1A	3002	1/1	0.92	0.09	47,47,47,47	0
57	MG	2a	1607	1/1	0.92	0.15	59,59,59,59	0
57	MG	2A	3182	1/1	0.92	0.21	56,56,56,56	0
57	MG	1A	3887	1/1	0.92	0.07	38,38,38,38	0
57	MG	2A	3185	1/1	0.92	0.21	57,57,57,57	0
57	MG	2A	3186	1/1	0.92	0.09	58,58,58,58	0
57	MG	2a	1615	1/1	0.92	0.11	58,58,58,58	0
57	MG	1a	1758	1/1	0.92	0.16	58,58,58,58	0
57	MG	1A	3362	1/1	0.92	0.37	53,53,53,53	0
57	MG	2a	1620	1/1	0.92	0.15	65,65,65,65	0
57	MG	1A	3603	1/1	0.92	0.42	66,66,66,66	0
57	MG	1A	3611	1/1	0.92	0.09	49,49,49,49	0
57	MG	2A	3490	1/1	0.92	0.07	43,43,43,43	0
57	MG	1A	3626	1/1	0.92	0.12	56,56,56,56	0
57	MG	2A	3198	1/1	0.92	0.11	46,46,46,46	0
57	MG	2A	3496	1/1	0.92	0.18	44,44,44,44	0
57	MG	2A	3498	1/1	0.92	0.09	71,71,71,71	0
57	MG	1P	205	1/1	0.92	0.15	54,54,54,54	0
57	MG	1A	3907	1/1	0.92	0.09	24,24,24,24	0
57	MG	1A	3456	1/1	0.92	0.08	51,51,51,51	0
57	MG	1A	3915	1/1	0.92	0.09	60,60,60,60	0
57	MG	1R	206	1/1	0.92	0.07	32,32,32,32	0
57	MG	1a	1779	1/1	0.92	0.18	63,63,63,63	0
57	MG	1A	3366	1/1	0.92	0.06	32,32,32,32	0
57	MG	2A	3214	1/1	0.92	0.13	41,41,41,41	0
57	MG	1a	1783	1/1	0.92	0.12	47,47,47,47	0
57	MG	2A	3533	1/1	0.92	0.12	44,44,44,44	0
57	MG	1A	3001	1/1	0.92	0.07	39,39,39,39	0
57	MG	2A	3218	1/1	0.92	0.12	56,56,56,56	0
57	MG	2A	3541	1/1	0.92	0.14	44,44,44,44	0
57	MG	2a	1644	1/1	0.92	0.07	63,63,63,63	0
57	MG	1X	106	1/1	0.92	0.08	53,53,53,53	0
57	MG	1a	1792	1/1	0.92	0.15	74,74,74,74	0
57	MG	1A	3041	1/1	0.92	0.13	49,49,49,49	0
57	MG	10	104	1/1	0.92	0.12	61,61,61,61	0
57	MG	2a	1650	1/1	0.92	0.13	73,73,73,73	0
57	MG	2A	3229	1/1	0.92	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	10	106	1/1	0.92	0.09	45,45,45,45	0
57	MG	1A	3372	1/1	0.92	0.10	50,50,50,50	0
57	MG	1A	3260	1/1	0.92	0.11	51,51,51,51	0
57	MG	1A	3305	1/1	0.92	0.23	58,58,58,58	0
57	MG	1A	3307	1/1	0.92	0.13	43,43,43,43	0
57	MG	1A	3661	1/1	0.92	0.12	42,42,42,42	0
57	MG	1A	3662	1/1	0.92	0.08	46,46,46,46	0
57	MG	1A	3475	1/1	0.92	0.24	42,42,42,42	0
57	MG	1A	3477	1/1	0.92	0.09	40,40,40,40	0
57	MG	1A	3067	1/1	0.92	0.08	30,30,30,30	0
57	MG	2a	1669	1/1	0.92	0.23	54,54,54,54	0
57	MG	1b	301	1/1	0.92	0.14	70,70,70,70	0
57	MG	17	105	1/1	0.92	0.26	55,55,55,55	0
57	MG	18	104	1/1	0.92	0.18	58,58,58,58	0
57	MG	1A	3389	1/1	0.92	0.13	54,54,54,54	0
57	MG	2A	3605	1/1	0.92	0.07	68,68,68,68	0
57	MG	1A	3263	1/1	0.92	0.08	44,44,44,44	0
57	MG	2A	3610	1/1	0.92	0.09	46,46,46,46	0
57	MG	1A	3951	1/1	0.92	0.07	29,29,29,29	0
57	MG	1A	3397	1/1	0.92	0.22	60,60,60,60	0
57	MG	2A	3618	1/1	0.92	0.09	41,41,41,41	0
57	MG	1a	1613	1/1	0.92	0.20	48,48,48,48	0
57	MG	1A	3068	1/1	0.92	0.23	51,51,51,51	0
57	MG	2a	1691	1/1	0.92	0.15	52,52,52,52	0
57	MG	2A	3636	1/1	0.92	0.09	38,38,38,38	0
57	MG	1A	3166	1/1	0.92	0.12	41,41,41,41	0
57	MG	1x	101	1/1	0.92	0.27	65,65,65,65	0
57	MG	1A	3710	1/1	0.92	0.09	21,21,21,21	0
57	MG	2A	3267	1/1	0.92	0.12	52,52,52,52	0
57	MG	2A	3269	1/1	0.92	0.22	61,61,61,61	0
57	MG	2a	1704	1/1	0.92	0.10	80,80,80,80	0
57	MG	1A	3713	1/1	0.92	0.10	40,40,40,40	0
57	MG	2A	3274	1/1	0.92	0.09	80,80,80,80	0
57	MG	1A	3327	1/1	0.92	0.10	32,32,32,32	0
57	MG	2A	3662	1/1	0.92	0.13	73,73,73,73	0
57	MG	1x	112	1/1	0.92	0.24	54,54,54,54	0
57	MG	1A	3506	1/1	0.92	0.09	65,65,65,65	0
57	MG	2A	3284	1/1	0.92	0.22	67,67,67,67	0
57	MG	2A	3285	1/1	0.92	0.20	51,51,51,51	0
57	MG	2A	3287	1/1	0.92	0.11	52,52,52,52	0
57	MG	2A	3003	1/1	0.92	0.28	59,59,59,59	0
57	MG	2A	3005	1/1	0.92	0.16	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3015	1/1	0.92	0.26	54,54,54,54	0
57	MG	1A	3719	1/1	0.92	0.09	21,21,21,21	0
57	MG	1A	3328	1/1	0.92	0.19	58,58,58,58	0
57	MG	2A	3298	1/1	0.92	0.16	64,64,64,64	0
57	MG	2A	3683	1/1	0.92	0.13	32,32,32,32	0
57	MG	2A	3023	1/1	0.92	0.20	53,53,53,53	0
57	MG	2A	3685	1/1	0.92	0.14	45,45,45,45	0
57	MG	2A	3686	1/1	0.92	0.15	77,77,77,77	0
57	MG	2A	3688	1/1	0.92	0.20	53,53,53,53	0
57	MG	1A	3409	1/1	0.92	0.23	43,43,43,43	0
57	MG	1A	3410	1/1	0.92	0.08	43,43,43,43	0
57	MG	1A	3249	1/1	0.92	0.09	49,49,49,49	0
57	MG	2a	1739	1/1	0.92	0.24	74,74,74,74	0
57	MG	1A	3280	1/1	0.92	0.13	49,49,49,49	0
57	MG	1A	3528	1/1	0.92	0.12	54,54,54,54	0
57	MG	1a	1646	1/1	0.92	0.16	55,55,55,55	0
57	MG	2A	3705	1/1	0.92	0.09	49,49,49,49	0
57	MG	1A	4002	1/1	0.92	0.07	67,67,67,67	0
57	MG	2A	3711	1/1	0.92	0.13	45,45,45,45	0
57	MG	2A	3307	1/1	0.92	0.17	39,39,39,39	0
57	MG	2a	1752	1/1	0.92	0.06	65,65,65,65	0
57	MG	2a	1753	1/1	0.92	0.18	62,62,62,62	0
57	MG	1A	4005	1/1	0.92	0.08	56,56,56,56	0
57	MG	2A	3310	1/1	0.92	0.12	70,70,70,70	0
57	MG	1A	3766	1/1	0.92	0.12	37,37,37,37	0
57	MG	1a	1653	1/1	0.92	0.16	48,48,48,48	0
57	MG	2A	3723	1/1	0.92	0.08	53,53,53,53	0
57	MG	2A	3048	1/1	0.92	0.13	31,31,31,31	0
57	MG	2A	3049	1/1	0.92	0.15	40,40,40,40	0
57	MG	1A	4010	1/1	0.92	0.16	51,51,51,51	0
57	MG	1A	4012	1/1	0.92	0.13	48,48,48,48	0
57	MG	2A	3053	1/1	0.92	0.25	62,62,62,62	0
57	MG	1a	1657	1/1	0.92	0.08	53,53,53,53	0
57	MG	2a	1772	1/1	0.92	0.07	52,52,52,52	0
57	MG	2A	3740	1/1	0.92	0.15	46,46,46,46	0
57	MG	2A	3056	1/1	0.92	0.13	55,55,55,55	0
57	MG	2a	1779	1/1	0.92	0.17	55,55,55,55	0
57	MG	2A	3744	1/1	0.92	0.12	67,67,67,67	0
57	MG	2A	3328	1/1	0.92	0.16	81,81,81,81	0
57	MG	1A	3416	1/1	0.92	0.10	64,64,64,64	0
57	MG	2A	3750	1/1	0.92	0.14	47,47,47,47	0
57	MG	2A	3058	1/1	0.92	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
57	MG	1A	3417	1/1	0.92	0.10	44,44,44,44	0
57	MG	2A	3758	1/1	0.92	0.19	57,57,57,57	0
57	MG	2a	1790	1/1	0.92	0.17	60,60,60,60	0
57	MG	2A	3761	1/1	0.92	0.10	50,50,50,50	0
57	MG	1A	3418	1/1	0.92	0.11	50,50,50,50	0
57	MG	2A	3768	1/1	0.92	0.23	60,60,60,60	0
57	MG	1A	3534	1/1	0.92	0.29	32,32,32,32	0
57	MG	1A	3803	1/1	0.92	0.07	59,59,59,59	0
57	MG	2A	3774	1/1	0.92	0.14	59,59,59,59	0
57	MG	2a	1799	1/1	0.92	0.27	59,59,59,59	0
57	MG	2A	3341	1/1	0.92	0.11	55,55,55,55	0
57	MG	1A	3536	1/1	0.92	0.29	55,55,55,55	0
57	MG	1A	3540	1/1	0.92	0.10	29,29,29,29	0
57	MG	2A	3074	1/1	0.92	0.10	43,43,43,43	0
57	MG	2A	3078	1/1	0.92	0.19	55,55,55,55	0
57	MG	2a	1807	1/1	0.92	0.09	59,59,59,59	0
57	MG	2A	3354	1/1	0.92	0.08	40,40,40,40	0
57	MG	1a	1671	1/1	0.92	0.18	53,53,53,53	0
57	MG	1A	3811	1/1	0.92	0.08	46,46,46,46	0
57	MG	1a	1674	1/1	0.92	0.20	45,45,45,45	0
57	MG	1A	3421	1/1	0.92	0.20	41,41,41,41	0
57	MG	2a	1816	1/1	0.92	0.15	43,43,43,43	0
57	MG	1A	3548	1/1	0.92	0.09	44,44,44,44	0
57	MG	1A	3816	1/1	0.92	0.09	40,40,40,40	0
57	MG	2a	1820	1/1	0.92	0.13	55,55,55,55	0
57	MG	1a	1680	1/1	0.92	0.10	60,60,60,60	0
57	MG	1a	1681	1/1	0.92	0.17	51,51,51,51	0
57	MG	2d	301	1/1	0.92	0.17	53,53,53,53	0
57	MG	1A	4071	1/1	0.92	0.07	46,46,46,46	0
57	MG	2A	3807	1/1	0.92	0.10	52,52,52,52	0
57	MG	2A	3814	1/1	0.92	0.16	58,58,58,58	0
57	MG	2A	3816	1/1	0.92	0.08	54,54,54,54	0
57	MG	2A	3368	1/1	0.92	0.09	45,45,45,45	0
57	MG	1A	3817	1/1	0.92	0.43	41,41,41,41	0
57	MG	2l	202	1/1	0.92	0.18	69,69,69,69	0
57	MG	1A	3827	1/1	0.92	0.19	52,52,52,52	0
57	MG	2q	201	1/1	0.92	0.20	66,66,66,66	0
57	MG	2A	3374	1/1	0.92	0.17	58,58,58,58	0
57	MG	2r	101	1/1	0.92	0.08	61,61,61,61	0
57	MG	2t	201	1/1	0.92	0.15	48,48,48,48	0
57	MG	1A	4076	1/1	0.92	0.14	57,57,57,57	0
57	MG	1A	4079	1/1	0.92	0.15	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1691	1/1	0.92	0.23	53,53,53,53	0
57	MG	2A	3104	1/1	0.92	0.15	47,47,47,47	0
57	MG	1a	1693	1/1	0.92	0.25	50,50,50,50	0
57	MG	1A	3549	1/1	0.92	0.20	55,55,55,55	0
57	MG	1A	3281	1/1	0.92	0.13	48,48,48,48	0
57	MG	1A	3836	1/1	0.92	0.15	45,45,45,45	0
57	MG	1A	4085	1/1	0.92	0.26	42,42,42,42	0
57	MG	1A	3556	1/1	0.92	0.08	50,50,50,50	0
57	MG	2A	3390	1/1	0.92	0.06	51,51,51,51	0
57	MG	2A	3395	1/1	0.92	0.15	45,45,45,45	0
57	MG	2A	3853	1/1	0.92	0.26	62,62,62,62	0
57	MG	1A	3838	1/1	0.92	0.10	29,29,29,29	0
57	MG	27	101	1/1	0.93	0.10	48,48,48,48	0
57	MG	1a	1687	1/1	0.93	0.28	49,49,49,49	0
57	MG	2A	3568	1/1	0.93	0.10	40,40,40,40	0
57	MG	1B	229	1/1	0.93	0.17	56,56,56,56	0
57	MG	1A	3236	1/1	0.93	0.08	32,32,32,32	0
57	MG	2A	3574	1/1	0.93	0.12	44,44,44,44	0
57	MG	1A	3440	1/1	0.93	0.14	55,55,55,55	0
57	MG	2A	3063	1/1	0.93	0.21	56,56,56,56	0
57	MG	2A	3291	1/1	0.93	0.21	59,59,59,59	0
57	MG	2A	3582	1/1	0.93	0.07	38,38,38,38	0
57	MG	1A	3368	1/1	0.93	0.10	52,52,52,52	0
57	MG	1A	3083	1/1	0.93	0.19	25,25,25,25	0
57	MG	2A	3587	1/1	0.93	0.10	55,55,55,55	0
57	MG	2A	3068	1/1	0.93	0.29	60,60,60,60	0
57	MG	1A	3120	1/1	0.93	0.09	40,40,40,40	0
57	MG	1A	3450	1/1	0.93	0.06	28,28,28,28	0
57	MG	2A	3072	1/1	0.93	0.08	57,57,57,57	0
57	MG	1E	311	1/1	0.93	0.12	45,45,45,45	0
57	MG	1E	312	1/1	0.93	0.04	46,46,46,46	0
57	MG	1A	3732	1/1	0.93	0.10	60,60,60,60	0
57	MG	2A	3607	1/1	0.93	0.07	33,33,33,33	0
57	MG	1F	305	1/1	0.93	0.08	34,34,34,34	0
57	MG	1A	3121	1/1	0.93	0.11	37,37,37,37	0
57	MG	1a	1711	1/1	0.93	0.14	54,54,54,54	0
57	MG	1A	3745	1/1	0.93	0.08	19,19,19,19	0
57	MG	1A	3748	1/1	0.93	0.07	17,17,17,17	0
57	MG	1N	201	1/1	0.93	0.07	47,47,47,47	0
57	MG	2A	3622	1/1	0.93	0.16	44,44,44,44	0
57	MG	1N	204	1/1	0.93	0.13	53,53,53,53	0
57	MG	2A	3626	1/1	0.93	0.09	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1718	1/1	0.93	0.22	60,60,60,60	0
57	MG	1A	3373	1/1	0.93	0.10	52,52,52,52	0
57	MG	2A	3638	1/1	0.93	0.08	46,46,46,46	0
57	MG	2A	3639	1/1	0.93	0.08	47,47,47,47	0
57	MG	2A	3317	1/1	0.93	0.10	48,48,48,48	0
57	MG	1A	3759	1/1	0.93	0.09	49,49,49,49	0
57	MG	1A	3183	1/1	0.93	0.09	41,41,41,41	0
57	MG	2A	3647	1/1	0.93	0.11	40,40,40,40	0
57	MG	2A	3100	1/1	0.93	0.13	34,34,34,34	0
57	MG	2A	3652	1/1	0.93	0.15	49,49,49,49	0
57	MG	1P	206	1/1	0.93	0.13	48,48,48,48	0
57	MG	1A	3190	1/1	0.93	0.15	25,25,25,25	0
57	MG	2A	3657	1/1	0.93	0.12	58,58,58,58	0
57	MG	1a	1729	1/1	0.93	0.10	58,58,58,58	0
57	MG	2A	3661	1/1	0.93	0.11	56,56,56,56	0
57	MG	2A	3106	1/1	0.93	0.18	48,48,48,48	0
57	MG	1A	3950	1/1	0.93	0.15	42,42,42,42	0
57	MG	2A	3330	1/1	0.93	0.08	55,55,55,55	0
57	MG	1a	1732	1/1	0.93	0.12	40,40,40,40	0
57	MG	1a	1734	1/1	0.93	0.08	46,46,46,46	0
57	MG	1A	3769	1/1	0.93	0.08	24,24,24,24	0
57	MG	2A	3336	1/1	0.93	0.21	58,58,58,58	0
57	MG	2A	3337	1/1	0.93	0.10	48,48,48,48	0
57	MG	1A	3382	1/1	0.93	0.06	52,52,52,52	0
57	MG	1A	3956	1/1	0.93	0.08	45,45,45,45	0
57	MG	1A	3084	1/1	0.93	0.09	33,33,33,33	0
57	MG	2a	1670	1/1	0.93	0.19	58,58,58,58	0
57	MG	1a	1739	1/1	0.93	0.16	54,54,54,54	0
57	MG	2A	3345	1/1	0.93	0.13	39,39,39,39	0
57	MG	1U	203	1/1	0.93	0.19	63,63,63,63	0
57	MG	2A	3123	1/1	0.93	0.07	74,74,74,74	0
57	MG	1U	206	1/1	0.93	0.15	48,48,48,48	0
57	MG	2A	3135	1/1	0.93	0.15	39,39,39,39	0
57	MG	1a	1752	1/1	0.93	0.10	56,56,56,56	0
57	MG	1a	1754	1/1	0.93	0.11	38,38,38,38	0
57	MG	1a	1756	1/1	0.93	0.20	57,57,57,57	0
57	MG	1U	209	1/1	0.93	0.17	38,38,38,38	0
57	MG	2a	1687	1/1	0.93	0.23	57,57,57,57	0
57	MG	2A	3694	1/1	0.93	0.06	41,41,41,41	0
57	MG	1U	210	1/1	0.93	0.08	37,37,37,37	0
57	MG	2A	3151	1/1	0.93	0.13	59,59,59,59	0
57	MG	2A	3703	1/1	0.93	0.10	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1V	206	1/1	0.93	0.10	39,39,39,39	0
57	MG	1A	3059	1/1	0.93	0.17	51,51,51,51	0
57	MG	1A	3961	1/1	0.93	0.07	49,49,49,49	0
57	MG	2a	1698	1/1	0.93	0.07	74,74,74,74	0
57	MG	2a	1700	1/1	0.93	0.23	60,60,60,60	0
57	MG	1Z	301	1/1	0.93	0.12	46,46,46,46	0
57	MG	2A	3370	1/1	0.93	0.15	66,66,66,66	0
57	MG	2A	3371	1/1	0.93	0.09	57,57,57,57	0
57	MG	2A	3163	1/1	0.93	0.12	39,39,39,39	0
57	MG	2A	3721	1/1	0.93	0.14	48,48,48,48	0
57	MG	1A	3796	1/1	0.93	0.15	45,45,45,45	0
57	MG	1a	1773	1/1	0.93	0.12	53,53,53,53	0
57	MG	1A	3800	1/1	0.93	0.08	21,21,21,21	0
57	MG	1A	3469	1/1	0.93	0.07	47,47,47,47	0
57	MG	2A	3377	1/1	0.93	0.14	53,53,53,53	0
57	MG	2A	3169	1/1	0.93	0.12	49,49,49,49	0
57	MG	1a	1776	1/1	0.93	0.09	67,67,67,67	0
57	MG	1A	3308	1/1	0.93	0.25	52,52,52,52	0
57	MG	1A	3981	1/1	0.93	0.07	27,27,27,27	0
57	MG	1A	3312	1/1	0.93	0.07	41,41,41,41	0
57	MG	1A	3020	1/1	0.93	0.14	43,43,43,43	0
57	MG	1A	3320	1/1	0.93	0.10	57,57,57,57	0
57	MG	1A	3401	1/1	0.93	0.08	38,38,38,38	0
57	MG	15	107	1/1	0.93	0.07	30,30,30,30	0
57	MG	2A	3391	1/1	0.93	0.13	51,51,51,51	0
57	MG	1A	3097	1/1	0.93	0.18	41,41,41,41	0
57	MG	1A	3045	1/1	0.93	0.16	51,51,51,51	0
57	MG	2A	3759	1/1	0.93	0.08	63,63,63,63	0
57	MG	1A	3111	1/1	0.93	0.08	30,30,30,30	0
57	MG	18	102	1/1	0.93	0.16	34,34,34,34	0
57	MG	2A	3406	1/1	0.93	0.11	44,44,44,44	0
57	MG	2A	3769	1/1	0.93	0.10	45,45,45,45	0
57	MG	1A	3617	1/1	0.93	0.17	54,54,54,54	0
57	MG	2A	3411	1/1	0.93	0.19	56,56,56,56	0
57	MG	1A	4003	1/1	0.93	0.09	48,48,48,48	0
57	MG	2A	3415	1/1	0.93	0.23	47,47,47,47	0
57	MG	1A	3618	1/1	0.93	0.14	36,36,36,36	0
57	MG	2a	1747	1/1	0.93	0.26	63,63,63,63	0
57	MG	2A	3778	1/1	0.93	0.12	52,52,52,52	0
57	MG	2A	3192	1/1	0.93	0.47	65,65,65,65	0
57	MG	1A	3205	1/1	0.93	0.09	51,51,51,51	0
57	MG	2A	3783	1/1	0.93	0.10	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3835	1/1	0.93	0.09	56,56,56,56	0
57	MG	1A	3155	1/1	0.93	0.38	36,36,36,36	0
57	MG	2A	3427	1/1	0.93	0.23	54,54,54,54	0
57	MG	2A	3788	1/1	0.93	0.14	41,41,41,41	0
57	MG	1A	3503	1/1	0.93	0.20	55,55,55,55	0
57	MG	1A	3635	1/1	0.93	0.06	39,39,39,39	0
57	MG	1A	3411	1/1	0.93	0.10	27,27,27,27	0
57	MG	1A	3215	1/1	0.93	0.14	40,40,40,40	0
57	MG	1A	3266	1/1	0.93	0.11	45,45,45,45	0
57	MG	1j	201	1/1	0.93	0.30	58,58,58,58	0
57	MG	1A	4031	1/1	0.93	0.06	45,45,45,45	0
57	MG	1A	3644	1/1	0.93	0.10	43,43,43,43	0
57	MG	2A	3803	1/1	0.93	0.12	43,43,43,43	0
57	MG	1A	3851	1/1	0.93	0.08	22,22,22,22	0
57	MG	2A	3813	1/1	0.93	0.14	49,49,49,49	0
57	MG	2a	1780	1/1	0.93	0.19	55,55,55,55	0
57	MG	1a	1632	1/1	0.93	0.13	51,51,51,51	0
57	MG	1A	4057	1/1	0.93	0.07	43,43,43,43	0
57	MG	1A	3508	1/1	0.93	0.13	49,49,49,49	0
57	MG	1A	4059	1/1	0.93	0.07	38,38,38,38	0
57	MG	2A	3825	1/1	0.93	0.08	61,61,61,61	0
57	MG	1A	4065	1/1	0.93	0.24	54,54,54,54	0
57	MG	1w	105	1/1	0.93	0.07	54,54,54,54	0
57	MG	1a	1643	1/1	0.93	0.12	38,38,38,38	0
57	MG	1A	3857	1/1	0.93	0.10	34,34,34,34	0
57	MG	2a	1793	1/1	0.93	0.11	51,51,51,51	0
57	MG	1A	4068	1/1	0.93	0.19	61,61,61,61	0
57	MG	1A	3649	1/1	0.93	0.16	39,39,39,39	0
57	MG	1A	3861	1/1	0.93	0.09	45,45,45,45	0
57	MG	1A	3652	1/1	0.93	0.10	39,39,39,39	0
57	MG	2A	3002	1/1	0.93	0.25	46,46,46,46	0
57	MG	1A	3866	1/1	0.93	0.14	43,43,43,43	0
57	MG	2A	3474	1/1	0.93	0.24	42,42,42,42	0
57	MG	2A	3475	1/1	0.93	0.30	51,51,51,51	0
57	MG	2A	3477	1/1	0.93	0.26	53,53,53,53	0
57	MG	2A	3478	1/1	0.93	0.14	51,51,51,51	0
57	MG	1A	3510	1/1	0.93	0.28	43,43,43,43	0
57	MG	2A	3480	1/1	0.93	0.08	53,53,53,53	0
57	MG	2A	3481	1/1	0.93	0.16	61,61,61,61	0
57	MG	1A	3220	1/1	0.93	0.08	38,38,38,38	0
57	MG	1A	3157	1/1	0.93	0.09	41,41,41,41	0
57	MG	1A	3077	1/1	0.93	0.23	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3243	1/1	0.93	0.07	51,51,51,51	0
57	MG	2A	3244	1/1	0.93	0.08	39,39,39,39	0
57	MG	1A	3524	1/1	0.93	0.07	29,29,29,29	0
57	MG	1A	3525	1/1	0.93	0.22	48,48,48,48	0
57	MG	2a	1819	1/1	0.93	0.10	56,56,56,56	0
57	MG	2A	3249	1/1	0.93	0.07	46,46,46,46	0
57	MG	2A	3250	1/1	0.93	0.06	53,53,53,53	0
57	MG	1A	3881	1/1	0.93	0.12	47,47,47,47	0
57	MG	2A	3502	1/1	0.93	0.13	60,60,60,60	0
57	MG	2B	216	1/1	0.93	0.09	54,54,54,54	0
57	MG	1A	3671	1/1	0.93	0.13	32,32,32,32	0
57	MG	1A	3673	1/1	0.93	0.06	21,21,21,21	0
57	MG	2A	3507	1/1	0.93	0.11	35,35,35,35	0
57	MG	1A	3230	1/1	0.93	0.14	48,48,48,48	0
57	MG	2D	301	1/1	0.93	0.15	53,53,53,53	0
57	MG	1A	3282	1/1	0.93	0.09	49,49,49,49	0
57	MG	2E	302	1/1	0.93	0.06	43,43,43,43	0
57	MG	2E	303	1/1	0.93	0.16	52,52,52,52	0
57	MG	1A	3283	1/1	0.93	0.19	34,34,34,34	0
57	MG	2A	3524	1/1	0.93	0.08	52,52,52,52	0
57	MG	1a	1673	1/1	0.93	0.19	52,52,52,52	0
57	MG	1A	3162	1/1	0.93	0.18	50,50,50,50	0
57	MG	1A	3292	1/1	0.93	0.17	41,41,41,41	0
57	MG	1B	212	1/1	0.93	0.10	43,43,43,43	0
57	MG	2A	3268	1/1	0.93	0.17	76,76,76,76	0
57	MG	2w	103	1/1	0.93	0.06	77,77,77,77	0
57	MG	1A	3904	1/1	0.93	0.29	34,34,34,34	0
57	MG	1A	3297	1/1	0.93	0.16	41,41,41,41	0
57	MG	1A	3909	1/1	0.93	0.15	44,44,44,44	0
57	MG	1B	224	1/1	0.93	0.05	36,36,36,36	0
57	MG	2A	3551	1/1	0.93	0.13	42,42,42,42	0
57	MG	2A	3553	1/1	0.93	0.14	42,42,42,42	0
57	MG	1A	3298	1/1	0.93	0.06	29,29,29,29	0
57	MG	2x	106	1/1	0.93	0.09	43,43,43,43	0
57	MG	1A	3437	1/1	0.93	0.16	48,48,48,48	0
57	MG	20	102	1/1	0.93	0.09	51,51,51,51	0
57	MG	2A	3282	1/1	0.93	0.07	50,50,50,50	0
59	ERY	2A	3857	51/51	0.93	0.13	26,54,66,69	0
57	MG	2A	3205	1/1	0.94	0.08	59,59,59,59	0
57	MG	2B	209	1/1	0.94	0.08	65,65,65,65	0
57	MG	2B	210	1/1	0.94	0.19	55,55,55,55	0
57	MG	1A	3765	1/1	0.94	0.10	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3473	1/1	0.94	0.06	58,58,58,58	0
57	MG	1A	3562	1/1	0.94	0.13	36,36,36,36	0
57	MG	1a	1785	1/1	0.94	0.14	37,37,37,37	0
57	MG	1A	3564	1/1	0.94	0.15	43,43,43,43	0
57	MG	1A	3345	1/1	0.94	0.12	61,61,61,61	0
57	MG	1A	3772	1/1	0.94	0.09	38,38,38,38	0
57	MG	2A	3217	1/1	0.94	0.28	40,40,40,40	0
57	MG	1A	3346	1/1	0.94	0.05	34,34,34,34	0
57	MG	2A	3482	1/1	0.94	0.18	42,42,42,42	0
57	MG	1A	3570	1/1	0.94	0.09	31,31,31,31	0
57	MG	1A	3572	1/1	0.94	0.07	48,48,48,48	0
57	MG	15	108	1/1	0.94	0.08	49,49,49,49	0
57	MG	1A	3218	1/1	0.94	0.07	47,47,47,47	0
57	MG	1A	3348	1/1	0.94	0.09	51,51,51,51	0
57	MG	2A	3492	1/1	0.94	0.06	38,38,38,38	0
57	MG	2E	306	1/1	0.94	0.08	36,36,36,36	0
57	MG	1A	3219	1/1	0.94	0.16	38,38,38,38	0
57	MG	2A	3494	1/1	0.94	0.14	47,47,47,47	0
57	MG	1A	3156	1/1	0.94	0.07	29,29,29,29	0
57	MG	1a	1805	1/1	0.94	0.12	65,65,65,65	0
57	MG	2A	3497	1/1	0.94	0.07	44,44,44,44	0
57	MG	1A	3285	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3447	1/1	0.94	0.11	47,47,47,47	0
57	MG	1a	1808	1/1	0.94	0.12	61,61,61,61	0
57	MG	1A	3024	1/1	0.94	0.15	32,32,32,32	0
57	MG	2U	202	1/1	0.94	0.05	41,41,41,41	0
57	MG	18	107	1/1	0.94	0.14	36,36,36,36	0
57	MG	1A	4019	1/1	0.94	0.10	49,49,49,49	0
57	MG	2A	3510	1/1	0.94	0.16	44,44,44,44	0
57	MG	1a	1605	1/1	0.94	0.08	63,63,63,63	0
57	MG	1A	4020	1/1	0.94	0.10	30,30,30,30	0
57	MG	20	103	1/1	0.94	0.11	65,65,65,65	0
57	MG	1a	1609	1/1	0.94	0.06	38,38,38,38	0
57	MG	25	101	1/1	0.94	0.10	51,51,51,51	0
57	MG	2A	3521	1/1	0.94	0.06	35,35,35,35	0
57	MG	2A	3523	1/1	0.94	0.10	39,39,39,39	0
57	MG	1a	1610	1/1	0.94	0.08	61,61,61,61	0
57	MG	27	104	1/1	0.94	0.18	50,50,50,50	0
57	MG	2A	3526	1/1	0.94	0.12	50,50,50,50	0
57	MG	2A	3245	1/1	0.94	0.09	55,55,55,55	0
57	MG	1a	1611	1/1	0.94	0.11	28,28,28,28	0
57	MG	1A	3363	1/1	0.94	0.21	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3248	1/1	0.94	0.09	51,51,51,51	0
57	MG	1a	1614	1/1	0.94	0.05	60,60,60,60	0
57	MG	1A	3815	1/1	0.94	0.08	59,59,59,59	0
57	MG	2a	1608	1/1	0.94	0.08	56,56,56,56	0
57	MG	2A	3537	1/1	0.94	0.12	42,42,42,42	0
57	MG	1A	4024	1/1	0.94	0.08	53,53,53,53	0
57	MG	1A	3364	1/1	0.94	0.10	41,41,41,41	0
57	MG	1A	3287	1/1	0.94	0.08	58,58,58,58	0
57	MG	1a	1624	1/1	0.94	0.21	44,44,44,44	0
57	MG	2a	1616	1/1	0.94	0.09	67,67,67,67	0
57	MG	1a	1625	1/1	0.94	0.18	43,43,43,43	0
57	MG	2A	3554	1/1	0.94	0.10	46,46,46,46	0
57	MG	2A	3259	1/1	0.94	0.08	70,70,70,70	0
57	MG	2A	3557	1/1	0.94	0.10	41,41,41,41	0
57	MG	2A	3559	1/1	0.94	0.07	32,32,32,32	0
57	MG	1a	1626	1/1	0.94	0.22	59,59,59,59	0
57	MG	1x	110	1/1	0.94	0.13	50,50,50,50	0
57	MG	1A	3819	1/1	0.94	0.08	18,18,18,18	0
57	MG	1A	4038	1/1	0.94	0.12	42,42,42,42	0
57	MG	2A	3265	1/1	0.94	0.08	58,58,58,58	0
57	MG	2a	1629	1/1	0.94	0.16	58,58,58,58	0
57	MG	2A	3570	1/1	0.94	0.07	39,39,39,39	0
57	MG	1A	3821	1/1	0.94	0.12	38,38,38,38	0
57	MG	1A	3826	1/1	0.94	0.18	48,48,48,48	0
57	MG	1a	1631	1/1	0.94	0.19	55,55,55,55	0
57	MG	2A	3271	1/1	0.94	0.10	43,43,43,43	0
57	MG	2A	3272	1/1	0.94	0.10	36,36,36,36	0
57	MG	2A	3580	1/1	0.94	0.14	48,48,48,48	0
57	MG	2A	3009	1/1	0.94	0.13	57,57,57,57	0
57	MG	1A	3592	1/1	0.94	0.13	34,34,34,34	0
57	MG	2A	3016	1/1	0.94	0.22	48,48,48,48	0
57	MG	1A	3288	1/1	0.94	0.08	47,47,47,47	0
57	MG	1A	3832	1/1	0.94	0.06	41,41,41,41	0
57	MG	2A	3280	1/1	0.94	0.13	39,39,39,39	0
57	MG	1A	4060	1/1	0.94	0.10	31,31,31,31	0
57	MG	2A	3027	1/1	0.94	0.22	51,51,51,51	0
57	MG	1A	3112	1/1	0.94	0.15	40,40,40,40	0
57	MG	1A	4066	1/1	0.94	0.14	51,51,51,51	0
57	MG	1A	3296	1/1	0.94	0.23	41,41,41,41	0
57	MG	2a	1649	1/1	0.94	0.11	70,70,70,70	0
57	MG	1A	3025	1/1	0.94	0.13	35,35,35,35	0
57	MG	1A	3604	1/1	0.94	0.11	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3037	1/1	0.94	0.09	33,33,33,33	0
57	MG	2a	1653	1/1	0.94	0.12	58,58,58,58	0
57	MG	2A	3611	1/1	0.94	0.18	41,41,41,41	0
57	MG	1A	3231	1/1	0.94	0.06	48,48,48,48	0
57	MG	1A	3612	1/1	0.94	0.10	21,21,21,21	0
57	MG	1A	3613	1/1	0.94	0.12	49,49,49,49	0
57	MG	1A	3468	1/1	0.94	0.19	45,45,45,45	0
57	MG	2A	3046	1/1	0.94	0.10	44,44,44,44	0
57	MG	1A	3377	1/1	0.94	0.27	37,37,37,37	0
57	MG	1A	4078	1/1	0.94	0.15	45,45,45,45	0
57	MG	2a	1664	1/1	0.94	0.18	44,44,44,44	0
57	MG	2A	3628	1/1	0.94	0.11	41,41,41,41	0
57	MG	2a	1667	1/1	0.94	0.30	57,57,57,57	0
57	MG	2A	3631	1/1	0.94	0.08	48,48,48,48	0
57	MG	1A	3623	1/1	0.94	0.17	16,16,16,16	0
57	MG	1A	3048	1/1	0.94	0.07	22,22,22,22	0
57	MG	1A	3627	1/1	0.94	0.12	32,32,32,32	0
57	MG	1A	3859	1/1	0.94	0.13	58,58,58,58	0
57	MG	2A	3640	1/1	0.94	0.08	57,57,57,57	0
57	MG	1A	4083	1/1	0.94	0.07	54,54,54,54	0
57	MG	2A	3308	1/1	0.94	0.08	45,45,45,45	0
57	MG	1A	4084	1/1	0.94	0.09	49,49,49,49	0
57	MG	1A	3234	1/1	0.94	0.19	53,53,53,53	0
57	MG	2A	3311	1/1	0.94	0.10	50,50,50,50	0
57	MG	2A	3313	1/1	0.94	0.11	52,52,52,52	0
57	MG	1A	3472	1/1	0.94	0.12	53,53,53,53	0
57	MG	1A	3473	1/1	0.94	0.18	61,61,61,61	0
57	MG	2a	1689	1/1	0.94	0.19	58,58,58,58	0
57	MG	2A	3061	1/1	0.94	0.17	48,48,48,48	0
57	MG	1B	205	1/1	0.94	0.21	51,51,51,51	0
57	MG	2A	3659	1/1	0.94	0.09	53,53,53,53	0
57	MG	1A	3636	1/1	0.94	0.08	17,17,17,17	0
57	MG	1A	3474	1/1	0.94	0.26	46,46,46,46	0
57	MG	1A	3061	1/1	0.94	0.12	58,58,58,58	0
57	MG	1A	3062	1/1	0.94	0.19	38,38,38,38	0
57	MG	1a	1679	1/1	0.94	0.07	71,71,71,71	0
57	MG	1A	3478	1/1	0.94	0.13	41,41,41,41	0
57	MG	1A	3387	1/1	0.94	0.16	37,37,37,37	0
57	MG	1A	3181	1/1	0.94	0.09	47,47,47,47	0
57	MG	2A	3077	1/1	0.94	0.13	48,48,48,48	0
57	MG	2A	3331	1/1	0.94	0.07	64,64,64,64	0
57	MG	1B	215	1/1	0.94	0.20	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3880	1/1	0.94	0.09	25,25,25,25	0
57	MG	1B	217	1/1	0.94	0.07	54,54,54,54	0
57	MG	2A	3085	1/1	0.94	0.09	50,50,50,50	0
57	MG	1A	3122	1/1	0.94	0.07	31,31,31,31	0
57	MG	2A	3338	1/1	0.94	0.06	49,49,49,49	0
57	MG	1A	3247	1/1	0.94	0.06	51,51,51,51	0
57	MG	2a	1716	1/1	0.94	0.14	57,57,57,57	0
57	MG	1A	3392	1/1	0.94	0.29	50,50,50,50	0
57	MG	1A	3659	1/1	0.94	0.08	37,37,37,37	0
57	MG	2A	3342	1/1	0.94	0.18	51,51,51,51	0
57	MG	1A	3497	1/1	0.94	0.13	59,59,59,59	0
57	MG	1A	3891	1/1	0.94	0.16	33,33,33,33	0
57	MG	2a	1724	1/1	0.94	0.13	55,55,55,55	0
57	MG	1a	1696	1/1	0.94	0.10	56,56,56,56	0
57	MG	1a	1697	1/1	0.94	0.12	44,44,44,44	0
57	MG	2A	3352	1/1	0.94	0.06	66,66,66,66	0
57	MG	2a	1729	1/1	0.94	0.10	52,52,52,52	0
57	MG	2a	1730	1/1	0.94	0.22	59,59,59,59	0
57	MG	1A	3395	1/1	0.94	0.08	41,41,41,41	0
57	MG	2A	3704	1/1	0.94	0.10	42,42,42,42	0
57	MG	1A	3896	1/1	0.94	0.13	45,45,45,45	0
57	MG	1a	1701	1/1	0.94	0.15	61,61,61,61	0
57	MG	1a	1702	1/1	0.94	0.15	41,41,41,41	0
57	MG	2A	3712	1/1	0.94	0.07	41,41,41,41	0
57	MG	2A	3102	1/1	0.94	0.07	56,56,56,56	0
57	MG	2a	1740	1/1	0.94	0.19	52,52,52,52	0
57	MG	2A	3715	1/1	0.94	0.06	51,51,51,51	0
57	MG	1A	3663	1/1	0.94	0.11	44,44,44,44	0
57	MG	1A	3188	1/1	0.94	0.27	40,40,40,40	0
57	MG	2A	3362	1/1	0.94	0.16	58,58,58,58	0
57	MG	1D	301	1/1	0.94	0.16	31,31,31,31	0
57	MG	1A	3063	1/1	0.94	0.18	33,33,33,33	0
57	MG	1E	303	1/1	0.94	0.17	32,32,32,32	0
57	MG	1E	308	1/1	0.94	0.08	21,21,21,21	0
57	MG	1A	3127	1/1	0.94	0.39	42,42,42,42	0
57	MG	1A	3315	1/1	0.94	0.15	33,33,33,33	0
57	MG	2A	3732	1/1	0.94	0.08	49,49,49,49	0
57	MG	2A	3114	1/1	0.94	0.09	56,56,56,56	0
57	MG	2a	1757	1/1	0.94	0.10	52,52,52,52	0
57	MG	1A	3675	1/1	0.94	0.07	33,33,33,33	0
57	MG	2A	3736	1/1	0.94	0.12	53,53,53,53	0
57	MG	1A	3251	1/1	0.94	0.09	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1762	1/1	0.94	0.22	57,57,57,57	0
57	MG	1A	3091	1/1	0.94	0.10	43,43,43,43	0
57	MG	1A	3095	1/1	0.94	0.18	41,41,41,41	0
57	MG	1G	202	1/1	0.94	0.11	38,38,38,38	0
57	MG	2A	3124	1/1	0.94	0.10	52,52,52,52	0
57	MG	2a	1768	1/1	0.94	0.10	73,73,73,73	0
57	MG	1a	1722	1/1	0.94	0.10	52,52,52,52	0
57	MG	1A	3701	1/1	0.94	0.09	25,25,25,25	0
57	MG	2A	3380	1/1	0.94	0.05	46,46,46,46	0
57	MG	2a	1774	1/1	0.94	0.07	63,63,63,63	0
57	MG	2A	3136	1/1	0.94	0.06	33,33,33,33	0
57	MG	1A	3131	1/1	0.94	0.18	39,39,39,39	0
57	MG	2a	1778	1/1	0.94	0.11	37,37,37,37	0
57	MG	1A	3141	1/1	0.94	0.14	18,18,18,18	0
57	MG	2A	3385	1/1	0.94	0.05	52,52,52,52	0
57	MG	1A	3412	1/1	0.94	0.09	30,30,30,30	0
57	MG	1a	1731	1/1	0.94	0.11	41,41,41,41	0
57	MG	1A	3258	1/1	0.94	0.08	61,61,61,61	0
57	MG	1A	3008	1/1	0.94	0.06	31,31,31,31	0
57	MG	1A	3716	1/1	0.94	0.08	48,48,48,48	0
57	MG	2A	3773	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	3051	1/1	0.94	0.23	38,38,38,38	0
57	MG	1A	3022	1/1	0.94	0.10	42,42,42,42	0
57	MG	2A	3398	1/1	0.94	0.23	53,53,53,53	0
57	MG	1R	202	1/1	0.94	0.10	27,27,27,27	0
57	MG	2A	3400	1/1	0.94	0.14	51,51,51,51	0
57	MG	2A	3781	1/1	0.94	0.07	56,56,56,56	0
57	MG	2A	3401	1/1	0.94	0.28	43,43,43,43	0
57	MG	2A	3402	1/1	0.94	0.23	48,48,48,48	0
57	MG	1A	3208	1/1	0.94	0.09	40,40,40,40	0
57	MG	1R	205	1/1	0.94	0.13	29,29,29,29	0
57	MG	1a	1745	1/1	0.94	0.15	55,55,55,55	0
57	MG	1A	3419	1/1	0.94	0.08	48,48,48,48	0
57	MG	2a	1802	1/1	0.94	0.10	39,39,39,39	0
57	MG	2A	3413	1/1	0.94	0.29	54,54,54,54	0
57	MG	1a	1748	1/1	0.94	0.10	53,53,53,53	0
57	MG	1a	1751	1/1	0.94	0.14	44,44,44,44	0
57	MG	2A	3416	1/1	0.94	0.28	45,45,45,45	0
57	MG	2A	3797	1/1	0.94	0.16	51,51,51,51	0
57	MG	1A	3420	1/1	0.94	0.15	28,28,28,28	0
57	MG	2a	1810	1/1	0.94	0.21	56,56,56,56	0
57	MG	2A	3418	1/1	0.94	0.07	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3726	1/1	0.94	0.10	22,22,22,22	0
57	MG	1a	1755	1/1	0.94	0.11	51,51,51,51	0
57	MG	1A	3337	1/1	0.94	0.17	42,42,42,42	0
57	MG	2A	3175	1/1	0.94	0.19	49,49,49,49	0
57	MG	2A	3808	1/1	0.94	0.06	29,29,29,29	0
57	MG	2A	3425	1/1	0.94	0.12	31,31,31,31	0
57	MG	2A	3176	1/1	0.94	0.13	42,42,42,42	0
57	MG	1U	204	1/1	0.94	0.12	46,46,46,46	0
57	MG	1A	3210	1/1	0.94	0.11	49,49,49,49	0
57	MG	1a	1759	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3823	1/1	0.94	0.09	52,52,52,52	0
57	MG	1a	1760	1/1	0.94	0.17	50,50,50,50	0
57	MG	2f	202	1/1	0.94	0.09	63,63,63,63	0
57	MG	1A	3212	1/1	0.94	0.12	55,55,55,55	0
57	MG	1a	1764	1/1	0.94	0.07	55,55,55,55	0
57	MG	2A	3437	1/1	0.94	0.09	45,45,45,45	0
57	MG	2A	3832	1/1	0.94	0.14	56,56,56,56	0
57	MG	1A	3743	1/1	0.94	0.07	60,60,60,60	0
57	MG	2A	3439	1/1	0.94	0.06	50,50,50,50	0
57	MG	1a	1766	1/1	0.94	0.08	65,65,65,65	0
57	MG	1V	202	1/1	0.94	0.30	49,49,49,49	0
57	MG	2q	203	1/1	0.94	0.15	60,60,60,60	0
57	MG	2A	3443	1/1	0.94	0.20	48,48,48,48	0
57	MG	1A	3545	1/1	0.94	0.23	48,48,48,48	0
57	MG	1V	207	1/1	0.94	0.07	56,56,56,56	0
57	MG	2A	3843	1/1	0.94	0.16	49,49,49,49	0
57	MG	2A	3844	1/1	0.94	0.17	53,53,53,53	0
57	MG	2A	3190	1/1	0.94	0.18	43,43,43,43	0
57	MG	2A	3453	1/1	0.94	0.14	68,68,68,68	0
57	MG	2A	3849	1/1	0.94	0.09	53,53,53,53	0
57	MG	1W	203	1/1	0.94	0.15	42,42,42,42	0
57	MG	1W	207	1/1	0.94	0.10	38,38,38,38	0
57	MG	1A	3104	1/1	0.94	0.12	33,33,33,33	0
57	MG	1A	3425	1/1	0.94	0.09	41,41,41,41	0
57	MG	2B	201	1/1	0.94	0.08	57,57,57,57	0
57	MG	1A	3753	1/1	0.94	0.10	38,38,38,38	0
57	MG	2A	3461	1/1	0.94	0.08	54,54,54,54	0
57	MG	2z	101	1/1	0.94	0.07	50,50,50,50	0
57	MG	10	103	1/1	0.94	0.11	43,43,43,43	0
57	MG	1A	3217	1/1	0.94	0.13	36,36,36,36	0
57	MG	2A	3202	1/1	0.94	0.06	49,49,49,49	0
57	MG	1A	3430	1/1	0.94	0.16	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1F	304	1/1	0.95	0.09	42,42,42,42	0
57	MG	1A	3908	1/1	0.95	0.09	23,23,23,23	0
57	MG	1A	3375	1/1	0.95	0.13	50,50,50,50	0
57	MG	2A	3839	1/1	0.95	0.10	41,41,41,41	0
57	MG	1A	3544	1/1	0.95	0.14	49,49,49,49	0
57	MG	2A	3167	1/1	0.95	0.10	48,48,48,48	0
57	MG	1G	201	1/1	0.95	0.09	36,36,36,36	0
57	MG	1A	3912	1/1	0.95	0.07	60,60,60,60	0
57	MG	1A	3711	1/1	0.95	0.09	41,41,41,41	0
57	MG	2A	3450	1/1	0.95	0.20	39,39,39,39	0
57	MG	2A	3451	1/1	0.95	0.11	38,38,38,38	0
57	MG	1I	201	1/1	0.95	0.07	53,53,53,53	0
57	MG	1A	3376	1/1	0.95	0.17	38,38,38,38	0
57	MG	1N	203	1/1	0.95	0.09	52,52,52,52	0
57	MG	1A	3715	1/1	0.95	0.08	50,50,50,50	0
57	MG	1a	1743	1/1	0.95	0.09	46,46,46,46	0
57	MG	2A	3855	1/1	0.95	0.15	63,63,63,63	0
57	MG	2A	3856	1/1	0.95	0.07	52,52,52,52	0
57	MG	1a	1744	1/1	0.95	0.10	48,48,48,48	0
57	MG	1A	3919	1/1	0.95	0.08	45,45,45,45	0
57	MG	2A	3179	1/1	0.95	0.15	43,43,43,43	0
57	MG	2A	3462	1/1	0.95	0.15	45,45,45,45	0
57	MG	1A	3317	1/1	0.95	0.14	47,47,47,47	0
57	MG	1P	204	1/1	0.95	0.19	35,35,35,35	0
57	MG	2A	3467	1/1	0.95	0.10	40,40,40,40	0
57	MG	1a	1750	1/1	0.95	0.12	40,40,40,40	0
57	MG	1A	3925	1/1	0.95	0.08	40,40,40,40	0
57	MG	1A	3318	1/1	0.95	0.12	37,37,37,37	0
57	MG	2A	3471	1/1	0.95	0.15	55,55,55,55	0
57	MG	1A	3551	1/1	0.95	0.12	23,23,23,23	0
57	MG	1Q	206	1/1	0.95	0.05	39,39,39,39	0
57	MG	1A	3552	1/1	0.95	0.08	42,42,42,42	0
57	MG	1R	201	1/1	0.95	0.18	38,38,38,38	0
57	MG	2A	3476	1/1	0.95	0.18	28,28,28,28	0
57	MG	1A	3049	1/1	0.95	0.07	34,34,34,34	0
57	MG	2A	3191	1/1	0.95	0.12	69,69,69,69	0
57	MG	1A	3724	1/1	0.95	0.12	53,53,53,53	0
57	MG	1A	3268	1/1	0.95	0.07	51,51,51,51	0
57	MG	1a	1762	1/1	0.95	0.09	49,49,49,49	0
57	MG	2D	304	1/1	0.95	0.21	47,47,47,47	0
57	MG	2A	3196	1/1	0.95	0.06	41,41,41,41	0
57	MG	1A	3452	1/1	0.95	0.06	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3321	1/1	0.95	0.17	34,34,34,34	0
57	MG	1A	3386	1/1	0.95	0.16	43,43,43,43	0
57	MG	1A	3946	1/1	0.95	0.10	32,32,32,32	0
57	MG	1A	3738	1/1	0.95	0.14	51,51,51,51	0
57	MG	2E	308	1/1	0.95	0.11	39,39,39,39	0
57	MG	1A	3948	1/1	0.95	0.06	29,29,29,29	0
57	MG	1A	3233	1/1	0.95	0.27	35,35,35,35	0
57	MG	1A	3567	1/1	0.95	0.06	38,38,38,38	0
57	MG	2F	303	1/1	0.95	0.12	57,57,57,57	0
57	MG	1A	3569	1/1	0.95	0.17	46,46,46,46	0
57	MG	2A	3211	1/1	0.95	0.16	41,41,41,41	0
57	MG	1A	3953	1/1	0.95	0.10	53,53,53,53	0
57	MG	2P	201	1/1	0.95	0.05	43,43,43,43	0
57	MG	2A	3213	1/1	0.95	0.12	54,54,54,54	0
57	MG	1A	3090	1/1	0.95	0.07	38,38,38,38	0
57	MG	2R	203	1/1	0.95	0.25	50,50,50,50	0
57	MG	2A	3501	1/1	0.95	0.14	45,45,45,45	0
57	MG	2T	203	1/1	0.95	0.05	38,38,38,38	0
57	MG	1W	202	1/1	0.95	0.10	46,46,46,46	0
57	MG	2A	3503	1/1	0.95	0.09	57,57,57,57	0
57	MG	1A	3460	1/1	0.95	0.12	40,40,40,40	0
57	MG	1A	3752	1/1	0.95	0.05	26,26,26,26	0
57	MG	1X	101	1/1	0.95	0.07	52,52,52,52	0
57	MG	1A	3958	1/1	0.95	0.09	53,53,53,53	0
57	MG	1X	107	1/1	0.95	0.08	48,48,48,48	0
57	MG	21	3501	1/1	0.95	0.48	51,51,51,51	0
57	MG	1A	3573	1/1	0.95	0.09	37,37,37,37	0
57	MG	2A	3517	1/1	0.95	0.09	45,45,45,45	0
57	MG	2A	3518	1/1	0.95	0.13	48,48,48,48	0
57	MG	2A	3519	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3235	1/1	0.95	0.13	39,39,39,39	0
57	MG	2A	3228	1/1	0.95	0.08	50,50,50,50	0
57	MG	2A	3522	1/1	0.95	0.10	32,32,32,32	0
57	MG	28	102	1/1	0.95	0.25	56,56,56,56	0
57	MG	2a	1601	1/1	0.95	0.14	43,43,43,43	0
57	MG	1A	3761	1/1	0.95	0.11	55,55,55,55	0
57	MG	1A	3576	1/1	0.95	0.10	34,34,34,34	0
57	MG	1A	3966	1/1	0.95	0.11	56,56,56,56	0
57	MG	1A	3763	1/1	0.95	0.13	49,49,49,49	0
57	MG	1A	3326	1/1	0.95	0.07	43,43,43,43	0
57	MG	10	109	1/1	0.95	0.13	60,60,60,60	0
57	MG	1A	3972	1/1	0.95	0.15	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	11	101	1/1	0.95	0.15	38,38,38,38	0
57	MG	2a	1611	1/1	0.95	0.14	51,51,51,51	0
57	MG	1A	3976	1/1	0.95	0.16	61,61,61,61	0
57	MG	13	101	1/1	0.95	0.17	37,37,37,37	0
57	MG	2A	3539	1/1	0.95	0.08	37,37,37,37	0
57	MG	13	103	1/1	0.95	0.07	49,49,49,49	0
57	MG	2A	3542	1/1	0.95	0.13	45,45,45,45	0
57	MG	1A	3979	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3580	1/1	0.95	0.23	35,35,35,35	0
57	MG	2A	3549	1/1	0.95	0.08	40,40,40,40	0
57	MG	15	104	1/1	0.95	0.27	32,32,32,32	0
57	MG	1A	3983	1/1	0.95	0.09	42,42,42,42	0
57	MG	1a	1810	1/1	0.95	0.13	59,59,59,59	0
57	MG	1a	1811	1/1	0.95	0.06	51,51,51,51	0
57	MG	1A	3466	1/1	0.95	0.11	37,37,37,37	0
57	MG	2A	3558	1/1	0.95	0.13	48,48,48,48	0
57	MG	1d	301	1/1	0.95	0.12	48,48,48,48	0
57	MG	2A	3560	1/1	0.95	0.17	59,59,59,59	0
57	MG	1e	201	1/1	0.95	0.27	56,56,56,56	0
57	MG	1A	3037	1/1	0.95	0.06	34,34,34,34	0
57	MG	1A	3393	1/1	0.95	0.13	62,62,62,62	0
57	MG	2A	3254	1/1	0.95	0.09	45,45,45,45	0
57	MG	1A	3990	1/1	0.95	0.05	32,32,32,32	0
57	MG	1m	3001	1/1	0.95	0.05	46,46,46,46	0
57	MG	16	102	1/1	0.95	0.14	62,62,62,62	0
57	MG	2A	3573	1/1	0.95	0.07	28,28,28,28	0
57	MG	1n	103	1/1	0.95	0.19	46,46,46,46	0
57	MG	1A	3773	1/1	0.95	0.06	37,37,37,37	0
57	MG	1A	3394	1/1	0.95	0.27	49,49,49,49	0
57	MG	2A	3577	1/1	0.95	0.06	28,28,28,28	0
57	MG	1A	3997	1/1	0.95	0.06	36,36,36,36	0
57	MG	2A	3579	1/1	0.95	0.10	54,54,54,54	0
57	MG	1A	3776	1/1	0.95	0.05	21,21,21,21	0
57	MG	1A	4000	1/1	0.95	0.14	41,41,41,41	0
57	MG	1A	3779	1/1	0.95	0.05	57,57,57,57	0
57	MG	1a	1601	1/1	0.95	0.08	53,53,53,53	0
57	MG	1A	3781	1/1	0.95	0.09	22,22,22,22	0
57	MG	2A	3588	1/1	0.95	0.13	35,35,35,35	0
57	MG	2A	3591	1/1	0.95	0.10	46,46,46,46	0
57	MG	2A	3592	1/1	0.95	0.06	41,41,41,41	0
57	MG	2A	3593	1/1	0.95	0.07	53,53,53,53	0
57	MG	1a	1603	1/1	0.95	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
57	MG	2A	3596	1/1	0.95	0.08	24,24,24,24	0
57	MG	1x	104	1/1	0.95	0.10	56,56,56,56	0
57	MG	1A	3789	1/1	0.95	0.06	24,24,24,24	0
57	MG	1A	3093	1/1	0.95	0.06	46,46,46,46	0
57	MG	1A	3795	1/1	0.95	0.12	49,49,49,49	0
57	MG	1x	111	1/1	0.95	0.26	53,53,53,53	0
57	MG	2A	3603	1/1	0.95	0.08	56,56,56,56	0
57	MG	1A	3284	1/1	0.95	0.06	46,46,46,46	0
57	MG	1A	3799	1/1	0.95	0.10	19,19,19,19	0
57	MG	2A	3608	1/1	0.95	0.09	24,24,24,24	0
57	MG	2a	1668	1/1	0.95	0.10	47,47,47,47	0
57	MG	2A	3281	1/1	0.95	0.12	45,45,45,45	0
57	MG	1A	3060	1/1	0.95	0.13	40,40,40,40	0
57	MG	1A	3245	1/1	0.95	0.04	47,47,47,47	0
57	MG	1a	1615	1/1	0.95	0.10	36,36,36,36	0
57	MG	2A	3613	1/1	0.95	0.14	50,50,50,50	0
57	MG	2A	3286	1/1	0.95	0.09	64,64,64,64	0
57	MG	2A	3615	1/1	0.95	0.09	44,44,44,44	0
57	MG	2A	3616	1/1	0.95	0.16	63,63,63,63	0
57	MG	2A	3006	1/1	0.95	0.11	51,51,51,51	0
57	MG	1A	3591	1/1	0.95	0.16	42,42,42,42	0
57	MG	2a	1681	1/1	0.95	0.17	52,52,52,52	0
57	MG	2A	3010	1/1	0.95	0.15	48,48,48,48	0
57	MG	2a	1683	1/1	0.95	0.18	51,51,51,51	0
57	MG	2A	3011	1/1	0.95	0.12	40,40,40,40	0
57	MG	2a	1685	1/1	0.95	0.16	46,46,46,46	0
57	MG	2A	3625	1/1	0.95	0.20	42,42,42,42	0
57	MG	2A	3012	1/1	0.95	0.04	49,49,49,49	0
57	MG	2A	3013	1/1	0.95	0.17	32,32,32,32	0
57	MG	2A	3630	1/1	0.95	0.17	54,54,54,54	0
57	MG	1a	1620	1/1	0.95	0.08	53,53,53,53	0
57	MG	2a	1692	1/1	0.95	0.20	61,61,61,61	0
57	MG	2A	3633	1/1	0.95	0.15	32,32,32,32	0
57	MG	1A	3808	1/1	0.95	0.63	32,32,32,32	0
57	MG	1A	4022	1/1	0.95	0.12	48,48,48,48	0
57	MG	1A	3335	1/1	0.95	0.41	42,42,42,42	0
57	MG	1A	3597	1/1	0.95	0.06	47,47,47,47	0
57	MG	2A	3025	1/1	0.95	0.15	44,44,44,44	0
57	MG	1A	3203	1/1	0.95	0.17	40,40,40,40	0
57	MG	1A	3158	1/1	0.95	0.11	25,25,25,25	0
57	MG	2A	3645	1/1	0.95	0.09	46,46,46,46	0
57	MG	1A	3291	1/1	0.95	0.20	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	4034	1/1	0.95	0.07	52,52,52,52	0
57	MG	1A	4036	1/1	0.95	0.12	52,52,52,52	0
57	MG	2A	3651	1/1	0.95	0.10	46,46,46,46	0
57	MG	2A	3033	1/1	0.95	0.06	44,44,44,44	0
57	MG	2A	3653	1/1	0.95	0.10	54,54,54,54	0
57	MG	1A	3005	1/1	0.95	0.06	44,44,44,44	0
57	MG	2a	1712	1/1	0.95	0.07	51,51,51,51	0
57	MG	2A	3036	1/1	0.95	0.07	50,50,50,50	0
57	MG	2a	1714	1/1	0.95	0.12	57,57,57,57	0
57	MG	1A	3075	1/1	0.95	0.06	37,37,37,37	0
57	MG	2A	3312	1/1	0.95	0.16	51,51,51,51	0
57	MG	1A	4040	1/1	0.95	0.09	32,32,32,32	0
57	MG	2a	1718	1/1	0.95	0.13	51,51,51,51	0
57	MG	2A	3040	1/1	0.95	0.20	44,44,44,44	0
57	MG	1A	3484	1/1	0.95	0.17	41,41,41,41	0
57	MG	1A	4045	1/1	0.95	0.07	51,51,51,51	0
57	MG	2a	1722	1/1	0.95	0.09	72,72,72,72	0
57	MG	2A	3669	1/1	0.95	0.07	62,62,62,62	0
57	MG	1A	4051	1/1	0.95	0.06	54,54,54,54	0
57	MG	1A	3485	1/1	0.95	0.13	49,49,49,49	0
57	MG	1a	1642	1/1	0.95	0.10	53,53,53,53	0
57	MG	1A	3488	1/1	0.95	0.13	47,47,47,47	0
57	MG	1A	3824	1/1	0.95	0.09	39,39,39,39	0
57	MG	1A	3342	1/1	0.95	0.14	41,41,41,41	0
57	MG	2a	1731	1/1	0.95	0.14	46,46,46,46	0
57	MG	1A	3491	1/1	0.95	0.09	38,38,38,38	0
57	MG	2A	3679	1/1	0.95	0.14	63,63,63,63	0
57	MG	1A	3413	1/1	0.95	0.07	41,41,41,41	0
57	MG	2a	1735	1/1	0.95	0.28	60,60,60,60	0
57	MG	1A	3098	1/1	0.95	0.10	35,35,35,35	0
57	MG	2A	3055	1/1	0.95	0.13	52,52,52,52	0
57	MG	1A	3495	1/1	0.95	0.06	51,51,51,51	0
57	MG	2A	3332	1/1	0.95	0.14	47,47,47,47	0
57	MG	1A	3167	1/1	0.95	0.10	57,57,57,57	0
57	MG	1A	3632	1/1	0.95	0.09	29,29,29,29	0
57	MG	2A	3687	1/1	0.95	0.09	45,45,45,45	0
57	MG	1A	3213	1/1	0.95	0.19	40,40,40,40	0
57	MG	1A	3052	1/1	0.95	0.12	37,37,37,37	0
57	MG	1A	3504	1/1	0.95	0.10	41,41,41,41	0
57	MG	2a	1746	1/1	0.95	0.23	62,62,62,62	0
57	MG	1a	1661	1/1	0.95	0.14	64,64,64,64	0
57	MG	1a	1664	1/1	0.95	0.16	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3178	1/1	0.95	0.15	32,32,32,32	0
57	MG	2a	1751	1/1	0.95	0.13	49,49,49,49	0
57	MG	1A	4077	1/1	0.95	0.06	45,45,45,45	0
57	MG	2A	3069	1/1	0.95	0.09	44,44,44,44	0
57	MG	2A	3701	1/1	0.95	0.08	47,47,47,47	0
57	MG	2a	1755	1/1	0.95	0.15	76,76,76,76	0
57	MG	1A	3079	1/1	0.95	0.08	43,43,43,43	0
57	MG	1A	3358	1/1	0.95	0.20	40,40,40,40	0
57	MG	1a	1669	1/1	0.95	0.08	56,56,56,56	0
57	MG	1A	3135	1/1	0.95	0.12	30,30,30,30	0
57	MG	2A	3075	1/1	0.95	0.06	40,40,40,40	0
57	MG	2A	3076	1/1	0.95	0.11	33,33,33,33	0
57	MG	1A	3852	1/1	0.95	0.12	25,25,25,25	0
57	MG	1A	3139	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3855	1/1	0.95	0.13	36,36,36,36	0
57	MG	2A	3082	1/1	0.95	0.11	55,55,55,55	0
57	MG	2A	3719	1/1	0.95	0.09	53,53,53,53	0
57	MG	1A	3648	1/1	0.95	0.08	64,64,64,64	0
57	MG	2A	3359	1/1	0.95	0.07	41,41,41,41	0
57	MG	1A	3185	1/1	0.95	0.08	38,38,38,38	0
57	MG	1A	3516	1/1	0.95	0.21	46,46,46,46	0
57	MG	1A	3518	1/1	0.95	0.07	32,32,32,32	0
57	MG	1A	3863	1/1	0.95	0.18	53,53,53,53	0
57	MG	2A	3728	1/1	0.95	0.12	54,54,54,54	0
57	MG	1A	3028	1/1	0.95	0.22	69,69,69,69	0
57	MG	1A	3144	1/1	0.95	0.45	40,40,40,40	0
57	MG	2a	1781	1/1	0.95	0.10	51,51,51,51	0
57	MG	1A	3660	1/1	0.95	0.08	42,42,42,42	0
57	MG	2A	3369	1/1	0.95	0.12	53,53,53,53	0
57	MG	1A	3521	1/1	0.95	0.20	43,43,43,43	0
57	MG	1A	3523	1/1	0.95	0.19	44,44,44,44	0
57	MG	2A	3739	1/1	0.95	0.08	47,47,47,47	0
57	MG	1A	3367	1/1	0.95	0.10	49,49,49,49	0
57	MG	1B	213	1/1	0.95	0.16	50,50,50,50	0
57	MG	2a	1789	1/1	0.95	0.19	60,60,60,60	0
57	MG	1A	3310	1/1	0.95	0.22	32,32,32,32	0
57	MG	2A	3745	1/1	0.95	0.08	54,54,54,54	0
57	MG	2A	3746	1/1	0.95	0.14	44,44,44,44	0
57	MG	1A	3431	1/1	0.95	0.14	40,40,40,40	0
57	MG	1A	3878	1/1	0.95	0.06	26,26,26,26	0
57	MG	1A	3879	1/1	0.95	0.10	30,30,30,30	0
57	MG	2A	3752	1/1	0.95	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
57	MG	1A	3432	1/1	0.95	0.12	29,29,29,29	0
57	MG	1A	3529	1/1	0.95	0.14	44,44,44,44	0
57	MG	2A	3756	1/1	0.95	0.14	65,65,65,65	0
57	MG	1B	225	1/1	0.95	0.20	49,49,49,49	0
57	MG	1A	3882	1/1	0.95	0.12	50,50,50,50	0
57	MG	1A	3434	1/1	0.95	0.12	34,34,34,34	0
57	MG	2A	3762	1/1	0.95	0.07	48,48,48,48	0
57	MG	2A	3764	1/1	0.95	0.08	52,52,52,52	0
57	MG	2a	1806	1/1	0.95	0.07	50,50,50,50	0
57	MG	2A	3765	1/1	0.95	0.06	35,35,35,35	0
57	MG	2A	3111	1/1	0.95	0.20	50,50,50,50	0
57	MG	1A	3679	1/1	0.95	0.08	18,18,18,18	0
57	MG	1A	3680	1/1	0.95	0.09	21,21,21,21	0
57	MG	1a	1704	1/1	0.95	0.08	50,50,50,50	0
57	MG	1A	3682	1/1	0.95	0.06	16,16,16,16	0
57	MG	1a	1707	1/1	0.95	0.32	56,56,56,56	0
57	MG	2A	3117	1/1	0.95	0.14	38,38,38,38	0
57	MG	2A	3394	1/1	0.95	0.12	28,28,28,28	0
57	MG	1A	3265	1/1	0.95	0.11	47,47,47,47	0
57	MG	1A	3314	1/1	0.95	0.23	50,50,50,50	0
57	MG	1B	235	1/1	0.95	0.09	59,59,59,59	0
57	MG	1A	3018	1/1	0.95	0.12	31,31,31,31	0
57	MG	2A	3126	1/1	0.95	0.12	64,64,64,64	0
57	MG	2A	3128	1/1	0.95	0.13	43,43,43,43	0
57	MG	2A	3131	1/1	0.95	0.05	40,40,40,40	0
57	MG	2A	3133	1/1	0.95	0.10	46,46,46,46	0
57	MG	2f	201	1/1	0.95	0.11	54,54,54,54	0
57	MG	1A	3695	1/1	0.95	0.08	22,22,22,22	0
57	MG	2A	3407	1/1	0.95	0.30	53,53,53,53	0
57	MG	2A	3409	1/1	0.95	0.19	44,44,44,44	0
57	MG	1A	3899	1/1	0.95	0.15	60,60,60,60	0
57	MG	1D	312	1/1	0.95	0.07	28,28,28,28	0
57	MG	2A	3412	1/1	0.95	0.12	45,45,45,45	0
57	MG	2A	3796	1/1	0.95	0.07	41,41,41,41	0
57	MG	2o	101	1/1	0.95	0.14	54,54,54,54	0
57	MG	1E	301	1/1	0.95	0.17	44,44,44,44	0
57	MG	1A	3316	1/1	0.95	0.23	53,53,53,53	0
57	MG	2A	3141	1/1	0.95	0.14	37,37,37,37	0
57	MG	2A	3145	1/1	0.95	0.22	40,40,40,40	0
57	MG	2A	3146	1/1	0.95	0.07	35,35,35,35	0
57	MG	1E	305	1/1	0.95	0.10	40,40,40,40	0
57	MG	2A	3805	1/1	0.95	0.11	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1E	307	1/1	0.95	0.08	41,41,41,41	0
57	MG	2A	3420	1/1	0.95	0.14	49,49,49,49	0
57	MG	1A	3902	1/1	0.95	0.09	40,40,40,40	0
57	MG	2A	3150	1/1	0.95	0.11	54,54,54,54	0
57	MG	1A	3903	1/1	0.95	0.15	29,29,29,29	0
57	MG	2A	3153	1/1	0.95	0.08	43,43,43,43	0
57	MG	1A	3439	1/1	0.95	0.13	47,47,47,47	0
57	MG	2A	3156	1/1	0.95	0.09	63,63,63,63	0
57	MG	2A	3157	1/1	0.95	0.13	67,67,67,67	0
57	MG	1a	1724	1/1	0.95	0.15	50,50,50,50	0
57	MG	2A	3431	1/1	0.95	0.18	43,43,43,43	0
57	MG	2A	3828	1/1	0.95	0.08	53,53,53,53	0
57	MG	1A	3542	1/1	0.95	0.11	32,32,32,32	0
57	MG	1a	1727	1/1	0.95	0.10	43,43,43,43	0
57	MG	2A	3162	1/1	0.95	0.16	41,41,41,41	0
57	MG	2A	3835	1/1	0.95	0.10	52,52,52,52	0
57	MG	1A	3103	1/1	0.96	0.05	56,56,56,56	0
57	MG	2E	301	1/1	0.96	0.08	55,55,55,55	0
57	MG	1A	4075	1/1	0.96	0.06	46,46,46,46	0
57	MG	2A	3266	1/1	0.96	0.11	51,51,51,51	0
57	MG	2A	3547	1/1	0.96	0.06	41,41,41,41	0
57	MG	1A	3868	1/1	0.96	0.15	31,31,31,31	0
57	MG	2A	3020	1/1	0.96	0.11	42,42,42,42	0
57	MG	1a	1634	1/1	0.96	0.15	46,46,46,46	0
57	MG	1A	3869	1/1	0.96	0.28	39,39,39,39	0
57	MG	2A	3024	1/1	0.96	0.08	55,55,55,55	0
57	MG	1A	3163	1/1	0.96	0.09	42,42,42,42	0
57	MG	2A	3026	1/1	0.96	0.04	42,42,42,42	0
57	MG	2F	304	1/1	0.96	0.07	33,33,33,33	0
57	MG	2A	3275	1/1	0.96	0.08	55,55,55,55	0
57	MG	1A	3449	1/1	0.96	0.06	30,30,30,30	0
57	MG	2A	3562	1/1	0.96	0.05	35,35,35,35	0
57	MG	2A	3277	1/1	0.96	0.15	46,46,46,46	0
57	MG	1a	1639	1/1	0.96	0.08	46,46,46,46	0
57	MG	1a	1640	1/1	0.96	0.10	49,49,49,49	0
57	MG	2R	201	1/1	0.96	0.04	46,46,46,46	0
57	MG	2A	3567	1/1	0.96	0.11	46,46,46,46	0
57	MG	1a	1641	1/1	0.96	0.06	58,58,58,58	0
57	MG	1A	3691	1/1	0.96	0.06	23,23,23,23	0
57	MG	2U	201	1/1	0.96	0.13	55,55,55,55	0
57	MG	2A	3032	1/1	0.96	0.05	41,41,41,41	0
57	MG	2V	201	1/1	0.96	0.07	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3085	1/1	0.96	0.15	37,37,37,37	0
57	MG	1A	3547	1/1	0.96	0.06	35,35,35,35	0
57	MG	1A	3698	1/1	0.96	0.07	22,22,22,22	0
57	MG	1A	3378	1/1	0.96	0.04	38,38,38,38	0
57	MG	2A	3288	1/1	0.96	0.11	53,53,53,53	0
57	MG	1A	3703	1/1	0.96	0.09	19,19,19,19	0
57	MG	2A	3039	1/1	0.96	0.05	55,55,55,55	0
57	MG	1A	3132	1/1	0.96	0.05	32,32,32,32	0
57	MG	1A	3455	1/1	0.96	0.06	51,51,51,51	0
57	MG	2A	3293	1/1	0.96	0.16	62,62,62,62	0
57	MG	2A	3042	1/1	0.96	0.10	48,48,48,48	0
57	MG	2A	3585	1/1	0.96	0.05	41,41,41,41	0
57	MG	1B	204	1/1	0.96	0.04	30,30,30,30	0
57	MG	1A	3214	1/1	0.96	0.05	36,36,36,36	0
57	MG	1A	3709	1/1	0.96	0.07	24,24,24,24	0
57	MG	28	103	1/1	0.96	0.14	41,41,41,41	0
57	MG	1B	207	1/1	0.96	0.27	47,47,47,47	0
57	MG	1A	3554	1/1	0.96	0.06	46,46,46,46	0
57	MG	1A	3886	1/1	0.96	0.06	33,33,33,33	0
57	MG	1a	1662	1/1	0.96	0.05	33,33,33,33	0
57	MG	2A	3051	1/1	0.96	0.07	60,60,60,60	0
57	MG	1a	1663	1/1	0.96	0.14	51,51,51,51	0
57	MG	2A	3598	1/1	0.96	0.12	59,59,59,59	0
57	MG	1A	3457	1/1	0.96	0.05	46,46,46,46	0
57	MG	2a	1609	1/1	0.96	0.10	61,61,61,61	0
57	MG	1A	3888	1/1	0.96	0.07	23,23,23,23	0
57	MG	1A	3712	1/1	0.96	0.12	30,30,30,30	0
57	MG	1A	3168	1/1	0.96	0.10	30,30,30,30	0
57	MG	1A	3714	1/1	0.96	0.05	43,43,43,43	0
57	MG	2A	3604	1/1	0.96	0.13	43,43,43,43	0
57	MG	1A	3558	1/1	0.96	0.16	36,36,36,36	0
57	MG	1A	3897	1/1	0.96	0.04	31,31,31,31	0
57	MG	2a	1617	1/1	0.96	0.08	66,66,66,66	0
57	MG	1A	3134	1/1	0.96	0.07	42,42,42,42	0
57	MG	1A	3384	1/1	0.96	0.04	48,48,48,48	0
57	MG	1A	3172	1/1	0.96	0.23	29,29,29,29	0
57	MG	1A	3175	1/1	0.96	0.04	22,22,22,22	0
57	MG	1A	3720	1/1	0.96	0.09	48,48,48,48	0
57	MG	2A	3066	1/1	0.96	0.06	35,35,35,35	0
57	MG	1B	227	1/1	0.96	0.09	54,54,54,54	0
57	MG	2A	3322	1/1	0.96	0.08	85,85,85,85	0
57	MG	2A	3323	1/1	0.96	0.15	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3323	1/1	0.96	0.20	43,43,43,43	0
57	MG	1A	3273	1/1	0.96	0.13	24,24,24,24	0
57	MG	1A	3390	1/1	0.96	0.13	55,55,55,55	0
57	MG	1A	3571	1/1	0.96	0.06	50,50,50,50	0
57	MG	2A	3073	1/1	0.96	0.10	47,47,47,47	0
57	MG	1A	3274	1/1	0.96	0.45	35,35,35,35	0
57	MG	1a	1683	1/1	0.96	0.12	44,44,44,44	0
57	MG	1A	3911	1/1	0.96	0.08	40,40,40,40	0
57	MG	1A	3731	1/1	0.96	0.12	56,56,56,56	0
57	MG	1A	3110	1/1	0.96	0.25	33,33,33,33	0
57	MG	1A	3574	1/1	0.96	0.07	40,40,40,40	0
57	MG	1D	303	1/1	0.96	0.08	33,33,33,33	0
57	MG	1D	306	1/1	0.96	0.09	35,35,35,35	0
57	MG	1a	1692	1/1	0.96	0.17	42,42,42,42	0
57	MG	1A	3179	1/1	0.96	0.11	38,38,38,38	0
57	MG	2a	1643	1/1	0.96	0.07	48,48,48,48	0
57	MG	1A	3740	1/1	0.96	0.06	47,47,47,47	0
57	MG	2A	3642	1/1	0.96	0.06	45,45,45,45	0
57	MG	1A	3742	1/1	0.96	0.08	50,50,50,50	0
57	MG	2A	3644	1/1	0.96	0.34	39,39,39,39	0
57	MG	1A	3227	1/1	0.96	0.05	46,46,46,46	0
57	MG	2A	3090	1/1	0.96	0.15	47,47,47,47	0
57	MG	1A	3926	1/1	0.96	0.11	39,39,39,39	0
57	MG	2A	3648	1/1	0.96	0.11	67,67,67,67	0
57	MG	1A	3578	1/1	0.96	0.27	27,27,27,27	0
57	MG	1A	3928	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3348	1/1	0.96	0.08	51,51,51,51	0
57	MG	1E	310	1/1	0.96	0.08	58,58,58,58	0
57	MG	1A	3929	1/1	0.96	0.06	55,55,55,55	0
57	MG	2a	1657	1/1	0.96	0.14	56,56,56,56	0
57	MG	1A	3930	1/1	0.96	0.08	44,44,44,44	0
57	MG	1E	313	1/1	0.96	0.07	48,48,48,48	0
57	MG	1a	1706	1/1	0.96	0.14	41,41,41,41	0
57	MG	1A	3931	1/1	0.96	0.05	35,35,35,35	0
57	MG	2A	3660	1/1	0.96	0.07	51,51,51,51	0
57	MG	1A	3746	1/1	0.96	0.12	26,26,26,26	0
57	MG	2a	1665	1/1	0.96	0.22	43,43,43,43	0
57	MG	1A	3023	1/1	0.96	0.04	17,17,17,17	0
57	MG	2A	3105	1/1	0.96	0.07	59,59,59,59	0
57	MG	2A	3665	1/1	0.96	0.09	56,56,56,56	0
57	MG	2A	3668	1/1	0.96	0.06	58,58,58,58	0
57	MG	2A	3360	1/1	0.96	0.17	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1F	307	1/1	0.96	0.09	29,29,29,29	0
57	MG	1A	3229	1/1	0.96	0.11	45,45,45,45	0
57	MG	2A	3363	1/1	0.96	0.13	43,43,43,43	0
57	MG	1A	3072	1/1	0.96	0.27	37,37,37,37	0
57	MG	2A	3674	1/1	0.96	0.06	38,38,38,38	0
57	MG	1A	3182	1/1	0.96	0.12	60,60,60,60	0
57	MG	1A	3754	1/1	0.96	0.07	60,60,60,60	0
57	MG	1A	3757	1/1	0.96	0.09	25,25,25,25	0
57	MG	1A	3943	1/1	0.96	0.10	61,61,61,61	0
57	MG	1A	3402	1/1	0.96	0.11	49,49,49,49	0
57	MG	1A	3143	1/1	0.96	0.11	50,50,50,50	0
57	MG	1A	3036	1/1	0.96	0.05	34,34,34,34	0
57	MG	1A	3483	1/1	0.96	0.06	43,43,43,43	0
57	MG	2a	1686	1/1	0.96	0.12	41,41,41,41	0
57	MG	1A	3186	1/1	0.96	0.14	55,55,55,55	0
57	MG	2A	3120	1/1	0.96	0.12	46,46,46,46	0
57	MG	2A	3121	1/1	0.96	0.20	64,64,64,64	0
57	MG	1O	204	1/1	0.96	0.07	63,63,63,63	0
57	MG	1P	203	1/1	0.96	0.19	29,29,29,29	0
57	MG	1a	1726	1/1	0.96	0.08	57,57,57,57	0
57	MG	2A	3125	1/1	0.96	0.09	40,40,40,40	0
57	MG	1A	3407	1/1	0.96	0.05	45,45,45,45	0
57	MG	1A	3768	1/1	0.96	0.07	41,41,41,41	0
57	MG	2A	3129	1/1	0.96	0.17	50,50,50,50	0
57	MG	2A	3696	1/1	0.96	0.07	50,50,50,50	0
57	MG	2A	3698	1/1	0.96	0.07	39,39,39,39	0
57	MG	2a	1701	1/1	0.96	0.09	44,44,44,44	0
57	MG	2A	3130	1/1	0.96	0.07	72,72,72,72	0
57	MG	1A	3952	1/1	0.96	0.05	46,46,46,46	0
57	MG	2A	3132	1/1	0.96	0.11	43,43,43,43	0
57	MG	1Q	202	1/1	0.96	0.07	34,34,34,34	0
57	MG	1A	3486	1/1	0.96	0.07	39,39,39,39	0
57	MG	1Q	205	1/1	0.96	0.08	43,43,43,43	0
57	MG	2A	3708	1/1	0.96	0.08	48,48,48,48	0
57	MG	1A	3289	1/1	0.96	0.09	29,29,29,29	0
57	MG	2A	3392	1/1	0.96	0.12	40,40,40,40	0
57	MG	1A	3290	1/1	0.96	0.21	40,40,40,40	0
57	MG	1A	3490	1/1	0.96	0.17	49,49,49,49	0
57	MG	2A	3140	1/1	0.96	0.20	38,38,38,38	0
57	MG	1A	3016	1/1	0.96	0.19	51,51,51,51	0
57	MG	2A	3142	1/1	0.96	0.13	42,42,42,42	0
57	MG	1A	3189	1/1	0.96	0.06	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3294	1/1	0.96	0.15	31,31,31,31	0
57	MG	1A	3240	1/1	0.96	0.07	39,39,39,39	0
57	MG	1A	3783	1/1	0.96	0.06	26,26,26,26	0
57	MG	2A	3405	1/1	0.96	0.09	41,41,41,41	0
57	MG	1S	202	1/1	0.96	0.14	57,57,57,57	0
57	MG	1A	3965	1/1	0.96	0.08	41,41,41,41	0
57	MG	2A	3408	1/1	0.96	0.11	45,45,45,45	0
57	MG	1A	3496	1/1	0.96	0.12	54,54,54,54	0
57	MG	2A	3731	1/1	0.96	0.05	47,47,47,47	0
57	MG	1A	3094	1/1	0.96	0.07	18,18,18,18	0
57	MG	2A	3733	1/1	0.96	0.10	49,49,49,49	0
57	MG	1A	3501	1/1	0.96	0.12	31,31,31,31	0
57	MG	1A	3971	1/1	0.96	0.05	30,30,30,30	0
57	MG	1a	1753	1/1	0.96	0.10	54,54,54,54	0
57	MG	1A	3615	1/1	0.96	0.04	48,48,48,48	0
57	MG	1V	201	1/1	0.96	0.31	28,28,28,28	0
57	MG	1A	3974	1/1	0.96	0.07	29,29,29,29	0
57	MG	2A	3161	1/1	0.96	0.23	38,38,38,38	0
57	MG	2A	3743	1/1	0.96	0.13	55,55,55,55	0
57	MG	1A	3975	1/1	0.96	0.08	28,28,28,28	0
57	MG	1A	3616	1/1	0.96	0.09	23,23,23,23	0
57	MG	1W	201	1/1	0.96	0.07	29,29,29,29	0
57	MG	1A	3350	1/1	0.96	0.14	52,52,52,52	0
57	MG	2A	3748	1/1	0.96	0.06	42,42,42,42	0
57	MG	2A	3422	1/1	0.96	0.08	53,53,53,53	0
57	MG	1a	1761	1/1	0.96	0.05	35,35,35,35	0
57	MG	1A	3351	1/1	0.96	0.15	48,48,48,48	0
57	MG	1W	204	1/1	0.96	0.06	42,42,42,42	0
57	MG	2A	3426	1/1	0.96	0.14	38,38,38,38	0
57	MG	1A	3619	1/1	0.96	0.12	37,37,37,37	0
57	MG	1A	3352	1/1	0.96	0.07	46,46,46,46	0
57	MG	1X	105	1/1	0.96	0.05	38,38,38,38	0
57	MG	2A	3172	1/1	0.96	0.10	37,37,37,37	0
57	MG	1A	3192	1/1	0.96	0.23	25,25,25,25	0
57	MG	2A	3432	1/1	0.96	0.18	45,45,45,45	0
57	MG	1A	3007	1/1	0.96	0.08	26,26,26,26	0
57	MG	2A	3766	1/1	0.96	0.08	47,47,47,47	0
57	MG	1a	1770	1/1	0.96	0.10	65,65,65,65	0
57	MG	1a	1771	1/1	0.96	0.05	67,67,67,67	0
57	MG	1A	3630	1/1	0.96	0.09	52,52,52,52	0
57	MG	1A	3355	1/1	0.96	0.08	46,46,46,46	0
57	MG	1Z	302	1/1	0.96	0.06	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1761	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3440	1/1	0.96	0.10	42,42,42,42	0
57	MG	10	101	1/1	0.96	0.09	36,36,36,36	0
57	MG	1A	3356	1/1	0.96	0.10	42,42,42,42	0
57	MG	1A	3509	1/1	0.96	0.08	41,41,41,41	0
57	MG	2A	3777	1/1	0.96	0.09	43,43,43,43	0
57	MG	2A	3183	1/1	0.96	0.06	46,46,46,46	0
57	MG	2A	3447	1/1	0.96	0.06	39,39,39,39	0
57	MG	1A	3357	1/1	0.96	0.07	42,42,42,42	0
57	MG	1A	3511	1/1	0.96	0.04	35,35,35,35	0
57	MG	1A	3637	1/1	0.96	0.07	35,35,35,35	0
57	MG	1a	1781	1/1	0.96	0.12	44,44,44,44	0
57	MG	2a	1776	1/1	0.96	0.13	45,45,45,45	0
57	MG	1A	3820	1/1	0.96	0.05	31,31,31,31	0
57	MG	1A	3194	1/1	0.96	0.05	44,44,44,44	0
57	MG	2A	3787	1/1	0.96	0.08	61,61,61,61	0
57	MG	1A	4004	1/1	0.96	0.13	50,50,50,50	0
57	MG	2A	3456	1/1	0.96	0.12	69,69,69,69	0
57	MG	2A	3790	1/1	0.96	0.06	41,41,41,41	0
57	MG	1a	1788	1/1	0.96	0.10	40,40,40,40	0
57	MG	11	102	1/1	0.96	0.08	55,55,55,55	0
57	MG	1A	3514	1/1	0.96	0.15	33,33,33,33	0
57	MG	12	101	1/1	0.96	0.09	36,36,36,36	0
57	MG	1A	3359	1/1	0.96	0.16	33,33,33,33	0
57	MG	2A	3197	1/1	0.96	0.06	48,48,48,48	0
57	MG	2A	3799	1/1	0.96	0.06	34,34,34,34	0
57	MG	13	102	1/1	0.96	0.10	39,39,39,39	0
57	MG	1A	4009	1/1	0.96	0.06	48,48,48,48	0
57	MG	13	104	1/1	0.96	0.09	48,48,48,48	0
57	MG	1A	3517	1/1	0.96	0.14	30,30,30,30	0
57	MG	1A	3828	1/1	0.96	0.10	48,48,48,48	0
57	MG	15	103	1/1	0.96	0.15	36,36,36,36	0
57	MG	1A	3829	1/1	0.96	0.11	49,49,49,49	0
57	MG	2A	3809	1/1	0.96	0.05	52,52,52,52	0
57	MG	2A	3812	1/1	0.96	0.16	54,54,54,54	0
57	MG	1A	3151	1/1	0.96	0.05	31,31,31,31	0
57	MG	1A	3428	1/1	0.96	0.13	45,45,45,45	0
57	MG	2A	3210	1/1	0.96	0.14	42,42,42,42	0
57	MG	1A	3196	1/1	0.96	0.10	35,35,35,35	0
57	MG	1A	3834	1/1	0.96	0.13	46,46,46,46	0
57	MG	1A	3650	1/1	0.96	0.06	33,33,33,33	0
57	MG	1A	3153	1/1	0.96	0.08	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	17	103	1/1	0.96	0.10	31,31,31,31	0
57	MG	17	104	1/1	0.96	0.09	36,36,36,36	0
57	MG	1A	3006	1/1	0.96	0.06	30,30,30,30	0
57	MG	2A	3829	1/1	0.96	0.10	38,38,38,38	0
57	MG	1A	3365	1/1	0.96	0.09	39,39,39,39	0
57	MG	2A	3484	1/1	0.96	0.11	43,43,43,43	0
57	MG	2A	3219	1/1	0.96	0.21	59,59,59,59	0
57	MG	2A	3834	1/1	0.96	0.09	55,55,55,55	0
57	MG	2A	3221	1/1	0.96	0.12	42,42,42,42	0
57	MG	18	103	1/1	0.96	0.19	49,49,49,49	0
57	MG	2A	3489	1/1	0.96	0.10	49,49,49,49	0
57	MG	1A	3839	1/1	0.96	0.10	46,46,46,46	0
57	MG	1A	3081	1/1	0.96	0.12	37,37,37,37	0
57	MG	1A	3842	1/1	0.96	0.07	46,46,46,46	0
57	MG	2a	1823	1/1	0.96	0.13	59,59,59,59	0
57	MG	1n	101	1/1	0.96	0.27	46,46,46,46	0
57	MG	1A	4037	1/1	0.96	0.06	50,50,50,50	0
57	MG	2A	3230	1/1	0.96	0.15	51,51,51,51	0
57	MG	1A	3306	1/1	0.96	0.13	49,49,49,49	0
57	MG	1A	3009	1/1	0.96	0.07	32,32,32,32	0
57	MG	1r	101	1/1	0.96	0.18	51,51,51,51	0
57	MG	1A	3029	1/1	0.96	0.15	24,24,24,24	0
57	MG	2A	3235	1/1	0.96	0.07	47,47,47,47	0
57	MG	1a	1604	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3848	1/1	0.96	0.13	44,44,44,44	0
57	MG	1A	3849	1/1	0.96	0.10	56,56,56,56	0
57	MG	1A	4046	1/1	0.96	0.07	34,34,34,34	0
57	MG	2A	3508	1/1	0.96	0.20	50,50,50,50	0
57	MG	1A	4048	1/1	0.96	0.09	18,18,18,18	0
57	MG	1A	4050	1/1	0.96	0.08	23,23,23,23	0
57	MG	2A	3515	1/1	0.96	0.08	46,46,46,46	0
57	MG	1a	1612	1/1	0.96	0.04	67,67,67,67	0
57	MG	1A	3850	1/1	0.96	0.05	50,50,50,50	0
57	MG	1A	4053	1/1	0.96	0.08	42,42,42,42	0
57	MG	1A	3530	1/1	0.96	0.09	36,36,36,36	0
57	MG	1A	3309	1/1	0.96	0.08	34,34,34,34	0
57	MG	1a	1618	1/1	0.96	0.04	52,52,52,52	0
57	MG	1A	3668	1/1	0.96	0.06	52,52,52,52	0
57	MG	1A	3160	1/1	0.96	0.07	28,28,28,28	0
57	MG	1A	3129	1/1	0.96	0.12	30,30,30,30	0
57	MG	1A	3858	1/1	0.96	0.07	57,57,57,57	0
57	MG	2A	3004	1/1	0.96	0.35	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3672	1/1	0.96	0.11	21,21,21,21	0
57	MG	1A	3444	1/1	0.96	0.08	42,42,42,42	0
57	MG	1A	3445	1/1	0.96	0.34	44,44,44,44	0
57	MG	1A	3539	1/1	0.96	0.16	36,36,36,36	0
57	MG	1A	3864	1/1	0.96	0.10	31,31,31,31	0
57	MG	1A	3374	1/1	0.96	0.06	41,41,41,41	0
57	MG	1A	4073	1/1	0.96	0.12	42,42,42,42	0
59	ERY	1A	4087	51/51	0.96	0.10	25,42,54,59	0
57	MG	2A	3014	1/1	0.96	0.11	41,41,41,41	0
60	ZN	14	102	1/1	0.96	0.11	118,118,118,118	0
60	ZN	24	501	1/1	0.96	0.13	137,137,137,137	0
60	ZN	2n	501	1/1	0.96	0.05	94,94,94,94	0
57	MG	2E	307	1/1	0.97	0.10	45,45,45,45	0
57	MG	1A	3042	1/1	0.97	0.04	21,21,21,21	0
57	MG	1a	1645	1/1	0.97	0.11	39,39,39,39	0
57	MG	1A	3728	1/1	0.97	0.16	49,49,49,49	0
57	MG	1A	3198	1/1	0.97	0.06	29,29,29,29	0
57	MG	2A	3043	1/1	0.97	0.07	49,49,49,49	0
57	MG	1A	3590	1/1	0.97	0.10	24,24,24,24	0
57	MG	2F	305	1/1	0.97	0.18	51,51,51,51	0
57	MG	2A	3295	1/1	0.97	0.10	55,55,55,55	0
57	MG	1a	1650	1/1	0.97	0.13	48,48,48,48	0
57	MG	2A	3297	1/1	0.97	0.25	35,35,35,35	0
57	MG	1a	1651	1/1	0.97	0.06	44,44,44,44	0
57	MG	1A	3901	1/1	0.97	0.06	46,46,46,46	0
57	MG	1A	3360	1/1	0.97	0.15	39,39,39,39	0
57	MG	1A	3500	1/1	0.97	0.19	37,37,37,37	0
57	MG	1A	3593	1/1	0.97	0.05	38,38,38,38	0
57	MG	2T	201	1/1	0.97	0.09	57,57,57,57	0
57	MG	1A	3159	1/1	0.97	0.08	36,36,36,36	0
57	MG	1a	1658	1/1	0.97	0.10	47,47,47,47	0
57	MG	1A	3741	1/1	0.97	0.06	34,34,34,34	0
57	MG	1B	219	1/1	0.97	0.07	45,45,45,45	0
57	MG	1B	221	1/1	0.97	0.04	40,40,40,40	0
57	MG	1B	222	1/1	0.97	0.06	36,36,36,36	0
57	MG	1B	223	1/1	0.97	0.05	30,30,30,30	0
57	MG	2X	101	1/1	0.97	0.06	68,68,68,68	0
57	MG	1A	3080	1/1	0.97	0.08	41,41,41,41	0
57	MG	1A	3064	1/1	0.97	0.12	41,41,41,41	0
57	MG	2A	3060	1/1	0.97	0.08	46,46,46,46	0
57	MG	1A	3054	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3601	1/1	0.97	0.14	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3747	1/1	0.97	0.07	27,27,27,27	0
57	MG	23	102	1/1	0.97	0.06	56,56,56,56	0
57	MG	1A	3602	1/1	0.97	0.24	34,34,34,34	0
57	MG	1B	230	1/1	0.97	0.08	41,41,41,41	0
57	MG	1A	3429	1/1	0.97	0.09	37,37,37,37	0
57	MG	2A	3319	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3918	1/1	0.97	0.05	26,26,26,26	0
57	MG	1A	3751	1/1	0.97	0.08	43,43,43,43	0
57	MG	1A	3921	1/1	0.97	0.05	50,50,50,50	0
57	MG	1A	3922	1/1	0.97	0.04	17,17,17,17	0
57	MG	1A	3013	1/1	0.97	0.14	23,23,23,23	0
57	MG	1B	237	1/1	0.97	0.05	31,31,31,31	0
57	MG	1A	3605	1/1	0.97	0.14	37,37,37,37	0
57	MG	1A	3606	1/1	0.97	0.04	38,38,38,38	0
57	MG	1D	304	1/1	0.97	0.15	47,47,47,47	0
57	MG	1D	305	1/1	0.97	0.04	22,22,22,22	0
57	MG	2A	3617	1/1	0.97	0.04	35,35,35,35	0
57	MG	1A	3755	1/1	0.97	0.07	38,38,38,38	0
57	MG	2A	3619	1/1	0.97	0.12	61,61,61,61	0
57	MG	1D	308	1/1	0.97	0.17	31,31,31,31	0
57	MG	2A	3080	1/1	0.97	0.10	46,46,46,46	0
57	MG	1D	310	1/1	0.97	0.04	45,45,45,45	0
57	MG	1A	3756	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3084	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3607	1/1	0.97	0.09	34,34,34,34	0
57	MG	1A	3608	1/1	0.97	0.04	28,28,28,28	0
57	MG	1a	1690	1/1	0.97	0.22	51,51,51,51	0
57	MG	1E	302	1/1	0.97	0.16	35,35,35,35	0
57	MG	2A	3634	1/1	0.97	0.13	50,50,50,50	0
57	MG	2A	3635	1/1	0.97	0.10	47,47,47,47	0
57	MG	1A	3609	1/1	0.97	0.06	24,24,24,24	0
57	MG	1A	3610	1/1	0.97	0.06	34,34,34,34	0
57	MG	2a	1623	1/1	0.97	0.10	44,44,44,44	0
57	MG	2A	3091	1/1	0.97	0.04	44,44,44,44	0
57	MG	2A	3344	1/1	0.97	0.06	44,44,44,44	0
57	MG	1A	3252	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3253	1/1	0.97	0.08	39,39,39,39	0
57	MG	1A	3433	1/1	0.97	0.14	55,55,55,55	0
57	MG	2A	3350	1/1	0.97	0.26	42,42,42,42	0
57	MG	1A	3936	1/1	0.97	0.08	48,48,48,48	0
57	MG	1A	3937	1/1	0.97	0.05	44,44,44,44	0
57	MG	1a	1699	1/1	0.97	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3938	1/1	0.97	0.08	58,58,58,58	0
57	MG	1A	3767	1/1	0.97	0.06	35,35,35,35	0
57	MG	1F	302	1/1	0.97	0.10	59,59,59,59	0
57	MG	1A	3614	1/1	0.97	0.07	17,17,17,17	0
57	MG	1A	3204	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3942	1/1	0.97	0.04	40,40,40,40	0
57	MG	1F	308	1/1	0.97	0.28	35,35,35,35	0
57	MG	1F	309	1/1	0.97	0.07	48,48,48,48	0
57	MG	2A	3656	1/1	0.97	0.14	50,50,50,50	0
57	MG	1A	3164	1/1	0.97	0.16	36,36,36,36	0
57	MG	2A	3109	1/1	0.97	0.14	43,43,43,43	0
57	MG	1A	3771	1/1	0.97	0.10	42,42,42,42	0
57	MG	1A	3945	1/1	0.97	0.06	47,47,47,47	0
57	MG	1a	1712	1/1	0.97	0.12	42,42,42,42	0
57	MG	1A	3313	1/1	0.97	0.15	36,36,36,36	0
57	MG	1A	3107	1/1	0.97	0.06	32,32,32,32	0
57	MG	1G	204	1/1	0.97	0.10	38,38,38,38	0
57	MG	2A	3667	1/1	0.97	0.12	42,42,42,42	0
57	MG	1A	3515	1/1	0.97	0.13	33,33,33,33	0
57	MG	1A	3109	1/1	0.97	0.33	31,31,31,31	0
57	MG	1N	202	1/1	0.97	0.06	42,42,42,42	0
57	MG	1A	3777	1/1	0.97	0.08	21,21,21,21	0
57	MG	1A	3778	1/1	0.97	0.05	28,28,28,28	0
57	MG	1A	3625	1/1	0.97	0.05	27,27,27,27	0
57	MG	1A	3056	1/1	0.97	0.19	41,41,41,41	0
57	MG	1O	203	1/1	0.97	0.08	56,56,56,56	0
57	MG	1A	3954	1/1	0.97	0.10	24,24,24,24	0
57	MG	2A	3677	1/1	0.97	0.16	38,38,38,38	0
57	MG	1A	3782	1/1	0.97	0.06	28,28,28,28	0
57	MG	2a	1662	1/1	0.97	0.09	48,48,48,48	0
57	MG	2A	3127	1/1	0.97	0.06	46,46,46,46	0
57	MG	2A	3381	1/1	0.97	0.07	55,55,55,55	0
57	MG	1A	3211	1/1	0.97	0.14	46,46,46,46	0
57	MG	1A	3784	1/1	0.97	0.07	54,54,54,54	0
57	MG	1A	3787	1/1	0.97	0.04	52,52,52,52	0
57	MG	1A	3628	1/1	0.97	0.06	34,34,34,34	0
57	MG	1A	3960	1/1	0.97	0.10	54,54,54,54	0
57	MG	2A	3387	1/1	0.97	0.07	51,51,51,51	0
57	MG	1a	1733	1/1	0.97	0.05	39,39,39,39	0
57	MG	2a	1672	1/1	0.97	0.08	64,64,64,64	0
57	MG	1A	3629	1/1	0.97	0.09	31,31,31,31	0
57	MG	2A	3689	1/1	0.97	0.08	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3794	1/1	0.97	0.08	49,49,49,49	0
57	MG	1A	3963	1/1	0.97	0.06	68,68,68,68	0
57	MG	1A	3169	1/1	0.97	0.12	38,38,38,38	0
57	MG	2A	3393	1/1	0.97	0.11	51,51,51,51	0
57	MG	2a	1679	1/1	0.97	0.15	46,46,46,46	0
57	MG	1A	3442	1/1	0.97	0.08	40,40,40,40	0
57	MG	1A	3797	1/1	0.97	0.05	17,17,17,17	0
57	MG	1A	3443	1/1	0.97	0.06	37,37,37,37	0
57	MG	2A	3397	1/1	0.97	0.21	39,39,39,39	0
57	MG	1A	3633	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3262	1/1	0.97	0.27	42,42,42,42	0
57	MG	1A	3802	1/1	0.97	0.06	40,40,40,40	0
57	MG	1a	1746	1/1	0.97	0.10	50,50,50,50	0
57	MG	1A	3973	1/1	0.97	0.07	21,21,21,21	0
57	MG	2A	3707	1/1	0.97	0.10	53,53,53,53	0
57	MG	1U	201	1/1	0.97	0.10	27,27,27,27	0
57	MG	2A	3709	1/1	0.97	0.05	51,51,51,51	0
57	MG	1a	1749	1/1	0.97	0.13	41,41,41,41	0
57	MG	1A	3137	1/1	0.97	0.23	31,31,31,31	0
57	MG	2A	3152	1/1	0.97	0.08	47,47,47,47	0
57	MG	1A	3804	1/1	0.97	0.04	41,41,41,41	0
57	MG	1U	205	1/1	0.97	0.04	40,40,40,40	0
57	MG	1A	3805	1/1	0.97	0.06	38,38,38,38	0
57	MG	1U	207	1/1	0.97	0.19	30,30,30,30	0
57	MG	1U	208	1/1	0.97	0.28	33,33,33,33	0
57	MG	1A	3806	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3138	1/1	0.97	0.06	27,27,27,27	0
57	MG	1A	3982	1/1	0.97	0.06	23,23,23,23	0
57	MG	1A	3034	1/1	0.97	0.33	31,31,31,31	0
57	MG	2A	3724	1/1	0.97	0.14	45,45,45,45	0
57	MG	2A	3725	1/1	0.97	0.05	45,45,45,45	0
57	MG	1V	204	1/1	0.97	0.14	38,38,38,38	0
57	MG	1V	205	1/1	0.97	0.05	43,43,43,43	0
57	MG	1A	3984	1/1	0.97	0.14	17,17,17,17	0
57	MG	2A	3729	1/1	0.97	0.09	43,43,43,43	0
57	MG	1A	3527	1/1	0.97	0.06	48,48,48,48	0
57	MG	1A	3216	1/1	0.97	0.08	39,39,39,39	0
57	MG	1A	3069	1/1	0.97	0.06	26,26,26,26	0
57	MG	1A	3643	1/1	0.97	0.06	39,39,39,39	0
57	MG	1a	1767	1/1	0.97	0.10	54,54,54,54	0
57	MG	1A	3113	1/1	0.97	0.08	31,31,31,31	0
57	MG	1W	205	1/1	0.97	0.13	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3993	1/1	0.97	0.07	31,31,31,31	0
57	MG	1A	3645	1/1	0.97	0.06	22,22,22,22	0
57	MG	1X	103	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3269	1/1	0.97	0.11	29,29,29,29	0
57	MG	2A	3742	1/1	0.97	0.05	39,39,39,39	0
57	MG	1A	3453	1/1	0.97	0.10	47,47,47,47	0
57	MG	2a	1725	1/1	0.97	0.06	49,49,49,49	0
57	MG	1A	3271	1/1	0.97	0.08	37,37,37,37	0
57	MG	2A	3433	1/1	0.97	0.23	46,46,46,46	0
57	MG	1Y	201	1/1	0.97	0.14	43,43,43,43	0
57	MG	1A	3011	1/1	0.97	0.08	33,33,33,33	0
57	MG	1A	3822	1/1	0.97	0.05	26,26,26,26	0
57	MG	1A	3823	1/1	0.97	0.06	27,27,27,27	0
57	MG	1A	3651	1/1	0.97	0.06	37,37,37,37	0
57	MG	10	102	1/1	0.97	0.17	46,46,46,46	0
57	MG	2A	3753	1/1	0.97	0.07	38,38,38,38	0
57	MG	1a	1782	1/1	0.97	0.05	47,47,47,47	0
57	MG	1A	3825	1/1	0.97	0.04	37,37,37,37	0
57	MG	1A	4006	1/1	0.97	0.07	61,61,61,61	0
57	MG	2A	3757	1/1	0.97	0.08	42,42,42,42	0
57	MG	10	105	1/1	0.97	0.05	39,39,39,39	0
57	MG	1A	3146	1/1	0.97	0.06	27,27,27,27	0
57	MG	2A	3446	1/1	0.97	0.10	27,27,27,27	0
57	MG	1A	4008	1/1	0.97	0.09	44,44,44,44	0
57	MG	1a	1791	1/1	0.97	0.08	32,32,32,32	0
57	MG	1A	3537	1/1	0.97	0.13	26,26,26,26	0
57	MG	2A	3193	1/1	0.97	0.05	37,37,37,37	0
57	MG	1A	3655	1/1	0.97	0.06	49,49,49,49	0
57	MG	1A	3538	1/1	0.97	0.13	30,30,30,30	0
57	MG	1A	4013	1/1	0.97	0.09	35,35,35,35	0
57	MG	1A	4015	1/1	0.97	0.06	44,44,44,44	0
57	MG	2A	3771	1/1	0.97	0.08	50,50,50,50	0
57	MG	1A	3331	1/1	0.97	0.04	30,30,30,30	0
57	MG	1A	4018	1/1	0.97	0.04	47,47,47,47	0
57	MG	1A	3831	1/1	0.97	0.16	29,29,29,29	0
57	MG	1A	3221	1/1	0.97	0.04	31,31,31,31	0
57	MG	1a	1803	1/1	0.97	0.05	38,38,38,38	0
57	MG	1A	3541	1/1	0.97	0.11	35,35,35,35	0
57	MG	2A	3463	1/1	0.97	0.12	45,45,45,45	0
57	MG	2A	3204	1/1	0.97	0.04	52,52,52,52	0
57	MG	2A	3780	1/1	0.97	0.04	41,41,41,41	0
57	MG	1A	3278	1/1	0.97	0.09	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3334	1/1	0.97	0.12	41,41,41,41	0
57	MG	1A	3092	1/1	0.97	0.19	47,47,47,47	0
57	MG	2A	3209	1/1	0.97	0.19	62,62,62,62	0
57	MG	1A	3666	1/1	0.97	0.05	20,20,20,20	0
57	MG	1A	3462	1/1	0.97	0.09	51,51,51,51	0
57	MG	15	105	1/1	0.97	0.30	35,35,35,35	0
57	MG	1A	4030	1/1	0.97	0.11	47,47,47,47	0
57	MG	2a	1770	1/1	0.97	0.05	68,68,68,68	0
57	MG	1A	3336	1/1	0.97	0.07	39,39,39,39	0
57	MG	1A	3464	1/1	0.97	0.25	30,30,30,30	0
57	MG	1A	4035	1/1	0.97	0.09	16,16,16,16	0
57	MG	2A	3792	1/1	0.97	0.05	47,47,47,47	0
57	MG	1A	3465	1/1	0.97	0.15	41,41,41,41	0
57	MG	1A	3225	1/1	0.97	0.06	21,21,21,21	0
57	MG	1A	3398	1/1	0.97	0.10	37,37,37,37	0
57	MG	2A	3220	1/1	0.97	0.13	49,49,49,49	0
57	MG	1l	202	1/1	0.97	0.11	40,40,40,40	0
57	MG	1A	3676	1/1	0.97	0.10	46,46,46,46	0
57	MG	1A	3553	1/1	0.97	0.15	36,36,36,36	0
57	MG	2A	3224	1/1	0.97	0.10	34,34,34,34	0
57	MG	2A	3485	1/1	0.97	0.07	44,44,44,44	0
57	MG	18	101	1/1	0.97	0.10	48,48,48,48	0
57	MG	2A	3804	1/1	0.97	0.06	34,34,34,34	0
57	MG	1A	3399	1/1	0.97	0.15	35,35,35,35	0
57	MG	1A	3116	1/1	0.97	0.06	34,34,34,34	0
57	MG	1A	3684	1/1	0.97	0.09	43,43,43,43	0
57	MG	1A	3184	1/1	0.97	0.06	35,35,35,35	0
57	MG	2A	3810	1/1	0.97	0.12	38,38,38,38	0
57	MG	2a	1792	1/1	0.97	0.12	33,33,33,33	0
57	MG	2A	3811	1/1	0.97	0.07	40,40,40,40	0
57	MG	1A	4049	1/1	0.97	0.09	35,35,35,35	0
57	MG	1A	3119	1/1	0.97	0.09	28,28,28,28	0
57	MG	1A	3560	1/1	0.97	0.09	35,35,35,35	0
57	MG	1A	3693	1/1	0.97	0.07	29,29,29,29	0
57	MG	1A	4054	1/1	0.97	0.04	25,25,25,25	0
57	MG	1w	106	1/1	0.97	0.06	66,66,66,66	0
57	MG	1A	4056	1/1	0.97	0.07	44,44,44,44	0
57	MG	2A	3824	1/1	0.97	0.07	26,26,26,26	0
57	MG	1A	3561	1/1	0.97	0.34	34,34,34,34	0
57	MG	1a	1606	1/1	0.97	0.16	60,60,60,60	0
57	MG	1A	3150	1/1	0.97	0.16	26,26,26,26	0
57	MG	1x	106	1/1	0.97	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1x	108	1/1	0.97	0.08	22,22,22,22	0
57	MG	1a	1608	1/1	0.97	0.15	56,56,56,56	0
57	MG	2A	3831	1/1	0.97	0.12	55,55,55,55	0
57	MG	1A	3696	1/1	0.97	0.04	25,25,25,25	0
57	MG	1A	3697	1/1	0.97	0.05	55,55,55,55	0
57	MG	2A	3509	1/1	0.97	0.07	30,30,30,30	0
57	MG	1A	4063	1/1	0.97	0.09	53,53,53,53	0
57	MG	2a	1813	1/1	0.97	0.14	45,45,45,45	0
57	MG	1A	3862	1/1	0.97	0.05	29,29,29,29	0
57	MG	2A	3512	1/1	0.97	0.17	54,54,54,54	0
57	MG	1A	3187	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3699	1/1	0.97	0.06	24,24,24,24	0
57	MG	1A	3700	1/1	0.97	0.04	25,25,25,25	0
57	MG	2A	3251	1/1	0.97	0.23	45,45,45,45	0
57	MG	1a	1616	1/1	0.97	0.04	42,42,42,42	0
57	MG	1A	3405	1/1	0.97	0.09	38,38,38,38	0
57	MG	2A	3007	1/1	0.97	0.06	40,40,40,40	0
57	MG	2a	1824	1/1	0.97	0.13	47,47,47,47	0
57	MG	2A	3008	1/1	0.97	0.06	47,47,47,47	0
57	MG	2A	3256	1/1	0.97	0.05	50,50,50,50	0
57	MG	1A	3702	1/1	0.97	0.15	26,26,26,26	0
57	MG	2A	3525	1/1	0.97	0.08	28,28,28,28	0
57	MG	1a	1619	1/1	0.97	0.07	54,54,54,54	0
57	MG	1A	3343	1/1	0.97	0.05	42,42,42,42	0
57	MG	2A	3528	1/1	0.97	0.08	34,34,34,34	0
57	MG	1A	3476	1/1	0.97	0.06	31,31,31,31	0
57	MG	1A	3705	1/1	0.97	0.07	27,27,27,27	0
57	MG	2A	3532	1/1	0.97	0.14	44,44,44,44	0
57	MG	1A	3012	1/1	0.97	0.11	32,32,32,32	0
57	MG	1A	3707	1/1	0.97	0.04	17,17,17,17	0
57	MG	2A	3535	1/1	0.97	0.09	45,45,45,45	0
57	MG	1A	3408	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3152	1/1	0.97	0.07	36,36,36,36	0
57	MG	2A	3538	1/1	0.97	0.08	40,40,40,40	0
57	MG	2A	3019	1/1	0.97	0.06	35,35,35,35	0
57	MG	1A	3039	1/1	0.97	0.11	28,28,28,28	0
57	MG	1A	3481	1/1	0.97	0.08	26,26,26,26	0
57	MG	2A	3022	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3482	1/1	0.97	0.13	28,28,28,28	0
57	MG	1A	3191	1/1	0.97	0.20	27,27,27,27	0
57	MG	1A	3349	1/1	0.97	0.09	53,53,53,53	0
57	MG	1A	3154	1/1	0.97	0.06	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3552	1/1	0.97	0.06	37,37,37,37	0
57	MG	1A	3238	1/1	0.97	0.20	33,33,33,33	0
57	MG	1A	3487	1/1	0.97	0.07	39,39,39,39	0
57	MG	1a	1635	1/1	0.97	0.22	67,67,67,67	0
57	MG	1A	4086	1/1	0.97	0.20	36,36,36,36	0
57	MG	1A	3239	1/1	0.97	0.15	47,47,47,47	0
57	MG	1A	3076	1/1	0.97	0.04	33,33,33,33	0
57	MG	2D	305	1/1	0.97	0.21	45,45,45,45	0
57	MG	1A	3123	1/1	0.97	0.06	37,37,37,37	0
57	MG	2A	3283	1/1	0.97	0.07	53,53,53,53	0
57	MG	2A	3034	1/1	0.97	0.07	30,30,30,30	0
57	MG	1A	3242	1/1	0.97	0.13	37,37,37,37	0
57	MG	1A	3019	1/1	0.97	0.19	41,41,41,41	0
57	MG	1A	3895	1/1	0.97	0.04	37,37,37,37	0
57	MG	1A	3244	1/1	0.97	0.09	33,33,33,33	0
57	MG	2A	3347	1/1	0.98	0.09	42,42,42,42	0
57	MG	1A	4052	1/1	0.98	0.05	39,39,39,39	0
57	MG	2A	3349	1/1	0.98	0.07	39,39,39,39	0
57	MG	1a	1675	1/1	0.98	0.15	44,44,44,44	0
57	MG	1T	203	1/1	0.98	0.05	42,42,42,42	0
57	MG	1A	3385	1/1	0.98	0.06	25,25,25,25	0
57	MG	1U	202	1/1	0.98	0.10	29,29,29,29	0
57	MG	1A	3106	1/1	0.98	0.05	27,27,27,27	0
57	MG	2A	3760	1/1	0.98	0.05	40,40,40,40	0
57	MG	1A	4055	1/1	0.98	0.07	29,29,29,29	0
57	MG	1A	3920	1/1	0.98	0.05	38,38,38,38	0
57	MG	2A	3763	1/1	0.98	0.03	39,39,39,39	0
57	MG	1A	3807	1/1	0.98	0.07	24,24,24,24	0
57	MG	1A	3017	1/1	0.98	0.12	54,54,54,54	0
57	MG	1A	3550	1/1	0.98	0.18	33,33,33,33	0
57	MG	1a	1685	1/1	0.98	0.11	35,35,35,35	0
57	MG	2A	3555	1/1	0.98	0.07	30,30,30,30	0
57	MG	1A	3035	1/1	0.98	0.15	37,37,37,37	0
57	MG	1A	3170	1/1	0.98	0.04	42,42,42,42	0
57	MG	1U	211	1/1	0.98	0.35	34,34,34,34	0
57	MG	1A	3621	1/1	0.98	0.07	24,24,24,24	0
57	MG	1A	3813	1/1	0.98	0.05	50,50,50,50	0
57	MG	2A	3561	1/1	0.98	0.06	35,35,35,35	0
57	MG	1V	203	1/1	0.98	0.21	28,28,28,28	0
57	MG	1A	3493	1/1	0.98	0.06	30,30,30,30	0
57	MG	2A	3564	1/1	0.98	0.07	38,38,38,38	0
57	MG	2A	3017	1/1	0.98	0.07	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3624	1/1	0.98	0.10	30,30,30,30	0
57	MG	1A	3293	1/1	0.98	0.12	29,29,29,29	0
57	MG	1A	3207	1/1	0.98	0.07	31,31,31,31	0
57	MG	1A	3818	1/1	0.98	0.04	38,38,38,38	0
57	MG	1A	3295	1/1	0.98	0.18	35,35,35,35	0
57	MG	1A	3557	1/1	0.98	0.26	46,46,46,46	0
57	MG	1A	3140	1/1	0.98	0.15	29,29,29,29	0
57	MG	1A	3559	1/1	0.98	0.07	41,41,41,41	0
57	MG	1A	3499	1/1	0.98	0.16	24,24,24,24	0
57	MG	1A	3209	1/1	0.98	0.25	31,31,31,31	0
57	MG	1a	1703	1/1	0.98	0.08	52,52,52,52	0
57	MG	1X	102	1/1	0.98	0.20	34,34,34,34	0
57	MG	1A	3003	1/1	0.98	0.03	27,27,27,27	0
57	MG	1X	104	1/1	0.98	0.05	33,33,33,33	0
57	MG	2A	3581	1/1	0.98	0.10	40,40,40,40	0
57	MG	1A	3563	1/1	0.98	0.14	31,31,31,31	0
57	MG	2A	3795	1/1	0.98	0.07	43,43,43,43	0
57	MG	1A	3396	1/1	0.98	0.04	30,30,30,30	0
57	MG	2A	3207	1/1	0.98	0.05	46,46,46,46	0
57	MG	1A	3173	1/1	0.98	0.32	40,40,40,40	0
57	MG	1A	3174	1/1	0.98	0.05	30,30,30,30	0
57	MG	1A	3727	1/1	0.98	0.12	52,52,52,52	0
57	MG	1A	3638	1/1	0.98	0.03	21,21,21,21	0
57	MG	1A	3729	1/1	0.98	0.11	41,41,41,41	0
57	MG	1A	3142	1/1	0.98	0.09	35,35,35,35	0
57	MG	2a	1693	1/1	0.98	0.04	57,57,57,57	0
57	MG	2A	3594	1/1	0.98	0.06	47,47,47,47	0
57	MG	1A	3568	1/1	0.98	0.08	40,40,40,40	0
57	MG	2A	3806	1/1	0.98	0.09	39,39,39,39	0
57	MG	1B	202	1/1	0.98	0.11	38,38,38,38	0
57	MG	1A	3451	1/1	0.98	0.06	35,35,35,35	0
57	MG	2a	1699	1/1	0.98	0.06	60,60,60,60	0
57	MG	1A	3733	1/1	0.98	0.05	40,40,40,40	0
57	MG	1A	3734	1/1	0.98	0.03	31,31,31,31	0
57	MG	1A	3176	1/1	0.98	0.08	25,25,25,25	0
57	MG	1A	3177	1/1	0.98	0.08	24,24,24,24	0
57	MG	1A	3840	1/1	0.98	0.04	42,42,42,42	0
57	MG	1A	3015	1/1	0.98	0.14	26,26,26,26	0
57	MG	1A	3646	1/1	0.98	0.06	17,17,17,17	0
57	MG	1A	3843	1/1	0.98	0.12	44,44,44,44	0
57	MG	2A	3819	1/1	0.98	0.13	62,62,62,62	0
57	MG	2A	3606	1/1	0.98	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
57	MG	2A	3225	1/1	0.98	0.27	32,32,32,32	0
57	MG	2A	3404	1/1	0.98	0.07	31,31,31,31	0
57	MG	1A	3010	1/1	0.98	0.06	34,34,34,34	0
57	MG	1a	1728	1/1	0.98	0.04	50,50,50,50	0
57	MG	1A	3259	1/1	0.98	0.12	33,33,33,33	0
57	MG	12	102	1/1	0.98	0.11	45,45,45,45	0
57	MG	1A	3744	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3847	1/1	0.98	0.06	18,18,18,18	0
57	MG	1A	3512	1/1	0.98	0.13	34,34,34,34	0
57	MG	1A	3145	1/1	0.98	0.08	26,26,26,26	0
57	MG	1A	3087	1/1	0.98	0.11	32,32,32,32	0
57	MG	1A	3040	1/1	0.98	0.12	27,27,27,27	0
57	MG	15	101	1/1	0.98	0.10	33,33,33,33	0
57	MG	15	102	1/1	0.98	0.08	33,33,33,33	0
57	MG	2A	3621	1/1	0.98	0.07	44,44,44,44	0
57	MG	1B	220	1/1	0.98	0.05	43,43,43,43	0
57	MG	1A	3653	1/1	0.98	0.07	40,40,40,40	0
57	MG	2A	3624	1/1	0.98	0.10	39,39,39,39	0
57	MG	1A	3853	1/1	0.98	0.08	31,31,31,31	0
57	MG	1A	3969	1/1	0.98	0.06	34,34,34,34	0
57	MG	2A	3627	1/1	0.98	0.12	48,48,48,48	0
57	MG	2A	3067	1/1	0.98	0.05	38,38,38,38	0
57	MG	2A	3845	1/1	0.98	0.11	39,39,39,39	0
57	MG	2A	3629	1/1	0.98	0.08	35,35,35,35	0
57	MG	2A	3847	1/1	0.98	0.08	30,30,30,30	0
57	MG	1A	3750	1/1	0.98	0.04	49,49,49,49	0
57	MG	1A	3089	1/1	0.98	0.07	36,36,36,36	0
57	MG	1A	3856	1/1	0.98	0.06	39,39,39,39	0
57	MG	2A	3851	1/1	0.98	0.07	40,40,40,40	0
57	MG	1A	3311	1/1	0.98	0.08	40,40,40,40	0
57	MG	1A	3656	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3222	1/1	0.98	0.11	42,42,42,42	0
57	MG	1A	3977	1/1	0.98	0.05	39,39,39,39	0
57	MG	1A	3978	1/1	0.98	0.06	55,55,55,55	0
57	MG	17	106	1/1	0.98	0.03	35,35,35,35	0
57	MG	1A	3658	1/1	0.98	0.05	44,44,44,44	0
57	MG	1A	3980	1/1	0.98	0.04	30,30,30,30	0
57	MG	1A	3583	1/1	0.98	0.04	30,30,30,30	0
57	MG	1A	3031	1/1	0.98	0.06	40,40,40,40	0
57	MG	2a	1749	1/1	0.98	0.14	44,44,44,44	0
57	MG	2A	3081	1/1	0.98	0.04	39,39,39,39	0
57	MG	1A	3758	1/1	0.98	0.04	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3032	1/1	0.98	0.12	21,21,21,21	0
57	MG	1B	238	1/1	0.98	0.04	44,44,44,44	0
57	MG	1A	3760	1/1	0.98	0.14	49,49,49,49	0
57	MG	1A	3226	1/1	0.98	0.16	30,30,30,30	0
57	MG	2A	3650	1/1	0.98	0.05	57,57,57,57	0
57	MG	1A	3867	1/1	0.98	0.04	25,25,25,25	0
57	MG	2A	3263	1/1	0.98	0.22	36,36,36,36	0
57	MG	1A	3522	1/1	0.98	0.15	26,26,26,26	0
57	MG	1A	3664	1/1	0.98	0.04	32,32,32,32	0
57	MG	1D	307	1/1	0.98	0.11	32,32,32,32	0
57	MG	1A	3070	1/1	0.98	0.12	19,19,19,19	0
57	MG	2a	1763	1/1	0.98	0.10	58,58,58,58	0
57	MG	2A	3448	1/1	0.98	0.05	45,45,45,45	0
57	MG	1D	309	1/1	0.98	0.07	40,40,40,40	0
57	MG	1A	3995	1/1	0.98	0.07	28,28,28,28	0
57	MG	2D	302	1/1	0.98	0.10	41,41,41,41	0
57	MG	2A	3270	1/1	0.98	0.06	44,44,44,44	0
57	MG	1A	3871	1/1	0.98	0.13	24,24,24,24	0
57	MG	2A	3096	1/1	0.98	0.05	46,46,46,46	0
57	MG	2A	3663	1/1	0.98	0.03	33,33,33,33	0
57	MG	1A	3872	1/1	0.98	0.08	36,36,36,36	0
57	MG	2a	1773	1/1	0.98	0.10	43,43,43,43	0
57	MG	1A	3071	1/1	0.98	0.06	22,22,22,22	0
57	MG	2A	3666	1/1	0.98	0.09	52,52,52,52	0
57	MG	1A	3667	1/1	0.98	0.04	26,26,26,26	0
57	MG	1A	3043	1/1	0.98	0.08	26,26,26,26	0
57	MG	2A	3458	1/1	0.98	0.03	28,28,28,28	0
57	MG	1E	304	1/1	0.98	0.07	25,25,25,25	0
57	MG	1A	3272	1/1	0.98	0.06	41,41,41,41	0
57	MG	1E	306	1/1	0.98	0.04	35,35,35,35	0
57	MG	1A	3670	1/1	0.98	0.08	27,27,27,27	0
57	MG	1A	3073	1/1	0.98	0.05	14,14,14,14	0
57	MG	1E	309	1/1	0.98	0.12	16,16,16,16	0
57	MG	1A	3369	1/1	0.98	0.05	24,24,24,24	0
57	MG	2F	306	1/1	0.98	0.11	49,49,49,49	0
57	MG	1A	3594	1/1	0.98	0.12	21,21,21,21	0
57	MG	1A	3595	1/1	0.98	0.04	25,25,25,25	0
57	MG	1A	3596	1/1	0.98	0.07	33,33,33,33	0
57	MG	1A	3883	1/1	0.98	0.04	33,33,33,33	0
57	MG	1a	1786	1/1	0.98	0.04	43,43,43,43	0
57	MG	1a	1787	1/1	0.98	0.08	50,50,50,50	0
57	MG	1A	3057	1/1	0.98	0.12	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2R	202	1/1	0.98	0.05	44,44,44,44	0
57	MG	1F	303	1/1	0.98	0.19	34,34,34,34	0
57	MG	2R	204	1/1	0.98	0.05	36,36,36,36	0
57	MG	1A	3276	1/1	0.98	0.05	34,34,34,34	0
57	MG	1A	3125	1/1	0.98	0.22	31,31,31,31	0
57	MG	2A	3118	1/1	0.98	0.06	47,47,47,47	0
57	MG	1a	1793	1/1	0.98	0.05	55,55,55,55	0
57	MG	1F	306	1/1	0.98	0.04	42,42,42,42	0
57	MG	1A	3780	1/1	0.98	0.06	49,49,49,49	0
57	MG	1A	3683	1/1	0.98	0.05	24,24,24,24	0
57	MG	1A	4017	1/1	0.98	0.05	39,39,39,39	0
57	MG	1F	310	1/1	0.98	0.08	36,36,36,36	0
57	MG	2Y	201	1/1	0.98	0.13	37,37,37,37	0
57	MG	1A	3889	1/1	0.98	0.06	54,54,54,54	0
57	MG	1A	3126	1/1	0.98	0.22	34,34,34,34	0
57	MG	2A	3697	1/1	0.98	0.06	20,20,20,20	0
57	MG	1a	1801	1/1	0.98	0.09	59,59,59,59	0
57	MG	1F	313	1/1	0.98	0.04	30,30,30,30	0
57	MG	1A	3685	1/1	0.98	0.06	46,46,46,46	0
57	MG	1A	3893	1/1	0.98	0.04	39,39,39,39	0
57	MG	1A	3279	1/1	0.98	0.07	39,39,39,39	0
57	MG	2a	1815	1/1	0.98	0.12	45,45,45,45	0
57	MG	26	101	1/1	0.98	0.14	41,41,41,41	0
57	MG	2A	3491	1/1	0.98	0.08	34,34,34,34	0
57	MG	1A	3785	1/1	0.98	0.06	48,48,48,48	0
57	MG	2A	3706	1/1	0.98	0.09	55,55,55,55	0
57	MG	1H	201	1/1	0.98	0.13	41,41,41,41	0
57	MG	1A	3786	1/1	0.98	0.10	18,18,18,18	0
57	MG	1A	3044	1/1	0.98	0.08	30,30,30,30	0
57	MG	1A	3788	1/1	0.98	0.06	37,37,37,37	0
57	MG	1A	4028	1/1	0.98	0.04	22,22,22,22	0
57	MG	2a	1825	1/1	0.98	0.09	53,53,53,53	0
57	MG	2A	3138	1/1	0.98	0.18	37,37,37,37	0
57	MG	1A	4029	1/1	0.98	0.03	41,41,41,41	0
57	MG	2A	3714	1/1	0.98	0.05	42,42,42,42	0
57	MG	2A	3500	1/1	0.98	0.08	49,49,49,49	0
57	MG	1A	3535	1/1	0.98	0.08	24,24,24,24	0
57	MG	1a	1649	1/1	0.98	0.05	45,45,45,45	0
57	MG	1A	3790	1/1	0.98	0.03	39,39,39,39	0
57	MG	2A	3143	1/1	0.98	0.22	44,44,44,44	0
57	MG	2A	3320	1/1	0.98	0.06	45,45,45,45	0
57	MG	2A	3506	1/1	0.98	0.14	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2l	203	1/1	0.98	0.06	63,63,63,63	0
57	MG	2A	3144	1/1	0.98	0.20	46,46,46,46	0
57	MG	1A	4033	1/1	0.98	0.11	58,58,58,58	0
57	MG	1A	3791	1/1	0.98	0.04	35,35,35,35	0
57	MG	1P	202	1/1	0.98	0.15	28,28,28,28	0
57	MG	1a	1654	1/1	0.98	0.13	39,39,39,39	0
57	MG	1A	3792	1/1	0.98	0.08	20,20,20,20	0
57	MG	1A	3692	1/1	0.98	0.07	22,22,22,22	0
57	MG	1A	3426	1/1	0.98	0.16	36,36,36,36	0
57	MG	1A	3033	1/1	0.98	0.05	28,28,28,28	0
57	MG	1Q	201	1/1	0.98	0.12	34,34,34,34	0
57	MG	1A	3099	1/1	0.98	0.10	24,24,24,24	0
57	MG	1Q	203	1/1	0.98	0.09	40,40,40,40	0
57	MG	1A	3046	1/1	0.98	0.08	27,27,27,27	0
57	MG	1A	4042	1/1	0.98	0.03	26,26,26,26	0
57	MG	1A	4043	1/1	0.98	0.04	46,46,46,46	0
57	MG	2A	3738	1/1	0.98	0.05	51,51,51,51	0
57	MG	1A	3102	1/1	0.98	0.05	38,38,38,38	0
57	MG	1A	3078	1/1	0.98	0.05	18,18,18,18	0
57	MG	1A	3381	1/1	0.98	0.06	62,62,62,62	0
57	MG	1A	4047	1/1	0.98	0.11	11,11,11,11	0
57	MG	1x	103	1/1	0.98	0.14	52,52,52,52	0
57	MG	1R	204	1/1	0.98	0.11	26,26,26,26	0
57	MG	2A	3530	1/1	0.98	0.05	49,49,49,49	0
57	MG	1A	3914	1/1	0.98	0.06	36,36,36,36	0
57	MG	1A	3047	1/1	0.98	0.04	28,28,28,28	0
57	MG	1x	107	1/1	0.98	0.05	35,35,35,35	0
57	MG	1A	3165	1/1	0.98	0.05	30,30,30,30	0
57	MG	1A	3105	1/1	0.98	0.07	27,27,27,27	0
60	ZN	25	102	1/1	0.98	0.03	80,80,80,80	0
57	MG	2A	3751	1/1	0.98	0.07	58,58,58,58	0
57	MG	1A	4064	1/1	0.99	0.03	33,33,33,33	0
57	MG	1A	3764	1/1	0.99	0.06	28,28,28,28	0
57	MG	1A	4011	1/1	0.99	0.04	31,31,31,31	0
57	MG	1A	3640	1/1	0.99	0.09	34,34,34,34	0
57	MG	2A	3545	1/1	0.99	0.05	37,37,37,37	0
57	MG	2A	3546	1/1	0.99	0.03	25,25,25,25	0
57	MG	2A	3702	1/1	0.99	0.07	34,34,34,34	0
57	MG	1A	3117	1/1	0.99	0.06	49,49,49,49	0
57	MG	2A	3548	1/1	0.99	0.05	34,34,34,34	0
57	MG	1A	4014	1/1	0.99	0.06	26,26,26,26	0
57	MG	1a	1740	1/1	0.99	0.04	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1741	1/1	0.99	0.08	25,25,25,25	0
57	MG	1A	3118	1/1	0.99	0.06	22,22,22,22	0
57	MG	2A	3154	1/1	0.99	0.08	31,31,31,31	0
57	MG	1D	302	1/1	0.99	0.04	26,26,26,26	0
57	MG	2A	3632	1/1	0.99	0.02	39,39,39,39	0
57	MG	1A	3577	1/1	0.99	0.03	38,38,38,38	0
57	MG	2A	3092	1/1	0.99	0.04	37,37,37,37	0
57	MG	1A	3620	1/1	0.99	0.08	37,37,37,37	0
57	MG	2D	303	1/1	0.99	0.05	29,29,29,29	0
57	MG	1A	3344	1/1	0.99	0.13	41,41,41,41	0
57	MG	2A	3716	1/1	0.99	0.04	33,33,33,33	0
57	MG	1A	3970	1/1	0.99	0.08	22,22,22,22	0
57	MG	1A	3622	1/1	0.99	0.05	32,32,32,32	0
57	MG	1A	3735	1/1	0.99	0.03	26,26,26,26	0
57	MG	1A	3736	1/1	0.99	0.05	20,20,20,20	0
57	MG	1A	3737	1/1	0.99	0.07	66,66,66,66	0
57	MG	1A	3775	1/1	0.99	0.03	51,51,51,51	0
57	MG	1A	3275	1/1	0.99	0.27	29,29,29,29	0
57	MG	1A	4026	1/1	0.99	0.07	24,24,24,24	0
57	MG	1A	3892	1/1	0.99	0.06	43,43,43,43	0
57	MG	1A	3498	1/1	0.99	0.13	26,26,26,26	0
57	MG	1A	3082	1/1	0.99	0.18	33,33,33,33	0
57	MG	1A	3674	1/1	0.99	0.12	17,17,17,17	0
57	MG	2A	3572	1/1	0.99	0.03	36,36,36,36	0
57	MG	1T	202	1/1	0.99	0.14	40,40,40,40	0
57	MG	1A	3038	1/1	0.99	0.13	18,18,18,18	0
57	MG	1A	4032	1/1	0.99	0.05	20,20,20,20	0
57	MG	1A	3026	1/1	0.99	0.05	39,39,39,39	0
57	MG	1A	3677	1/1	0.99	0.10	20,20,20,20	0
57	MG	2A	3815	1/1	0.99	0.07	26,26,26,26	0
57	MG	1A	3678	1/1	0.99	0.06	21,21,21,21	0
57	MG	1A	3985	1/1	0.99	0.08	30,30,30,30	0
57	MG	2A	3818	1/1	0.99	0.08	21,21,21,21	0
57	MG	1A	3986	1/1	0.99	0.07	32,32,32,32	0
57	MG	2A	3820	1/1	0.99	0.09	57,57,57,57	0
57	MG	1A	3330	1/1	0.99	0.05	40,40,40,40	0
57	MG	2A	3822	1/1	0.99	0.05	45,45,45,45	0
57	MG	1A	3014	1/1	0.99	0.04	30,30,30,30	0
57	MG	2A	3583	1/1	0.99	0.06	34,34,34,34	0
57	MG	1A	3681	1/1	0.99	0.04	24,24,24,24	0
57	MG	1A	4041	1/1	0.99	0.02	23,23,23,23	0
57	MG	17	101	1/1	0.99	0.03	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	17	102	1/1	0.99	0.05	25,25,25,25	0
57	MG	2A	3513	1/1	0.99	0.04	32,32,32,32	0
57	MG	2A	3589	1/1	0.99	0.02	27,27,27,27	0
57	MG	2A	3590	1/1	0.99	0.06	31,31,31,31	0
57	MG	2A	3514	1/1	0.99	0.08	58,58,58,58	0
57	MG	1A	3133	1/1	0.99	0.19	35,35,35,35	0
57	MG	1A	3991	1/1	0.99	0.04	23,23,23,23	0
57	MG	1A	3086	1/1	0.99	0.10	31,31,31,31	0
57	MG	1A	3906	1/1	0.99	0.02	29,29,29,29	0
57	MG	1A	3994	1/1	0.99	0.05	21,21,21,21	0
57	MG	1a	1715	1/1	0.99	0.04	49,49,49,49	0
57	MG	1A	3021	1/1	0.99	0.03	20,20,20,20	0
57	MG	1A	3136	1/1	0.99	0.03	32,32,32,32	0
57	MG	1A	3686	1/1	0.99	0.03	26,26,26,26	0
57	MG	1A	3998	1/1	0.99	0.07	25,25,25,25	0
57	MG	1A	3237	1/1	0.99	0.08	23,23,23,23	0
57	MG	1A	3688	1/1	0.99	0.09	22,22,22,22	0
57	MG	1A	3689	1/1	0.99	0.05	17,17,17,17	0
57	MG	1A	3913	1/1	0.99	0.05	30,30,30,30	0
57	MG	1W	206	1/1	0.99	0.07	24,24,24,24	0
57	MG	1A	3721	1/1	0.99	0.04	29,29,29,29	0
57	MG	1A	3197	1/1	0.99	0.05	18,18,18,18	0
57	MG	2A	3464	1/1	0.99	0.06	48,48,48,48	0
57	MG	1A	3723	1/1	0.99	0.07	40,40,40,40	0
57	MG	1A	3224	1/1	0.99	0.05	20,20,20,20	0
57	MG	1A	3270	1/1	0.99	0.21	26,26,26,26	0
57	MG	1A	3100	1/1	0.99	0.04	31,31,31,31	0
57	MG	1A	4061	1/1	0.99	0.11	41,41,41,41	0
60	ZN	1Y	203	1/1	0.99	0.03	69,69,69,69	0
57	MG	1A	4062	1/1	0.99	0.08	33,33,33,33	0
60	ZN	15	110	1/1	0.99	0.04	43,43,43,43	0
60	ZN	16	103	1/1	0.99	0.03	41,41,41,41	0
60	ZN	19	501	1/1	0.99	0.09	56,56,56,56	0
60	ZN	1n	104	1/1	0.99	0.03	55,55,55,55	0
60	ZN	2Y	202	1/1	0.99	0.03	103,103,103,103	0
57	MG	1A	3108	1/1	0.99	0.08	25,25,25,25	0
57	MG	2A	3540	1/1	0.99	0.07	32,32,32,32	0
60	ZN	26	102	1/1	0.99	0.04	59,59,59,59	0
60	ZN	29	501	1/1	0.99	0.03	66,66,66,66	0
57	MG	2A	3695	1/1	0.99	0.03	45,45,45,45	0
61	SF4	1d	302	8/8	0.99	0.04	46,48,60,61	0
61	SF4	2d	303	8/8	0.99	0.03	57,71,80,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3550	1/1	1.00	0.10	29,29,29,29	0
57	MG	1A	3924	1/1	1.00	0.05	17,17,17,17	0
57	MG	1P	201	1/1	1.00	0.10	26,26,26,26	0
57	MG	1A	3798	1/1	1.00	0.04	22,22,22,22	0
57	MG	1a	1790	1/1	1.00	0.03	37,37,37,37	0
57	MG	1A	3905	1/1	1.00	0.03	28,28,28,28	0

6.5 Other polymers

There are no such residues in this entry.