Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2025 – 11:35 PM EDT

PDB ID	:	9MTQ / pdb_00009mtq
Title	:	Crystal structure of the wild-type Thermus thermophilus 70S ribosome in complex with mRNA, A-site GGD-mutant Release Factor 1, and P-site fMEAAA KC-peptidyl-tRNAcys at 2.55A resolution
Authors	:	Aleksandrova, E.V.; Syroegin, E.A.; Basu, R.S.; Vassilevski, A.A.; Gagnon, M.G.; Polikanov, Y.S.
Deposited on	:	2025-01-12
Resolution	:	2.55 Å(reported)

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

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

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

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

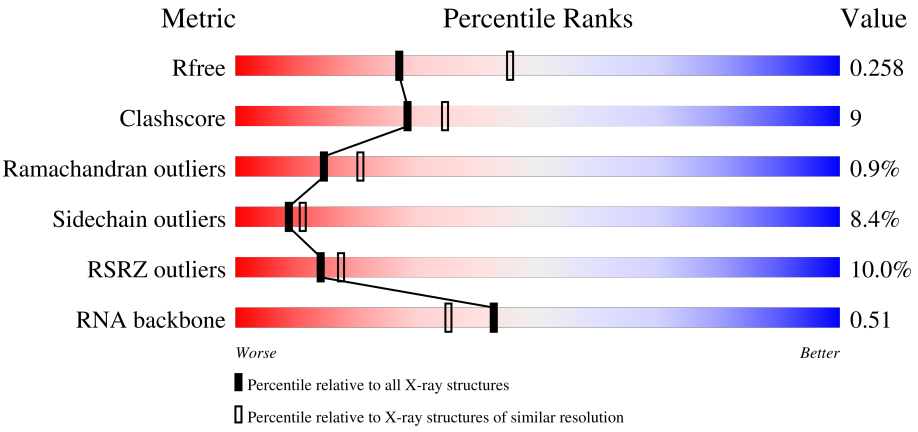
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 2.55 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	1004 (2.54-2.54)
Clashscore	180529	1055 (2.54-2.54)
Ramachandran outliers	177936	1048 (2.54-2.54)
Sidechain outliers	177891	1048 (2.54-2.54)
RSRZ outliers	164620	1004 (2.54-2.54)
RNA backbone	3690	1040 (2.80-2.28)

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	5% 64% 27% 7%
1	2A	2915	4% 59% 30% 6%
2	1B	121	69% 26%

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Mol	Chain	Length	Quality of chain
2	2B	121	2% 64% 27% 7%
3	1D	276	% 82% 15%
3	2D	276	% 76% 21%
4	1E	206	2% 79% 19%
4	2E	206	2% 82% 16%
5	1F	210	69% 24%
5	2F	210	2% 61% 31%
6	1G	182	16% 63% 34%
6	2G	182	18% 60% 32% 7%
7	1H	180	2% 75% 21%
7	2H	180	24% 62% 31%
8	1I	148	8% 70% 26%
8	2I	148	20% 61% 30% 6%
9	1N	140	% 84% 14%
9	2N	140	4% 74% 26%
10	1O	122	80% 17%
10	2O	122	78% 21%
11	1P	150	% 79% 17%
11	2P	150	% 78% 20%
12	1Q	141	4% 87% 13%
12	2Q	141	6% 74% 24%
13	1R	118	85% 14%
13	2R	118	81% 18%
14	1S	112	2% 74% 21%
14	2S	112	11% 71% 23%

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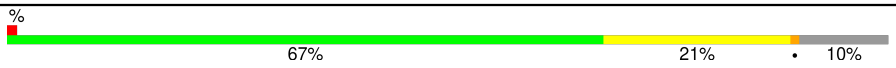
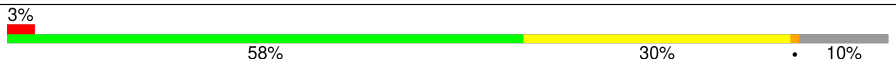
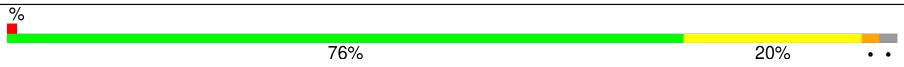
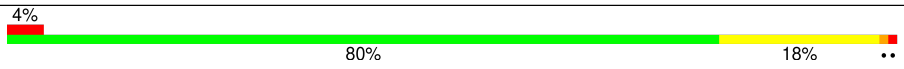
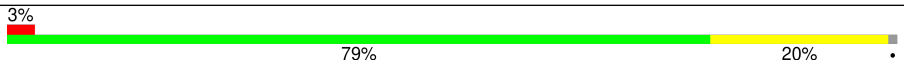
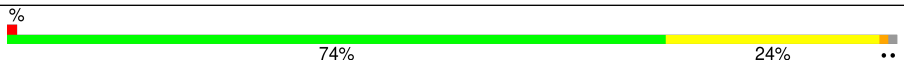
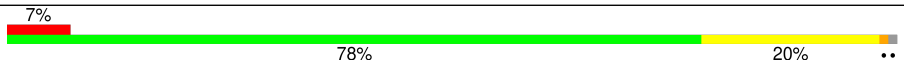
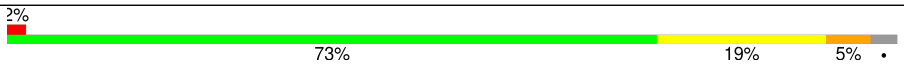
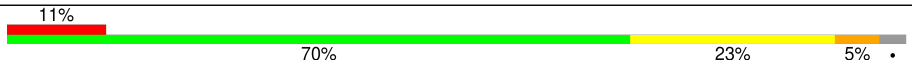
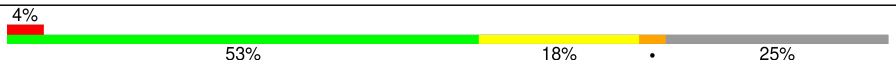
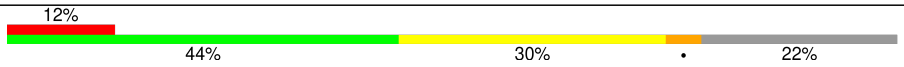
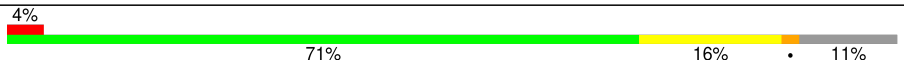
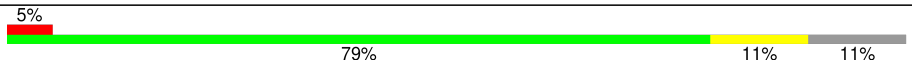
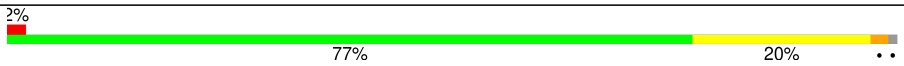
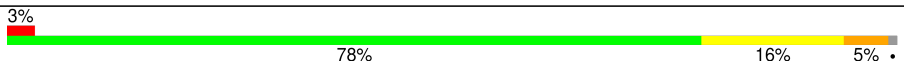
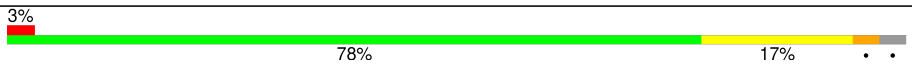
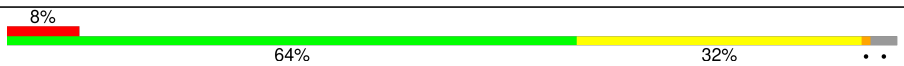
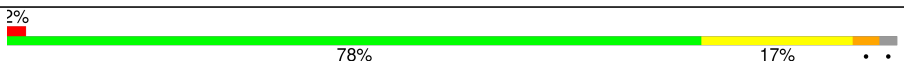
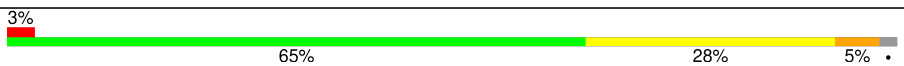
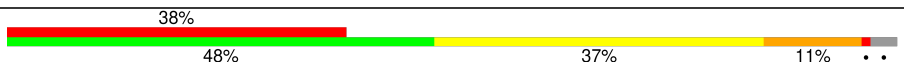
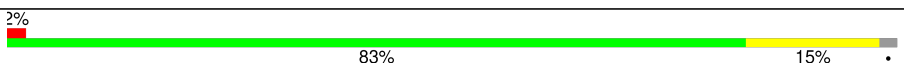
Mol	Chain	Length	Quality of chain
15	1T	146	
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	

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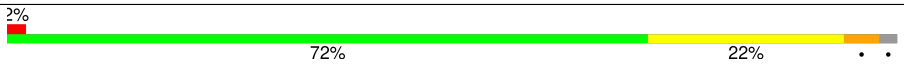
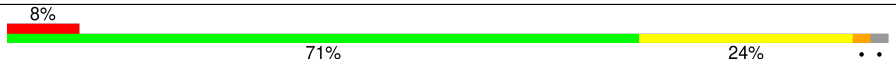
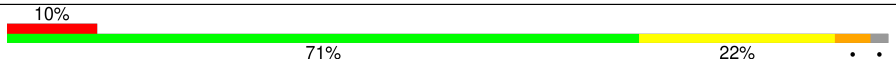
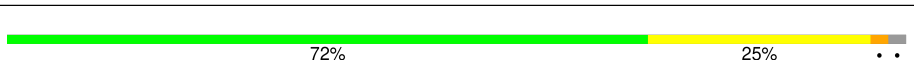
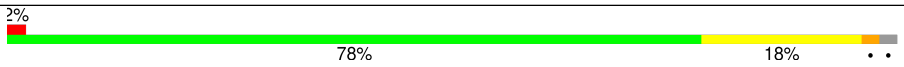
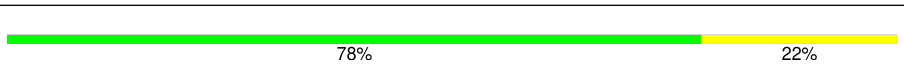
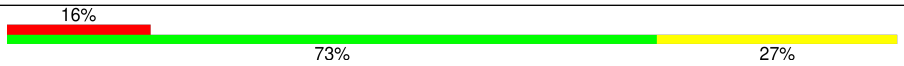
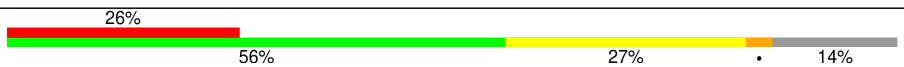
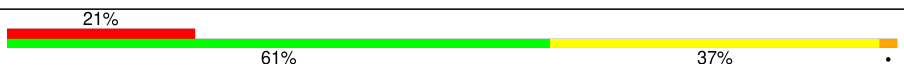
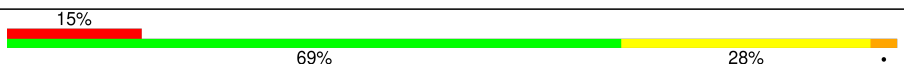
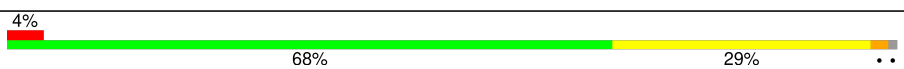
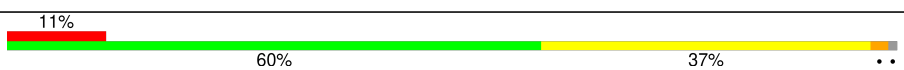
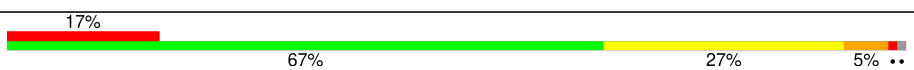
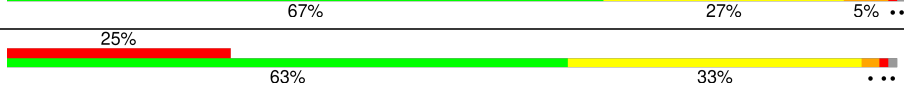
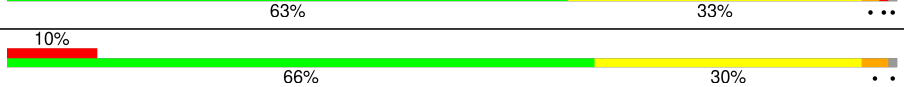
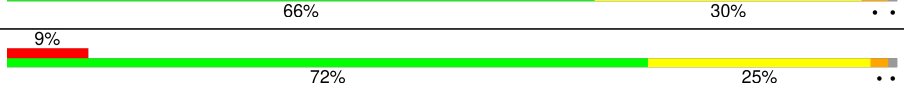
Mol	Chain	Length	Quality of chain
27	25	60	
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	

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Mol	Chain	Length	Quality of chain
40	1i	128	21% 53% 41% 5%
40	2i	128	56% 54% 38% 8%
41	1j	105	34% 51% 36% 5% 8%
41	2j	105	63% 52% 34% 5% 9%
42	1k	129	8% 72% 14% 12%
42	2k	129	11% 58% 29% 12%
43	1l	132	7% 60% 30% 8%
43	2l	132	5% 70% 21% 8%
44	1m	126	49% 55% 29% 10% 6%
44	2m	126	31% 43% 46% 8%
45	1n	61	41% 61% 36%
45	2n	61	59% 61% 36%
46	1o	89	20% 70% 26%
46	2o	89	15% 70% 26%
47	1p	88	34% 47% 43% 7%
47	2p	88	14% 63% 27% 7%
48	1q	105	15% 64% 30% 6%
48	2q	105	3% 80% 14% 6%
49	1r	88	6% 63% 15% 23%
49	2r	88	8% 55% 20% 23%
50	1s	93	66% 44% 40% 5% 11%
50	2s	93	47% 44% 42% 11%
51	1t	106	18% 55% 34% 9%
51	2t	106	15% 58% 30% 9%
52	1u	27	41% 59% 22% 15%

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Mol	Chain	Length	Quality of chain
52	2u	27	33% 52% 33% 15%
53	1v	24	17% 29% 25% 46%
53	2v	24	29% 33% 17% 46%
54	1w	354	% 49% 18% 30%
54	2w	354	4% 46% 23% 29%
55	1x	74	57% 38%
55	2x	74	66% 26% 8%
56	1z	7	29% 57% 14% 29%
56	2z	7	29% 57% 43%

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	3239	-	-	-	X
57	MG	2A	3259	-	-	-	X
57	MG	2A	3435	-	-	-	X
57	MG	2a	1645	-	-	-	X

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 297259 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	76	Total	C	N	O	S	0	0	0
			604	373	128	102	1			
22	20	76	Total	C	N	O	S	0	0	0
			604	373	128	102	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	118	Total	C	N	O	S	0	0	0
			919	566	190	161	2			
44	2m	116	Total	C	N	O	S	0	0	0
			907	558	188	159	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 CYS-Stop 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 protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	249	Total	C	N	O	S	0	0	0
			1937	1197	359	372	9			
54	2w	253	Total	C	N	O	S	0	0	0
			1955	1208	360	378	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1w	230	ASP	GLN	engineered mutation	UNP P96077
2w	230	ASP	GLN	engineered mutation	UNP P96077

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	74	Total	C	N	O	P	S	0	0	0
			1577	704	281	517	74	1			
55	2x	74	Total	C	N	O	P	S	0	0	0
			1577	704	281	517	74	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	1z	5	Total	C	N	O	S	0	0	0
			30	18	6	5	1			
56	2z	4	Total	C	N	O	S	0	0	0
			25	15	5	4	1			

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1088	Total	Mg	0	0
			1088	1088		
57	1B	36	Total	Mg	0	0
			36	36		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1D	13	Total Mg 13 13	0	0
57	1E	15	Total Mg 15 15	0	0
57	1F	15	Total Mg 15 15	0	0
57	1G	4	Total Mg 4 4	0	0
57	1I	1	Total Mg 1 1	0	0
57	1N	6	Total Mg 6 6	0	0
57	1O	4	Total Mg 4 4	0	0
57	1P	4	Total Mg 4 4	0	0
57	1Q	8	Total Mg 8 8	0	0
57	1R	5	Total Mg 5 5	0	0
57	1S	3	Total Mg 3 3	0	0
57	1T	2	Total Mg 2 2	0	0
57	1U	10	Total Mg 10 10	0	0
57	1V	6	Total Mg 6 6	0	0
57	1W	6	Total Mg 6 6	0	0
57	1X	5	Total Mg 5 5	0	0
57	1Y	4	Total Mg 4 4	0	0
57	1Z	2	Total Mg 2 2	0	0
57	10	8	Total Mg 8 8	0	0
57	11	4	Total Mg 4 4	0	0
57	12	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	13	4	Total Mg 4 4	0	0
57	15	8	Total Mg 8 8	0	0
57	16	1	Total Mg 1 1	0	0
57	17	6	Total Mg 6 6	0	0
57	18	4	Total Mg 4 4	0	0
57	19	1	Total Mg 1 1	0	0
57	1a	223	Total Mg 223 223	0	0
57	1b	1	Total Mg 1 1	0	0
57	1d	1	Total Mg 1 1	0	0
57	1e	3	Total Mg 3 3	0	0
57	1f	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	1	Total Mg 1 1	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	1v	1	Total Mg 1 1	0	0
57	1w	2	Total Mg 2 2	0	0
57	1x	13	Total Mg 13 13	0	0
57	2A	853	Total Mg 853 853	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2B	22	Total Mg 22 22	0	0
57	2D	9	Total Mg 9 9	0	0
57	2E	9	Total Mg 9 9	0	0
57	2F	9	Total Mg 9 9	0	0
57	2G	1	Total Mg 1 1	0	0
57	2N	1	Total Mg 1 1	0	0
57	2O	2	Total Mg 2 2	0	0
57	2P	1	Total Mg 1 1	0	0
57	2Q	4	Total Mg 4 4	0	0
57	2R	2	Total Mg 2 2	0	0
57	2T	3	Total Mg 3 3	0	0
57	2U	2	Total Mg 2 2	0	0
57	2V	2	Total Mg 2 2	0	0
57	2W	2	Total Mg 2 2	0	0
57	2X	2	Total Mg 2 2	0	0
57	2Z	1	Total Mg 1 1	0	0
57	20	2	Total Mg 2 2	0	0
57	21	1	Total Mg 1 1	0	0
57	23	3	Total Mg 3 3	0	0
57	25	7	Total Mg 7 7	0	0
57	26	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	27	2	Total Mg 2 2	0	0
57	28	4	Total Mg 4 4	0	0
57	29	1	Total Mg 1 1	0	0
57	2a	176	Total Mg 176 176	0	0
57	2d	2	Total Mg 2 2	0	0
57	2e	1	Total Mg 1 1	0	0
57	2f	3	Total Mg 3 3	0	0
57	2g	1	Total Mg 1 1	0	0
57	2i	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	2	Total Mg 2 2	0	0
57	2q	3	Total Mg 3 3	0	0
57	2t	1	Total Mg 1 1	0	0
57	2v	2	Total Mg 2 2	0	0
57	2w	1	Total Mg 1 1	0	0
57	2x	10	Total Mg 10 10	0	0

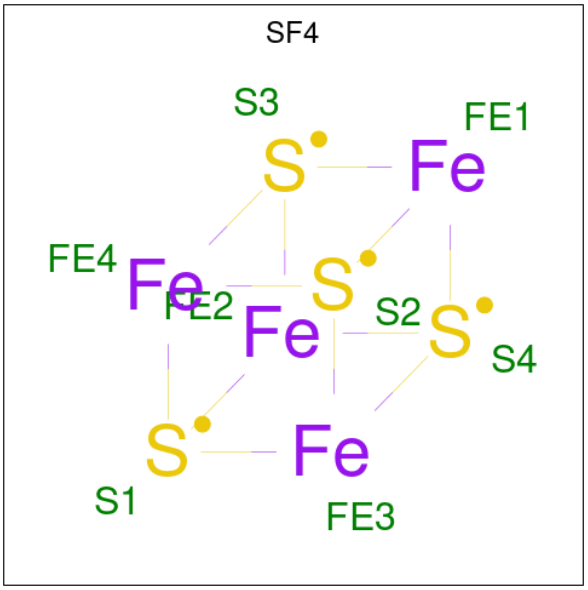
- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1Y	1	Total Zn 1 1	0	0
59	14	1	Total Zn 1 1	0	0
59	15	1	Total Zn 1 1	0	0
59	16	1	Total Zn 1 1	0	0
59	19	1	Total Zn 1 1	0	0
59	1n	1	Total Zn 1 1	0	0
59	2Y	1	Total Zn 1 1	0	0
59	24	1	Total Zn 1 1	0	0
59	25	1	Total Zn 1 1	0	0
59	26	1	Total Zn 1 1	0	0
59	29	1	Total Zn 1 1	0	0
59	2n	1	Total Zn 1 1	0	0

- Molecule 60 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1d	1	Total Fe S 8 4 4	0	0
60	2d	1	Total Fe S 8 4 4	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1A	2032	Total O 2032 2032	0	0
61	1B	62	Total O 62 62	0	0
61	1D	24	Total O 24 24	0	0
61	1E	31	Total O 31 31	0	0
61	1F	15	Total O 15 15	0	0
61	1G	7	Total O 7 7	0	0
61	1H	2	Total O 2 2	0	0
61	1I	1	Total O 1 1	0	0
61	1N	5	Total O 5 5	0	0
61	1O	7	Total O 7 7	0	0
61	1P	20	Total O 20 20	0	0
61	1Q	7	Total O 7 7	0	0
61	1R	15	Total O 15 15	0	0
61	1S	4	Total O 4 4	0	0
61	1T	9	Total O 9 9	0	0
61	1U	13	Total O 13 13	0	0
61	1V	9	Total O 9 9	0	0
61	1W	11	Total O 11 11	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1X	4	Total O 4 4	0	0
61	1Y	2	Total O 2 2	0	0
61	1Z	1	Total O 1 1	0	0
61	10	9	Total O 9 9	0	0
61	11	10	Total O 10 10	0	0
61	12	3	Total O 3 3	0	0
61	13	4	Total O 4 4	0	0
61	15	5	Total O 5 5	0	0
61	16	1	Total O 1 1	0	0
61	17	6	Total O 6 6	0	0
61	18	10	Total O 10 10	0	0
61	1a	289	Total O 289 289	0	0
61	1d	1	Total O 1 1	0	0
61	1j	1	Total O 1 1	0	0
61	1l	4	Total O 4 4	0	0
61	1q	2	Total O 2 2	0	0
61	1v	5	Total O 5 5	0	0
61	1w	5	Total O 5 5	0	0
61	1x	24	Total O 24 24	0	0
61	2A	1200	Total O 1200 1200	0	0
61	2B	20	Total O 20 20	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	2D	23	Total O 23 23	0	0
61	2E	12	Total O 12 12	0	0
61	2F	15	Total O 15 15	0	0
61	2I	2	Total O 2 2	0	0
61	2O	3	Total O 3 3	0	0
61	2P	14	Total O 14 14	0	0
61	2Q	1	Total O 1 1	0	0
61	2R	3	Total O 3 3	0	0
61	2T	4	Total O 4 4	0	0
61	2U	3	Total O 3 3	0	0
61	2W	2	Total O 2 2	0	0
61	2X	3	Total O 3 3	0	0
61	2Z	1	Total O 1 1	0	0
61	20	2	Total O 2 2	0	0
61	21	7	Total O 7 7	0	0
61	22	1	Total O 1 1	0	0
61	23	2	Total O 2 2	0	0
61	25	1	Total O 1 1	0	0
61	27	3	Total O 3 3	0	0
61	28	2	Total O 2 2	0	0
61	29	1	Total O 1 1	0	0

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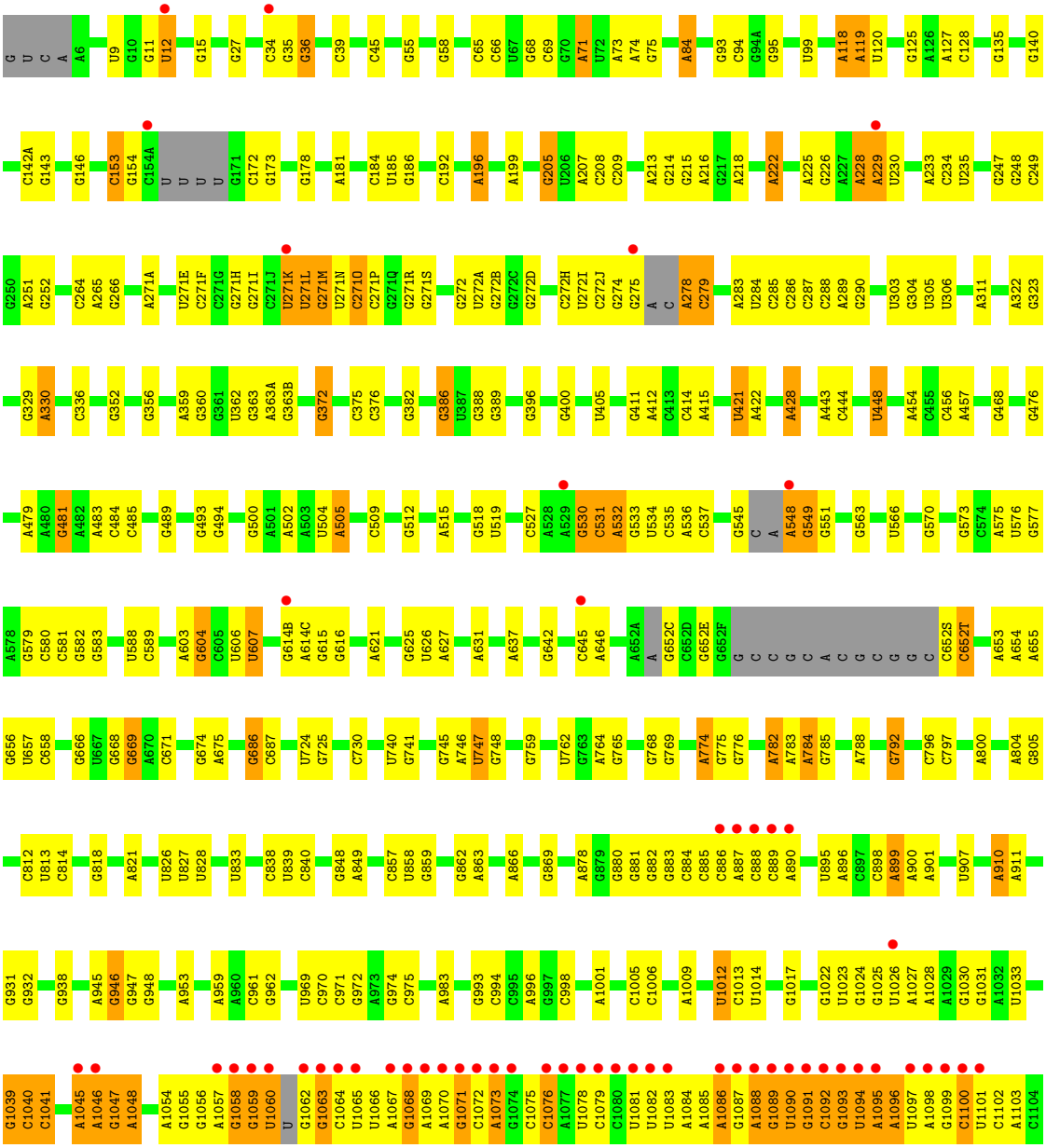
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	2a	152	Total O 152 152	0	0
61	2e	2	Total O 2 2	0	0
61	2j	1	Total O 1 1	0	0
61	2l	5	Total O 5 5	0	0
61	2o	1	Total O 1 1	0	0
61	2q	2	Total O 2 2	0	0
61	2t	1	Total O 1 1	0	0
61	2v	1	Total O 1 1	0	0
61	2w	3	Total O 3 3	0	0
61	2x	28	Total O 28 28	0	0
61	2z	1	Total O 1 1	0	0

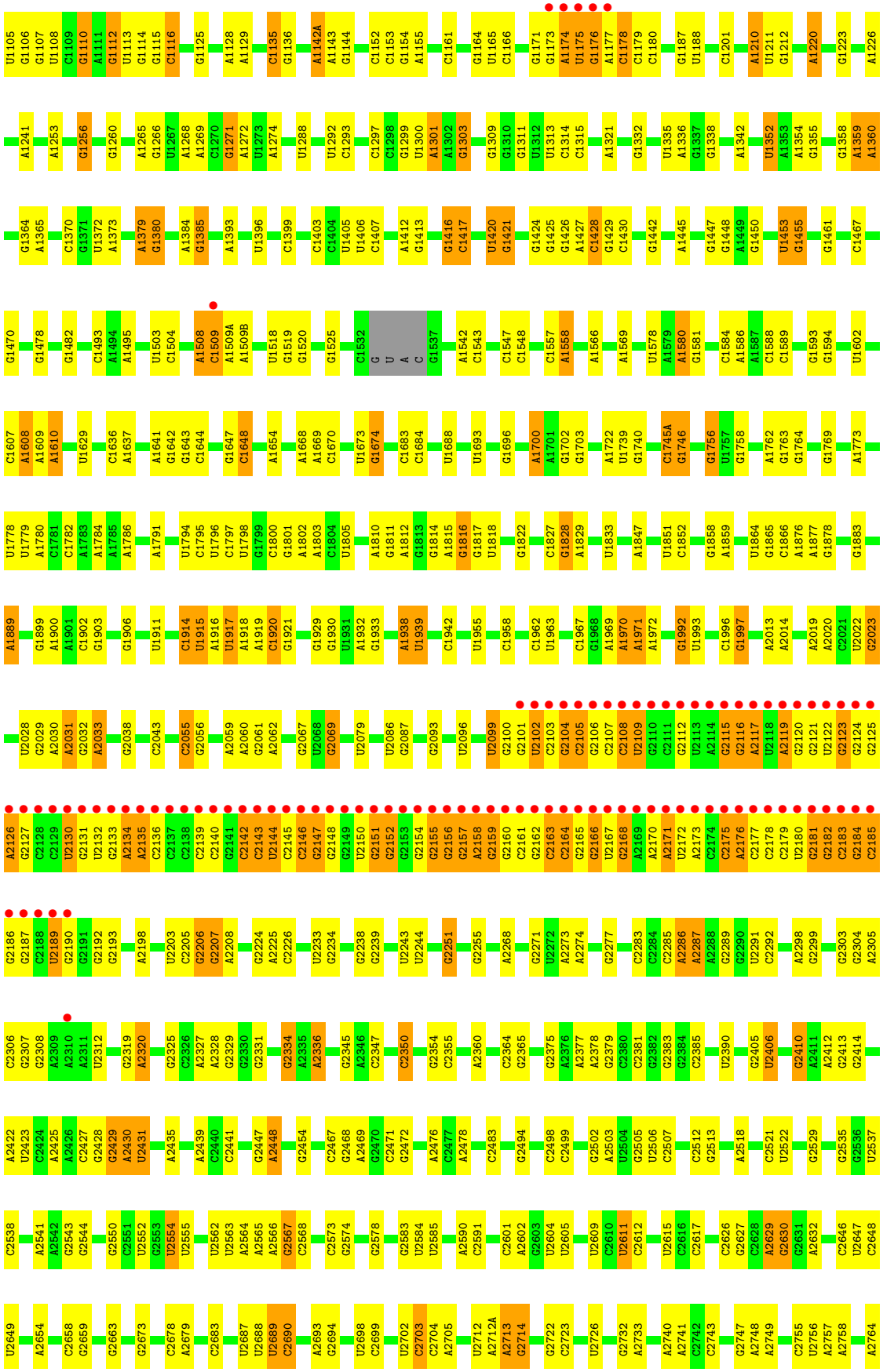
3 Residue-property plots (i)

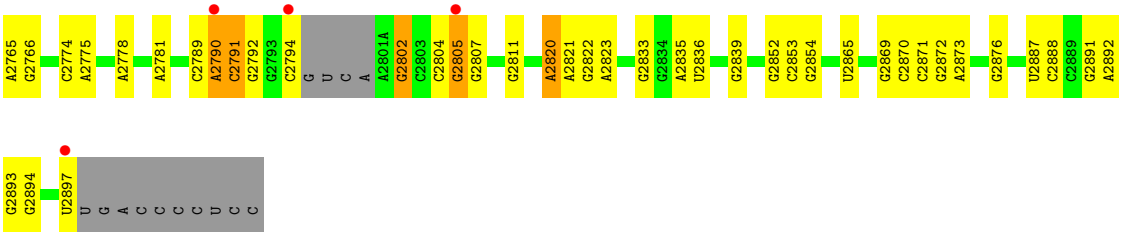
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

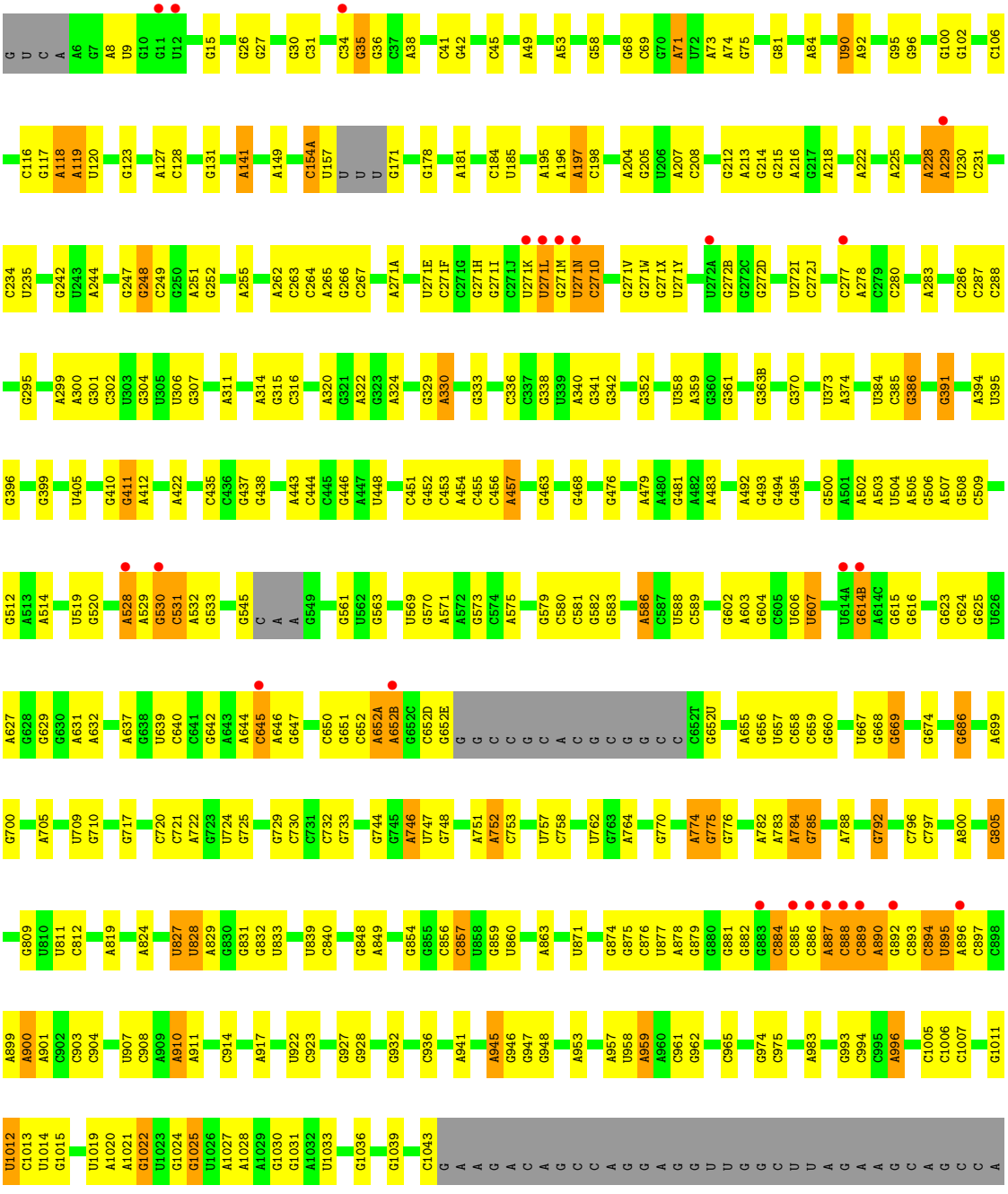


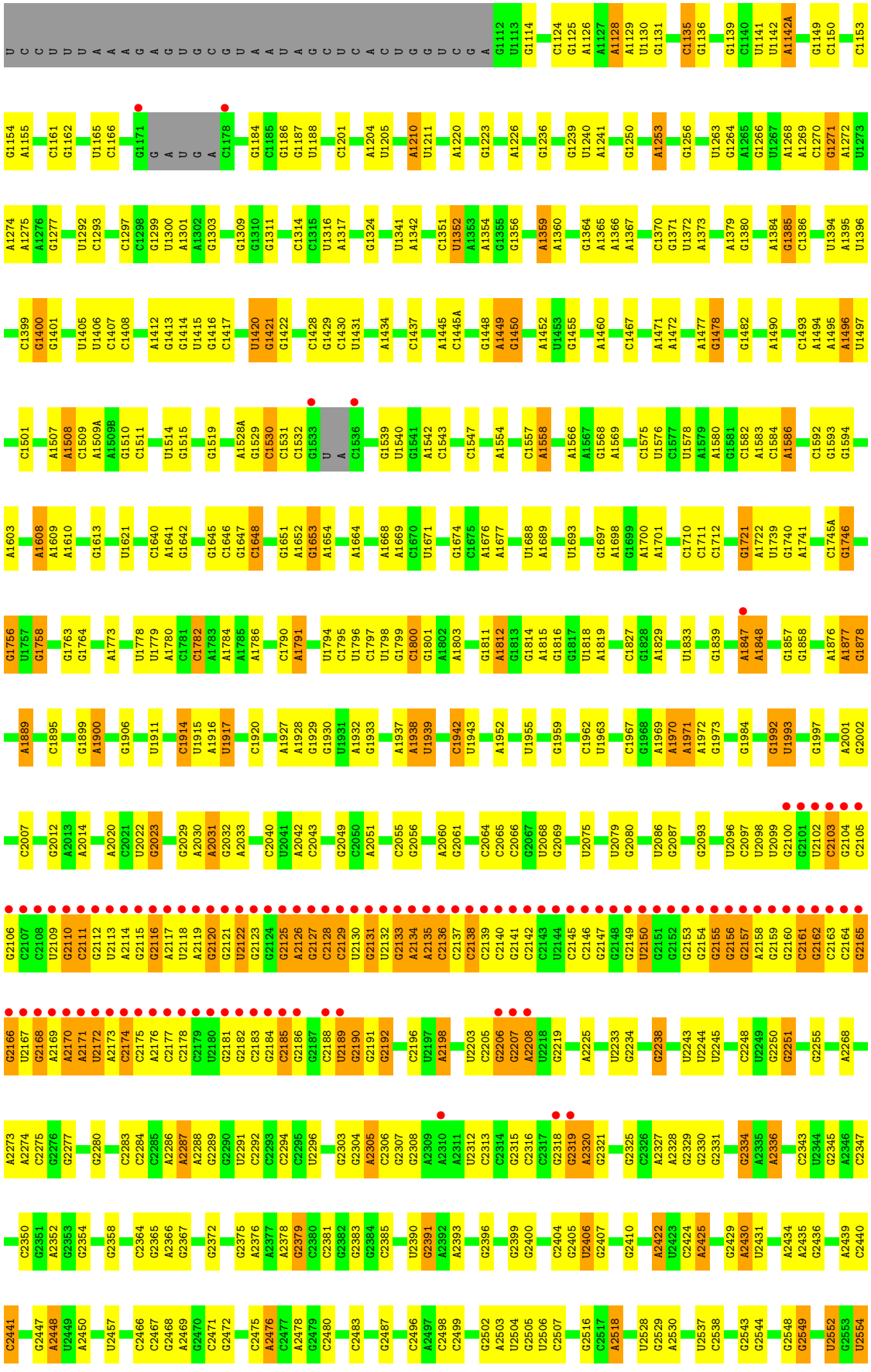


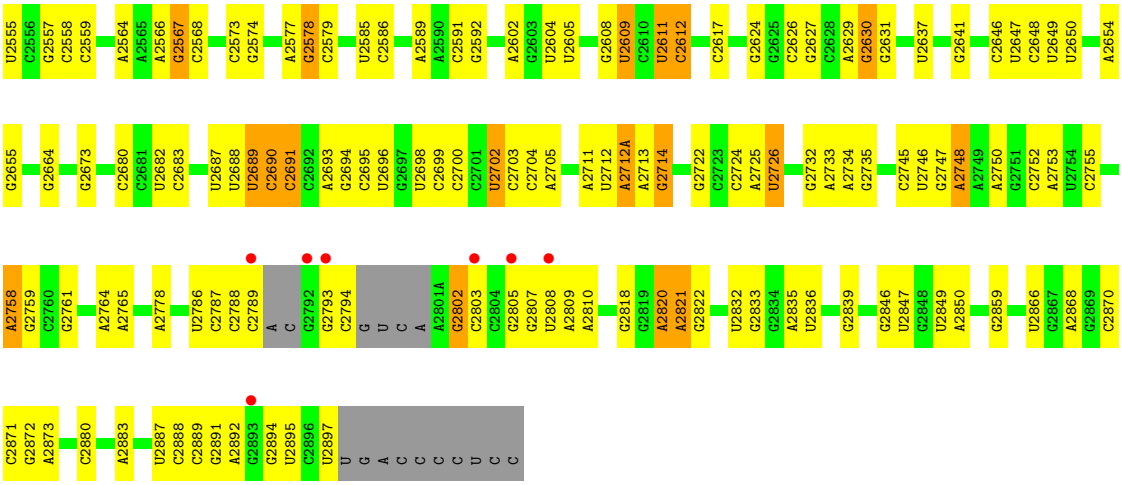


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

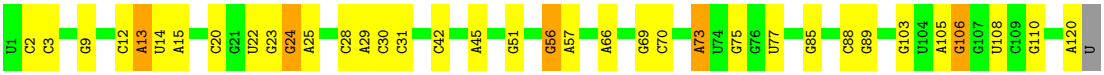






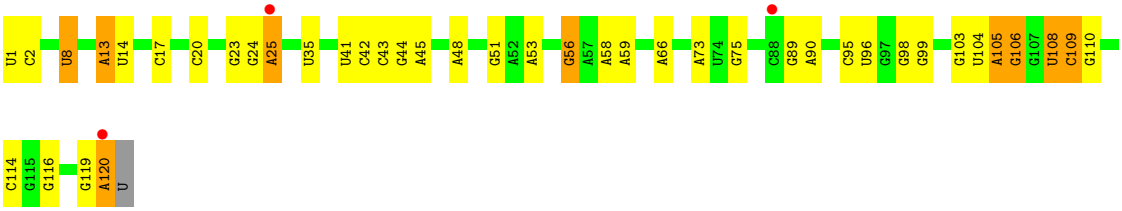
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



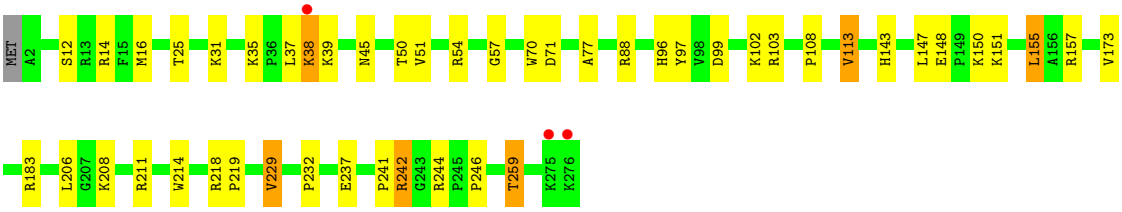
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



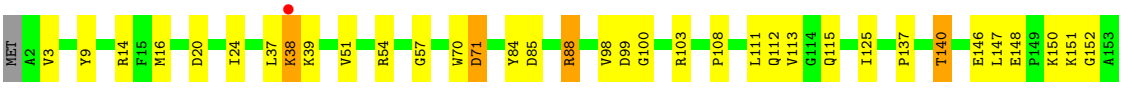
• Molecule 3: 50S ribosomal protein L2

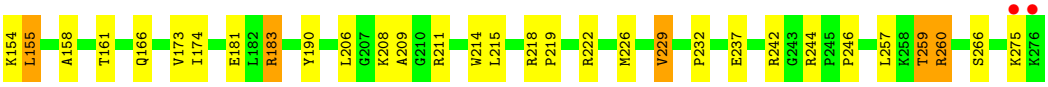
Chain 1D:



• Molecule 3: 50S ribosomal protein L2

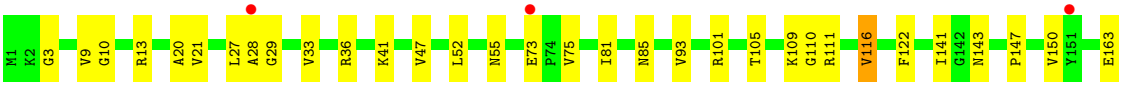
Chain 2D:

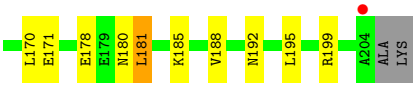




• Molecule 4: 50S ribosomal protein L3

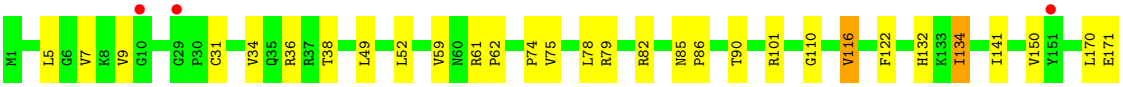
Chain 1E:

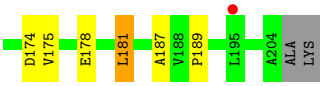




• Molecule 4: 50S ribosomal protein L3

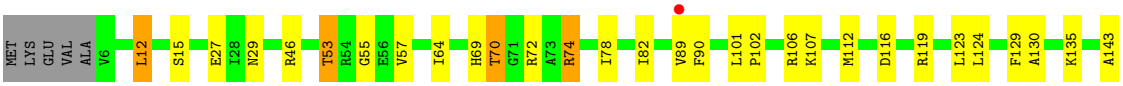
Chain 2E:

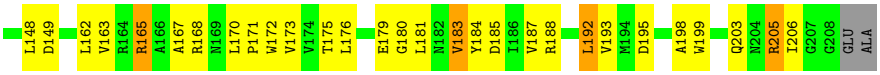




• Molecule 5: 50S ribosomal protein L4

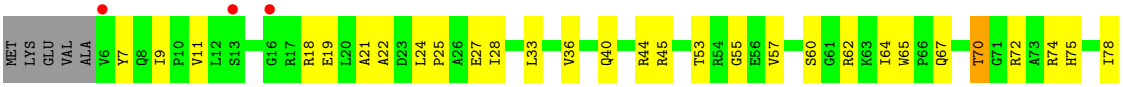
Chain 1F:

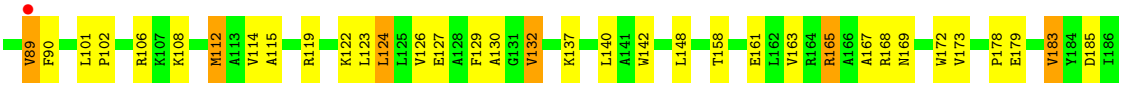


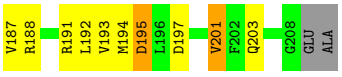


• Molecule 5: 50S ribosomal protein L4

Chain 2F:

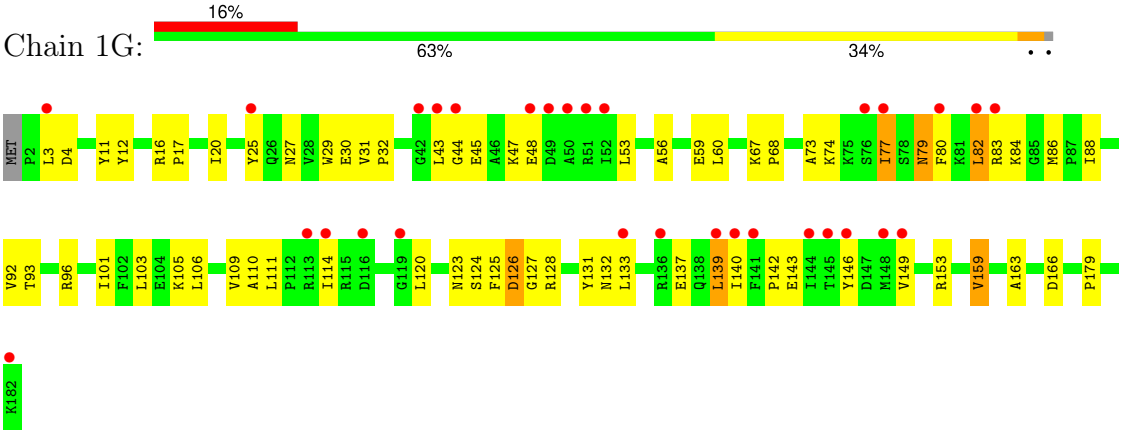






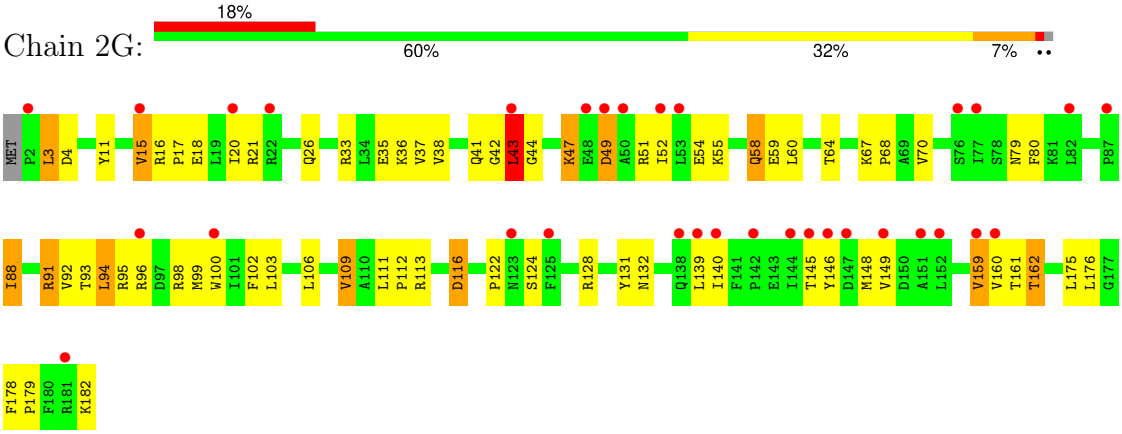
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



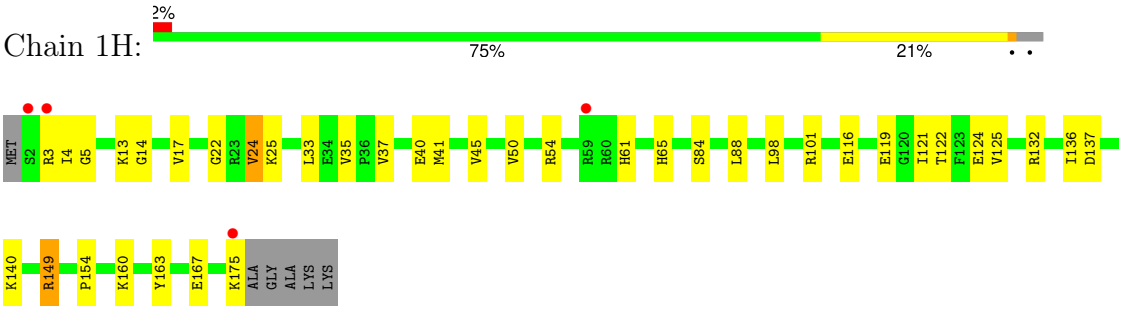
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



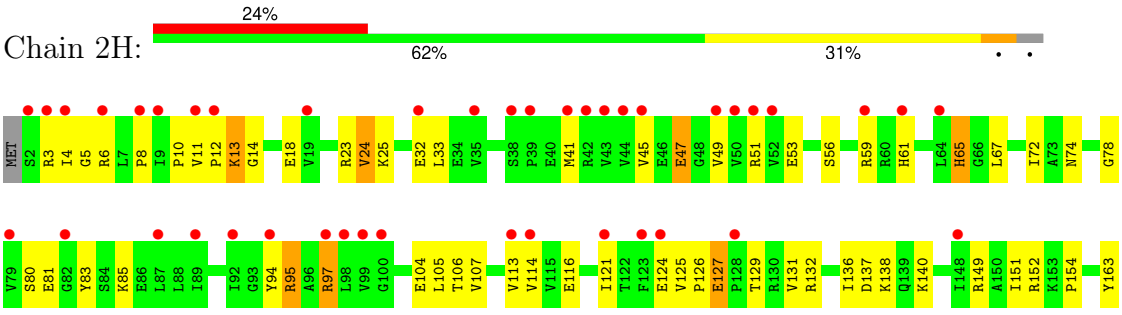
• Molecule 7: 50S ribosomal protein L6

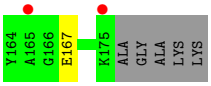
Chain 1H:



• Molecule 7: 50S ribosomal protein L6

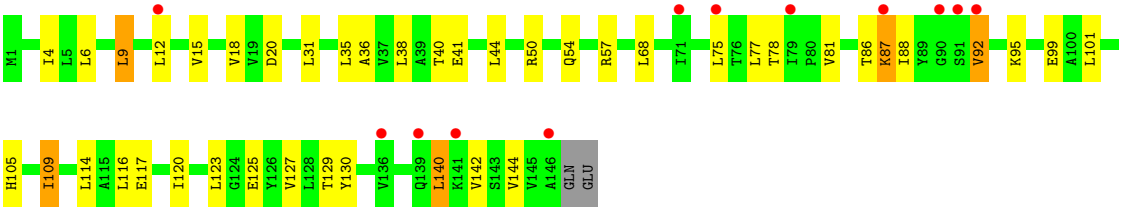
Chain 2H:





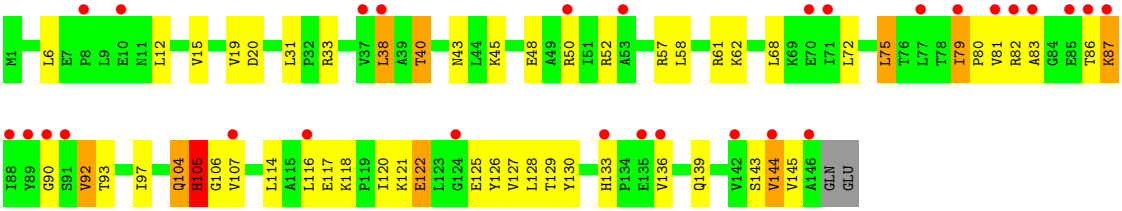
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



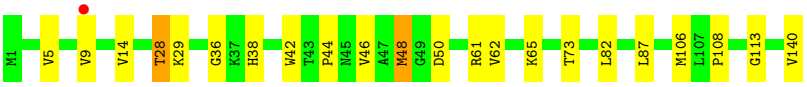
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



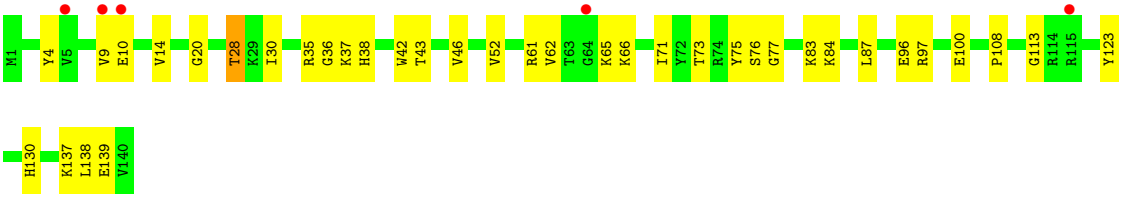
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



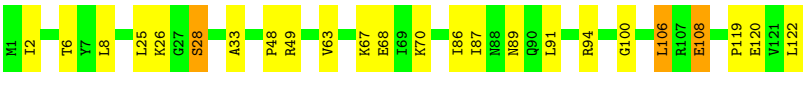
• Molecule 9: 50S ribosomal protein L13

Chain 2N:



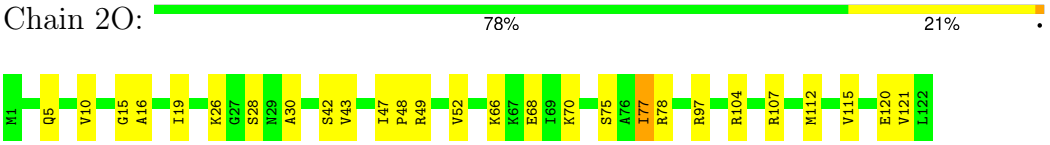
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



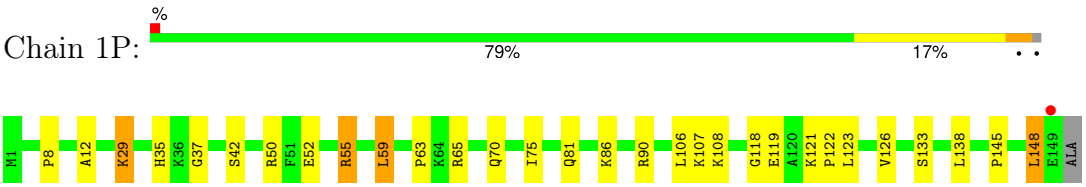
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



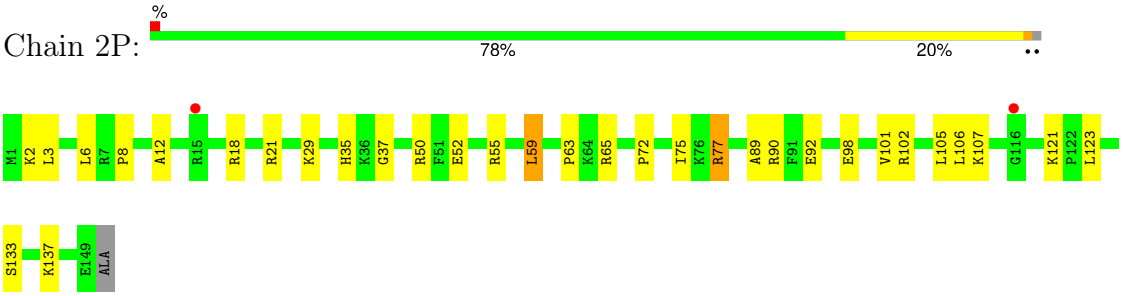
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



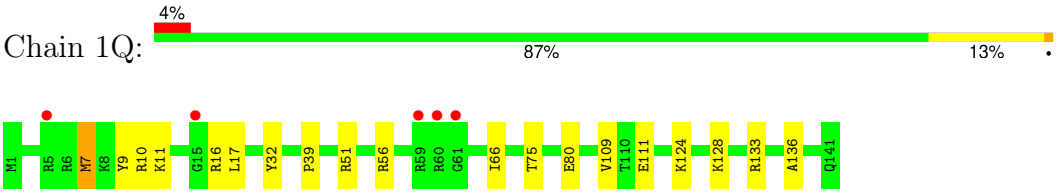
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



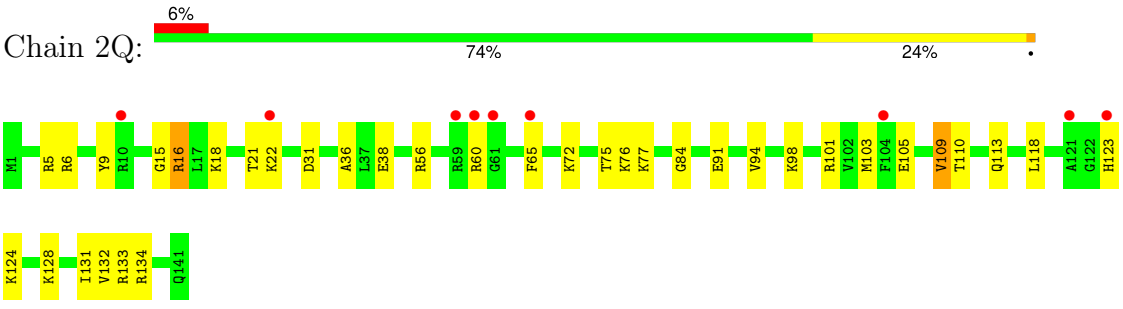
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



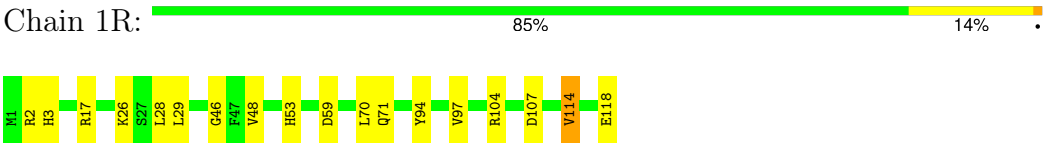
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



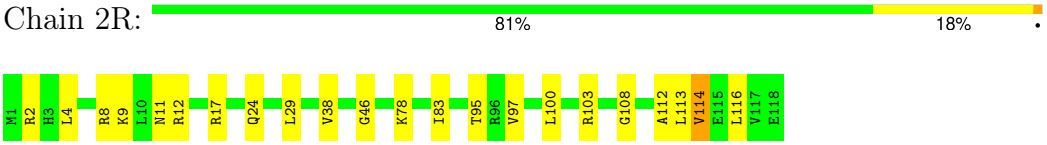
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



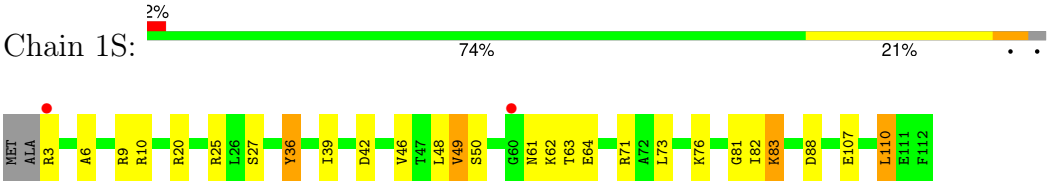
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



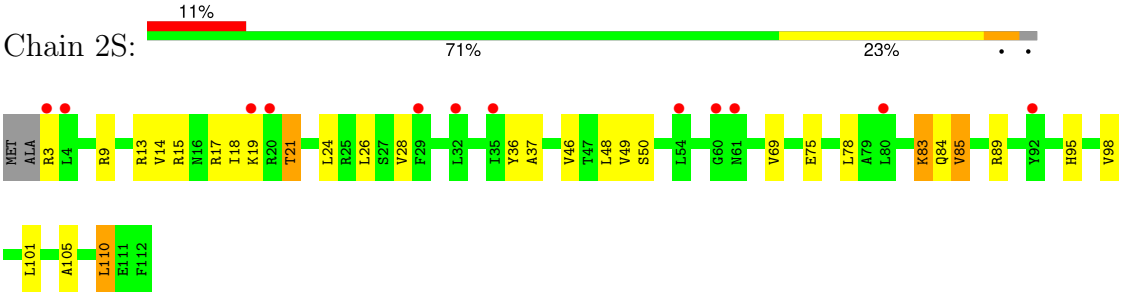
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



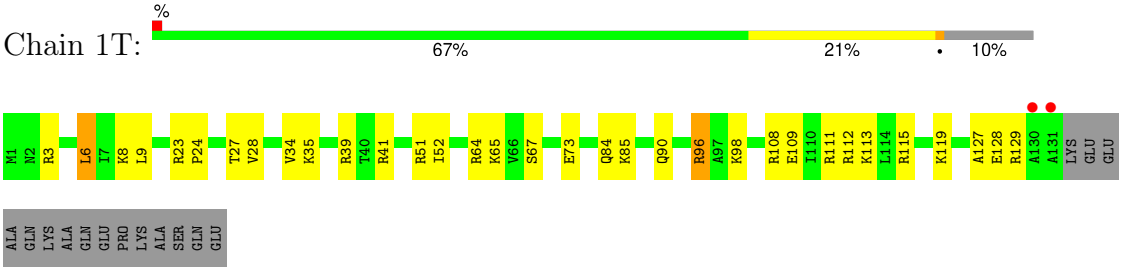
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



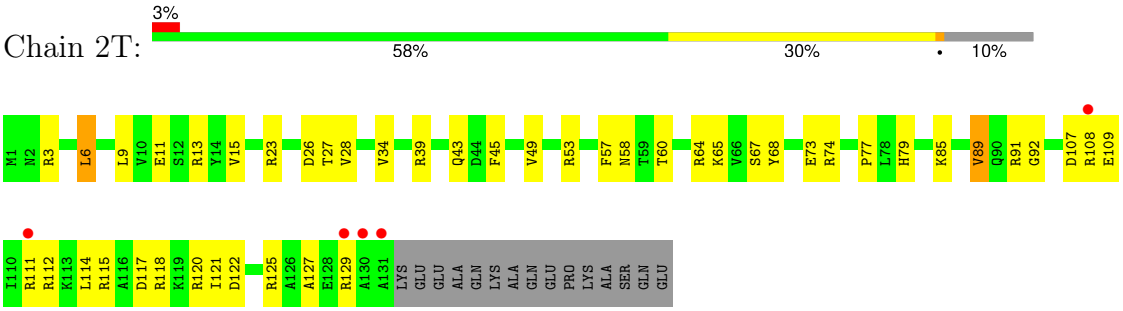
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



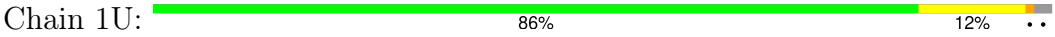
• Molecule 15: 50S ribosomal protein L19

Chain 2T:



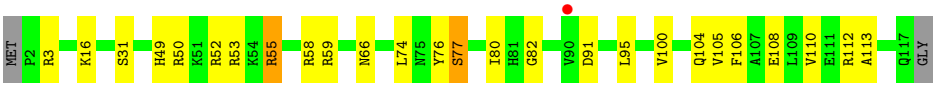
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



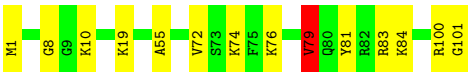
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



• Molecule 17: 50S ribosomal protein L21

Chain 1V:

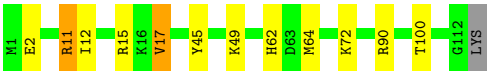


• Molecule 17: 50S ribosomal protein L21

Chain 2V:

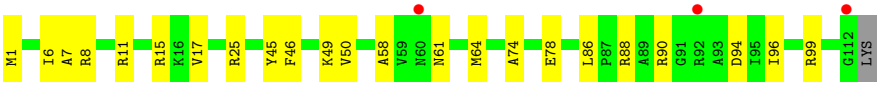
• Molecule 18: 50S ribosomal protein L22

Chain 1W:



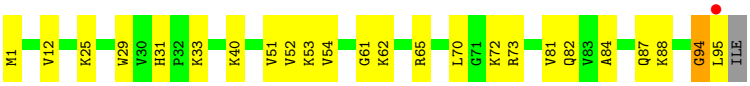
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



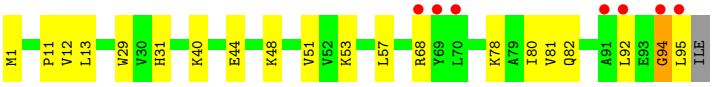
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



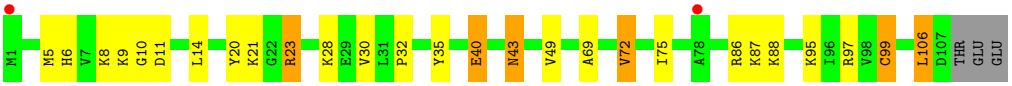
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



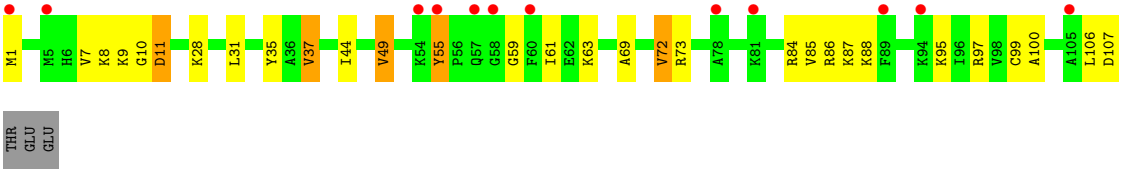
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



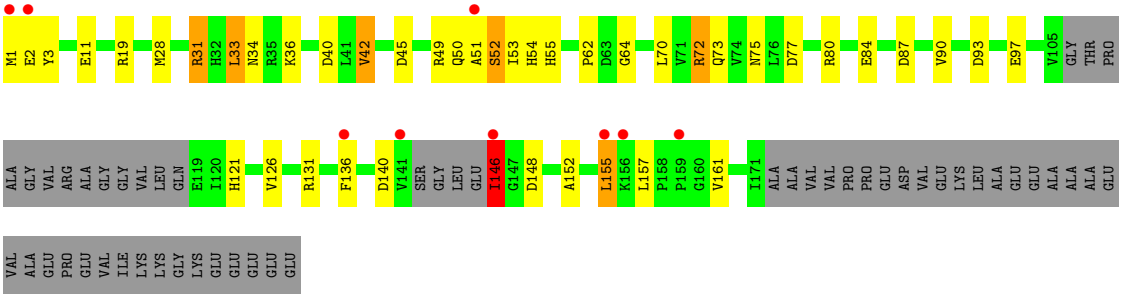
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



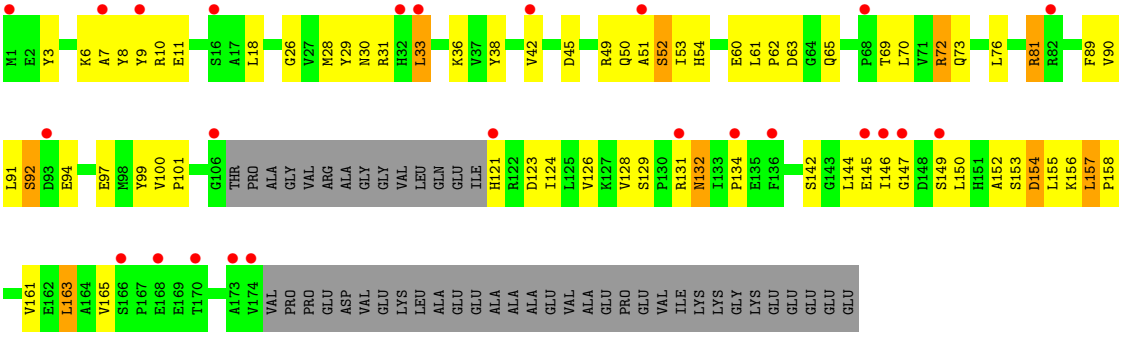
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



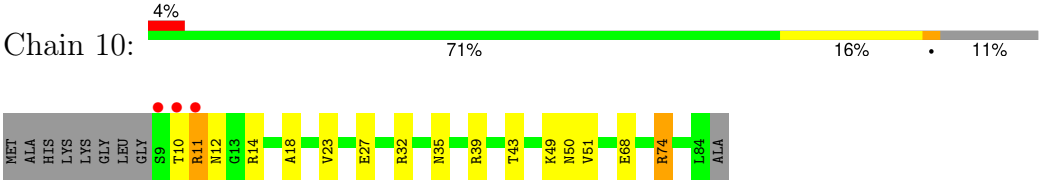
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



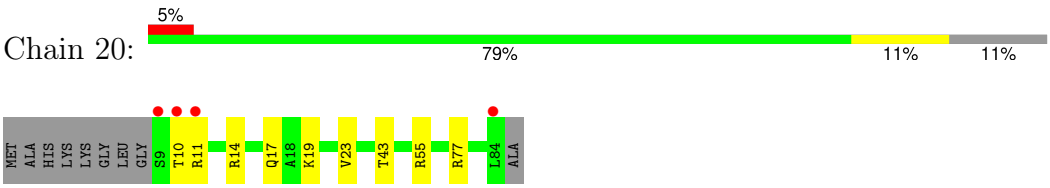
• Molecule 22: 50S ribosomal protein L27

Chain 10:



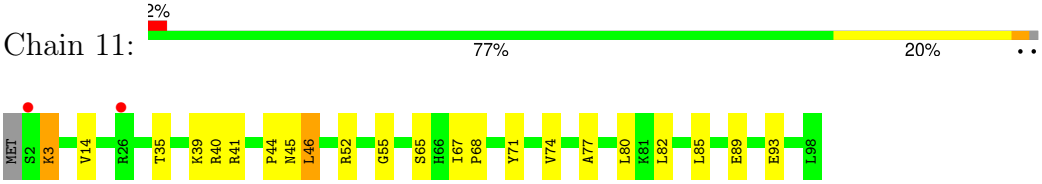
• Molecule 22: 50S ribosomal protein L27

Chain 20:



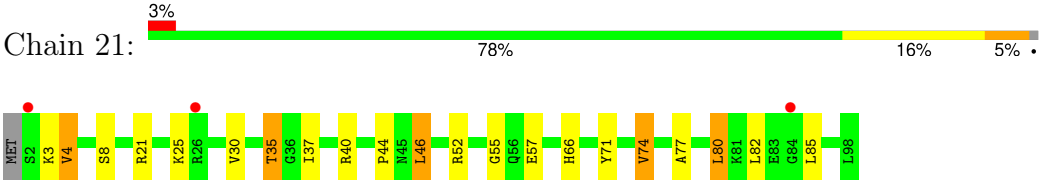
• Molecule 23: 50S ribosomal protein L28

Chain 11:



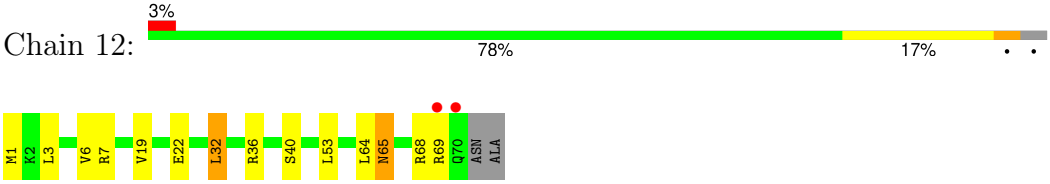
• Molecule 23: 50S ribosomal protein L28

Chain 21:



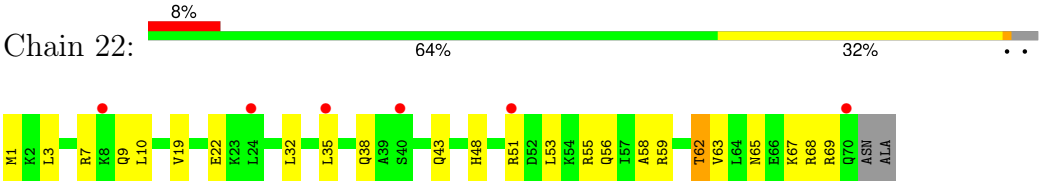
• Molecule 24: 50S ribosomal protein L29

Chain 12:



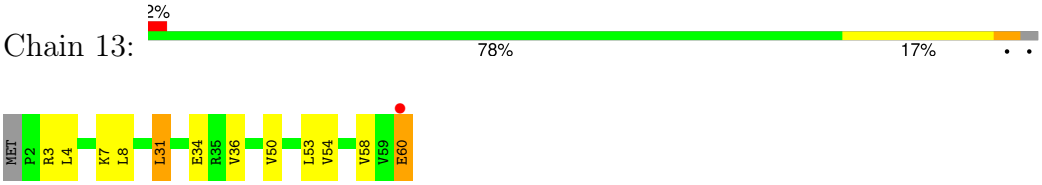
• Molecule 24: 50S ribosomal protein L29

Chain 22:



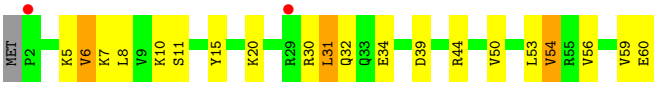
• Molecule 25: 50S ribosomal protein L30

Chain 13:



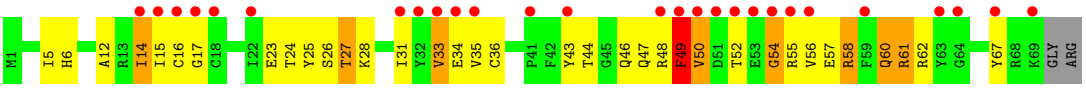
• Molecule 25: 50S ribosomal protein L30

Chain 23:



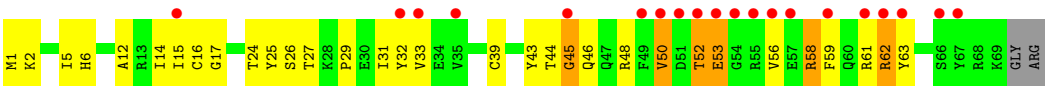
• Molecule 26: 50S ribosomal protein L31

Chain 14:



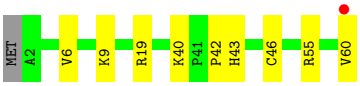
• Molecule 26: 50S ribosomal protein L31

Chain 24:



• Molecule 27: 50S ribosomal protein L32

Chain 15:

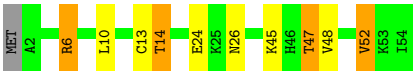


• Molecule 27: 50S ribosomal protein L32

Chain 25:

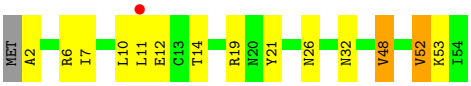
• Molecule 28: 50S ribosomal protein L33

Chain 16:



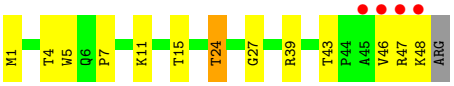
• Molecule 28: 50S ribosomal protein L33

Chain 26:



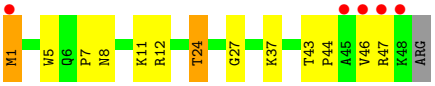
• Molecule 29: 50S ribosomal protein L34

Chain 17:



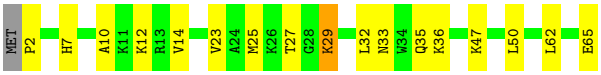
• Molecule 29: 50S ribosomal protein L34

Chain 27:



• Molecule 30: 50S ribosomal protein L35

Chain 18:



• Molecule 30: 50S ribosomal protein L35

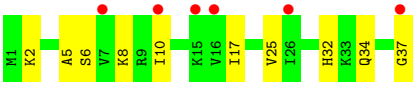
Chain 28:

• Molecule 31: 50S ribosomal protein L36

Chain 19:

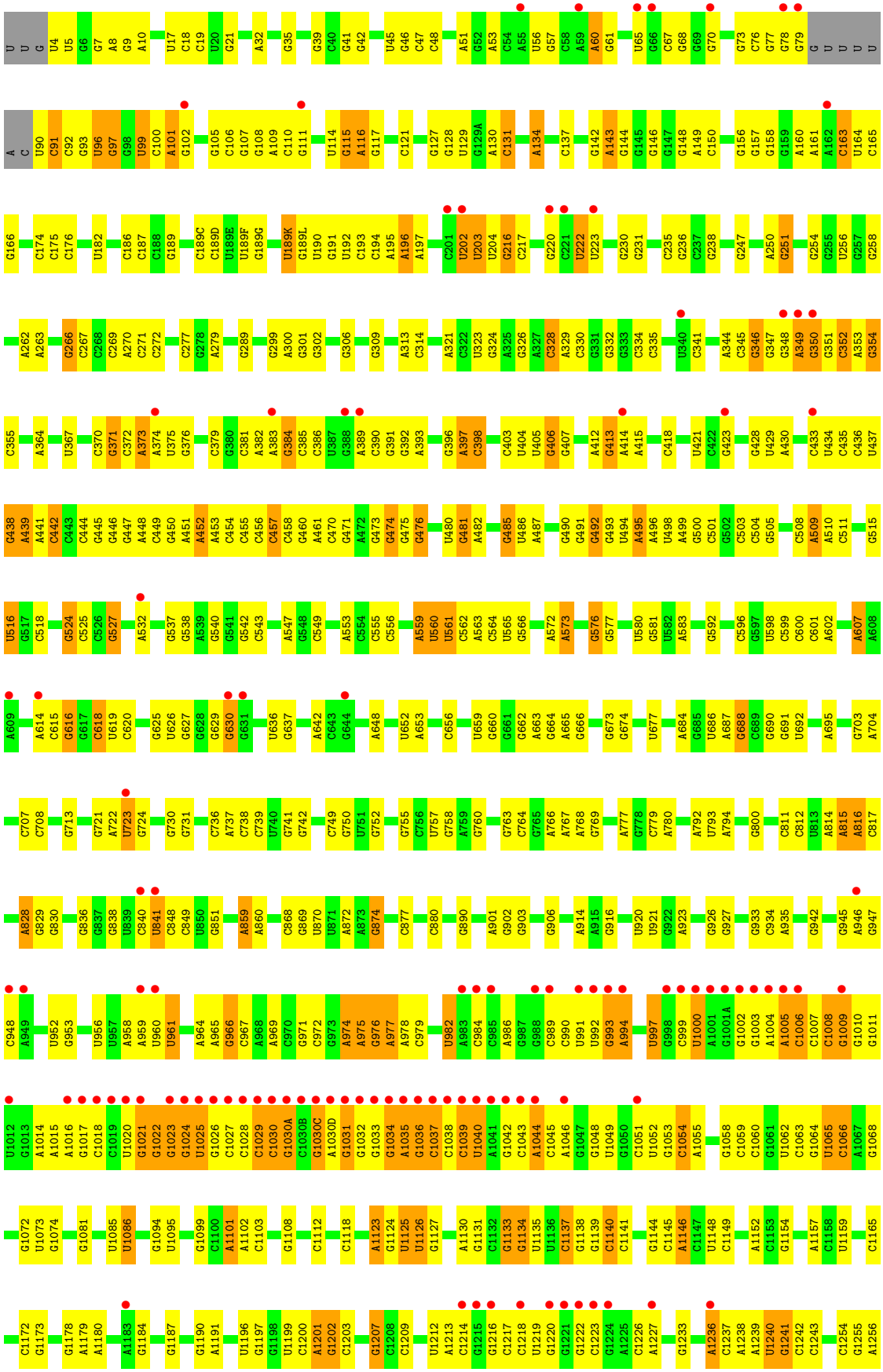
• Molecule 31: 50S ribosomal protein L36

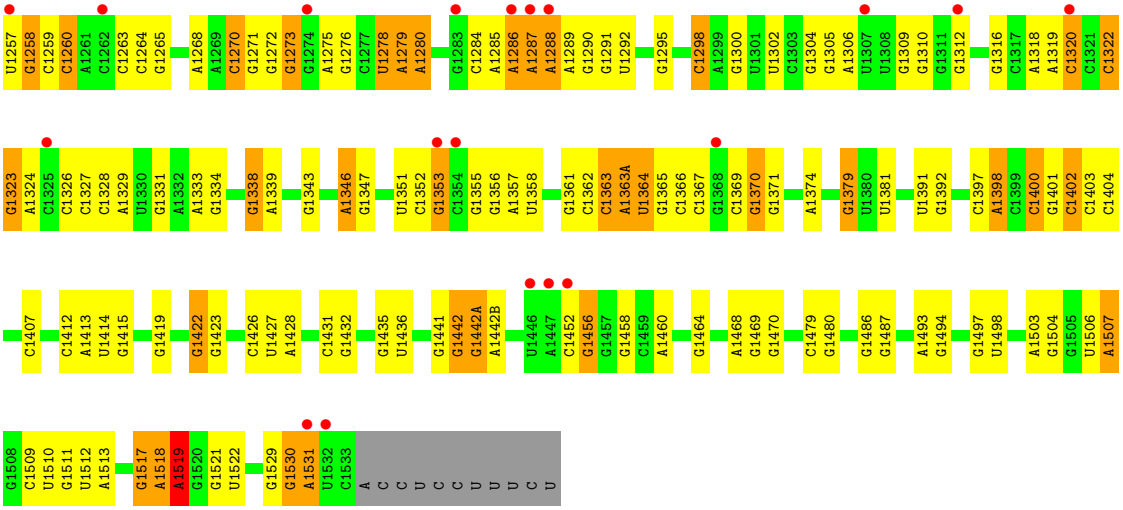
Chain 29:



• Molecule 32: 16S Ribosomal RNA

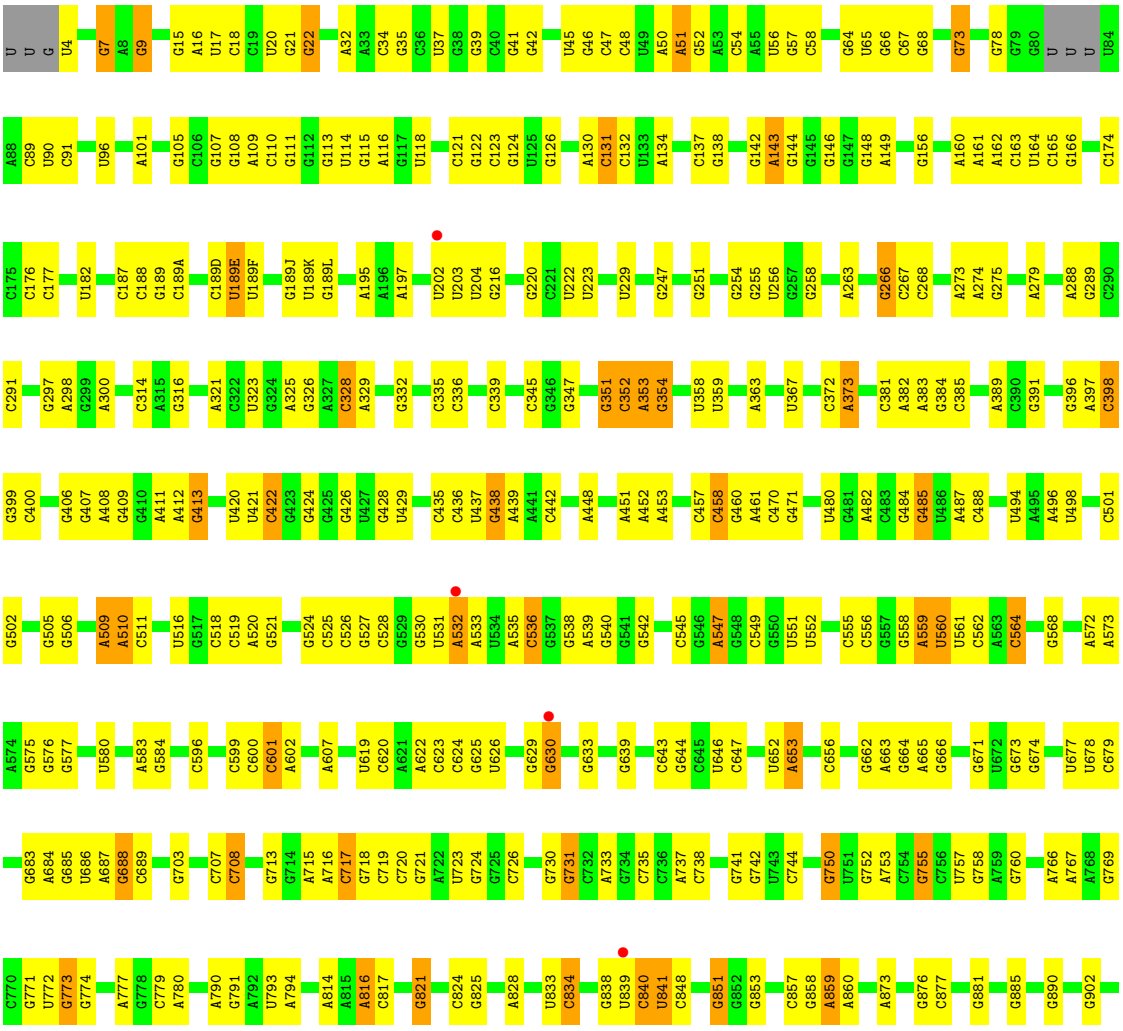
Chain 1a:

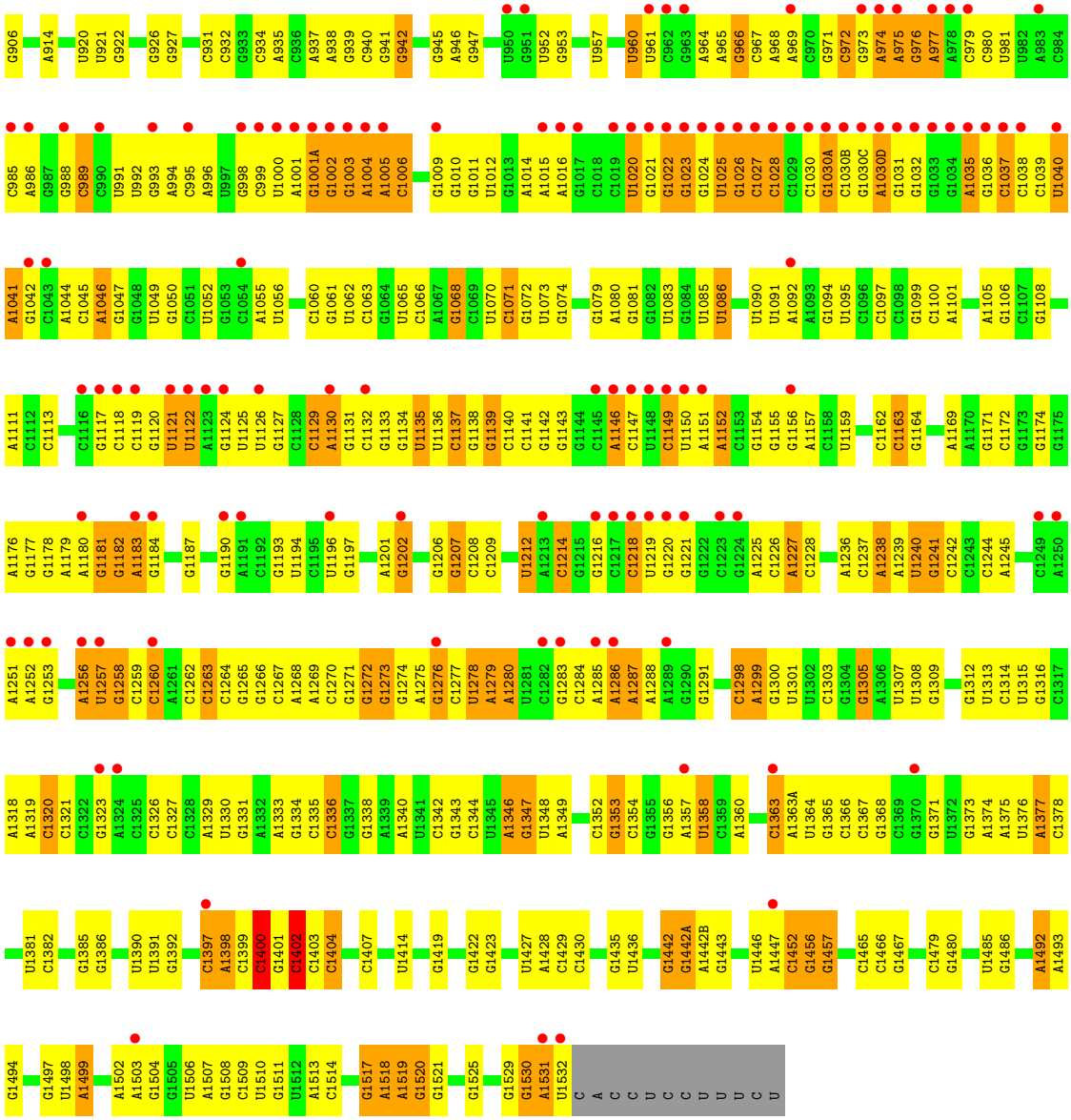




• Molecule 32: 16S Ribosomal RNA

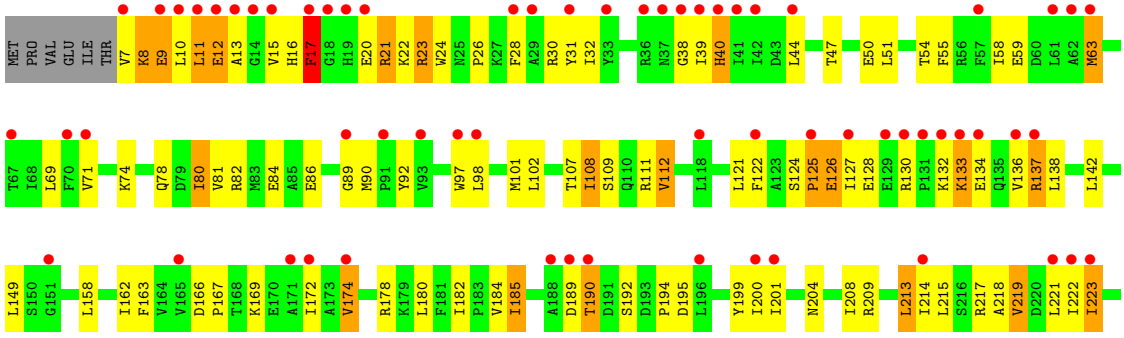
Chain 2a:

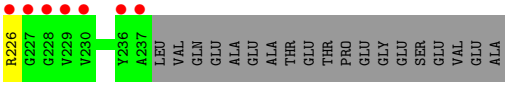




• Molecule 33: 30S ribosomal protein S2

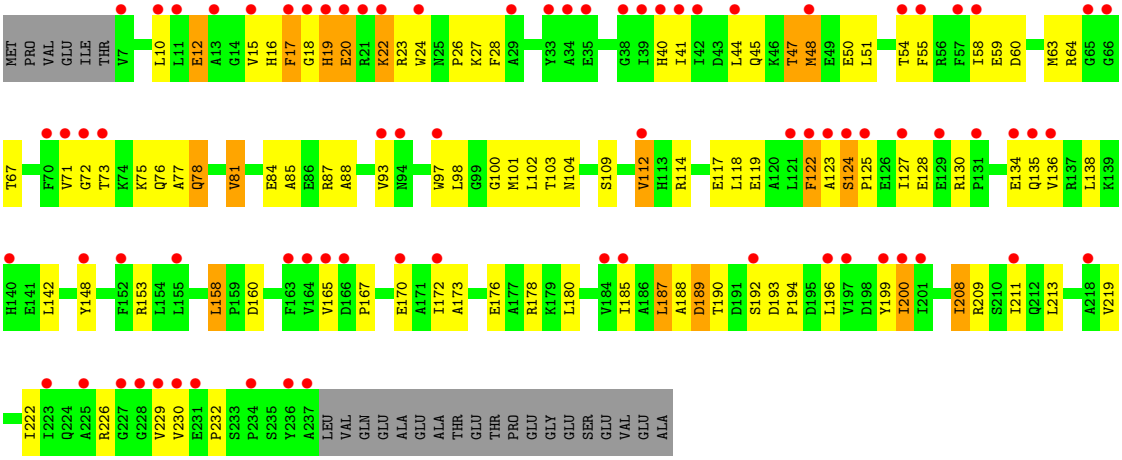
Chain 1b:





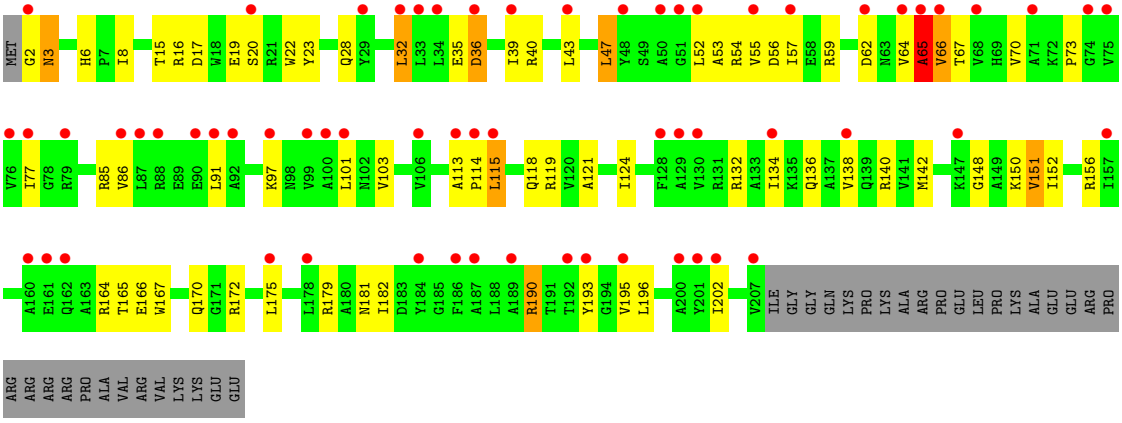
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



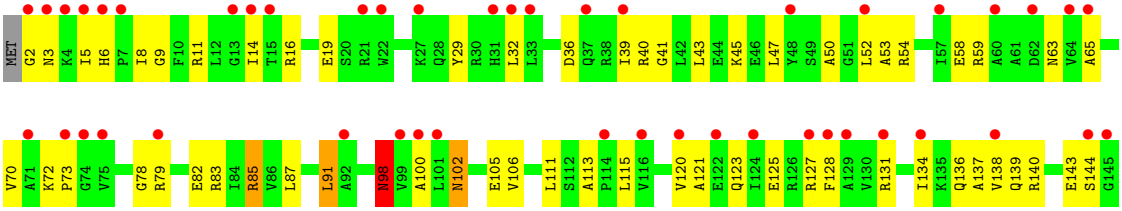
• Molecule 34: 30S ribosomal protein S3

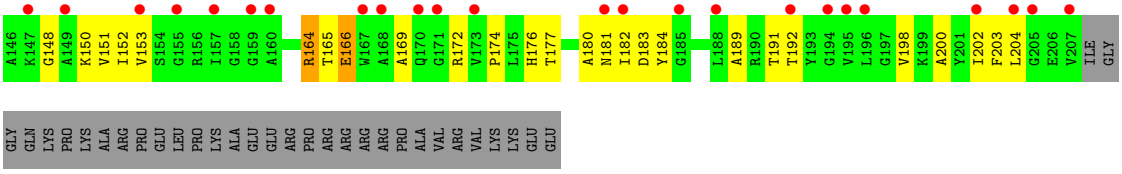
Chain 1c:



• Molecule 34: 30S ribosomal protein S3

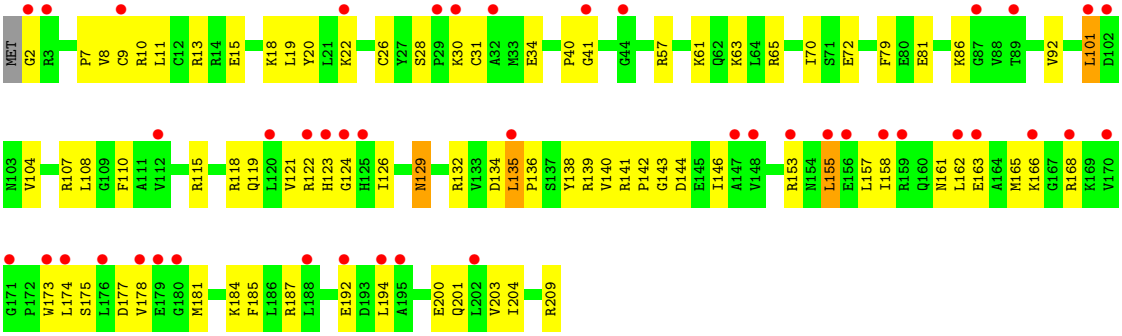
Chain 2c:





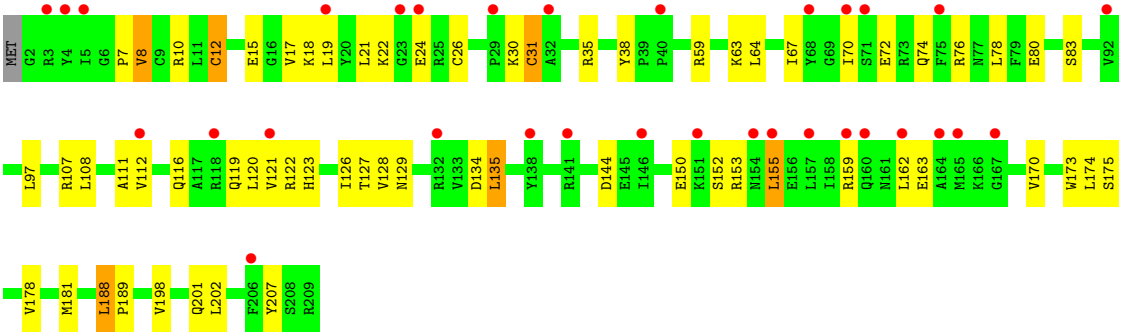
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



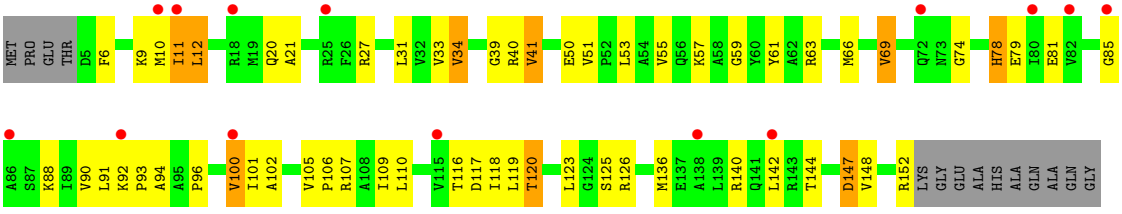
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



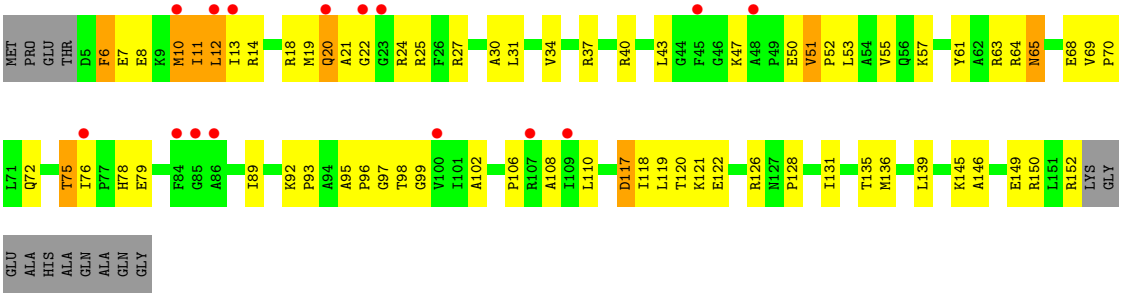
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



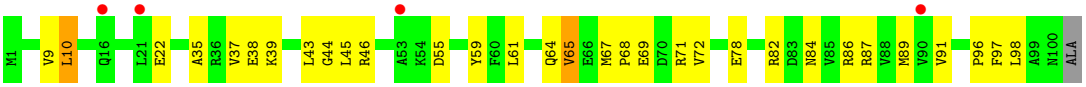
• Molecule 36: 30S ribosomal protein S5

Chain 2e:



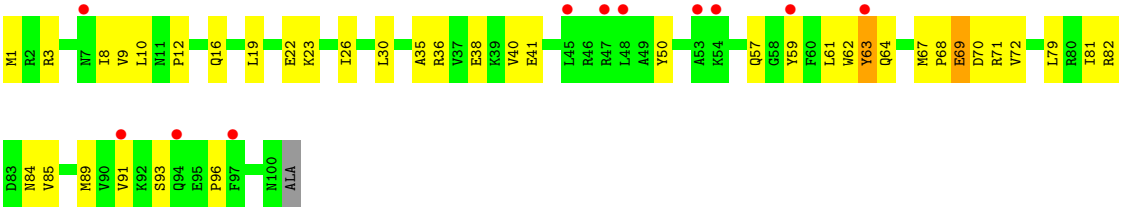
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



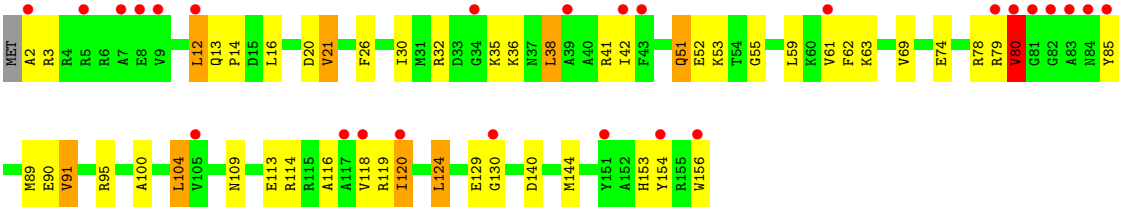
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



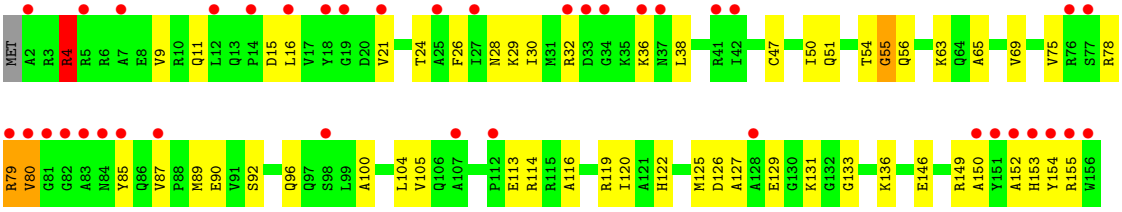
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



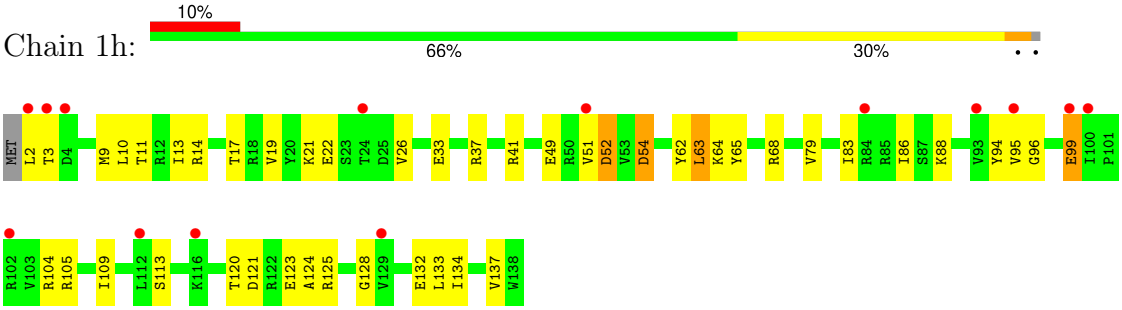
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



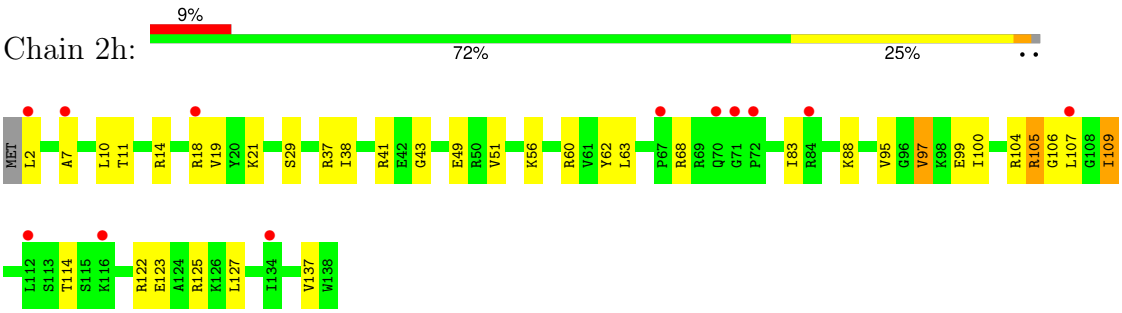
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



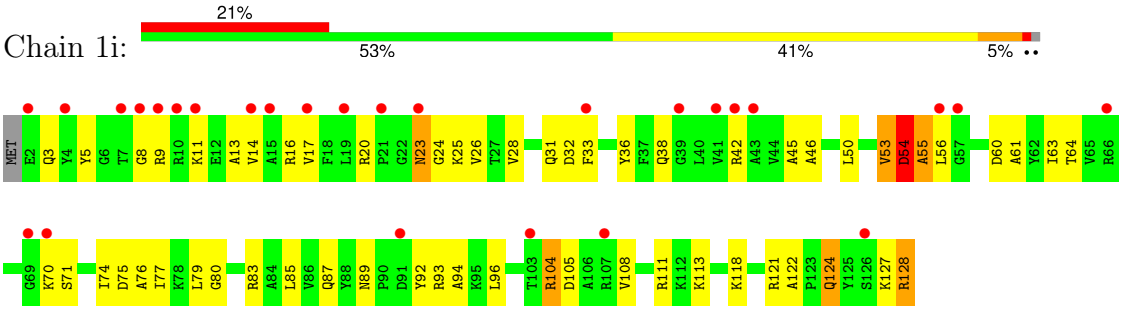
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



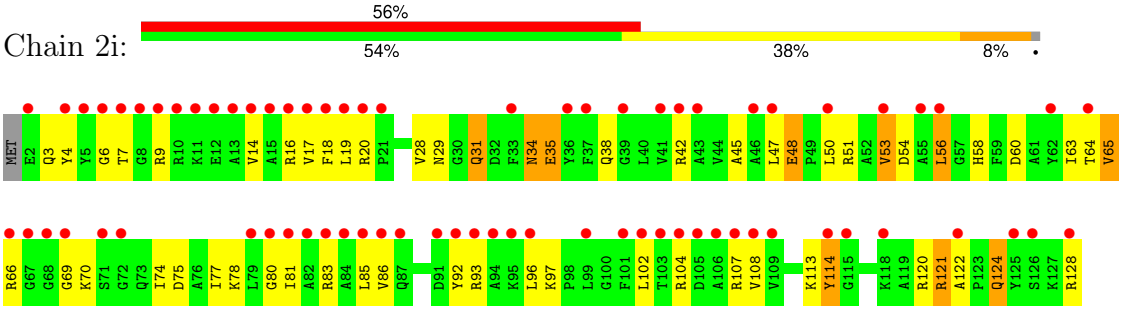
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



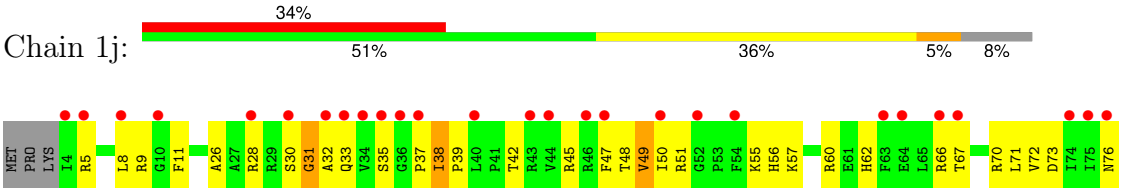
• Molecule 40: 30S ribosomal protein S9

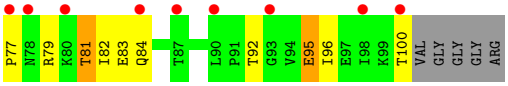
Chain 2i:



• Molecule 41: 30S ribosomal protein S10

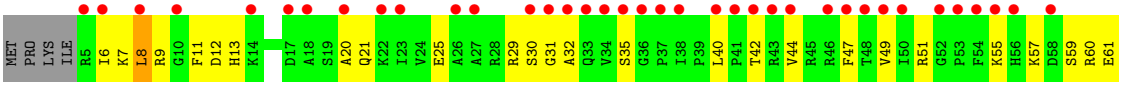
Chain 1j:

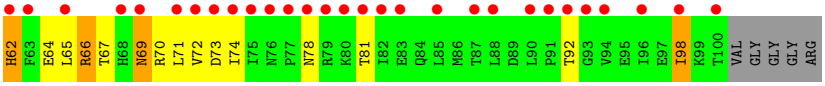




• Molecule 41: 30S ribosomal protein S10

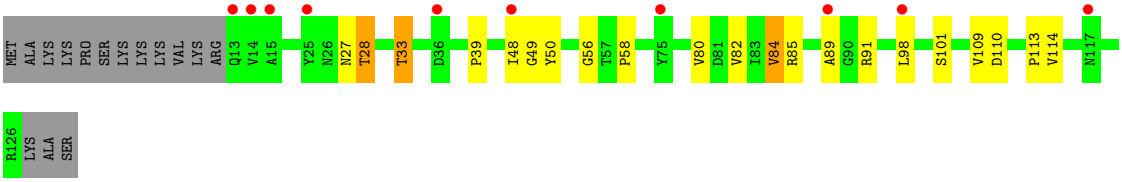
Chain 2j:





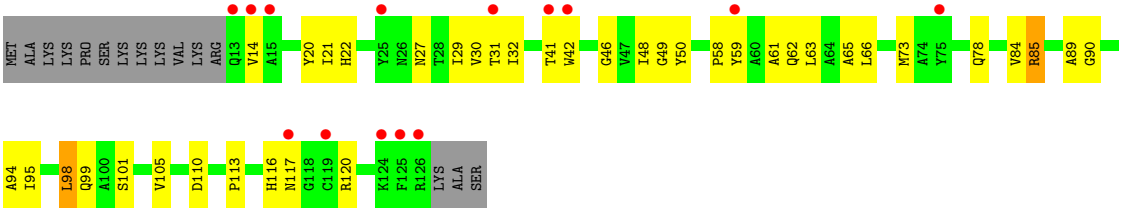
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



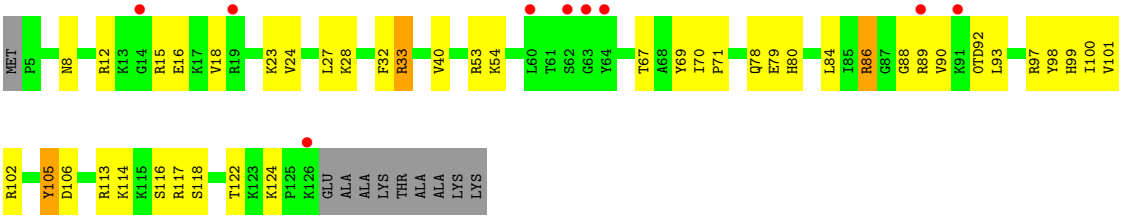
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



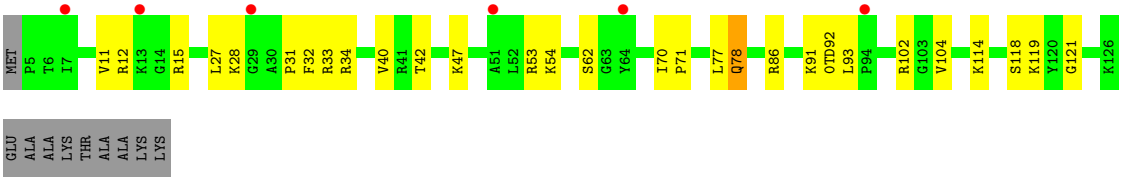
• Molecule 43: 30S ribosomal protein S12

Chain 1l:

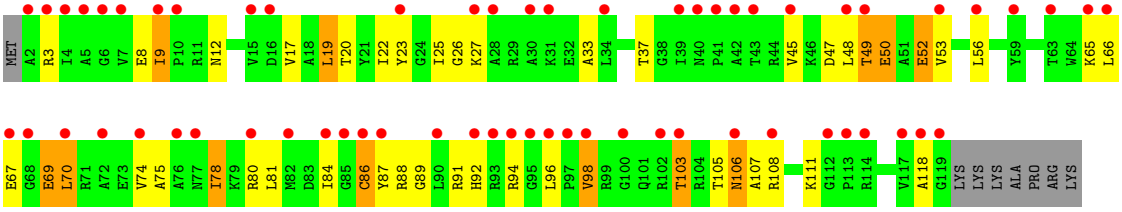


• Molecule 43: 30S ribosomal protein S12

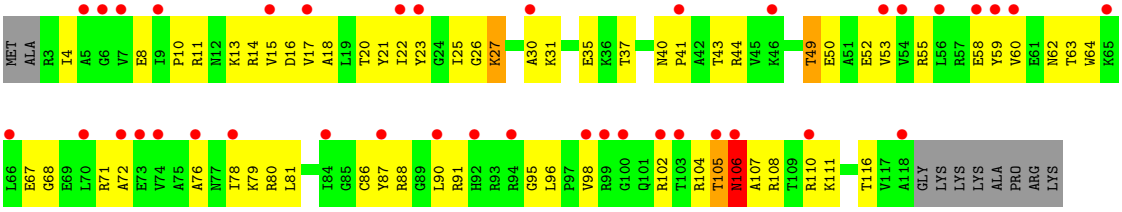
Chain 2l:



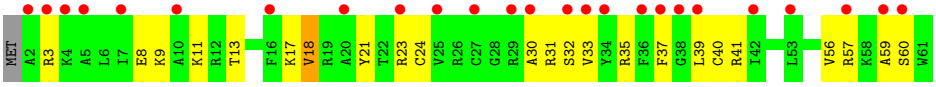
• Molecule 44: 30S ribosomal protein S13



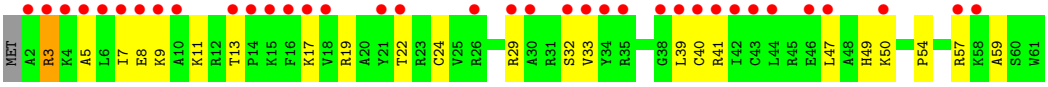
• Molecule 44: 30S ribosomal protein S13



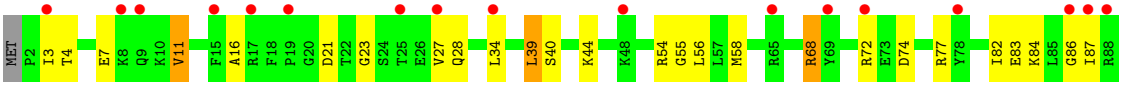
• Molecule 45: 30S ribosomal protein S14 type Z



• Molecule 45: 30S ribosomal protein S14 type Z



• Molecule 46: 30S ribosomal protein S15

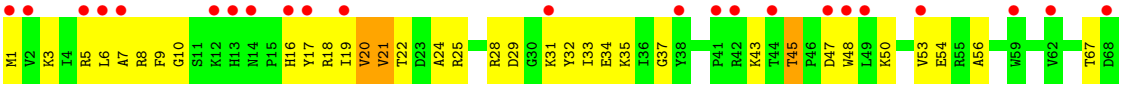


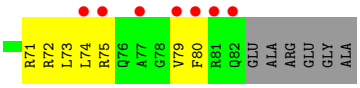
• Molecule 46: 30S ribosomal protein S15

Chain 2o:

• Molecule 47: 30S ribosomal protein S16

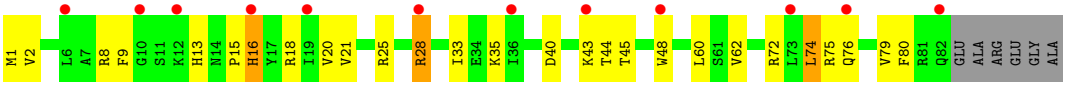
Chain 1p:





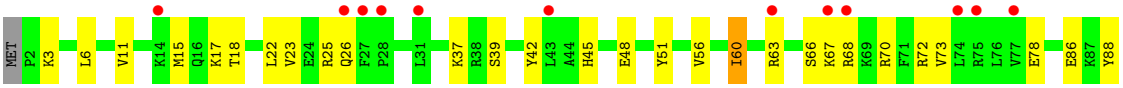
• Molecule 47: 30S ribosomal protein S16

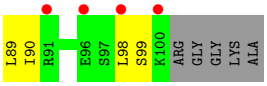
Chain 2p:



• Molecule 48: 30S ribosomal protein S17

Chain 1q:



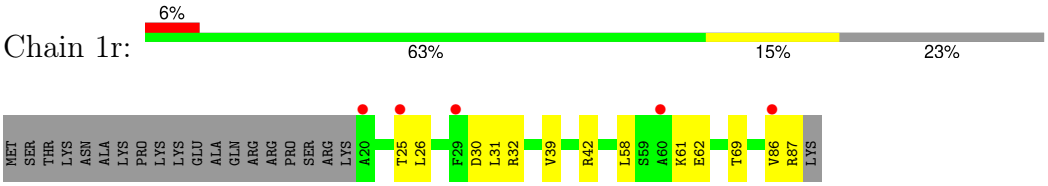


• Molecule 48: 30S ribosomal protein S17

Chain 2q:

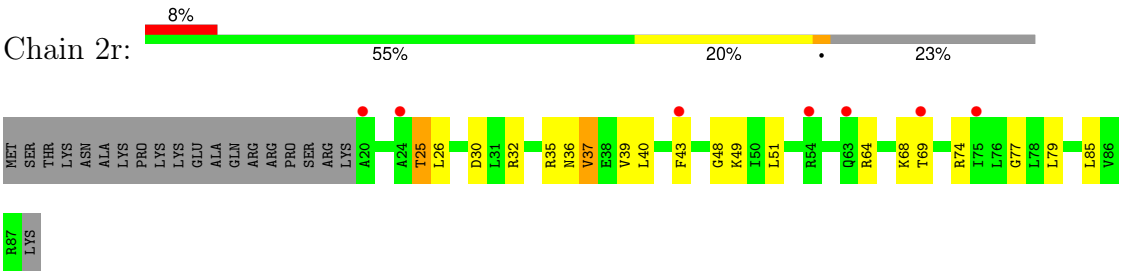
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



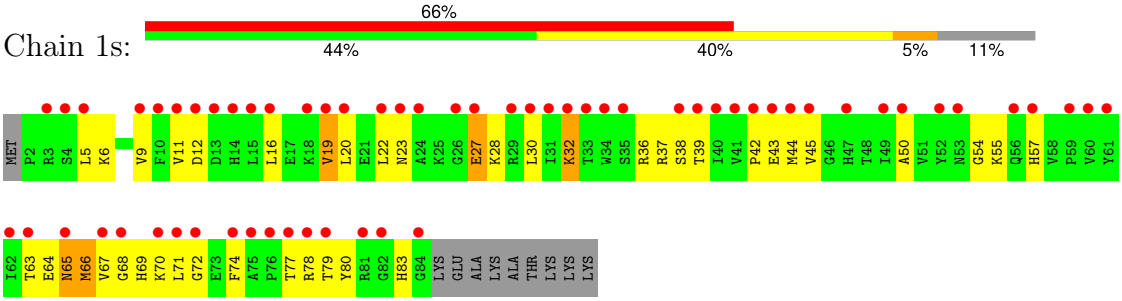
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



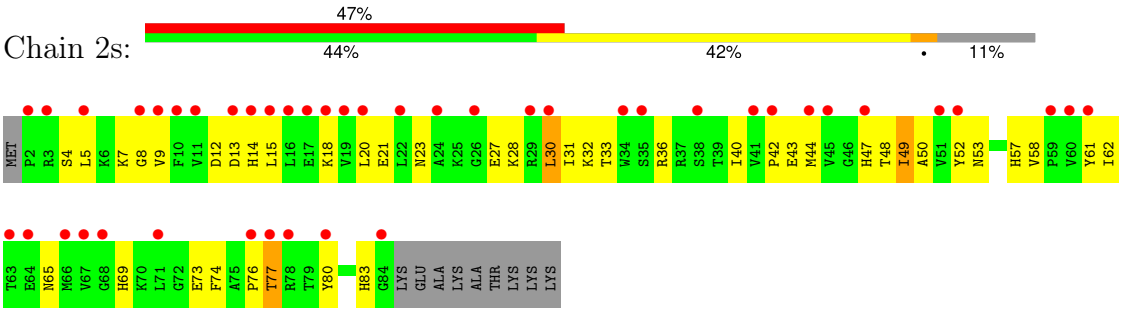
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



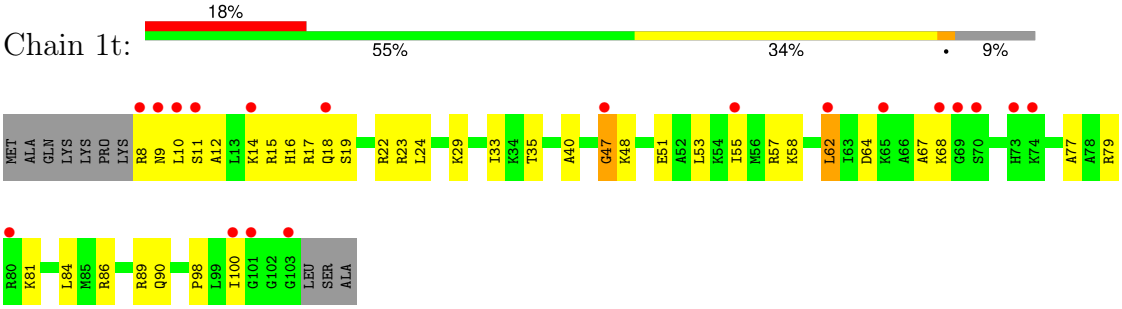
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



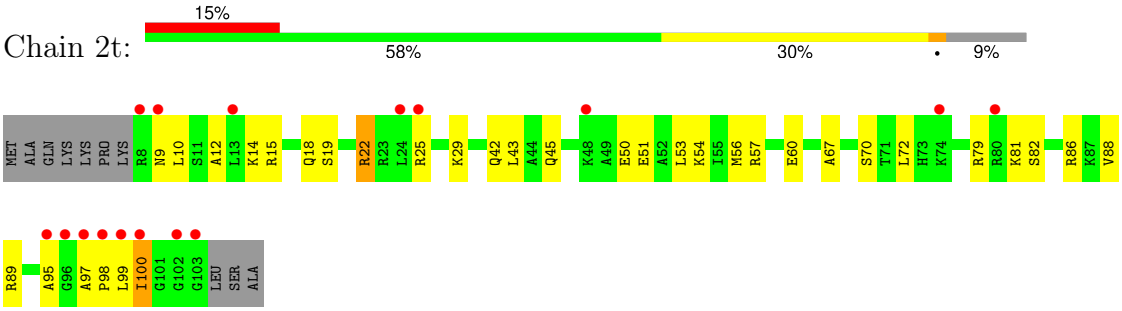
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



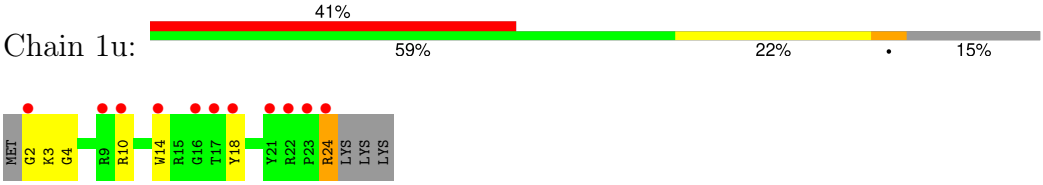
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



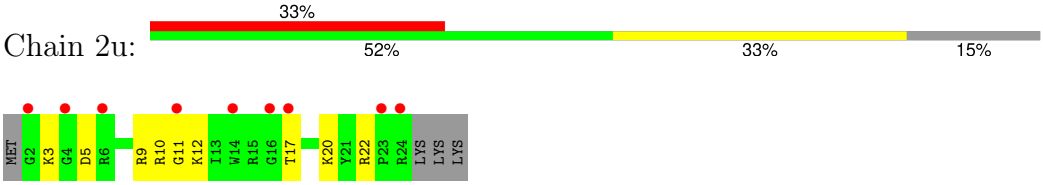
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



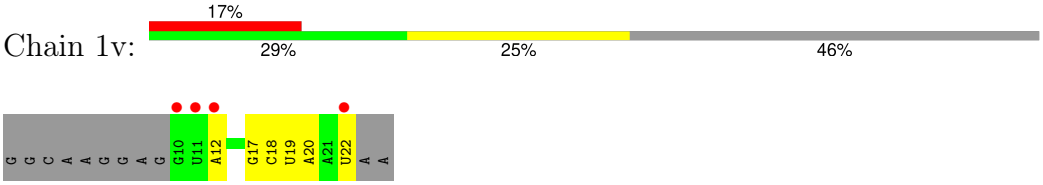
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



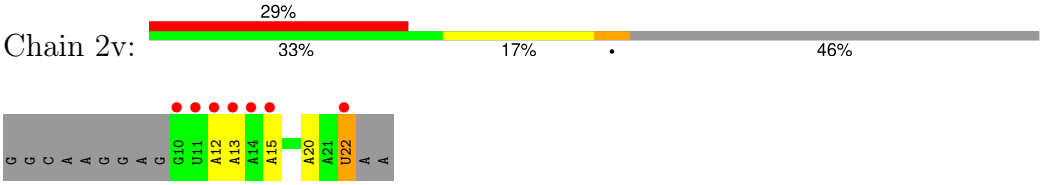
• Molecule 53: CYS-Stop mRNA

Chain 1v:



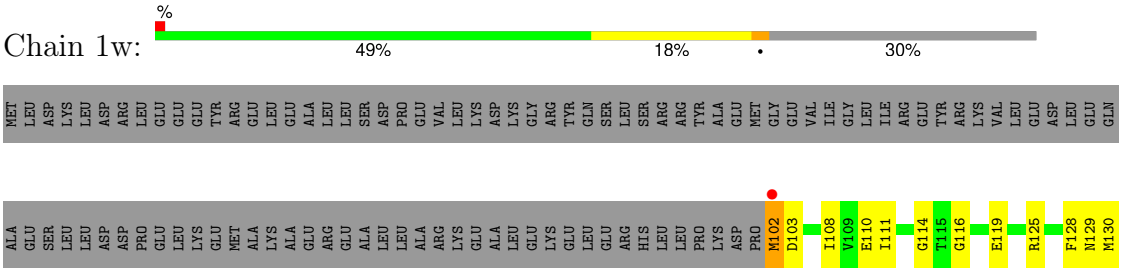
• Molecule 53: CYS-Stop mRNA

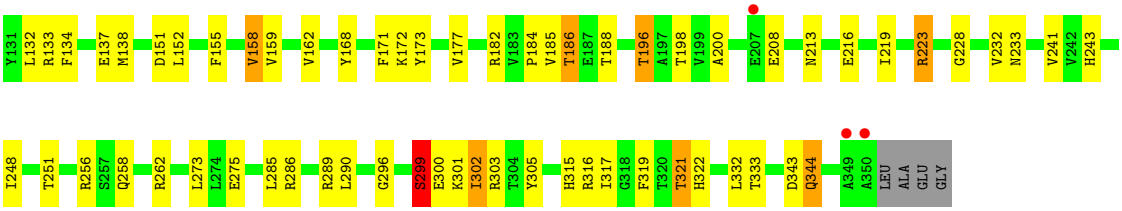
Chain 2v:



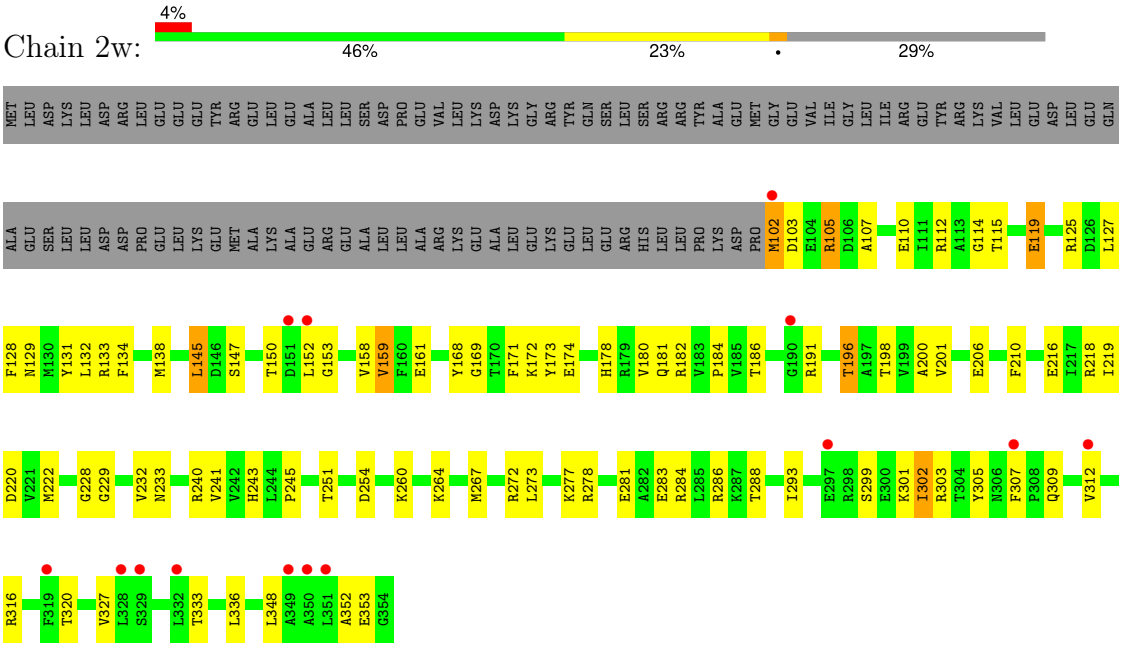
• Molecule 54: Peptide chain release factor 1

Chain 1w:

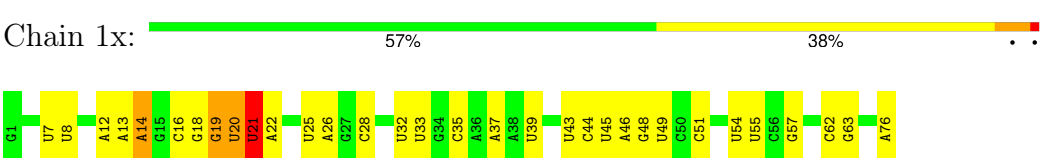




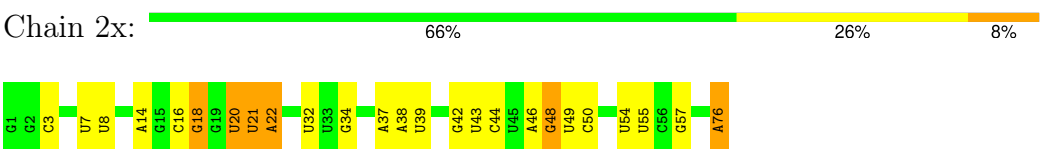
• Molecule 54: Peptide chain release factor 1



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



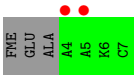
• Molecule 55: P-site Peptidyl-tRNA fMEAAAKC-tRNAcys RNA-part



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

• Molecule 56: P-site Peptidyl-tRNA fMEAAAKC-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	208.96Å 448.05Å 615.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	122.56 – 2.55 122.56 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.6 (122.56-2.55) 98.6 (122.56-2.55)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.22 (at 2.55Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.216 , 0.257 0.218 , 0.258	Depositor DCC
R_{free} test set	92899 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	52.1	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	297259	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.86% 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: OMU, G7M, MG, 0TD, PSU, OMG, 4OC, MA6, 4SU, 2MA, 5MC, 2MG, 8AN, MIA, UR3, OMC, H2U, 5MU, K, SF4, M2G, ZN

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	0.29	0/69011	0.47	1/107720 (0.0%)
1	2A	0.23	0/67295	0.41	1/105042 (0.0%)
2	1B	0.22	0/2882	0.40	0/4494
2	2B	0.19	0/2879	0.36	0/4487
3	1D	0.28	0/2186	0.52	0/2944
3	2D	0.23	0/2186	0.47	1/2944 (0.0%)
4	1E	0.26	0/1592	0.52	0/2149
4	2E	0.22	0/1592	0.44	0/2149
5	1F	0.26	0/1619	0.49	0/2193
5	2F	0.21	0/1615	0.43	0/2188
6	1G	0.20	0/1448	0.43	0/1957
6	2G	0.19	0/1453	0.43	0/1963
7	1H	0.21	0/1356	0.42	0/1834
7	2H	0.19	0/1356	0.38	0/1834
8	1I	0.19	0/1112	0.42	0/1514
8	2I	0.19	0/1079	0.39	0/1475
9	1N	0.27	0/1144	0.45	0/1543
9	2N	0.20	0/1144	0.41	0/1543
10	1O	0.26	0/943	0.46	0/1269
10	2O	0.21	0/943	0.44	0/1269
11	1P	0.27	0/1152	0.50	0/1533
11	2P	0.21	0/1152	0.46	0/1533
12	1Q	0.27	0/1143	0.50	0/1527
12	2Q	0.22	0/1143	0.43	0/1527
13	1R	0.26	0/982	0.50	0/1312
13	2R	0.22	0/982	0.43	0/1312
14	1S	0.23	0/883	0.45	0/1176
14	2S	0.19	0/880	0.43	0/1172
15	1T	0.25	0/1105	0.46	0/1477
15	2T	0.21	0/1097	0.43	0/1468
16	1U	0.27	0/977	0.47	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
16	2U	0.19	0/977	0.40	0/1301
17	1V	0.24	0/782	0.45	0/1049
17	2V	0.17	0/782	0.38	0/1049
18	1W	0.28	0/897	0.46	0/1205
18	2W	0.21	0/897	0.42	0/1205
19	1X	0.26	0/764	0.53	2/1025 (0.2%)
19	2X	0.19	0/764	0.48	2/1025 (0.2%)
20	1Y	0.23	0/819	0.47	0/1095
20	2Y	0.20	0/819	0.42	0/1095
21	1Z	0.22	0/1267	0.50	0/1717
21	2Z	0.21	0/1299	0.45	0/1763
22	10	0.27	0/612	0.47	0/816
22	20	0.22	0/612	0.45	0/816
23	11	0.27	0/762	0.45	0/1014
23	21	0.23	0/762	0.40	0/1014
24	12	0.23	0/590	0.45	0/781
24	22	0.19	0/590	0.38	0/781
25	13	0.25	0/474	0.47	0/635
25	23	0.20	0/469	0.42	0/630
26	14	0.24	0/565	0.59	2/761 (0.3%)
26	24	0.24	0/545	0.55	0/737
27	15	0.24	0/469	0.50	0/635
27	25	0.22	0/469	0.44	0/635
28	16	0.27	0/460	0.50	0/613
28	26	0.21	0/456	0.46	0/608
29	17	0.32	0/426	0.56	0/561
29	27	0.24	0/426	0.48	0/561
30	18	0.27	0/525	0.48	0/691
30	28	0.21	0/525	0.38	0/691
31	19	0.30	0/310	0.51	0/407
31	29	0.19	0/310	0.44	0/407
32	1a	0.20	0/35795	0.39	1/55864 (0.0%)
32	2a	0.20	1/35886 (0.0%)	0.38	3/56005 (0.0%)
33	1b	0.22	0/1881	0.51	0/2542
33	2b	0.23	0/1860	0.47	0/2518
34	1c	0.21	0/1572	0.46	2/2126 (0.1%)
34	2c	0.21	0/1566	0.43	0/2119
35	1d	0.20	0/1685	0.42	0/2262
35	2d	0.20	0/1704	0.44	0/2284
36	1e	0.20	0/1145	0.45	0/1543
36	2e	0.21	0/1149	0.45	0/1548
37	1f	0.18	0/823	0.42	0/1115
37	2f	0.18	0/829	0.40	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.18	0/1250	0.43	0/1679
38	2g	0.21	0/1254	0.43	0/1683
39	1h	0.18	0/1108	0.40	0/1494
39	2h	0.18	0/1108	0.41	0/1494
40	1i	0.19	0/1002	0.44	0/1346
40	2i	0.21	0/997	0.45	0/1343
41	1j	0.25	0/722	0.47	0/982
41	2j	0.22	0/727	0.48	0/988
42	1k	0.19	0/844	0.41	0/1145
42	2k	0.18	0/848	0.40	0/1149
43	1l	0.20	0/937	0.45	0/1260
43	2l	0.19	0/937	0.44	0/1260
44	1m	0.21	0/929	0.50	0/1250
44	2m	0.22	0/917	0.45	0/1234
45	1n	0.19	0/501	0.48	0/664
45	2n	0.19	0/501	0.44	0/664
46	1o	0.19	0/739	0.38	0/985
46	2o	0.18	0/739	0.43	0/985
47	1p	0.19	0/697	0.44	0/939
47	2p	0.18	0/693	0.45	0/935
48	1q	0.20	0/836	0.41	0/1117
48	2q	0.17	0/836	0.40	0/1117
49	1r	0.20	0/560	0.41	0/746
49	2r	0.18	0/560	0.38	0/746
50	1s	0.22	0/667	0.52	0/900
50	2s	0.21	0/661	0.51	0/893
51	1t	0.20	0/730	0.43	0/965
51	2t	0.20	0/729	0.45	0/965
52	1u	0.22	0/203	0.43	0/266
52	2u	0.22	0/203	0.46	0/266
53	1v	0.25	0/310	0.44	0/480
53	2v	0.24	0/310	0.45	0/480
54	1w	0.22	0/1965	0.44	0/2648
54	2w	0.20	0/1983	0.39	0/2671
55	1x	0.23	0/1555	0.36	0/2419
55	2x	0.23	1/1555 (0.1%)	0.37	0/2419
56	1z	0.35	0/29	0.60	0/37
56	2z	0.30	0/24	0.51	0/30
All	All	0.24	2/313816 (0.0%)	0.43	15/468865 (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
11	1P	0	1
11	2P	0	1
21	1Z	0	2
26	14	0	1
33	1b	0	2
33	2b	0	2
All	All	0	9

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	527	G7M	O3'-P	5.13	1.61	1.56
55	2x	8	4SU	O3'-P	5.02	1.61	1.56

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1992	G	C2'-C3'-O3'	7.29	120.44	109.50
1	2A	1992	G	C2'-C3'-O3'	6.52	119.28	109.50
32	2a	1272	G	N1-C2-N2	-6.18	97.66	116.20
32	2a	1263	C	N1-C2-O2	5.99	136.85	118.90
34	1c	65	ALA	CA-C-N	5.83	132.46	121.97
34	1c	65	ALA	C-N-CA	5.83	132.46	121.97
32	2a	1272	G	N3-C2-N2	5.30	135.79	119.90
32	1a	266	G	C2'-C3'-O3'	5.26	117.40	109.50
3	2D	98	VAL	N-CA-C	-5.23	104.35	111.89
19	1X	94	GLY	CA-C-N	5.17	131.00	121.70
19	1X	94	GLY	C-N-CA	5.17	131.00	121.70
26	14	54	GLY	CA-C-N	5.14	131.35	121.54
26	14	54	GLY	C-N-CA	5.14	131.35	121.54
19	2X	94	GLY	CA-C-N	5.11	130.90	121.70
19	2X	94	GLY	C-N-CA	5.11	130.90	121.70

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	14	52	THR	Peptide
11	1P	35	HIS	Peptide
21	1Z	136	PHE	Peptide

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Mol	Chain	Res	Type	Group
21	1Z	146	ILE	Peptide
33	1b	122	PHE	Peptide
33	1b	9	GLU	Peptide
11	2P	35	HIS	Peptide
33	2b	124	SER	Peptide
33	2b	22	LYS	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	31196	617	0
1	2A	60322	0	30426	647	0
2	1B	2577	0	1305	26	0
2	2B	2575	0	1303	26	0
3	1D	2136	0	2218	41	0
3	2D	2136	0	2218	49	0
4	1E	1559	0	1618	22	0
4	2E	1559	0	1618	21	0
5	1F	1584	0	1625	40	0
5	2F	1580	0	1619	46	0
6	1G	1423	0	1436	53	0
6	2G	1428	0	1438	47	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	40	0
8	1I	1097	0	1140	24	0
8	2I	1064	0	1082	37	0
9	1N	1117	0	1184	10	0
9	2N	1117	0	1184	19	0
10	1O	933	0	996	16	0
10	2O	933	0	996	18	0
11	1P	1135	0	1212	22	0
11	2P	1135	0	1212	24	0
12	1Q	1122	0	1179	12	0
12	2Q	1122	0	1179	24	0
13	1R	968	0	1033	14	0
13	2R	968	0	1033	16	0
14	1S	873	0	927	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	2S	870	0	923	20	0
15	1T	1091	0	1151	18	0
15	2T	1083	0	1136	30	0
16	1U	959	0	1019	12	0
16	2U	959	0	1019	19	0
17	1V	771	0	830	11	0
17	2V	771	0	830	11	0
18	1W	886	0	940	8	0
18	2W	886	0	940	12	0
19	1X	750	0	814	16	0
19	2X	750	0	814	12	0
20	1Y	806	0	881	17	0
20	2Y	806	0	881	20	0
21	1Z	1240	0	1240	29	0
21	2Z	1271	0	1273	43	0
22	10	604	0	619	15	0
22	20	604	0	619	7	0
23	11	755	0	826	15	0
23	21	755	0	826	18	0
24	12	588	0	643	8	0
24	22	588	0	643	13	0
25	13	469	0	518	5	0
25	23	464	0	514	12	0
26	14	552	0	533	29	0
26	24	532	0	503	27	0
27	15	455	0	465	4	0
27	25	455	0	465	4	0
28	16	453	0	473	6	0
28	26	449	0	469	6	0
29	17	418	0	467	9	0
29	27	418	0	467	9	0
30	18	517	0	582	13	0
30	28	517	0	582	14	0
31	19	307	0	335	5	0
31	29	307	0	335	8	0
32	1a	32246	0	16292	494	0
32	2a	32327	0	16338	500	0
33	1b	1846	0	1867	77	0
33	2b	1825	0	1828	59	0
34	1c	1548	0	1535	44	0
34	2c	1542	0	1517	57	0
35	1d	1655	0	1672	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	2d	1674	0	1714	42	0
36	1e	1129	0	1185	44	0
36	2e	1133	0	1191	50	0
37	1f	810	0	804	17	0
37	2f	816	0	808	24	0
38	1g	1231	0	1238	40	0
38	2g	1235	0	1249	37	0
39	1h	1088	0	1126	37	0
39	2h	1088	0	1126	28	0
40	1i	983	0	986	40	0
40	2i	978	0	966	41	0
41	1j	709	0	650	34	0
41	2j	714	0	672	32	0
42	1k	829	0	825	13	0
42	2k	833	0	836	30	0
43	1l	932	0	981	28	0
43	2l	932	0	981	19	0
44	1m	919	0	951	41	0
44	2m	907	0	934	49	0
45	1n	492	0	529	16	0
45	2n	492	0	529	24	0
46	1o	728	0	760	14	0
46	2o	728	0	760	17	0
47	1p	681	0	697	35	0
47	2p	677	0	686	15	0
48	1q	823	0	891	23	0
48	2q	823	0	891	10	0
49	1r	555	0	618	8	0
49	2r	555	0	618	15	0
50	1s	652	0	662	36	0
50	2s	646	0	644	37	0
51	1t	728	0	798	27	0
51	2t	727	0	796	25	0
52	1u	199	0	208	6	0
52	2u	199	0	208	8	0
53	1v	277	0	140	4	0
53	2v	277	0	140	3	0
54	1w	1937	0	1919	45	0
54	2w	1955	0	1927	50	0
55	1x	1577	0	801	14	0
55	2x	1577	0	801	11	0
56	1z	30	0	32	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2z	25	0	27	0	0
57	10	8	0	0	0	0
57	11	4	0	0	0	0
57	12	2	0	0	0	0
57	13	4	0	0	0	0
57	15	8	0	0	0	0
57	16	1	0	0	0	0
57	17	6	0	0	0	0
57	18	4	0	0	0	0
57	19	1	0	0	0	0
57	1A	1088	0	0	0	0
57	1B	36	0	0	0	0
57	1D	13	0	0	0	0
57	1E	15	0	0	0	0
57	1F	15	0	0	0	0
57	1G	4	0	0	0	0
57	1I	1	0	0	0	0
57	1N	6	0	0	0	0
57	1O	4	0	0	0	0
57	1P	4	0	0	0	0
57	1Q	8	0	0	0	0
57	1R	5	0	0	0	0
57	1S	3	0	0	0	0
57	1T	2	0	0	0	0
57	1U	10	0	0	0	0
57	1V	6	0	0	0	0
57	1W	6	0	0	0	0
57	1X	5	0	0	0	0
57	1Y	4	0	0	0	0
57	1Z	2	0	0	0	0
57	1a	223	0	0	0	0
57	1b	1	0	0	0	0
57	1d	1	0	0	0	0
57	1e	3	0	0	0	0
57	1f	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	1	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	1v	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1w	2	0	0	0	0
57	1x	13	0	0	0	0
57	20	2	0	0	0	0
57	21	1	0	0	0	0
57	23	3	0	0	0	0
57	25	7	0	0	0	0
57	26	1	0	0	0	0
57	27	2	0	0	0	0
57	28	4	0	0	0	0
57	29	1	0	0	0	0
57	2A	853	0	0	0	0
57	2B	22	0	0	0	0
57	2D	9	0	0	0	0
57	2E	9	0	0	0	0
57	2F	9	0	0	0	0
57	2G	1	0	0	0	0
57	2N	1	0	0	0	0
57	2O	2	0	0	0	0
57	2P	1	0	0	0	0
57	2Q	4	0	0	0	0
57	2R	2	0	0	0	0
57	2T	3	0	0	0	0
57	2U	2	0	0	0	0
57	2V	2	0	0	0	0
57	2W	2	0	0	0	0
57	2X	2	0	0	0	0
57	2Z	1	0	0	0	0
57	2a	176	0	0	0	0
57	2d	2	0	0	0	0
57	2e	1	0	0	0	0
57	2f	3	0	0	0	0
57	2g	1	0	0	0	0
57	2i	1	0	0	0	0
57	2j	1	0	0	0	0
57	2k	1	0	0	0	0
57	2l	2	0	0	0	0
57	2q	3	0	0	0	0
57	2t	1	0	0	0	0
57	2v	2	0	0	0	0
57	2w	1	0	0	0	0
57	2x	10	0	0	0	0
58	1A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	14	1	0	0	0	0
59	15	1	0	0	0	0
59	16	1	0	0	0	0
59	19	1	0	0	0	0
59	1Y	1	0	0	0	0
59	1n	1	0	0	0	0
59	24	1	0	0	0	0
59	25	1	0	0	0	0
59	26	1	0	0	0	0
59	29	1	0	0	0	0
59	2Y	1	0	0	0	0
59	2n	1	0	0	0	0
60	1d	8	0	0	0	0
60	2d	8	0	0	0	0
61	10	9	0	0	0	0
61	11	10	0	0	0	0
61	12	3	0	0	0	0
61	13	4	0	0	0	0
61	15	5	0	0	0	0
61	16	1	0	0	0	0
61	17	6	0	0	0	0
61	18	10	0	0	0	0
61	1A	2032	0	0	76	0
61	1B	62	0	0	0	0
61	1D	24	0	0	1	0
61	1E	31	0	0	4	0
61	1F	15	0	0	0	0
61	1G	7	0	0	2	0
61	1H	2	0	0	0	0
61	1I	1	0	0	0	0
61	1N	5	0	0	0	0
61	1O	7	0	0	0	0
61	1P	20	0	0	1	0
61	1Q	7	0	0	0	0
61	1R	15	0	0	2	0
61	1S	4	0	0	0	0
61	1T	9	0	0	0	0
61	1U	13	0	0	1	0
61	1V	9	0	0	0	0
61	1W	11	0	0	0	0
61	1X	4	0	0	0	0
61	1Y	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	1Z	1	0	0	0	0
61	1a	289	0	0	25	0
61	1d	1	0	0	0	0
61	1j	1	0	0	0	0
61	1l	4	0	0	0	0
61	1q	2	0	0	0	0
61	1v	5	0	0	0	0
61	1w	5	0	0	1	0
61	1x	24	0	0	3	0
61	20	2	0	0	0	0
61	21	7	0	0	1	0
61	22	1	0	0	0	0
61	23	2	0	0	0	0
61	25	1	0	0	0	0
61	27	3	0	0	0	0
61	28	2	0	0	1	0
61	29	1	0	0	0	0
61	2A	1200	0	0	76	0
61	2B	20	0	0	1	0
61	2D	23	0	0	1	0
61	2E	12	0	0	0	0
61	2F	15	0	0	1	0
61	2I	2	0	0	0	0
61	2O	3	0	0	0	0
61	2P	14	0	0	0	0
61	2Q	1	0	0	0	0
61	2R	3	0	0	2	0
61	2T	4	0	0	0	0
61	2U	3	0	0	0	0
61	2W	2	0	0	0	0
61	2X	3	0	0	0	0
61	2Z	1	0	0	0	0
61	2a	152	0	0	9	0
61	2e	2	0	0	0	0
61	2j	1	0	0	0	0
61	2l	5	0	0	1	0
61	2o	1	0	0	0	0
61	2q	2	0	0	0	0
61	2t	1	0	0	0	0
61	2v	1	0	0	0	0
61	2w	3	0	0	0	0
61	2x	28	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	2z	1	0	0	0	0
All	All	297259	0	197120	4158	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 9.

All (4158) 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	1.33	1.26
32:1a:1035:A:H2'	32:1a:1036:G:H21	1.21	1.04
1:1A:1082:U:O4	1:1A:1086:A:N1	1.95	0.99
1:2A:2589:A:OP1	61:2A:3903:HOH:O	1.83	0.94
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.50	0.94
1:2A:784:A:OP2	61:2A:3903:HOH:O	1.86	0.93
29:17:24:THR:HG22	29:17:27:GLY:H	1.34	0.92
1:1A:2499:C:OP1	61:1A:4102:HOH:O	1.84	0.92
50:1s:27:GLU:HB2	50:1s:28:LYS:HA	1.53	0.91
32:2a:1086:U:H3	32:2a:1099:G:H22	1.17	0.89
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.55	0.89
1:2A:2104:G:H1	1:2A:2185:C:H42	1.18	0.88
32:1a:1025:U:H3	32:1a:1036:G:H1	1.22	0.88
32:1a:1441:G:H5"	32:1a:1442:G:H5'	1.57	0.86
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.54	0.86
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.10	0.86
1:1A:962:G:OP1	61:1A:4104:HOH:O	1.93	0.86
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.57	0.86
1:1A:2427:C:OP1	61:1A:4103:HOH:O	1.93	0.85
10:1O:48:PRO:HB3	32:1a:1422:G:H5'	1.58	0.85
32:1a:975:A:H4'	32:1a:976:G:H5"	1.57	0.85
33:1b:178:ARG:HH22	39:1h:68:ARG:HH12	1.25	0.85
1:2A:1664:A:OP1	61:2A:3904:HOH:O	1.94	0.85
50:2s:27:GLU:HB3	50:2s:28:LYS:HB3	1.58	0.84
29:27:24:THR:HG22	29:27:27:GLY:H	1.41	0.84
32:1a:405:U:O4	35:1d:2:GLY:N	2.11	0.84
1:2A:1689:A:H62	1:2A:1698:A:H2	1.25	0.84
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.10	0.84
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.11	0.84
32:1a:1401:G:OP1	61:1a:1901:HOH:O	1.96	0.84
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.60	0.84
32:1a:1222:G:H5"	50:1s:78:ARG:HE	1.43	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:959:A:HO2'	32:1a:984:C:HO2'	1.24	0.83
1:1A:505:A:OP2	61:1A:4105:HOH:O	1.96	0.83
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.60	0.83
1:2A:1354:A:H5"	3:2D:38:LYS:HD3	1.61	0.82
1:2A:783:A:OP2	61:2A:3903:HOH:O	1.95	0.82
32:1a:451:A:H61	32:1a:481:G:H5'	1.45	0.82
44:1m:19:LEU:HD21	44:1m:56:LEU:HD21	1.61	0.82
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.62	0.82
32:1a:1366:C:O2'	41:1j:60:ARG:NH1	2.12	0.81
54:2w:169:GLY:HA2	54:2w:172:LYS:HE3	1.62	0.81
33:2b:76:GLN:HB3	33:2b:208:ILE:HG12	1.62	0.81
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.12	0.81
39:2h:11:THR:HG22	39:2h:14:ARG:HH12	1.44	0.81
1:2A:336:C:HO2'	20:2Y:35:TYR:HH	1.26	0.80
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.63	0.80
42:2k:48:ILE:HG12	42:2k:63:LEU:HB3	1.63	0.80
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.12	0.80
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.15	0.80
41:2j:6:ILE:HG12	41:2j:98:ILE:HG22	1.64	0.80
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.14	0.80
32:2a:1316:G:H5"	45:2n:17:LYS:HD2	1.63	0.80
7:2H:3:ARG:HD3	7:2H:6:ARG:HH21	1.47	0.80
1:2A:1352:U:OP2	61:2A:3905:HOH:O	2.00	0.80
40:2i:3:GLN:HG2	40:2i:20:ARG:HH21	1.47	0.79
1:1A:1072:C:O2	1:1A:1092:C:N4	2.15	0.79
32:2a:975:A:H4'	32:2a:976:G:H5"	1.65	0.79
32:1a:959:A:O2'	32:1a:984:C:O2'	1.99	0.79
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.65	0.79
34:2c:70:VAL:HG12	34:2c:72:LYS:H	1.47	0.79
32:2a:664:G:H22	32:2a:741:G:H1	1.31	0.79
1:1A:741:G:OP2	61:1A:4109:HOH:O	2.01	0.79
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.15	0.79
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.56	0.79
32:1a:1286:A:H8	32:1a:1287:A:H4'	1.48	0.79
33:2b:230:VAL:HG22	33:2b:232:PRO:HD2	1.64	0.78
1:1A:1670:C:OP2	61:1A:4107:HOH:O	2.01	0.78
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.64	0.78
32:1a:664:G:H22	32:1a:741:G:H1	1.30	0.78
1:1A:11:G:H2'	1:1A:12:U:H5"	1.63	0.78
1:2A:775:G:O3'	61:2A:3906:HOH:O	2.02	0.78
1:1A:1332:G:OP1	61:1A:4106:HOH:O	2.01	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1865:G:OP1	61:1A:4108:HOH:O	2.01	0.78
61:1E:402:HOH:O	13:1R:3:HIS:NE2	2.16	0.78
1:1A:948:G:OP1	61:1A:4104:HOH:O	2.00	0.78
1:2A:1204:A:H2	1:2A:1241:A:H62	1.29	0.78
15:1T:41:ARG:NH2	32:1a:346:G:OP1	2.16	0.77
39:1h:11:THR:HG22	39:1h:14:ARG:HH12	1.48	0.77
40:1i:128:ARG:NH2	55:1x:33:U:OP2	2.18	0.77
2:2B:66:A:H61	2:2B:109:C:H5'	1.48	0.77
32:1a:21:G:OP1	61:1a:1902:HOH:O	2.01	0.77
1:2A:1970:A:OP1	61:2A:3908:HOH:O	2.03	0.77
1:1A:1041:C:H42	1:1A:1114:G:H1	1.30	0.77
34:2c:47:LEU:HB2	34:2c:52:LEU:HD12	1.66	0.77
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.65	0.77
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.31	0.77
1:1A:1647:G:OP1	61:1A:4111:HOH:O	2.03	0.77
11:2P:52:GLU:OE1	11:2P:55:ARG:NH1	2.18	0.77
34:2c:79:ARG:H	34:2c:82:GLU:HB3	1.49	0.77
1:1A:2447:G:OP2	61:1A:4110:HOH:O	2.02	0.76
40:1i:53:VAL:O	40:1i:55:ALA:N	2.18	0.76
32:1a:79:G:H22	32:1a:90:U:H1'	1.51	0.76
32:1a:330:C:O2	61:1a:1903:HOH:O	2.04	0.76
32:2a:953:G:H5'	32:2a:965:A:H61	1.50	0.76
1:2A:1021:A:H62	1:2A:1141:U:H3	1.32	0.76
1:2A:792:G:O6	61:2A:3907:HOH:O	2.02	0.76
1:2A:832:G:OP1	61:2A:3909:HOH:O	2.03	0.76
41:2j:7:LYS:HB3	41:2j:71:LEU:HD12	1.68	0.76
1:1A:826:U:OP1	61:1A:4103:HOH:O	2.03	0.76
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.50	0.76
1:2A:2130:U:H4'	1:2A:2133:G:H4'	1.68	0.76
1:1A:1352:U:OP2	61:1A:4113:HOH:O	2.05	0.75
54:1w:119:GLU:HG3	54:1w:184:PRO:HB3	1.68	0.75
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.50	0.75
32:2a:677:U:H3	32:2a:713:G:H22	1.35	0.75
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.18	0.75
48:1q:45:HIS:HB3	48:1q:72:ARG:HG2	1.68	0.75
44:2m:31:LYS:O	44:2m:35:GLU:N	2.15	0.75
28:16:13:CYS:SG	28:16:47:THR:HG21	2.27	0.75
34:1c:43:LEU:HD23	34:1c:47:LEU:HD21	1.69	0.75
32:1a:1029:C:H42	32:1a:1032:G:H1	1.31	0.75
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.20	0.75
1:1A:2794:C:H42	1:1A:2802:G:H1	1.35	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:456:C:O2'	19:2X:68:ARG:NH1	2.20	0.74
54:1w:258:GLN:HE21	54:1w:262:ARG:HH12	1.32	0.74
36:2e:89:ILE:HG12	36:2e:135:THR:HG22	1.68	0.74
1:1A:1023:U:OP2	61:1A:4112:HOH:O	2.05	0.74
34:1c:134:ILE:HG23	34:1c:151:VAL:HG13	1.67	0.74
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.36	0.74
32:1a:964:A:OP1	61:1a:1904:HOH:O	2.05	0.74
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.69	0.74
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.70	0.74
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.20	0.74
1:2A:2448:A:OP1	61:2A:3910:HOH:O	2.04	0.74
1:1A:1271:G:OP2	61:1A:4111:HOH:O	2.05	0.74
1:1A:1311:G:H2'	29:17:47:ARG:HH22	1.53	0.74
44:1m:105:THR:OG1	44:1m:106:ASN:N	2.21	0.74
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.21	0.74
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.20	0.73
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.20	0.73
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.22	0.73
4:1E:110:GLY:O	61:1E:402:HOH:O	2.05	0.73
3:1D:39:LYS:NZ	3:1D:57:GLY:O	2.20	0.73
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.70	0.73
32:1a:56:U:H2'	32:1a:57:G:C8	2.23	0.73
1:2A:1648:C:OP1	61:2A:3911:HOH:O	2.05	0.73
32:2a:9:G:OP2	36:2e:121:LYS:NZ	2.21	0.73
6:1G:109:VAL:HG11	26:14:14:ILE:HD13	1.71	0.73
32:2a:1256:A:N6	32:2a:1278:U:O2'	2.21	0.73
32:2a:266:G:H5"	32:2a:268:C:H41	1.52	0.73
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.69	0.73
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.19	0.73
32:1a:56:U:H2'	32:1a:57:G:H8	1.53	0.73
32:2a:533:A:OP1	61:2a:1801:HOH:O	2.07	0.73
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.21	0.73
1:2A:1812:A:OP2	61:2A:3912:HOH:O	2.05	0.73
44:2m:80:ARG:HH12	50:2s:69:HIS:HE1	1.36	0.73
32:2a:717:C:H4'	42:2k:117:ASN:HD22	1.54	0.73
1:1A:271(R):G:O6	61:1A:4115:HOH:O	2.07	0.72
1:1A:1071:G:H21	1:1A:1089:G:H22	1.35	0.72
38:1g:78:ARG:HG2	38:1g:79:ARG:H	1.53	0.72
50:2s:30:LEU:HD21	50:2s:32:LYS:HG3	1.71	0.72
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.69	0.72
38:1g:51:GLN:HA	38:1g:55:GLY:HA2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:50:ILE:HA	41:1j:60:ARG:HG2	1.71	0.72
1:1A:782:A:N1	61:1A:4156:HOH:O	2.23	0.72
54:1w:258:GLN:HE21	54:1w:262:ARG:NH1	1.88	0.72
26:24:16:CYS:SG	26:24:17:GLY:N	2.61	0.72
38:2g:126:ASP:HB3	38:2g:131:LYS:HB2	1.71	0.72
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.23	0.72
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.71	0.72
1:1A:2550:G:OP1	61:1A:4107:HOH:O	2.07	0.72
55:1x:12:A:OP2	61:1x:201:HOH:O	2.07	0.72
1:1A:1315:C:OP2	61:1A:4106:HOH:O	2.08	0.72
1:1A:2428:G:OP1	61:1A:4103:HOH:O	2.08	0.72
47:1p:45:THR:HG23	47:1p:47:ASP:H	1.53	0.72
1:2A:2504:U:OP2	61:2A:3913:HOH:O	2.07	0.72
7:2H:3:ARG:HH21	7:2H:65:HIS:HB3	1.55	0.71
22:10:10:THR:HG22	22:10:12:ASN:H	1.55	0.71
37:1f:35:ALA:HB1	37:1f:65:VAL:HG11	1.72	0.71
15:2T:107:ASP:OD2	15:2T:111:ARG:NH1	2.24	0.71
32:1a:677:U:H3	32:1a:713:G:H22	1.38	0.71
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.71	0.71
22:10:11:ARG:O	22:10:14:ARG:NH2	2.23	0.71
41:1j:26:ALA:HB1	41:1j:84:GLN:HE22	1.56	0.71
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.71	0.71
1:2A:2049:G:N7	61:2A:3967:HOH:O	2.24	0.71
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.24	0.71
1:2A:948:G:OP1	61:2A:3916:HOH:O	2.09	0.71
32:2a:1083:U:OP2	61:2a:1802:HOH:O	2.08	0.71
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.23	0.71
1:1A:998:C:OP1	61:1A:4114:HOH:O	2.07	0.71
1:1A:2181:G:H2'	1:1A:2182:G:C8	2.26	0.71
1:2A:1226:A:OP1	17:2V:84:LYS:NZ	2.23	0.71
55:1x:13:A:N7	61:1x:203:HOH:O	2.24	0.71
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.23	0.71
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.25	0.70
32:1a:407:G:H5"	35:1d:115:ARG:HB3	1.73	0.70
1:1A:1056:G:H4'	1:1A:1086:A:H1'	1.73	0.70
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.71	0.70
32:1a:1125:U:H4'	41:1j:5:ARG:HH12	1.56	0.70
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.24	0.70
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	1.71	0.70
32:2a:363:A:OP2	43:2l:34:ARG:NH1	2.24	0.70
1:1A:2116:G:H2'	1:1A:2117:A:C5	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2822:G:OP2	61:1E:402:HOH:O	2.08	0.70
32:1a:1029:C:N4	32:1a:1032:G:H1	1.90	0.70
1:2A:304:G:O6	61:2A:3914:HOH:O	2.08	0.70
8:2I:62:LYS:HE2	8:2I:133:HIS:HE1	1.56	0.70
32:2a:542:G:OP1	35:2d:10:ARG:NH2	2.24	0.70
1:1A:1014:U:OP2	61:1A:4116:HOH:O	2.10	0.70
1:2A:1124:C:OP1	61:2A:3915:HOH:O	2.09	0.70
25:23:59:VAL:HG22	25:23:60:GLU:H	1.57	0.70
22:20:11:ARG:O	22:20:14:ARG:NH2	2.23	0.70
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.73	0.70
34:1c:59:ARG:HG2	34:1c:64:VAL:HG12	1.72	0.70
45:1n:8:GLU:HG2	45:1n:11:LYS:HZ1	1.56	0.70
54:1w:114:GLY:HA3	54:1w:196:THR:HG22	1.71	0.70
18:2W:25:ARG:NH2	18:2W:74:ALA:O	2.24	0.70
32:2a:986:A:N3	50:2s:52:TYR:OH	2.20	0.70
15:1T:39:ARG:NH2	32:1a:345:C:OP2	2.24	0.70
1:2A:2478:A:OP2	31:29:2:LYS:NZ	2.21	0.70
1:1A:146:G:OP2	61:1A:4117:HOH:O	2.10	0.70
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.71	0.70
6:2G:109:VAL:HG23	26:24:33:VAL:HG21	1.73	0.70
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.19	0.70
1:2A:370:G:N7	61:2A:3970:HOH:O	2.24	0.70
34:2c:73:PRO:HD3	34:2c:105:GLU:HG3	1.74	0.69
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.25	0.69
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.25	0.69
26:14:57:GLU:OE1	26:14:58:ARG:NH1	2.26	0.69
32:1a:1005:A:OP2	32:1a:1006:C:N4	2.22	0.69
1:2A:2104:G:H1	1:2A:2185:C:N4	1.88	0.69
32:1a:1402:4OC:OP2	61:1a:1901:HOH:O	2.08	0.69
39:2h:37:ARG:HH21	39:2h:38:ILE:HD11	1.58	0.69
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.74	0.69
28:26:12:GLU:OE1	28:26:19:ARG:NH1	2.25	0.69
32:2a:1272:G:N2	32:2a:1273:G:C5	2.60	0.69
32:1a:1220:G:N2	50:1s:54:GLY:O	2.25	0.69
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.40	0.69
54:2w:114:GLY:HA3	54:2w:196:THR:HG22	1.75	0.69
1:1A:1970:A:OP1	61:1A:4120:HOH:O	2.11	0.69
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.25	0.69
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.74	0.69
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.26	0.69
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:81:G:N7	61:2A:3979:HOH:O	2.26	0.69
1:2A:336:C:O2'	20:2Y:35:TYR:OH	2.08	0.69
15:1T:84:GLN:HG2	15:1T:85:LYS:HG2	1.75	0.69
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.26	0.69
38:2g:113:GLU:HB2	38:2g:119:ARG:HG2	1.74	0.69
32:1a:1217:C:H5"	45:1n:9:LYS:HD2	1.75	0.68
1:2A:805:G:OP1	61:2A:3919:HOH:O	2.11	0.68
10:2O:49:ARG:NH2	32:2a:1423:G:OP1	2.24	0.68
1:1A:1447:G:N7	61:1A:4172:HOH:O	2.26	0.68
32:1a:116:A:OP1	61:1a:1905:HOH:O	2.12	0.68
32:1a:490:G:OP2	35:1d:132:ARG:NH2	2.26	0.68
32:2a:35:G:O2'	43:2l:118:SER:O	2.11	0.68
32:1a:972:C:O2'	41:1j:55:LYS:O	2.11	0.68
1:2A:965:C:OP2	61:2A:3917:HOH:O	2.10	0.68
1:2A:2499:C:OP1	61:2A:3910:HOH:O	2.12	0.68
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.26	0.68
18:1W:12:ILE:HD13	18:1W:17:VAL:HG13	1.75	0.68
32:1a:142:G:H2'	32:1a:143:A:C8	2.29	0.68
32:1a:1456:G:N2	51:1t:51:GLU:OE2	2.25	0.68
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.59	0.68
33:2b:55:PHE:HD1	33:2b:58:ILE:HD11	1.59	0.68
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.29	0.68
1:1A:745:G:O6	61:1A:4121:HOH:O	2.11	0.68
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.29	0.68
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.27	0.68
1:2A:1299:G:N7	61:2A:3981:HOH:O	2.26	0.68
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.27	0.68
32:1a:142:G:H2'	32:1a:143:A:H8	1.58	0.68
32:1a:376:G:H5"	47:1p:5:ARG:HB2	1.76	0.68
1:2A:2171:A:N3	1:2A:2172:U:N3	2.39	0.68
1:1A:1024:G:OP2	61:1A:4112:HOH:O	2.12	0.68
19:1X:1:MET:HE1	24:12:22:GLU:HA	1.76	0.68
1:2A:1833:U:OP1	61:2A:3918:HOH:O	2.11	0.68
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.75	0.68
1:2A:330:A:H2	1:2A:1210:A:HO2'	1.40	0.68
1:2A:1568:G:N7	61:2A:3985:HOH:O	2.27	0.68
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.74	0.67
33:2b:178:ARG:HH22	39:2h:68:ARG:HH22	1.43	0.67
55:2x:50:C:OP2	61:2x:201:HOH:O	2.11	0.67
32:1a:1366:C:HO2'	41:1j:60:ARG:HH12	1.39	0.67
44:1m:81:LEU:HD22	44:1m:88:ARG:HB2	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:762:U:OP1	61:1A:4118:HOH:O	2.10	0.67
1:1A:2130:U:H2'	1:1A:2158:A:H61	1.59	0.67
32:1a:1298:C:OP2	38:1g:114:ARG:NH2	2.27	0.67
1:2A:2624:G:N7	61:2A:3989:HOH:O	2.28	0.67
4:2E:110:GLY:O	61:2R:301:HOH:O	2.11	0.67
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.58	0.67
37:2f:1:MET:HE2	37:2f:68:PRO:HD3	1.77	0.67
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.77	0.67
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.77	0.67
32:2a:972:C:OP1	61:2a:1804:HOH:O	2.13	0.67
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.12	0.67
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	1.76	0.67
1:1A:833:U:O2	11:1P:55:ARG:NH2	2.27	0.67
35:1d:101:LEU:HD13	35:1d:138:TYR:HB3	1.75	0.67
32:2a:1130:A:H4'	40:2i:3:GLN:HE22	1.59	0.67
54:2w:348:LEU:HA	54:2w:352:ALA:HB3	1.77	0.67
1:1A:1071:G:H22	1:1A:1100:C:H42	1.43	0.67
32:1a:128:G:O2'	48:1q:3:LYS:NZ	2.28	0.67
32:1a:1381:U:H1'	38:1g:79:ARG:HB3	1.75	0.67
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.28	0.67
32:2a:1060:C:H5"	41:2j:51:ARG:HG2	1.77	0.67
1:1A:947:G:OP2	61:1A:4123:HOH:O	2.12	0.67
1:1A:1648:C:OP1	61:1A:4111:HOH:O	2.12	0.67
1:2A:875:G:H5"	21:2Z:149:SER:HB3	1.77	0.67
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.22	0.67
1:2A:1959:G:N7	61:2A:3984:HOH:O	2.27	0.67
1:2A:2711:A:OP2	61:2A:3920:HOH:O	2.12	0.67
54:2w:240:ARG:HB2	54:2w:251:THR:HG22	1.77	0.67
1:1A:1009:A:OP2	61:1A:4122:HOH:O	2.12	0.67
33:1b:178:ARG:HH12	39:1h:68:ARG:HH22	1.43	0.67
1:2A:1324:G:N7	61:2A:3993:HOH:O	2.28	0.67
7:2H:97:ARG:NH2	7:2H:104:GLU:OE1	2.25	0.67
32:1a:455:C:H42	32:1a:476:G:H1	1.42	0.66
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.77	0.66
39:2h:41:ARG:NH2	39:2h:123:GLU:OE2	2.28	0.66
1:2A:962:G:OP1	61:2A:3916:HOH:O	2.13	0.66
32:2a:972:C:O2'	41:2j:55:LYS:O	2.13	0.66
41:2j:64:GLU:OE2	41:2j:66:ARG:NH1	2.28	0.66
1:2A:2141:G:H1	1:2A:2150:U:H3	1.42	0.66
32:2a:113:G:H1'	32:2a:354:G:H5'	1.77	0.66
43:2l:40:VAL:HG21	43:2l:78:GLN:HA	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1669:A:OP2	61:1A:4107:HOH:O	2.13	0.66
32:1a:352:C:O2'	32:1a:354:G:OP1	2.14	0.66
3:1D:206:LEU:O	3:1D:211:ARG:HD3	1.96	0.66
32:1a:1402:4OC:OP1	61:1a:1907:HOH:O	2.14	0.66
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.76	0.66
1:1A:2145:C:O2'	1:1A:2147:G:O6	2.13	0.66
1:2A:1250:G:N7	11:2P:18:ARG:NH2	2.43	0.66
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.78	0.66
38:2g:69:VAL:HG21	38:2g:104:LEU:HD21	1.78	0.66
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.78	0.66
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.29	0.66
1:1A:1673:U:OP1	61:1A:4127:HOH:O	2.13	0.66
54:1w:110:GLU:HB2	54:1w:200:ALA:HB3	1.75	0.66
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.76	0.66
44:2m:76:ALA:HA	44:2m:79:LYS:HB3	1.78	0.66
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.28	0.66
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.27	0.66
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.77	0.66
36:2e:51:VAL:HG23	36:2e:52:PRO:HD3	1.77	0.66
1:1A:642:G:OP2	61:1A:4128:HOH:O	2.14	0.65
32:1a:160:A:H1'	32:1a:344:A:C5	2.31	0.65
47:1p:71:ARG:HA	47:1p:74:LEU:HD12	1.78	0.65
21:2Z:92:SER:OG	21:2Z:94:GLU:OE1	2.14	0.65
32:2a:1272:G:N2	32:2a:1273:G:N7	2.44	0.65
1:1A:2774:C:OP2	61:1A:4125:HOH:O	2.13	0.65
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.31	0.65
1:2A:204:A:N3	61:2A:3998:HOH:O	2.29	0.65
1:2A:1253:A:OP1	61:2A:3922:HOH:O	2.14	0.65
1:1A:1971:A:OP1	61:1A:4120:HOH:O	2.13	0.65
1:1A:2469:A:O2'	12:1Q:56:ARG:NE	2.29	0.65
32:1a:382:A:H2'	32:1a:383:A:H8	1.62	0.65
32:1a:382:A:H2'	32:1a:383:A:C8	2.31	0.65
35:1d:122:ARG:NH1	35:1d:134:ASP:O	2.28	0.65
39:1h:83:ILE:HG13	39:1h:137:VAL:HG22	1.78	0.65
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.78	0.65
2:1B:45:A:OP2	6:1G:96:ARG:NH2	2.30	0.65
3:2D:237:GLU:OE2	61:2D:401:HOH:O	2.13	0.65
42:2k:48:ILE:O	42:2k:50:TYR:N	2.29	0.65
4:1E:29:GLY:HA3	61:1E:407:HOH:O	1.95	0.65
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.28	0.65
33:1b:40:HIS:HB3	33:1b:190:THR:HG21	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:20:GLU:OE1	33:2b:23:ARG:NH1	2.29	0.65
54:2w:216:GLU:HB2	54:2w:245:PRO:HD3	1.79	0.65
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.32	0.65
33:1b:15:VAL:HG13	33:1b:209:ARG:HG2	1.78	0.65
5:2F:124:LEU:HB3	5:2F:193:VAL:HG22	1.78	0.65
17:2V:1:MET:HE3	17:2V:43:GLU:H	1.62	0.65
32:2a:1178:G:N2	32:2a:1181:G:OP2	2.30	0.65
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.31	0.65
1:1A:2255:G:OP2	61:1A:4126:HOH:O	2.13	0.65
1:1A:2350:C:OP2	61:1A:4129:HOH:O	2.14	0.65
1:2A:2548:G:O6	61:2A:3921:HOH:O	2.12	0.65
5:1F:123:LEU:HD13	5:1F:192:LEU:HD13	1.76	0.65
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.79	0.65
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.25	0.65
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.57	0.65
1:1A:135:G:N7	61:1A:4195:HOH:O	2.30	0.65
1:1A:2467:C:OP2	61:1A:4130:HOH:O	2.15	0.65
32:1a:100:C:H2'	32:1a:101:A:C8	2.31	0.65
32:1a:1086:U:H3	32:1a:1099:G:H22	1.43	0.65
32:1a:1130:A:OP1	40:1i:16:ARG:NH2	2.23	0.65
1:2A:53:A:OP2	61:2A:3925:HOH:O	2.15	0.65
26:24:62:ARG:HA	26:24:62:ARG:CZ	2.27	0.65
33:2b:73:THR:OG1	33:2b:170:GLU:OE2	2.09	0.65
1:1A:1017:G:N7	61:1A:4187:HOH:O	2.29	0.64
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE2	2.14	0.64
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.30	0.64
33:2b:60:ASP:O	33:2b:64:ARG:N	2.29	0.64
35:2d:111:ALA:HB2	35:2d:120:LEU:HD22	1.77	0.64
1:1A:1071:G:H21	1:1A:1089:G:N2	1.95	0.64
1:1A:1342:A:OP2	61:1A:4131:HOH:O	2.15	0.64
1:1A:2431:U:O4	61:1A:4119:HOH:O	2.10	0.64
32:1a:1209:C:O2'	32:1a:1214:C:N4	2.23	0.64
33:1b:127:ILE:HG22	33:1b:130:ARG:H	1.62	0.64
40:1i:128:ARG:NH1	55:1x:35:C:OP1	2.29	0.64
47:1p:72:ARG:HH21	47:1p:73:LEU:HD21	1.63	0.64
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.15	0.64
48:2q:81:ARG:HH21	48:2q:84:LEU:HD21	1.62	0.64
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.62	0.64
32:1a:1329:A:H5"	44:1m:26:GLY:H	1.63	0.64
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.77	0.64
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:30:SER:HB3	41:1j:81:THR:HG23	1.79	0.64
49:1r:26:LEU:HD21	49:1r:39:VAL:HG13	1.79	0.64
21:2Z:11:GLU:O	21:2Z:36:LYS:NZ	2.28	0.64
33:2b:54:THR:HG22	33:2b:199:TYR:HB3	1.78	0.64
1:1A:607:U:OP1	5:1F:102:PRO:HA	1.98	0.64
32:1a:1352:C:OP1	52:1u:3:LYS:NZ	2.27	0.64
1:1A:9:U:H3	1:1A:2629:A:H2	1.43	0.64
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.62	0.64
32:2a:134:A:H61	47:2p:25:ARG:HH12	1.46	0.64
43:2l:86:ARG:NH1	61:2l:301:HOH:O	2.29	0.64
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.79	0.64
1:1A:748:G:O6	18:1W:90:ARG:NH1	2.31	0.64
32:1a:812:C:N3	61:1a:1931:HOH:O	2.29	0.64
21:2Z:145:GLU:HG3	21:2Z:146:ILE:H	1.62	0.64
26:24:43:TYR:O	26:24:45:GLY:N	2.31	0.64
34:2c:153:VAL:HG22	34:2c:198:VAL:HG12	1.78	0.64
53:1v:20:A:N6	54:1w:186:THR:OG1	2.30	0.64
1:2A:446:G:OP1	16:2U:3:ARG:NH1	2.29	0.64
1:2A:2029:G:OP1	61:2A:3924:HOH:O	2.15	0.64
8:2I:38:LEU:H	8:2I:38:LEU:HD12	1.62	0.64
32:2a:1129:C:OP1	40:2i:16:ARG:NH1	2.31	0.64
41:2j:32:ALA:HB3	41:2j:74:ILE:HD11	1.80	0.64
1:1A:2448:A:OP1	61:1A:4102:HOH:O	2.15	0.64
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.31	0.64
1:2A:1973:G:OP1	61:2A:3923:HOH:O	2.15	0.64
2:2B:103:G:O6	61:2B:301:HOH:O	2.15	0.64
32:2a:316:G:OP2	32:2a:351:G:O2'	2.15	0.64
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.62	0.64
32:1a:757:U:H2'	32:1a:758:G:O4'	1.97	0.64
38:1g:14:PRO:HG3	38:1g:21:VAL:HG13	1.78	0.64
32:2a:17:U:H2'	32:2a:18:C:C6	2.33	0.64
34:1c:152:ILE:HG23	34:1c:167:TRP:HB3	1.78	0.63
1:2A:2198:A:OP1	8:2I:33:ARG:NH2	2.31	0.63
6:2G:35:GLU:HB3	6:2G:36:LYS:HE3	1.80	0.63
1:1A:1093:G:H3'	1:1A:1094:U:H5"	1.79	0.63
32:2a:297:G:N2	32:2a:300:A:OP2	2.29	0.63
41:2j:30:SER:HB2	41:2j:81:THR:HB	1.80	0.63
3:1D:237:GLU:OE2	61:1D:401:HOH:O	2.15	0.63
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.80	0.63
35:1d:28:SER:OG	35:1d:30:LYS:HG2	1.98	0.63
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.64	0.63
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.31	0.63
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.80	0.63
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.14	0.63
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.25	0.63
50:1s:36:ARG:HB3	50:1s:72:GLY:HA3	1.79	0.63
1:2A:452:G:N7	61:2A:4006:HOH:O	2.31	0.63
1:2A:2334:G:H5'	14:2S:9:ARG:HG2	1.81	0.63
33:2b:158:LEU:HD21	33:2b:180:LEU:HD13	1.80	0.63
1:1A:1314:C:OP1	61:1A:4106:HOH:O	2.15	0.63
1:1A:2134:A:H4'	1:1A:2159:G:H21	1.63	0.63
32:1a:1312:G:H5'	50:1s:5:LEU:HD23	1.80	0.63
50:1s:20:LEU:HD11	50:1s:43:GLU:HG2	1.80	0.63
54:1w:129:ASN:O	54:1w:133:ARG:HG3	1.99	0.63
1:2A:2724:C:N4	61:2A:3974:HOH:O	2.30	0.63
32:2a:1149:C:OP2	40:2i:9:ARG:NH1	2.31	0.63
32:1a:601:C:H2'	32:1a:602:A:H8	1.64	0.63
1:2A:1434:A:H61	1:2A:1558:A:H62	1.45	0.63
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.34	0.62
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	1.81	0.62
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.80	0.62
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.80	0.62
1:1A:1045:A:H1'	1:1A:1047:G:C4	2.34	0.62
20:1Y:11:ASP:OD2	20:1Y:97:ARG:NH2	2.29	0.62
26:14:34:GLU:HG2	26:14:35:VAL:HG23	1.81	0.62
32:2a:964:A:O2'	41:2j:55:LYS:NZ	2.25	0.62
36:2e:152:ARG:HB3	39:2h:43:GLY:HA3	1.81	0.62
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.31	0.62
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.15	0.62
32:2a:1132:C:H2'	32:2a:1133:G:H8	1.64	0.62
36:2e:20:GLN:NE2	36:2e:21:ALA:O	2.32	0.62
1:1A:2658:C:OP1	7:1H:160:LYS:NZ	2.32	0.62
32:1a:942:G:H21	40:1i:124:GLN:NE2	1.97	0.62
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.35	0.62
1:1A:2134:A:H2'	1:1A:2135:A:H8	1.64	0.62
5:1F:165:ARG:HA	5:1F:168:ARG:HD2	1.80	0.62
33:2b:118:LEU:HD22	33:2b:142:LEU:HB2	1.81	0.62
35:2d:153:ARG:HH11	35:2d:181:MET:HE3	1.64	0.62
47:2p:74:LEU:HD23	47:2p:79:VAL:HG11	1.81	0.62
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.82	0.62
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:48:ILE:O	42:1k:50:TYR:N	2.29	0.62
32:1a:430:A:H4'	35:1d:7:PRO:HG3	1.81	0.62
32:2a:222:U:H2'	32:2a:223:U:C6	2.34	0.62
32:2a:1521:G:N3	61:2a:1814:HOH:O	2.31	0.62
33:2b:16:HIS:CD2	33:2b:18:GLY:H	2.17	0.62
26:14:61:ARG:HG2	26:14:62:ARG:N	2.14	0.62
44:1m:50:GLU:HA	44:1m:53:VAL:HB	1.80	0.62
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.27	0.62
32:1a:656:C:O2'	46:1o:28:GLN:OE1	2.16	0.62
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.81	0.62
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.82	0.62
32:2a:1263:C:N3	32:2a:1272:G:O6	2.33	0.62
32:2a:1278:U:H5'	32:2a:1279:A:H5'	1.80	0.62
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.00	0.62
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.64	0.62
1:2A:1721:G:H8	1:2A:1741:A:H62	1.46	0.62
38:2g:50:ILE:HG13	38:2g:125:MET:HG3	1.81	0.62
14:1S:61:ASN:HD22	14:1S:64:GLU:H	1.48	0.61
37:1f:38:GLU:HB2	37:1f:64:GLN:HG2	1.80	0.61
1:2A:2822:G:OP2	61:2A:3929:HOH:O	2.16	0.61
41:2j:8:LEU:HG	41:2j:70:ARG:HB2	1.82	0.61
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.00	0.61
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.33	0.61
1:1A:2109:U:O4	1:1A:2179:C:N4	2.34	0.61
32:1a:504:C:OP1	61:1a:1912:HOH:O	2.16	0.61
7:2H:3:ARG:NH1	7:2H:4:ILE:H	1.98	0.61
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.82	0.61
1:1A:500:G:N7	61:1A:4198:HOH:O	2.31	0.61
1:1A:1971:A:OP2	3:1D:242:ARG:NH2	2.33	0.61
1:1A:2306:C:O2	61:1A:4124:HOH:O	2.12	0.61
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.33	0.61
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.81	0.61
2:2B:106:G:H5'	21:2Z:31:ARG:HG2	1.82	0.61
42:2k:61:ALA:HB1	42:2k:94:ALA:HB2	1.83	0.61
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.36	0.61
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.81	0.61
44:2m:105:THR:O	44:2m:105:THR:OG1	2.16	0.61
36:1e:78:HIS:CE1	36:1e:142:LEU:HD23	2.35	0.61
33:2b:93:VAL:HG21	33:2b:97:TRP:HD1	1.66	0.61
1:2A:2100:G:H1	1:2A:2189:U:H3	1.48	0.61
23:21:77:ALA:HA	23:21:80:LEU:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:102:ARG:HH21	44:2m:105:THR:HG23	1.65	0.61
54:2w:254:ASP:OD2	54:2w:264:LYS:NZ	2.28	0.61
1:1A:1068:G:C8	1:1A:1096:A:H1'	2.35	0.61
1:1A:1071:G:H22	1:1A:1100:C:N4	1.98	0.61
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.82	0.61
1:2A:1309:G:H4'	29:27:7:PRO:HB2	1.82	0.61
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	1.82	0.61
54:2w:110:GLU:HG2	54:2w:159:VAL:HG13	1.83	0.61
32:1a:961:U:OP2	32:1a:1223:C:O2'	2.12	0.61
32:2a:519:C:O5'	54:2w:301:LYS:NZ	2.30	0.61
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.66	0.61
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.35	0.61
32:1a:35:G:O2'	43:1l:118:SER:O	2.14	0.61
32:1a:1030:C:H42	32:1a:1031:G:H1	1.49	0.61
38:1g:69:VAL:HG21	38:1g:104:LEU:HD11	1.83	0.61
39:1h:9:MET:HG3	39:1h:26:VAL:HG21	1.82	0.61
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.83	0.61
41:2j:6:ILE:HB	41:2j:72:VAL:HG23	1.83	0.61
47:2p:18:ARG:HD3	47:2p:35:LYS:HD3	1.83	0.61
51:2t:43:LEU:HD13	51:2t:51:GLU:HB3	1.81	0.61
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.82	0.61
32:2a:673:G:H2'	32:2a:674:G:C8	2.36	0.61
1:1A:1071:G:H1'	1:1A:1089:G:C5	2.35	0.60
32:1a:196:A:OP1	51:1t:68:LYS:NZ	2.34	0.60
32:1a:560:U:O2'	32:1a:561:U:OP2	2.18	0.60
32:1a:1035:A:H2'	32:1a:1036:G:N2	2.05	0.60
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.34	0.60
32:2a:1060:C:C5	34:2c:2:GLY:HA3	2.35	0.60
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.34	0.60
1:1A:2375:G:O2'	1:1A:2377:A:N7	2.33	0.60
32:1a:1240:U:OP1	38:1g:119:ARG:NH2	2.32	0.60
14:2S:37:ALA:HB2	14:2S:101:LEU:HD11	1.82	0.60
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.36	0.60
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.36	0.60
33:2b:27:LYS:NZ	33:2b:193:ASP:OD1	2.31	0.60
12:1Q:10:ARG:HH11	12:1Q:11:LYS:HE2	1.66	0.60
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.84	0.60
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.33	0.60
3:2D:137:PRO:O	3:2D:140:THR:OG1	2.18	0.60
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.16	0.60
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.48	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:71:A:N7	19:1X:31:HIS:HE1	1.99	0.60
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.82	0.60
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.82	0.60
40:1i:20:ARG:O	40:1i:60:ASP:N	2.30	0.60
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.33	0.60
33:1b:74:LYS:HD2	33:1b:166:ASP:HB2	1.83	0.60
41:1j:55:LYS:O	41:1j:57:LYS:N	2.34	0.60
1:2A:1857:G:N7	61:2A:4008:HOH:O	2.31	0.60
7:2H:10:PRO:HA	7:2H:49:VAL:HG22	1.83	0.60
33:2b:15:VAL:HG13	33:2b:209:ARG:HG2	1.83	0.60
32:1a:1030(D):A:C8	32:1a:1031:G:H1'	2.36	0.60
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.36	0.60
1:2A:1993:U:OP2	61:2A:3930:HOH:O	2.16	0.60
34:2c:5:ILE:HD11	45:2n:49:HIS:HE1	1.66	0.60
1:1A:1309:G:H4'	29:17:7:PRO:HB2	1.84	0.60
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.84	0.60
32:1a:573:A:OP2	61:1a:1909:HOH:O	2.16	0.60
44:1m:65:LYS:HG2	44:1m:69:GLU:HG2	1.84	0.60
54:1w:177:VAL:HG22	54:1w:198:THR:HG22	1.83	0.60
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.84	0.60
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.36	0.60
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.83	0.60
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.84	0.60
32:2a:538:G:H5"	43:2l:114:LYS:HB2	1.82	0.60
1:1A:192:C:OP1	61:1A:4133:HOH:O	2.17	0.60
32:1a:830:G:O6	61:1a:1906:HOH:O	2.12	0.60
6:2G:11:TYR:OH	6:2G:16:ARG:NH1	2.34	0.60
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.37	0.60
2:1B:14:U:OP2	2:1B:70:C:O2'	2.20	0.60
1:2A:1311:G:H2'	29:27:47:ARG:HH22	1.66	0.60
1:1A:382:G:O6	61:1A:4132:HOH:O	2.16	0.60
1:2A:2518:A:OP2	61:2A:3928:HOH:O	2.16	0.60
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.84	0.60
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.82	0.60
38:2g:16:LEU:HD11	40:2i:45:ALA:HB2	1.84	0.60
32:1a:53:A:OP2	61:1a:1910:HOH:O	2.16	0.59
54:1w:299:SER:O	54:1w:301:LYS:N	2.35	0.59
1:2A:1342:A:OP2	61:2A:3933:HOH:O	2.17	0.59
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.36	0.59
7:2H:80:SER:OG	7:2H:81:GLU:N	2.32	0.59
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:93:ASP:HB2	21:1Z:131:ARG:HH22	1.66	0.59
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.36	0.59
38:1g:74:GLU:OE2	38:1g:95:ARG:NE	2.32	0.59
1:2A:668:G:H5'	1:2A:669:G:OP2	2.02	0.59
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.19	0.59
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.33	0.59
32:2a:744:C:O2'	32:2a:851:G:N2	2.35	0.59
1:1A:2632:A:O2'	1:1A:2811:G:O2'	2.18	0.59
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.17	0.59
21:2Z:10:ARG:NH2	21:2Z:26:GLY:O	2.35	0.59
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.15	0.59
51:2t:50:GLU:HB2	51:2t:99:LEU:HD13	1.83	0.59
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.85	0.59
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.25	0.59
38:1g:38:LEU:HA	38:1g:41:ARG:HD2	1.85	0.59
32:2a:558:G:O6	61:2a:1803:HOH:O	2.11	0.59
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.84	0.59
39:2h:106:GLY:O	39:2h:122:ARG:NH2	2.35	0.59
40:2i:114:TYR:HE1	41:2j:60:ARG:H	1.50	0.59
54:2w:127:LEU:HD13	54:2w:178:HIS:HD2	1.68	0.59
1:1A:530:G:N1	1:1A:2023:G:OP1	2.28	0.59
1:1A:1915:5MU:H1'	54:1w:286:ARG:HD2	1.84	0.59
47:1p:43:LYS:HA	47:1p:48:TRP:CD1	2.37	0.59
1:2A:307:G:H21	1:2A:330:A:H62	1.50	0.59
1:2A:2166:G:N7	1:2A:2168:G:N2	2.51	0.59
5:2F:70:THR:HG22	5:2F:72:ARG:H	1.67	0.59
8:1I:75:LEU:HD22	8:1I:105:HIS:HD2	1.68	0.59
32:1a:438:G:O2'	32:1a:494:U:O4	2.20	0.59
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.68	0.59
55:1x:44:C:N4	61:1x:205:HOH:O	2.34	0.59
1:2A:2306:C:N4	6:2G:42:GLY:O	2.35	0.59
32:1a:814:A:H2'	32:1a:816:A:H5"	1.85	0.59
1:1A:1072:C:H1'	1:1A:1092:C:H41	1.68	0.59
32:1a:953:G:H5'	32:1a:965:A:H61	1.67	0.59
37:2f:68:PRO:HG2	37:2f:71:ARG:HD2	1.85	0.59
1:1A:1082:U:N3	1:1A:1086:A:N6	2.12	0.59
1:1A:2079:U:O3'	23:11:35:THR:OG1	2.21	0.59
7:1H:40:GLU:OE2	7:1H:61:HIS:NE2	2.34	0.59
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.84	0.59
34:1c:138:VAL:HG23	34:1c:151:VAL:HG12	1.85	0.59
39:1h:17:THR:HG22	39:1h:63:LEU:HG	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1420:U:HO2'	1:2A:1421:G:P	2.26	0.59
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.37	0.59
8:2I:125:GLU:OE2	8:2I:143:SER:OG	2.18	0.59
19:2X:94:GLY:H	19:2X:95:LEU:HB2	1.66	0.59
32:2a:839:U:H3'	32:2a:840:C:H5'	1.85	0.59
8:1I:4:ILE:HD11	8:1I:44:LEU:HD23	1.85	0.59
61:1a:1901:HOH:O	53:1v:19:U:OP1	2.17	0.59
41:1j:9:ARG:NH2	41:1j:95:GLU:OE2	2.36	0.59
1:2A:1900:A:OP2	61:2A:3932:HOH:O	2.16	0.59
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.03	0.59
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.33	0.59
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.85	0.59
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.83	0.59
36:2e:136:MET:HA	36:2e:139:LEU:HD12	1.85	0.59
39:2h:19:VAL:HG23	39:2h:21:LYS:HG3	1.85	0.59
1:1A:400:G:N7	61:1A:4205:HOH:O	2.32	0.58
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.85	0.58
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.37	0.58
32:1a:598:U:H4'	39:1h:94:TYR:CD2	2.38	0.58
32:1a:1209:C:HO2'	32:1a:1214:C:H42	1.49	0.58
35:1d:19:LEU:HD21	35:1d:63:LYS:HG2	1.85	0.58
1:2A:1971:A:OP1	61:2A:3908:HOH:O	2.15	0.58
7:2H:51:ARG:NH1	7:2H:53:GLU:OE2	2.35	0.58
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.38	0.58
32:2a:1119:C:OP2	40:2i:9:ARG:NH2	2.37	0.58
38:2g:24:THR:O	38:2g:28:ASN:ND2	2.36	0.58
1:1A:1702:G:N7	61:1A:4204:HOH:O	2.32	0.58
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.38	0.58
32:1a:538:G:H5"	43:1l:114:LYS:HB2	1.84	0.58
3:2D:71:ASP:HB3	3:2D:103:ARG:HH12	1.68	0.58
44:2m:23:TYR:HD2	44:2m:67:GLU:HA	1.68	0.58
1:1A:588:U:H2'	1:1A:589:C:C6	2.38	0.58
32:1a:299:G:O6	61:1a:1908:HOH:O	2.14	0.58
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.83	0.58
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.83	0.58
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.84	0.58
15:2T:91:ARG:HB2	15:2T:121:ILE:HG13	1.85	0.58
15:2T:127:ALA:C	15:2T:129:ARG:H	2.10	0.58
32:2a:353:A:H5'	32:2a:353:A:H8	1.66	0.58
32:2a:1030(D):A:H3'	32:2a:1031:G:H8	1.67	0.58
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.20	0.58
1:1A:1859:A:N6	1:1A:1883:G:O2'	2.36	0.58
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.85	0.58
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.86	0.58
10:1O:2:ILE:HB	10:1O:33:ALA:HB3	1.85	0.58
32:1a:986:A:H1'	50:1s:55:LYS:HA	1.85	0.58
42:2k:63:LEU:HD23	42:2k:66:LEU:HD12	1.84	0.58
32:1a:559:A:H4'	32:1a:560:U:H5"	1.85	0.58
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.36	0.58
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.34	0.58
34:2c:150:LYS:HE3	34:2c:152:ILE:HD11	1.84	0.58
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.51	0.58
32:1a:324:G:N7	61:1a:1938:HOH:O	2.32	0.58
32:1a:1414:U:H3	32:1a:1486:G:H1	1.50	0.58
48:1q:6:LEU:HD23	48:1q:23:VAL:HG11	1.85	0.58
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.85	0.58
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.37	0.58
32:2a:1163:C:H2'	32:2a:1164:G:C8	2.38	0.58
32:2a:1221:G:O3'	50:2s:77:THR:OG1	2.16	0.58
54:2w:312:VAL:HG21	54:2w:327:VAL:HG21	1.86	0.58
11:1P:86:LYS:HB3	11:1P:118:GLY:HA3	1.84	0.58
32:1a:1264:C:H2'	32:1a:1265:G:H8	1.68	0.58
1:2A:1621:U:OP1	61:2A:3934:HOH:O	2.17	0.58
32:1a:17:U:H2'	32:1a:18:C:C6	2.38	0.58
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.04	0.58
50:1s:27:GLU:CB	50:1s:28:LYS:HA	2.31	0.58
1:2A:38:A:OP1	61:2A:3938:HOH:O	2.17	0.58
1:2A:632:A:OP1	61:2A:3937:HOH:O	2.17	0.58
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.68	0.58
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	1.85	0.58
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.86	0.58
1:1A:272:G:O2'	1:1A:421:U:OP2	2.15	0.58
1:1A:881:G:H2'	1:1A:882:G:O4'	2.04	0.58
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.37	0.58
32:1a:189(F):U:O2	48:1q:63:ARG:NH2	2.36	0.58
32:1a:454:C:OP1	47:1p:75:ARG:NH2	2.34	0.58
40:1i:9:ARG:HG2	40:1i:14:VAL:HG12	1.86	0.58
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.50	0.58
28:26:11:LEU:HB2	28:26:21:TYR:HB2	1.86	0.58
36:2e:8:GLU:HA	36:2e:34:VAL:HG12	1.86	0.58
44:2m:104:ARG:HG2	44:2m:105:THR:HG22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1089:G:N2	1:1A:1090:U:O4	2.31	0.57
1:1A:2105:C:H2'	1:1A:2106:G:H8	1.69	0.57
20:1Y:14:LEU:HB2	20:1Y:75:ILE:HD11	1.86	0.57
8:2I:57:ARG:O	8:2I:61:ARG:NH1	2.37	0.57
26:24:61:ARG:HH21	50:2s:42:PRO:HD3	1.69	0.57
32:2a:664:G:P	49:2r:64:ARG:HH21	2.27	0.57
34:2c:98:ASN:HD22	34:2c:98:ASN:N	2.01	0.57
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.69	0.57
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.37	0.57
23:11:14:VAL:HG11	23:11:39:LYS:HE2	1.86	0.57
32:1a:1323:G:H4'	32:1a:1363:C:N3	2.19	0.57
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.36	0.57
32:2a:501:C:H2'	32:2a:502:G:C8	2.38	0.57
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	1.85	0.57
23:11:52:ARG:NH1	23:11:55:GLY:O	2.37	0.57
37:1f:43:LEU:HD23	37:1f:46:ARG:CZ	2.34	0.57
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	1.84	0.57
1:1A:821:A:H2'	1:1A:946:G:H5"	1.86	0.57
32:1a:537:G:H5"	43:1l:113:ARG:NH1	2.19	0.57
21:2Z:45:ASP:OD1	21:2Z:49:ARG:NE	2.38	0.57
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.86	0.57
1:1A:1602:U:O4	61:1A:4131:HOH:O	2.16	0.57
6:1G:83:ARG:O	6:1G:86:MET:HG3	2.04	0.57
32:1a:269:C:H2'	32:1a:270:A:C8	2.40	0.57
32:1a:642:A:N3	39:1h:113:SER:OG	2.33	0.57
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.40	0.57
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.39	0.57
34:1c:132:ARG:NH1	34:1c:136:GLN:OE1	2.38	0.57
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.40	0.57
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.38	0.57
1:2A:1241:A:OP2	61:2A:3941:HOH:O	2.18	0.57
1:2A:2430:A:H2'	1:2A:2430:A:N3	2.18	0.57
26:24:62:ARG:HA	26:24:62:ARG:NH1	2.19	0.57
32:2a:1268:A:H2'	32:2a:1269:A:C8	2.40	0.57
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.85	0.57
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	1.85	0.57
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.68	0.57
47:1p:53:VAL:HG12	47:1p:79:VAL:HG22	1.85	0.57
5:2F:165:ARG:HG2	5:2F:168:ARG:HH21	1.70	0.57
6:2G:96:ARG:O	6:2G:100:TRP:HD1	1.87	0.57
32:2a:176:C:H2'	32:2a:177:C:H6	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:652:U:O4	32:2a:752:G:O2'	2.23	0.57
32:2a:1309:G:OP1	44:2m:88:ARG:NH1	2.37	0.57
39:2h:11:THR:HG22	39:2h:14:ARG:NH1	2.18	0.57
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.40	0.57
1:2A:1914:C:N3	54:2w:286:ARG:NH2	2.53	0.57
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.05	0.57
1:1A:1399:C:OP1	19:1X:25:LYS:NZ	2.38	0.57
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.04	0.57
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.38	0.57
35:1d:61:LYS:NZ	35:1d:72:GLU:OE1	2.30	0.57
32:2a:67:C:H2'	32:2a:68:G:C8	2.39	0.57
32:2a:1271:G:N2	32:2a:1272:G:N7	2.53	0.57
49:2r:35:ARG:O	49:2r:37:VAL:N	2.38	0.57
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.23	0.57
32:1a:1319:A:O2'	32:1a:1323:G:N7	2.31	0.57
32:2a:1209:C:O2'	32:2a:1214:C:N4	2.38	0.57
37:2f:3:ARG:HB3	37:2f:93:SER:HB2	1.86	0.57
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.40	0.57
12:1Q:136:ALA:HB1	21:1Z:52:SER:HB3	1.87	0.57
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.86	0.57
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.13	0.57
44:1m:19:LEU:HB3	44:1m:25:ILE:HG21	1.87	0.57
1:2A:752:A:H3'	29:27:1:MET:HE1	1.86	0.57
1:2A:1371:G:O6	61:2A:3942:HOH:O	2.18	0.57
1:2A:2134:A:H2	1:2A:2159:G:H1'	1.69	0.57
1:2A:2552:OMU:OP2	61:2A:3936:HOH:O	2.17	0.57
5:2F:25:PRO:HD2	5:2F:115:ALA:HB2	1.86	0.57
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.87	0.57
5:2F:192:LEU:HD21	5:2F:194:MET:HE2	1.87	0.57
26:24:48:ARG:HD2	26:24:52:THR:HG23	1.87	0.57
32:2a:448:A:P	32:2a:485:G:H22	2.28	0.57
32:2a:580:U:OP2	61:2a:1805:HOH:O	2.18	0.57
34:2c:19:GLU:O	34:2c:40:ARG:NH2	2.37	0.57
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.20	0.56
1:1A:2122:U:H2'	1:1A:2123:G:O4'	2.05	0.56
32:1a:79:G:H1'	32:1a:91:C:O2	2.04	0.56
32:1a:673:G:H2'	32:1a:674:G:C8	2.40	0.56
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.39	0.56
39:1h:121:ASP:HB2	39:1h:125:ARG:HH22	1.70	0.56
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.70	0.56
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:8:GLU:OE2	36:2e:63:ARG:NH1	2.38	0.56
1:1A:969:U:H2'	1:1A:970:C:C6	2.40	0.56
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.39	0.56
32:1a:473:G:H2'	32:1a:474:G:H8	1.70	0.56
32:1a:946:A:H2'	32:1a:947:G:C8	2.40	0.56
32:1a:1226:C:O2'	44:1m:111:LYS:NZ	2.38	0.56
54:1w:256:ARG:O	61:1w:501:HOH:O	2.17	0.56
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.22	0.56
1:2A:2114:A:N3	1:2A:2168:G:H1'	2.20	0.56
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.86	0.56
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.40	0.56
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.87	0.56
33:1b:15:VAL:HG11	33:1b:213:LEU:HD12	1.87	0.56
1:2A:570:G:O6	61:2A:3910:HOH:O	2.13	0.56
1:2A:1452:A:OP2	61:2A:3943:HOH:O	2.18	0.56
1:2A:2127:G:C6	1:2A:2161:C:C4	2.93	0.56
7:2H:18:GLU:HB3	7:2H:25:LYS:HB2	1.86	0.56
11:2P:59:LEU:HD21	30:28:10:ALA:HA	1.87	0.56
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.35	0.56
21:2Z:63:ASP:OD2	21:2Z:65:GLN:NE2	2.36	0.56
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.71	0.56
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.85	0.56
49:2r:26:LEU:HD21	49:2r:39:VAL:HG13	1.86	0.56
1:1A:271(H):G:H2'	1:1A:271(I):G:C8	2.41	0.56
1:1A:800:A:H8	1:1A:800:A:OP1	1.88	0.56
34:1c:52:LEU:HD11	34:1c:55:VAL:HG23	1.88	0.56
35:1d:121:VAL:HG11	35:1d:136:PRO:HA	1.87	0.56
39:1h:64:LYS:HD2	39:1h:79:VAL:HG21	1.88	0.56
39:1h:113:SER:HB2	39:1h:134:ILE:HD11	1.87	0.56
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.39	0.56
1:2A:2162:G:O2'	1:2A:2172:U:H5'	2.05	0.56
3:2D:206:LEU:O	3:2D:211:ARG:HD3	2.05	0.56
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.05	0.56
32:2a:90:U:H2'	32:2a:91:C:C6	2.40	0.56
32:2a:1132:C:H2'	32:2a:1133:G:C8	2.39	0.56
54:2w:219:ILE:HG12	54:2w:241:VAL:HG12	1.86	0.56
1:1A:993:G:H5"	16:1U:50:ARG:HH21	1.70	0.56
32:1a:158:G:H1	32:1a:163:C:H42	1.52	0.56
32:1a:1053:G:N7	32:1a:1200:C:H5"	2.21	0.56
33:1b:59:GLU:HB2	33:1b:221:LEU:HD11	1.87	0.56
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:321:THR:OG1	54:1w:322:HIS:N	2.38	0.56
1:2A:248:G:OP1	61:2A:3940:HOH:O	2.17	0.56
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.41	0.56
1:2A:1603:A:OP1	61:2A:3939:HOH:O	2.17	0.56
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.88	0.56
32:2a:1286:A:H62	32:2a:1354:C:H5"	1.70	0.56
42:2k:84:VAL:HG21	42:2k:95:ILE:HD11	1.88	0.56
32:1a:381:C:H2'	32:1a:382:A:O4'	2.06	0.56
42:1k:33:THR:HA	42:1k:39:PRO:HA	1.87	0.56
1:2A:212:G:H2'	1:2A:213:A:O4'	2.06	0.56
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.41	0.56
21:2Z:30:ASN:HB3	21:2Z:90:VAL:HB	1.87	0.56
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.88	0.56
54:2w:110:GLU:OE1	54:2w:112:ARG:NH1	2.37	0.56
32:1a:117:G:N7	61:1a:1941:HOH:O	2.33	0.56
1:2A:2887:U:H2'	1:2A:2888:C:H6	1.71	0.56
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.04	0.56
33:2b:19:HIS:CE1	33:2b:20:GLU:HG3	2.41	0.56
51:2t:25:ARG:HG2	51:2t:29:LYS:HE3	1.88	0.56
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.21	0.56
32:1a:160:A:H2'	32:1a:161:A:O4'	2.06	0.56
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.40	0.56
54:1w:173:TYR:OH	54:1w:343:ASP:OD2	2.19	0.56
32:2a:1218:C:OP2	45:2n:9:LYS:NZ	2.32	0.56
50:2s:18:LYS:HA	50:2s:21:GLU:HB2	1.87	0.56
1:1A:1364:G:OP2	23:11:3:LYS:HG3	2.06	0.56
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.06	0.56
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.41	0.56
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.06	0.56
44:1m:3:ARG:H	44:1m:8:GLU:HA	1.70	0.56
50:1s:65:ASN:OD1	50:1s:65:ASN:N	2.38	0.56
54:1w:102:MET:HE3	54:1w:103:ASP:HB2	1.87	0.56
54:1w:130:MET:HE3	54:1w:332:LEU:HD11	1.88	0.56
1:2A:1472:A:N6	1:2A:1519:G:O2'	2.39	0.56
25:23:15:TYR:O	25:23:20:LYS:NZ	2.38	0.56
32:2a:539:A:H2'	32:2a:540:G:C8	2.41	0.56
32:2a:689:C:OP1	42:2k:27:ASN:ND2	2.39	0.56
32:2a:1285:A:H5'	32:2a:1286:A:C2	2.40	0.56
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.06	0.56
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.88	0.56
7:1H:101:ARG:NH2	7:1H:121:ILE:O	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:19:2:LYS:NZ	31:19:31:LYS:O	2.35	0.56
32:1a:450:G:OP1	47:1p:43:LYS:NZ	2.39	0.56
32:1a:460:G:N2	32:1a:471:G:N7	2.54	0.56
38:1g:35:LYS:HE3	38:1g:38:LEU:HD23	1.88	0.56
61:2A:3909:HOH:O	11:2P:37:GLY:HA3	2.06	0.56
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.87	0.56
32:2a:1316:G:N1	32:2a:1319:A:OP2	2.37	0.56
42:2k:31:THR:HG22	42:2k:42:TRP:HB2	1.88	0.56
1:1A:336:C:O2'	20:1Y:35:TYR:OH	2.22	0.55
4:1E:9:VAL:HG13	15:1T:3:ARG:HG2	1.88	0.55
22:10:32:ARG:H	22:10:35:ASN:ND2	2.03	0.55
32:1a:486:U:H2'	32:1a:487:A:H8	1.71	0.55
32:1a:1118:C:OP1	40:1i:104:ARG:NH1	2.39	0.55
36:1e:148:VAL:O	36:1e:152:ARG:N	2.29	0.55
38:1g:113:GLU:HB2	38:1g:119:ARG:HG2	1.87	0.55
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.41	0.55
1:2A:2136:C:C4	1:2A:2155:G:C6	2.94	0.55
1:2A:2196:C:OP2	61:2A:3935:HOH:O	2.17	0.55
32:2a:1329:A:H5"	44:2m:26:GLY:H	1.71	0.55
32:2a:1347:G:H5"	40:2i:107:ARG:HB3	1.88	0.55
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.06	0.55
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.39	0.55
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.70	0.55
1:1A:1914:C:H1'	54:1w:290:LEU:HD11	1.89	0.55
1:1A:2100:G:H2'	1:1A:2101:G:O4'	2.06	0.55
1:1A:2567:G:O6	61:1A:4134:HOH:O	2.17	0.55
32:2a:90:U:H2'	32:2a:91:C:H6	1.70	0.55
32:2a:562:C:H1'	43:2l:15:ARG:HB3	1.88	0.55
32:2a:975:A:H5'	32:2a:975:A:H8	1.71	0.55
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.06	0.55
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	1.88	0.55
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.06	0.55
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.88	0.55
1:2A:247:G:H4'	1:2A:386:G:C5	2.40	0.55
1:2A:1223:G:N2	1:2A:1226:A:OP2	2.29	0.55
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.72	0.55
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.39	0.55
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.30	0.55
50:2s:28:LYS:HD3	50:2s:47:HIS:HA	1.86	0.55
1:1A:1420:U:O2'	1:1A:1421:G:OP1	2.20	0.55
1:1A:2794:C:N4	1:1A:2802:G:H1	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:81:GLU:HG2	36:1e:90:VAL:HG22	1.88	0.55
1:2A:644:A:H4'	1:2A:645:C:C5	2.41	0.55
1:2A:2121:G:H1	1:2A:2177:C:H42	1.54	0.55
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.88	0.55
6:2G:54:GLU:O	6:2G:58:GLN:N	2.38	0.55
32:2a:533:A:O2'	32:2a:535:A:OP2	2.19	0.55
32:2a:1239:A:H4'	32:2a:1240:U:H5"	1.88	0.55
49:2r:48:GLY:O	49:2r:74:ARG:NH2	2.39	0.55
32:1a:375:U:O2	47:1p:28:ARG:NH1	2.40	0.55
32:1a:1108:G:O6	61:1a:1911:HOH:O	2.16	0.55
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.41	0.55
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.88	0.55
35:1d:124:GLY:C	35:1d:126:ILE:H	2.15	0.55
38:1g:116:ALA:O	38:1g:120:ILE:HG12	2.06	0.55
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.87	0.55
54:1w:111:ILE:HB	54:1w:158:VAL:HG23	1.87	0.55
1:2A:774:A:H2'	1:2A:774:A:N3	2.20	0.55
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.88	0.55
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.41	0.55
1:1A:747:U:O2	1:1A:2014:A:H1'	2.06	0.55
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.42	0.55
3:1D:211:ARG:HG2	3:1D:214:TRP:CZ3	2.41	0.55
34:1c:62:ASP:HA	34:1c:97:LYS:HD2	1.89	0.55
1:2A:1971:A:OP2	3:2D:242:ARG:NH2	2.39	0.55
26:24:59:PHE:O	26:24:62:ARG:NH2	2.38	0.55
32:2a:1271:G:C2	32:2a:1272:G:N7	2.75	0.55
32:2a:1314:C:H2'	32:2a:1315:U:C6	2.42	0.55
1:1A:2134:A:H1'	1:1A:2159:G:H1'	1.88	0.55
32:1a:148:G:H2'	32:1a:149:A:C8	2.42	0.55
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.21	0.55
35:1d:157:LEU:HD23	35:1d:161:ASN:HD21	1.71	0.55
1:2A:582:G:OP2	61:2A:3946:HOH:O	2.18	0.55
1:2A:2114:A:H2	1:2A:2171:A:H61	1.54	0.55
32:2a:1327:C:OP1	52:2u:12:LYS:NZ	2.40	0.55
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.41	0.55
33:2b:84:GLU:HB3	33:2b:219:VAL:HG11	1.88	0.55
43:2l:27:LEU:HA	43:2l:33:ARG:HG3	1.88	0.55
54:2w:105:ARG:HB3	54:2w:105:ARG:HH21	1.72	0.55
54:2w:228:GLY:HA3	54:2w:232:VAL:HB	1.89	0.55
1:1A:2507:C:H4'	54:1w:233:ASN:O	2.06	0.55
7:1H:3:ARG:HE	7:1H:54:ARG:HH12	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:46:GLN:HB3	26:14:48:ARG:HG2	1.89	0.55
36:1e:102:ALA:HB1	36:1e:106:PRO:HB2	1.89	0.55
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.88	0.55
1:2A:623:G:H2'	1:2A:624:C:C6	2.42	0.55
1:2A:1528(A):A:H2'	1:2A:1529:G:O4'	2.07	0.55
8:2I:104:GLN:OE1	8:2I:105:HIS:NE2	2.39	0.55
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.87	0.55
42:2k:85:ARG:HD3	42:2k:113:PRO:HD3	1.89	0.55
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.35	0.55
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.88	0.55
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.88	0.55
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.88	0.55
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.88	0.55
1:2A:2127:G:C2	1:2A:2161:C:C2	2.95	0.55
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.41	0.55
21:2Z:157:LEU:HG	21:2Z:161:VAL:HG23	1.88	0.55
39:2h:100:ILE:O	39:2h:125:ARG:NH1	2.40	0.55
32:1a:164:U:H2'	32:1a:165:C:C6	2.42	0.55
32:1a:473:G:H2'	32:1a:474:G:C8	2.42	0.55
43:1l:27:LEU:HA	43:1l:33:ARG:HG3	1.89	0.55
54:1w:285:LEU:HD21	54:1w:289:ARG:HH22	1.72	0.55
54:1w:344:GLN:HA	54:1w:344:GLN:HE21	1.72	0.55
1:2A:531:C:OP1	1:2A:561:G:N1	2.37	0.55
1:2A:652(D):C:H2'	1:2A:652(E):G:C8	2.42	0.55
9:2N:20:GLY:HA2	9:2N:61:ARG:HG2	1.89	0.55
32:2a:352:C:H4'	32:2a:354:G:OP1	2.06	0.55
32:2a:1004:A:N6	32:2a:1037:C:O2	2.39	0.55
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.42	0.54
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.42	0.54
33:1b:9:GLU:O	33:1b:11:LEU:N	2.40	0.54
36:1e:91:LEU:HB3	36:1e:118:ILE:HD11	1.89	0.54
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.40	0.54
1:2A:1125:G:H5'	31:29:37:GLY:HA2	1.89	0.54
1:2A:2159:G:H2'	1:2A:2160:G:H8	1.73	0.54
1:2A:2207:G:H3'	1:2A:2208:A:H5"	1.89	0.54
1:2A:2319:G:H22	14:2S:3:ARG:HE	1.55	0.54
32:2a:601:C:H2'	32:2a:602:A:C8	2.42	0.54
33:2b:167:PRO:HD3	33:2b:187:LEU:O	2.07	0.54
46:1o:82:ILE:O	46:1o:86:GLY:N	2.40	0.54
55:1x:16:C:O2'	55:1x:19:G:OP1	2.17	0.54
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2849:U:O4	15:2T:23:ARG:NH1	2.30	0.54
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.39	0.54
23:21:52:ARG:NH1	23:21:55:GLY:O	2.40	0.54
44:2m:50:GLU:CD	44:2m:50:GLU:H	2.16	0.54
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.88	0.54
1:1A:1069:A:H1'	1:1A:1096:A:H4'	1.88	0.54
26:14:15:ILE:O	26:14:33:VAL:N	2.41	0.54
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.89	0.54
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.89	0.54
9:2N:36:GLY:HA2	9:2N:38:HIS:CE1	2.43	0.54
50:2s:48:THR:HG22	50:2s:61:TYR:HB2	1.90	0.54
1:1A:288:C:H2'	1:1A:289:A:H8	1.71	0.54
1:1A:1067:A:H2'	1:1A:1068:G:H5"	1.89	0.54
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.07	0.54
28:16:14:THR:HB	28:16:48:VAL:O	2.07	0.54
32:1a:576:G:OP2	61:1a:1915:HOH:O	2.18	0.54
1:2A:581:C:H2'	1:2A:582:G:C8	2.43	0.54
1:2A:1697:G:OP2	1:2A:1698:A:O2'	2.23	0.54
1:2A:2099:U:H3	1:2A:2190:G:H1	1.54	0.54
7:2H:24:VAL:HG21	7:2H:72:ILE:HG12	1.90	0.54
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.42	0.54
17:2V:1:MET:HE1	17:2V:44:LYS:H	1.72	0.54
17:1V:8:GLY:O	17:1V:10:LYS:NZ	2.39	0.54
34:1c:150:LYS:HE3	34:1c:152:ILE:HD11	1.89	0.54
1:2A:1671:U:OP2	61:2A:3944:HOH:O	2.18	0.54
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.40	0.54
1:2A:2698:U:O4	61:2A:3931:HOH:O	2.16	0.54
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.90	0.54
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.07	0.54
50:2s:53:ASN:HB2	50:2s:77:THR:HA	1.90	0.54
1:1A:2743:C:OP1	31:19:33:LYS:NZ	2.34	0.54
32:1a:501:C:H1'	32:1a:549:C:H1'	1.88	0.54
1:2A:686:G:N2	1:2A:788:A:H61	2.05	0.54
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.90	0.54
21:2Z:7:ALA:O	21:2Z:62:PRO:HD3	2.07	0.54
42:2k:20:TYR:O	42:2k:30:VAL:HA	2.08	0.54
1:1A:2175:C:H2'	1:1A:2176:A:C8	2.43	0.54
1:1A:2285:C:OP2	28:16:6:ARG:NH1	2.41	0.54
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.25	0.54
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.89	0.54
32:1a:96:U:H2'	32:1a:97:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:164:U:H2'	32:1a:165:C:H6	1.73	0.54
32:1a:1123:A:O2'	41:1j:37:PRO:O	2.25	0.54
32:1a:1320:C:O2	50:1s:36:ARG:NH2	2.41	0.54
33:1b:32:ILE:HD13	33:1b:40:HIS:CD2	2.43	0.54
33:1b:59:GLU:O	33:1b:63:MET:N	2.37	0.54
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.89	0.54
36:1e:148:VAL:O	36:1e:152:ARG:HG2	2.06	0.54
6:2G:51:ARG:HA	6:2G:51:ARG:HH11	1.73	0.54
32:2a:137:C:H2'	32:2a:138:G:H8	1.73	0.54
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.27	0.54
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.43	0.54
54:2w:128:PHE:CZ	54:2w:132:LEU:HD11	2.43	0.54
1:1A:1071:G:N3	1:1A:1089:G:N1	2.55	0.54
1:1A:1226:A:OP1	17:1V:84:LYS:NZ	2.38	0.54
1:1A:1359:A:H2	1:1A:1372:U:O4	1.91	0.54
1:1A:2155:G:H3'	1:1A:2156:G:H8	1.73	0.54
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.24	0.54
54:1w:317:ILE:HG13	54:1w:319:PHE:H	1.72	0.54
10:2O:97:ARG:NH1	32:2a:339:C:OP2	2.38	0.54
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.20	0.54
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.43	0.54
34:2c:174:PRO:HD2	34:2c:182:ILE:HD11	1.90	0.54
1:1A:272(J):C:H2'	1:1A:274:G:H8	1.72	0.54
1:1A:674:G:O2'	5:1F:74:ARG:HD3	2.07	0.54
1:1A:1364:G:P	23:11:3:LYS:HG3	2.47	0.54
1:1A:2105:C:H2'	1:1A:2106:G:C8	2.42	0.54
32:1a:277:C:OP1	48:1q:68:ARG:NH2	2.41	0.54
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.40	0.54
35:1d:10:ARG:HB2	35:1d:40:PRO:HG3	1.88	0.54
38:1g:80:VAL:HG11	38:1g:154:TYR:CD2	2.42	0.54
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.43	0.54
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.73	0.54
8:2I:79:ILE:HD12	8:2I:144:VAL:HG13	1.90	0.54
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.72	0.54
32:2a:1027:C:H2'	32:2a:1028:C:C6	2.43	0.54
33:2b:12:GLU:HB2	33:2b:213:LEU:HD21	1.90	0.54
39:2h:109:ILE:HG23	39:2h:137:VAL:HB	1.90	0.54
1:1A:616:G:H5'	5:1F:205:ARG:HE	1.73	0.54
1:1A:1091:G:H2'	1:1A:1092:C:C6	2.43	0.54
1:1A:2336:A:H61	22:10:43:THR:HG22	1.73	0.54
32:1a:373:A:H2'	32:1a:374:A:H8	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:24:GLY:N	40:1i:60:ASP:OD1	2.41	0.54
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.41	0.54
38:2g:152:ALA:O	38:2g:155:ARG:HD3	2.08	0.54
1:1A:271(K):U:O2	8:1I:50:ARG:HG3	2.08	0.53
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.40	0.53
4:1E:33:VAL:HG13	4:1E:47:VAL:HG23	1.90	0.53
32:1a:8:A:N6	35:1d:209:ARG:HB2	2.23	0.53
36:1e:11:ILE:HD13	36:1e:105:VAL:HG13	1.90	0.53
1:2A:373:U:H2'	1:2A:374:A:H8	1.73	0.53
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.90	0.53
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.43	0.53
32:2a:1414:U:H3	32:2a:1486:G:H1	1.55	0.53
33:2b:55:PHE:CD1	33:2b:58:ILE:HD11	2.42	0.53
1:1A:2116:G:N2	1:1A:2162:G:OP1	2.40	0.53
8:1I:9:LEU:HD11	8:1I:35:LEU:HD13	1.90	0.53
32:1a:309:G:O2'	32:1a:607:A:N1	2.41	0.53
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.91	0.53
1:2A:2391:G:O6	1:2A:2425:A:H8	1.91	0.53
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.08	0.53
21:2Z:153:SER:OG	21:2Z:154:ASP:N	2.40	0.53
32:2a:15:G:H21	36:2e:18:ARG:HA	1.73	0.53
1:1A:1071:G:H1'	1:1A:1089:G:C6	2.43	0.53
1:1A:2119:A:H61	1:1A:2168:G:H8	1.56	0.53
32:1a:600:C:H2'	32:1a:601:C:H6	1.74	0.53
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.42	0.53
44:1m:33:ALA:O	44:1m:37:THR:N	2.40	0.53
50:1s:19:VAL:HG21	50:1s:44:MET:HA	1.90	0.53
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.23	0.53
36:2e:95:ALA:O	36:2e:97:GLY:N	2.41	0.53
49:2r:25:THR:O	49:2r:25:THR:OG1	2.23	0.53
54:2w:229:GLY:HA3	55:2x:76:8AN:H3'	1.91	0.53
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.43	0.53
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.43	0.53
47:1p:8:ARG:HG2	47:1p:17:TYR:CE1	2.43	0.53
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.43	0.53
32:2a:1314:C:H2'	32:2a:1315:U:H6	1.74	0.53
33:2b:40:HIS:HB3	33:2b:190:THR:HG21	1.90	0.53
1:1A:185:U:H4'	1:1A:218:A:H4'	1.91	0.53
1:1A:271(H):G:H2'	1:1A:271(I):G:H8	1.72	0.53
2:1B:66:A:H61	2:1B:108:U:H2'	1.73	0.53
11:1P:8:PRO:HB2	11:1P:12:ALA:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.42	0.53
39:1h:11:THR:HG22	39:1h:14:ARG:NH1	2.21	0.53
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.73	0.53
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.90	0.53
32:2a:54:C:N4	32:2a:353:A:OP2	2.38	0.53
1:1A:205:G:O6	23:11:39:LYS:NZ	2.42	0.53
6:1G:137:GLU:HB2	6:1G:140:ILE:HD13	1.91	0.53
6:1G:142:PRO:HB3	26:14:14:ILE:HD11	1.91	0.53
8:1I:77:LEU:HB3	8:1I:142:VAL:HG22	1.91	0.53
20:1Y:28:LYS:HD2	20:1Y:40:GLU:HG3	1.91	0.53
23:11:82:LEU:HA	23:11:85:LEU:HD12	1.90	0.53
32:1a:456:C:H2'	32:1a:457:C:C6	2.43	0.53
33:1b:55:PHE:CE1	33:1b:218:ALA:HA	2.44	0.53
36:1e:136:MET:HB3	36:1e:140:ARG:HH21	1.73	0.53
37:1f:10:LEU:HD11	37:1f:61:LEU:HD22	1.90	0.53
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.44	0.53
3:2D:232:PRO:HB3	3:2D:244:ARG:CZ	2.39	0.53
19:2X:11:PRO:HG2	19:2X:13:LEU:HD21	1.91	0.53
32:2a:130:A:O2'	32:2a:131:C:O5'	2.24	0.53
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.24	0.53
35:2d:7:PRO:HB2	35:2d:10:ARG:HD2	1.89	0.53
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.08	0.53
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.44	0.53
33:2b:47:THR:O	33:2b:51:LEU:N	2.30	0.53
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.08	0.53
41:2j:8:LEU:HD11	41:2j:20:ALA:HB2	1.91	0.53
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.74	0.53
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.40	0.53
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.89	0.53
3:1D:25:THR:HG21	3:1D:113:VAL:HG11	1.91	0.53
32:1a:41:G:H2'	32:1a:42:G:C8	2.44	0.53
32:1a:96:U:H2'	32:1a:97:G:H8	1.73	0.53
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.91	0.53
35:1d:175:SER:HB3	35:1d:184:LYS:HB3	1.89	0.53
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.44	0.53
1:2A:514:A:N3	1:2A:581:C:O2'	2.38	0.53
1:2A:2134:A:O2'	1:2A:2159:G:N2	2.42	0.53
6:2G:44:GLY:HA2	6:2G:88:ILE:HG22	1.91	0.53
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.90	0.53
35:2d:107:ARG:HH21	35:2d:173:TRP:HH2	1.55	0.53
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1470:G:N2	1:1A:1520:G:OP2	2.32	0.53
24:12:1:MET:HE3	24:12:6:VAL:HG22	1.91	0.53
26:14:16:CYS:HB2	26:14:36:CYS:HB3	1.91	0.53
32:1a:45:U:H2'	32:1a:46:G:C8	2.43	0.53
32:1a:990:C:H2'	32:1a:991:U:C6	2.44	0.53
37:1f:44:GLY:HA2	37:1f:59:TYR:CZ	2.44	0.53
1:2A:271(A):A:N1	1:2A:272(D):G:O2'	2.37	0.53
1:2A:2096:U:H2'	1:2A:2097:C:C6	2.44	0.53
21:2Z:145:GLU:HG3	21:2Z:146:ILE:N	2.23	0.53
32:2a:707:C:O2'	32:2a:708:C:H5'	2.09	0.53
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.89	0.53
44:2m:68:GLY:O	44:2m:72:ALA:N	2.42	0.53
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.44	0.53
1:1A:1902:C:H5'	3:1D:246:PRO:HD3	1.90	0.53
1:1A:2865:U:OP2	15:1T:119:LYS:NZ	2.41	0.53
14:1S:61:ASN:HD22	14:1S:64:GLU:HG3	1.73	0.53
18:1W:11:ARG:HA	18:1W:100:THR:HG22	1.91	0.53
47:1p:53:VAL:HA	47:1p:56:ALA:HB3	1.91	0.53
1:2A:751:A:H5'	18:2W:90:ARG:HA	1.91	0.53
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.44	0.53
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.09	0.53
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.73	0.53
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.09	0.53
50:2s:44:MET:HB3	50:2s:62:ILE:HD12	1.91	0.53
1:1A:2115:G:H1	1:1A:2119:A:P	2.33	0.52
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.23	0.52
32:1a:989:C:H42	32:1a:1216:G:H1	1.56	0.52
33:1b:8:LYS:O	33:1b:217:ARG:NH1	2.41	0.52
33:1b:17:PHE:HA	33:1b:44:LEU:HD21	1.90	0.52
43:1l:117:ARG:NH2	43:1l:124:LYS:HB2	2.24	0.52
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.42	0.52
30:28:23:VAL:HG13	30:28:47:LYS:HB3	1.90	0.52
1:1A:2139:C:H2'	1:1A:2140:C:O4'	2.10	0.52
32:1a:583:A:N6	32:1a:758:G:O2'	2.43	0.52
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.44	0.52
32:1a:1202:G:H2'	32:1a:1203:C:O4'	2.09	0.52
32:1a:1226:C:H4'	50:1s:80:TYR:OH	2.09	0.52
33:1b:28:PHE:HD1	33:1b:194:PRO:HG3	1.73	0.52
47:1p:22:THR:HA	47:1p:33:ILE:HG13	1.89	0.52
1:2A:839:U:H2'	1:2A:840:C:C6	2.43	0.52
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:38:LEU:HB2	8:2I:40:THR:HG22	1.91	0.52
21:2Z:155:LEU:O	21:2Z:156:LYS:NZ	2.32	0.52
44:2m:27:LYS:HE2	44:2m:30:ALA:HB3	1.92	0.52
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.43	0.52
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.09	0.52
32:1a:192:U:H4'	51:1t:57:ARG:HD2	1.91	0.52
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.42	0.52
36:1e:93:PRO:HG2	39:1h:105:ARG:NH1	2.24	0.52
55:1x:7:U:O2'	55:1x:49:U:OP2	2.18	0.52
1:2A:154(A):C:H42	1:2A:171:G:H1	1.56	0.52
1:2A:1645:G:H5"	1:2A:1646:C:H5'	1.92	0.52
1:2A:1790:C:H5"	1:2A:1791:A:OP1	2.09	0.52
1:2A:2393:A:H5"	11:2P:63:PRO:HB3	1.90	0.52
14:2S:26:LEU:HB2	14:2S:85:VAL:CG1	2.39	0.52
26:24:61:ARG:NH1	50:2s:9:VAL:HG21	2.24	0.52
33:2b:134:GLU:O	33:2b:138:LEU:HG	2.10	0.52
34:2c:120:VAL:HG11	34:2c:137:ALA:HB2	1.91	0.52
1:1A:2134:A:O2'	1:1A:2135:A:OP1	2.27	0.52
6:1G:103:LEU:HA	6:1G:106:LEU:HB3	1.92	0.52
32:1a:448:A:OP2	32:1a:485:G:N1	2.26	0.52
32:1a:800:G:O6	61:1a:1916:HOH:O	2.18	0.52
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.45	0.52
35:1d:104:VAL:HG11	35:1d:146:ILE:HD13	1.90	0.52
40:1i:50:LEU:HD23	40:1i:85:LEU:HD11	1.91	0.52
51:1t:16:HIS:O	51:1t:19:SER:OG	2.23	0.52
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.41	0.52
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.25	0.52
32:2a:56:U:H2'	32:2a:57:G:C8	2.45	0.52
32:2a:559:A:H4'	32:2a:560:U:H5"	1.91	0.52
32:2a:1348:U:H2'	32:2a:1349:A:H8	1.75	0.52
1:1A:2124:G:H3'	1:1A:2125:G:H8	1.75	0.52
6:1G:67:LYS:HD3	26:14:5:ILE:HD12	1.92	0.52
32:1a:149:A:H2'	32:1a:150:C:C6	2.44	0.52
32:1a:598:U:H2'	32:1a:599:C:C6	2.45	0.52
36:1e:39:GLY:HA2	36:1e:69:VAL:HG13	1.91	0.52
1:2A:1420:U:O2'	1:2A:1421:G:O5'	2.18	0.52
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.25	0.52
17:2V:1:MET:HG2	17:2V:99:ILE:HD12	1.91	0.52
32:2a:45:U:H2'	32:2a:46:G:C8	2.45	0.52
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.45	0.52
34:2c:70:VAL:HG12	34:2c:72:LYS:N	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2541:A:OP2	61:1A:4135:HOH:O	2.18	0.52
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.06	0.52
32:1a:236:G:H5"	48:1q:42:TYR:OH	2.10	0.52
44:1m:3:ARG:HG2	44:1m:9:ILE:HD11	1.91	0.52
1:2A:242:G:C8	30:28:5:LYS:HG2	2.45	0.52
1:2A:493:G:H2'	1:2A:494:G:O4'	2.10	0.52
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.10	0.52
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.10	0.52
1:2A:2135:A:H5"	1:2A:2160:G:H1'	1.91	0.52
1:2A:2365:G:O6	30:28:43:GLN:NE2	2.38	0.52
13:2R:78:LYS:HE2	13:2R:83:ILE:HD11	1.90	0.52
19:2X:1:MET:HE1	24:22:22:GLU:HA	1.92	0.52
32:2a:624:C:H2'	32:2a:625:G:H8	1.75	0.52
32:2a:988:G:H2'	32:2a:989:C:O4'	2.09	0.52
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.25	0.52
43:2l:70:ILE:HD13	43:2l:77:LEU:HD12	1.91	0.52
1:1A:84:A:H5'	20:1Y:8:LYS:HB3	1.91	0.52
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.91	0.52
1:1A:2099:U:H3	1:1A:2190:G:H1	1.57	0.52
1:1A:2144:U:H3	1:1A:2147:G:H22	1.56	0.52
1:1A:2184:G:H2'	1:1A:2185:C:O4'	2.10	0.52
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.44	0.52
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	1.92	0.52
1:2A:2284:C:OP2	28:26:2:ALA:N	2.42	0.52
2:2B:8:U:H6	2:2B:8:U:H5"	1.75	0.52
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.43	0.52
11:2P:89:ALA:HA	11:2P:121:LYS:HE2	1.92	0.52
32:2a:877:C:H5"	39:2h:88:LYS:HD3	1.91	0.52
32:2a:1194:U:H4'	36:2e:22:GLY:HA2	1.92	0.52
46:2o:43:LEU:HD12	46:2o:56:LEU:HD13	1.90	0.52
54:2w:110:GLU:HB2	54:2w:200:ALA:HB3	1.92	0.52
1:1A:208:C:H2'	1:1A:209:C:C6	2.44	0.52
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.42	0.52
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.44	0.52
32:1a:564:C:OP1	43:1l:15:ARG:NE	2.43	0.52
32:1a:1305:G:H5"	52:1u:4:GLY:HA3	1.92	0.52
33:1b:82:ARG:HD2	33:1b:92:TYR:OH	2.10	0.52
1:2A:1031:G:H5"	31:29:8:LYS:HE3	1.91	0.52
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.09	0.52
1:2A:2098:U:H3	1:2A:2191:G:H1	1.56	0.52
1:2A:2127:G:O2'	1:2A:2173:A:N3	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:125:ARG:NH2	32:2a:1443:G:H5'	2.24	0.52
32:2a:1073:U:H2'	32:2a:1074:G:C8	2.44	0.52
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.74	0.52
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.45	0.52
1:1A:376:C:OP2	61:1A:4138:HOH:O	2.19	0.52
1:1A:671:C:N4	61:1A:4306:HOH:O	2.43	0.52
1:1A:848:G:H2'	1:1A:849:A:C8	2.44	0.52
1:1A:1041:C:N4	1:1A:1114:G:H1	2.05	0.52
1:1A:1062:G:C2	1:1A:1088:A:H2'	2.45	0.52
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.45	0.52
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.45	0.52
48:1q:88:TYR:CD2	48:1q:89:LEU:HD23	2.43	0.52
1:2A:1412:A:H2'	1:2A:1413:G:H8	1.74	0.52
6:2G:16:ARG:HB2	6:2G:17:PRO:HD3	1.92	0.52
7:2H:95:ARG:NH1	7:2H:97:ARG:HD3	2.25	0.52
24:22:10:LEU:HD21	24:22:59:ARG:HG2	1.90	0.52
32:2a:501:C:H2'	32:2a:502:G:H8	1.74	0.52
32:2a:1121:U:H2'	32:2a:1122:U:C6	2.44	0.52
32:2a:1141:C:H2'	32:2a:1142:G:H8	1.75	0.52
32:2a:1321:C:H4'	44:2m:87:TYR:CZ	2.45	0.52
9:1N:38:HIS:NE2	9:1N:50:ASP:OD2	2.42	0.52
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.90	0.52
34:1c:23:TYR:HA	41:1j:11:PHE:CE2	2.45	0.52
45:1n:37:PHE:HB3	45:1n:39:LEU:HD12	1.91	0.52
46:1o:68:ARG:O	46:1o:72:ARG:HG3	2.10	0.52
54:1w:302:ILE:HG13	54:1w:316:ARG:HD3	1.92	0.52
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.45	0.52
7:2H:3:ARG:NH2	7:2H:65:HIS:HB3	2.23	0.52
31:29:10:ILE:HD12	31:29:32:HIS:HA	1.91	0.52
32:2a:51:A:N1	32:2a:314:C:O2'	2.39	0.52
32:2a:263:A:OP1	51:2t:79:ARG:NH1	2.42	0.52
32:2a:1193:G:O2'	36:2e:25:ARG:NH2	2.43	0.52
32:2a:1397:C:O2'	32:2a:1398:A:OP1	2.28	0.52
38:2g:146:GLU:OE1	38:2g:149:ARG:HD2	2.10	0.52
1:1A:228:A:H3'	1:1A:229:A:C5'	2.40	0.51
1:1A:1031:G:N3	31:19:36:GLN:NE2	2.51	0.51
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.75	0.51
1:1A:1056:G:H5"	1:1A:1086:A:C8	2.45	0.51
1:1A:2130:U:H2'	1:1A:2158:A:N6	2.25	0.51
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.43	0.51
34:1c:39:ILE:HG22	34:1c:43:LEU:HD12	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:23:TYR:HE2	44:1m:70:LEU:HB3	1.75	0.51
44:1m:45:VAL:HG13	44:1m:48:LEU:HD12	1.92	0.51
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.45	0.51
8:2I:75:LEU:HD11	8:2I:105:HIS:ND1	2.25	0.51
11:2P:8:PRO:HB2	11:2P:12:ALA:HB3	1.92	0.51
32:2a:1025:U:H1'	32:2a:1026:G:N7	2.25	0.51
32:2a:1258:G:H2'	32:2a:1259:C:C6	2.45	0.51
32:2a:1320:C:O2	50:2s:36:ARG:NH2	2.43	0.51
33:2b:87:ARG:NH2	33:2b:232:PRO:O	2.35	0.51
1:1A:1827:C:C2'	1:1A:1828:G:H5'	2.40	0.51
32:1a:334:C:H2'	32:1a:335:C:C6	2.45	0.51
32:1a:508:C:OP1	35:1d:209:ARG:NH2	2.42	0.51
32:1a:601:C:H2'	32:1a:602:A:C8	2.44	0.51
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.27	0.51
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.91	0.51
50:1s:22:LEU:HB3	50:1s:27:GLU:HB3	1.92	0.51
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.26	0.51
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	1.90	0.51
32:2a:1499:A:H1'	32:2a:1520:G:H5'	1.90	0.51
35:2d:64:LEU:HD13	35:2d:198:VAL:HG21	1.91	0.51
1:1A:2494:G:O2'	12:1Q:80:GLU:HA	2.10	0.51
8:1I:4:ILE:HG12	8:1I:18:VAL:HG12	1.92	0.51
32:1a:41:G:H2'	32:1a:42:G:H8	1.75	0.51
32:1a:1426:C:H2'	32:1a:1427:U:C6	2.45	0.51
32:1a:1521:G:H2'	32:1a:1522:U:C6	2.45	0.51
37:1f:69:GLU:OE1	37:1f:69:GLU:N	2.34	0.51
50:1s:32:LYS:HB2	50:1s:57:HIS:CE1	2.46	0.51
54:1w:151:ASP:OD1	54:1w:151:ASP:N	2.44	0.51
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.57	0.51
32:2a:1060:C:H2'	32:2a:1061:G:H8	1.76	0.51
32:2a:1225:A:H2'	32:2a:1225:A:N3	2.25	0.51
32:2a:1452:C:H5'	32:2a:1457:G:C4	2.45	0.51
1:1A:359:A:H2'	1:1A:360:G:O4'	2.10	0.51
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.38	0.51
1:1A:2319:G:H22	14:1S:3:ARG:NE	2.07	0.51
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.11	0.51
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.56	0.51
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.26	0.51
9:1N:73:THR:HB	9:1N:82:LEU:HD11	1.91	0.51
32:1a:390:C:O3'	47:1p:28:ARG:NH2	2.38	0.51
32:1a:1035:A:N3	32:1a:1036:G:N2	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1144:G:N2	32:1a:1146:A:H62	2.07	0.51
38:1g:16:LEU:HD11	40:1i:45:ALA:HB2	1.92	0.51
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.75	0.51
1:2A:674:G:H1'	5:2F:74:ARG:HD3	1.91	0.51
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.43	0.51
32:2a:946:A:H2'	32:2a:947:G:C8	2.45	0.51
35:2d:111:ALA:HB1	35:2d:116:GLN:HG2	1.92	0.51
1:1A:272(H):C:H2'	1:1A:272(I):U:C6	2.46	0.51
1:1A:1580:A:OP2	1:1A:1580:A:H8	1.93	0.51
3:1D:211:ARG:HG2	3:1D:214:TRP:CE3	2.46	0.51
21:1Z:73:GLN:HB3	21:1Z:87:ASP:HB2	1.92	0.51
21:1Z:93:ASP:CB	21:1Z:131:ARG:HH22	2.23	0.51
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.92	0.51
32:2a:176:C:H2'	32:2a:177:C:C6	2.45	0.51
32:2a:411:A:OP2	35:2d:30:LYS:HD3	2.09	0.51
32:2a:413:G:N7	35:2d:35:ARG:NH2	2.59	0.51
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.46	0.51
47:2p:75:ARG:HB2	47:2p:80:PHE:HD2	1.73	0.51
50:2s:20:LEU:HD23	50:2s:23:ASN:HD22	1.74	0.51
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.08	0.51
32:1a:60:A:N1	32:1a:107:G:O2'	2.42	0.51
32:1a:413:G:N2	32:1a:428:G:H1'	2.26	0.51
32:1a:1318:A:O2'	50:1s:37:ARG:HD2	2.11	0.51
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.46	0.51
32:1a:1400:5MC:O2	54:1w:188:THR:HG21	2.11	0.51
50:1s:45:VAL:HG11	50:1s:64:GLU:HG3	1.91	0.51
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.11	0.51
2:2B:44:G:OP1	6:2G:98:ARG:NH2	2.44	0.51
5:2F:28:ILE:HG23	5:2F:112:MET:HG2	1.93	0.51
10:2O:68:GLU:HB3	10:2O:78:ARG:HD3	1.91	0.51
32:2a:164:U:H2'	32:2a:165:C:C6	2.46	0.51
34:2c:111:LEU:HD11	34:2c:144:SER:O	2.11	0.51
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.43	0.51
41:2j:55:LYS:O	41:2j:57:LYS:N	2.44	0.51
44:2m:60:VAL:HG23	44:2m:64:TRP:CE3	2.45	0.51
53:2v:20:A:N6	54:2w:186:THR:OG1	2.44	0.51
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.08	0.51
32:1a:392:G:H2'	32:1a:393:A:C8	2.45	0.51
33:1b:138:LEU:O	33:1b:142:LEU:N	2.44	0.51
44:1m:118:ALA:HB1	55:1x:28:C:H4'	1.92	0.51
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:211:ARG:HG2	3:2D:214:TRP:CZ3	2.45	0.51
32:2a:382:A:H2'	32:2a:383:A:C8	2.46	0.51
32:2a:1002:G:H1	32:2a:1038:C:H42	1.59	0.51
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.75	0.51
39:2h:7:ALA:O	39:2h:11:THR:HG23	2.10	0.51
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.46	0.51
6:1G:139:LEU:HD21	6:1G:146:TYR:N	2.25	0.51
32:1a:190:U:H2'	32:1a:191:G:H8	1.76	0.51
32:1a:250:A:H4'	32:1a:251:G:O5'	2.09	0.51
32:1a:446:G:O6	61:1a:1913:HOH:O	2.17	0.51
32:1a:828:A:H2'	32:1a:829:G:O4'	2.11	0.51
43:1l:69:TYR:HB2	43:1l:90:VAL:HG21	1.91	0.51
51:1t:9:ASN:OD1	51:1t:10:LEU:N	2.44	0.51
1:2A:391:G:O2'	1:2A:410:G:OP1	2.25	0.51
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.11	0.51
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.10	0.51
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.45	0.51
32:2a:666:G:H5'	32:2a:726:C:H1'	1.92	0.51
32:2a:1227:A:OP2	44:2m:111:LYS:HE3	2.11	0.51
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.11	0.51
38:2g:116:ALA:O	38:2g:120:ILE:HD12	2.11	0.51
1:1A:2038:G:O6	61:1A:4137:HOH:O	2.19	0.51
1:1A:2289:G:OP1	61:1A:4139:HOH:O	2.19	0.51
1:1A:2336:A:H61	22:10:43:THR:CG2	2.24	0.51
2:1B:13:A:N1	2:1B:69:G:O2'	2.36	0.51
2:1B:31:C:H4'	6:1G:29:TRP:CH2	2.46	0.51
32:1a:390:C:H2'	32:1a:391:G:C8	2.46	0.51
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.93	0.51
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.29	0.51
35:1d:107:ARG:HD2	35:1d:173:TRP:HH2	1.76	0.51
49:1r:58:LEU:HB3	49:1r:62:GLU:HB2	1.92	0.51
1:2A:721:C:H2'	1:2A:722:A:C8	2.45	0.51
1:2A:922:U:H2'	1:2A:923:C:C6	2.46	0.51
32:2a:110:C:H2'	32:2a:111:G:O4'	2.11	0.51
38:2g:90:GLU:H	38:2g:90:GLU:CD	2.19	0.51
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.46	0.51
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.11	0.51
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.75	0.51
32:1a:524:G:H2'	32:1a:525:C:C6	2.46	0.51
32:1a:1379:G:O6	38:1g:2:ALA:N	2.44	0.51
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:219:VAL:O	33:1b:223:ILE:HG12	2.11	0.51
35:1d:15:GLU:O	35:1d:63:LYS:NZ	2.43	0.51
36:1e:147:ASP:OD1	36:1e:147:ASP:N	2.44	0.51
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.27	0.51
33:2b:45:GLN:O	33:2b:48:MET:HG3	2.11	0.51
35:2d:129:ASN:HD21	35:2d:144:ASP:HA	1.76	0.51
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.11	0.51
36:2e:50:GLU:OE1	36:2e:51:VAL:HG22	2.11	0.51
1:1A:1057:A:H2'	1:1A:1058:G:O4'	2.11	0.50
1:1A:1166:C:O2'	61:1A:4140:HOH:O	2.19	0.50
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.34	0.50
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.45	0.50
10:1O:87:ILE:HD12	10:1O:91:LEU:HA	1.92	0.50
32:1a:629:G:H2'	32:1a:630:G:O4'	2.11	0.50
46:1o:39:LEU:HB3	46:1o:56:LEU:HD12	1.92	0.50
52:1u:18:TYR:CG	52:1u:24:ARG:HG2	2.46	0.50
1:2A:463:G:OP2	61:2A:3948:HOH:O	2.19	0.50
1:2A:2135:A:C4	1:2A:2136:C:H5	2.29	0.50
1:2A:2238:G:H5"	61:2A:4451:HOH:O	2.11	0.50
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.11	0.50
21:2Z:158:PRO:O	21:2Z:161:VAL:HG22	2.10	0.50
32:2a:328:C:H4'	32:2a:329:A:H5'	1.93	0.50
32:2a:520:A:N1	32:2a:536:C:H1'	2.26	0.50
33:2b:219:VAL:HA	33:2b:222:ILE:HD12	1.93	0.50
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.46	0.50
37:2f:82:ARG:HB2	37:2f:85:VAL:HG23	1.93	0.50
54:2w:119:GLU:CD	54:2w:184:PRO:HB3	2.36	0.50
4:1E:109:LYS:O	4:1E:111:ARG:NH1	2.42	0.50
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.93	0.50
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.92	0.50
32:1a:903:G:OP1	61:1a:1914:HOH:O	2.18	0.50
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.11	0.50
32:1a:1226:C:H3'	44:1m:96:LEU:HD21	1.93	0.50
35:1d:129:ASN:N	35:1d:129:ASN:OD1	2.42	0.50
38:1g:42:ILE:HD12	38:1g:116:ALA:HB3	1.94	0.50
50:1s:36:ARG:NH2	50:1s:72:GLY:O	2.44	0.50
1:2A:271(L):U:H5'	8:2I:50:ARG:HH11	1.75	0.50
1:2A:422:A:OP2	61:2A:3950:HOH:O	2.20	0.50
1:2A:724:U:H2'	1:2A:725:G:O4'	2.12	0.50
1:2A:1739:U:O2'	1:2A:1740:G:H8	1.94	0.50
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:106:LEU:O	6:2G:111:LEU:HG	2.11	0.50
32:2a:323:U:H4'	51:2t:22:ARG:HG3	1.92	0.50
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.46	0.50
32:2a:1201:A:H4'	32:2a:1202:G:O5'	2.11	0.50
33:2b:118:LEU:HB3	33:2b:142:LEU:HD12	1.92	0.50
48:2q:53:LEU:HD23	48:2q:85:VAL:HG11	1.93	0.50
1:1A:249:C:O2	30:18:12:LYS:NZ	2.35	0.50
1:1A:1027:A:N3	61:1A:4217:HOH:O	2.34	0.50
1:1A:1056:G:H5"	1:1A:1086:A:H8	1.77	0.50
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.92	0.50
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.11	0.50
1:1A:2121:G:H1	1:1A:2177:C:H42	1.60	0.50
2:1B:75:G:H22	21:1Z:73:GLN:HE21	1.58	0.50
32:1a:562:C:O2	43:1l:16:GLU:N	2.44	0.50
32:1a:1065:U:H4'	32:1a:1066:C:O5'	2.11	0.50
32:1a:1298:C:H2'	38:1g:114:ARG:HH22	1.76	0.50
36:1e:51:VAL:O	36:1e:55:VAL:HG23	2.11	0.50
38:1g:91:VAL:HG12	38:1g:95:ARG:HB3	1.91	0.50
44:1m:80:ARG:HH12	50:1s:69:HIS:HE1	1.60	0.50
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.92	0.50
1:2A:1876:A:OP2	1:2A:1876:A:H8	1.94	0.50
7:2H:47:GLU:O	7:2H:47:GLU:HG3	2.10	0.50
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.45	0.50
9:2N:137:LYS:NZ	9:2N:139:GLU:OE2	2.34	0.50
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.92	0.50
12:2Q:16:ARG:HG3	12:2Q:18:LYS:HG3	1.93	0.50
32:2a:991:U:O2'	32:2a:1212:U:N3	2.44	0.50
54:2w:182:ARG:HB3	54:2w:307:PHE:HB2	1.92	0.50
26:14:58:ARG:O	26:14:61:ARG:HD3	2.11	0.50
33:1b:215:LEU:O	33:1b:219:VAL:HG22	2.11	0.50
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.36	0.50
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.47	0.50
16:2U:49:HIS:HA	16:2U:52:ARG:HB2	1.92	0.50
32:2a:408:A:H4'	35:2d:112:VAL:HG21	1.93	0.50
32:2a:1237:C:H3'	32:2a:1336:C:H41	1.77	0.50
32:2a:1360:A:H8	32:2a:1360:A:OP1	1.94	0.50
32:2a:1381:U:H2'	32:2a:1382:C:H6	1.75	0.50
35:2d:19:LEU:HD11	35:2d:63:LYS:HG2	1.94	0.50
36:2e:93:PRO:HG2	39:2h:105:ARG:CZ	2.42	0.50
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.12	0.50
32:1a:10:A:OP2	36:1e:126:ARG:HD2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:98:LEU:HB2	33:1b:101:MET:HE3	1.93	0.50
35:1d:101:LEU:HD23	35:1d:121:VAL:HG13	1.93	0.50
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.94	0.50
42:1k:98:LEU:O	42:1k:101:SER:OG	2.26	0.50
1:2A:330:A:H2	1:2A:1210:A:O2'	1.92	0.50
1:2A:468:G:H4'	5:2F:62:ARG:HH12	1.76	0.50
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.11	0.50
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.12	0.50
32:2a:876:G:H1'	39:2h:11:THR:HG21	1.94	0.50
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.93	0.50
32:2a:1374:A:OP1	38:2g:36:LYS:NZ	2.44	0.50
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.26	0.50
38:2g:153:HIS:HA	38:2g:155:ARG:NH1	2.26	0.50
1:1A:1068:G:H2'	1:1A:1096:A:O2'	2.11	0.50
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.11	0.50
1:1A:2134:A:H2'	1:1A:2135:A:C8	2.45	0.50
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.47	0.50
32:1a:110:C:H2'	32:1a:111:G:O4'	2.11	0.50
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.28	0.50
32:1a:923:A:OP1	36:1e:21:ALA:HB2	2.12	0.50
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.28	0.50
33:1b:13:ALA:HA	33:1b:17:PHE:HB3	1.93	0.50
39:2h:97:VAL:HA	39:2h:100:ILE:HD11	1.94	0.50
40:2i:47:LEU:HB3	40:2i:50:LEU:HD11	1.94	0.50
55:2x:18:G:O2'	55:2x:57:G:N2	2.34	0.50
1:1A:1256:G:H1'	5:1F:82:ILE:HD11	1.94	0.50
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.11	0.50
1:1A:2115:G:H1'	1:1A:2171:A:N6	2.26	0.50
1:1A:2126:A:N6	1:1A:2163:C:H4'	2.26	0.50
1:1A:2166:G:H2'	1:1A:2167:U:C5	2.46	0.50
1:1A:2206:G:H3'	1:1A:2207:G:H8	1.74	0.50
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	1.93	0.50
26:14:58:ARG:HD3	50:1s:65:ASN:C	2.37	0.50
32:1a:76:C:H2'	32:1a:77:G:C8	2.47	0.50
32:1a:737:A:H2'	32:1a:738:C:C6	2.46	0.50
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.45	0.50
51:1t:10:LEU:HG	51:1t:12:ALA:H	1.77	0.50
54:1w:196:THR:HG21	54:1w:296:GLY:O	2.12	0.50
1:2A:295:G:O5'	20:2Y:1:MET:HE3	2.12	0.50
1:2A:1311:G:H2'	29:27:47:ARG:NH2	2.27	0.50
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:37:LYS:HG3	9:2N:42:TRP:NE1	2.27	0.50
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.52	0.50
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD21	1.93	0.50
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.43	0.50
32:2a:1072:G:OP1	36:2e:57:LYS:NZ	2.44	0.50
1:1A:2144:U:H3	1:1A:2147:G:N2	2.10	0.50
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.93	0.50
12:1Q:51:ARG:HD3	12:1Q:66:ILE:HD11	1.93	0.50
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.47	0.50
1:2A:1036:G:P	7:2H:59:ARG:HD2	2.52	0.50
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	1.92	0.50
2:2B:105:A:OP1	21:2Z:72:ARG:NH1	2.45	0.50
3:2D:260:ARG:NH2	3:2D:266:SER:OG	2.43	0.50
32:2a:881:G:P	43:2l:12:ARG:HH22	2.34	0.50
39:2h:10:LEU:HD13	39:2h:83:ILE:HG12	1.93	0.50
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.46	0.50
1:1A:127:A:H5"	1:1A:128:C:C6	2.47	0.50
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.46	0.50
3:1D:71:ASP:CB	3:1D:103:ARG:HH12	2.25	0.50
25:13:7:LYS:HG3	25:13:34:GLU:HG3	1.94	0.50
32:1a:1199:U:OP1	61:1a:1917:HOH:O	2.20	0.50
32:1a:1305:G:H1	32:1a:1331:G:H1'	1.77	0.50
46:1o:40:SER:O	46:1o:44:LYS:HG3	2.12	0.50
1:2A:500:G:N1	1:2A:503:A:OP2	2.44	0.50
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.93	0.50
1:2A:2747:G:O6	1:2A:2755:C:H5"	2.12	0.50
8:2I:57:ARG:HB2	8:2I:61:ARG:HH12	1.77	0.50
8:2I:79:ILE:HD11	8:2I:144:VAL:HG22	1.94	0.50
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.11	0.50
14:2S:14:VAL:HG11	14:2S:89:ARG:HG2	1.94	0.50
40:2i:70:LYS:O	40:2i:74:ILE:N	2.34	0.50
1:1A:226:G:N2	1:1A:228:A:H62	2.10	0.49
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.77	0.49
6:1G:56:ALA:O	6:1G:59:GLU:HG2	2.12	0.49
8:1I:6:LEU:HG	8:1I:36:ALA:HA	1.94	0.49
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.12	0.49
11:1P:42:SER:O	61:1P:301:HOH:O	2.18	0.49
13:1R:53:HIS:ND1	13:1R:94:TYR:OH	2.38	0.49
32:1a:392:G:H2'	32:1a:393:A:H8	1.76	0.49
32:1a:1030(D):A:H3'	32:1a:1031:G:O4'	2.12	0.49
32:1a:1172:C:H2'	32:1a:1173:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.44	0.49
43:1l:8:ASN:O	43:1l:12:ARG:HG3	2.12	0.49
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.94	0.49
44:1m:49:THR:N	44:1m:52:GLU:OE1	2.44	0.49
6:2G:109:VAL:O	6:2G:113:ARG:HB2	2.11	0.49
8:2I:114:LEU:HD23	8:2I:130:TYR:HB2	1.94	0.49
25:23:39:ASP:OD2	25:23:44:ARG:NH1	2.45	0.49
30:28:30:ARG:NH1	61:28:201:HOH:O	2.41	0.49
34:2c:43:LEU:HB3	34:2c:47:LEU:HD12	1.93	0.49
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.12	0.49
1:1A:527:C:N3	61:1A:4212:HOH:O	2.34	0.49
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.12	0.49
19:1X:72:LYS:HG2	19:1X:73:ARG:O	2.12	0.49
32:1a:108:G:N7	61:1a:1942:HOH:O	2.34	0.49
32:1a:1272:G:H2'	32:1a:1273:G:O4'	2.12	0.49
33:1b:102:LEU:HD23	33:1b:182:ILE:HD12	1.94	0.49
36:1e:11:ILE:HG23	36:1e:105:VAL:HG22	1.93	0.49
46:1o:11:VAL:HG21	46:1o:34:LEU:HD22	1.95	0.49
1:2A:8:A:H2'	1:2A:9:U:C6	2.46	0.49
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.22	0.49
1:2A:2134:A:OP2	1:2A:2157:G:N2	2.45	0.49
7:2H:56:SER:HB3	7:2H:61:HIS:ND1	2.28	0.49
10:2O:26:LYS:O	10:2O:30:ALA:HB2	2.12	0.49
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.27	0.49
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.46	0.49
34:2c:102:ASN:OD1	34:2c:102:ASN:N	2.45	0.49
51:2t:50:GLU:O	51:2t:100:ILE:HD11	2.12	0.49
26:14:16:CYS:SG	26:14:17:GLY:N	2.85	0.49
32:1a:1137:C:H5'	32:1a:1138:G:C4	2.47	0.49
33:1b:126:GLU:HG3	33:1b:127:ILE:HG13	1.94	0.49
37:1f:97:PHE:O	49:1r:31:LEU:N	2.36	0.49
44:1m:105:THR:OG1	44:1m:106:ASN:ND2	2.45	0.49
1:2A:324:A:N6	1:2A:338:G:O2'	2.45	0.49
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.12	0.49
24:22:1:MET:SD	24:22:56:GLN:NE2	2.86	0.49
32:2a:555:C:H2'	32:2a:556:C:C6	2.47	0.49
32:2a:1005:A:N6	32:2a:1024:G:O2'	2.45	0.49
34:2c:181:ASN:ND2	34:2c:204:LEU:HD12	2.27	0.49
44:2m:23:TYR:HB3	44:2m:67:GLU:HB3	1.94	0.49
1:1A:579:G:H2'	1:1A:580:C:C6	2.48	0.49
1:1A:759:G:OP2	61:1A:4141:HOH:O	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:910:A:N1	1:1A:2277:G:H1’	2.28	0.49
1:1A:1301:A:C8	1:1A:1303:G:C8	3.00	0.49
1:1A:1593:G:H2’	1:1A:1594:G:C8	2.47	0.49
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.44	0.49
15:1T:127:ALA:C	15:1T:129:ARG:H	2.20	0.49
32:1a:405:U:H5”	32:1a:495:A:H2	1.77	0.49
32:1a:625:G:H4’	47:1p:16:HIS:CD2	2.47	0.49
32:1a:1363(A):A:H4’	32:1a:1364:U:H2’	1.93	0.49
35:1d:119:GLN:HG2	35:1d:123:HIS:HD2	1.77	0.49
51:1t:58:LYS:HE3	51:1t:62:LEU:HD11	1.95	0.49
1:2A:286:C:H2’	1:2A:287:C:C6	2.47	0.49
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.47	0.49
1:2A:1019:U:O2’	1:2A:1021:A:H2	1.95	0.49
1:2A:1779:U:H2’	61:2A:4402:HOH:O	2.11	0.49
1:2A:1939:5MU:OP1	1:2A:2604:U:O2’	2.28	0.49
1:2A:2693:A:H2’	1:2A:2694:G:C8	2.48	0.49
5:2F:108:LYS:HE2	5:2F:112:MET:HE1	1.92	0.49
32:2a:437:U:H5’	35:2d:155:LEU:HD21	1.95	0.49
32:2a:601:C:H2’	32:2a:602:A:H8	1.77	0.49
32:2a:1238:A:H2	32:2a:1241:G:N3	2.09	0.49
44:2m:20:THR:HA	44:2m:25:ILE:O	2.12	0.49
54:2w:145:LEU:HD21	54:2w:161:GLU:HB3	1.94	0.49
1:1A:271(E):U:H2’	1:1A:271(F):C:C6	2.48	0.49
1:1A:1210:A:H5”	1:1A:1212:G:O4’	2.12	0.49
1:1A:1274:A:N3	1:1A:1297:C:H1’	2.27	0.49
1:1A:1803:A:H4’	3:1D:259:THR:HG23	1.93	0.49
1:1A:2563:U:H4’	10:1O:28:SER:HA	1.94	0.49
23:11:44:PRO:HB2	23:11:46:LEU:HD13	1.93	0.49
37:1f:89:MET:HG2	37:1f:91:VAL:HG23	1.94	0.49
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.11	0.49
54:1w:213:ASN:O	54:1w:216:GLU:HG2	2.13	0.49
1:2A:2159:G:H2’	1:2A:2160:G:C8	2.47	0.49
1:2A:2245:U:O2’	1:2A:2436:G:OP2	2.25	0.49
1:2A:2405:G:H5’	11:2P:75:ILE:HD13	1.94	0.49
32:2a:1002:G:C2	32:2a:1003:G:H1’	2.47	0.49
32:2a:1260:C:P	32:2a:1284:C:H4’	2.52	0.49
32:2a:1399:C:H4’	32:2a:1400:5MC:H5”	1.94	0.49
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.78	0.49
40:2i:51:ARG:HG2	40:2i:56:LEU:HD21	1.94	0.49
42:2k:58:PRO:HA	42:2k:90:GLY:HA3	1.94	0.49
42:2k:65:ALA:HB1	42:2k:98:LEU:HD23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.94	0.49
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.95	0.49
32:1a:1049:U:C6	32:1a:1201:A:H5'	2.48	0.49
33:1b:21:ARG:HB2	33:1b:38:GLY:O	2.13	0.49
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.44	0.49
40:1i:5:TYR:H	40:1i:87:GLN:NE2	2.11	0.49
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.47	0.49
1:2A:2122:U:H2'	1:2A:2123:G:C8	2.47	0.49
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.11	0.49
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.43	0.49
3:2D:85:ASP:OD2	3:2D:88:ARG:HD2	2.13	0.49
24:22:3:LEU:O	24:22:7:ARG:HG3	2.13	0.49
32:2a:1130:A:H5'	40:2i:18:PHE:CZ	2.48	0.49
44:2m:23:TYR:CZ	44:2m:71:ARG:HG3	2.48	0.49
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.76	0.49
1:1A:428:A:H8	1:1A:428:A:OP2	1.96	0.49
1:1A:654:A:OP2	61:1A:4136:HOH:O	2.18	0.49
1:1A:2154:G:H2'	1:1A:2155:G:O4'	2.12	0.49
1:1A:2155:G:H3'	1:1A:2156:G:C8	2.47	0.49
32:1a:148:G:H2'	32:1a:149:A:H8	1.78	0.49
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.94	0.49
32:1a:1327:C:H2'	32:1a:1328:C:C6	2.48	0.49
1:2A:1592:C:H2'	1:2A:1593:G:H8	1.77	0.49
3:2D:112:GLN:O	3:2D:115:GLN:HG2	2.13	0.49
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.13	0.49
14:2S:26:LEU:HB2	14:2S:85:VAL:HG11	1.94	0.49
17:2V:74:LYS:HB2	17:2V:83:ARG:HB2	1.95	0.49
32:2a:373:A:H61	32:2a:391:G:H1'	1.77	0.49
32:2a:1038:C:H2'	32:2a:1039:C:C6	2.47	0.49
50:2s:31:ILE:O	50:2s:49:ILE:HG13	2.13	0.49
1:1A:1161:C:O2'	17:1V:8:GLY:HA2	2.12	0.49
1:1A:1805:U:O2	3:1D:50:THR:HB	2.13	0.49
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.94	0.49
32:1a:600:C:H2'	32:1a:601:C:C6	2.46	0.49
1:2A:234:C:H2'	1:2A:235:U:C6	2.47	0.49
1:2A:320:A:H4'	1:2A:322:A:C8	2.47	0.49
1:2A:1364:G:P	23:21:3:LYS:HG3	2.53	0.49
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.36	0.49
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.28	0.49
20:2Y:11:ASP:OD2	20:2Y:97:ARG:NH2	2.32	0.49
20:2Y:37:VAL:HG22	20:2Y:69:ALA:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.93	0.49
32:2a:64:G:H4'	32:2a:65:U:H3'	1.94	0.49
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.46	0.49
51:2t:10:LEU:HB3	51:2t:12:ALA:H	1.76	0.49
1:1A:484:C:H2'	1:1A:485:C:C6	2.48	0.49
1:1A:740:U:H2'	1:1A:741:G:C8	2.47	0.49
1:1A:1069:A:H2'	1:1A:1073:A:C8	2.47	0.49
1:1A:2703:C:H2'	1:1A:2704:C:H6	1.78	0.49
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.13	0.49
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.28	0.49
32:1a:397:A:H3'	32:1a:397:A:N3	2.27	0.49
32:1a:618:C:H5'	32:1a:619:U:H5"	1.95	0.49
35:1d:142:PRO:HB3	35:1d:187:ARG:HA	1.95	0.49
40:1i:32:ASP:OD1	40:1i:33:PHE:N	2.45	0.49
40:1i:111:ARG:O	40:1i:113:LYS:NZ	2.46	0.49
1:2A:657:U:H2'	1:2A:658:C:C6	2.47	0.49
1:2A:1356:G:OP2	61:2A:3949:HOH:O	2.20	0.49
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.13	0.49
1:2A:2138:C:H2'	1:2A:2139:C:O4'	2.13	0.49
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.77	0.49
6:2G:68:PRO:HB3	6:2G:92:VAL:HB	1.94	0.49
1:1A:1058:G:N2	1:1A:1081:U:O2	2.46	0.49
1:1A:1827:C:H2'	1:1A:1828:G:H5'	1.94	0.49
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	1.94	0.49
8:1I:123:LEU:HA	8:1I:144:VAL:HG23	1.95	0.49
32:1a:673:G:O3'	37:1f:87:ARG:NH2	2.46	0.49
32:1a:977:A:H1'	32:1a:982:U:O4	2.13	0.49
1:2A:116:C:H2'	1:2A:117:G:O4'	2.13	0.49
5:2F:67:GLN:NE2	61:2F:401:HOH:O	2.46	0.49
26:24:2:LYS:HB2	26:24:5:ILE:HD11	1.94	0.49
32:2a:921:U:H2'	32:2a:922:G:O4'	2.13	0.49
32:2a:1307:U:H2'	32:2a:1308:U:C6	2.48	0.49
34:2c:70:VAL:O	34:2c:106:VAL:N	2.34	0.49
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.46	0.49
37:2f:9:VAL:HA	37:2f:59:TYR:O	2.12	0.49
51:2t:82:SER:O	51:2t:86:ARG:HG3	2.12	0.49
1:1A:2304:G:H22	1:1A:2312:U:H3	1.60	0.48
8:1I:116:LEU:HD11	8:1I:120:ILE:HG12	1.95	0.48
32:1a:1029:C:N3	32:1a:1032:G:N2	2.59	0.48
35:1d:20:TYR:HA	35:1d:26:CYS:SG	2.52	0.48
38:1g:26:PHE:HE1	38:1g:104:LEU:HD23	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:729:G:C8	3:2D:208:LYS:HD2	2.48	0.48
1:2A:1022:G:N7	9:2N:66:LYS:HE2	2.28	0.48
32:2a:108:G:N1	51:2t:15:ARG:HG2	2.28	0.48
32:2a:977:A:O2'	32:2a:980:C:N4	2.47	0.48
32:2a:1111:A:N1	34:2c:177:THR:OG1	2.40	0.48
40:2i:20:ARG:O	40:2i:60:ASP:N	2.29	0.48
51:2t:9:ASN:OD1	51:2t:9:ASN:N	2.46	0.48
1:1A:272(J):C:H2'	1:1A:274:G:C8	2.47	0.48
4:1E:101:ARG:NH2	4:1E:171:GLU:HB2	2.27	0.48
6:1G:131:TYR:HE2	6:1G:133:LEU:HD23	1.78	0.48
32:1a:115:G:H4'	32:1a:116:A:O5'	2.12	0.48
32:1a:1218:C:OP2	45:1n:9:LYS:NZ	2.36	0.48
32:1a:1324:A:H4'	32:1a:1362:C:H4'	1.96	0.48
34:1c:20:SER:OG	34:1c:40:ARG:NH2	2.39	0.48
34:1c:57:ILE:HG12	34:1c:66:VAL:HG12	1.95	0.48
34:1c:91:LEU:HD22	34:1c:101:LEU:HD12	1.94	0.48
47:1p:37:GLY:HA3	47:1p:50:LYS:O	2.13	0.48
1:2A:2129:C:H42	1:2A:2159:G:H1	1.61	0.48
8:2I:129:THR:HG22	8:2I:139:GLN:HE22	1.78	0.48
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.77	0.48
32:2a:384:G:H2'	32:2a:385:C:C6	2.48	0.48
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.78	0.48
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.48	0.48
32:2a:1366:C:HO2'	41:2j:60:ARG:HH22	1.58	0.48
38:2g:16:LEU:HD12	40:2i:42:ARG:HA	1.96	0.48
40:2i:34:ASN:N	40:2i:34:ASN:OD1	2.46	0.48
41:2j:61:GLU:OE1	45:2n:49:HIS:NE2	2.40	0.48
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.95	0.48
44:2m:50:GLU:HA	44:2m:53:VAL:HB	1.94	0.48
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.13	0.48
54:2w:218:ARG:NH1	54:2w:220:ASP:OD2	2.45	0.48
3:1D:242:ARG:N	3:1D:242:ARG:HD3	2.29	0.48
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.94	0.48
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.27	0.48
17:1V:55:ALA:CB	17:1V:101:GLY:HA2	2.43	0.48
32:1a:1172:C:H2'	32:1a:1173:G:H8	1.77	0.48
34:1c:35:GLU:O	34:1c:39:ILE:HG13	2.14	0.48
1:2A:570:G:H2'	1:2A:2030:A:C5	2.47	0.48
1:2A:796:C:H2'	1:2A:797:C:C6	2.48	0.48
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.12	0.48
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:625:G:H4'	47:2p:16:HIS:CG	2.49	0.48
32:2a:937:A:OP2	61:2a:1806:HOH:O	2.20	0.48
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.35	0.48
34:2c:50:ALA:HB1	34:2c:70:VAL:HG11	1.95	0.48
41:2j:7:LYS:HE2	41:2j:9:ARG:HH11	1.78	0.48
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.94	0.48
1:1A:2166:G:H2'	1:1A:2167:U:H5	1.76	0.48
6:1G:73:ALA:HB2	6:1G:82:LEU:HD11	1.95	0.48
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.95	0.48
32:1a:334:C:H2'	32:1a:335:C:H6	1.78	0.48
32:1a:1270:C:H2'	32:1a:1271:G:H8	1.76	0.48
32:1a:1304:G:OP1	52:1u:2:GLY:N	2.45	0.48
39:1h:49:GLU:HG2	39:1h:62:TYR:HE2	1.77	0.48
41:1j:28:ARG:HA	41:1j:31:GLY:HA2	1.95	0.48
48:1q:88:TYR:HD2	48:1q:89:LEU:HD23	1.79	0.48
51:1t:57:ARG:NH1	51:1t:100:ILE:HD12	2.27	0.48
1:2A:483:A:O2'	20:2Y:59:GLY:N	2.46	0.48
1:2A:645:C:H5"	1:2A:646:A:OP2	2.13	0.48
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.42	0.48
1:2A:1494:A:H2'	1:2A:1495:A:C8	2.48	0.48
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.79	0.48
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.48	0.48
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.95	0.48
18:2W:6:ILE:HG22	18:2W:8:ARG:HG3	1.96	0.48
32:2a:1049:U:C6	32:2a:1201:A:H5'	2.49	0.48
34:2c:123:GLN:HB3	34:2c:128:PHE:HD2	1.76	0.48
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.13	0.48
2:1B:24:G:N7	2:1B:56:G:H2'	2.28	0.48
32:1a:1030(C):G:N7	32:1a:1031:G:N2	2.62	0.48
32:1a:1414:U:H2'	32:1a:1415:G:H8	1.79	0.48
34:1c:121:ALA:O	34:1c:124:ILE:HG12	2.13	0.48
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.96	0.48
42:1k:84:VAL:HG23	42:1k:110:ASP:HA	1.95	0.48
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.49	0.48
2:2B:14:U:H1'	2:2B:108:U:O2'	2.13	0.48
3:2D:211:ARG:HG2	3:2D:214:TRP:CE3	2.49	0.48
1:1A:185:U:H2'	1:1A:186:G:C8	2.49	0.48
1:1A:548:A:N6	17:1V:19:LYS:H	2.11	0.48
1:1A:1779:U:H2'	61:1A:4636:HOH:O	2.14	0.48
1:1A:1914:C:OP1	61:1A:4142:HOH:O	2.20	0.48
2:1B:106:G:H5'	21:1Z:31:ARG:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.94	0.48
32:1a:187:C:O2'	51:1t:89:ARG:HD3	2.14	0.48
34:1c:142:MET:HG3	34:1c:170:GLN:HB3	1.95	0.48
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.28	0.48
47:1p:74:LEU:HB2	47:1p:80:PHE:HE2	1.77	0.48
51:1t:47:GLY:N	51:1t:48:LYS:HB2	2.28	0.48
1:2A:784:A:H5'	1:2A:785:G:OP1	2.13	0.48
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.49	0.48
1:2A:2839:G:C5'	13:2R:46:GLY:HA2	2.43	0.48
4:2E:141:ILE:HD12	4:2E:150:VAL:HG21	1.95	0.48
32:2a:37:U:O2'	32:2a:547:A:N1	2.39	0.48
32:2a:187:C:O2'	51:2t:89:ARG:HD3	2.13	0.48
32:2a:457:C:H2'	32:2a:458:C:C6	2.47	0.48
32:2a:977:A:O2'	32:2a:979:C:OP2	2.30	0.48
32:2a:1038:C:H2'	32:2a:1039:C:H6	1.79	0.48
32:2a:1239:A:H62	32:2a:1299:A:N6	2.11	0.48
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.96	0.48
54:2w:134:PHE:CZ	54:2w:138:MET:HE2	2.48	0.48
1:1A:2124:G:H3'	1:1A:2125:G:C8	2.49	0.48
3:1D:70:TRP:CE2	3:1D:150:LYS:HD3	2.49	0.48
6:1G:43:LEU:O	6:1G:45:GLU:N	2.47	0.48
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.79	0.48
24:12:64:LEU:O	24:12:68:ARG:HG2	2.14	0.48
32:1a:447:G:O2'	32:1a:487:A:N6	2.41	0.48
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.49	0.48
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.38	0.48
40:1i:46:ALA:HB1	40:1i:77:ILE:HG22	1.95	0.48
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.48	0.48
1:2A:747:U:O2	1:2A:2014:A:H1'	2.13	0.48
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.28	0.48
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.31	0.48
11:2P:121:LYS:HE3	11:2P:123:LEU:HD11	1.95	0.48
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.95	0.48
32:2a:718:G:H5'	42:2k:117:ASN:CG	2.39	0.48
32:2a:1106:G:H5"	34:2c:172:ARG:HG2	1.96	0.48
33:2b:88:ALA:HB1	33:2b:222:ILE:HG21	1.94	0.48
1:1A:271(L):U:H4'	8:1I:50:ARG:NH2	2.29	0.48
1:1A:774:A:N3	1:1A:774:A:H2'	2.28	0.48
1:1A:1420:U:HO2'	1:1A:1421:G:P	2.36	0.48
6:1G:77:ILE:HG13	6:1G:82:LEU:HD23	1.94	0.48
6:1G:146:TYR:O	6:1G:149:VAL:HG12	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:29:LYS:HD2	9:1N:140:VAL:HB	1.96	0.48
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.29	0.48
32:1a:279:A:C5	48:1q:98:LEU:HD23	2.49	0.48
32:1a:434:U:H2'	32:1a:435:C:C6	2.48	0.48
32:1a:1072:G:H2'	32:1a:1073:U:C6	2.48	0.48
32:1a:1355:G:H2'	32:1a:1356:G:C8	2.49	0.48
54:1w:303:ARG:HD2	54:1w:305:TYR:OH	2.14	0.48
1:2A:468:G:OP2	29:27:37:LYS:NZ	2.43	0.48
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.96	0.48
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.48	0.48
12:2Q:31:ASP:HA	12:2Q:134:ARG:HH11	1.78	0.48
32:2a:717:C:H4'	42:2k:117:ASN:ND2	2.27	0.48
32:2a:1092:A:H5"	38:2g:4:ARG:NH1	2.28	0.48
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.14	0.48
36:2e:12:LEU:HD12	36:2e:128:PRO:HB2	1.95	0.48
39:2h:105:ARG:HD2	39:2h:105:ARG:HA	1.64	0.48
42:2k:21:ILE:HG12	42:2k:30:VAL:HG22	1.95	0.48
44:2m:106:ASN:HB3	44:2m:107:ALA:H	1.41	0.48
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.13	0.48
54:2w:105:ARG:HB3	54:2w:105:ARG:NH2	2.29	0.48
1:1A:222:A:H3'	1:1A:421:U:H5'	1.95	0.48
1:1A:1299:G:N7	61:1A:4227:HOH:O	2.35	0.48
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.24	0.48
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.14	0.48
1:1A:2627:G:O2'	1:1A:2781:A:N1	2.41	0.48
10:1O:86:ILE:HG22	10:1O:94:ARG:HD3	1.95	0.48
20:1Y:30:VAL:O	20:1Y:32:PRO:HD3	2.14	0.48
26:14:28:LYS:HB2	26:14:31:ILE:HD11	1.96	0.48
32:1a:230:G:O2'	47:1p:25:ARG:NH2	2.46	0.48
32:1a:736:C:H2'	32:1a:737:A:C8	2.48	0.48
32:1a:952:U:H2'	32:1a:953:G:C8	2.49	0.48
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.96	0.48
41:1j:81:THR:C	41:1j:83:GLU:H	2.20	0.48
48:1q:51:TYR:CE2	48:1q:73:VAL:HG21	2.49	0.48
54:1w:134:PHE:CE1	54:1w:138:MET:HE3	2.49	0.48
1:2A:588:U:H2'	1:2A:589:C:C6	2.49	0.48
6:2G:18:GLU:OE2	6:2G:21:ARG:NH2	2.36	0.48
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.96	0.48
10:2O:75:SER:OG	15:2T:74:ARG:NH2	2.47	0.48
32:2a:1265:G:C2	32:2a:1271:G:C2	3.01	0.48
44:2m:37:THR:O	44:2m:55:ARG:NH1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.13	0.48
3:1D:96:HIS:CD2	3:1D:102:LYS:HG2	2.49	0.48
32:1a:263:A:OP1	51:1t:79:ARG:NH1	2.46	0.48
32:1a:396:G:O2'	32:1a:398:C:OP1	2.28	0.48
32:1a:475:G:N3	32:1a:475:G:H2'	2.29	0.48
32:1a:553:A:H5"	43:1l:24:VAL:HG21	1.95	0.48
32:1a:708:C:OP1	42:1k:85:ARG:NH2	2.47	0.48
32:1a:767:A:H2'	32:1a:768:A:O4'	2.14	0.48
32:1a:859:A:H2'	32:1a:860:A:O4'	2.14	0.48
32:1a:1004:A:O2'	32:1a:1038:C:O2	2.17	0.48
32:1a:1288:A:H2'	32:1a:1289:A:C8	2.48	0.48
54:1w:299:SER:C	54:1w:301:LYS:H	2.20	0.48
7:2H:33:LEU:HD21	7:2H:136:ILE:HG13	1.96	0.48
10:2O:104:ARG:HH22	15:2T:43:GLN:HE22	1.61	0.48
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.49	0.48
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.13	0.48
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.14	0.48
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.96	0.48
38:2g:47:CYS:O	38:2g:50:ILE:HG22	2.14	0.48
41:2j:25:GLU:OE2	41:2j:29:ARG:NH1	2.47	0.48
20:1Y:6:HIS:HE1	20:1Y:72:VAL:O	1.97	0.47
21:1Z:152:ALA:O	21:1Z:155:LEU:HB2	2.14	0.47
32:1a:238:G:OP1	48:1q:25:ARG:NH2	2.47	0.47
32:1a:328:C:H4'	32:1a:329:A:H5'	1.95	0.47
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.95	0.47
1:2A:1756:G:H4'	1:2A:1758:G:O4'	2.14	0.47
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.49	0.47
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.95	0.47
8:2I:83:ALA:HB1	8:2I:87:LYS:O	2.14	0.47
21:2Z:129:SER:HB3	21:2Z:132:ASN:HD21	1.79	0.47
32:2a:130:A:H5'	48:2q:63:ARG:HD3	1.96	0.47
32:2a:134:A:N6	47:2p:25:ARG:HH12	2.11	0.47
32:2a:922:G:H1'	36:2e:19:MET:HB2	1.96	0.47
32:2a:1326:C:H5"	52:2u:12:LYS:HE2	1.97	0.47
1:1A:626:U:O4	11:1P:107:LYS:HE2	2.14	0.47
1:1A:796:C:H2'	1:1A:797:C:C6	2.49	0.47
1:1A:1179:C:H2'	1:1A:1180:C:H6	1.78	0.47
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.08	0.47
6:1G:120:LEU:HD22	6:1G:133:LEU:HD22	1.96	0.47
32:1a:107:G:H2'	32:1a:108:G:O4'	2.14	0.47
32:1a:997:U:H3	32:1a:1044:A:H61	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1358:U:OP1	45:1n:35:ARG:HG3	2.13	0.47
34:1c:53:ALA:HB2	34:1c:115:LEU:HD23	1.95	0.47
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.96	0.47
1:2A:614(B):G:H1'	5:2F:44:ARG:HD2	1.94	0.47
1:2A:2154:G:N7	1:2A:2156:G:N2	2.61	0.47
1:2A:2206:G:H3'	1:2A:2207:G:N7	2.27	0.47
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.49	0.47
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.42	0.47
2:2B:98:G:H3'	2:2B:99:G:H8	1.79	0.47
32:2a:148:G:H2'	32:2a:149:A:C8	2.48	0.47
32:2a:1163:C:H2'	32:2a:1164:G:H8	1.78	0.47
32:2a:1329:A:H5"	44:2m:26:GLY:N	2.29	0.47
36:2e:50:GLU:HG3	36:2e:52:PRO:HD2	1.96	0.47
54:2w:147:SER:HA	54:2w:158:VAL:HG12	1.95	0.47
1:1A:582:G:H2'	1:1A:583:G:C8	2.49	0.47
1:1A:1040:C:H2'	1:1A:1041:C:O4'	2.15	0.47
1:1A:2125:G:H21	1:1A:2173:A:H62	1.62	0.47
1:1A:2673:G:O2'	10:1O:26:LYS:NZ	2.47	0.47
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.49	0.47
32:1a:509:A:N3	32:1a:543:C:O2'	2.42	0.47
32:1a:1006:C:H2'	32:1a:1007:C:C6	2.49	0.47
32:1a:1034:G:H2'	32:1a:1035:A:O4'	2.15	0.47
32:1a:1068:G:N2	32:1a:1191:A:N3	2.51	0.47
44:1m:70:LEU:O	44:1m:74:VAL:HG22	2.14	0.47
50:1s:50:ALA:O	50:1s:57:HIS:ND1	2.35	0.47
1:2A:127:A:H5"	1:2A:128:C:C6	2.49	0.47
1:2A:748:G:O6	18:2W:90:ARG:NH1	2.48	0.47
1:2A:927:G:H2'	1:2A:928:G:O4'	2.14	0.47
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.29	0.47
1:2A:2788:C:O2'	1:2A:2809:A:N3	2.47	0.47
7:2H:127:GLU:C	7:2H:129:THR:H	2.22	0.47
9:2N:73:THR:HA	9:2N:83:LYS:O	2.14	0.47
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.14	0.47
22:20:43:THR:HG23	22:20:43:THR:O	2.15	0.47
24:22:38:GLN:HG2	24:22:43:GLN:O	2.15	0.47
32:2a:979:C:O2	45:2n:19:ARG:NE	2.37	0.47
32:2a:1010:G:C2	32:2a:1020:U:H1'	2.50	0.47
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.49	0.47
2:1B:42:C:O2	6:1G:93:THR:N	2.35	0.47
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.96	0.47
21:1Z:45:ASP:O	21:1Z:49:ARG:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:72:ARG:HD3	21:1Z:72:ARG:HA	1.52	0.47
32:1a:1008:C:H2'	32:1a:1009:G:O4'	2.14	0.47
35:1d:155:LEU:HD12	35:1d:158:ILE:HG12	1.96	0.47
1:2A:1027:A:C6	1:2A:1126:A:C4	3.03	0.47
1:2A:1187:G:H5"	17:2V:81:TYR:CE1	2.49	0.47
2:2B:13:A:O2'	2:2B:14:U:H3'	2.14	0.47
32:2a:453:A:H4'	47:2p:72:ARG:HG3	1.96	0.47
33:2b:103:THR:HG23	33:2b:176:GLU:HB3	1.95	0.47
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.31	0.47
44:2m:23:TYR:CE2	44:2m:71:ARG:HG3	2.50	0.47
44:2m:60:VAL:HG23	44:2m:64:TRP:CZ3	2.50	0.47
1:1A:1045:A:OP1	1:1A:1046:A:H3'	2.15	0.47
32:1a:193:C:H2'	32:1a:194:C:C6	2.49	0.47
32:1a:1005:A:N6	32:1a:1024:G:O2'	2.47	0.47
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.39	0.47
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.29	0.47
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.49	0.47
1:2A:2164:C:C4	1:2A:2165:G:H1'	2.50	0.47
1:2A:2758:A:C4	7:2H:67:LEU:HD21	2.50	0.47
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.15	0.47
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.14	0.47
32:2a:1129:C:OP2	40:2i:66:ARG:NH1	2.46	0.47
1:1A:2186:G:O2'	1:1A:2187:G:H5'	2.15	0.47
1:1A:2412:A:H2'	1:1A:2413:G:O4'	2.14	0.47
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.97	0.47
25:13:8:LEU:HG	25:13:31:LEU:HD12	1.97	0.47
26:14:26:SER:OG	26:14:27:THR:N	2.47	0.47
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.97	0.47
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.25	0.47
40:1i:11:LYS:C	40:1i:13:ALA:H	2.22	0.47
54:1w:125:ARG:HG3	54:1w:155:PHE:CE2	2.50	0.47
1:2A:586:A:H5'	5:2F:89:VAL:HG21	1.96	0.47
1:2A:639:U:H2'	1:2A:640:C:C6	2.50	0.47
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.50	0.47
14:2S:18:ILE:O	14:2S:21:THR:HG23	2.15	0.47
26:24:24:THR:OG1	26:24:25:TYR:N	2.42	0.47
32:2a:575:G:O2'	32:2a:821:G:H5'	2.15	0.47
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.15	0.47
32:2a:1320:C:H1'	50:2s:73:GLU:HG3	1.95	0.47
32:2a:1456:G:O6	51:2t:54:LYS:NZ	2.34	0.47
1:1A:570:G:O6	61:1A:4102:HOH:O	2.19	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.14	0.47
1:1A:2233:U:H2'	1:1A:2234:G:C8	2.49	0.47
4:1E:28:ALA:HB3	4:1E:93:VAL:CG1	2.44	0.47
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.97	0.47
16:1U:50:ARG:HH22	17:1V:72:VAL:HG22	1.79	0.47
22:10:43:THR:O	22:10:43:THR:HG23	2.15	0.47
26:14:58:ARG:HB2	50:1s:67:VAL:HB	1.96	0.47
32:1a:348:G:C2'	32:1a:349:A:H5'	2.45	0.47
32:1a:1226:C:H2'	44:1m:103:THR:HB	1.97	0.47
32:1a:1369:C:H2'	32:1a:1370:G:C8	2.50	0.47
33:1b:21:ARG:H	33:1b:21:ARG:HH21	1.61	0.47
33:1b:71:VAL:HG11	33:1b:97:TRP:HE1	1.79	0.47
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.48	0.47
34:1c:113:ALA:HB3	34:1c:114:PRO:HD3	1.97	0.47
36:1e:41:VAL:O	36:1e:66:MET:HA	2.15	0.47
38:1g:89:MET:HG3	38:1g:156:TRP:CZ2	2.50	0.47
38:1g:113:GLU:HB3	38:1g:118:VAL:HG13	1.96	0.47
51:1t:58:LYS:O	51:1t:62:LEU:HD12	2.15	0.47
1:2A:370:G:OP2	61:2A:3950:HOH:O	2.20	0.47
1:2A:1811:G:H2'	1:2A:1812:A:O4'	2.15	0.47
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.50	0.47
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.49	0.47
6:2G:33:ARG:NH2	6:2G:162:THR:HG21	2.30	0.47
11:2P:92:GLU:OE2	11:2P:121:LYS:NZ	2.48	0.47
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD11	1.96	0.47
26:24:15:ILE:HB	26:24:32:TYR:CD1	2.50	0.47
26:24:58:ARG:HG3	50:2s:65:ASN:HA	1.96	0.47
32:2a:266:G:H2'	32:2a:266:G:N3	2.29	0.47
32:2a:411:A:P	35:2d:30:LYS:HD3	2.54	0.47
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.50	0.47
32:2a:966:M2G:HM22	55:2x:34:G:H5'	1.95	0.47
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.50	0.47
33:2b:128:GLU:HA	33:2b:135:GLN:NE2	2.30	0.47
34:2c:19:GLU:HG2	34:2c:54:ARG:NE	2.30	0.47
34:2c:59:ARG:O	41:2j:92:THR:OG1	2.23	0.47
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.79	0.47
35:2d:12:CYS:SG	35:2d:19:LEU:N	2.73	0.47
38:2g:150:ALA:HA	42:2k:59:TYR:HB3	1.97	0.47
42:2k:99:GLN:HG2	42:2k:105:VAL:HG11	1.97	0.47
52:2u:10:ARG:HH11	52:2u:10:ARG:HG3	1.80	0.47
54:2w:103:ASP:HB3	54:2w:169:GLY:HA3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:180:VAL:HG23	54:2w:305:TYR:HB2	1.96	0.47
1:1A:857:C:H4'	22:10:23:VAL:HG21	1.97	0.47
1:1A:1812:A:O2'	3:1D:45:ASN:N	2.46	0.47
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.50	0.47
1:1A:2790:A:H5'	1:1A:2893:G:H21	1.79	0.47
2:1B:103:G:N2	21:1Z:73:GLN:HE22	2.08	0.47
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.48	0.47
15:1T:51:ARG:HG3	15:1T:98:LYS:HD2	1.97	0.47
26:14:60:GLN:H	26:14:60:GLN:HG2	1.40	0.47
32:1a:370:C:H2'	32:1a:371:G:C8	2.50	0.47
32:1a:947:G:C6	32:1a:948:C:C4	3.03	0.47
34:1c:32:LEU:O	34:1c:36:ASP:HB2	2.15	0.47
1:2A:770:G:OP2	61:2A:3954:HOH:O	2.21	0.47
1:2A:1652:A:N6	13:2R:11:ASN:OD1	2.44	0.47
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.78	0.47
5:2F:101:LEU:HD23	5:2F:106:ARG:HG2	1.96	0.47
36:2e:98:THR:HB	36:2e:117:ASP:HB3	1.97	0.47
37:2f:70:ASP:OD1	37:2f:70:ASP:N	2.45	0.47
46:2o:5:LYS:HB2	46:2o:5:LYS:HE2	1.68	0.47
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.15	0.47
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.42	0.47
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.97	0.47
21:1Z:51:ALA:HA	21:1Z:55:HIS:HD2	1.80	0.47
32:1a:129:U:H5'	48:1q:3:LYS:HZ1	1.80	0.47
32:1a:302:G:O2'	32:1a:556:C:H5"	2.15	0.47
32:1a:1187:G:H4'	40:1i:111:ARG:HH11	1.80	0.47
33:1b:28:PHE:CD1	33:1b:194:PRO:HG3	2.50	0.47
33:1b:51:LEU:HD21	33:1b:201:ILE:HG23	1.97	0.47
35:1d:177:ASP:O	35:1d:181:MET:N	2.38	0.47
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.48	0.47
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.15	0.47
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.50	0.47
1:2A:1710:C:H5'	1:2A:2859:G:H1'	1.97	0.47
1:2A:2712(A):A:OP2	61:2A:3920:HOH:O	2.20	0.47
32:2a:841:U:H6	32:2a:841:U:P	2.38	0.47
32:2a:921:U:O2'	36:2e:19:MET:O	2.33	0.47
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.29	0.47
1:1A:1179:C:H2'	1:1A:1180:C:C6	2.50	0.47
7:1H:22:GLY:HA2	7:1H:37:VAL:O	2.15	0.47
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.15	0.47
32:1a:1017:G:H2'	32:1a:1018:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1048:G:N2	32:1a:1214:C:O2	2.48	0.47
32:1a:1333:A:H3'	32:1a:1334:G:H8	1.80	0.47
36:1e:6:PHE:HB3	36:1e:34:VAL:HG13	1.96	0.47
36:1e:148:VAL:C	36:1e:152:ARG:HG2	2.40	0.47
37:1f:9:VAL:HB	37:1f:87:ARG:HB2	1.96	0.47
1:2A:646:A:H2'	1:2A:647:G:O4'	2.15	0.47
1:2A:2113:U:H3'	1:2A:2115:G:N2	2.30	0.47
1:2A:2507:C:H4'	54:2w:233:ASN:O	2.15	0.47
26:24:12:ALA:HB3	26:24:24:THR:HG23	1.96	0.47
32:2a:457:C:H2'	32:2a:458:C:H6	1.80	0.47
32:2a:952:U:H4'	32:2a:964:A:N1	2.30	0.47
32:2a:1517:G:H2'	32:2a:1518:MA6:H8	1.97	0.47
43:2l:31:PRO:HB2	43:2l:32:PHE:CD2	2.49	0.47
1:1A:71:A:H5"	1:1A:73:A:C8	2.49	0.46
1:1A:228:A:H8	1:1A:229:A:H5'	1.79	0.46
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.30	0.46
1:1A:1062:G:N3	1:1A:1062:G:H2'	2.29	0.46
1:1A:1082:U:C4	1:1A:1086:A:N1	2.80	0.46
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.30	0.46
6:1G:123:ASN:O	61:1G:301:HOH:O	2.21	0.46
14:1S:25:ARG:HD3	14:1S:42:ASP:OD1	2.15	0.46
23:11:80:LEU:HB3	23:11:82:LEU:HG	1.97	0.46
32:1a:216:G:H2'	32:1a:217:C:C6	2.50	0.46
32:1a:537:G:H5"	43:1l:113:ARG:HH12	1.80	0.46
32:1a:880:C:OP1	43:1l:8:ASN:ND2	2.47	0.46
32:1a:975:A:H5'	32:1a:975:A:H8	1.80	0.46
32:1a:1030:C:C4	32:1a:1030(A):G:H1'	2.49	0.46
39:1h:13:ILE:O	39:1h:17:THR:HG23	2.15	0.46
50:1s:63:THR:OG1	50:1s:66:MET:SD	2.63	0.46
51:1t:53:LEU:O	51:1t:57:ARG:HG3	2.15	0.46
1:2A:384:U:H2'	1:2A:385:C:H6	1.79	0.46
1:2A:476:G:H4'	1:2A:502:A:N1	2.29	0.46
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.50	0.46
1:2A:2116:G:N7	1:2A:2166:G:N1	2.62	0.46
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.49	0.46
25:23:8:LEU:O	25:23:32:GLN:N	2.40	0.46
33:2b:15:VAL:HA	33:2b:209:ARG:HH11	1.80	0.46
36:2e:78:HIS:HB3	39:2h:107:LEU:HD12	1.97	0.46
1:1A:264:C:O2'	1:1A:265:A:H2'	2.14	0.46
1:1A:1405:U:H2'	1:1A:1406:U:H6	1.80	0.46
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:107:LYS:HG3	5:1F:206:ILE:HA	1.98	0.46
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.65	0.46
32:1a:1053:G:O2'	32:1a:1199:U:OP2	2.27	0.46
34:1c:73:PRO:O	34:1c:77:ILE:HG12	2.16	0.46
38:1g:20:ASP:OD2	38:1g:63:LYS:NZ	2.44	0.46
40:1i:3:GLN:HG2	40:1i:20:ARG:NE	2.30	0.46
51:1t:40:ALA:HB2	51:1t:55:ILE:HG22	1.97	0.46
1:2A:1341:U:OP2	1:2A:1394:U:O2'	2.29	0.46
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.50	0.46
1:2A:2112:G:C6	1:2A:2113:U:H1'	2.50	0.46
1:2A:2207:G:C3'	1:2A:2208:A:H5"	2.45	0.46
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.15	0.46
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.15	0.46
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.96	0.46
21:2Z:100:VAL:HG11	21:2Z:134:PRO:HG2	1.97	0.46
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.47	0.46
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.30	0.46
34:2c:131:ARG:HD3	34:2c:166:GLU:OE2	2.15	0.46
37:2f:16:GLN:H	37:2f:16:GLN:CD	2.23	0.46
39:2h:38:ILE:HD12	39:2h:41:ARG:HH21	1.80	0.46
39:2h:51:VAL:HG21	39:2h:60:ARG:HB2	1.96	0.46
1:1A:1338:G:O2'	1:1A:1393:A:N1	2.37	0.46
8:1I:140:LEU:HD23	8:1I:140:LEU:HA	1.79	0.46
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	1.96	0.46
18:1W:62:HIS:O	18:1W:64:MET:HG3	2.15	0.46
32:1a:323:U:O3'	51:1t:22:ARG:HD3	2.14	0.46
32:1a:690:G:C6	32:1a:691:G:C6	3.04	0.46
32:1a:920:U:H2'	32:1a:921:U:C6	2.50	0.46
32:1a:1233:G:O2'	32:1a:1365:G:OP1	2.30	0.46
33:1b:101:MET:HG3	33:1b:108:ILE:HD12	1.97	0.46
35:1d:192:GLU:C	35:1d:194:LEU:H	2.21	0.46
36:1e:94:ALA:HB2	36:1e:119:LEU:HG	1.97	0.46
44:1m:78:ILE:HA	44:1m:81:LEU:HD12	1.97	0.46
44:1m:92:HIS:CE1	44:1m:98:VAL:HG21	2.50	0.46
1:2A:709:U:H2'	1:2A:710:G:C8	2.50	0.46
1:2A:996:A:O3'	16:2U:91:ASP:HB2	2.15	0.46
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.50	0.46
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.31	0.46
32:2a:532:A:N6	32:2a:1206:G:O2'	2.48	0.46
32:2a:974:A:P	45:2n:41:ARG:HH21	2.38	0.46
32:2a:1291:G:O2'	40:2i:38:GLN:O	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:119:GLU:HG3	33:2b:153:ARG:HH12	1.80	0.46
44:2m:59:TYR:CE1	44:2m:63:THR:HG21	2.49	0.46
1:1A:99:U:O4	20:1Y:8:LYS:NZ	2.41	0.46
1:1A:251:A:C5	1:1A:252:G:H1'	2.50	0.46
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.51	0.46
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.51	0.46
5:1F:181:LEU:O	5:1F:205:ARG:NH2	2.39	0.46
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.97	0.46
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.97	0.46
26:14:58:ARG:HG3	50:1s:67:VAL:HG23	1.97	0.46
32:1a:203:U:OP2	32:1a:203:U:H2'	2.15	0.46
32:1a:376:G:OP2	47:1p:67:THR:HG21	2.15	0.46
34:1c:119:ARG:HH12	34:1c:140:ARG:NE	2.12	0.46
38:1g:62:PHE:HA	38:1g:124:LEU:HD23	1.97	0.46
1:2A:27:G:N2	1:2A:512:G:H1'	2.30	0.46
1:2A:271(V):G:H2'	1:2A:271(W):G:O4'	2.16	0.46
1:2A:492:A:OP2	61:2A:3955:HOH:O	2.21	0.46
1:2A:784:A:N6	3:2D:229:VAL:HG11	2.30	0.46
1:2A:1024:G:OP2	61:2A:3953:HOH:O	2.21	0.46
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.81	0.46
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.44	0.46
1:2A:2365:G:O6	30:28:39:LYS:HE3	2.16	0.46
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.30	0.46
2:2B:104:U:H2'	2:2B:105:A:H5"	1.97	0.46
2:2B:119:G:H5'	2:2B:120:A:OP2	2.16	0.46
5:2F:28:ILE:HD13	5:2F:119:ARG:HH21	1.81	0.46
32:2a:109:A:C6	32:2a:326:G:C6	3.04	0.46
32:2a:662:G:H2'	32:2a:663:A:C8	2.51	0.46
32:2a:1312:G:H5'	50:2s:5:LEU:HD11	1.98	0.46
33:2b:81:VAL:O	33:2b:85:ALA:N	2.45	0.46
37:2f:22:GLU:OE2	37:2f:84:ASN:ND2	2.49	0.46
38:2g:65:ALA:O	38:2g:69:VAL:HG23	2.15	0.46
40:2i:97:LYS:HA	40:2i:102:LEU:HD22	1.97	0.46
1:1A:536:A:H2'	1:1A:537:C:C6	2.51	0.46
1:1A:652(S):C:H2'	1:1A:652(T):C:C6	2.51	0.46
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.97	0.46
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.50	0.46
1:1A:2146:C:H5"	1:1A:2147:G:C5	2.50	0.46
61:1A:4406:HOH:O	11:1P:37:GLY:HA3	2.15	0.46
2:1B:77:U:OP1	21:1Z:19:ARG:NH1	2.40	0.46
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.97	0.46
32:1a:389:A:C6	32:1a:390:C:H1'	2.51	0.46
32:1a:441:A:H3'	32:1a:442:C:H6	1.81	0.46
32:1a:499:A:H4'	32:1a:500:G:OP1	2.15	0.46
34:1c:193:TYR:HE1	34:1c:196:LEU:HD11	1.80	0.46
1:2A:299:A:N1	1:2A:322:A:O2'	2.37	0.46
1:2A:476:G:N1	1:2A:479:A:OP2	2.48	0.46
1:2A:2304:G:H22	1:2A:2312:U:H3	1.64	0.46
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.45	0.46
28:26:14:THR:OG1	28:26:48:VAL:HG13	2.15	0.46
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.80	0.46
32:2a:1257:U:H5'	32:2a:1258:G:H5'	1.98	0.46
32:2a:1390:U:H2'	32:2a:1391:U:C6	2.50	0.46
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	1.98	0.46
1:1A:2147:G:H3'	1:1A:2147:G:N3	2.31	0.46
2:1B:13:A:O2'	2:1B:14:U:H3'	2.16	0.46
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.16	0.46
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	1.98	0.46
32:1a:262:A:C6	32:1a:263:A:C6	3.04	0.46
32:1a:999:C:H2'	32:1a:1000:U:O4'	2.15	0.46
32:1a:1005:A:C2	32:1a:1025:U:H1'	2.50	0.46
35:1d:65:ARG:HD2	35:1d:72:GLU:HA	1.97	0.46
36:1e:96:PRO:HA	36:1e:117:ASP:OD2	2.16	0.46
37:1f:22:GLU:OE2	37:1f:82:ARG:NH2	2.40	0.46
43:1l:84:LEU:HB2	43:1l:105:TYR:CE2	2.51	0.46
1:2A:625:G:O6	11:2P:107:LYS:NZ	2.39	0.46
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.30	0.46
6:2G:36:LYS:HG2	6:2G:160:VAL:HB	1.96	0.46
7:2H:3:ARG:CZ	7:2H:5:GLY:H	2.29	0.46
24:22:63:VAL:O	24:22:67:LYS:HG2	2.16	0.46
32:2a:438:G:O2'	32:2a:494:U:O4	2.28	0.46
32:2a:1265:G:C6	32:2a:1266:G:C6	3.04	0.46
44:2m:91:ARG:HB2	44:2m:98:VAL:HG12	1.98	0.46
1:1A:27:G:N2	1:1A:512:G:H1'	2.31	0.46
1:1A:226:G:H21	1:1A:228:A:H62	1.62	0.46
1:1A:388:G:O2'	1:1A:389:G:N7	2.46	0.46
1:1A:2319:G:C2	14:1S:3:ARG:HA	2.51	0.46
5:1F:199:TRP:O	5:1F:203:GLN:HG2	2.15	0.46
32:1a:620:C:C2	35:1d:135:LEU:HG	2.51	0.46
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.63	0.46
1:2A:800:A:H8	1:2A:800:A:OP1	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2552:OMU:H2'	1:2A:2554:U:H5"	1.98	0.46
5:2F:188:ARG:HG2	11:2P:3:LEU:HD11	1.97	0.46
32:2a:165:C:H2'	32:2a:166:G:H8	1.80	0.46
32:2a:279:A:C5	48:2q:98:LEU:HD23	2.51	0.46
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.18	0.46
32:2a:1005:A:H3'	32:2a:1006:C:C6	2.50	0.46
32:2a:1265:G:C4	32:2a:1271:G:N2	2.84	0.46
44:2m:14:ARG:HB3	44:2m:41:PRO:O	2.16	0.46
48:2q:6:LEU:HD22	48:2q:23:VAL:HG11	1.98	0.46
1:1A:1005:C:H5"	61:1A:4148:HOH:O	2.16	0.46
1:1A:2312:U:OP1	6:1G:73:ALA:HA	2.16	0.46
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.29	0.46
6:1G:103:LEU:HD23	6:1G:106:LEU:HD23	1.96	0.46
9:1N:36:GLY:HA2	9:1N:38:HIS:CE1	2.51	0.46
10:1O:108:GLU:H	10:1O:108:GLU:HG2	1.52	0.46
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.30	0.46
32:1a:1064:G:H1'	32:1a:1190:G:N2	2.31	0.46
32:1a:1442:G:O2'	32:1a:1442(A):G:O5'	2.33	0.46
33:1b:30:ARG:HG3	33:1b:31:TYR:CD1	2.51	0.46
39:1h:2:LEU:HD23	39:1h:3:THR:N	2.30	0.46
1:2A:207:A:H2'	1:2A:208:C:O4'	2.16	0.46
1:2A:890:A:H2'	1:2A:892:G:C8	2.51	0.46
11:2P:98:GLU:O	11:2P:102:ARG:HD3	2.15	0.46
16:2U:108:GLU:O	16:2U:112:ARG:HG2	2.16	0.46
32:2a:1002:G:C6	32:2a:1003:G:H8	2.34	0.46
36:2e:43:LEU:H	36:2e:65:ASN:HD22	1.64	0.46
36:2e:68:GLU:OE1	36:2e:70:PRO:HG3	2.15	0.46
1:1A:185:U:H2'	1:1A:186:G:H8	1.81	0.46
1:1A:2151:G:H2'	1:1A:2152:G:C8	2.51	0.46
1:1A:2562:U:H4'	10:1O:25:LEU:HD21	1.97	0.46
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.15	0.46
7:1H:101:ARG:HH12	7:1H:122:THR:HG22	1.81	0.46
32:1a:1291:G:OP1	38:1g:41:ARG:NH2	2.49	0.46
33:1b:127:ILE:HG22	33:1b:130:ARG:N	2.29	0.46
1:2A:530:G:C5	1:2A:2022:U:H5"	2.51	0.46
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	1.98	0.46
8:2I:87:LYS:H	8:2I:87:LYS:HD3	1.81	0.46
32:2a:56:U:H2'	32:2a:57:G:H8	1.79	0.46
32:2a:1129:C:H42	32:2a:1143:G:H1	1.64	0.46
32:2a:1155:G:H2'	32:2a:1156:G:O4'	2.16	0.46
35:2d:8:VAL:HG13	35:2d:21:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:19:LEU:HD23	37:2f:23:LYS:HD2	1.98	0.46
1:1A:222:A:H5"	1:1A:421:U:OP1	2.16	0.46
21:1Z:146:ILE:N	21:1Z:148:ASP:H	2.13	0.46
32:1a:614:A:H2'	32:1a:615:C:C6	2.51	0.46
32:1a:1004:A:H62	32:1a:1036:G:N2	2.14	0.46
32:1a:1060:C:H5"	41:1j:51:ARG:HG2	1.98	0.46
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.51	0.46
32:1a:1426:C:H2'	32:1a:1427:U:H6	1.80	0.46
39:1h:96:GLY:N	39:1h:99:GLU:OE1	2.49	0.46
41:1j:81:THR:O	41:1j:83:GLU:N	2.50	0.46
44:1m:87:TYR:O	44:1m:91:ARG:HG3	2.15	0.46
48:1q:26:GLN:HG2	48:1q:37:LYS:HG2	1.98	0.46
1:2A:828:U:H4'	1:2A:831:G:N1	2.31	0.46
1:2A:1142:U:H5"	1:2A:1142(A):A:C8	2.51	0.46
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.51	0.46
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.48	0.46
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.16	0.46
8:2I:129:THR:HG22	8:2I:139:GLN:NE2	2.31	0.46
20:2Y:86:ARG:HD2	20:2Y:100:ALA:HA	1.96	0.46
32:2a:1162:C:H2'	32:2a:1163:C:C6	2.51	0.46
32:2a:1273:G:C6	32:2a:1274:G:C4	3.03	0.46
36:2e:11:ILE:HD11	36:2e:108:ALA:HB3	1.97	0.46
1:1A:652(C):G:N2	1:1A:653:A:H1'	2.31	0.45
1:1A:1557:C:H5"	1:1A:1558:A:OP2	2.16	0.45
1:1A:2160:G:N2	1:1A:2173:A:O2'	2.49	0.45
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.14	0.45
3:1D:38:LYS:HD2	3:1D:38:LYS:HA	1.71	0.45
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.98	0.45
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.16	0.45
32:1a:109:A:H2'	32:1a:326:G:N2	2.31	0.45
32:1a:383:A:C5	32:1a:384:G:H1'	2.50	0.45
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.32	0.45
33:1b:133:LYS:O	33:1b:136:VAL:HG22	2.16	0.45
47:1p:18:ARG:NH1	47:1p:32:TYR:OH	2.49	0.45
48:1q:86:GLU:O	48:1q:90:ILE:HG13	2.16	0.45
1:2A:1582:C:O2'	1:2A:1586:A:N3	2.47	0.45
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	1.98	0.45
3:2D:71:ASP:CB	3:2D:103:ARG:HH12	2.29	0.45
3:2D:211:ARG:O	3:2D:215:LEU:HG	2.16	0.45
6:2G:124:SER:HB2	6:2G:131:TYR:CE1	2.51	0.45
11:2P:65:ARG:HD2	30:28:25:MET:SD	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:132:VAL:HB	21:2Z:81:ARG:NH2	2.31	0.45
32:2a:526:C:OP2	43:2l:91:LYS:HE3	2.16	0.45
32:2a:688:G:H5'	42:2k:46:GLY:C	2.41	0.45
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.78	0.45
33:2b:97:TRP:HZ2	33:2b:102:LEU:HD13	1.81	0.45
43:2l:119:LYS:C	43:2l:121:GLY:H	2.24	0.45
44:2m:49:THR:O	44:2m:52:GLU:N	2.34	0.45
46:2o:4:THR:OG1	46:2o:7:GLU:HG3	2.16	0.45
50:2s:33:THR:HG21	50:2s:49:ILE:HD11	1.98	0.45
1:1A:305:U:H2'	1:1A:306:U:C6	2.51	0.45
1:1A:414:C:H2'	1:1A:415:A:C8	2.51	0.45
1:1A:657:U:H2'	1:1A:658:C:C6	2.52	0.45
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.32	0.45
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.52	0.45
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.52	0.45
11:1P:126:VAL:HG12	11:1P:148:LEU:HD13	1.98	0.45
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.51	0.45
32:1a:175:C:H2'	32:1a:176:C:H6	1.82	0.45
32:1a:626:U:C2	32:1a:627:G:C8	3.04	0.45
33:1b:134:GLU:HA	33:1b:137:ARG:HD3	1.98	0.45
39:1h:124:ALA:O	39:1h:128:GLY:N	2.49	0.45
55:1x:43:U:H2'	55:1x:44:C:C6	2.51	0.45
1:2A:602:G:O2'	1:2A:655:A:N6	2.49	0.45
15:2T:122:ASP:OD2	32:2a:1442(A):G:O2'	2.31	0.45
32:2a:160:A:H2'	32:2a:161:A:O4'	2.16	0.45
32:2a:646:U:H2'	32:2a:647:C:C6	2.51	0.45
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.52	0.45
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.16	0.45
51:2t:67:ALA:HA	51:2t:72:LEU:O	2.16	0.45
54:2w:210:PHE:HD1	54:2w:277:LYS:HD3	1.81	0.45
1:1A:548:A:H1'	1:1A:549:G:OP1	2.15	0.45
1:1A:826:U:H4'	11:1P:55:ARG:HB3	1.97	0.45
1:1A:1508:A:O2'	1:1A:1509:C:OP1	2.28	0.45
1:1A:1769:G:O2'	1:1A:1958:C:OP1	2.24	0.45
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.31	0.45
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.51	0.45
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.16	0.45
6:1G:125:PHE:N	61:1G:301:HOH:O	2.50	0.45
13:1R:71:GLN:NE2	61:1R:302:HOH:O	2.48	0.45
14:1S:39:ILE:HD11	14:1S:73:LEU:HD21	1.98	0.45
14:1S:61:ASN:ND2	14:1S:63:THR:HB	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:49:PHE:HB3	26:14:50:VAL:H	1.60	0.45
28:16:10:LEU:HB2	28:16:52:VAL:HG12	1.99	0.45
32:1a:1343:G:H4'	40:1i:122:ALA:HB3	1.97	0.45
33:1b:162:ILE:HD11	33:1b:184:VAL:HG13	1.98	0.45
37:1f:67:MET:HG3	37:1f:68:PRO:HD2	1.99	0.45
1:2A:506:G:O3'	1:2A:507:A:H8	1.99	0.45
1:2A:824:A:H1'	1:2A:2358:G:N7	2.31	0.45
8:2I:40:THR:HG23	8:2I:43:ASN:OD1	2.17	0.45
32:2a:583:A:H2'	32:2a:584:G:O4'	2.15	0.45
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.31	0.45
1:1A:483:A:O2'	20:1Y:49:VAL:O	2.31	0.45
14:1S:61:ASN:ND2	14:1S:64:GLU:HG3	2.31	0.45
18:1W:45:TYR:CZ	18:1W:49:LYS:HE3	2.52	0.45
32:1a:406:G:N2	35:1d:119:GLN:HE22	2.14	0.45
32:1a:652:U:O4	32:1a:752:G:O2'	2.27	0.45
32:1a:1140:C:H2'	32:1a:1141:C:H6	1.82	0.45
47:1p:9:PHE:HB2	47:1p:16:HIS:O	2.16	0.45
1:2A:571:A:N6	1:2A:2499:C:O3'	2.49	0.45
1:2A:652:C:C2'	1:2A:652(A):A:H5'	2.46	0.45
1:2A:667:U:O2	30:28:2:PRO:HD2	2.17	0.45
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.32	0.45
1:2A:2110:G:O2'	1:2A:2120:G:O5'	2.34	0.45
1:2A:2128:C:H4'	1:2A:2174:C:H4'	1.98	0.45
1:2A:2135:A:H2'	1:2A:2136:C:H5"	1.98	0.45
1:2A:2303:G:O2'	6:2G:132:ASN:HB2	2.17	0.45
1:2A:2626:C:H2'	1:2A:2627:G:O4'	2.16	0.45
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.51	0.45
21:2Z:3:TYR:CD2	21:2Z:51:ALA:HB2	2.51	0.45
21:2Z:128:VAL:HB	21:2Z:161:VAL:HG12	1.98	0.45
32:2a:352:C:OP2	61:2a:1807:HOH:O	2.21	0.45
32:2a:707:C:H2'	32:2a:708:C:C6	2.51	0.45
1:1A:125:G:O2'	29:17:48:LYS:HE3	2.17	0.45
1:1A:1876:A:H2'	1:1A:1877:A:C8	2.52	0.45
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.51	0.45
32:1a:114:U:O2'	32:1a:115:G:H5'	2.17	0.45
32:1a:444:C:H2'	32:1a:445:G:C8	2.52	0.45
32:1a:453:A:C5	32:1a:454:C:C4	3.04	0.45
32:1a:890:G:O2'	32:1a:906:G:O6	2.24	0.45
32:1a:1051:C:H2'	32:1a:1052:U:C6	2.52	0.45
32:1a:1258:G:H2'	32:1a:1259:C:C6	2.51	0.45
32:1a:1412:C:H2'	32:1a:1413:A:H8	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:8:VAL:HA	35:1d:11:LEU:HD13	1.99	0.45
36:1e:88:LYS:HB3	36:1e:123:LEU:HB2	1.99	0.45
41:1j:50:ILE:HD11	41:1j:57:LYS:HD3	1.98	0.45
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.99	0.45
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.51	0.45
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.99	0.45
6:2G:103:LEU:HD22	6:2G:178:PHE:HZ	1.82	0.45
26:24:14:ILE:HA	26:24:31:ILE:O	2.17	0.45
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.52	0.45
32:2a:1263:C:C4	32:2a:1272:G:O6	2.69	0.45
33:2b:28:PHE:CD1	33:2b:194:PRO:HG3	2.51	0.45
54:2w:278:ARG:HA	54:2w:281:GLU:HG2	1.99	0.45
1:1A:234:C:H2'	1:1A:235:U:C6	2.52	0.45
1:1A:479:A:N3	1:1A:481:G:H5"	2.31	0.45
1:1A:548:A:H61	17:1V:19:LYS:H	1.64	0.45
1:1A:1115:G:H2'	1:1A:1116:C:O4'	2.16	0.45
1:1A:2167:U:H3	1:1A:2171:A:H62	1.63	0.45
22:10:49:LYS:HG2	22:10:50:ASN:ND2	2.32	0.45
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.99	0.45
32:1a:414:A:H2'	32:1a:415:A:C8	2.52	0.45
32:1a:1112:C:H1'	34:1c:179:ARG:HH11	1.80	0.45
32:1a:1226:C:P	44:1m:91:ARG:HH22	2.39	0.45
33:1b:81:VAL:HG12	33:1b:215:LEU:HD21	1.98	0.45
39:1h:94:TYR:CE1	39:1h:132:GLU:HB2	2.52	0.45
47:1p:28:ARG:HG3	47:1p:29:ASP:N	2.31	0.45
54:1w:182:ARG:O	54:1w:184:PRO:HD3	2.17	0.45
1:2A:197:A:N6	1:2A:2430:A:O2'	2.48	0.45
1:2A:848:G:OP1	61:2A:3952:HOH:O	2.20	0.45
1:2A:959:A:N3	1:2A:2457:U:O2'	2.40	0.45
1:2A:1011:G:OP1	16:2U:77:SER:OG	2.34	0.45
3:2D:146:GLU:HG2	3:2D:152:GLY:C	2.42	0.45
12:2Q:18:LYS:O	12:2Q:98:LYS:NZ	2.20	0.45
14:2S:28:VAL:HG11	14:2S:98:VAL:HG13	1.99	0.45
21:2Z:30:ASN:HA	21:2Z:89:PHE:CE1	2.51	0.45
32:2a:20:U:H2'	32:2a:21:G:O4'	2.15	0.45
32:2a:358:U:H2'	32:2a:359:U:C6	2.51	0.45
32:2a:407:G:H2'	32:2a:408:A:C8	2.51	0.45
32:2a:653:A:O4'	39:2h:56:LYS:HE2	2.17	0.45
32:2a:683:G:H2'	32:2a:684:A:C8	2.51	0.45
32:2a:1046:A:H3'	32:2a:1047:G:H8	1.81	0.45
34:2c:121:ALA:HB1	34:2c:189:ALA:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:36:ARG:NH2	37:2f:38:GLU:OE2	2.48	0.45
51:2t:42:GLN:O	51:2t:45:GLN:HB3	2.17	0.45
1:1A:213:A:H2'	1:1A:214:G:O4'	2.17	0.45
1:1A:583:G:OP2	16:1U:10:ARG:NH1	2.45	0.45
1:1A:668:G:H5'	1:1A:669:G:OP2	2.16	0.45
1:1A:1412:A:H2'	1:1A:1413:G:C8	2.51	0.45
1:1A:1802:A:N1	1:1A:1822:G:H1'	2.32	0.45
1:1A:2104:G:H1	1:1A:2185:C:H42	1.65	0.45
1:1A:2143:C:H2'	1:1A:2144:U:C4'	2.47	0.45
3:1D:16:MET:HE3	3:1D:16:MET:HB2	1.83	0.45
19:1X:84:ALA:HB3	19:1X:87:GLN:CD	2.42	0.45
26:14:24:THR:OG1	26:14:25:TYR:N	2.50	0.45
32:1a:1309:G:OP1	44:1m:92:HIS:HE1	2.00	0.45
43:1l:53:ARG:CB	43:1l:93:LEU:HD11	2.47	0.45
43:1l:79:GLU:HG2	43:1l:80:HIS:CD2	2.51	0.45
50:1s:23:ASN:HA	50:1s:27:GLU:OE1	2.17	0.45
54:1w:162:VAL:HG11	54:1w:171:PHE:CE1	2.51	0.45
1:2A:307:G:H21	1:2A:330:A:N6	2.14	0.45
1:2A:340:A:H2'	1:2A:341:G:O4'	2.17	0.45
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.16	0.45
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.51	0.45
1:2A:1359:A:C2	1:2A:1372:U:O4	2.70	0.45
1:2A:2305:A:H2'	1:2A:2306:C:O4'	2.17	0.45
4:2E:5:LEU:HD21	4:2E:79:ARG:HB2	1.98	0.45
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.16	0.45
12:2Q:72:LYS:HB3	12:2Q:94:VAL:HG22	1.97	0.45
20:2Y:49:VAL:HG21	20:2Y:61:ILE:HG23	1.99	0.45
32:2a:109:A:H2'	32:2a:326:G:N2	2.31	0.45
32:2a:118:U:H3'	32:2a:288:A:H61	1.82	0.45
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.52	0.45
32:2a:824:C:H2'	32:2a:825:G:C8	2.52	0.45
32:2a:1267:C:O2	52:2u:20:LYS:HE3	2.16	0.45
33:2b:122:PHE:HD2	33:2b:142:LEU:HD13	1.82	0.45
34:2c:52:LEU:HD23	34:2c:53:ALA:N	2.31	0.45
10:1O:67:LYS:NZ	10:1O:68:GLU:OE2	2.49	0.45
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.51	0.45
32:1a:441:A:H3'	32:1a:442:C:C6	2.51	0.45
32:1a:565:U:H3'	32:1a:566:G:H2'	1.99	0.45
32:1a:1021:G:O2'	32:1a:1022:G:OP2	2.29	0.45
35:1d:9:CYS:O	35:1d:13:ARG:HG3	2.17	0.45
35:1d:158:ILE:O	35:1d:162:LEU:HG	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:39:GLY:O	36:1e:40:ARG:HD2	2.16	0.45
42:1k:109:VAL:HG22	49:1r:86:VAL:HG22	1.99	0.45
43:1l:88:GLY:O	43:1l:99:HIS:HD2	2.00	0.45
1:2A:1359:A:H2	1:2A:1372:U:O4	2.00	0.45
1:2A:1422:G:H1'	1:2A:1496:A:N1	2.31	0.45
1:2A:2390:U:P	30:28:35:GLN:HE22	2.40	0.45
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.52	0.45
1:2A:2680:C:H5'	4:2E:189:PRO:HA	1.99	0.45
3:2D:147:LEU:HD13	3:2D:155:LEU:HD21	1.99	0.45
8:2I:87:LYS:HE2	8:2I:87:LYS:HB2	1.68	0.45
9:2N:14:VAL:HG11	9:2N:138:LEU:HD12	1.98	0.45
32:2a:57:G:H2'	32:2a:58:C:O4'	2.16	0.45
32:2a:131:C:H2'	32:2a:132:C:C6	2.52	0.45
33:2b:97:TRP:HH2	33:2b:176:GLU:CD	2.25	0.45
37:2f:10:LEU:HD23	37:2f:85:VAL:HA	1.98	0.45
49:2r:40:LEU:HB3	49:2r:79:LEU:HD11	1.98	0.45
54:2w:302:ILE:HD12	54:2w:302:ILE:HA	1.76	0.45
55:2x:42:G:H2'	55:2x:43:U:O4'	2.17	0.45
1:1A:284:U:H2'	1:1A:285:C:C6	2.52	0.45
1:1A:1039:G:H1	1:1A:1116:C:N4	2.15	0.45
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.98	0.45
1:1A:2583:G:H2'	1:1A:2584:U:O4'	2.16	0.45
2:1B:2:C:H2'	2:1B:3:C:C6	2.52	0.45
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.98	0.45
13:1R:118:GLU:H	13:1R:118:GLU:CD	2.24	0.45
32:1a:271:C:H2'	32:1a:272:C:C6	2.52	0.45
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.17	0.45
35:1d:108:LEU:HB3	35:1d:110:PHE:CE1	2.51	0.45
40:1i:23:ASN:ND2	40:1i:25:LYS:HG2	2.32	0.45
47:1p:3:LYS:HD2	47:1p:24:ALA:HB2	1.97	0.45
54:1w:299:SER:C	54:1w:301:LYS:N	2.72	0.45
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.81	0.45
1:2A:848:G:H2'	1:2A:849:A:C8	2.52	0.45
1:2A:884:C:H2'	1:2A:885:C:O4'	2.17	0.45
1:2A:908:C:OP1	12:2Q:22:LYS:HE2	2.17	0.45
1:2A:1263:U:C4	1:2A:1264:G:C6	3.05	0.45
1:2A:2126:A:H4'	1:2A:2127:G:OP1	2.15	0.45
1:2A:2169:A:H2'	1:2A:2170:A:C8	2.51	0.45
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.32	0.45
1:2A:2391:G:O2'	1:2A:2422:A:N7	2.50	0.45
32:2a:335:C:H2'	32:2a:336:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:685:G:C2	32:2a:686:U:C4	3.05	0.45
32:2a:1429:C:H2'	32:2a:1430:C:C6	2.52	0.45
1:1A:93:G:H2'	1:1A:94:C:H6	1.82	0.45
1:1A:1176:G:H21	1:1A:1178:C:P	2.40	0.45
1:1A:2164:C:N4	1:1A:2166:G:H22	2.15	0.45
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.34	0.45
6:1G:105:LYS:NZ	26:14:25:TYR:O	2.38	0.45
27:15:42:PRO:HB2	27:15:43:HIS:ND1	2.32	0.45
32:1a:99:U:H2'	32:1a:100:C:C6	2.52	0.45
32:1a:1037:C:H2'	32:1a:1038:C:C6	2.52	0.45
32:1a:1309:G:P	44:1m:88:ARG:HH21	2.40	0.45
33:1b:223:ILE:HG12	33:1b:223:ILE:H	1.47	0.45
39:1h:49:GLU:O	39:1h:51:VAL:HG23	2.16	0.45
39:1h:51:VAL:HG12	39:1h:52:ASP:N	2.32	0.45
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.17	0.45
1:2A:2888:C:H2'	1:2A:2889:C:H6	1.82	0.45
15:2T:45:PHE:CZ	15:2T:74:ARG:HG3	2.52	0.45
25:23:7:LYS:HE3	25:23:32:GLN:HE21	1.81	0.45
32:2a:735:C:OP1	49:2r:68:LYS:NZ	2.49	0.45
32:2a:1049:U:C5	32:2a:1201:A:H5'	2.52	0.45
32:2a:1298:C:N4	38:2g:114:ARG:HB3	2.32	0.45
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.32	0.45
42:2k:21:ILE:HD12	42:2k:95:ILE:HG13	1.99	0.45
43:2l:42:THR:HA	43:2l:53:ARG:O	2.16	0.45
44:2m:10:PRO:HG3	44:2m:21:TYR:CD2	2.52	0.45
44:2m:23:TYR:CD2	44:2m:67:GLU:HA	2.52	0.45
54:2w:171:PHE:O	54:2w:201:VAL:HG21	2.16	0.45
54:2w:173:TYR:O	54:2w:316:ARG:NH2	2.50	0.45
55:2x:48:G:H3'	61:2x:201:HOH:O	2.16	0.45
1:1A:288:C:H2'	1:1A:289:A:C8	2.52	0.44
1:1A:2298:A:H2'	1:1A:2299:G:O4'	2.18	0.44
61:1A:4785:HOH:O	5:1F:70:THR:HG23	2.16	0.44
7:1H:3:ARG:HD2	7:1H:3:ARG:HA	1.78	0.44
14:1S:6:ALA:O	14:1S:10:ARG:HD3	2.16	0.44
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.51	0.44
18:1W:2:GLU:OE2	18:1W:72:LYS:NZ	2.31	0.44
23:11:67:ILE:N	23:11:68:PRO:HD2	2.32	0.44
26:14:44:THR:O	26:14:47:GLN:HB2	2.17	0.44
32:1a:956:U:P	54:1w:133:ARG:HH22	2.40	0.44
32:1a:1260:C:O5'	32:1a:1284:C:H4'	2.17	0.44
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:32:ARG:HH21	38:1g:109:ASN:HD21	1.65	0.44
44:1m:75:ALA:HA	44:1m:78:ILE:HD11	1.99	0.44
44:1m:84:ILE:HG13	50:1s:74:PHE:HE1	1.82	0.44
47:1p:7:ALA:HB3	47:1p:18:ARG:HB2	1.99	0.44
54:1w:110:GLU:HG2	54:1w:159:VAL:HG22	1.99	0.44
1:2A:306:U:H2'	1:2A:307:G:O4'	2.17	0.44
1:2A:903:C:H2'	1:2A:904:C:H6	1.82	0.44
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.16	0.44
1:2A:2163:C:H2'	1:2A:2164:C:H5'	1.99	0.44
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.52	0.44
2:2B:48:A:H4'	14:2S:95:HIS:CD2	2.52	0.44
6:2G:79:ASN:H	6:2G:79:ASN:HD22	1.65	0.44
7:2H:8:PRO:O	7:2H:10:PRO:HD3	2.16	0.44
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.72	0.44
32:2a:599:C:H5"	39:2h:95:VAL:O	2.18	0.44
32:2a:715:A:H2'	32:2a:716:A:C8	2.52	0.44
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.33	0.44
32:2a:973:G:H3'	32:2a:974:A:H5"	1.99	0.44
35:2d:128:VAL:HG12	35:2d:129:ASN:HD22	1.82	0.44
35:2d:150:GLU:C	35:2d:152:SER:H	2.25	0.44
1:1A:818:G:H4'	1:1A:838:C:O3'	2.16	0.44
1:1A:1039:G:H1	1:1A:1116:C:H42	1.63	0.44
1:1A:2115:G:H1'	1:1A:2171:A:H61	1.82	0.44
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.52	0.44
14:1S:71:ARG:NH1	14:1S:107:GLU:OE1	2.48	0.44
15:1T:96:ARG:HB3	15:1T:96:ARG:CZ	2.47	0.44
32:1a:838:G:N2	32:1a:849:C:C2	2.86	0.44
34:1c:19:GLU:HA	34:1c:54:ARG:HH21	1.82	0.44
47:1p:5:ARG:HE	47:1p:22:THR:HG23	1.82	0.44
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.18	0.44
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.31	0.44
26:24:53:GLU:H	26:24:53:GLU:HG3	1.49	0.44
27:25:41:PRO:O	27:25:44:THR:OG1	2.23	0.44
32:2a:41:G:H2'	32:2a:42:G:C8	2.52	0.44
32:2a:421:U:H3'	32:2a:422:C:H6	1.83	0.44
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.53	0.44
32:2a:1313:U:P	50:2s:5:LEU:HD12	2.57	0.44
50:2s:52:TYR:HD1	50:2s:57:HIS:CD2	2.36	0.44
1:1A:142(A):C:H2'	1:1A:143:G:O4'	2.17	0.44
1:1A:604:G:OP2	11:1P:90:ARG:NH1	2.50	0.44
1:1A:724:U:H2'	1:1A:725:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1920:OMC:HM22	1:1A:1921:G:O4'	2.17	0.44
1:1A:2590:A:H2'	1:1A:2591:C:C6	2.52	0.44
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.52	0.44
4:1E:181:LEU:HD21	15:1T:6:LEU:HD12	1.99	0.44
11:1P:121:LYS:O	11:1P:123:LEU:N	2.50	0.44
14:1S:81:GLY:O	14:1S:83:LYS:HD2	2.18	0.44
15:1T:8:LYS:HE3	15:1T:8:LYS:HB3	1.78	0.44
32:1a:190:U:H2'	32:1a:191:G:C8	2.52	0.44
32:1a:349:A:H2'	32:1a:350:G:H5"	1.98	0.44
32:1a:580:U:H2'	32:1a:581:G:O4'	2.17	0.44
32:1a:1010:G:H2'	32:1a:1011:G:O4'	2.16	0.44
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.17	0.44
32:1a:1284:C:H3'	32:1a:1285:A:H8	1.83	0.44
33:1b:21:ARG:O	33:1b:23:ARG:N	2.44	0.44
51:1t:29:LYS:O	51:1t:33:ILE:HG13	2.16	0.44
1:2A:218:A:C2	1:2A:235:U:H4'	2.52	0.44
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.83	0.44
1:2A:1815:A:H8	1:2A:1815:A:OP1	2.01	0.44
1:2A:1818:U:O4	3:2D:154:LYS:HD2	2.17	0.44
1:2A:2330:G:H2'	1:2A:2331:G:O4'	2.16	0.44
6:2G:41:GLN:O	6:2G:43:LEU:HD22	2.16	0.44
25:23:6:VAL:HG13	25:23:56:VAL:HG22	1.99	0.44
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.99	0.44
32:2a:509:A:H2'	32:2a:510:A:C8	2.52	0.44
32:2a:530:G:O2'	54:2w:181:GLN:NE2	2.50	0.44
32:2a:985:C:H2'	32:2a:986:A:C8	2.53	0.44
33:2b:188:ALA:HB1	33:2b:192:SER:HB2	2.00	0.44
36:2e:76:ILE:HD13	36:2e:118:ILE:HD11	1.98	0.44
36:2e:146:ALA:O	36:2e:150:ARG:HG2	2.17	0.44
37:2f:89:MET:HG2	37:2f:91:VAL:HG23	1.98	0.44
54:2w:303:ARG:HD2	54:2w:305:TYR:OH	2.17	0.44
1:1A:207:A:H2'	1:1A:208:C:O4'	2.16	0.44
1:1A:900:A:H2'	1:1A:901:A:O4'	2.17	0.44
1:1A:1071:G:H2'	1:1A:1072:C:C6	2.52	0.44
1:1A:1424:G:H2'	1:1A:1425:G:O4'	2.17	0.44
1:1A:1851:U:H2'	1:1A:1852:C:O4'	2.17	0.44
1:1A:1889:A:N1	1:1A:2234:G:H1'	2.32	0.44
1:1A:2106:G:H2'	1:1A:2107:C:C6	2.53	0.44
1:1A:2355:C:H1'	22:10:39:ARG:HH21	1.83	0.44
5:1F:195:ASP:HB2	5:1F:198:ALA:H	1.83	0.44
8:1I:95:LYS:NZ	8:1I:99:GLU:OE2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:56:VAL:O	26:14:60:GLN:HG3	2.17	0.44
32:1a:67:C:H2'	32:1a:68:G:C8	2.53	0.44
32:1a:598:U:H2'	32:1a:599:C:H6	1.83	0.44
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.53	0.44
34:1c:190:ARG:H	34:1c:190:ARG:HG3	1.57	0.44
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.42	0.44
42:1k:91:ARG:NH2	49:1r:87:ARG:HH21	2.15	0.44
1:2A:876:C:H2'	1:2A:877:U:O4'	2.18	0.44
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.53	0.44
1:2A:1812:A:H5"	61:2A:3912:HOH:O	2.17	0.44
1:2A:2786:U:O2'	4:2E:62:PRO:O	2.28	0.44
3:2D:166:GLN:HB2	3:2D:174:ILE:HG22	2.00	0.44
7:2H:6:ARG:HG3	7:2H:65:HIS:HE1	1.81	0.44
32:2a:399:G:H2'	32:2a:400:C:C6	2.53	0.44
32:2a:757:U:H2'	32:2a:758:G:O4'	2.16	0.44
32:2a:953:G:H5'	32:2a:965:A:N6	2.26	0.44
32:2a:975:A:H5'	32:2a:975:A:C8	2.53	0.44
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.52	0.44
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.99	0.44
34:2c:29:TYR:OH	45:2n:54:PRO:O	2.36	0.44
39:2h:49:GLU:HG3	39:2h:62:TYR:HE2	1.82	0.44
47:2p:8:ARG:HB2	47:2p:28:ARG:NE	2.32	0.44
1:1A:1063:G:H1	1:1A:1075:C:H42	1.65	0.44
1:1A:1091:G:O6	1:1A:1100:C:N3	2.51	0.44
1:1A:1152:C:H4'	16:1U:77:SER:HA	1.99	0.44
1:1A:1426:G:N7	3:1D:31:LYS:NZ	2.57	0.44
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.33	0.44
24:12:53:LEU:HD12	24:12:53:LEU:HA	1.76	0.44
32:1a:414:A:H2'	32:1a:415:A:H8	1.83	0.44
32:1a:455:C:N4	32:1a:476:G:H1	2.13	0.44
32:1a:592:G:C6	32:1a:648:A:C6	3.06	0.44
32:1a:993:G:H2'	32:1a:993:G:N3	2.32	0.44
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.52	0.44
34:1c:65:ALA:O	34:1c:66:VAL:HG22	2.18	0.44
36:1e:78:HIS:HE1	36:1e:142:LEU:HD23	1.82	0.44
38:1g:12:LEU:H	38:1g:12:LEU:HG	1.62	0.44
41:1j:5:ARG:HG3	41:1j:73:ASP:OD1	2.18	0.44
50:1s:39:THR:HG23	50:1s:68:GLY:O	2.17	0.44
1:2A:68:G:H2'	1:2A:69:C:O4'	2.17	0.44
1:2A:141:A:C8	1:2A:1408:C:O2'	2.71	0.44
1:2A:732:C:H2'	1:2A:733:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:907:U:O2'	12:2Q:101:ARG:NH2	2.41	0.44
1:2A:2467:C:H4'	12:2Q:123:HIS:CG	2.53	0.44
1:2A:2680:C:H1'	4:2E:187:ALA:HB1	1.99	0.44
8:2I:122:GLU:O	8:2I:126:TYR:OH	2.31	0.44
15:2T:6:LEU:HD12	15:2T:6:LEU:HA	1.72	0.44
32:2a:678:U:H2'	32:2a:679:C:C6	2.53	0.44
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.32	0.44
32:2a:1492:A:C8	43:2l:47:LYS:HG3	2.53	0.44
35:2d:159:ARG:O	35:2d:163:GLU:HB2	2.17	0.44
36:2e:6:PHE:HD1	36:2e:6:PHE:HA	1.68	0.44
37:2f:12:PRO:HG3	37:2f:57:GLN:O	2.17	0.44
41:2j:59:SER:C	41:2j:60:ARG:HG2	2.42	0.44
44:2m:16:ASP:HB2	44:2m:30:ALA:HB1	2.00	0.44
51:2t:18:GLN:O	51:2t:22:ARG:HG2	2.18	0.44
1:1A:11:G:C2'	1:1A:12:U:H5"	2.43	0.44
1:1A:2055:C:O2	61:1A:4144:HOH:O	2.20	0.44
1:1A:2390:U:P	30:18:35:GLN:HE22	2.41	0.44
2:1B:22:U:H2'	2:1B:23:G:C8	2.53	0.44
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.48	0.44
11:1P:81:GLN:OE1	11:1P:106:LEU:HD12	2.18	0.44
26:14:14:ILE:HG13	26:14:31:ILE:HB	2.00	0.44
32:1a:109:A:C6	32:1a:326:G:C6	3.06	0.44
32:1a:384:G:H2'	32:1a:385:C:C6	2.53	0.44
32:1a:1006:C:N4	32:1a:1023:G:H1	2.15	0.44
34:1c:36:ASP:OD1	34:1c:57:ILE:HG21	2.18	0.44
35:1d:181:MET:HE3	35:1d:181:MET:HB2	1.70	0.44
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.51	0.44
51:1t:86:ARG:HB3	51:1t:90:GLN:NE2	2.33	0.44
54:1w:219:ILE:HG12	54:1w:241:VAL:HG12	1.98	0.44
54:1w:258:GLN:NE2	54:1w:262:ARG:HH12	2.07	0.44
1:2A:2134:A:C2	1:2A:2159:G:H1'	2.49	0.44
2:2B:114:C:H4'	14:2S:46:VAL:HG12	1.99	0.44
6:2G:37:VAL:HG21	6:2G:103:LEU:HD11	2.00	0.44
10:2O:107:ARG:HG3	10:2O:112:MET:HE1	2.00	0.44
14:2S:15:ARG:O	14:2S:19:LYS:HG3	2.18	0.44
17:2V:14:VAL:HG12	17:2V:18:LEU:HD23	1.99	0.44
32:2a:148:G:H2'	32:2a:149:A:H8	1.83	0.44
32:2a:1275:A:H2'	32:2a:1276:G:O4'	2.16	0.44
32:2a:1278:U:H5'	32:2a:1279:A:C5'	2.45	0.44
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.83	0.44
1:1A:93:G:H2'	1:1A:94:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:284:U:H2'	1:1A:285:C:H6	1.83	0.44
1:1A:375:C:H2'	1:1A:376:C:C6	2.53	0.44
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.83	0.44
1:1A:2203:U:O4'	3:1D:151:LYS:HE2	2.17	0.44
4:1E:27:LEU:HD12	4:1E:180:ASN:O	2.17	0.44
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.53	0.44
32:1a:222:U:H2'	32:1a:223:U:C6	2.53	0.44
32:1a:975:A:N1	41:1j:48:THR:HB	2.33	0.44
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.33	0.44
32:1a:1367:C:H5'	41:1j:60:ARG:CZ	2.47	0.44
33:1b:86:GLU:C	33:1b:89:GLY:H	2.26	0.44
43:1l:32:PHE:CD1	43:1l:86:ARG:HB3	2.53	0.44
43:1l:40:VAL:HG21	43:1l:78:GLN:HA	1.99	0.44
1:2A:894:C:HO2'	1:2A:895:U:H6	1.65	0.44
1:2A:1364:G:C8	23:21:3:LYS:HD2	2.52	0.44
1:2A:1394:U:H2'	1:2A:1395:A:O4'	2.17	0.44
1:2A:2064:C:H2'	1:2A:2065:C:C6	2.53	0.44
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.53	0.44
1:2A:2752:C:H2'	1:2A:2753:A:O4'	2.18	0.44
5:2F:9:ILE:HG12	5:2F:123:LEU:HD23	1.99	0.44
6:2G:47:LYS:NZ	6:2G:80:PHE:O	2.38	0.44
15:2T:92:GLY:O	15:2T:120:ARG:NH2	2.50	0.44
21:2Z:63:ASP:CG	21:2Z:65:GLN:HE21	2.24	0.44
32:2a:487:A:H2'	32:2a:488:C:O4'	2.18	0.44
32:2a:620:C:C2	35:2d:135:LEU:HG	2.53	0.44
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.17	0.44
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.82	0.44
32:2a:1371:G:O3'	40:2i:69:GLY:HA3	2.18	0.44
32:2a:1508:G:H2'	32:2a:1509:C:O4'	2.17	0.44
34:2c:136:GLN:HG3	34:2c:140:ARG:CZ	2.48	0.44
37:2f:96:PRO:HB3	49:2r:30:ASP:CG	2.42	0.44
41:2j:25:GLU:O	41:2j:29:ARG:HG2	2.17	0.44
1:1A:581:C:H2'	1:1A:582:G:C8	2.53	0.44
1:1A:606:U:H4'	1:1A:658:C:H4'	2.00	0.44
1:1A:1001:A:OP2	61:1A:4147:HOH:O	2.21	0.44
1:1A:1288:U:O2'	1:1A:1647:G:N2	2.50	0.44
1:1A:1372:U:H2'	1:1A:1373:A:O4'	2.18	0.44
5:1F:102:PRO:O	5:1F:106:ARG:HG3	2.17	0.44
15:1T:108:ARG:NH2	15:1T:112:ARG:HD3	2.33	0.44
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.17	0.44
32:1a:1278:U:H5"	32:1a:1279:A:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:114:PRO:O	34:1c:118:GLN:NE2	2.48	0.44
35:1d:163:GLU:O	35:1d:166:LYS:HG3	2.18	0.44
35:1d:165:MET:SD	35:1d:168:ARG:HD2	2.58	0.44
38:1g:80:VAL:HG11	38:1g:154:TYR:CG	2.53	0.44
40:1i:11:LYS:H	40:1i:104:ARG:HH21	1.66	0.44
45:1n:24:CYS:HB2	45:1n:40:CYS:HB3	1.99	0.44
1:2A:453:C:O2	1:2A:457:A:O2'	2.33	0.44
1:2A:705:A:H1'	3:2D:9:TYR:CE2	2.53	0.44
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.41	0.44
6:2G:47:LYS:HG3	6:2G:49:ASP:H	1.82	0.44
6:2G:116:ASP:OD2	44:2m:68:GLY:HA3	2.17	0.44
9:2N:138:LEU:HD23	9:2N:138:LEU:HA	1.85	0.44
23:21:82:LEU:HA	23:21:85:LEU:HD12	2.00	0.44
24:22:58:ALA:O	24:22:62:THR:OG1	2.35	0.44
26:24:12:ALA:HB2	26:24:26:SER:HB3	2.00	0.44
32:2a:254:G:OP1	48:2q:67:LYS:O	2.35	0.44
32:2a:1130:A:H2'	32:2a:1131:G:C8	2.53	0.44
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.99	0.44
34:2c:183:ASP:OD2	34:2c:184:TYR:N	2.51	0.44
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.99	0.44
1:1A:184:C:H2'	1:1A:185:U:C6	2.52	0.44
1:1A:515:A:H2	1:1A:1260:G:N3	2.16	0.44
1:1A:2033:A:OP1	61:1A:4145:HOH:O	2.21	0.44
4:1E:13:ARG:HD2	4:1E:20:ALA:HB1	1.99	0.44
7:1H:17:VAL:HG21	7:1H:50:VAL:HG21	2.00	0.44
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.53	0.44
32:1a:157:G:H2'	32:1a:158:G:C8	2.53	0.44
33:1b:167:PRO:HG2	33:1b:192:SER:HB3	2.00	0.44
38:1g:69:VAL:HG21	38:1g:104:LEU:CD1	2.47	0.44
40:1i:94:ALA:C	40:1i:96:LEU:H	2.26	0.44
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.17	0.44
1:2A:2750:A:O2'	1:2A:2752:C:N4	2.44	0.44
32:2a:7:G:H5'	32:2a:298:A:O4'	2.18	0.44
32:2a:300:A:O2'	32:2a:564:C:N3	2.48	0.44
32:2a:1342:C:H1'	40:2i:124:GLN:NE2	2.33	0.44
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.53	0.44
37:2f:26:ILE:O	37:2f:30:LEU:HG	2.17	0.44
47:2p:40:ASP:OD2	47:2p:44:THR:OG1	2.35	0.44
54:2w:198:THR:HG21	54:2w:293:ILE:HG23	1.98	0.44
1:1A:1005:C:O2'	9:1N:28:THR:HG21	2.18	0.43
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2102:U:H2'	1:1A:2103:C:C5	2.53	0.43
6:1G:11:TYR:O	6:1G:16:ARG:HG2	2.18	0.43
6:1G:68:PRO:HB3	6:1G:92:VAL:HB	1.99	0.43
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.52	0.43
25:13:50:VAL:HB	25:13:53:LEU:HD12	2.00	0.43
32:1a:235:C:H5'	48:1q:70:ARG:HG2	2.00	0.43
32:1a:515:G:H2'	32:1a:516:PSU:O4'	2.17	0.43
32:1a:868:C:H2'	32:1a:869:G:O4'	2.18	0.43
32:1a:1397:C:H4'	32:1a:1398:A:O5'	2.17	0.43
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.53	0.43
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.18	0.43
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.52	0.43
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.18	0.43
35:1d:118:ARG:HG3	35:1d:136:PRO:HB3	2.00	0.43
41:1j:45:ARG:HD3	41:1j:47:PHE:CZ	2.52	0.43
44:1m:80:ARG:HH12	50:1s:69:HIS:CE1	2.35	0.43
54:1w:168:TYR:O	54:1w:172:LYS:HB3	2.18	0.43
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.19	0.43
8:2I:80:PRO:HB3	8:2I:145:VAL:HG23	2.00	0.43
32:2a:73:G:H1	32:2a:96:U:H3	1.65	0.43
32:2a:325:A:H2'	32:2a:326:G:O4'	2.18	0.43
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.32	0.43
36:2e:27:ARG:HB2	36:2e:27:ARG:HH11	1.83	0.43
40:2i:53:VAL:HG21	40:2i:85:LEU:HD13	2.00	0.43
46:2o:25:THR:HA	46:2o:28:GLN:HB2	1.99	0.43
1:1A:55:G:O2'	1:1A:127:A:N1	2.46	0.43
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.18	0.43
1:1A:1268:A:C2	1:1A:2013:A:C4	3.06	0.43
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.18	0.43
1:1A:2158:A:H4'	1:1A:2159:G:OP1	2.16	0.43
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.19	0.43
1:1A:2712:U:OP1	1:1A:2714:G:H4'	2.18	0.43
6:1G:101:ILE:HD13	26:14:25:TYR:HB2	2.01	0.43
10:1O:100:GLY:O	10:1O:119:PRO:HD2	2.17	0.43
29:17:1:MET:HE2	29:17:1:MET:HB3	1.93	0.43
32:1a:1055:A:H2'	34:1c:156:ARG:HD2	1.99	0.43
32:1a:1217:C:OP1	45:1n:9:LYS:HD3	2.18	0.43
32:1a:1268:A:N3	32:1a:1326:C:O2'	2.49	0.43
32:1a:1285:A:H4'	32:1a:1286:A:O5'	2.17	0.43
39:1h:33:GLU:O	39:1h:37:ARG:N	2.43	0.43
44:1m:20:THR:HA	44:1m:25:ILE:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:9:PHE:HB3	47:1p:10:GLY:H	1.63	0.43
1:2A:30:G:H2'	1:2A:31:C:C6	2.53	0.43
1:2A:468:G:O2'	5:2F:62:ARG:NH2	2.50	0.43
1:2A:656:G:H2'	1:2A:657:U:O4'	2.18	0.43
1:2A:1449:A:H5'	1:2A:1450:G:OP2	2.19	0.43
1:2A:1827:C:O2'	1:2A:1970:A:N3	2.47	0.43
5:2F:122:LYS:HB3	5:2F:191:ARG:HA	1.99	0.43
6:2G:44:GLY:N	6:2G:88:ILE:O	2.51	0.43
33:2b:122:PHE:HD1	33:2b:122:PHE:HA	1.64	0.43
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	2.00	0.43
1:1A:389:G:O6	11:1P:70:GLN:HB2	2.17	0.43
1:1A:2180:U:H2'	1:1A:2181:G:O4'	2.18	0.43
4:1E:21:VAL:HG13	4:1E:185:LYS:HD2	2.01	0.43
32:1a:19:C:OP1	36:1e:125:SER:OG	2.36	0.43
32:1a:976:G:OP1	45:1n:32:SER:N	2.25	0.43
32:1a:1191:A:OP2	34:1c:3:ASN:ND2	2.52	0.43
32:1a:1319:A:H4'	32:1a:1320:C:OP1	2.17	0.43
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	1.99	0.43
40:1i:11:LYS:O	40:1i:13:ALA:N	2.50	0.43
54:1w:243:HIS:CD2	54:1w:273:LEU:HD11	2.54	0.43
55:1x:20:H2U:H4'	55:1x:21:H2U:OP2	2.14	0.43
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.53	0.43
1:2A:1399:C:O2'	1:2A:1400:G:H5'	2.18	0.43
1:2A:2175:C:H2'	1:2A:2176:A:C8	2.53	0.43
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.53	0.43
7:2H:125:VAL:HG22	7:2H:131:VAL:HG22	2.00	0.43
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.83	0.43
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	2.00	0.43
32:2a:358:U:H2'	32:2a:359:U:H6	1.82	0.43
38:2g:54:THR:O	38:2g:56:GLN:N	2.51	0.43
38:2g:122:HIS:O	38:2g:125:MET:HB2	2.17	0.43
39:2h:83:ILE:HG13	39:2h:137:VAL:HG22	2.00	0.43
44:2m:22:ILE:HD13	44:2m:25:ILE:HD12	2.01	0.43
45:2n:47:LEU:HD23	45:2n:47:LEU:HA	1.88	0.43
49:2r:43:PHE:O	49:2r:51:LEU:HD12	2.18	0.43
1:1A:476:G:H4'	1:1A:502:A:N1	2.33	0.43
1:1A:768:G:O2'	1:1A:1379:A:N1	2.44	0.43
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.18	0.43
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.18	0.43
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.83	0.43
1:1A:2659:G:O2'	7:1H:175:LYS:NZ	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2774:C:H2'	1:1A:2775:A:O4'	2.18	0.43
2:1B:51:G:N7	14:1S:62:LYS:NZ	2.57	0.43
2:1B:73:A:N1	21:1Z:34:ASN:ND2	2.67	0.43
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.00	0.43
32:1a:189:G:C6	32:1a:189(L):G:C6	3.07	0.43
32:1a:663:A:H5'	32:1a:836:G:OP1	2.18	0.43
33:1b:12:GLU:OE1	33:1b:12:GLU:N	2.50	0.43
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.84	0.43
39:1h:94:TYR:HE1	39:1h:132:GLU:HB2	1.82	0.43
55:1x:19:G:C4	55:1x:57:G:N2	2.86	0.43
1:2A:492:A:H2'	1:2A:493:G:O4'	2.18	0.43
4:2E:36:ARG:NH1	4:2E:86:PRO:O	2.41	0.43
7:2H:94:TYR:HA	7:2H:106:THR:O	2.18	0.43
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.52	0.43
24:22:35:LEU:HD23	24:22:35:LEU:HA	1.81	0.43
32:2a:420:U:H2'	32:2a:422:C:C5	2.53	0.43
32:2a:551:U:H2'	32:2a:552:U:C6	2.53	0.43
32:2a:737:A:H2'	32:2a:738:C:C6	2.53	0.43
32:2a:790:A:OP1	55:2x:38:A:O2'	2.35	0.43
32:2a:833:U:H2'	32:2a:834:C:H6	1.83	0.43
32:2a:957:U:H1'	32:2a:960:U:C4	2.54	0.43
33:2b:178:ARG:NH2	39:2h:68:ARG:HH22	2.12	0.43
35:2d:19:LEU:HB3	35:2d:21:LEU:HD21	2.00	0.43
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.51	0.43
44:2m:14:ARG:HB2	44:2m:17:VAL:HG23	2.00	0.43
45:2n:24:CYS:SG	45:2n:40:CYS:N	2.92	0.43
47:2p:13:HIS:C	47:2p:15:PRO:HD3	2.43	0.43
1:1A:271(M):G:N2	8:1I:50:ARG:HH11	2.17	0.43
1:1A:1060:U:O2	1:1A:1062:G:H1'	2.19	0.43
1:1A:1815:A:H8	1:1A:1815:A:OP1	2.02	0.43
1:1A:2555:U:O2	54:1w:223:ARG:HB2	2.18	0.43
1:1A:2853:C:H2'	1:1A:2854:G:C8	2.53	0.43
16:1U:17:ILE:HG23	16:1U:39:LEU:HD12	2.01	0.43
20:1Y:5:MET:HE2	20:1Y:5:MET:HB2	1.88	0.43
30:18:62:LEU:HB3	30:18:65:GLU:HG2	2.01	0.43
32:1a:73:G:C6	32:1a:76:C:C4	3.06	0.43
32:1a:300:A:O2'	32:1a:564:C:N3	2.47	0.43
32:1a:872:A:C8	32:1a:874:G:C8	3.07	0.43
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.19	0.43
33:1b:12:GLU:H	33:1b:12:GLU:CD	2.25	0.43
35:1d:10:ARG:HG3	35:1d:11:LEU:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:78:HIS:HE1	36:1e:142:LEU:HA	1.83	0.43
38:1g:69:VAL:HG12	38:1g:100:ALA:HA	2.00	0.43
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.49	0.43
1:2A:106:C:H1'	20:2Y:1:MET:HE2	2.00	0.43
1:2A:448:U:O4	1:2A:583:G:H1'	2.18	0.43
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.33	0.43
1:2A:1711:C:H2'	1:2A:1712:C:C6	2.54	0.43
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.51	0.43
1:2A:2396:G:H1'	23:21:30:VAL:HG12	2.01	0.43
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.52	0.43
1:2A:2641:G:H5"	9:2N:76:SER:HB3	2.00	0.43
1:2A:2821:A:OP2	61:2R:301:HOH:O	2.21	0.43
2:2B:95:C:H2'	2:2B:96:U:C6	2.53	0.43
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.49	0.43
7:2H:8:PRO:HB3	7:2H:51:ARG:CG	2.46	0.43
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.27	0.43
26:24:58:ARG:HE	26:24:58:ARG:HB3	1.58	0.43
26:24:61:ARG:O	26:24:62:ARG:HB2	2.17	0.43
32:2a:451:A:N6	32:2a:480:U:H2'	2.33	0.43
32:2a:838:G:H1	32:2a:848:C:H42	1.65	0.43
32:2a:941:G:H2'	32:2a:942:G:O4'	2.18	0.43
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.49	0.43
34:2c:19:GLU:HG2	34:2c:54:ARG:HE	1.84	0.43
40:2i:9:ARG:HB3	40:2i:104:ARG:NH1	2.34	0.43
45:2n:47:LEU:HD23	45:2n:50:LYS:HD2	2.01	0.43
51:2t:89:ARG:HE	51:2t:89:ARG:HB3	1.63	0.43
1:1A:247:G:H4'	1:1A:386:G:C5	2.53	0.43
1:1A:468:G:N7	29:17:39:ARG:NH2	2.64	0.43
1:1A:1223:G:N2	1:1A:1226:A:OP2	2.47	0.43
1:1A:1903:G:OP1	3:1D:241:PRO:HB2	2.19	0.43
1:1A:1914:C:O2	54:1w:290:LEU:HD11	2.19	0.43
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.33	0.43
5:1F:72:ARG:HE	5:1F:72:ARG:HB3	1.68	0.43
8:1I:38:LEU:C	8:1I:40:THR:H	2.27	0.43
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	2.01	0.43
27:15:40:LYS:HD3	27:15:46:CYS:HA	2.00	0.43
32:1a:106:C:O2'	32:1a:379:C:H5"	2.19	0.43
32:1a:110:C:O2'	47:1p:25:ARG:O	2.29	0.43
32:1a:269:C:H2'	32:1a:270:A:H8	1.82	0.43
34:1c:17:ASP:O	34:1c:54:ARG:NH2	2.31	0.43
34:1c:175:LEU:HD23	34:1c:182:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:144:THR:O	36:1e:148:VAL:HG22	2.18	0.43
38:1g:62:PHE:CD1	38:1g:124:LEU:HD21	2.52	0.43
39:1h:54:ASP:N	39:1h:54:ASP:OD1	2.51	0.43
47:1p:6:LEU:HB3	47:1p:17:TYR:HB3	1.99	0.43
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.19	0.43
1:2A:2207:G:H2'	1:2A:2208:A:H2	1.84	0.43
1:2A:2655:G:O2'	1:2A:2664:G:O6	2.34	0.43
12:2Q:77:LYS:NZ	12:2Q:84:GLY:O	2.30	0.43
32:2a:107:G:H2'	32:2a:108:G:O4'	2.19	0.43
32:2a:124:G:H4'	32:2a:291:C:O2'	2.19	0.43
32:2a:354:G:O2'	32:2a:389:A:OP1	2.29	0.43
32:2a:730:G:C5	32:2a:731:G:H1'	2.53	0.43
32:2a:1518:MA6:H93	32:2a:1519:MA6:C9	2.46	0.43
35:2d:8:VAL:HG11	35:2d:21:LEU:HB2	2.01	0.43
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.18	0.43
35:2d:188:LEU:HD12	35:2d:188:LEU:HA	1.86	0.43
38:2g:78:ARG:NH1	38:2g:154:TYR:O	2.52	0.43
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.18	0.43
54:2w:243:HIS:CG	54:2w:273:LEU:HD11	2.53	0.43
1:1A:882:G:H2'	1:1A:883:G:H8	1.83	0.43
1:1A:2116:G:H5"	1:1A:2117:A:N7	2.32	0.43
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.54	0.43
1:1A:2789:C:H1'	1:1A:2892:A:C2	2.54	0.43
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.82	0.43
6:1G:43:LEU:C	6:1G:45:GLU:H	2.27	0.43
32:1a:130:A:C8	48:1q:63:ARG:HG3	2.53	0.43
32:1a:636:U:H2'	32:1a:637:G:H8	1.83	0.43
32:1a:1058:G:C6	32:1a:1059:C:C4	3.07	0.43
32:1a:1367:C:H4'	41:1j:48:THR:HG21	2.01	0.43
35:1d:81:GLU:OE1	35:1d:139:ARG:NH2	2.46	0.43
44:1m:81:LEU:O	44:1m:89:GLY:HA3	2.19	0.43
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.70	0.43
1:2A:384:U:H2'	1:2A:385:C:C6	2.53	0.43
1:2A:399:G:OP2	61:2A:3956:HOH:O	2.21	0.43
1:2A:437:G:H2'	1:2A:438:G:C8	2.53	0.43
1:2A:448:U:C4	1:2A:583:G:H1'	2.53	0.43
1:2A:616:G:OP2	5:2F:106:ARG:NH1	2.41	0.43
1:2A:839:U:H2'	1:2A:840:C:H6	1.84	0.43
1:2A:1277:G:O2'	13:2R:24:GLN:HG2	2.18	0.43
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.35	0.43
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.53	0.43
6:2G:11:TYR:O	6:2G:16:ARG:HG3	2.18	0.43
19:2X:44:GLU:O	19:2X:48:LYS:N	2.43	0.43
23:21:77:ALA:HB1	23:21:82:LEU:HD11	2.00	0.43
33:2b:109:SER:HA	33:2b:112:VAL:HG13	2.01	0.43
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.59	0.43
35:2d:153:ARG:HB3	35:2d:181:MET:HE1	2.01	0.43
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.99	0.43
38:2g:92:SER:O	38:2g:96:GLN:HG3	2.18	0.43
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.19	0.43
51:2t:57:ARG:HH12	51:2t:100:ILE:HD12	1.83	0.43
1:1A:534:U:H2'	1:1A:535:C:C6	2.54	0.43
1:1A:1056:G:C2'	1:1A:1103:A:H61	2.32	0.43
1:1A:1814:G:C4'	3:1D:51:VAL:HG21	2.49	0.43
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.19	0.43
1:1A:2161:C:O2'	1:1A:2162:G:H8	2.02	0.43
1:1A:2563:U:O2	1:1A:2565:A:H8	2.01	0.43
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.83	0.43
5:1F:149:ASP:OD1	5:1F:149:ASP:N	2.42	0.43
6:1G:111:LEU:HD23	6:1G:114:ILE:HD12	2.00	0.43
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.61	0.43
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.93	0.43
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.54	0.43
24:12:3:LEU:HA	24:12:3:LEU:HD23	1.82	0.43
32:1a:616:G:OP2	35:1d:141:ARG:NH1	2.49	0.43
32:1a:1118:C:P	40:1i:104:ARG:HH11	2.41	0.43
36:1e:110:LEU:HD13	36:1e:118:ILE:HD13	2.01	0.43
47:1p:19:ILE:H	47:1p:19:ILE:HG13	1.61	0.43
48:1q:56:VAL:N	48:1q:78:GLU:O	2.50	0.43
1:2A:271(N):U:O2'	1:2A:271(O):C:H5'	2.19	0.43
1:2A:721:C:H2'	1:2A:722:A:H8	1.84	0.43
1:2A:1494:A:C6	1:2A:1495:A:C6	3.07	0.43
1:2A:2131:G:H5"	1:2A:2133:G:O4'	2.18	0.43
2:2B:58:A:H2'	2:2B:59:A:O4'	2.19	0.43
10:2O:104:ARG:HH22	15:2T:43:GLN:NE2	2.16	0.43
15:2T:127:ALA:C	15:2T:129:ARG:N	2.75	0.43
32:2a:255:G:H2'	32:2a:256:U:C6	2.54	0.43
32:2a:411:A:O2'	32:2a:413:G:H5'	2.19	0.43
32:2a:622:A:C8	32:2a:623:C:C6	3.07	0.43
32:2a:857:C:H2'	32:2a:858:G:O4'	2.18	0.43
32:2a:976:G:OP1	45:2n:32:SER:N	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.46	0.43
32:2a:1244:C:OP1	52:2u:9:ARG:HB2	2.19	0.43
33:2b:60:ASP:HA	33:2b:63:MET:HE3	2.00	0.43
34:2c:113:ALA:HB2	34:2c:202:ILE:HG13	2.01	0.43
36:2e:7:GLU:OE1	36:2e:37:ARG:NE	2.51	0.43
37:2f:8:ILE:HD11	37:2f:79:LEU:HD13	2.00	0.43
40:2i:114:TYR:HD1	41:2j:60:ARG:HG3	1.83	0.43
45:2n:3:ARG:O	45:2n:7:ILE:HG13	2.18	0.43
1:1A:68:G:H2'	1:1A:69:C:O4'	2.18	0.43
1:1A:1069:A:H4'	1:1A:1070:A:H5"	2.00	0.43
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.84	0.43
1:1A:2429:G:OP1	61:1A:4103:HOH:O	2.21	0.43
2:1B:29:A:C2	2:1B:30:C:C2	3.07	0.43
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.48	0.43
6:1G:74:LYS:O	6:1G:84:LYS:HG3	2.19	0.43
8:1I:114:LEU:HD12	8:1I:114:LEU:HA	1.85	0.43
21:1Z:77:ASP:OD2	21:1Z:80:ARG:HD2	2.18	0.43
23:11:77:ALA:HB1	23:11:82:LEU:HD11	2.01	0.43
32:1a:79:G:N1	32:1a:90:U:C2	2.87	0.43
32:1a:438:G:H4'	35:1d:123:HIS:ND1	2.34	0.43
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.87	0.43
33:1b:80:ILE:O	33:1b:84:GLU:HG2	2.18	0.43
35:1d:104:VAL:O	35:1d:108:LEU:HB2	2.18	0.43
1:2A:141:A:H8	1:2A:1408:C:O2'	2.01	0.43
1:2A:686:G:H21	1:2A:788:A:H61	1.67	0.43
1:2A:746:A:H2'	1:2A:2612:C:H5"	2.01	0.43
1:2A:860:U:H1'	1:2A:2268:A:H5'	2.00	0.43
1:2A:1790:C:H4'	3:2D:209:ALA:HB2	2.01	0.43
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.18	0.43
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.18	0.43
1:2A:2712:U:H2'	1:2A:2714:G:H5"	2.01	0.43
3:2D:39:LYS:NZ	3:2D:57:GLY:O	2.44	0.43
5:2F:11:VAL:HB	5:2F:18:ARG:HG3	2.01	0.43
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.19	0.43
12:2Q:109:VAL:HG22	12:2Q:113:GLN:OE1	2.18	0.43
13:2R:12:ARG:O	13:2R:17:ARG:NH1	2.52	0.43
21:2Z:150:LEU:HD23	21:2Z:150:LEU:HA	1.88	0.43
31:29:32:HIS:O	31:29:34:GLN:HG3	2.19	0.43
32:2a:381:C:H2'	32:2a:382:A:O4'	2.19	0.43
32:2a:718:G:C8	42:2k:116:HIS:HB3	2.54	0.43
32:2a:833:U:O2'	32:2a:834:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1035:A:HO2'	32:2a:1036:G:H8	1.67	0.43
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.53	0.43
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.54	0.43
45:2n:8:GLU:HA	45:2n:11:LYS:HE2	2.00	0.43
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.19	0.43
47:2p:8:ARG:HB2	47:2p:28:ARG:HE	1.83	0.43
54:2w:348:LEU:HA	54:2w:352:ALA:CB	2.48	0.43
1:1A:566:U:H5"	11:1P:29:LYS:HE3	2.01	0.43
1:1A:1359:A:C2	1:1A:1372:U:O4	2.70	0.43
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.33	0.43
1:1A:2107:C:H42	1:1A:2182:G:H1	1.65	0.43
6:1G:43:LEU:HD12	6:1G:53:LEU:HD22	2.00	0.43
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	2.01	0.43
21:1Z:3:TYR:CE2	21:1Z:51:ALA:HB2	2.54	0.43
21:1Z:33:LEU:HD11	21:1Z:90:VAL:HG21	2.01	0.43
32:1a:271:C:H2'	32:1a:272:C:H6	1.84	0.43
32:1a:688:G:O2'	32:1a:704:A:N1	2.39	0.43
32:1a:730:G:C5	32:1a:731:G:H1'	2.54	0.43
32:1a:1243:C:C2	32:1a:1295:G:N2	2.87	0.43
33:1b:134:GLU:O	33:1b:138:LEU:HG	2.19	0.43
1:2A:118:A:O5'	1:2A:119:A:H5"	2.19	0.43
1:2A:320:A:H4'	1:2A:322:A:N7	2.34	0.43
1:2A:606:U:H4'	1:2A:658:C:H4'	2.00	0.43
1:2A:958:U:O2	2:2B:90:A:O2'	2.30	0.43
1:2A:1414:G:C6	1:2A:1415:U:C4	3.06	0.43
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	2.01	0.43
1:2A:2375:G:N2	1:2A:2378:A:OP2	2.43	0.43
1:2A:2577:A:OP2	27:25:3:LYS:NZ	2.42	0.43
9:2N:71:ILE:HG21	9:2N:84:LYS:HB3	2.01	0.43
10:2O:19:ILE:HG22	10:2O:43:VAL:HA	2.00	0.43
14:2S:83:LYS:HD2	14:2S:84:GLN:H	1.84	0.43
26:24:5:ILE:HG13	26:24:6:HIS:CD2	2.54	0.43
32:2a:161:A:H2'	32:2a:162:A:C8	2.54	0.43
32:2a:859:A:H2'	32:2a:860:A:O4'	2.19	0.43
32:2a:1030(D):A:H3'	32:2a:1031:G:C8	2.50	0.43
32:2a:1085:U:H3'	32:2a:1086:U:C6	2.53	0.43
32:2a:1363(A):A:H4'	32:2a:1364:U:H2'	2.01	0.43
41:2j:74:ILE:HD12	41:2j:74:ILE:HA	1.81	0.43
1:1A:570:G:H2'	1:1A:2030:A:N7	2.34	0.42
1:1A:1416:G:O2'	1:1A:1417:C:OP2	2.26	0.42
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2108:C:O2'	1:1A:2109:U:H5'	2.19	0.42
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.54	0.42
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.53	0.42
19:1X:94:GLY:H	19:1X:95:LEU:C	2.27	0.42
32:1a:721:G:H4'	32:1a:722:A:O4'	2.19	0.42
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.19	0.42
32:1a:1316:G:H4'	45:1n:18:VAL:HG13	2.00	0.42
32:1a:1530:G:H4'	32:1a:1530:G:OP1	2.19	0.42
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	2.00	0.42
39:1h:11:THR:HG22	39:1h:14:ARG:HH22	1.84	0.42
55:1x:62:C:H2'	55:1x:63:G:H8	1.84	0.42
1:2A:26:G:C6	1:2A:27:G:N1	2.87	0.42
1:2A:58:G:O2'	1:2A:73:A:N1	2.39	0.42
1:2A:315:G:H2'	1:2A:316:C:C6	2.54	0.42
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.51	0.42
1:2A:1745(A):C:H5'	1:2A:1746:G:OP2	2.19	0.42
1:2A:2116:G:C6	1:2A:2172:U:H5	2.37	0.42
1:2A:2251:OMG:H1'	1:2A:2251:OMG:HM23	1.69	0.42
6:2G:11:TYR:HA	6:2G:15:VAL:HG22	2.01	0.42
6:2G:122:PRO:HG3	6:2G:182:LYS:C	2.44	0.42
8:2I:6:LEU:C	8:2I:15:VAL:HG13	2.43	0.42
10:2O:77:ILE:HD12	15:2T:74:ARG:HG2	2.01	0.42
12:2Q:118:LEU:HD12	12:2Q:131:ILE:HG23	2.00	0.42
16:2U:55:ARG:O	16:2U:59:ARG:HG3	2.18	0.42
20:2Y:97:ARG:HB2	20:2Y:106:LEU:HB2	2.01	0.42
32:2a:22:G:H4'	32:2a:885:G:C8	2.54	0.42
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.18	0.42
32:2a:1385:G:H2'	32:2a:1386:G:H8	1.84	0.42
33:2b:75:LYS:HA	33:2b:78:GLN:HG2	2.01	0.42
40:2i:63:ILE:HD13	40:2i:77:ILE:HG23	2.01	0.42
44:2m:11:ARG:C	44:2m:13:LYS:H	2.26	0.42
53:2v:22:U:OP2	54:2w:191:ARG:NH1	2.52	0.42
1:1A:818:G:H5'	1:1A:839:U:OP1	2.18	0.42
1:1A:839:U:H2'	1:1A:840:C:C6	2.54	0.42
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.34	0.42
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	2.01	0.42
32:1a:70:G:H1	32:1a:99:U:H3	1.68	0.42
32:1a:448:A:H2'	32:1a:449:C:C6	2.55	0.42
32:1a:1085:U:H3'	32:1a:1086:U:C6	2.54	0.42
32:1a:1220:G:O3'	50:1s:36:ARG:HD3	2.18	0.42
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:59:GLY:O	36:1e:63:ARG:HD2	2.19	0.42
41:1j:45:ARG:HD3	41:1j:47:PHE:HZ	1.84	0.42
44:1m:3:ARG:HB2	44:1m:8:GLU:HA	2.00	0.42
46:1o:4:THR:HG1	46:1o:7:GLU:HG3	1.82	0.42
1:2A:262:A:H2'	1:2A:263:C:O4'	2.19	0.42
1:2A:829:A:N7	1:2A:2248:C:H5'	2.34	0.42
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.18	0.42
1:2A:2137:C:H1'	1:2A:2138:C:H5'	2.00	0.42
1:2A:2466:C:H5"	31:29:6:SER:HB2	2.01	0.42
7:2H:3:ARG:HA	7:2H:3:ARG:HH11	1.82	0.42
7:2H:5:GLY:HA3	7:2H:65:HIS:CG	2.55	0.42
12:2Q:76:LYS:HB3	12:2Q:91:GLU:HG3	2.00	0.42
21:2Z:8:TYR:HB2	21:2Z:38:TYR:CE2	2.54	0.42
21:2Z:146:ILE:HA	21:2Z:147:GLY:HA2	1.54	0.42
23:21:3:LYS:HB3	23:21:4:VAL:H	1.56	0.42
32:2a:448:A:OP2	32:2a:485:G:N1	2.43	0.42
32:2a:600:C:C2	32:2a:639:G:C2	3.06	0.42
32:2a:1125:U:H6	32:2a:1126:U:O2'	2.02	0.42
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.19	0.42
34:2c:41:GLY:O	34:2c:45:LYS:HG3	2.18	0.42
35:2d:15:GLU:OE1	35:2d:59:ARG:NE	2.52	0.42
35:2d:108:LEU:HD21	35:2d:174:LEU:HB3	2.01	0.42
38:2g:78:ARG:HH21	38:2g:79:ARG:NH2	2.17	0.42
40:2i:92:TYR:O	40:2i:96:LEU:HB2	2.18	0.42
44:2m:86:CYS:HA	50:2s:73:GLU:O	2.18	0.42
1:1A:655:A:H2'	1:1A:656:G:O4'	2.19	0.42
1:1A:686:G:N2	1:1A:788:A:H61	2.17	0.42
1:1A:1833:U:O2'	1:1A:1969:A:N1	2.48	0.42
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.52	0.42
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.27	0.42
30:18:33:ASN:HA	30:18:36:LYS:HD2	2.01	0.42
31:19:13:LYS:HG3	31:19:28:GLU:OE2	2.19	0.42
32:1a:189(C):C:H2'	32:1a:189(D):C:O4'	2.19	0.42
32:1a:418:C:H1'	32:1a:540:G:O2'	2.19	0.42
32:1a:841:U:O2	32:1a:841:U:H2'	2.19	0.42
32:1a:1014:A:C2	32:1a:1219:U:H1'	2.55	0.42
32:1a:1351:U:O4	40:1i:118:LYS:NZ	2.52	0.42
34:1c:85:ARG:HG3	34:1c:86:VAL:N	2.32	0.42
38:1g:153:HIS:CE1	42:1k:58:PRO:HD2	2.54	0.42
40:1i:23:ASN:ND2	40:1i:23:ASN:H	2.17	0.42
41:1j:32:ALA:HB1	41:1j:76:ASN:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	2.01	0.42
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.34	0.42
50:1s:27:GLU:CG	50:1s:28:LYS:HG2	2.49	0.42
1:2A:118:A:N3	1:2A:178:G:H1'	2.34	0.42
1:2A:652(B):A:N6	1:2A:655:A:N3	2.67	0.42
1:2A:887:A:H2'	1:2A:889:C:OP2	2.19	0.42
1:2A:1270:C:H5"	1:2A:1271:G:O5'	2.19	0.42
1:2A:1782:C:H1'	1:2A:2609:U:H5"	2.00	0.42
3:2D:242:ARG:HG2	3:2D:246:PRO:HG3	2.01	0.42
15:2T:57:PHE:HA	15:2T:79:HIS:HD2	1.84	0.42
16:2U:16:LYS:HE2	16:2U:16:LYS:HB3	1.83	0.42
23:21:52:ARG:NH2	23:21:57:GLU:HB2	2.34	0.42
32:2a:1041:A:H2'	32:2a:1042:G:C8	2.55	0.42
32:2a:1080:A:OP1	36:2e:47:LYS:HD3	2.19	0.42
32:2a:1182:G:H4'	32:2a:1183:A:H5"	2.01	0.42
33:2b:19:HIS:HE1	33:2b:189:ASP:OD2	2.01	0.42
39:2h:104:ARG:HD3	39:2h:104:ARG:HA	1.81	0.42
53:2v:15:A:H8	53:2v:15:A:O5'	2.02	0.42
54:2w:129:ASN:O	54:2w:133:ARG:HG3	2.18	0.42
1:1A:2251:OMG:H1'	1:1A:2251:OMG:HM23	1.81	0.42
1:1A:2648:C:H2'	1:1A:2649:U:C6	2.55	0.42
2:1B:66:A:N6	2:1B:108:U:H2'	2.34	0.42
2:1B:75:G:H22	21:1Z:73:GLN:NE2	2.17	0.42
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.32	0.42
26:14:12:ALA:HB2	26:14:26:SER:HB3	2.02	0.42
32:1a:270:A:H2'	32:1a:271:C:O4'	2.19	0.42
32:1a:493:G:H2'	32:1a:494:U:C5	2.54	0.42
32:1a:1239:A:C4	32:1a:1298:C:N4	2.87	0.42
36:1e:92:LYS:N	36:1e:119:LEU:O	2.45	0.42
50:1s:42:PRO:HA	50:1s:45:VAL:HG23	2.01	0.42
55:1x:13:A:H2'	55:1x:14:A:H5"	2.00	0.42
1:2A:2136:C:C5	1:2A:2155:G:O6	2.72	0.42
1:2A:2183:C:H2'	1:2A:2184:G:C8	2.54	0.42
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.19	0.42
1:2A:2832:U:OP2	61:2A:3957:HOH:O	2.21	0.42
5:2F:122:LYS:HD2	5:2F:191:ARG:HG2	2.02	0.42
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.18	0.42
12:2Q:56:ARG:HE	12:2Q:56:ARG:HB3	1.77	0.42
21:2Z:45:ASP:O	21:2Z:49:ARG:HG2	2.18	0.42
32:2a:256:U:OP1	48:2q:17:LYS:NZ	2.42	0.42
32:2a:890:G:O2'	32:2a:906:G:O6	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1151:A:H5"	41:2j:42:THR:HG23	2.02	0.42
32:2a:1206:G:C6	32:2a:1207:2MG:C5	3.07	0.42
32:2a:1279:A:H5"	32:2a:1280:A:OP1	2.19	0.42
33:2b:27:LYS:HB2	33:2b:194:PRO:HD2	2.00	0.42
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.19	0.42
50:2s:15:LEU:H	50:2s:15:LEU:HD23	1.83	0.42
1:1A:272(I):U:H2'	1:1A:272(J):C:C6	2.55	0.42
1:1A:1063:G:N2	1:1A:1076:C:O2'	2.53	0.42
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.20	0.42
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.20	0.42
1:1A:2703:C:H2'	1:1A:2704:C:C6	2.54	0.42
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.20	0.42
3:1D:38:LYS:HE2	3:1D:39:LYS:N	2.34	0.42
8:1I:31:LEU:HD21	8:1I:38:LEU:HG	2.01	0.42
10:1O:63:VAL:HA	10:1O:106:LEU:HD11	1.99	0.42
21:1Z:62:PRO:C	21:1Z:64:GLY:H	2.26	0.42
30:18:50:LEU:HD23	30:18:50:LEU:HA	1.84	0.42
32:1a:235:C:H2'	32:1a:236:G:H8	1.85	0.42
32:1a:486:U:H2'	32:1a:487:A:C8	2.51	0.42
33:1b:21:ARG:HB3	33:1b:39:ILE:HG12	2.00	0.42
33:1b:50:GLU:HB3	33:1b:200:ILE:O	2.19	0.42
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.51	0.42
41:1j:81:THR:C	41:1j:83:GLU:N	2.78	0.42
44:1m:52:GLU:H	44:1m:52:GLU:HG3	1.70	0.42
44:1m:65:LYS:O	44:1m:66:LEU:HD23	2.19	0.42
51:1t:55:ILE:HD13	51:1t:55:ILE:HA	1.92	0.42
1:2A:251:A:C5	1:2A:252:G:H1'	2.55	0.42
1:2A:1372:U:H2'	1:2A:1373:A:O4'	2.19	0.42
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.20	0.42
1:2A:1510:G:H2'	1:2A:1511:C:C6	2.55	0.42
1:2A:1530:C:H42	1:2A:1539:G:H1	1.68	0.42
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.32	0.42
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.34	0.42
2:2B:1:U:H2'	2:2B:2:C:C6	2.54	0.42
6:2G:38:VAL:HG22	6:2G:93:THR:HG22	2.02	0.42
23:21:37:ILE:O	61:21:201:HOH:O	2.22	0.42
32:2a:51:A:H61	32:2a:314:C:H1'	1.85	0.42
32:2a:437:U:O2'	35:2d:123:HIS:HD2	2.02	0.42
32:2a:545:C:O2'	32:2a:549:C:OP1	2.26	0.42
32:2a:551:U:H2'	32:2a:552:U:H6	1.84	0.42
32:2a:942:G:C2	32:2a:1342:C:C2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1259:C:O2'	32:2a:1283:G:N3	2.51	0.42
32:2a:1375:A:C5	32:2a:1376:U:C4	3.07	0.42
33:2b:167:PRO:HG3	33:2b:188:ALA:HB2	2.01	0.42
37:2f:62:TRP:CH2	37:2f:64:GLN:HB2	2.54	0.42
38:2g:29:LYS:O	38:2g:105:VAL:HG11	2.19	0.42
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.52	0.42
44:2m:40:ASN:ND2	44:2m:43:THR:HG23	2.34	0.42
45:2n:24:CYS:SG	45:2n:39:LEU:HA	2.60	0.42
54:2w:198:THR:HB	54:2w:293:ILE:HG12	2.01	0.42
1:1A:576:U:H2'	1:1A:577:G:C8	2.53	0.42
1:1A:675:A:C8	1:1A:804:A:C6	3.08	0.42
1:1A:1006:C:O2'	9:1N:106:MET:HB3	2.20	0.42
1:1A:1091:G:N1	1:1A:1100:C:O2	2.53	0.42
1:1A:1421:G:N2	1:1A:1495:A:N1	2.61	0.42
1:1A:1547:C:H2'	1:1A:1548:C:C6	2.54	0.42
1:1A:2271:G:OP1	22:10:18:ALA:HB1	2.20	0.42
6:1G:12:TYR:HA	6:1G:16:ARG:CG	2.50	0.42
10:1O:120:GLU:OE2	10:1O:122:LEU:HD21	2.20	0.42
15:1T:27:THR:HB	15:1T:90:GLN:HB3	2.02	0.42
21:1Z:70:LEU:HD23	21:1Z:70:LEU:HA	1.85	0.42
26:14:54:GLY:C	26:14:56:VAL:HA	2.44	0.42
30:18:29:LYS:HE2	30:18:29:LYS:HB2	1.80	0.42
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.49	0.42
33:1b:215:LEU:HD12	33:1b:215:LEU:HA	1.89	0.42
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.19	0.42
54:1w:228:GLY:HA3	54:1w:232:VAL:HB	2.02	0.42
1:2A:720:C:H2'	1:2A:721:C:C6	2.55	0.42
1:2A:757:U:H2'	1:2A:758:C:O4'	2.19	0.42
1:2A:1651:G:N2	1:2A:2007:C:C2	2.88	0.42
1:2A:2649:U:H2'	1:2A:2650:U:C6	2.54	0.42
4:2E:9:VAL:HG13	15:2T:3:ARG:HG2	2.02	0.42
5:2F:126:VAL:HG11	5:2F:142:TRP:CH2	2.54	0.42
5:2F:148:LEU:HD21	5:2F:191:ARG:HH21	1.84	0.42
5:2F:178:PRO:HG2	5:2F:179:GLU:OE2	2.19	0.42
7:2H:105:LEU:HB3	7:2H:107:VAL:HG13	2.00	0.42
8:2I:90:GLY:O	8:2I:121:LYS:HE3	2.20	0.42
32:2a:1005:A:H5"	32:2a:1006:C:H5	1.84	0.42
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.54	0.42
32:2a:1149:C:OP1	40:2i:14:VAL:HG11	2.19	0.42
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.02	0.42
32:2a:1264:C:N4	32:2a:1265:G:O6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:97:LEU:HD23	35:2d:97:LEU:HA	1.84	0.42
41:2j:44:VAL:HG22	41:2j:66:ARG:HB3	2.02	0.42
54:2w:260:LYS:HD3	54:2w:260:LYS:HA	1.78	0.42
1:1A:784:A:C8	1:1A:792:G:C5	3.07	0.42
1:1A:1091:G:C2	1:1A:1101:U:H1'	2.54	0.42
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.51	0.42
1:1A:2287:A:O2'	1:1A:2289:G:N7	2.49	0.42
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.19	0.42
2:1B:12:C:N3	22:10:74:ARG:NH2	2.63	0.42
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.19	0.42
6:1G:25:TYR:HB3	6:1G:30:GLU:HB2	2.01	0.42
8:1I:54:GLN:HE21	8:1I:57:ARG:NH2	2.18	0.42
10:1O:2:ILE:HG13	10:1O:8:LEU:HD21	2.01	0.42
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.39	0.42
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.20	0.42
32:1a:1148:U:O4'	40:1i:16:ARG:HD2	2.19	0.42
32:1a:1319:A:H61	32:1a:1361:G:N2	2.18	0.42
35:1d:124:GLY:C	35:1d:126:ILE:N	2.78	0.42
37:1f:84:ASN:O	37:1f:86:ARG:HG3	2.20	0.42
1:2A:588:U:H1'	5:2F:90:PHE:CG	2.55	0.42
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.20	0.42
1:2A:2722:G:H5'	13:2R:4:LEU:HD12	2.00	0.42
8:2I:52:ARG:HE	8:2I:52:ARG:HB2	1.43	0.42
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.35	0.42
32:2a:524:G:H2'	32:2a:525:C:C6	2.54	0.42
32:2a:771:G:N7	61:2a:1821:HOH:O	2.37	0.42
32:2a:922:G:N3	32:2a:1398:A:H2	2.17	0.42
32:2a:1240:U:OP2	38:2g:116:ALA:N	2.53	0.42
32:2a:1256:A:H4'	32:2a:1257:U:H4'	2.01	0.42
32:2a:1315:U:OP2	50:2s:7:LYS:NZ	2.38	0.42
38:2g:153:HIS:ND1	42:2k:58:PRO:HD2	2.34	0.42
42:2k:98:LEU:O	42:2k:101:SER:OG	2.28	0.42
42:2k:116:HIS:O	42:2k:117:ASN:HB2	2.20	0.42
46:2o:62:GLN:O	46:2o:66:LEU:HG	2.20	0.42
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.55	0.42
1:1A:898:C:H5'	1:1A:899:A:OP2	2.20	0.42
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.35	0.42
1:1A:2062:A:C2	56:1z:5:ALA:HB1	2.55	0.42
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.55	0.42
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.37	0.42
32:1a:457:C:H2'	32:1a:458:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:684:A:O2'	42:1k:39:PRO:O	2.25	0.42
32:1a:1005:A:H5"	32:1a:1006:C:C5	2.55	0.42
32:1a:1053:G:O5'	32:1a:1054:C:H3'	2.19	0.42
32:1a:1133:G:H2'	32:1a:1134:G:C8	2.55	0.42
32:1a:1370:G:C2	32:1a:1371:G:C8	3.08	0.42
34:1c:8:ILE:HD12	34:1c:16:ARG:HG3	2.02	0.42
35:1d:22:LYS:HB2	35:1d:26:CYS:SG	2.60	0.42
35:1d:173:TRP:CZ3	35:1d:174:LEU:HG	2.55	0.42
36:1e:144:THR:OG1	36:1e:147:ASP:OD1	2.34	0.42
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.55	0.42
1:2A:1529:G:C6	1:2A:1530:C:N4	2.88	0.42
1:2A:1539:G:H2'	1:2A:1540:U:O4'	2.20	0.42
1:2A:1920:OMC:O5'	1:2A:1920:OMC:H6	2.02	0.42
1:2A:2162:G:H2'	1:2A:2163:C:O4'	2.20	0.42
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.20	0.42
2:2B:24:G:N7	2:2B:56:G:H2'	2.35	0.42
7:2H:121:ILE:HD13	7:2H:121:ILE:HA	1.91	0.42
21:2Z:54:HIS:ND1	21:2Z:101:PRO:HG3	2.35	0.42
32:2a:945:G:C2	32:2a:946:A:C8	3.07	0.42
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.20	0.42
34:2c:85:ARG:HB2	34:2c:85:ARG:CZ	2.50	0.42
36:2e:40:ARG:NH1	36:2e:68:GLU:HA	2.35	0.42
40:2i:81:ILE:O	40:2i:85:LEU:HG	2.19	0.42
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.85	0.42
44:2m:108:ARG:HA	44:2m:108:ARG:HD3	1.86	0.42
46:2o:80:ALA:O	46:2o:83:GLU:HG3	2.20	0.42
54:2w:102:MET:HB3	54:2w:103:ASP:H	1.47	0.42
54:2w:302:ILE:HG13	54:2w:316:ARG:NE	2.34	0.42
1:1A:9:U:N3	1:1A:2629:A:H2	2.15	0.42
1:1A:228:A:H2'	1:1A:230:U:O4'	2.19	0.42
1:1A:1091:G:C5	1:1A:1092:C:C4	3.07	0.42
1:1A:1338:G:N7	19:1X:62:LYS:NZ	2.53	0.42
4:1E:141:ILE:HD12	4:1E:150:VAL:HG21	2.02	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.50	0.42
7:1H:54:ARG:HD3	7:1H:65:HIS:ND1	2.34	0.42
12:1Q:7:MET:HB3	12:1Q:7:MET:HE3	1.80	0.42
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	2.02	0.42
32:1a:435:C:H2'	32:1a:436:C:C6	2.55	0.42
32:1a:815:A:N7	32:1a:1509:C:O2'	2.49	0.42
32:1a:958:A:C2	50:1s:55:LYS:HB2	2.55	0.42
32:1a:975:A:H4'	32:1a:976:G:C5'	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1236:A:H2'	32:1a:1237:C:C6	2.55	0.42
32:1a:1254:C:H2'	32:1a:1255:G:O4'	2.20	0.42
32:1a:1289:A:H2'	32:1a:1290:G:H5'	2.02	0.42
40:1i:28:VAL:O	40:1i:31:GLN:N	2.52	0.42
48:1q:3:LYS:HB2	48:1q:60:ILE:HD11	2.02	0.42
1:2A:631:A:H2'	1:2A:632:A:O4'	2.20	0.42
1:2A:1501:C:O4'	3:2D:100:GLY:HA2	2.20	0.42
1:2A:2366:A:H2'	1:2A:2367:G:O4'	2.20	0.42
3:2D:20:ASP:OD1	3:2D:20:ASP:N	2.50	0.42
5:2F:7:TYR:O	5:2F:21:ALA:HA	2.20	0.42
5:2F:65:TRP:CZ2	5:2F:75:HIS:HD2	2.38	0.42
11:2P:133:SER:O	11:2P:137:LYS:HG3	2.20	0.42
15:2T:26:ASP:O	15:2T:49:VAL:HG22	2.20	0.42
24:22:51:ARG:O	24:22:55:ARG:HG2	2.19	0.42
32:2a:189(D):C:H2'	32:2a:189(E):U:O4'	2.20	0.42
32:2a:1022:G:H2'	32:2a:1023:G:C8	2.55	0.42
32:2a:1099:G:C6	32:2a:1100:C:C4	3.08	0.42
32:2a:1264:C:C4	32:2a:1272:G:O6	2.73	0.42
33:2b:93:VAL:HG21	33:2b:97:TRP:CD1	2.50	0.42
38:2g:100:ALA:O	38:2g:104:LEU:HG	2.20	0.42
41:2j:12:ASP:OD1	41:2j:13:HIS:N	2.53	0.42
51:2t:56:MET:HG3	51:2t:88:VAL:HG21	2.02	0.42
1:1A:65:C:H2'	1:1A:66:C:C6	2.55	0.42
1:1A:286:C:H2'	1:1A:287:C:C6	2.55	0.42
1:1A:948:G:H5'	61:1A:4518:HOH:O	2.20	0.42
1:1A:1654:A:C1'	1:1A:2823:A:H5'	2.50	0.42
1:1A:2405:G:O2'	1:1A:2406:U:OP1	2.30	0.42
1:1A:2512:C:H2'	1:1A:2513:G:O4'	2.20	0.42
10:1O:49:ARG:NH2	32:1a:1423:G:OP1	2.38	0.42
32:1a:439:A:C5	32:1a:441:A:H1'	2.55	0.42
32:1a:456:C:H2'	32:1a:457:C:H6	1.84	0.42
33:1b:21:ARG:HA	33:1b:39:ILE:HA	2.02	0.42
35:1d:79:PHE:CE1	35:1d:204:ILE:HD13	2.55	0.42
44:1m:86:CYS:SG	44:1m:87:TYR:N	2.93	0.42
1:2A:863:A:OP1	12:2Q:22:LYS:HG3	2.19	0.42
1:2A:1927:A:H2'	1:2A:1928:A:C8	2.55	0.42
1:2A:2399:G:H2'	1:2A:2400:G:O4'	2.20	0.42
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.52	0.42
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.55	0.42
2:2B:104:U:O2'	21:2Z:29:TYR:OH	2.24	0.42
4:2E:34:VAL:HG21	4:2E:78:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:124:LEU:HD22	5:2F:124:LEU:HA	1.81	0.42
8:2I:93:THR:O	8:2I:97:ILE:HG13	2.20	0.42
32:2a:625:G:H2'	32:2a:626:U:H6	1.84	0.42
32:2a:991:U:HO2'	32:2a:1212:U:H3	1.65	0.42
32:2a:1002:G:N2	32:2a:1039:C:C2	2.87	0.42
32:2a:1040:U:O4	32:2a:1041:A:N6	2.53	0.42
32:2a:1225:A:H5"	32:2a:1226:C:OP2	2.20	0.42
32:2a:1272:G:N2	32:2a:1273:G:C8	2.88	0.42
34:2c:87:LEU:O	34:2c:91:LEU:N	2.44	0.42
34:2c:127:ARG:HH12	34:2c:191:THR:HB	1.84	0.42
35:2d:70:ILE:HD11	35:2d:74:GLN:HB3	2.00	0.42
40:2i:45:ALA:HA	40:2i:48:GLU:OE1	2.20	0.42
54:2w:284:ARG:O	54:2w:288:THR:HG23	2.20	0.42
1:1A:65:C:H2'	1:1A:66:C:H6	1.84	0.41
1:1A:303:U:H2'	1:1A:304:G:C8	2.55	0.41
1:1A:372:G:H8	23:11:65:SER:O	2.03	0.41
1:1A:687:C:H1'	29:17:4:THR:HG22	2.01	0.41
1:1A:813:U:H2'	1:1A:814:C:C6	2.55	0.41
1:1A:1142(A):A:C4	1:1A:1144:G:N7	2.88	0.41
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.55	0.41
1:1A:2790:A:N3	1:1A:2790:A:H2'	2.33	0.41
15:1T:64:ARG:HB2	15:1T:73:GLU:HG2	2.02	0.41
20:1Y:14:LEU:HD12	20:1Y:23:ARG:O	2.19	0.41
21:1Z:1:MET:N	21:1Z:2:GLU:HA	2.35	0.41
31:19:25:VAL:O	31:19:33:LYS:HA	2.20	0.41
32:1a:948:C:OP2	44:1m:106:ASN:HB3	2.19	0.41
32:1a:974:A:O4'	45:1n:31:ARG:HD3	2.20	0.41
32:1a:979:C:H42	45:1n:18:VAL:HB	1.84	0.41
32:1a:993:G:O2'	32:1a:994:A:N7	2.52	0.41
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.55	0.41
32:1a:1292:U:P	38:1g:41:ARG:HH22	2.44	0.41
33:1b:125:PRO:O	33:1b:126:GLU:C	2.63	0.41
35:1d:122:ARG:HD2	35:1d:122:ARG:HA	1.65	0.41
50:1s:38:SER:C	50:1s:70:LYS:HD3	2.45	0.41
51:1t:67:ALA:HB2	51:1t:77:ALA:HB2	2.00	0.41
1:2A:302:C:OP2	20:2Y:73:ARG:NH1	2.41	0.41
1:2A:314:A:H2'	1:2A:315:G:C8	2.55	0.41
1:2A:1399:C:C2'	1:2A:1400:G:H5'	2.50	0.41
1:2A:1405:U:H2'	1:2A:1406:U:H6	1.82	0.41
1:2A:2097:C:H2'	1:2A:2098:U:C6	2.55	0.41
1:2A:2109:U:C2'	1:2A:2110:G:H5'	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.85	0.41
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	2.02	0.41
14:2S:24:LEU:HB2	14:2S:85:VAL:HG22	2.01	0.41
18:2W:45:TYR:CZ	18:2W:49:LYS:HE3	2.55	0.41
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.35	0.41
32:2a:1004:A:H5"	32:2a:1024:G:H22	1.84	0.41
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	2.01	0.41
36:2e:19:MET:SD	36:2e:24:ARG:HB3	2.59	0.41
36:2e:40:ARG:HH11	36:2e:68:GLU:HA	1.85	0.41
45:2n:11:LYS:HE3	45:2n:11:LYS:HB2	1.92	0.41
1:1A:271(M):G:H21	8:1I:50:ARG:HH11	1.68	0.41
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.68	0.41
1:1A:857:C:N4	1:1A:858:U:O4	2.54	0.41
1:1A:2105:C:C2	1:1A:2106:G:C8	3.07	0.41
1:1A:2471:C:H2'	1:1A:2472:G:O4'	2.20	0.41
1:1A:2543:G:H2'	1:1A:2544:G:C8	2.55	0.41
5:1F:176:LEU:HD13	5:1F:181:LEU:HA	2.02	0.41
12:1Q:17:LEU:HB3	12:1Q:39:PRO:HB2	2.02	0.41
32:1a:256:U:P	48:1q:17:LYS:HZ2	2.43	0.41
32:1a:403:C:H2'	32:1a:404:U:H6	1.85	0.41
32:1a:457:C:H2'	32:1a:458:C:H6	1.85	0.41
32:1a:1304:G:C5	32:1a:1305:G:C6	3.08	0.41
1:2A:263:C:H2'	1:2A:264:C:O4'	2.20	0.41
1:2A:659:C:H2'	1:2A:660:G:H8	1.86	0.41
1:2A:827:U:O2'	1:2A:2068:U:C2	2.67	0.41
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.65	0.41
1:2A:2699:C:H2'	1:2A:2700:C:O4'	2.20	0.41
1:2A:2836:U:C4	1:2A:2883:A:N6	2.87	0.41
2:2B:43:C:C4	2:2B:45:A:C6	3.07	0.41
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.55	0.41
4:2E:31:CYS:HB3	4:2E:49:LEU:HB3	2.02	0.41
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	2.02	0.41
6:2G:176:LEU:HD23	6:2G:176:LEU:HA	1.94	0.41
11:2P:63:PRO:HB2	30:28:30:ARG:NH2	2.35	0.41
12:2Q:133:ARG:HG2	12:2Q:134:ARG:N	2.35	0.41
13:2R:100:LEU:HD21	13:2R:113:LEU:HD23	2.01	0.41
15:2T:64:ARG:NH1	15:2T:73:GLU:OE2	2.54	0.41
18:2W:58:ALA:HB1	18:2W:64:MET:HB2	2.02	0.41
18:2W:86:LEU:HD22	18:2W:96:ILE:HD11	2.01	0.41
32:2a:939:G:H2'	32:2a:940:C:C6	2.54	0.41
32:2a:1146:A:H2'	32:2a:1147:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:76:ARG:NH2	35:2d:80:GLU:OE2	2.53	0.41
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.59	0.41
54:2w:131:TYR:CE1	54:2w:174:GLU:HG3	2.55	0.41
55:2x:76:8AN:N3	61:2x:205:HOH:O	2.37	0.41
1:1A:58:G:O2'	1:1A:73:A:N1	2.48	0.41
1:1A:118:A:H3'	1:1A:119:A:H5"	2.02	0.41
1:1A:2203:U:O2'	1:1A:2205:C:H5'	2.21	0.41
1:1A:2334:G:O6	22:10:74:ARG:NH1	2.47	0.41
1:1A:2748:A:H2'	1:1A:2749:A:O4'	2.20	0.41
1:1A:2804:C:H2'	1:1A:2805:G:C8	2.55	0.41
1:1A:2820:A:C8	4:1E:109:LYS:HE2	2.55	0.41
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	2.02	0.41
23:11:44:PRO:O	23:11:46:LEU:N	2.53	0.41
24:12:32:LEU:HD13	24:12:36:ARG:NH1	2.35	0.41
29:17:11:LYS:HE3	29:17:15:THR:OG1	2.20	0.41
32:1a:1318:A:H1'	50:1s:37:ARG:HH11	1.85	0.41
32:1a:1322:C:N4	61:1a:1925:HOH:O	2.54	0.41
33:1b:74:LYS:O	33:1b:78:GLN:HG2	2.20	0.41
33:1b:219:VAL:HG12	33:1b:222:ILE:HD12	2.03	0.41
35:1d:153:ARG:CB	35:1d:181:MET:HE1	2.49	0.41
36:1e:100:VAL:HG13	36:1e:107:ARG:NH1	2.36	0.41
37:1f:39:LYS:HB2	37:1f:64:GLN:HB3	2.02	0.41
54:1w:128:PHE:CZ	54:1w:132:LEU:HD11	2.55	0.41
1:2A:118:A:H1'	1:2A:178:G:O4'	2.20	0.41
1:2A:443:A:N7	5:2F:45:ARG:HG2	2.34	0.41
1:2A:569:U:C4	1:2A:570:G:C6	3.08	0.41
1:2A:1688:U:H1'	1:2A:1701:A:C6	2.56	0.41
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.54	0.41
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.55	0.41
6:2G:3:LEU:HD22	26:24:25:TYR:CE1	2.54	0.41
7:2H:25:LYS:HB3	7:2H:25:LYS:HE2	1.74	0.41
11:2P:90:ARG:HH12	11:2P:105:LEU:HD21	1.85	0.41
18:2W:78:GLU:OE2	18:2W:99:ARG:HD3	2.21	0.41
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG11	2.02	0.41
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	2.00	0.41
32:2a:373:A:O2'	32:2a:451:A:N7	2.52	0.41
32:2a:552:U:O2	43:2l:31:PRO:HB3	2.20	0.41
32:2a:876:G:C1'	39:2h:11:THR:HG21	2.50	0.41
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.34	0.41
33:2b:59:GLU:HG2	33:2b:63:MET:HE2	2.02	0.41
42:2k:62:GLN:O	42:2k:66:LEU:HG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:9:PHE:N	47:2p:16:HIS:O	2.51	0.41
1:1A:581:C:H5"	61:1U:306:HOH:O	2.20	0.41
1:1A:1024:G:O2'	1:1A:1144:G:O2'	2.38	0.41
1:1A:1030:G:OP2	12:1Q:128:LYS:NZ	2.53	0.41
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.20	0.41
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.52	0.41
1:1A:2096:U:H3	1:1A:2193:G:H1	1.69	0.41
32:1a:202:U:O2'	32:1a:203:U:O5'	2.36	0.41
32:1a:503:C:OP2	43:1l:116:SER:OG	2.30	0.41
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.19	0.41
44:1m:23:TYR:CE2	44:1m:70:LEU:HB3	2.54	0.41
46:1o:4:THR:OG1	46:1o:7:GLU:HG3	2.21	0.41
53:1v:17:G:C6	53:1v:18:C:N4	2.89	0.41
1:2A:195:A:H2'	1:2A:198:C:N4	2.36	0.41
1:2A:579:G:H2'	1:2A:580:C:C6	2.55	0.41
1:2A:586:A:N1	1:2A:809:G:O2'	2.35	0.41
1:2A:1448:G:H2'	1:2A:1449:A:C8	2.56	0.41
1:2A:1799:G:O2'	3:2D:181:GLU:OE2	2.35	0.41
1:2A:2125:G:H22	1:2A:2172:U:P	2.44	0.41
3:2D:70:TRP:HB3	3:2D:190:TYR:CE2	2.55	0.41
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	2.02	0.41
5:2F:89:VAL:HG12	5:2F:90:PHE:CD2	2.55	0.41
6:2G:67:LYS:HD2	26:24:5:ILE:HB	2.02	0.41
20:2Y:28:LYS:HB3	20:2Y:28:LYS:HE2	1.84	0.41
26:24:46:GLN:HB3	26:24:48:ARG:NH1	2.36	0.41
28:26:10:LEU:HB2	28:26:52:VAL:HG12	2.02	0.41
32:2a:189:G:C6	32:2a:189(L):G:C6	3.09	0.41
32:2a:625:G:H2'	32:2a:626:U:C6	2.55	0.41
32:2a:643:C:H2'	32:2a:644:G:H8	1.86	0.41
32:2a:938:A:C6	32:2a:939:G:C5	3.08	0.41
32:2a:1287:A:H61	32:2a:1371:G:C1'	2.31	0.41
32:2a:1320:C:N4	50:2s:36:ARG:HB2	2.35	0.41
32:2a:1323:G:H4'	32:2a:1363:C:C2	2.55	0.41
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.35	0.41
32:2a:1530:G:H2'	32:2a:1531:A:O4'	2.20	0.41
34:2c:139:GLN:NE2	34:2c:143:GLU:HG3	2.34	0.41
35:2d:15:GLU:HB3	35:2d:63:LYS:HG3	2.01	0.41
44:2m:10:PRO:HD2	44:2m:18:ALA:HB1	2.03	0.41
1:1A:271(A):A:N1	1:1A:272(D):G:O2'	2.50	0.41
1:1A:1636:C:H2'	1:1A:1637:A:C8	2.56	0.41
1:1A:2521:C:C4	1:1A:2522:U:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2554:U:H2'	1:1A:2555:U:C6	2.56	0.41
6:1G:143:GLU:HG2	26:14:27:THR:OG1	2.21	0.41
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.55	0.41
40:1i:79:LEU:HG	40:1i:83:ARG:HD2	2.02	0.41
55:1x:25:U:H2'	55:1x:26:A:O4'	2.21	0.41
1:2A:35:G:H2'	1:2A:36:G:O4'	2.20	0.41
1:2A:519:U:H2'	1:2A:520:G:H8	1.85	0.41
1:2A:882:G:H1	1:2A:894:C:H42	1.67	0.41
1:2A:945:A:C4	1:2A:2448:A:C2	3.08	0.41
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.20	0.41
1:2A:1153:C:H5'	16:2U:76:TYR:HE2	1.86	0.41
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.55	0.41
1:2A:2182:G:H2'	1:2A:2183:C:C6	2.56	0.41
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.56	0.41
1:2A:2528:U:H2'	1:2A:2530:A:O5'	2.20	0.41
1:2A:2558:C:H2'	1:2A:2559:C:O4'	2.21	0.41
1:2A:2689:U:H4'	1:2A:2690:C:H5'	2.03	0.41
7:2H:152:ARG:HA	7:2H:152:ARG:HD3	1.72	0.41
8:2I:45:LYS:O	8:2I:48:GLU:N	2.54	0.41
8:2I:104:GLN:C	8:2I:106:GLY:H	2.29	0.41
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	2.02	0.41
10:2O:10:VAL:HG11	10:2O:16:ALA:HB3	2.02	0.41
17:2V:34:GLU:HA	17:2V:57:VAL:O	2.21	0.41
18:2W:7:ALA:HB2	18:2W:50:VAL:HG22	2.01	0.41
32:2a:409:G:OP1	35:2d:24:GLU:N	2.53	0.41
32:2a:1005:A:H3'	32:2a:1006:C:H6	1.84	0.41
33:2b:100:GLY:O	33:2b:104:ASN:N	2.44	0.41
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.31	0.41
40:2i:114:TYR:H	40:2i:114:TYR:HD2	1.69	0.41
1:1A:289:A:H2'	1:1A:290:G:O4'	2.21	0.41
1:1A:330:A:N7	1:1A:1210:A:O2'	2.46	0.41
1:1A:1756:G:H4'	1:1A:1758:G:O4'	2.20	0.41
1:1A:2142:C:H2'	1:1A:2143:C:C6	2.55	0.41
1:1A:2156:G:H2'	1:1A:2157:G:C2	2.56	0.41
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.55	0.41
1:1A:2853:C:H2'	1:1A:2854:G:H8	1.84	0.41
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	2.03	0.41
21:1Z:40:ASP:OD2	21:1Z:42:VAL:HG22	2.20	0.41
32:1a:196:A:N3	32:1a:222:U:H1'	2.36	0.41
32:1a:945:G:C2	32:1a:946:A:C8	3.08	0.41
32:1a:1310:G:OP2	44:1m:88:ARG:NH2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1431:C:H2'	32:1a:1432:G:O4'	2.20	0.41
33:1b:21:ARG:H	33:1b:21:ARG:NH2	2.19	0.41
33:1b:132:LYS:O	33:1b:136:VAL:HG13	2.21	0.41
34:1c:164:ARG:HG2	34:1c:165:THR:H	1.85	0.41
36:1e:90:VAL:O	36:1e:120:THR:HA	2.19	0.41
43:1l:86:ARG:HG2	43:1l:101:VAL:HG22	2.03	0.41
43:1l:97:ARG:HB2	43:1l:98:TYR:CE2	2.56	0.41
44:1m:3:ARG:HD3	44:1m:8:GLU:OE2	2.20	0.41
45:1n:32:SER:O	45:1n:40:CYS:HA	2.21	0.41
1:2A:287:C:H2'	1:2A:288:C:H6	1.85	0.41
1:2A:358:U:H2'	1:2A:359:A:H8	1.85	0.41
1:2A:899:A:O2'	1:2A:900:A:H5'	2.20	0.41
1:2A:1186:G:H2'	1:2A:1187:G:O4'	2.21	0.41
1:2A:1351:C:H2'	1:2A:1352:U:C6	2.56	0.41
1:2A:1529:G:O6	1:2A:1530:C:N4	2.54	0.41
1:2A:1669:A:O3'	1:2A:2549:G:H5"	2.21	0.41
1:2A:1814:G:C4'	3:2D:51:VAL:HG21	2.51	0.41
1:2A:2075:U:OP2	1:2A:2238:G:O2'	2.35	0.41
1:2A:2255:G:O2'	55:2x:3:C:H5'	2.20	0.41
1:2A:2466:C:H5'	31:29:5:ALA:HB3	2.01	0.41
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.21	0.41
5:2F:178:PRO:HB2	5:2F:201:VAL:CG2	2.51	0.41
6:2G:146:TYR:O	6:2G:149:VAL:HG12	2.21	0.41
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	2.02	0.41
16:2U:82:GLY:HA3	16:2U:113:ALA:HB1	2.02	0.41
32:2a:16:A:N3	32:2a:1080:A:O2'	2.44	0.41
32:2a:435:C:H2'	32:2a:436:C:C6	2.55	0.41
32:2a:718:G:H5'	42:2k:117:ASN:ND2	2.36	0.41
32:2a:980:C:H3'	32:2a:981:U:C6	2.55	0.41
32:2a:994:A:N7	32:2a:1216:G:H4'	2.35	0.41
32:2a:1072:G:H2'	32:2a:1073:U:C6	2.56	0.41
32:2a:1364:U:O2'	32:2a:1365:G:H5'	2.21	0.41
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.55	0.41
40:2i:29:ASN:OD1	40:2i:65:VAL:N	2.53	0.41
43:2l:54:LYS:N	43:2l:54:LYS:HD2	2.35	0.41
45:2n:29:ARG:HD2	45:2n:40:CYS:SG	2.60	0.41
51:2t:53:LEU:HD12	51:2t:98:PRO:O	2.20	0.41
54:2w:125:ARG:HD2	54:2w:153:GLY:O	2.20	0.41
1:1A:625:G:N7	11:1P:107:LYS:NZ	2.65	0.41
1:1A:666:G:N2	30:18:2:PRO:O	2.54	0.41
1:1A:971:C:H2'	1:1A:972:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1059:G:OP2	1:1A:1059:G:H8	2.03	0.41
1:1A:1094:U:O3'	1:1A:1095:A:H8	2.04	0.41
1:1A:1358:G:N1	1:1A:1372:U:OP2	2.46	0.41
1:1A:1918:A:O2'	1:1A:1920:OMC:N4	2.54	0.41
1:1A:2789:C:H1'	1:1A:2892:A:H2	1.86	0.41
6:1G:43:LEU:HD22	6:1G:153:ARG:HD2	2.03	0.41
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.20	0.41
32:1a:4:U:O4	39:1h:105:ARG:HD2	2.20	0.41
32:1a:741:G:H2'	32:1a:742:G:O4'	2.20	0.41
32:1a:1178:G:OP1	40:1i:93:ARG:NH1	2.53	0.41
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.56	0.41
35:1d:166:LYS:HG2	35:1d:178:VAL:HG11	2.02	0.41
38:1g:32:ARG:HH21	38:1g:109:ASN:ND2	2.19	0.41
40:1i:23:ASN:O	40:1i:25:LYS:NZ	2.53	0.41
1:2A:230:U:H2'	1:2A:231:C:C6	2.55	0.41
1:2A:271(X):G:C2	1:2A:271(Y):U:O4	2.73	0.41
1:2A:887:A:H2'	1:2A:887:A:N3	2.36	0.41
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.20	0.41
1:2A:1400:G:H2'	1:2A:1401:G:O4'	2.20	0.41
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	2.03	0.41
16:2U:112:ARG:NH2	17:2V:47:VAL:HB	2.36	0.41
21:2Z:91:LEU:HD23	21:2Z:91:LEU:HA	1.80	0.41
23:21:44:PRO:HB2	23:21:46:LEU:HD12	2.02	0.41
26:24:26:SER:OG	26:24:27:THR:N	2.54	0.41
32:2a:67:C:H2'	32:2a:68:G:H8	1.82	0.41
32:2a:126:G:H5'	32:2a:633:G:N2	2.36	0.41
32:2a:165:C:H2'	32:2a:166:G:C8	2.54	0.41
32:2a:841:U:H6	32:2a:841:U:OP2	2.03	0.41
32:2a:973:G:O3'	45:2n:41:ARG:NH2	2.51	0.41
32:2a:1002:G:H3'	32:2a:1003:G:H4'	2.03	0.41
32:2a:1014:A:H4'	50:2s:14:HIS:NE2	2.35	0.41
32:2a:1026:G:O6	32:2a:1036:G:N1	2.54	0.41
32:2a:1085:U:H3'	32:2a:1086:U:C5	2.55	0.41
32:2a:1240:U:C2	38:2g:32:ARG:HD3	2.55	0.41
32:2a:1375:A:C6	32:2a:1376:U:C4	3.08	0.41
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.56	0.41
33:2b:50:GLU:HB3	33:2b:200:ILE:O	2.20	0.41
36:2e:10:MET:HE3	36:2e:13:ILE:HD11	2.03	0.41
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.29	0.41
55:2x:14:A:C2	55:2x:22:A:C8	3.09	0.41
1:1A:118:A:N3	1:1A:178:G:H1'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:278:A:H2'	1:1A:279:C:C6	2.56	0.41
1:1A:1012:U:C5	9:1N:28:THR:HG21	2.56	0.41
1:1A:1087:G:C8	1:1A:1087:G:O5'	2.74	0.41
1:1A:1354:A:H5"	3:1D:38:LYS:HD3	2.03	0.41
1:1A:2177:C:H2'	1:1A:2178:C:O4'	2.21	0.41
2:1B:88:C:H2'	2:1B:89:G:O4'	2.21	0.41
5:1F:135:LYS:HA	5:1F:135:LYS:HD2	1.94	0.41
32:1a:73:G:H1	32:1a:96:U:H3	1.69	0.41
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.55	0.41
32:1a:1134:G:N1	32:1a:1141:C:N3	2.69	0.41
41:1j:38:ILE:HG13	41:1j:71:LEU:O	2.20	0.41
42:1k:56:GLY:O	42:1k:89:ALA:HB3	2.19	0.41
51:1t:11:SER:O	51:1t:15:ARG:N	2.49	0.41
1:2A:228:A:O2'	1:2A:229:A:H4'	2.21	0.41
1:2A:699:A:H2'	1:2A:700:G:O4'	2.20	0.41
1:2A:1128:A:O4'	1:2A:2516:G:O2'	2.38	0.41
2:2B:41:U:H5	6:2G:70:VAL:H	1.69	0.41
6:2G:102:PHE:CE2	6:2G:106:LEU:HD22	2.56	0.41
8:2I:62:LYS:HE2	8:2I:133:HIS:CE1	2.43	0.41
19:2X:94:GLY:N	19:2X:95:LEU:HB2	2.34	0.41
22:20:17:GLN:HB2	22:20:19:LYS:NZ	2.35	0.41
32:2a:275:G:O5'	48:2q:14:LYS:HB3	2.21	0.41
32:2a:920:U:H2'	32:2a:921:U:C6	2.55	0.41
32:2a:995:C:O2'	32:2a:996:A:H5'	2.21	0.41
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.36	0.41
32:2a:1141:C:C2	32:2a:1142:G:C8	3.09	0.41
32:2a:1258:G:H2'	32:2a:1259:C:H6	1.85	0.41
33:2b:72:GLY:HA3	33:2b:81:VAL:HG11	2.02	0.41
1:1A:322:A:OP1	5:1F:168:ARG:HD3	2.21	0.41
1:1A:551:G:O2'	1:1A:1220:A:N3	2.43	0.41
1:1A:581:C:H2'	1:1A:582:G:H8	1.86	0.41
1:1A:1101:U:H2'	1:1A:1102:C:C6	2.56	0.41
1:1A:1643:G:H2'	1:1A:1644:C:O4'	2.20	0.41
1:1A:2067:G:O2'	1:1A:2069:G:H5'	2.21	0.41
1:1A:2135:A:N6	1:1A:2156:G:O2'	2.54	0.41
1:1A:2740:A:H2'	1:1A:2741:A:C8	2.56	0.41
5:1F:89:VAL:HG12	5:1F:90:PHE:CD2	2.56	0.41
8:1I:81:VAL:HG21	8:1I:88:ILE:HD13	2.03	0.41
8:1I:87:LYS:H	8:1I:87:LYS:HG3	1.50	0.41
19:1X:94:GLY:N	19:1X:95:LEU:HB2	2.31	0.41
32:1a:165:C:H2'	32:1a:166:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:452:A:O4'	47:1p:72:ARG:NH1	2.53	0.41
32:1a:779:C:H2'	32:1a:780:A:O4'	2.21	0.41
32:1a:811:C:O2'	32:1a:901:A:N1	2.50	0.41
32:1a:1304:G:OP2	61:1a:1918:HOH:O	2.22	0.41
32:1a:1338:G:C6	32:1a:1339:A:C6	3.09	0.41
34:1c:62:ASP:O	34:1c:97:LYS:HB2	2.21	0.41
35:1d:143:GLY:N	35:1d:185:PHE:O	2.49	0.41
38:1g:80:VAL:HG21	38:1g:85:TYR:CD2	2.56	0.41
38:1g:104:LEU:HA	38:1g:104:LEU:HD12	1.77	0.41
51:1t:8:ARG:HD3	51:1t:8:ARG:HA	1.97	0.41
1:2A:90:U:H1'	1:2A:92:A:C8	2.56	0.41
1:2A:295:G:H5'	20:2Y:1:MET:HG2	2.02	0.41
1:2A:528:A:N1	1:2A:2042:A:H2'	2.36	0.41
1:2A:642:G:H21	1:2A:646:A:H2	1.67	0.41
1:2A:1154:G:OP1	16:2U:58:ARG:HG2	2.21	0.41
1:2A:1782:C:O2	1:2A:2608:G:O2'	2.31	0.41
1:2A:2103:C:H2'	1:2A:2104:G:O4'	2.21	0.41
1:2A:2161:C:H2'	1:2A:2162:G:O4'	2.20	0.41
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.55	0.41
1:2A:2471:C:H2'	1:2A:2472:G:O4'	2.21	0.41
1:2A:2702:U:H4'	1:2A:2703:C:OP1	2.21	0.41
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.21	0.41
2:2B:24:G:H4'	2:2B:25:A:C8	2.56	0.41
3:2D:158:ALA:O	3:2D:161:THR:OG1	2.37	0.41
7:2H:11:VAL:HG12	7:2H:12:PRO:O	2.21	0.41
7:2H:74:ASN:O	7:2H:78:GLY:N	2.54	0.41
8:2I:121:LYS:HE2	8:2I:121:LYS:HB3	1.85	0.41
21:2Z:144:LEU:HD23	21:2Z:144:LEU:HA	1.85	0.41
23:21:71:TYR:O	23:21:74:VAL:HG22	2.21	0.41
26:24:61:ARG:HH11	50:2s:9:VAL:HG21	1.85	0.41
32:2a:34:C:H2'	32:2a:35:G:C8	2.56	0.41
32:2a:229:U:H5"	47:2p:33:ILE:HD13	2.02	0.41
32:2a:396:G:O2'	32:2a:398:C:OP1	2.23	0.41
32:2a:413:G:H21	32:2a:428:G:H1'	1.86	0.41
32:2a:766:A:H2'	32:2a:767:A:O4'	2.21	0.41
32:2a:772:U:H2'	32:2a:773:G:O4'	2.20	0.41
32:2a:1134:G:C2	32:2a:1135:U:H1'	2.56	0.41
32:2a:1134:G:N1	32:2a:1135:U:H1'	2.35	0.41
32:2a:1244:C:H2'	32:2a:1245:A:C8	2.56	0.41
32:2a:1326:C:H2'	32:2a:1327:C:C6	2.55	0.41
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1363(A):A:H1'	32:2a:1365:G:N7	2.36	0.41
32:2a:1485:U:H2'	32:2a:1486:G:C8	2.56	0.41
33:2b:97:TRP:CH2	33:2b:173:ALA:HA	2.56	0.41
50:2s:74:PHE:O	50:2s:76:PRO:HD3	2.21	0.41
1:1A:196:A:H2'	1:1A:196:A:N3	2.35	0.41
1:1A:518:G:H2'	1:1A:519:U:C6	2.56	0.41
1:1A:1818:U:OP2	3:1D:157:ARG:NH2	2.48	0.41
1:1A:2360:A:H8	1:1A:2360:A:O5'	2.04	0.41
1:1A:2626:C:H2'	1:1A:2627:G:O4'	2.21	0.41
1:1A:2791:C:H2'	1:1A:2792:G:C8	2.56	0.41
1:1A:2820:A:P	13:1R:2:ARG:HH22	2.44	0.41
5:1F:179:GLU:CD	5:1F:179:GLU:H	2.29	0.41
7:1H:98:LEU:HG	7:1H:125:VAL:HG23	2.02	0.41
13:1R:2:ARG:N	61:1R:304:HOH:O	2.54	0.41
24:12:3:LEU:O	24:12:7:ARG:HG3	2.21	0.41
32:1a:8:A:C6	35:1d:209:ARG:HB2	2.56	0.41
32:1a:555:C:H2'	32:1a:556:C:C6	2.56	0.41
32:1a:691:G:H2'	32:1a:692:U:C6	2.56	0.41
33:1b:174:VAL:O	33:1b:178:ARG:HG3	2.20	0.41
45:1n:21:TYR:HE1	45:1n:23:ARG:NE	2.18	0.41
48:1q:15:MET:HB3	48:1q:18:THR:HB	2.02	0.41
51:1t:64:ASP:OD1	51:1t:81:LYS:HD2	2.21	0.41
54:1w:302:ILE:HG13	54:1w:316:ARG:CD	2.50	0.41
1:2A:184:C:H2'	1:2A:185:U:C6	2.56	0.41
1:2A:881:G:H1	1:2A:895:U:H3	1.68	0.41
1:2A:947:G:H2'	1:2A:948:G:C8	2.55	0.41
1:2A:2191:G:H2'	1:2A:2192:G:O4'	2.21	0.41
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.55	0.41
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	2.03	0.41
4:2E:181:LEU:HD11	15:2T:6:LEU:HG	2.03	0.41
5:2F:22:ALA:HB1	5:2F:24:LEU:HD13	2.03	0.41
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.21	0.41
25:23:5:LYS:NZ	25:23:34:GLU:OE2	2.46	0.41
25:23:6:VAL:O	25:23:34:GLU:HA	2.21	0.41
32:2a:4:U:O4	39:2h:105:ARG:HD2	2.21	0.41
32:2a:814:A:H2'	32:2a:816:A:H5"	2.01	0.41
32:2a:1177:G:H2'	32:2a:1178:G:O4'	2.21	0.41
32:2a:1479:C:H2'	32:2a:1480:G:H8	1.86	0.41
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.88	0.41
34:2c:98:ASN:HD22	34:2c:98:ASN:H	1.68	0.41
35:2d:119:GLN:HG2	35:2d:123:HIS:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:51:VAL:O	36:2e:55:VAL:HG23	2.21	0.41
50:2s:20:LEU:HD23	50:2s:23:ASN:ND2	2.36	0.41
50:2s:40:ILE:H	50:2s:40:ILE:HG13	1.69	0.41
1:1A:153:C:H2'	1:1A:154:G:C8	2.55	0.40
1:1A:234:C:H2'	1:1A:235:U:H6	1.85	0.40
1:1A:493:G:H2'	1:1A:494:G:O4'	2.20	0.40
1:1A:531:C:H4'	1:1A:532:A:H5"	2.02	0.40
1:1A:768:G:C6	1:1A:769:G:C5	3.09	0.40
1:1A:1265:A:H3'	27:15:19:ARG:HH21	1.85	0.40
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.57	0.40
1:1A:1335:U:H2'	1:1A:1336:A:O4'	2.20	0.40
1:1A:1668:A:O2'	1:1A:1674:G:N7	2.46	0.40
1:1A:1745(A):C:H5'	1:1A:1746:G:OP2	2.21	0.40
1:1A:2206:G:H5"	1:1A:2207:G:N7	2.36	0.40
1:1A:2303:G:O2'	6:1G:132:ASN:HB2	2.22	0.40
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.26	0.40
3:1D:108:PRO:HG3	3:1D:143:HIS:CE1	2.57	0.40
6:1G:56:ALA:HA	6:1G:59:GLU:HG2	2.03	0.40
24:12:65:ASN:O	24:12:69:ARG:HG3	2.21	0.40
33:1b:89:GLY:O	33:1b:90:MET:HE2	2.21	0.40
38:1g:13:GLN:NE2	38:1g:14:PRO:HD2	2.36	0.40
40:1i:8:GLY:C	40:1i:76:ALA:HB1	2.46	0.40
41:1j:55:LYS:HE2	41:1j:55:LYS:HB3	1.75	0.40
53:1v:19:U:N3	54:1w:116:GLY:O	2.50	0.40
1:2A:373:U:H2'	1:2A:374:A:C8	2.54	0.40
1:2A:519:U:H2'	1:2A:520:G:C8	2.56	0.40
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.85	0.40
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.57	0.40
1:2A:1676:A:H2'	1:2A:1677:A:O4'	2.21	0.40
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.56	0.40
1:2A:2250:G:O2'	1:2A:2496:C:OP1	2.32	0.40
1:2A:2471:C:N4	1:2A:2476:A:O2'	2.54	0.40
61:2A:4728:HOH:O	23:21:3:LYS:HE2	2.20	0.40
2:2B:89:G:H2'	2:2B:90:A:C8	2.57	0.40
7:2H:83:TYR:CE2	7:2H:138:LYS:HB2	2.56	0.40
8:2I:117:GLU:HG3	8:2I:118:LYS:H	1.86	0.40
9:2N:75:TYR:CE2	9:2N:77:GLY:HA2	2.56	0.40
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.30	0.40
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.81	0.40
25:23:11:SER:HA	25:23:31:LEU:HD11	2.02	0.40
32:2a:460:G:N2	32:2a:471:G:OP2	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:629:G:H2'	32:2a:630:G:O4'	2.21	0.40
32:2a:779:C:H2'	32:2a:780:A:O4'	2.21	0.40
32:2a:1466:C:H2'	32:2a:1467:G:O4'	2.21	0.40
33:2b:114:ARG:NH1	33:2b:117:GLU:OE1	2.52	0.40
33:2b:122:PHE:CD2	33:2b:142:LEU:HD13	2.57	0.40
36:2e:131:ILE:O	36:2e:135:THR:HG23	2.20	0.40
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.57	0.40
45:2n:32:SER:O	45:2n:40:CYS:HA	2.21	0.40
1:1A:880:G:C2	1:1A:881:G:C8	3.09	0.40
1:1A:1113:U:H2'	1:1A:1114:G:H8	1.85	0.40
1:1A:1683:C:H2'	1:1A:1684:C:C6	2.56	0.40
1:1A:2032:G:OP2	1:1A:2454:G:O2'	2.30	0.40
5:1F:29:ASN:HB3	5:1F:112:MET:HE1	2.03	0.40
5:1F:170:LEU:HD13	5:1F:172:TRP:CZ2	2.56	0.40
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	2.03	0.40
6:1G:127:GLY:HA2	6:1G:166:ASP:OD2	2.21	0.40
25:13:4:LEU:O	25:13:36:VAL:HA	2.20	0.40
32:1a:738:C:H2'	32:1a:739:C:H6	1.86	0.40
32:1a:1468:A:H2'	32:1a:1469:G:O4'	2.20	0.40
33:1b:55:PHE:HA	33:1b:58:ILE:HD12	2.02	0.40
34:1c:22:TRP:CG	34:1c:59:ARG:HB2	2.56	0.40
35:1d:18:LYS:HD3	35:1d:20:TYR:CZ	2.57	0.40
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	2.03	0.40
40:1i:54:ASP:O	40:1i:56:LEU:N	2.54	0.40
51:1t:14:LYS:HG3	51:1t:17:ARG:HH21	1.86	0.40
1:2A:244:A:C2	1:2A:255:A:C4	3.09	0.40
1:2A:280:C:C2	1:2A:361:G:C2	3.08	0.40
1:2A:797:C:OP1	5:2F:60:SER:OG	2.38	0.40
1:2A:910:A:N1	1:2A:2277:G:H1'	2.36	0.40
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.20	0.40
1:2A:2336:A:H61	22:20:43:THR:CG2	2.34	0.40
3:2D:222:ARG:O	3:2D:226:MET:HG3	2.21	0.40
19:2X:57:LEU:HD11	19:2X:78:LYS:HE2	2.03	0.40
23:21:80:LEU:HB3	23:21:82:LEU:HD21	2.02	0.40
29:27:8:ASN:HB3	29:27:11:LYS:HB3	2.02	0.40
32:2a:187:C:H2'	32:2a:188:C:C6	2.55	0.40
44:2m:11:ARG:H	44:2m:11:ARG:HG3	1.63	0.40
51:2t:97:ALA:HB1	51:2t:98:PRO:HD2	2.04	0.40
55:2x:7:U:O2'	55:2x:49:U:OP2	2.29	0.40
1:1A:35:G:H2'	1:1A:36:G:O4'	2.22	0.40
1:1A:39:C:O2	5:1F:46:ARG:NH2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:862:G:H2'	1:1A:863:A:O4'	2.22	0.40
1:1A:1153:C:H2'	1:1A:1154:G:O4'	2.22	0.40
1:1A:1313:U:H2'	1:1A:1610:A:C2	2.57	0.40
1:1A:2028:U:H2'	1:1A:2029:G:O4'	2.21	0.40
1:1A:2189:U:H2'	1:1A:2190:G:H8	1.86	0.40
4:1E:10:GLY:HA2	4:1E:192:ASN:OD1	2.21	0.40
6:1G:47:LYS:NZ	6:1G:80:PHE:O	2.49	0.40
32:1a:262:A:H2'	32:1a:263:A:C8	2.56	0.40
32:1a:385:C:H2'	32:1a:386:C:C6	2.56	0.40
32:1a:508:C:P	35:1d:209:ARG:HH21	2.44	0.40
32:1a:659:U:H2'	32:1a:660:G:H8	1.87	0.40
32:1a:723:U:O2'	32:1a:724:G:H5'	2.21	0.40
32:1a:763:G:H2'	32:1a:764:C:C6	2.57	0.40
32:1a:966:M2G:HM11	40:1i:127:LYS:HD3	2.03	0.40
32:1a:1326:C:H2'	32:1a:1327:C:C6	2.56	0.40
32:1a:1402:4OC:H2'	32:1a:1403:C:O4'	2.22	0.40
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.56	0.40
1:2A:1575:C:H2'	1:2A:1576:U:C6	2.56	0.40
1:2A:1815:A:P	3:2D:54:ARG:HH22	2.43	0.40
1:2A:1942:5MC:OP2	1:2A:1943:U:O2'	2.31	0.40
1:2A:2134:A:H2'	1:2A:2134:A:N3	2.36	0.40
2:2B:66:A:N6	2:2B:109:C:H5'	2.25	0.40
21:2Z:6:LYS:H	21:2Z:6:LYS:HG3	1.64	0.40
25:23:50:VAL:O	25:23:54:VAL:HB	2.21	0.40
32:2a:114:U:O2'	32:2a:115:G:H5'	2.21	0.40
32:2a:122:G:H2'	32:2a:123:C:O4'	2.22	0.40
32:2a:273:A:N6	32:2a:274:A:C6	2.89	0.40
32:2a:1001:A:H2'	32:2a:1001(A):G:C8	2.57	0.40
33:2b:130:ARG:HD3	33:2b:130:ARG:HA	1.89	0.40
34:2c:5:ILE:HD11	45:2n:49:HIS:CE1	2.50	0.40
34:2c:8:ILE:HG13	34:2c:9:GLY:N	2.36	0.40
37:2f:8:ILE:HB	37:2f:61:LEU:HB2	2.03	0.40
38:2g:80:VAL:HG22	38:2g:85:TYR:HE2	1.87	0.40
43:2l:53:ARG:HD2	43:2l:93:LEU:HD11	2.04	0.40
50:2s:40:ILE:HG23	50:2s:62:ILE:HD13	2.03	0.40
51:2t:54:LYS:HB3	51:2t:54:LYS:HE2	1.80	0.40
54:2w:115:THR:HG22	54:2w:196:THR:HB	2.03	0.40
1:1A:448:U:O4	1:1A:583:G:H1'	2.21	0.40
1:1A:614(C):A:C4	5:1F:180:GLY:HA3	2.56	0.40
1:1A:1107:G:H2'	1:1A:1108:U:C6	2.56	0.40
1:1A:1629:U:O4	61:1A:4143:HOH:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2019:A:N7	27:15:9:LYS:HE2	2.37	0.40
1:1A:2059:A:O2'	5:1F:69:HIS:HD2	2.04	0.40
1:1A:2678:C:H2'	1:1A:2679:A:O4'	2.21	0.40
5:1F:124:LEU:O	5:1F:193:VAL:HA	2.21	0.40
23:11:71:TYR:O	23:11:74:VAL:HG22	2.21	0.40
32:1a:8:A:H5'	36:1e:101:ILE:HG22	2.04	0.40
32:1a:131:C:O2'	32:1a:262:A:N3	2.50	0.40
32:1a:403:C:H2'	32:1a:404:U:C6	2.56	0.40
32:1a:491:G:H2'	32:1a:492:G:O4'	2.22	0.40
32:1a:763:G:H2'	32:1a:764:C:H6	1.86	0.40
40:1i:36:TYR:O	40:1i:70:LYS:NZ	2.48	0.40
47:1p:21:VAL:HG22	47:1p:33:ILE:HB	2.04	0.40
1:2A:391:G:H1'	1:2A:411:G:O4'	2.21	0.40
1:2A:394:A:O2'	1:2A:395:U:H5'	2.21	0.40
1:2A:629:G:H5"	1:2A:650:C:O2'	2.21	0.40
1:2A:871:U:OP1	12:2Q:5:ARG:HG3	2.22	0.40
1:2A:2307:G:N1	6:2G:43:LEU:O	2.51	0.40
1:2A:2725:A:H1'	1:2A:2726:U:H2'	2.03	0.40
6:2G:111:LEU:HB2	6:2G:112:PRO:HD3	2.02	0.40
8:2I:104:GLN:O	8:2I:106:GLY:N	2.54	0.40
8:2I:133:HIS:HB3	8:2I:136:VAL:HB	2.04	0.40
10:2O:77:ILE:HG13	10:2O:78:ARG:N	2.35	0.40
32:2a:143:A:H2	32:2a:220:G:H1	1.70	0.40
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.56	0.40
32:2a:1124:G:N2	32:2a:1125:U:O4	2.53	0.40
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.56	0.40
34:2c:184:TYR:HA	34:2c:200:ALA:O	2.22	0.40
36:2e:99:GLY:O	36:2e:117:ASP:HA	2.21	0.40
36:2e:145:LYS:O	36:2e:149:GLU:HB2	2.21	0.40
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.56	0.40
40:2i:31:GLN:NE2	40:2i:35:GLU:OE1	2.55	0.40
44:2m:22:ILE:HB	44:2m:25:ILE:HD12	2.03	0.40
44:2m:80:ARG:NH1	50:2s:65:ASN:O	2.51	0.40
54:2w:107:ALA:HB2	54:2w:168:TYR:HA	2.02	0.40
1:1A:172:C:H2'	1:1A:173:G:C8	2.56	0.40
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.57	0.40
1:1A:2184:G:C6	1:1A:2185:C:C4	3.10	0.40
2:1B:28:C:OP1	14:1S:36:TYR:OH	2.25	0.40
3:1D:218:ARG:HB3	3:1D:219:PRO:HD2	2.04	0.40
23:11:89:GLU:O	23:11:93:GLU:HG2	2.21	0.40
32:1a:313:A:H2'	32:1a:314:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:707:C:H5”	42:1k:85:ARG:HH12	1.87	0.40
32:1a:1036:G:H3’	32:1a:1037:C:C6	2.56	0.40
32:1a:1275:A:H2’	32:1a:1276:G:O4’	2.21	0.40
32:1a:1286:A:H2’	32:1a:1287:A:H4’	2.03	0.40
37:1f:37:VAL:HA	37:1f:65:VAL:HG13	2.03	0.40
43:1l:113:ARG:HB3	43:1l:122:THR:HG21	2.03	0.40
1:2A:41:C:H2’	1:2A:42:G:C8	2.57	0.40
1:2A:71:A:N7	19:2X:31:HIS:CE1	2.89	0.40
1:2A:659:C:H2’	1:2A:660:G:C8	2.57	0.40
1:2A:792:G:O2’	1:2A:2440:C:N3	2.49	0.40
1:2A:854:G:O6	61:2A:3945:HOH:O	2.18	0.40
1:2A:888:C:H2’	1:2A:889:C:C4	2.56	0.40
1:2A:1668:A:H4’	1:2A:1669:A:O5’	2.21	0.40
1:2A:2691:C:O3’	1:2A:2871:C:H4’	2.21	0.40
1:2A:2850:A:OP2	1:2A:2866:U:H5	2.05	0.40
15:2T:27:THR:HB	15:2T:89:VAL:HG22	2.04	0.40
21:2Z:100:VAL:O	21:2Z:124:ILE:HG22	2.22	0.40
32:2a:137:C:H2’	32:2a:138:G:C8	2.53	0.40
32:2a:298:A:OP1	32:2a:298:A:H8	2.04	0.40
32:2a:790:A:C6	32:2a:791:G:C6	3.09	0.40
32:2a:1030(A):G:H2’	32:2a:1030(C):G:OP2	2.21	0.40
38:2g:75:VAL:HA	38:2g:87:VAL:O	2.21	0.40
44:2m:106:ASN:HD22	44:2m:106:ASN:HA	1.61	0.40
45:2n:24:CYS:HB2	45:2n:40:CYS:HB3	2.03	0.40
46:2o:70:LEU:HD11	46:2o:77:ARG:HB2	2.03	0.40
49:2r:43:PHE:C	49:2r:51:LEU:HD12	2.46	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%)	262 (96%)	11 (4%)	0	100 100
3	2D	273/276 (99%)	257 (94%)	15 (6%)	1 (0%)	30 40
4	1E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	25 34
4	2E	202/206 (98%)	191 (95%)	10 (5%)	1 (0%)	25 34
5	1F	201/210 (96%)	194 (96%)	6 (3%)	1 (0%)	25 34
5	2F	201/210 (96%)	187 (93%)	11 (6%)	3 (2%)	8 11
6	1G	179/182 (98%)	167 (93%)	10 (6%)	2 (1%)	12 15
6	2G	179/182 (98%)	154 (86%)	21 (12%)	4 (2%)	5 5
7	1H	172/180 (96%)	162 (94%)	10 (6%)	0	100 100
7	2H	172/180 (96%)	157 (91%)	13 (8%)	2 (1%)	11 14
8	1I	144/148 (97%)	129 (90%)	14 (10%)	1 (1%)	19 26
8	2I	144/148 (97%)	125 (87%)	17 (12%)	2 (1%)	9 12
9	1N	138/140 (99%)	136 (99%)	2 (1%)	0	100 100
9	2N	138/140 (99%)	133 (96%)	5 (4%)	0	100 100
10	1O	120/122 (98%)	112 (93%)	8 (7%)	0	100 100
10	2O	120/122 (98%)	112 (93%)	7 (6%)	1 (1%)	16 23
11	1P	147/150 (98%)	141 (96%)	4 (3%)	2 (1%)	9 12
11	2P	147/150 (98%)	136 (92%)	9 (6%)	2 (1%)	9 12
12	1Q	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	19 26
12	2Q	139/141 (99%)	131 (94%)	5 (4%)	3 (2%)	5 5
13	1R	116/118 (98%)	114 (98%)	2 (2%)	0	100 100
13	2R	116/118 (98%)	113 (97%)	3 (3%)	0	100 100
14	1S	108/112 (96%)	103 (95%)	5 (5%)	0	100 100
14	2S	108/112 (96%)	101 (94%)	7 (6%)	0	100 100
15	1T	129/146 (88%)	122 (95%)	7 (5%)	0	100 100
15	2T	129/146 (88%)	122 (95%)	7 (5%)	0	100 100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
16	2U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
17	1V	99/101 (98%)	95 (96%)	2 (2%)	2 (2%)	6 6
17	2V	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	13 18
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100 100
18	2W	110/113 (97%)	103 (94%)	7 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	1X	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
19	2X	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
20	1Y	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
20	2Y	105/110 (96%)	96 (91%)	7 (7%)	2 (2%)	6	7
21	1Z	148/206 (72%)	132 (89%)	13 (9%)	3 (2%)	6	6
21	2Z	156/206 (76%)	140 (90%)	14 (9%)	2 (1%)	10	13
22	10	74/85 (87%)	71 (96%)	3 (4%)	0	100	100
22	20	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
23	11	95/98 (97%)	91 (96%)	2 (2%)	2 (2%)	5	6
23	21	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	14	67/71 (94%)	54 (81%)	11 (16%)	2 (3%)	3	2
26	24	67/71 (94%)	52 (78%)	8 (12%)	7 (10%)	0	0
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	25	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	51 (100%)	0	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%)	62 (100%)	0	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	197 (86%)	25 (11%)	7 (3%)	3	2
33	2b	229/256 (90%)	199 (87%)	24 (10%)	6 (3%)	4	3
34	1c	204/239 (85%)	174 (85%)	28 (14%)	2 (1%)	13	18
34	2c	204/239 (85%)	178 (87%)	23 (11%)	3 (2%)	8	11
35	1d	206/209 (99%)	184 (89%)	22 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
35	2d	206/209 (99%)	190 (92%)	16 (8%)	0	100 100
36	1e	146/162 (90%)	133 (91%)	11 (8%)	2 (1%)	9 12
36	2e	146/162 (90%)	131 (90%)	12 (8%)	3 (2%)	5 6
37	1f	98/101 (97%)	95 (97%)	3 (3%)	0	100 100
37	2f	98/101 (97%)	93 (95%)	4 (4%)	1 (1%)	13 18
38	1g	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	10 13
38	2g	153/156 (98%)	134 (88%)	17 (11%)	2 (1%)	10 13
39	1h	135/138 (98%)	130 (96%)	5 (4%)	0	100 100
39	2h	135/138 (98%)	130 (96%)	5 (4%)	0	100 100
40	1i	125/128 (98%)	107 (86%)	16 (13%)	2 (2%)	8 10
40	2i	125/128 (98%)	108 (86%)	15 (12%)	2 (2%)	8 10
41	1j	95/105 (90%)	78 (82%)	11 (12%)	6 (6%)	1 0
41	2j	94/105 (90%)	81 (86%)	11 (12%)	2 (2%)	5 6
42	1k	112/129 (87%)	99 (88%)	12 (11%)	1 (1%)	14 21
42	2k	112/129 (87%)	98 (88%)	12 (11%)	2 (2%)	7 8
43	1l	119/132 (90%)	111 (93%)	7 (6%)	1 (1%)	16 23
43	2l	119/132 (90%)	117 (98%)	2 (2%)	0	100 100
44	1m	116/126 (92%)	104 (90%)	10 (9%)	2 (2%)	7 9
44	2m	114/126 (90%)	100 (88%)	13 (11%)	1 (1%)	14 21
45	1n	58/61 (95%)	54 (93%)	3 (5%)	1 (2%)	7 9
45	2n	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
46	1o	86/89 (97%)	83 (96%)	3 (4%)	0	100 100
46	2o	86/89 (97%)	84 (98%)	2 (2%)	0	100 100
47	1p	80/88 (91%)	66 (82%)	14 (18%)	0	100 100
47	2p	80/88 (91%)	72 (90%)	8 (10%)	0	100 100
48	1q	97/105 (92%)	88 (91%)	9 (9%)	0	100 100
48	2q	97/105 (92%)	90 (93%)	7 (7%)	0	100 100
49	1r	66/88 (75%)	60 (91%)	6 (9%)	0	100 100
49	2r	66/88 (75%)	63 (96%)	2 (3%)	1 (2%)	8 11
50	1s	81/93 (87%)	70 (86%)	11 (14%)	0	100 100
50	2s	81/93 (87%)	73 (90%)	5 (6%)	3 (4%)	2 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	1t	94/106 (89%)	86 (92%)	6 (6%)	2 (2%)	5 6
51	2t	94/106 (89%)	88 (94%)	5 (5%)	1 (1%)	12 15
52	1u	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
52	2u	21/27 (78%)	16 (76%)	5 (24%)	0	100 100
54	1w	247/354 (70%)	238 (96%)	6 (2%)	3 (1%)	11 14
54	2w	251/354 (71%)	234 (93%)	16 (6%)	1 (0%)	30 40
56	1z	3/7 (43%)	3 (100%)	0	0	100 100
56	2z	2/7 (29%)	2 (100%)	0	0	100 100
All	All	11848/12850 (92%)	10976 (93%)	765 (6%)	107 (1%)	14 21

All (107) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
23	11	3	LYS
26	14	55	ARG
33	1b	10	LEU
33	1b	17	PHE
33	1b	126	GLU
34	1c	66	VAL
38	1g	80	VAL
40	1i	54	ASP
44	1m	67	GLU
44	1m	107	ALA
5	2F	130	ALA
6	2G	43	LEU
7	2H	126	PRO
26	24	44	THR
26	24	56	VAL
26	24	62	ARG
33	2b	22	LYS
44	2m	106	ASN
6	1G	44	GLY
21	1Z	52	SER
26	14	49	PHE
36	1e	85	GLY
40	1i	55	ALA
41	1j	31	GLY
41	1j	56	HIS

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Mol	Chain	Res	Type
42	1k	49	GLY
54	1w	299	SER
6	2G	47	LYS
6	2G	52	ILE
8	2I	104	GLN
17	2V	79	VAL
21	2Z	142	SER
26	24	45	GLY
26	24	50	VAL
33	2b	17	PHE
33	2b	78	GLN
40	2i	56	LEU
41	2j	31	GLY
42	2k	49	GLY
49	2r	36	ASN
50	2s	13	ASP
6	1G	126	ASP
11	1P	29	LYS
12	1Q	16	ARG
17	1V	100	ARG
33	1b	22	LYS
34	1c	65	ALA
38	1g	130	GLY
45	1n	60	SER
54	1w	137	GLU
4	2E	52	LEU
5	2F	195	ASP
11	2P	29	LYS
12	2Q	16	ARG
12	2Q	60	ARG
21	2Z	52	SER
26	24	39	CYS
33	2b	20	GLU
34	2c	91	LEU
34	2c	98	ASN
36	2e	65	ASN
38	2g	4	ARG
38	2g	55	GLY
42	2k	89	ALA
54	2w	299	SER
4	1E	52	LEU
8	1I	86	THR

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Mol	Chain	Res	Type
23	11	45	ASN
33	1b	20	GLU
41	1j	79	ARG
54	1w	300	GLU
6	2G	49	ASP
8	2I	105	HIS
20	2Y	11	ASP
33	2b	123	ALA
33	2b	125	PRO
34	2c	100	ALA
36	2e	96	PRO
41	2j	78	ASN
50	2s	12	ASP
21	1Z	53	ILE
41	1j	33	GLN
41	1j	77	PRO
43	1l	105	TYR
10	2O	5	GLN
40	2i	121	ARG
51	2t	95	ALA
21	1Z	157	LEU
33	1b	125	PRO
41	1j	82	ILE
51	1t	47	GLY
3	2D	257	LEU
7	2H	65	HIS
11	2P	6	LEU
26	24	29	PRO
36	2e	69	VAL
20	2Y	55	TYR
17	1V	79	VAL
36	1e	69	VAL
51	1t	98	PRO
12	2Q	15	GLY
33	1b	124	SER
5	2F	89	VAL
37	2f	40	VAL
50	2s	8	GLY
11	1P	122	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	1D	215/218 (99%)	205 (95%)	10 (5%)	22 32
3	2D	215/218 (99%)	200 (93%)	15 (7%)	12 16
4	1E	164/166 (99%)	153 (93%)	11 (7%)	13 17
4	2E	164/166 (99%)	155 (94%)	9 (6%)	18 25
5	1F	160/166 (96%)	147 (92%)	13 (8%)	9 12
5	2F	159/166 (96%)	140 (88%)	19 (12%)	4 4
6	1G	143/156 (92%)	134 (94%)	9 (6%)	15 19
6	2G	143/156 (92%)	122 (85%)	21 (15%)	2 2
7	1H	144/148 (97%)	136 (94%)	8 (6%)	17 24
7	2H	144/148 (97%)	131 (91%)	13 (9%)	8 9
8	1I	113/124 (91%)	97 (86%)	16 (14%)	2 2
8	2I	105/124 (85%)	88 (84%)	17 (16%)	2 1
9	1N	118/119 (99%)	109 (92%)	9 (8%)	11 14
9	2N	118/119 (99%)	110 (93%)	8 (7%)	13 17
10	1O	100/100 (100%)	96 (96%)	4 (4%)	27 40
10	2O	100/100 (100%)	96 (96%)	4 (4%)	27 40
11	1P	115/116 (99%)	109 (95%)	6 (5%)	19 27
11	2P	115/116 (99%)	110 (96%)	5 (4%)	25 36
12	1Q	111/111 (100%)	108 (97%)	3 (3%)	40 57
12	2Q	111/111 (100%)	106 (96%)	5 (4%)	23 34
13	1R	101/101 (100%)	99 (98%)	2 (2%)	50 69
13	2R	101/101 (100%)	99 (98%)	2 (2%)	50 69
14	1S	86/88 (98%)	79 (92%)	7 (8%)	9 12
14	2S	85/88 (97%)	73 (86%)	12 (14%)	3 2
15	1T	115/127 (91%)	107 (93%)	8 (7%)	12 16
15	2T	113/127 (89%)	102 (90%)	11 (10%)	6 7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
16	1U	93/94 (99%)	90 (97%)	3 (3%)	34 49
16	2U	93/94 (99%)	88 (95%)	5 (5%)	18 25
17	1V	80/82 (98%)	78 (98%)	2 (2%)	42 60
17	2V	80/82 (98%)	73 (91%)	7 (9%)	8 10
18	1W	90/92 (98%)	88 (98%)	2 (2%)	47 65
18	2W	90/92 (98%)	86 (96%)	4 (4%)	24 35
19	1X	77/78 (99%)	73 (95%)	4 (5%)	19 27
19	2X	77/78 (99%)	74 (96%)	3 (4%)	27 41
20	1Y	85/91 (93%)	76 (89%)	9 (11%)	5 6
20	2Y	85/91 (93%)	76 (89%)	9 (11%)	5 6
21	1Z	135/179 (75%)	123 (91%)	12 (9%)	8 9
21	2Z	137/179 (76%)	119 (87%)	18 (13%)	3 2
22	10	61/67 (91%)	59 (97%)	2 (3%)	33 48
22	20	61/67 (91%)	60 (98%)	1 (2%)	58 75
23	11	80/83 (96%)	77 (96%)	3 (4%)	28 41
23	21	80/83 (96%)	73 (91%)	7 (9%)	8 10
24	12	65/67 (97%)	61 (94%)	4 (6%)	15 20
24	22	65/67 (97%)	61 (94%)	4 (6%)	15 20
25	13	51/52 (98%)	47 (92%)	4 (8%)	10 13
25	23	50/52 (96%)	47 (94%)	3 (6%)	16 21
26	14	59/63 (94%)	49 (83%)	10 (17%)	1 1
26	24	53/63 (84%)	47 (89%)	6 (11%)	4 5
27	15	50/52 (96%)	47 (94%)	3 (6%)	16 21
27	25	50/52 (96%)	47 (94%)	3 (6%)	16 21
28	16	51/52 (98%)	46 (90%)	5 (10%)	6 7
28	26	50/52 (96%)	45 (90%)	5 (10%)	6 7
29	17	41/42 (98%)	38 (93%)	3 (7%)	11 15
29	27	41/42 (98%)	37 (90%)	4 (10%)	6 7
30	18	54/55 (98%)	51 (94%)	3 (6%)	17 24
30	28	54/55 (98%)	51 (94%)	3 (6%)	17 24
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
31	29	34/34 (100%)	33 (97%)	1 (3%)	37 54
33	1b	192/220 (87%)	161 (84%)	31 (16%)	2 1
33	2b	187/220 (85%)	159 (85%)	28 (15%)	2 2
34	1c	142/188 (76%)	129 (91%)	13 (9%)	7 9
34	2c	140/188 (74%)	128 (91%)	12 (9%)	8 10
35	1d	169/181 (93%)	155 (92%)	14 (8%)	9 12
35	2d	173/181 (96%)	155 (90%)	18 (10%)	5 6
36	1e	113/123 (92%)	101 (89%)	12 (11%)	5 6
36	2e	114/123 (93%)	102 (90%)	12 (10%)	5 6
37	1f	84/90 (93%)	77 (92%)	7 (8%)	9 12
37	2f	85/90 (94%)	81 (95%)	4 (5%)	22 32
38	1g	119/127 (94%)	100 (84%)	19 (16%)	2 1
38	2g	120/127 (94%)	109 (91%)	11 (9%)	7 9
39	1h	114/119 (96%)	106 (93%)	8 (7%)	12 16
39	2h	114/119 (96%)	104 (91%)	10 (9%)	8 10
40	1i	90/99 (91%)	76 (84%)	14 (16%)	2 1
40	2i	89/99 (90%)	71 (80%)	18 (20%)	1 1
41	1j	66/92 (72%)	56 (85%)	10 (15%)	2 2
41	2j	69/92 (75%)	61 (88%)	8 (12%)	4 4
42	1k	82/99 (83%)	76 (93%)	6 (7%)	11 15
42	2k	83/99 (84%)	76 (92%)	7 (8%)	9 11
43	1l	96/108 (89%)	88 (92%)	8 (8%)	9 12
43	2l	96/108 (89%)	91 (95%)	5 (5%)	19 27
44	1m	89/101 (88%)	72 (81%)	17 (19%)	1 1
44	2m	88/101 (87%)	78 (89%)	10 (11%)	4 4
45	1n	49/50 (98%)	42 (86%)	7 (14%)	2 2
45	2n	49/50 (98%)	44 (90%)	5 (10%)	6 6
46	1o	78/80 (98%)	70 (90%)	8 (10%)	6 6
46	2o	78/80 (98%)	73 (94%)	5 (6%)	14 19
47	1p	69/74 (93%)	62 (90%)	7 (10%)	6 7
47	2p	68/74 (92%)	57 (84%)	11 (16%)	2 1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
48	1q	94/97 (97%)	90 (96%)	4 (4%)	25 36
48	2q	94/97 (97%)	93 (99%)	1 (1%)	70 82
49	1r	59/77 (77%)	57 (97%)	2 (3%)	32 47
49	2r	59/77 (77%)	57 (97%)	2 (3%)	32 47
50	1s	69/80 (86%)	56 (81%)	13 (19%)	1 1
50	2s	67/80 (84%)	62 (92%)	5 (8%)	11 15
51	1t	70/82 (85%)	66 (94%)	4 (6%)	17 23
51	2t	70/82 (85%)	66 (94%)	4 (6%)	17 23
52	1u	18/22 (82%)	17 (94%)	1 (6%)	17 24
52	2u	18/22 (82%)	18 (100%)	0	100 100
54	1w	204/299 (68%)	186 (91%)	18 (9%)	8 10
54	2w	204/299 (68%)	185 (91%)	19 (9%)	7 8
56	1z	2/3 (67%)	2 (100%)	0	100 100
56	2z	2/3 (67%)	2 (100%)	0	100 100
All	All	9699/10668 (91%)	8881 (92%)	818 (8%)	9 11

All (818) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	37	LEU
3	1D	38	LYS
3	1D	99	ASP
3	1D	113	VAL
3	1D	155	LEU
3	1D	173	VAL
3	1D	183	ARG
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	41	LYS
4	1E	55	ASN
4	1E	73	GLU
4	1E	75	VAL
4	1E	116	VAL
4	1E	163	GLU
4	1E	170	LEU
4	1E	178	GLU

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Mol	Chain	Res	Type
4	1E	181	LEU
4	1E	188	VAL
4	1E	195	LEU
5	1F	12	LEU
5	1F	15	SER
5	1F	27	GLU
5	1F	53	THR
5	1F	57	VAL
5	1F	70	THR
5	1F	74	ARG
5	1F	162	LEU
5	1F	165	ARG
5	1F	175	THR
5	1F	183	VAL
5	1F	192	LEU
5	1F	205	ARG
6	1G	3	LEU
6	1G	4	ASP
6	1G	31	VAL
6	1G	60	LEU
6	1G	77	ILE
6	1G	79	ASN
6	1G	82	LEU
6	1G	139	LEU
6	1G	159	VAL
7	1H	24	VAL
7	1H	25	LYS
7	1H	45	VAL
7	1H	84	SER
7	1H	88	LEU
7	1H	116	GLU
7	1H	119	GLU
7	1H	149	ARG
8	1I	9	LEU
8	1I	12	LEU
8	1I	15	VAL
8	1I	20	ASP
8	1I	41	GLU
8	1I	68	LEU
8	1I	78	THR
8	1I	87	LYS
8	1I	92	VAL

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Mol	Chain	Res	Type
8	1I	101	LEU
8	1I	109	ILE
8	1I	117	GLU
8	1I	125	GLU
8	1I	127	VAL
8	1I	129	THR
8	1I	140	LEU
9	1N	5	VAL
9	1N	9	VAL
9	1N	14	VAL
9	1N	28	THR
9	1N	48	MET
9	1N	61	ARG
9	1N	62	VAL
9	1N	65	LYS
9	1N	87	LEU
10	1O	28	SER
10	1O	89	ASN
10	1O	106	LEU
10	1O	108	GLU
11	1P	55	ARG
11	1P	59	LEU
11	1P	75	ILE
11	1P	119	GLU
11	1P	133	SER
11	1P	148	LEU
12	1Q	7	MET
12	1Q	75	THR
12	1Q	109	VAL
13	1R	29	LEU
13	1R	114	VAL
14	1S	36	TYR
14	1S	46	VAL
14	1S	49	VAL
14	1S	50	SER
14	1S	76	LYS
14	1S	83	LYS
14	1S	110	LEU
15	1T	6	LEU
15	1T	9	LEU
15	1T	23	ARG
15	1T	28	VAL

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Mol	Chain	Res	Type
15	1T	34	VAL
15	1T	35	LYS
15	1T	96	ARG
15	1T	128	GLU
16	1U	74	LEU
16	1U	77	SER
16	1U	95	LEU
17	1V	1	MET
17	1V	79	VAL
18	1W	11	ARG
18	1W	17	VAL
19	1X	52	VAL
19	1X	65	ARG
19	1X	70	LEU
19	1X	88	LYS
20	1Y	21	LYS
20	1Y	23	ARG
20	1Y	40	GLU
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	86	ARG
20	1Y	88	LYS
20	1Y	99	CYS
20	1Y	106	LEU
21	1Z	28	MET
21	1Z	31	ARG
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	50	GLN
21	1Z	72	ARG
21	1Z	121	HIS
21	1Z	126	VAL
21	1Z	140	ASP
21	1Z	146	ILE
21	1Z	155	LEU
21	1Z	161	VAL
22	10	11	ARG
22	10	74	ARG
23	11	40	ARG
23	11	41	ARG
23	11	46	LEU
24	12	19	VAL

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Mol	Chain	Res	Type
24	12	32	LEU
24	12	40	SER
24	12	65	ASN
25	13	31	LEU
25	13	54	VAL
25	13	58	VAL
25	13	60	GLU
26	14	14	ILE
26	14	23	GLU
26	14	27	THR
26	14	33	VAL
26	14	49	PHE
26	14	50	VAL
26	14	58	ARG
26	14	60	GLN
26	14	61	ARG
26	14	67	TYR
27	15	6	VAL
27	15	55	ARG
27	15	60	VAL
28	16	6	ARG
28	16	14	THR
28	16	45	LYS
28	16	47	THR
28	16	52	VAL
29	17	24	THR
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	29	LYS
30	18	32	LEU
31	19	17	ILE
33	1b	7	VAL
33	1b	8	LYS
33	1b	11	LEU
33	1b	12	GLU
33	1b	17	PHE
33	1b	21	ARG
33	1b	23	ARG
33	1b	40	HIS
33	1b	47	THR
33	1b	63	MET

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Mol	Chain	Res	Type
33	1b	69	LEU
33	1b	80	ILE
33	1b	107	THR
33	1b	108	ILE
33	1b	111	ARG
33	1b	112	VAL
33	1b	121	LEU
33	1b	128	GLU
33	1b	133	LYS
33	1b	137	ARG
33	1b	158	LEU
33	1b	172	ILE
33	1b	174	VAL
33	1b	185	ILE
33	1b	189	ASP
33	1b	190	THR
33	1b	208	ILE
33	1b	213	LEU
33	1b	219	VAL
33	1b	223	ILE
33	1b	226	ARG
34	1c	3	ASN
34	1c	28	GLN
34	1c	32	LEU
34	1c	36	ASP
34	1c	47	LEU
34	1c	70	VAL
34	1c	103	VAL
34	1c	115	LEU
34	1c	151	VAL
34	1c	166	GLU
34	1c	190	ARG
34	1c	195	VAL
34	1c	202	ILE
35	1d	31	CYS
35	1d	34	GLU
35	1d	57	ARG
35	1d	70	ILE
35	1d	86	LYS
35	1d	92	VAL
35	1d	101	LEU
35	1d	129	ASN

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Mol	Chain	Res	Type
35	1d	135	LEU
35	1d	144	ASP
35	1d	155	LEU
35	1d	200	GLU
35	1d	201	GLN
35	1d	203	VAL
36	1e	9	LYS
36	1e	10	MET
36	1e	11	ILE
36	1e	12	LEU
36	1e	27	ARG
36	1e	34	VAL
36	1e	41	VAL
36	1e	78	HIS
36	1e	79	GLU
36	1e	100	VAL
36	1e	120	THR
36	1e	147	ASP
37	1f	10	LEU
37	1f	45	LEU
37	1f	55	ASP
37	1f	65	VAL
37	1f	72	VAL
37	1f	78	GLU
37	1f	98	LEU
38	1g	12	LEU
38	1g	21	VAL
38	1g	30	ILE
38	1g	36	LYS
38	1g	38	LEU
38	1g	51	GLN
38	1g	52	GLU
38	1g	53	LYS
38	1g	59	LEU
38	1g	61	VAL
38	1g	80	VAL
38	1g	90	GLU
38	1g	91	VAL
38	1g	104	LEU
38	1g	120	ILE
38	1g	124	LEU
38	1g	129	GLU

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Mol	Chain	Res	Type
38	1g	140	ASP
38	1g	144	MET
39	1h	19	VAL
39	1h	22	GLU
39	1h	52	ASP
39	1h	54	ASP
39	1h	63	LEU
39	1h	95	VAL
39	1h	99	GLU
39	1h	109	ILE
40	1i	23	ASN
40	1i	38	GLN
40	1i	53	VAL
40	1i	54	ASP
40	1i	64	THR
40	1i	74	ILE
40	1i	75	ASP
40	1i	89	ASN
40	1i	92	TYR
40	1i	104	ARG
40	1i	105	ASP
40	1i	108	VAL
40	1i	124	GLN
40	1i	128	ARG
41	1j	8	LEU
41	1j	38	ILE
41	1j	42	THR
41	1j	49	VAL
41	1j	66	ARG
41	1j	81	THR
41	1j	92	THR
41	1j	95	GLU
41	1j	96	ILE
41	1j	100	THR
42	1k	28	THR
42	1k	33	THR
42	1k	80	VAL
42	1k	82	VAL
42	1k	84	VAL
42	1k	114	VAL
43	1l	18	VAL
43	1l	23	LYS

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Mol	Chain	Res	Type
43	1l	28	LYS
43	1l	33	ARG
43	1l	67	THR
43	1l	86	ARG
43	1l	89	ARG
43	1l	106	ASP
44	1m	9	ILE
44	1m	12	ASN
44	1m	19	LEU
44	1m	22	ILE
44	1m	27	LYS
44	1m	47	ASP
44	1m	49	THR
44	1m	50	GLU
44	1m	52	GLU
44	1m	69	GLU
44	1m	70	LEU
44	1m	78	ILE
44	1m	86	CYS
44	1m	94	ARG
44	1m	98	VAL
44	1m	103	THR
44	1m	106	ASN
45	1n	3	ARG
45	1n	13	THR
45	1n	17	LYS
45	1n	18	VAL
45	1n	33	VAL
45	1n	56	VAL
45	1n	57	ARG
46	1o	3	ILE
46	1o	11	VAL
46	1o	27	VAL
46	1o	39	LEU
46	1o	68	ARG
46	1o	83	GLU
46	1o	84	LYS
46	1o	87	ILE
47	1p	1	MET
47	1p	20	VAL
47	1p	21	VAL
47	1p	31	LYS

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Mol	Chain	Res	Type
47	1p	34	GLU
47	1p	45	THR
47	1p	54	GLU
48	1q	11	VAL
48	1q	48	GLU
48	1q	60	ILE
48	1q	99	SER
49	1r	25	THR
49	1r	42	ARG
50	1s	6	LYS
50	1s	9	VAL
50	1s	12	ASP
50	1s	19	VAL
50	1s	27	GLU
50	1s	30	LEU
50	1s	32	LYS
50	1s	65	ASN
50	1s	66	MET
50	1s	71	LEU
50	1s	77	THR
50	1s	79	THR
50	1s	83	HIS
51	1t	23	ARG
51	1t	24	LEU
51	1t	62	LEU
51	1t	84	LEU
52	1u	24	ARG
54	1w	102	MET
54	1w	108	ILE
54	1w	152	LEU
54	1w	158	VAL
54	1w	185	VAL
54	1w	186	THR
54	1w	196	THR
54	1w	208	GLU
54	1w	223	ARG
54	1w	248	ILE
54	1w	251	THR
54	1w	275	GLU
54	1w	299	SER
54	1w	302	ILE
54	1w	315	HIS

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Mol	Chain	Res	Type
54	1w	321	THR
54	1w	333	THR
54	1w	344	GLN
3	2D	3	VAL
3	2D	37	LEU
3	2D	38	LYS
3	2D	71	ASP
3	2D	88	ARG
3	2D	99	ASP
3	2D	113	VAL
3	2D	140	THR
3	2D	155	LEU
3	2D	173	VAL
3	2D	183	ARG
3	2D	229	VAL
3	2D	259	THR
3	2D	260	ARG
3	2D	275	LYS
4	2E	7	VAL
4	2E	38	THR
4	2E	75	VAL
4	2E	90	THR
4	2E	116	VAL
4	2E	134	ILE
4	2E	170	LEU
4	2E	178	GLU
4	2E	181	LEU
5	2F	19	GLU
5	2F	27	GLU
5	2F	33	LEU
5	2F	57	VAL
5	2F	70	THR
5	2F	112	MET
5	2F	114	VAL
5	2F	124	LEU
5	2F	127	GLU
5	2F	132	VAL
5	2F	137	LYS
5	2F	140	LEU
5	2F	158	THR
5	2F	165	ARG
5	2F	183	VAL

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Mol	Chain	Res	Type
5	2F	195	ASP
5	2F	197	ASP
5	2F	201	VAL
5	2F	203	GLN
6	2G	3	LEU
6	2G	4	ASP
6	2G	15	VAL
6	2G	26	GLN
6	2G	43	LEU
6	2G	58	GLN
6	2G	59	GLU
6	2G	88	ILE
6	2G	91	ARG
6	2G	94	LEU
6	2G	95	ARG
6	2G	109	VAL
6	2G	116	ASP
6	2G	139	LEU
6	2G	140	ILE
6	2G	145	THR
6	2G	148	MET
6	2G	159	VAL
6	2G	161	THR
6	2G	162	THR
6	2G	175	LEU
7	2H	13	LYS
7	2H	23	ARG
7	2H	24	VAL
7	2H	32	GLU
7	2H	41	MET
7	2H	45	VAL
7	2H	47	GLU
7	2H	85	LYS
7	2H	95	ARG
7	2H	97	ARG
7	2H	114	VAL
7	2H	116	GLU
7	2H	127	GLU
8	2I	20	ASP
8	2I	38	LEU
8	2I	40	THR
8	2I	58	LEU

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Mol	Chain	Res	Type
8	2I	68	LEU
8	2I	75	LEU
8	2I	79	ILE
8	2I	81	VAL
8	2I	82	ARG
8	2I	86	THR
8	2I	87	LYS
8	2I	92	VAL
8	2I	105	HIS
8	2I	116	LEU
8	2I	122	GLU
8	2I	127	VAL
8	2I	144	VAL
9	2N	9	VAL
9	2N	10	GLU
9	2N	28	THR
9	2N	43	THR
9	2N	46	VAL
9	2N	62	VAL
9	2N	65	LYS
9	2N	87	LEU
10	2O	28	SER
10	2O	52	VAL
10	2O	66	LYS
10	2O	77	ILE
11	2P	2	LYS
11	2P	59	LEU
11	2P	77	ARG
11	2P	101	VAL
11	2P	106	LEU
12	2Q	6	ARG
12	2Q	21	THR
12	2Q	38	GLU
12	2Q	75	THR
12	2Q	109	VAL
13	2R	29	LEU
13	2R	114	VAL
14	2S	13	ARG
14	2S	21	THR
14	2S	36	TYR
14	2S	48	LEU
14	2S	49	VAL

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Mol	Chain	Res	Type
14	2S	50	SER
14	2S	69	VAL
14	2S	75	GLU
14	2S	78	LEU
14	2S	83	LYS
14	2S	85	VAL
14	2S	110	LEU
15	2T	6	LEU
15	2T	9	LEU
15	2T	13	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	85	LYS
15	2T	89	VAL
15	2T	108	ARG
15	2T	114	LEU
15	2T	115	ARG
15	2T	118	ARG
16	2U	31	SER
16	2U	55	ARG
16	2U	74	LEU
16	2U	77	SER
16	2U	95	LEU
17	2V	1	MET
17	2V	15	GLU
17	2V	33	VAL
17	2V	46	VAL
17	2V	51	VAL
17	2V	53	GLU
17	2V	79	VAL
18	2W	1	MET
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
19	2X	80	ILE
19	2X	81	VAL
19	2X	92	LEU
20	2Y	8	LYS
20	2Y	31	LEU
20	2Y	37	VAL
20	2Y	49	VAL
20	2Y	55	TYR

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Mol	Chain	Res	Type
20	2Y	72	VAL
20	2Y	88	LYS
20	2Y	99	CYS
20	2Y	107	ASP
21	2Z	18	LEU
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	50	GLN
21	2Z	60	GLU
21	2Z	70	LEU
21	2Z	72	ARG
21	2Z	76	LEU
21	2Z	81	ARG
21	2Z	92	SER
21	2Z	121	HIS
21	2Z	126	VAL
21	2Z	131	ARG
21	2Z	132	ASN
21	2Z	154	ASP
21	2Z	157	LEU
21	2Z	163	LEU
21	2Z	165	VAL
22	20	10	THR
23	21	4	VAL
23	21	21	ARG
23	21	35	THR
23	21	40	ARG
23	21	46	LEU
23	21	74	VAL
23	21	80	LEU
24	22	19	VAL
24	22	32	LEU
24	22	53	LEU
24	22	62	THR
25	23	6	VAL
25	23	31	LEU
25	23	54	VAL
26	24	1	MET
26	24	50	VAL
26	24	52	THR
26	24	53	GLU
26	24	58	ARG

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Mol	Chain	Res	Type
26	24	63	TYR
27	25	6	VAL
27	25	33	CYS
27	25	58	LEU
28	26	7	ILE
28	26	32	ASN
28	26	48	VAL
28	26	52	VAL
28	26	53	LYS
29	27	1	MET
29	27	24	THR
29	27	43	THR
29	27	46	VAL
30	28	14	VAL
30	28	23	VAL
30	28	32	LEU
31	29	17	ILE
33	2b	10	LEU
33	2b	12	GLU
33	2b	19	HIS
33	2b	41	ILE
33	2b	44	LEU
33	2b	47	THR
33	2b	48	MET
33	2b	67	THR
33	2b	71	VAL
33	2b	81	VAL
33	2b	112	VAL
33	2b	122	PHE
33	2b	124	SER
33	2b	127	ILE
33	2b	136	VAL
33	2b	148	TYR
33	2b	158	LEU
33	2b	160	ASP
33	2b	165	VAL
33	2b	172	ILE
33	2b	185	ILE
33	2b	187	LEU
33	2b	189	ASP
33	2b	196	LEU
33	2b	200	ILE

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Mol	Chain	Res	Type
33	2b	208	ILE
33	2b	226	ARG
33	2b	229	VAL
34	2c	14	ILE
34	2c	16	ARG
34	2c	39	ILE
34	2c	85	ARG
34	2c	98	ASN
34	2c	102	ASN
34	2c	115	LEU
34	2c	125	GLU
34	2c	138	VAL
34	2c	164	ARG
34	2c	166	GLU
34	2c	192	THR
35	2d	8	VAL
35	2d	12	CYS
35	2d	17	VAL
35	2d	31	CYS
35	2d	67	ILE
35	2d	78	LEU
35	2d	83	SER
35	2d	126	ILE
35	2d	127	THR
35	2d	135	LEU
35	2d	155	LEU
35	2d	162	LEU
35	2d	170	VAL
35	2d	175	SER
35	2d	178	VAL
35	2d	188	LEU
35	2d	201	GLN
35	2d	202	LEU
36	2e	6	PHE
36	2e	10	MET
36	2e	11	ILE
36	2e	12	LEU
36	2e	20	GLN
36	2e	51	VAL
36	2e	53	LEU
36	2e	64	ARG
36	2e	75	THR

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Mol	Chain	Res	Type
36	2e	79	GLU
36	2e	117	ASP
36	2e	120	THR
37	2f	41	GLU
37	2f	63	TYR
37	2f	69	GLU
37	2f	72	VAL
38	2g	4	ARG
38	2g	9	VAL
38	2g	11	GLN
38	2g	15	ASP
38	2g	21	VAL
38	2g	38	LEU
38	2g	63	LYS
38	2g	79	ARG
38	2g	80	VAL
38	2g	89	MET
38	2g	129	GLU
39	2h	2	LEU
39	2h	18	ARG
39	2h	29	SER
39	2h	63	LEU
39	2h	97	VAL
39	2h	99	GLU
39	2h	105	ARG
39	2h	109	ILE
39	2h	114	THR
39	2h	127	LEU
40	2i	7	THR
40	2i	31	GLN
40	2i	34	ASN
40	2i	35	GLU
40	2i	48	GLU
40	2i	53	VAL
40	2i	54	ASP
40	2i	58	HIS
40	2i	65	VAL
40	2i	75	ASP
40	2i	78	LYS
40	2i	83	ARG
40	2i	86	VAL
40	2i	93	ARG

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Mol	Chain	Res	Type
40	2i	108	VAL
40	2i	114	TYR
40	2i	124	GLN
40	2i	128	ARG
41	2j	8	LEU
41	2j	21	GLN
41	2j	47	PHE
41	2j	62	HIS
41	2j	65	LEU
41	2j	66	ARG
41	2j	69	ASN
41	2j	98	ILE
42	2k	14	VAL
42	2k	32	ILE
42	2k	41	THR
42	2k	73	MET
42	2k	78	GLN
42	2k	85	ARG
42	2k	98	LEU
43	2l	11	VAL
43	2l	28	LYS
43	2l	62	SER
43	2l	78	GLN
43	2l	104	VAL
44	2m	4	ILE
44	2m	8	GLU
44	2m	15	VAL
44	2m	27	LYS
44	2m	49	THR
44	2m	90	LEU
44	2m	96	LEU
44	2m	105	THR
44	2m	106	ASN
44	2m	116	THR
45	2n	3	ARG
45	2n	13	THR
45	2n	22	THR
45	2n	33	VAL
45	2n	57	ARG
46	2o	5	LYS
46	2o	39	LEU
46	2o	83	GLU

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Mol	Chain	Res	Type
46	2o	84	LYS
46	2o	87	ILE
47	2p	1	MET
47	2p	2	VAL
47	2p	16	HIS
47	2p	20	VAL
47	2p	21	VAL
47	2p	28	ARG
47	2p	45	THR
47	2p	60	LEU
47	2p	62	VAL
47	2p	74	LEU
47	2p	76	GLN
48	2q	57	VAL
49	2r	25	THR
49	2r	37	VAL
50	2s	30	LEU
50	2s	43	GLU
50	2s	49	ILE
50	2s	77	THR
50	2s	83	HIS
51	2t	19	SER
51	2t	22	ARG
51	2t	70	SER
51	2t	100	ILE
54	2w	102	MET
54	2w	105	ARG
54	2w	119	GLU
54	2w	145	LEU
54	2w	150	THR
54	2w	152	LEU
54	2w	159	VAL
54	2w	196	THR
54	2w	206	GLU
54	2w	222	MET
54	2w	267	MET
54	2w	272	ARG
54	2w	283	GLU
54	2w	302	ILE
54	2w	309	GLN
54	2w	320	THR
54	2w	333	THR

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Mol	Chain	Res	Type
54	2w	336	LEU
54	2w	353	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (143) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	126	GLN
4	1E	48	GLN
4	1E	121	ASN
5	1F	69	HIS
5	1F	203	GLN
5	1F	204	ASN
8	1I	54	GLN
8	1I	104	GLN
8	1I	105	HIS
9	1N	94	HIS
12	1Q	12	GLN
13	1R	71	GLN
13	1R	91	GLN
14	1S	61	ASN
15	1T	58	ASN
16	1U	72	HIS
16	1U	94	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	43	ASN
21	1Z	32	HIS
21	1Z	55	HIS
21	1Z	73	GLN
21	1Z	151	HIS
22	10	35	ASN
22	10	50	ASN
23	11	19	GLN
30	18	35	GLN
33	1b	16	HIS
33	1b	37	ASN
33	1b	40	HIS
33	1b	94	ASN
33	1b	140	HIS
33	1b	146	GLN

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Mol	Chain	Res	Type
34	1c	98	ASN
34	1c	123	GLN
35	1d	77	ASN
35	1d	123	HIS
35	1d	161	ASN
36	1e	20	GLN
36	1e	78	HIS
36	1e	141	GLN
37	1f	18	GLN
37	1f	32	ASN
37	1f	100	ASN
38	1g	13	GLN
38	1g	28	ASN
38	1g	109	ASN
38	1g	148	ASN
38	1g	153	HIS
40	1i	23	ASN
40	1i	73	GLN
40	1i	124	GLN
41	1j	56	HIS
41	1j	62	HIS
41	1j	84	GLN
42	1k	93	GLN
42	1k	117	ASN
43	1l	80	HIS
43	1l	99	HIS
44	1m	77	ASN
44	1m	106	ASN
45	1n	49	HIS
47	1p	14	ASN
49	1r	36	ASN
49	1r	63	GLN
50	1s	23	ASN
50	1s	69	HIS
51	1t	90	GLN
54	1w	129	ASN
54	1w	178	HIS
54	1w	189	GLN
54	1w	258	GLN
54	1w	344	GLN
4	2E	48	GLN
4	2E	55	ASN

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Mol	Chain	Res	Type
6	2G	79	ASN
8	2I	74	ASN
8	2I	133	HIS
8	2I	139	GLN
9	2N	94	HIS
10	2O	5	GLN
12	2Q	12	GLN
12	2Q	89	ASN
12	2Q	123	HIS
13	2R	50	HIS
15	2T	43	GLN
15	2T	58	ASN
15	2T	79	HIS
16	2U	72	HIS
16	2U	94	ASN
18	2W	60	ASN
19	2X	31	HIS
20	2Y	6	HIS
20	2Y	43	ASN
21	2Z	73	GLN
21	2Z	132	ASN
21	2Z	151	HIS
24	22	9	GLN
25	23	32	GLN
28	26	32	ASN
33	2b	16	HIS
33	2b	95	GLN
34	2c	98	ASN
34	2c	123	GLN
34	2c	139	GLN
34	2c	181	ASN
35	2d	77	ASN
35	2d	116	GLN
35	2d	123	HIS
35	2d	125	HIS
35	2d	129	ASN
35	2d	201	GLN
36	2e	65	ASN
37	2f	32	ASN
38	2g	51	GLN
38	2g	110	GLN
38	2g	153	HIS

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Mol	Chain	Res	Type
40	2i	3	GLN
40	2i	31	GLN
40	2i	38	GLN
41	2j	33	GLN
41	2j	56	HIS
42	2k	62	GLN
42	2k	99	GLN
42	2k	104	GLN
42	2k	117	ASN
43	2l	80	HIS
44	2m	106	ASN
46	2o	62	GLN
47	2p	65	GLN
49	2r	63	GLN
50	2s	23	ASN
50	2s	69	HIS
50	2s	83	HIS
51	2t	18	GLN
51	2t	42	GLN
51	2t	75	ASN
54	2w	253	GLN
54	2w	258	GLN
54	2w	315	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	438 (15%)	31 (1%)
1	2A	2791/2915 (95%)	437 (15%)	26 (0%)
2	1B	119/121 (98%)	12 (10%)	0
2	2B	118/121 (97%)	19 (16%)	0
32	1a	1497/1521 (98%)	295 (19%)	0
32	2a	1501/1521 (98%)	299 (19%)	0
53	1v	10/24 (41%)	2 (20%)	0
53	2v	10/24 (41%)	3 (30%)	0
55	1x	72/74 (97%)	9 (12%)	0
55	2x	72/74 (97%)	8 (11%)	0
All	All	9054/9310 (97%)	1522 (16%)	57 (0%)

All (1522) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	15	G
1	1A	34	C
1	1A	36	G
1	1A	45	C
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	84	A
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	140	G
1	1A	153	C
1	1A	181	A
1	1A	196	A
1	1A	199	A
1	1A	205	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
1	1A	233	A
1	1A	248	G
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(S)	G
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	283	A
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	352	G
1	1A	356	G

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Mol	Chain	Res	Type
1	1A	362	U
1	1A	363	G
1	1A	363(A)	A
1	1A	363(B)	G
1	1A	372	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	421	U
1	1A	422	A
1	1A	428	A
1	1A	444	C
1	1A	448	U
1	1A	454	A
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	509	C
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(E)	G
1	1A	652(T)	C

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Mol	Chain	Res	Type
1	1A	669	G
1	1A	686	G
1	1A	730	C
1	1A	746	A
1	1A	747	U
1	1A	764	A
1	1A	765	G
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	783	A
1	1A	784	A
1	1A	785	G
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G
1	1A	866	A
1	1A	869	G
1	1A	878	A
1	1A	884	C
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	895	U
1	1A	896	A
1	1A	899	A
1	1A	907	U
1	1A	910	A
1	1A	931	G
1	1A	932	G
1	1A	938	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C

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Mol	Chain	Res	Type
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1022	G
1	1A	1026	U
1	1A	1033	U
1	1A	1039	G
1	1A	1040	C
1	1A	1041	C
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1055	G
1	1A	1058	G
1	1A	1059	G
1	1A	1060	U
1	1A	1063	G
1	1A	1064	C
1	1A	1066	U
1	1A	1068	G
1	1A	1071	G
1	1A	1073	A
1	1A	1076	C
1	1A	1078	U
1	1A	1079	C
1	1A	1083	U
1	1A	1084	A
1	1A	1085	A
1	1A	1086	A
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	G
1	1A	1092	C
1	1A	1093	G
1	1A	1094	U
1	1A	1095	A

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Mol	Chain	Res	Type
1	1A	1096	A
1	1A	1097	U
1	1A	1098	A
1	1A	1099	G
1	1A	1100	C
1	1A	1110	G
1	1A	1112	G
1	1A	1116	C
1	1A	1128	A
1	1A	1129	A
1	1A	1135	C
1	1A	1136	G
1	1A	1142(A)	A
1	1A	1143	A
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	1211	U
1	1A	1220	A
1	1A	1241	A
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1321	A
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1403	C
1	1A	1416	G

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Mol	Chain	Res	Type
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	1453	U
1	1A	1455	G
1	1A	1461	G
1	1A	1467	C
1	1A	1478	G
1	1A	1482	G
1	1A	1493	C
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1509(B)	A
1	1A	1525	G
1	1A	1543	C
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1648	C
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1740	G
1	1A	1745(A)	C
1	1A	1746	G
1	1A	1756	G
1	1A	1762	A
1	1A	1763	G

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Mol	Chain	Res	Type
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	1828	G
1	1A	1829	A
1	1A	1847	A
1	1A	1858	G
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1914	C
1	1A	1929	G
1	1A	1930	G
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1992	G
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2033	A
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2093	G
1	1A	2099	U
1	1A	2102	U

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Mol	Chain	Res	Type
1	1A	2104	G
1	1A	2105	C
1	1A	2108	C
1	1A	2109	U
1	1A	2112	G
1	1A	2115	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2120	G
1	1A	2123	G
1	1A	2126	A
1	1A	2127	G
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2136	C
1	1A	2142	C
1	1A	2143	C
1	1A	2144	U
1	1A	2146	C
1	1A	2147	G
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	2163	C
1	1A	2164	C
1	1A	2165	G
1	1A	2166	G
1	1A	2168	G
1	1A	2170	A
1	1A	2171	A
1	1A	2172	U

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Mol	Chain	Res	Type
1	1A	2175	C
1	1A	2176	A
1	1A	2181	G
1	1A	2182	G
1	1A	2183	C
1	1A	2184	G
1	1A	2185	C
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	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2283	C
1	1A	2286	A
1	1A	2287	A
1	1A	2305	A
1	1A	2307	G
1	1A	2308	G
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2354	G
1	1A	2379	G
1	1A	2383	G
1	1A	2385	C
1	1A	2406	U
1	1A	2410	G
1	1A	2414	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

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Mol	Chain	Res	Type
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2476	A
1	1A	2478	A
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2578	G
1	1A	2585	U
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2615	U
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2663	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	2726	U
1	1A	2733	A
1	1A	2757	A
1	1A	2758	A
1	1A	2764	A
1	1A	2765	A

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Mol	Chain	Res	Type
1	1A	2766	G
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2805	G
1	1A	2807	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2836	U
1	1A	2872	G
1	1A	2873	A
1	1A	2876	G
1	1A	2894	G
1	1A	2897	U
2	1B	9	G
2	1B	13	A
2	1B	15	A
2	1B	20	C
2	1B	24	G
2	1B	25	A
2	1B	56	G
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
2	1B	120	A
32	1a	5	U
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	51	A
32	1a	60	A
32	1a	61	G
32	1a	65	U
32	1a	78	G
32	1a	91	C

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Mol	Chain	Res	Type
32	1a	92	C
32	1a	93	G
32	1a	96	U
32	1a	97	G
32	1a	99	U
32	1a	101	A
32	1a	102	G
32	1a	105	G
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	127	G
32	1a	131	C
32	1a	134	A
32	1a	137	C
32	1a	143	A
32	1a	144	G
32	1a	146	G
32	1a	156	G
32	1a	163	C
32	1a	174	C
32	1a	182	U
32	1a	186	C
32	1a	189(G)	G
32	1a	189(K)	U
32	1a	195	A
32	1a	196	A
32	1a	197	A
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	220	G
32	1a	222	U
32	1a	231	G
32	1a	247	G
32	1a	251	G
32	1a	254	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G

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Mol	Chain	Res	Type
32	1a	301	G
32	1a	306	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	341	C
32	1a	346	G
32	1a	347	G
32	1a	349	A
32	1a	350	G
32	1a	351	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	355	C
32	1a	364	A
32	1a	367	U
32	1a	371	G
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	421	U
32	1a	423	G
32	1a	429	U
32	1a	433	C
32	1a	438	G
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	457	C
32	1a	461	A
32	1a	470	C
32	1a	474	G
32	1a	476	G
32	1a	480	U
32	1a	481	G
32	1a	482	A

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Mol	Chain	Res	Type
32	1a	485	G
32	1a	492	G
32	1a	495	A
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	524	G
32	1a	527	G7M
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	560	U
32	1a	561	U
32	1a	563	A
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	607	A
32	1a	616	G
32	1a	618	C
32	1a	630	G
32	1a	653	A
32	1a	662	G
32	1a	665	A
32	1a	666	G
32	1a	686	U
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	703	G
32	1a	723	U
32	1a	749	C
32	1a	755	G
32	1a	760	G
32	1a	766	A
32	1a	777	A

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Mol	Chain	Res	Type
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	851	G
32	1a	859	A
32	1a	870	U
32	1a	874	G
32	1a	902	G
32	1a	914	A
32	1a	916	G
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	935	A
32	1a	960	U
32	1a	961	U
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	978	A
32	1a	982	U
32	1a	992	U
32	1a	993	G
32	1a	994	A
32	1a	997	U
32	1a	1000	U
32	1a	1002	G
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1008	C
32	1a	1009	G

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Mol	Chain	Res	Type
32	1a	1020	U
32	1a	1021	G
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1034	G
32	1a	1035	A
32	1a	1036	G
32	1a	1037	C
32	1a	1039	C
32	1a	1040	U
32	1a	1042	G
32	1a	1043	C
32	1a	1044	A
32	1a	1045	C
32	1a	1046	A
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1081	G
32	1a	1086	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1103	C
32	1a	1123	A
32	1a	1124	G
32	1a	1125	U
32	1a	1126	U
32	1a	1127	G
32	1a	1131	G
32	1a	1133	G

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Mol	Chain	Res	Type
32	1a	1134	G
32	1a	1135	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1146	A
32	1a	1152	A
32	1a	1154	G
32	1a	1157	A
32	1a	1159	U
32	1a	1165	C
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1207	2MG
32	1a	1212	U
32	1a	1213	A
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1240	U
32	1a	1241	G
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C
32	1a	1273	G
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1288	A
32	1a	1298	C
32	1a	1300	G
32	1a	1302	U
32	1a	1306	A
32	1a	1320	C
32	1a	1322	C

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Mol	Chain	Res	Type
32	1a	1323	G
32	1a	1338	G
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1363(A)	A
32	1a	1364	U
32	1a	1370	G
32	1a	1379	G
32	1a	1398	A
32	1a	1419	G
32	1a	1422	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1442(B)	A
32	1a	1452	C
32	1a	1456	G
32	1a	1460	A
32	1a	1493	A
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1506	U
32	1a	1507	A
32	1a	1517	G
32	1a	1519	MA6
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
53	1v	12	A
53	1v	22	U
55	1x	14	A
55	1x	18	G
55	1x	19	G
55	1x	21	H2U
55	1x	22	A
55	1x	45	U
55	1x	46	A
55	1x	48	G
55	1x	51	C
1	2A	15	G

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Mol	Chain	Res	Type
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	49	A
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	90	U
1	2A	95	G
1	2A	100	G
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	123	G
1	2A	131	G
1	2A	141	A
1	2A	149	A
1	2A	154(A)	C
1	2A	157	U
1	2A	181	A
1	2A	196	A
1	2A	197	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	248	G
1	2A	249	C
1	2A	265	A
1	2A	267	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G

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Mol	Chain	Res	Type
1	2A	272(I)	U
1	2A	272(J)	C
1	2A	277	C
1	2A	278	A
1	2A	283	A
1	2A	311	A
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	342	G
1	2A	352	G
1	2A	363(B)	G
1	2A	386	G
1	2A	391	G
1	2A	396	G
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	435	C
1	2A	444	C
1	2A	451	C
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	481	G
1	2A	504	U
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	603	A
1	2A	604	G
1	2A	607	U

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Mol	Chain	Res	Type
1	2A	614(B)	G
1	2A	615	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	651	G
1	2A	652(A)	A
1	2A	652(B)	A
1	2A	652(U)	G
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	730	C
1	2A	753	C
1	2A	762	U
1	2A	764	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	833	U
1	2A	857	C
1	2A	859	G
1	2A	874	G
1	2A	878	A
1	2A	879	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	894	C
1	2A	895	U

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Mol	Chain	Res	Type
1	2A	896	A
1	2A	897	C
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	936	C
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	983	A
1	2A	996	A
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1025	G
1	2A	1033	U
1	2A	1039	G
1	2A	1043	C
1	2A	1114	G
1	2A	1128	A
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142(A)	A
1	2A	1155	A
1	2A	1205	U
1	2A	1210	A
1	2A	1211	U
1	2A	1220	A
1	2A	1236	G
1	2A	1253	A

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Mol	Chain	Res	Type
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1275	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1370	C
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1400	G
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1437	C
1	2A	1445	A
1	2A	1445(A)	C
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1478	G
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1531	C

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Mol	Chain	Res	Type
1	2A	1532	C
1	2A	1543	C
1	2A	1547	C
1	2A	1554	A
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1609	A
1	2A	1613	G
1	2A	1640	C
1	2A	1647	G
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G
1	2A	1700	A
1	2A	1721	G
1	2A	1722	A
1	2A	1746	G
1	2A	1756	G
1	2A	1758	G
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1812	A
1	2A	1816	G
1	2A	1819	A
1	2A	1829	A
1	2A	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1858	G

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Mol	Chain	Res	Type
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1895	C
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
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	1984	G
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2032	G
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2080	G
1	2A	2093	G
1	2A	2103	C
1	2A	2110	G
1	2A	2111	C
1	2A	2116	G
1	2A	2117	A
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U

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Mol	Chain	Res	Type
1	2A	2125	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	2136	C
1	2A	2138	C
1	2A	2140	C
1	2A	2142	C
1	2A	2146	C
1	2A	2147	G
1	2A	2149	G
1	2A	2150	U
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	2162	G
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2170	A
1	2A	2171	A
1	2A	2172	U
1	2A	2174	C
1	2A	2178	C
1	2A	2181	G
1	2A	2185	C
1	2A	2188	C
1	2A	2189	U
1	2A	2190	G
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G

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Mol	Chain	Res	Type
1	2A	2207	G
1	2A	2208	A
1	2A	2219	G
1	2A	2225	A
1	2A	2275	C
1	2A	2280	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2305	A
1	2A	2308	G
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2372	G
1	2A	2376	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2391	G
1	2A	2406	U
1	2A	2407	G
1	2A	2410	G
1	2A	2422	A
1	2A	2424	C
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2431	U
1	2A	2434	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2468	G

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Mol	Chain	Res	Type
1	2A	2469	A
1	2A	2476	A
1	2A	2480	C
1	2A	2487	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2529	G
1	2A	2549	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2574	G
1	2A	2578	G
1	2A	2585	U
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2629	A
1	2A	2630	G
1	2A	2654	A
1	2A	2673	G
1	2A	2689	U
1	2A	2690	C
1	2A	2691	C
1	2A	2702	U
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2748	A
1	2A	2758	A
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2789	C

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Mol	Chain	Res	Type
1	2A	2793	G
1	2A	2794	C
1	2A	2802	G
1	2A	2808	U
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2873	A
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2895	U
1	2A	2897	U
2	2B	8	U
2	2B	13	A
2	2B	17	C
2	2B	20	C
2	2B	23	G
2	2B	25	A
2	2B	35	U
2	2B	42	C
2	2B	51	G
2	2B	53	A
2	2B	56	G
2	2B	73	A
2	2B	105	A
2	2B	106	G
2	2B	108	U
2	2B	109	C
2	2B	110	G
2	2B	116	G
2	2B	120	A
32	2a	7	G
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C

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Mol	Chain	Res	Type
32	2a	50	A
32	2a	51	A
32	2a	52	G
32	2a	66	G
32	2a	73	G
32	2a	78	G
32	2a	89	C
32	2a	101	A
32	2a	105	G
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	142	G
32	2a	143	A
32	2a	144	G
32	2a	146	G
32	2a	156	G
32	2a	163	C
32	2a	174	C
32	2a	182	U
32	2a	189(A)	C
32	2a	189(E)	U
32	2a	189(F)	U
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	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	347	G
32	2a	351	G
32	2a	352	C

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Mol	Chain	Res	Type
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	422	C
32	2a	424	G
32	2a	429	U
32	2a	438	G
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	482	A
32	2a	484	G
32	2a	485	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	528	C
32	2a	531	U
32	2a	532	A
32	2a	536	C
32	2a	547	A
32	2a	559	A
32	2a	560	U
32	2a	561	U
32	2a	564	C
32	2a	568	G

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Mol	Chain	Res	Type
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	601	C
32	2a	607	A
32	2a	630	G
32	2a	653	A
32	2a	665	A
32	2a	671	G
32	2a	687	A
32	2a	688	G
32	2a	703	G
32	2a	708	C
32	2a	717	C
32	2a	720	C
32	2a	721	G
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	733	A
32	2a	750	G
32	2a	753	A
32	2a	755	G
32	2a	760	G
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	816	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	834	C
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	853	G
32	2a	859	A
32	2a	873	A

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Mol	Chain	Res	Type
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	935	A
32	2a	942	G
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	998	G
32	2a	999	C
32	2a	1000	U
32	2a	1001(A)	G
32	2a	1002	G
32	2a	1003	G
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1012	U
32	2a	1020	U
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	1030	C
32	2a	1030(A)	G

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Mol	Chain	Res	Type
32	2a	1030(B)	C
32	2a	1030(D)	A
32	2a	1032	G
32	2a	1035	A
32	2a	1037	C
32	2a	1040	U
32	2a	1041	A
32	2a	1044	A
32	2a	1045	C
32	2a	1046	A
32	2a	1050	G
32	2a	1056	U
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1071	C
32	2a	1081	G
32	2a	1086	U
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1113	C
32	2a	1117	G
32	2a	1120	G
32	2a	1121	U
32	2a	1122	U
32	2a	1127	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	1140	C
32	2a	1146	A
32	2a	1149	C
32	2a	1150	U
32	2a	1152	A
32	2a	1154	G
32	2a	1157	A
32	2a	1159	U

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Mol	Chain	Res	Type
32	2a	1163	C
32	2a	1171	G
32	2a	1172	C
32	2a	1174	G
32	2a	1181	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1208	C
32	2a	1212	U
32	2a	1214	C
32	2a	1218	C
32	2a	1220	G
32	2a	1227	A
32	2a	1228	C
32	2a	1236	A
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1253	G
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1262	C
32	2a	1270	C
32	2a	1273	G
32	2a	1276	G
32	2a	1277	C
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1286	A
32	2a	1287	A
32	2a	1298	C
32	2a	1299	A
32	2a	1300	G
32	2a	1301	U
32	2a	1303	C

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Mol	Chain	Res	Type
32	2a	1305	G
32	2a	1320	C
32	2a	1335	C
32	2a	1336	C
32	2a	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1358	U
32	2a	1363	C
32	2a	1368	G
32	2a	1377	A
32	2a	1378	C
32	2a	1397	C
32	2a	1398	A
32	2a	1400	5MC
32	2a	1402	4OC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1442(B)	A
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G
32	2a	1492	A
32	2a	1493	A
32	2a	1494	G
32	2a	1497	G
32	2a	1499	A
32	2a	1503	A
32	2a	1506	U
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	12	A
53	2v	13	A

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Mol	Chain	Res	Type
53	2v	22	U
55	2x	16	C
55	2x	18	G
55	2x	20	H2U
55	2x	21	H2U
55	2x	22	A
55	2x	44	C
55	2x	46	A
55	2x	48	G

All (57) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	266	G
1	1A	278	A
1	1A	548	A
1	1A	746	A
1	1A	764	A
1	1A	774	A
1	1A	827	U
1	1A	974	G
1	1A	1065	U
1	1A	1142(A)	A
1	1A	1174	A
1	1A	1176	G
1	1A	1210	A
1	1A	1211	U
1	1A	1379	A
1	1A	1420	U
1	1A	1442	G
1	1A	1508	A
1	1A	1608	A
1	1A	1992	G
1	1A	2134	A
1	1A	2158	A
1	1A	2181	G
1	1A	2183	C
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2601	C

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Mol	Chain	Res	Type
1	1A	2689	U
1	1A	2756	U
1	2A	196	A
1	2A	228	A
1	2A	266	G
1	2A	277	C
1	2A	528	A
1	2A	746	A
1	2A	752	A
1	2A	764	A
1	2A	774	A
1	2A	827	U
1	2A	856	C
1	2A	893	C
1	2A	896	A
1	2A	900	A
1	2A	1210	A
1	2A	1379	A
1	2A	1420	U
1	2A	1530	C
1	2A	1653	G
1	2A	1992	G
1	2A	2126	A
1	2A	2145	C
1	2A	2238	G
1	2A	2406	U
1	2A	2430	A
1	2A	2689	U

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

66 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	$\#\|Z\|>2$
32	G7M	1a	527	57,32	20,26,27	1.19	2 (10%)	16,39,42	0.58	0
55	PSU	2x	39	55	18,21,22	1.46	3 (16%)	21,30,33	1.64	3 (14%)
32	5MC	2a	967	32	19,22,23	1.74	3 (15%)	26,32,35	1.18	3 (11%)
32	UR3	1a	1498	32	19,22,23	1.04	1 (5%)	26,32,35	1.75	5 (19%)
1	2MA	2A	2503	57,1	18,25,26	0.74	0	20,37,40	1.98	4 (20%)
32	G7M	2a	527	57,32	20,26,27	1.16	2 (10%)	16,39,42	0.59	0
1	5MC	1A	1962	57,1	19,22,23	2.01	3 (15%)	26,32,35	1.18	3 (11%)
55	H2U	2x	20	55	18,21,22	0.90	1 (5%)	19,30,33	1.04	1 (5%)
32	5MC	2a	1400	32	19,22,23	1.73	3 (15%)	26,32,35	1.22	2 (7%)
32	M2G	1a	966	32	20,27,28	1.35	3 (15%)	19,40,43	1.06	2 (10%)
55	4SU	2x	8	55	18,21,22	1.81	5 (27%)	25,30,33	2.07	5 (20%)
1	PSU	2A	1911	1	18,21,22	1.40	3 (16%)	21,30,33	2.14	4 (19%)
55	5MU	1x	54	57,55	19,22,23	1.44	5 (26%)	27,32,35	1.78	5 (18%)
55	H2U	1x	21	55	18,21,22	1.04	2 (11%)	19,30,33	1.73	3 (15%)
1	PSU	2A	2605	1	18,21,22	1.41	3 (16%)	21,30,33	2.08	5 (23%)
1	PSU	1A	2605	57,1	18,21,22	1.37	2 (11%)	21,30,33	2.15	4 (19%)
1	PSU	1A	1911	1	18,21,22	1.38	2 (11%)	21,30,33	1.91	4 (19%)
32	5MC	1a	1407	32	19,22,23	1.73	3 (15%)	26,32,35	1.12	4 (15%)
1	PSU	2A	1917	1	18,21,22	1.38	2 (11%)	21,30,33	2.09	4 (19%)
1	OMG	2A	2251	57,1,55	19,26,27	0.88	1 (5%)	21,38,41	1.09	1 (4%)
55	5MU	2x	54	55	19,22,23	1.43	5 (26%)	27,32,35	1.83	6 (22%)
1	OMC	2A	1920	1	19,22,23	0.80	0	25,31,34	0.86	0
32	5MC	2a	1407	57,32	19,22,23	1.61	2 (10%)	26,32,35	1.23	3 (11%)
32	4OC	1a	1402	57,32	20,23,24	0.73	0	25,32,35	1.07	1 (4%)
1	5MU	1A	1915	1	19,22,23	1.39	6 (31%)	27,32,35	2.22	6 (22%)
1	5MU	2A	1939	1	19,22,23	1.48	5 (26%)	27,32,35	2.23	6 (22%)
1	OMU	1A	2552	57,1	19,22,23	1.16	1 (5%)	25,31,34	1.90	6 (24%)
1	OMU	2A	2552	57,1	19,22,23	1.18	2 (10%)	25,31,34	1.74	5 (20%)
43	0TD	2l	92	43	8,9,10	4.62	1 (12%)	6,11,13	4.83	3 (50%)
55	MIA	1x	37	55	17,24,32	0.91	1 (5%)	16,35,47	1.62	3 (18%)
1	PSU	1A	1917	1	18,21,22	1.40	3 (16%)	21,30,33	2.12	5 (23%)
32	PSU	1a	516	57,32	18,21,22	1.37	2 (11%)	21,30,33	2.17	4 (19%)
32	2MG	1a	1207	32	18,26,27	0.92	1 (5%)	16,38,41	1.22	1 (6%)
32	5MC	2a	1404	32	19,22,23	1.74	3 (15%)	26,32,35	1.12	2 (7%)
32	PSU	2a	516	57,32	18,21,22	1.35	3 (16%)	21,30,33	1.98	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
32	4OC	2a	1402	57,32	20,23,24	0.78	0	25,32,35	1.11	3 (12%)
32	5MC	1a	967	32	19,22,23	1.62	2 (10%)	26,32,35	1.10	2 (7%)
32	5MC	1a	1400	32	19,22,23	1.83	3 (15%)	26,32,35	1.19	3 (11%)
32	5MC	1a	1404	32	19,22,23	1.86	3 (15%)	26,32,35	1.18	4 (15%)
1	2MA	1A	2503	57,1	18,25,26	0.69	0	20,37,40	2.05	3 (15%)
1	5MC	2A	1962	1	19,22,23	1.52	3 (15%)	26,32,35	1.15	2 (7%)
55	8AN	2x	76	57,55,56	17,24,25	1.08	2 (11%)	13,35,38	2.76	2 (15%)
55	PSU	2x	32	55	18,21,22	1.32	2 (11%)	21,30,33	2.07	3 (14%)
32	UR3	2a	1498	32	19,22,23	1.02	2 (10%)	26,32,35	1.69	3 (11%)
1	5MU	1A	1939	1	19,22,23	1.52	4 (21%)	27,32,35	2.22	6 (22%)
55	PSU	1x	39	55	18,21,22	1.55	3 (16%)	21,30,33	1.74	3 (14%)
55	PSU	1x	55	55	18,21,22	1.32	2 (11%)	21,30,33	2.16	4 (19%)
55	8AN	1x	76	57,55,56	17,24,25	1.05	2 (11%)	13,35,38	2.76	2 (15%)
55	PSU	1x	32	55	18,21,22	1.33	2 (11%)	21,30,33	2.02	4 (19%)
32	M2G	2a	966	32	20,27,28	1.43	3 (15%)	19,40,43	1.05	1 (5%)
1	5MU	2A	1915	57,1	19,22,23	1.49	4 (21%)	27,32,35	2.04	5 (18%)
32	MA6	2a	1519	32	19,26,27	1.00	2 (10%)	18,38,41	2.03	3 (16%)
55	MIA	2x	37	55	17,24,32	0.99	1 (5%)	16,35,47	1.51	2 (12%)
55	H2U	2x	21	55	18,21,22	0.85	2 (11%)	19,30,33	0.85	1 (5%)
32	MA6	1a	1519	32	19,26,27	1.01	1 (5%)	18,38,41	1.91	3 (16%)
1	5MC	2A	1942	1	19,22,23	1.56	3 (15%)	26,32,35	1.18	2 (7%)
32	MA6	1a	1518	32	19,26,27	1.03	2 (10%)	18,38,41	2.09	3 (16%)
55	4SU	1x	8	55	18,21,22	2.07	4 (22%)	25,30,33	1.94	4 (16%)
1	5MC	1A	1942	57,1	19,22,23	1.56	3 (15%)	26,32,35	1.25	4 (15%)
1	OMG	1A	2251	57,1,55	19,26,27	0.93	1 (5%)	21,38,41	1.14	3 (14%)
55	H2U	1x	20	55	18,21,22	0.93	2 (11%)	19,30,33	1.03	2 (10%)
43	0TD	1l	92	43	8,9,10	4.53	2 (25%)	6,11,13	8.06	2 (33%)
32	2MG	2a	1207	32	18,26,27	0.93	1 (5%)	16,38,41	1.23	1 (6%)
32	MA6	2a	1518	32	19,26,27	1.02	2 (10%)	18,38,41	1.76	3 (16%)
55	PSU	2x	55	55	18,21,22	1.35	2 (11%)	21,30,33	2.13	4 (19%)
1	OMC	1A	1920	1	19,22,23	0.82	0	25,31,34	0.97	1 (4%)

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
32	G7M	1a	527	57,32	-	3/3/25/26	0/3/3/3
55	PSU	2x	39	55	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	57,1	-	1/3/25/26	0/3/3/3
32	G7M	2a	527	57,32	-	2/3/25/26	0/3/3/3
1	5MC	1A	1962	57,1	-	0/7/25/26	0/2/2/2
55	H2U	2x	20	55	-	2/7/38/39	0/2/2/2
32	5MC	2a	1400	32	-	2/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/7/29/30	0/3/3/3
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
55	5MU	1x	54	57,55	-	0/7/25/26	0/2/2/2
55	H2U	1x	21	55	-	6/7/38/39	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	57,1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	57,1,55	-	1/5/27/28	0/3/3/3
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
32	5MC	2a	1407	57,32	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	57,32	-	2/9/29/30	0/2/2/2
1	5MU	1A	1915	1	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	57,1	-	0/9/27/28	0/2/2/2
1	OMU	2A	2552	57,1	-	0/9/27/28	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
55	MIA	1x	37	55	-	1/3/25/34	0/3/3/3
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	57,32	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	57,32	-	2/7/25/26	0/2/2/2
32	4OC	2a	1402	57,32	-	2/9/29/30	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	2MA	1A	2503	57,1	-	1/3/25/26	0/3/3/3
1	5MC	2A	1962	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	8AN	2x	76	57,55,56	-	1/3/25/26	0/3/3/3
55	PSU	2x	32	55	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	1	-	0/7/25/26	0/2/2/2
55	PSU	1x	39	55	-	0/7/25/26	0/2/2/2
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
55	8AN	1x	76	57,55,56	-	1/3/25/26	0/3/3/3
55	PSU	1x	32	55	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/7/29/30	0/3/3/3
1	5MU	2A	1915	57,1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	3/7/29/30	0/3/3/3
55	MIA	2x	37	55	-	2/3/25/34	0/3/3/3
55	H2U	2x	21	55	-	4/7/38/39	0/2/2/2
32	MA6	1a	1519	32	-	3/7/29/30	0/3/3/3
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/7/29/30	0/3/3/3
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	57,1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	57,1,55	-	0/5/27/28	0/3/3/3
55	H2U	1x	20	55	-	2/7/38/39	0/2/2/2
43	0TD	1l	92	43	-	2/7/12/14	-
32	2MG	2a	1207	32	-	2/5/27/28	0/3/3/3
32	MA6	2a	1518	32	-	0/7/29/30	0/3/3/3
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
1	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2

All (149) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.57	1.69	1.82
43	1l	92	0TD	CB-SB	-12.15	1.70	1.82
1	1A	1962	5MC	C5-C4	7.66	1.49	1.44
32	1a	1404	5MC	C5-C4	6.88	1.49	1.44
32	1a	1400	5MC	C5-C4	6.79	1.49	1.44
32	2a	967	5MC	C5-C4	6.48	1.49	1.44
32	1a	1407	5MC	C5-C4	6.48	1.49	1.44
32	2a	1404	5MC	C5-C4	6.41	1.49	1.44
32	2a	1400	5MC	C5-C4	6.39	1.49	1.44
32	1a	967	5MC	C5-C4	5.89	1.48	1.44
32	2a	1407	5MC	C5-C4	5.56	1.48	1.44
1	1A	1942	5MC	C5-C4	5.44	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	1942	5MC	C5-C4	5.43	1.48	1.44
1	2A	1962	5MC	C5-C4	5.31	1.48	1.44
55	1x	8	4SU	C4-S4	-5.30	1.59	1.68
55	2x	8	4SU	C4-S4	-4.97	1.59	1.68
55	1x	8	4SU	C4-N3	-4.54	1.32	1.37
32	2a	966	M2G	C2-N3	4.39	1.36	1.30
32	1a	966	M2G	C2-N3	4.12	1.36	1.30
55	2x	39	PSU	C6-C5	3.68	1.39	1.35
1	1A	1911	PSU	C6-C5	3.67	1.39	1.35
55	1x	39	PSU	C6-C5	3.64	1.39	1.35
1	2A	2605	PSU	C6-C5	3.62	1.39	1.35
55	2x	55	PSU	C6-C5	3.61	1.39	1.35
32	1a	527	G7M	C5-C4	3.60	1.46	1.39
32	2a	527	G7M	C5-C4	3.50	1.46	1.39
1	2A	1917	PSU	C6-C5	3.48	1.39	1.35
32	2a	516	PSU	C6-C5	3.46	1.39	1.35
55	1x	55	PSU	C6-C5	3.43	1.39	1.35
1	1A	1939	5MU	C4-N3	-3.39	1.32	1.38
32	1a	516	PSU	C6-C5	3.38	1.39	1.35
1	1A	1917	PSU	C6-C5	3.36	1.39	1.35
1	2A	1911	PSU	C6-C5	3.29	1.38	1.35
55	1x	32	PSU	C6-C5	3.26	1.38	1.35
55	2x	32	PSU	C6-C5	3.22	1.38	1.35
55	1x	39	PSU	C4-N3	-3.20	1.32	1.38
32	2a	1407	5MC	C6-C5	3.15	1.39	1.34
1	2A	1915	5MU	C2-N1	3.13	1.43	1.38
1	1A	2605	PSU	C4-N3	-3.08	1.33	1.38
32	1a	1400	5MC	C6-C5	3.07	1.39	1.34
1	1A	1939	5MU	C2-N3	-3.05	1.32	1.38
55	2x	8	4SU	C4-N3	-3.05	1.34	1.37
32	1a	1404	5MC	C6-C5	3.03	1.39	1.34
1	1A	1942	5MC	C6-C5	3.01	1.39	1.34
1	2A	1939	5MU	C4-N3	-3.01	1.33	1.38
32	2a	1404	5MC	C6-C5	3.00	1.39	1.34
55	1x	8	4SU	C2-N3	-3.00	1.32	1.38
1	2A	1915	5MU	C6-C5	2.97	1.39	1.34
55	1x	8	4SU	C5-C4	-2.96	1.39	1.42
55	1x	54	5MU	C6-C5	2.94	1.39	1.34
1	1A	1915	5MU	C4-N3	-2.92	1.33	1.38
55	2x	39	PSU	C4-N3	-2.92	1.33	1.38
1	2A	1942	5MC	C6-C5	2.89	1.39	1.34
1	1A	1962	5MC	C6-C5	2.89	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2x	54	5MU	C4-N3	-2.86	1.33	1.38
32	2a	966	M2G	C2-N2	2.83	1.40	1.35
1	1A	1917	PSU	C4-N3	-2.82	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.79	1.33	1.38
55	2x	54	5MU	C6-C5	2.78	1.39	1.34
32	1a	966	M2G	C2-N2	2.77	1.40	1.35
1	2A	1939	5MU	C6-C5	2.77	1.39	1.34
55	2x	76	8AN	C6-C5	-2.74	1.33	1.43
55	2x	37	MIA	C2-N3	2.73	1.36	1.32
1	1A	1939	5MU	C6-C5	2.72	1.39	1.34
32	2a	1400	5MC	C6-C5	2.71	1.39	1.34
32	1a	967	5MC	C6-C5	2.70	1.39	1.34
1	2A	1917	PSU	C4-N3	-2.68	1.33	1.38
1	2A	1915	5MU	C4-N3	-2.67	1.33	1.38
55	1x	54	5MU	C4-N3	-2.67	1.33	1.38
55	2x	8	4SU	C5-C4	-2.65	1.39	1.42
1	2A	1939	5MU	C2-N3	-2.64	1.33	1.38
1	1A	1911	PSU	C4-N3	-2.64	1.33	1.38
55	1x	39	PSU	C2-N3	-2.63	1.33	1.37
55	2x	55	PSU	C4-N3	-2.62	1.33	1.38
1	1A	1915	5MU	C6-C5	2.61	1.38	1.34
32	1a	516	PSU	C4-N3	-2.59	1.34	1.38
1	2A	2605	PSU	C4-N3	-2.58	1.34	1.38
55	1x	32	PSU	C4-N3	-2.58	1.34	1.38
55	1x	21	H2U	C2-N3	-2.57	1.33	1.38
32	2a	967	5MC	C6-C5	2.54	1.38	1.34
1	1A	1939	5MU	C6-N1	-2.53	1.33	1.38
32	1a	1407	5MC	C6-C5	2.53	1.38	1.34
43	1l	92	0TD	CB-CA	-2.51	1.53	1.54
55	1x	76	8AN	C6-C5	-2.50	1.34	1.43
55	1x	20	H2U	C2-N3	-2.49	1.33	1.38
1	2A	1939	5MU	C6-N1	-2.46	1.33	1.38
55	2x	32	PSU	C4-N3	-2.46	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.45	1.33	1.38
1	2A	1962	5MC	C6-C5	2.45	1.38	1.34
1	1A	2552	OMU	C4-N3	-2.44	1.34	1.38
32	1a	1518	MA6	C6-C5	-2.43	1.41	1.44
32	2a	1207	2MG	C6-N1	-2.41	1.34	1.37
1	2A	1939	5MU	C4-C5	2.41	1.48	1.44
32	2a	1518	MA6	C6-C5	-2.40	1.41	1.44
1	2A	1915	5MU	C4-C5	2.40	1.48	1.44
55	1x	54	5MU	C4-C5	2.38	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1519	MA6	C6-C5	-2.37	1.41	1.44
32	1a	1207	2MG	C6-N1	-2.36	1.34	1.37
55	2x	21	H2U	C2-N3	-2.36	1.33	1.38
32	2a	516	PSU	C4-N3	-2.35	1.34	1.38
55	2x	20	H2U	C2-N3	-2.35	1.33	1.38
55	2x	54	5MU	C4-C5	2.34	1.48	1.44
32	2a	967	5MC	C6-N1	-2.34	1.34	1.38
1	2A	2552	OMU	C4-N3	-2.34	1.34	1.38
55	1x	37	MIA	C2-N3	2.33	1.35	1.32
1	1A	2251	OMG	C6-N1	-2.33	1.34	1.37
1	2A	2251	OMG	C6-N1	-2.31	1.34	1.37
32	1a	1404	5MC	C6-N1	-2.31	1.34	1.38
55	1x	54	5MU	C2-N1	2.31	1.42	1.38
1	1A	1962	5MC	C6-N1	-2.31	1.34	1.38
55	1x	55	PSU	C4-N3	-2.30	1.34	1.38
1	1A	2605	PSU	C6-C5	2.29	1.37	1.35
32	2a	1400	5MC	C6-N1	-2.28	1.34	1.38
55	2x	8	4SU	C2-N1	2.26	1.42	1.38
55	2x	54	5MU	C2-N3	-2.26	1.34	1.38
32	2a	1519	MA6	C6-C5	-2.25	1.41	1.44
55	2x	39	PSU	C2-N3	-2.24	1.33	1.37
32	1a	1407	5MC	C6-N1	-2.23	1.34	1.38
32	1a	1498	UR3	C2-N1	2.23	1.41	1.38
32	1a	527	G7M	C6-N1	-2.22	1.34	1.37
32	2a	966	M2G	C6-N1	-2.21	1.34	1.37
32	2a	527	G7M	C6-N1	-2.21	1.34	1.37
55	1x	76	8AN	C5-N7	-2.19	1.32	1.39
1	1A	1917	PSU	C2-N3	-2.18	1.33	1.37
1	1A	1915	5MU	C2-N3	-2.18	1.34	1.38
32	2a	1498	UR3	C2-N1	2.18	1.41	1.38
1	1A	1915	5MU	C2-N1	2.16	1.41	1.38
55	2x	21	H2U	C4-N3	-2.15	1.34	1.37
1	2A	2552	OMU	C2-N3	-2.14	1.34	1.38
32	1a	966	M2G	C6-N1	-2.13	1.34	1.37
32	2a	1404	5MC	C6-N1	-2.11	1.34	1.38
55	2x	54	5MU	C2-N1	2.10	1.41	1.38
32	2a	1518	MA6	C6-N1	2.10	1.35	1.32
55	1x	20	H2U	C4-N3	-2.10	1.34	1.37
1	1A	1915	5MU	C4-C5	2.09	1.48	1.44
32	2a	1498	UR3	C6-C5	2.09	1.39	1.35
55	2x	8	4SU	C2-N3	-2.08	1.34	1.38
1	2A	2605	PSU	C2-N3	-2.07	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1x	54	5MU	C2-N3	-2.07	1.34	1.38
32	2a	1519	MA6	C6-N1	2.06	1.35	1.32
55	2x	76	8AN	C5-N7	-2.06	1.32	1.39
32	1a	1518	MA6	C6-N1	2.06	1.35	1.32
1	2A	1942	5MC	C6-N1	-2.05	1.34	1.38
55	1x	21	H2U	C4-N3	-2.04	1.34	1.37
32	1a	1400	5MC	C6-N1	-2.04	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.04	1.34	1.38
32	2a	516	PSU	O4'-C1'	-2.03	1.41	1.43
1	1A	1942	5MC	C6-N1	-2.02	1.34	1.38
1	2A	1911	PSU	C2-N3	-2.01	1.34	1.37

All (206) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	1l	92	0TD	CSB-SB-CB	-19.33	67.63	102.36
43	2l	92	0TD	CSB-SB-CB	-11.05	82.50	102.36
55	1x	76	8AN	C4'-O4'-C1'	-7.10	103.42	109.92
1	2A	2503	2MA	C2-N3-C4	7.09	121.18	115.46
55	2x	76	8AN	C4'-O4'-C1'	-6.92	103.59	109.92
32	1a	516	PSU	N1-C2-N3	6.91	122.45	115.17
1	1A	2503	2MA	C2-N3-C4	6.91	121.03	115.46
32	2a	1498	UR3	C4-N3-C2	-6.86	119.06	124.58
1	1A	1917	PSU	N1-C2-N3	6.69	122.22	115.17
32	1a	1498	UR3	C4-N3-C2	-6.64	119.23	124.58
1	2A	1911	PSU	N1-C2-N3	6.64	122.17	115.17
55	2x	55	PSU	N1-C2-N3	6.63	122.16	115.17
1	2A	2605	PSU	N1-C2-N3	6.57	122.10	115.17
1	2A	1917	PSU	N1-C2-N3	6.56	122.09	115.17
55	1x	55	PSU	N1-C2-N3	6.54	122.06	115.17
55	2x	76	8AN	N3-C2-N1	-6.49	119.87	128.67
55	1x	76	8AN	N3-C2-N1	-6.48	119.88	128.67
1	1A	2605	PSU	N1-C2-N3	6.15	121.66	115.17
55	2x	32	PSU	N1-C2-N3	6.11	121.62	115.17
55	1x	32	PSU	N1-C2-N3	6.09	121.60	115.17
55	1x	8	4SU	C5-C4-N3	6.05	120.38	114.75
1	1A	1911	PSU	N1-C2-N3	5.87	121.36	115.17
32	2a	516	PSU	N1-C2-N3	5.86	121.35	115.17
55	2x	8	4SU	C5-C4-N3	5.83	120.18	114.75
32	1a	1518	MA6	N3-C2-N1	-5.79	120.81	128.67
55	1x	39	PSU	N1-C2-N3	5.76	121.25	115.17
1	1A	1915	5MU	N3-C2-N1	5.74	122.36	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2x	8	4SU	C4-N3-C2	-5.71	121.84	127.31
1	2A	1939	5MU	C4-N3-C2	-5.63	119.96	127.34
32	1a	1518	MA6	C2-N1-C6	5.56	122.29	116.84
1	1A	1939	5MU	C5-C4-N3	5.54	120.14	115.32
32	2a	1519	MA6	N3-C2-N1	-5.47	121.25	128.67
1	1A	1915	5MU	C4-N3-C2	-5.45	120.19	127.34
32	1a	1519	MA6	N3-C2-N1	-5.38	121.36	128.67
1	1A	1939	5MU	C4-N3-C2	-5.33	120.36	127.34
1	1A	2552	OMU	C4-N3-C2	-5.31	120.02	126.61
1	2A	1939	5MU	N3-C2-N1	5.16	121.61	114.89
55	1x	8	4SU	C4-N3-C2	-5.12	122.40	127.31
55	2x	39	PSU	N1-C2-N3	5.06	120.51	115.17
55	1x	21	H2U	N3-C2-N1	-5.00	111.62	116.65
1	2A	1939	5MU	C5-C4-N3	4.97	119.65	115.32
1	2A	1939	5MU	C5-C6-N1	-4.97	117.92	123.31
32	2a	1518	MA6	N3-C2-N1	-4.89	122.03	128.67
1	2A	1915	5MU	C4-N3-C2	-4.88	120.94	127.34
32	1a	1519	MA6	C2-N1-C6	4.81	121.56	116.84
1	1A	1939	5MU	C5-C6-N1	-4.81	118.09	123.31
1	2A	2552	OMU	C4-N3-C2	-4.76	120.70	126.61
32	2a	1519	MA6	C2-N1-C6	4.74	121.49	116.84
1	2A	1915	5MU	N3-C2-N1	4.74	121.06	114.89
55	2x	54	5MU	N3-C2-N1	4.74	121.06	114.89
1	1A	1939	5MU	N3-C2-N1	4.71	121.02	114.89
1	1A	2605	PSU	C4-N3-C2	-4.66	119.95	126.37
1	2A	1915	5MU	C5-C4-N3	4.65	119.36	115.32
1	2A	1911	PSU	C4-N3-C2	-4.57	120.07	126.37
55	2x	32	PSU	O2-C2-N1	-4.45	118.20	122.79
55	2x	55	PSU	C4-N3-C2	-4.44	120.26	126.37
55	1x	37	MIA	N3-C2-N1	-4.42	122.67	128.67
1	1A	1915	5MU	C5-C4-N3	4.40	119.15	115.32
55	1x	54	5MU	N3-C2-N1	4.33	120.53	114.89
55	1x	32	PSU	C4-N3-C2	-4.31	120.43	126.37
1	1A	1917	PSU	C4-N3-C2	-4.31	120.44	126.37
55	1x	55	PSU	C4-N3-C2	-4.28	120.47	126.37
1	2A	1917	PSU	C4-N3-C2	-4.28	120.47	126.37
32	1a	516	PSU	C4-N3-C2	-4.24	120.53	126.37
55	2x	54	5MU	C4-N3-C2	-4.23	121.80	127.34
1	1A	2552	OMU	N3-C2-N1	4.20	120.36	114.89
32	2a	1400	5MC	C5-C6-N1	-4.17	118.78	123.31
32	2a	1518	MA6	C2-N1-C6	4.17	120.92	116.84
55	2x	32	PSU	C4-N3-C2	-4.16	120.64	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2x	37	MIA	N3-C2-N1	-4.14	123.06	128.67
1	2A	2552	OMU	N3-C2-N1	4.08	120.20	114.89
55	1x	54	5MU	C4-N3-C2	-4.08	121.99	127.34
55	1x	55	PSU	O2-C2-N1	-4.06	118.60	122.79
1	1A	1939	5MU	O4-C4-C5	-4.01	120.33	124.92
32	2a	516	PSU	C4-N3-C2	-4.00	120.86	126.37
1	2A	2605	PSU	C4-N3-C2	-3.97	120.91	126.37
1	1A	2605	PSU	O2-C2-N1	-3.95	118.72	122.79
32	1a	516	PSU	O2-C2-N1	-3.94	118.73	122.79
1	1A	2552	OMU	C5-C4-N3	3.92	120.29	114.80
1	2A	1915	5MU	O4-C4-C5	-3.91	120.44	124.92
1	1A	1911	PSU	C4-N3-C2	-3.89	121.01	126.37
55	1x	54	5MU	C5-C4-N3	3.80	118.62	115.32
1	1A	1942	5MC	C5-C6-N1	-3.80	119.19	123.31
1	1A	1915	5MU	O4-C4-C5	-3.78	120.59	124.92
1	2A	2552	OMU	C5-C4-N3	3.77	120.08	114.80
32	1a	1400	5MC	C5-C6-N1	-3.76	119.23	123.31
55	2x	8	4SU	C5-C4-S4	-3.68	120.10	124.31
1	2A	1962	5MC	C5-C6-N1	-3.64	119.36	123.31
55	2x	54	5MU	C5-C4-N3	3.63	118.48	115.32
32	2a	1519	MA6	C4-C5-N7	-3.63	105.51	109.34
1	1A	1915	5MU	C5-C6-N1	-3.56	119.44	123.31
1	2A	1911	PSU	O2-C2-N1	-3.56	119.12	122.79
55	1x	21	H2U	C5-C6-N1	-3.54	100.82	111.52
32	2a	1404	5MC	C5-C6-N1	-3.51	119.50	123.31
1	2A	1917	PSU	O2-C2-N1	-3.50	119.18	122.79
32	2a	967	5MC	C5-C6-N1	-3.49	119.53	123.31
55	1x	54	5MU	O4-C4-C5	-3.39	121.04	124.92
55	2x	8	4SU	N3-C2-N1	3.38	119.29	114.89
1	2A	1939	5MU	O4-C4-C5	-3.36	121.07	124.92
1	1A	1962	5MC	C5-C6-N1	-3.35	119.68	123.31
1	2A	1915	5MU	C5-C6-N1	-3.34	119.69	123.31
1	1A	2552	OMU	O4-C4-C5	-3.31	119.46	125.16
32	2a	516	PSU	O2-C2-N1	-3.29	119.39	122.79
43	2l	92	0TD	OD2-CG-CB	3.27	120.21	113.15
1	2A	1942	5MC	C5-C6-N1	-3.24	119.80	123.31
55	2x	55	PSU	O2-C2-N1	-3.24	119.45	122.79
32	1a	967	5MC	C5-C6-N1	-3.24	119.80	123.31
55	1x	32	PSU	O2-C2-N1	-3.23	119.46	122.79
32	2a	1407	5MC	C5-C4-N3	-3.20	118.47	121.75
32	2a	1407	5MC	C5-C6-N1	-3.17	119.88	123.31
1	1A	1917	PSU	O2-C2-N1	-3.17	119.52	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2x	37	MIA	C4-C5-N7	-3.14	106.02	109.34
55	2x	54	5MU	C5-C6-N1	-3.11	119.94	123.31
1	1A	1915	5MU	O2-C2-N1	-3.10	118.76	122.80
43	1l	92	0TD	OD2-CG-CB	3.10	119.84	113.15
32	1a	1404	5MC	C5-C6-N1	-3.09	119.96	123.31
55	1x	8	4SU	N3-C2-N1	3.06	118.87	114.89
32	1a	1498	UR3	C5-C4-N3	3.05	119.06	115.04
32	1a	966	M2G	C8-N7-C5	3.03	107.71	102.55
55	2x	54	5MU	O4-C4-C5	-3.03	121.45	124.92
32	1a	1404	5MC	C5-C4-N3	-3.01	118.67	121.75
1	1A	2605	PSU	C5-C6-N1	-3.00	117.97	122.14
1	1A	2251	OMG	C8-N7-C5	3.00	107.66	102.55
55	1x	54	5MU	C5-C6-N1	-3.00	120.05	123.31
55	1x	37	MIA	C4-C5-N7	-2.97	106.20	109.34
1	2A	2605	PSU	O2-C2-N1	-2.96	119.73	122.79
55	2x	39	PSU	C4-N3-C2	-2.94	122.32	126.37
32	1a	1407	5MC	C5-C6-N1	-2.91	120.16	123.31
1	1A	1942	5MC	C5-C4-N3	-2.90	118.79	121.75
32	2a	966	M2G	C8-N7-C5	2.90	107.48	102.55
32	1a	1402	4OC	C6-C5-C4	2.89	120.48	117.00
32	1a	1518	MA6	C4-C5-N7	-2.89	106.28	109.34
32	1a	1207	2MG	C8-N7-C5	2.89	107.47	102.55
32	2a	1498	UR3	C5-C4-N3	2.87	118.82	115.04
1	2A	2251	OMG	C8-N7-C5	2.86	107.43	102.55
55	2x	20	H2U	C5-C6-N1	-2.86	102.87	111.52
55	1x	39	PSU	C4-N3-C2	-2.82	122.49	126.37
32	2a	1518	MA6	C4-C5-N7	-2.81	106.36	109.34
1	2A	2552	OMU	O4-C4-C5	-2.81	120.32	125.16
1	2A	1942	5MC	C5-C4-N3	-2.80	118.89	121.75
1	1A	2552	OMU	O2-C2-N1	-2.75	119.22	122.80
55	1x	20	H2U	C5-C6-N1	-2.72	103.28	111.52
1	1A	1911	PSU	O2-C2-N1	-2.69	120.02	122.79
1	1A	2503	2MA	C2-N1-C6	2.69	122.23	118.10
32	1a	1498	UR3	C6-N1-C2	-2.66	119.62	121.80
32	1a	1407	5MC	C5-C4-N3	-2.66	119.03	121.75
32	1a	1400	5MC	C5-C4-N3	-2.63	119.06	121.75
32	2a	1207	2MG	C8-N7-C5	2.61	106.99	102.55
1	2A	2503	2MA	C4-C5-N7	-2.60	106.58	109.34
32	1a	1519	MA6	C4-C5-N7	-2.60	106.59	109.34
55	1x	8	4SU	S4-C4-N3	-2.60	117.48	120.20
55	2x	55	PSU	C5-C6-N1	-2.60	118.53	122.14
32	1a	967	5MC	C5-C4-N3	-2.58	119.11	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	967	5MC	C5-C4-N3	-2.57	119.12	121.75
1	2A	2503	2MA	C2-N1-C6	2.57	122.05	118.10
32	2a	1402	4OC	O2-C2-N3	-2.57	118.28	122.33
1	2A	1962	5MC	C5-C4-N3	-2.57	119.12	121.75
32	2a	1404	5MC	C5-C4-N3	-2.53	119.16	121.75
55	1x	21	H2U	O4'-C1'-N1	2.51	112.71	109.30
32	2a	1400	5MC	C5-C4-N3	-2.50	119.19	121.75
32	2a	1407	5MC	O2-C2-N3	-2.50	118.39	122.33
1	2A	1911	PSU	C5-C6-N1	-2.46	118.73	122.14
1	1A	1962	5MC	CM5-C5-C6	-2.45	119.54	122.85
1	1A	1920	OMC	O2-C2-N3	-2.43	118.50	122.33
32	1a	1498	UR3	C3U-N3-C2	2.42	121.55	117.33
55	1x	32	PSU	C5-C6-N1	-2.39	118.82	122.14
1	1A	1939	5MU	O2-C2-N1	-2.38	119.70	122.80
55	1x	39	PSU	O2-C2-N3	-2.37	117.65	121.86
1	2A	1939	5MU	O2-C2-N1	-2.37	119.72	122.80
1	1A	2251	OMG	C5-C6-N1	2.35	118.55	114.07
32	1a	1407	5MC	CM5-C5-C6	-2.33	119.69	122.85
1	1A	1962	5MC	C5-C4-N3	-2.33	119.37	121.75
32	2a	516	PSU	O4'-C1'-C2'	2.32	108.36	105.15
1	1A	1917	PSU	C5-C6-N1	-2.31	118.94	122.14
55	2x	8	4SU	C1'-N1-C2	2.30	121.73	117.59
32	1a	1404	5MC	CM5-C5-C6	-2.29	119.75	122.85
32	2a	1402	4OC	C6-C5-C4	2.29	119.76	117.00
55	1x	55	PSU	C5-C6-N1	-2.29	118.97	122.14
32	1a	1498	UR3	C1'-N1-C2	2.27	120.76	117.04
1	2A	2552	OMU	O2-C2-N1	-2.27	119.85	122.80
1	2A	1917	PSU	C5-C6-N1	-2.25	119.02	122.14
32	1a	1400	5MC	O2-C2-N3	-2.21	118.84	122.33
32	2a	1402	4OC	CM4-N4-C4	-2.20	118.16	122.45
32	2a	967	5MC	CM5-C5-C6	-2.20	119.88	122.85
1	1A	1942	5MC	N1-C2-N3	2.18	122.59	118.80
32	1a	1404	5MC	O2-C2-N3	-2.17	118.91	122.33
55	2x	54	5MU	O2-C2-N1	-2.16	119.98	122.80
43	2l	92	0TD	OD1-CG-CB	-2.16	117.92	122.44
32	1a	966	M2G	C5-C6-N1	2.15	118.17	114.07
55	1x	37	MIA	C1'-N9-C4	-2.14	122.88	126.64
1	1A	1942	5MC	O2-C2-N3	-2.13	118.98	122.33
32	1a	1407	5MC	O2-C2-N3	-2.11	119.00	122.33
1	1A	1911	PSU	C6-C5-C4	-2.10	116.75	118.17
1	1A	2552	OMU	C5-C6-N1	-2.10	118.42	121.84
1	2A	2605	PSU	O2-C2-N3	-2.08	118.16	121.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	516	PSU	C5-C6-N1	-2.08	119.25	122.14
55	2x	21	H2U	O4-C4-N3	2.06	123.48	120.30
1	2A	2503	2MA	C5-C6-N1	-2.05	118.42	120.84
1	2A	2605	PSU	C5-C6-N1	-2.05	119.30	122.14
55	2x	39	PSU	C6-C5-C4	-2.04	116.80	118.17
1	1A	1917	PSU	O2-C2-N3	-2.03	118.25	121.86
55	1x	20	H2U	C5-C4-N3	2.03	118.84	116.69
1	1A	2503	2MA	N3-C2-N1	-2.02	122.23	125.77
32	1a	516	PSU	C5-C6-N1	-2.01	119.35	122.14
1	1A	2251	OMG	O6-C6-C5	-2.01	120.34	124.32
32	2a	1498	UR3	C3U-N3-C4	2.00	120.64	117.87

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	CA-CB-SB-CSB
43	1l	92	0TD	CG-CB-SB-CSB
1	2A	2251	OMG	C1'-C2'-O2'-CM2
32	2a	1207	2MG	N1-C2-N2-CM2
32	2a	1207	2MG	N3-C2-N2-CM2
32	2a	1400	5MC	O4'-C4'-C5'-O5'
55	1x	21	H2U	C3'-C4'-C5'-O5'
55	2x	76	8AN	C4'-C5'-O5'-P
55	1x	21	H2U	C2'-C1'-N1-C2
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
55	2x	21	H2U	C3'-C4'-C5'-O5'
55	1x	21	H2U	O4'-C4'-C5'-O5'
55	2x	21	H2U	O4'-C4'-C5'-O5'
55	1x	76	8AN	C4'-C5'-O5'-P
32	1a	1519	MA6	C3'-C4'-C5'-O5'
55	2x	20	H2U	O4'-C4'-C5'-O5'
55	2x	37	MIA	O4'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
55	1x	20	H2U	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
32	1a	1402	4OC	C3'-C4'-C5'-O5'
55	1x	21	H2U	C2'-C1'-N1-C6
55	1x	20	H2U	C3'-C4'-C5'-O5'
55	2x	20	H2U	C3'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
55	1x	21	H2U	O4'-C1'-N1-C6
55	1x	37	MIA	O4'-C4'-C5'-O5'
55	2x	21	H2U	C4'-C5'-O5'-P
32	2a	516	PSU	O4'-C1'-C5-C4
32	1a	1519	MA6	C4'-C5'-O5'-P
1	1A	2503	2MA	C4'-C5'-O5'-P
32	1a	527	G7M	C4'-C5'-O5'-P
43	2l	92	0TD	SB-CB-CG-OD2
55	2x	37	MIA	C3'-C4'-C5'-O5'
32	2a	516	PSU	O4'-C1'-C5-C6
43	2l	92	0TD	CG-CB-SB-CSB
1	1A	1920	OMC	C2'-C1'-N1-C2
55	1x	21	H2U	O4'-C1'-N1-C2
1	2A	2503	2MA	C4'-C5'-O5'-P
32	2a	1519	MA6	C4'-C5'-O5'-P
55	2x	21	H2U	C2'-C1'-N1-C2
1	2A	1920	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

27 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1400	5MC	1	0
32	1a	966	M2G	1	0
55	1x	21	H2U	1	0
1	2A	1917	PSU	1	0
1	2A	2251	OMG	1	0
1	2A	1920	OMC	1	0
32	1a	1402	4OC	4	0
1	1A	1915	5MU	1	0
1	2A	1939	5MU	1	0
1	2A	2552	OMU	2	0
1	1A	1917	PSU	1	0
32	1a	516	PSU	1	0
32	2a	1404	5MC	1	0
32	2a	1402	4OC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1400	5MC	1	0
55	2x	76	8AN	2	0
1	1A	1939	5MU	1	0
32	2a	966	M2G	1	0
32	2a	1519	MA6	2	0
32	1a	1519	MA6	1	0
1	2A	1942	5MC	1	0
32	1a	1518	MA6	1	0
1	1A	2251	OMG	1	0
55	1x	20	H2U	1	0
32	2a	1207	2MG	1	0
32	2a	1518	MA6	3	0
1	1A	1920	OMC	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2693 ligands modelled in this entry, 2691 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
60	SF4	1d	302	35	0,12,12	-	-	-		
60	SF4	2d	303	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
60	SF4	1d	302	35	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	SF4	2d	303	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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%)	-0.39	158 (5%) 32 35	20, 36, 93, 105	0
1	2A	2789/2915 (95%)	-0.01	131 (4%) 37 42	30, 53, 89, 105	0
2	1B	120/121 (99%)	-0.24	0 100 100	29, 50, 61, 83	0
2	2B	120/121 (99%)	0.73	3 (2%) 58 63	55, 73, 79, 91	0
3	1D	275/276 (99%)	-0.23	3 (1%) 77 80	21, 35, 52, 77	0
3	2D	275/276 (99%)	0.11	3 (1%) 77 80	28, 46, 59, 75	0
4	1E	204/206 (99%)	-0.15	4 (1%) 64 69	20, 40, 58, 75	0
4	2E	204/206 (99%)	0.37	4 (1%) 64 69	30, 54, 67, 74	0
5	1F	203/210 (96%)	-0.17	1 (0%) 87 90	19, 41, 65, 80	0
5	2F	203/210 (96%)	0.48	4 (1%) 64 69	33, 62, 75, 86	0
6	1G	181/182 (99%)	1.18	30 (16%) 5 6	49, 67, 77, 84	0
6	2G	181/182 (99%)	1.38	32 (17%) 4 6	62, 76, 83, 91	0
7	1H	174/180 (96%)	0.39	4 (2%) 61 65	36, 52, 64, 75	0
7	2H	174/180 (96%)	1.45	44 (25%) 2 3	65, 78, 85, 91	0
8	1I	146/148 (98%)	1.00	12 (8%) 19 22	44, 70, 78, 81	0
8	2I	146/148 (98%)	1.43	29 (19%) 3 5	53, 74, 81, 86	0
9	1N	140/140 (100%)	-0.13	1 (0%) 84 86	26, 39, 59, 75	0
9	2N	140/140 (100%)	0.60	5 (3%) 46 52	44, 60, 73, 82	0
10	1O	122/122 (100%)	-0.12	0 100 100	26, 39, 59, 66	0
10	2O	122/122 (100%)	0.17	0 100 100	41, 50, 65, 70	0
11	1P	149/150 (99%)	0.05	1 (0%) 84 86	20, 42, 63, 75	0
11	2P	149/150 (99%)	0.57	2 (1%) 74 77	33, 62, 77, 84	0
12	1Q	141/141 (100%)	0.05	5 (3%) 47 53	26, 39, 54, 61	0
12	2Q	141/141 (100%)	0.71	9 (6%) 27 30	42, 59, 68, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.27	0 100 100	26, 35, 50, 59	0
13	2R	118/118 (100%)	0.12	0 100 100	36, 50, 59, 70	0
14	1S	110/112 (98%)	0.25	2 (1%) 67 71	37, 48, 60, 67	0
14	2S	110/112 (98%)	1.17	12 (10%) 12 15	55, 67, 75, 77	0
15	1T	131/146 (89%)	0.09	2 (1%) 71 75	32, 45, 70, 80	0
15	2T	131/146 (89%)	0.42	5 (3%) 44 50	46, 55, 72, 79	0
16	1U	116/118 (98%)	-0.44	0 100 100	21, 30, 48, 56	0
16	2U	116/118 (98%)	0.38	1 (0%) 81 83	38, 55, 68, 76	0
17	1V	101/101 (100%)	-0.29	0 100 100	21, 41, 56, 65	0
17	2V	101/101 (100%)	0.74	4 (3%) 43 48	40, 65, 76, 83	0
18	1W	112/113 (99%)	-0.31	0 100 100	23, 32, 53, 75	0
18	2W	112/113 (99%)	0.25	3 (2%) 56 61	37, 47, 62, 83	0
19	1X	95/96 (98%)	-0.08	1 (1%) 77 80	25, 37, 58, 74	0
19	2X	95/96 (98%)	0.66	7 (7%) 22 25	46, 56, 73, 81	0
20	1Y	107/110 (97%)	0.34	2 (1%) 66 69	34, 48, 66, 76	0
20	2Y	107/110 (97%)	1.08	12 (11%) 11 14	57, 67, 78, 82	0
21	1Z	154/206 (74%)	0.65	9 (5%) 30 34	38, 57, 70, 75	0
21	2Z	160/206 (77%)	1.38	25 (15%) 6 7	58, 72, 79, 83	0
22	10	76/85 (89%)	-0.07	3 (3%) 44 49	26, 37, 57, 63	0
22	20	76/85 (89%)	0.75	4 (5%) 33 37	45, 58, 69, 73	0
23	11	97/98 (98%)	0.19	2 (2%) 63 68	27, 42, 66, 71	0
23	21	97/98 (98%)	0.49	3 (3%) 51 57	37, 52, 70, 76	0
24	12	70/72 (97%)	0.14	2 (2%) 54 58	33, 48, 59, 75	0
24	22	70/72 (97%)	0.96	6 (8%) 18 21	58, 67, 73, 81	0
25	13	59/60 (98%)	-0.20	1 (1%) 69 72	25, 34, 56, 71	0
25	23	59/60 (98%)	0.55	2 (3%) 48 53	48, 57, 68, 74	0
26	14	69/71 (97%)	1.67	27 (39%) 1 1	59, 81, 90, 91	0
26	24	69/71 (97%)	1.66	20 (28%) 1 2	72, 82, 90, 91	0
27	15	59/60 (98%)	-0.34	1 (1%) 69 72	22, 35, 50, 61	0
27	25	59/60 (98%)	0.27	2 (3%) 48 53	31, 49, 65, 78	0
28	16	53/54 (98%)	-0.25	0 100 100	31, 41, 52, 55	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.52	1 (1%) 66 69	47, 56, 64, 67	0
29	17	48/49 (97%)	-0.18	4 (8%) 19 22	21, 26, 55, 62	0
29	27	48/49 (97%)	-0.00	5 (10%) 13 16	30, 39, 62, 73	0
30	18	64/65 (98%)	-0.27	0 100 100	27, 33, 39, 51	0
30	28	64/65 (98%)	0.28	1 (1%) 70 74	41, 50, 57, 63	0
31	19	37/37 (100%)	0.05	0 100 100	31, 41, 53, 55	0
31	29	37/37 (100%)	1.03	6 (16%) 5 7	50, 63, 72, 74	0
32	1a	1488/1521 (97%)	0.82	126 (8%) 18 21	35, 72, 93, 104	0
32	2a	1491/1521 (98%)	0.71	124 (8%) 19 22	43, 72, 92, 104	0
33	1b	231/256 (90%)	1.70	70 (30%) 1 1	67, 78, 85, 88	0
33	2b	231/256 (90%)	1.77	78 (33%) 1 1	69, 80, 87, 91	0
34	1c	206/239 (86%)	1.70	63 (30%) 1 2	65, 78, 85, 88	0
34	2c	206/239 (86%)	1.75	70 (33%) 1 1	69, 80, 85, 88	0
35	1d	208/209 (99%)	1.45	44 (21%) 3 4	60, 75, 82, 84	0
35	2d	208/209 (99%)	1.29	32 (15%) 6 8	56, 70, 78, 83	0
36	1e	148/162 (91%)	1.03	14 (9%) 15 19	54, 68, 77, 82	0
36	2e	148/162 (91%)	1.05	15 (10%) 14 17	58, 70, 77, 80	0
37	1f	100/101 (99%)	0.87	4 (4%) 43 48	56, 68, 75, 77	0
37	2f	100/101 (99%)	1.09	11 (11%) 12 14	61, 72, 78, 81	0
38	1g	155/156 (99%)	1.22	26 (16%) 5 6	66, 75, 83, 89	0
38	2g	155/156 (99%)	1.52	39 (25%) 2 3	70, 79, 85, 90	0
39	1h	137/138 (99%)	1.05	14 (10%) 13 17	58, 71, 78, 80	0
39	2h	137/138 (99%)	1.05	12 (8%) 17 20	63, 70, 76, 81	0
40	1i	127/128 (99%)	1.56	27 (21%) 3 4	61, 77, 83, 87	0
40	2i	127/128 (99%)	2.37	72 (56%) 0 0	69, 82, 88, 90	0
41	1j	97/105 (92%)	1.84	36 (37%) 1 1	65, 79, 85, 87	0
41	2j	96/105 (91%)	2.43	66 (68%) 0 0	71, 83, 88, 91	0
42	1k	114/129 (88%)	0.92	10 (8%) 17 20	45, 67, 77, 82	0
42	2k	114/129 (88%)	1.13	14 (12%) 9 11	56, 72, 81, 84	0
43	1l	121/132 (91%)	0.91	9 (7%) 22 25	51, 59, 69, 75	0
43	2l	121/132 (91%)	0.72	6 (4%) 35 40	52, 60, 68, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	118/126 (93%)	2.13	62 (52%) 0 0	71, 80, 84, 87	0
44	2m	116/126 (92%)	1.73	39 (33%) 1 1	72, 80, 85, 86	0
45	1n	60/61 (98%)	1.96	25 (41%) 1 1	67, 77, 83, 86	0
45	2n	60/61 (98%)	2.45	36 (60%) 0 0	73, 81, 85, 87	0
46	1o	88/89 (98%)	1.22	18 (20%) 3 4	50, 68, 77, 79	0
46	2o	88/89 (98%)	1.19	13 (14%) 7 9	59, 70, 76, 78	0
47	1p	82/88 (93%)	1.84	30 (36%) 1 1	63, 74, 81, 85	0
47	2p	82/88 (93%)	1.40	12 (14%) 7 9	58, 68, 75, 79	0
48	1q	99/105 (94%)	1.31	16 (16%) 5 7	56, 67, 76, 79	0
48	2q	99/105 (94%)	0.89	3 (3%) 52 58	58, 65, 75, 79	0
49	1r	68/88 (77%)	0.83	5 (7%) 22 25	56, 67, 74, 80	0
49	2r	68/88 (77%)	1.12	7 (10%) 13 16	63, 70, 80, 83	0
50	1s	83/93 (89%)	2.50	61 (73%) 0 0	72, 83, 87, 91	0
50	2s	83/93 (89%)	2.05	44 (53%) 0 0	70, 83, 88, 90	0
51	1t	96/106 (90%)	1.47	19 (19%) 3 5	63, 72, 78, 82	0
51	2t	96/106 (90%)	1.18	16 (16%) 5 6	56, 66, 77, 80	0
52	1u	23/27 (85%)	2.22	11 (47%) 0 0	73, 78, 81, 85	0
52	2u	23/27 (85%)	1.92	9 (39%) 1 1	74, 79, 82, 83	0
53	1v	13/24 (54%)	1.44	4 (30%) 1 1	47, 58, 94, 96	0
53	2v	13/24 (54%)	1.72	7 (53%) 0 0	57, 65, 96, 98	0
54	1w	249/354 (70%)	0.34	4 (1%) 70 74	22, 57, 77, 87	0
54	2w	253/354 (71%)	0.66	14 (5%) 32 35	38, 66, 80, 93	0
55	1x	65/74 (87%)	0.06	0 100 100	26, 60, 80, 83	0
55	2x	65/74 (87%)	0.29	0 100 100	40, 70, 84, 85	0
56	1z	5/7 (71%)	2.06	2 (40%) 1 1	31, 32, 56, 72	0
56	2z	4/7 (57%)	1.50	2 (50%) 0 0	42, 45, 48, 54	0
All	All	21082/22160 (95%)	0.53	2101 (9%) 14 17	19, 61, 85, 105	0

All (2101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	2A	2147	G	9.6
1	1A	2113	U	8.0

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Mol	Chain	Res	Type	RSRZ
21	2Z	174	VAL	7.5
1	1A	2116	G	7.3
1	1A	2112	G	6.9
1	2A	2145	C	6.8
38	2g	83	ALA	6.8
40	2i	11	LYS	6.8
1	1A	2141	G	6.7
1	1A	2159	G	6.6
1	2A	2146	C	6.6
45	1n	2	ALA	6.6
34	2c	2	GLY	6.5
44	1m	2	ALA	6.5
33	1b	129	GLU	6.5
56	1z	3	ALA	6.4
50	1s	84	GLY	6.4
1	2A	2111	C	6.3
1	1A	2117	A	6.3
1	1A	1093	G	6.3
1	1A	2179	C	6.2
1	1A	2110	G	6.2
40	2i	7	THR	6.1
1	1A	2120	G	6.1
41	2j	47	PHE	5.9
45	2n	2	ALA	5.8
44	2m	118	ALA	5.8
1	1A	2111	C	5.7
50	1s	71	LEU	5.7
38	2g	81	GLY	5.7
1	2A	2117	A	5.6
1	1A	2114	A	5.6
50	1s	13	ASP	5.6
26	24	56	VAL	5.5
1	2A	2144	U	5.5
1	1A	2170	A	5.5
1	2A	2148	G	5.5
38	2g	82	GLY	5.5
1	1A	2119	A	5.5
1	2A	2158	A	5.5
1	1A	2121	G	5.5
44	2m	6	GLY	5.4
1	1A	2178	C	5.4
51	1t	103	GLY	5.4

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Mol	Chain	Res	Type	RSRZ
1	1A	2129	C	5.4
1	1A	2169	A	5.4
1	2A	2159	G	5.4
1	1A	1058	G	5.3
1	2A	2120	G	5.3
1	2A	2110	G	5.3
1	2A	2112	G	5.3
40	2i	14	VAL	5.3
38	2g	80	VAL	5.2
1	1A	2128	C	5.2
1	1A	2174	C	5.2
20	2Y	1	MET	5.2
41	2j	75	ILE	5.2
21	2Z	146	ILE	5.1
1	1A	2130	U	5.1
38	2g	84	ASN	5.1
45	2n	18	VAL	5.0
1	1A	2133	G	5.0
47	1p	82	GLN	5.0
1	2A	2133	G	5.0
1	2A	2137	C	5.0
1	2A	2115	G	5.0
1	1A	2158	A	5.0
1	1A	1100	C	4.9
1	1A	2108	C	4.9
1	1A	2145	C	4.9
1	2A	2140	C	4.9
15	1T	131	ALA	4.9
1	1A	2167	U	4.9
1	1A	1072	C	4.9
40	2i	102	LEU	4.9
1	1A	2135	A	4.9
44	2m	102	ARG	4.9
1	1A	2115	G	4.9
33	2b	10	LEU	4.9
43	1l	64	TYR	4.9
26	14	59	PHE	4.9
45	1n	7	ILE	4.8
1	1A	2173	A	4.8
1	2A	2134	A	4.8
1	1A	2147	G	4.8
1	1A	1098	A	4.8

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Mol	Chain	Res	Type	RSRZ
1	2A	2157	G	4.7
20	1Y	1	MET	4.7
1	2A	2131	G	4.7
38	1g	80	VAL	4.7
1	1A	2180	U	4.7
41	2j	77	PRO	4.7
44	1m	97	PRO	4.7
40	2i	104	ARG	4.6
52	1u	23	PRO	4.6
1	1A	2109	U	4.6
50	1s	9	VAL	4.6
40	2i	2	GLU	4.6
1	1A	1068	G	4.6
1	2A	2160	G	4.6
1	2A	2130	U	4.6
8	2I	146	ALA	4.6
47	2p	82	GLN	4.6
1	1A	2107	C	4.6
1	1A	1094	U	4.5
1	2A	2118	U	4.5
26	14	56	VAL	4.5
1	2A	2138	C	4.5
6	1G	139	LEU	4.5
40	2i	5	TYR	4.5
44	1m	119	GLY	4.5
45	2n	7	ILE	4.5
1	1A	2160	G	4.5
32	1a	1034	G	4.5
1	1A	2175	C	4.5
1	2A	2114	A	4.5
32	1a	1286	A	4.5
1	1A	1099	G	4.5
1	1A	2142	C	4.5
1	1A	2143	C	4.5
1	1A	2118	U	4.4
1	1A	2132	U	4.4
4	2E	151	TYR	4.4
32	2a	1034	G	4.4
38	1g	81	GLY	4.4
1	1A	2127	G	4.4
1	1A	2131	G	4.4
1	1A	2134	A	4.4

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Mol	Chain	Res	Type	RSRZ
41	2j	20	ALA	4.4
50	1s	33	THR	4.4
40	1i	2	GLU	4.4
1	1A	1071	G	4.4
1	2A	2177	C	4.3
32	2a	1532	U	4.3
33	2b	7	VAL	4.3
40	2i	10	ARG	4.3
52	2u	24	ARG	4.3
1	2A	2108	C	4.3
1	1A	1088	A	4.3
1	1A	1059	G	4.3
38	1g	85	TYR	4.3
40	2i	105	ASP	4.3
1	1A	2124	G	4.3
32	1a	1036	G	4.3
1	2A	2143	C	4.2
33	2b	44	LEU	4.2
33	2b	200	ILE	4.2
40	2i	15	ALA	4.2
50	1s	40	ILE	4.2
1	1A	1064	C	4.2
32	1a	1447	A	4.2
47	1p	2	VAL	4.2
32	1a	1021	G	4.2
20	2Y	54	LYS	4.2
51	1t	9	ASN	4.2
3	1D	276	LYS	4.2
1	1A	2166	G	4.2
52	2u	14	TRP	4.2
50	1s	62	ILE	4.2
32	2a	1030(B)	C	4.2
1	2A	2135	A	4.2
39	1h	2	LEU	4.1
12	2Q	60	ARG	4.1
40	2i	91	ASP	4.1
1	2A	2154	G	4.1
22	20	10	THR	4.1
26	24	49	PHE	4.1
33	1b	17	PHE	4.1
40	2i	109	VAL	4.1
1	1A	1069	A	4.1

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Mol	Chain	Res	Type	RSRZ
52	1u	21	TYR	4.1
33	1b	134	GLU	4.1
34	1c	99	VAL	4.1
7	2H	2	SER	4.1
1	2A	2123	G	4.1
40	2i	6	GLY	4.1
33	1b	229	VAL	4.1
34	1c	92	ALA	4.1
34	1c	48	TYR	4.0
22	10	9	SER	4.0
40	1i	8	GLY	4.0
41	2j	78	ASN	4.0
51	2t	103	GLY	4.0
1	1A	2181	G	4.0
1	2A	2156	G	4.0
33	1b	230	VAL	4.0
45	2n	33	VAL	4.0
56	1z	4	ALA	4.0
14	2S	3	ARG	4.0
34	2c	6	HIS	4.0
1	1A	2148	G	4.0
1	1A	2168	G	4.0
1	1A	1057	A	4.0
8	2I	86	THR	4.0
1	1A	2125	G	4.0
42	2k	14	VAL	4.0
32	1a	1028	C	4.0
23	21	2	SER	4.0
1	2A	2122	U	4.0
41	2j	100	THR	4.0
50	2s	9	VAL	4.0
8	2I	82	ARG	3.9
12	1Q	61	GLY	3.9
33	1b	132	LYS	3.9
32	1a	1027	C	3.9
45	2n	34	TYR	3.9
33	1b	127	ILE	3.9
1	1A	1082	U	3.9
1	2A	2113	U	3.9
32	1a	1000	U	3.9
33	1b	97	TRP	3.9
1	1A	1091	G	3.9

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Mol	Chain	Res	Type	RSRZ
23	11	2	SER	3.9
32	1a	1003	G	3.9
32	1a	1001	A	3.9
8	1I	79	ILE	3.9
1	1A	1087	G	3.9
53	1v	10	G	3.9
42	1k	14	VAL	3.9
1	1A	2122	U	3.9
41	2j	37	PRO	3.9
7	1H	2	SER	3.9
1	1A	1086	A	3.8
1	2A	1171	G	3.8
6	1G	149	VAL	3.8
17	2V	42	GLY	3.8
34	1c	2	GLY	3.8
38	1g	82	GLY	3.8
47	2p	19	ILE	3.8
6	2G	146	TYR	3.8
33	1b	165	VAL	3.8
50	1s	20	LEU	3.8
1	1A	2157	G	3.8
32	1a	1035	A	3.8
1	2A	2129	C	3.8
6	1G	42	GLY	3.8
32	2a	1202	G	3.8
33	1b	237	ALA	3.8
40	2i	43	ALA	3.8
32	1a	1030(B)	C	3.8
40	2i	67	GLY	3.8
50	2s	84	GLY	3.8
33	2b	134	GLU	3.8
1	2A	2109	U	3.8
40	2i	126	SER	3.8
27	25	60	VAL	3.8
41	2j	34	VAL	3.8
44	2m	7	VAL	3.8
35	1d	180	GLY	3.8
40	2i	12	GLU	3.8
53	2v	12	A	3.8
1	1A	2123	G	3.8
1	1A	1081	U	3.8
12	2Q	104	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
14	2S	32	LEU	3.8
33	1b	19	HIS	3.8
50	1s	45	VAL	3.8
38	2g	25	ALA	3.8
40	2i	8	GLY	3.8
52	2u	23	PRO	3.8
6	2G	50	ALA	3.8
1	2A	2119	A	3.8
1	1A	888	C	3.8
1	1A	1092	C	3.8
1	1A	1063	G	3.8
1	1A	2182	G	3.8
1	2A	2149	G	3.8
32	1a	1001(A)	G	3.8
32	2a	1030(A)	G	3.8
33	2b	163	PHE	3.7
56	2z	4	ALA	3.7
26	24	51	ASP	3.7
40	2i	42	ARG	3.7
1	1A	2144	U	3.7
32	1a	1024	G	3.7
34	1c	34	LEU	3.7
34	2c	195	VAL	3.7
33	1b	228	GLY	3.7
43	1l	126	LYS	3.7
42	1k	13	GLN	3.7
32	2a	1035	A	3.7
51	2t	13	LEU	3.7
1	2A	2105	C	3.7
40	2i	50	LEU	3.7
32	1a	1531	A	3.7
47	1p	41	PRO	3.7
1	2A	1536	C	3.7
26	24	63	TYR	3.7
32	1a	1029	C	3.7
41	2j	42	THR	3.7
1	1A	2149	G	3.7
32	1a	988	G	3.7
40	1i	19	LEU	3.6
7	2H	175	LYS	3.6
40	2i	21	PRO	3.6
32	1a	1025	U	3.6

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Mol	Chain	Res	Type	RSRZ
1	2A	2169	A	3.6
1	2A	2170	A	3.6
38	2g	156	TRP	3.6
44	1m	87	TYR	3.6
12	1Q	60	ARG	3.6
40	2i	9	ARG	3.6
50	2s	29	ARG	3.6
1	2A	2142	C	3.6
33	2b	41	ILE	3.6
1	2A	2155	G	3.6
33	1b	10	LEU	3.6
6	2G	149	VAL	3.6
38	2g	79	ARG	3.6
53	1v	22	U	3.6
1	1A	2146	C	3.6
6	2G	152	LEU	3.6
19	2X	95	LEU	3.6
45	2n	6	LEU	3.6
1	1A	2154	G	3.6
1	2A	2116	G	3.6
6	1G	76	SER	3.6
54	2w	297	GLU	3.6
40	1i	10	ARG	3.6
46	1o	89	GLY	3.6
35	2d	164	ALA	3.6
24	12	70	GLN	3.6
34	2c	37	GLN	3.6
41	1j	4	ILE	3.6
1	1A	1073	A	3.6
1	1A	889	C	3.6
51	1t	14	LYS	3.6
8	2I	38	LEU	3.6
41	2j	40	LEU	3.6
41	2j	30	SER	3.6
53	2v	10	G	3.6
34	1c	207	VAL	3.6
1	1A	2189	U	3.6
1	2A	2132	U	3.6
32	2a	1257	U	3.6
45	2n	4	LYS	3.5
34	2c	33	LEU	3.5
41	1j	77	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
40	2i	86	VAL	3.5
45	1n	33	VAL	3.5
45	2n	5	ALA	3.5
1	2A	2166	G	3.5
1	1A	1097	U	3.5
45	2n	21	TYR	3.5
33	2b	11	LEU	3.5
1	1A	229	A	3.5
32	2a	1447	A	3.5
44	1m	80	ARG	3.5
52	1u	9	ARG	3.5
1	1A	2139	C	3.5
32	1a	989	C	3.5
26	14	17	GLY	3.5
1	1A	2150	U	3.5
32	1a	1040	U	3.5
32	2a	1219	U	3.5
38	2g	16	LEU	3.5
40	2i	18	PHE	3.5
26	24	54	GLY	3.5
44	1m	100	GLY	3.5
41	2j	44	VAL	3.5
41	1j	74	ILE	3.5
26	14	51	ASP	3.5
26	14	67	TYR	3.5
34	1c	87	LEU	3.5
1	1A	1074	G	3.5
42	2k	117	ASN	3.5
26	14	35	VAL	3.5
33	1b	188	ALA	3.5
41	1j	75	ILE	3.5
54	2w	350	ALA	3.5
1	2A	2789	C	3.4
33	1b	11	LEU	3.4
41	1j	40	LEU	3.4
33	1b	236	TYR	3.4
50	2s	52	TYR	3.4
33	2b	125	PRO	3.4
41	1j	64	GLU	3.4
46	2o	86	GLY	3.4
45	1n	25	VAL	3.4
34	2c	192	THR	3.4

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Mol	Chain	Res	Type	RSRZ
45	1n	5	ALA	3.4
39	2h	112	LEU	3.4
32	2a	1397	C	3.4
40	2i	66	ARG	3.4
21	2Z	1	MET	3.4
44	1m	95	GLY	3.4
45	1n	32	SER	3.4
44	1m	28	ALA	3.4
50	1s	24	ALA	3.4
50	2s	16	LEU	3.4
1	1A	2176	A	3.4
42	2k	126	ARG	3.4
33	1b	131	PRO	3.4
1	1A	2138	C	3.4
1	2A	2136	C	3.4
26	24	67	TYR	3.4
32	1a	1354	C	3.4
32	2a	1019	C	3.4
32	2a	1029	C	3.4
38	1g	154	TYR	3.4
33	2b	22	LYS	3.4
41	2j	63	PHE	3.4
21	2Z	106	GLY	3.4
41	1j	44	VAL	3.4
21	2Z	51	ALA	3.4
41	2j	79	ARG	3.4
33	2b	48	MET	3.4
6	1G	146	TYR	3.4
1	1A	2140	C	3.4
1	2A	2139	C	3.4
32	1a	1038	C	3.4
1	1A	1060	U	3.4
7	2H	44	VAL	3.4
33	1b	172	ILE	3.4
33	2b	165	VAL	3.4
50	2s	60	VAL	3.4
44	1m	90	LEU	3.3
41	2j	55	LYS	3.3
27	25	59	GLU	3.3
1	1A	2165	G	3.3
32	1a	1026	G	3.3
50	2s	13	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	1A	1067	A	3.3
26	24	32	TYR	3.3
42	2k	75	TYR	3.3
33	2b	140	HIS	3.3
41	2j	93	GLY	3.3
44	1m	68	GLY	3.3
1	2A	2167	U	3.3
32	1a	1257	U	3.3
21	2Z	82	ARG	3.3
34	2c	129	ALA	3.3
44	2m	5	ALA	3.3
35	1d	194	LEU	3.3
45	2n	3	ARG	3.3
35	1d	102	ASP	3.3
7	2H	123	PHE	3.3
1	2A	2182	G	3.3
32	1a	1002	G	3.3
1	1A	887	A	3.3
32	1a	1030(D)	A	3.3
40	1i	39	GLY	3.3
53	1v	12	A	3.3
7	2H	45	VAL	3.3
33	2b	229	VAL	3.3
34	1c	75	VAL	3.3
1	2A	271(K)	U	3.3
52	1u	10	ARG	3.3
15	1T	130	ALA	3.3
8	2I	87	LYS	3.3
34	1c	36	ASP	3.3
6	1G	80	PHE	3.3
38	2g	154	TYR	3.3
40	2i	4	TYR	3.3
6	1G	52	ILE	3.3
34	2c	5	ILE	3.3
38	1g	156	TRP	3.3
1	2A	2121	G	3.3
6	1G	133	LEU	3.3
32	2a	1036	G	3.3
50	1s	15	LEU	3.3
50	2s	15	LEU	3.3
29	17	48	LYS	3.3
29	27	48	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	1A	1078	U	3.3
1	1A	2172	U	3.3
4	2E	29	GLY	3.3
33	2b	38	GLY	3.3
45	2n	38	GLY	3.3
50	2s	8	GLY	3.3
40	2i	83	ARG	3.2
45	2n	29	ARG	3.2
3	1D	38	LYS	3.2
33	2b	230	VAL	3.2
41	2j	72	VAL	3.2
1	2A	2173	A	3.2
41	2j	35	SER	3.2
1	2A	614(A)	U	3.2
1	2A	2165	G	3.2
32	2a	1033	G	3.2
1	1A	2103	C	3.2
1	1A	2177	C	3.2
33	2b	17	PHE	3.2
47	1p	81	ARG	3.2
33	1b	7	VAL	3.2
33	2b	237	ALA	3.2
50	1s	50	ALA	3.2
1	1A	1070	A	3.2
32	1a	630	G	3.2
32	1a	1030(A)	G	3.2
1	1A	2136	C	3.2
32	1a	1214	C	3.2
32	2a	1030	C	3.2
33	2b	21	ARG	3.2
33	2b	223	ILE	3.2
50	1s	16	LEU	3.2
9	2N	9	VAL	3.2
26	14	32	TYR	3.2
34	1c	55	VAL	3.2
34	1c	64	VAL	3.2
42	1k	75	TYR	3.2
38	1g	2	ALA	3.2
41	2j	26	ALA	3.2
26	24	52	THR	3.2
32	2a	1148	U	3.2
1	1A	2171	A	3.2

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Mol	Chain	Res	Type	RSRZ
1	1A	1062	G	3.2
1	1A	2156	G	3.2
20	2Y	60	PHE	3.2
32	1a	1033	G	3.2
1	2A	2183	C	3.2
32	1a	999	C	3.2
34	2c	159	GLY	3.2
44	1m	112	GLY	3.2
34	1c	157	ILE	3.2
40	2i	81	ILE	3.2
34	2c	153	VAL	3.2
44	1m	74	VAL	3.2
43	2l	64	TYR	3.2
26	14	52	THR	3.2
38	2g	14	PRO	3.2
33	2b	97	TRP	3.2
34	2c	144	SER	3.2
1	1A	1090	U	3.2
1	2A	2150	U	3.2
45	1n	29	ARG	3.2
47	1p	42	ARG	3.2
48	1q	68	ARG	3.2
33	2b	70	PHE	3.2
12	2Q	61	GLY	3.1
43	2l	29	GLY	3.1
6	2G	139	LEU	3.1
34	2c	32	LEU	3.1
42	1k	98	LEU	3.1
51	2t	99	LEU	3.1
1	1A	2188	C	3.1
1	2A	2141	G	3.1
5	2F	6	VAL	3.1
32	1a	1039	C	3.1
33	2b	136	VAL	3.1
41	2j	76	ASN	3.1
44	1m	77	ASN	3.1
8	2I	89	TYR	3.1
33	1b	33	TYR	3.1
50	1s	61	TYR	3.1
52	1u	18	TYR	3.1
41	1j	10	GLY	3.1
41	2j	36	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
6	2G	52	ILE	3.1
33	2b	39	ILE	3.1
33	2b	71	VAL	3.1
34	1c	106	VAL	3.1
42	1k	117	ASN	3.1
47	1p	14	ASN	3.1
50	1s	41	VAL	3.1
1	1A	2190	G	3.1
20	2Y	55	TYR	3.1
26	14	63	TYR	3.1
47	1p	17	TYR	3.1
7	1H	175	LYS	3.1
40	1i	126	SER	3.1
26	14	55	ARG	3.1
1	1A	2102	U	3.1
20	2Y	58	GLY	3.1
21	2Z	136	PHE	3.1
34	1c	77	ILE	3.1
39	2h	2	LEU	3.1
41	1j	36	GLY	3.1
44	1m	85	GLY	3.1
44	2m	100	GLY	3.1
53	2v	22	U	3.1
1	2A	2126	A	3.1
14	2S	61	ASN	3.1
21	2Z	145	GLU	3.1
34	2c	71	ALA	3.1
41	2j	32	ALA	3.1
45	2n	30	ALA	3.1
1	2A	2174	C	3.1
1	2A	2185	C	3.1
32	2a	1223	C	3.1
52	1u	24	ARG	3.1
1	1A	2151	G	3.1
1	2A	2151	G	3.1
32	1a	1224	G	3.1
38	2g	12	LEU	3.1
41	1j	8	LEU	3.1
41	2j	74	ILE	3.1
53	1v	11	U	3.1
8	2I	81	VAL	3.1
34	1c	86	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
50	2s	45	VAL	3.1
38	1g	151	TYR	3.1
51	1t	18	GLN	3.1
1	2A	2128	C	3.1
32	2a	1149	C	3.1
1	2A	2127	G	3.0
6	2G	53	LEU	3.0
33	1b	200	ILE	3.0
34	2c	57	ILE	3.0
46	2o	89	GLY	3.0
32	1a	1012	U	3.0
32	1a	1532	U	3.0
44	1m	53	VAL	3.0
33	1b	9	GLU	3.0
12	2Q	121	ALA	3.0
15	2T	130	ALA	3.0
34	2c	65	ALA	3.0
35	2d	154	ASN	3.0
40	2i	106	ALA	3.0
45	1n	10	ALA	3.0
6	1G	51	ARG	3.0
1	1A	1046	A	3.0
32	2a	1001	A	3.0
21	2Z	166	SER	3.0
22	20	9	SER	3.0
45	2n	39	LEU	3.0
50	1s	22	LEU	3.0
54	2w	351	LEU	3.0
8	1I	90	GLY	3.0
26	24	59	PHE	3.0
34	2c	185	GLY	3.0
35	2d	23	GLY	3.0
47	2p	10	GLY	3.0
1	1A	2162	G	3.0
1	2A	2125	G	3.0
1	2A	2318	G	3.0
7	2H	12	PRO	3.0
21	1Z	141	VAL	3.0
50	1s	32	LYS	3.0
33	2b	20	GLU	3.0
35	1d	179	GLU	3.0
1	2A	272(A)	U	3.0

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Mol	Chain	Res	Type	RSRZ
53	2v	11	U	3.0
25	23	29	ARG	3.0
35	2d	159	ARG	3.0
49	2r	20	ALA	3.0
41	2j	81	THR	3.0
45	2n	13	THR	3.0
45	2n	22	THR	3.0
33	2b	148	TYR	3.0
40	2i	36	TYR	3.0
1	1A	1095	A	3.0
32	1a	1005	A	3.0
34	1c	52	LEU	3.0
41	2j	8	LEU	3.0
51	1t	10	LEU	3.0
33	1b	227	GLY	3.0
33	2b	55	PHE	3.0
40	2i	72	GLY	3.0
44	1m	84	ILE	3.0
3	1D	275	LYS	3.0
33	1b	125	PRO	3.0
34	1c	62	ASP	3.0
7	2H	49	VAL	3.0
7	2H	114	VAL	3.0
8	2I	142	VAL	3.0
35	1d	192	GLU	3.0
40	2i	41	VAL	3.0
44	1m	67	GLU	3.0
18	2W	92	ARG	3.0
45	2n	10	ALA	3.0
50	1s	14	HIS	3.0
50	1s	47	HIS	3.0
1	2A	2153	G	3.0
32	2a	1032	G	3.0
20	2Y	57	GLN	3.0
6	1G	82	LEU	3.0
19	1X	95	LEU	3.0
33	1b	221	LEU	3.0
34	1c	32	LEU	3.0
35	1d	155	LEU	3.0
40	1i	56	LEU	3.0
32	2a	1251	A	3.0
32	2a	1531	A	3.0

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Mol	Chain	Res	Type	RSRZ
34	1c	186	PHE	3.0
34	2c	182	ILE	3.0
51	2t	102	GLY	3.0
50	2s	2	PRO	3.0
6	2G	147	ASP	3.0
34	1c	90	GLU	3.0
34	2c	62	ASP	3.0
50	1s	12	ASP	3.0
44	1m	102	ARG	3.0
32	2a	1363	C	3.0
24	22	70	GLN	3.0
44	2m	106	ASN	3.0
41	1j	87	THR	3.0
1	2A	2793	G	3.0
32	2a	1117	G	3.0
33	2b	33	TYR	2.9
40	2i	96	LEU	2.9
21	1Z	146	ILE	2.9
36	2e	85	GLY	2.9
1	1A	1077	A	2.9
1	2A	887	A	2.9
32	2a	1016	A	2.9
46	1o	72	ARG	2.9
51	2t	25	ARG	2.9
33	2b	93	VAL	2.9
34	2c	207	VAL	2.9
42	2k	13	GLN	2.9
50	1s	44	MET	2.9
8	2I	53	ALA	2.9
20	2Y	78	ALA	2.9
1	1A	886	C	2.9
1	1A	2161	C	2.9
1	2A	2178	C	2.9
40	2i	64	THR	2.9
51	2t	24	LEU	2.9
1	2A	2152	G	2.9
6	1G	25	TYR	2.9
6	2G	76	SER	2.9
32	2a	1002	G	2.9
32	2a	1024	G	2.9
6	2G	140	ILE	2.9
33	1b	214	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
36	2e	23	GLY	2.9
50	1s	74	PHE	2.9
7	2H	6	ARG	2.9
34	1c	88	ARG	2.9
1	1A	2126	A	2.9
1	2A	2176	A	2.9
27	15	60	VAL	2.9
32	1a	374	A	2.9
32	2a	1146	A	2.9
34	1c	195	VAL	2.9
54	2w	102	MET	2.9
33	2b	218	ALA	2.9
41	1j	78	ASN	2.9
46	1o	25	THR	2.9
1	1A	1101	U	2.9
8	1I	87	LYS	2.9
33	1b	133	LYS	2.9
41	2j	65	LEU	2.9
26	24	66	SER	2.9
31	29	10	ILE	2.9
41	1j	35	SER	2.9
44	1m	9	ILE	2.9
44	1m	23	TYR	2.9
44	2m	22	ILE	2.9
50	1s	49	ILE	2.9
26	14	49	PHE	2.9
33	2b	152	PHE	2.9
50	1s	26	GLY	2.9
25	23	2	PRO	2.9
45	2n	35	ARG	2.9
1	2A	2162	G	2.9
6	1G	48	GLU	2.9
21	1Z	2	GLU	2.9
26	14	50	VAL	2.9
33	1b	93	VAL	2.9
34	1c	68	VAL	2.9
44	2m	17	VAL	2.9
50	1s	60	VAL	2.9
6	1G	50	ALA	2.9
21	1Z	51	ALA	2.9
33	2b	123	ALA	2.9
34	2c	92	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
50	2s	24	ALA	2.9
50	1s	63	THR	2.9
35	1d	135	LEU	2.9
39	1h	112	LEU	2.9
50	1s	30	LEU	2.9
1	2A	888	C	2.9
33	1b	41	ILE	2.9
33	2b	127	ILE	2.9
47	1p	19	ILE	2.9
6	1G	83	ARG	2.9
6	1G	136	ARG	2.9
6	2G	142	PRO	2.9
14	1S	3	ARG	2.9
34	1c	74	GLY	2.9
36	2e	22	GLY	2.9
7	2H	41	MET	2.9
50	1s	11	VAL	2.9
1	1A	2104	G	2.9
1	1A	2152	G	2.9
32	2a	1031	G	2.9
32	2a	1184	G	2.9
33	1b	13	ALA	2.9
47	1p	48	TRP	2.9
14	2S	4	LEU	2.8
19	2X	92	LEU	2.8
33	1b	61	LEU	2.8
39	2h	107	LEU	2.8
43	1l	60	LEU	2.8
6	1G	114	ILE	2.8
8	2I	71	ILE	2.8
33	2b	201	ILE	2.8
36	2e	13	ILE	2.8
34	2c	74	GLY	2.8
34	2c	79	ARG	2.8
1	1A	1026	U	2.8
44	1m	6	GLY	2.8
1	1A	2137	C	2.8
32	1a	1043	C	2.8
32	2a	1119	C	2.8
33	2b	236	TYR	2.8
46	1o	69	TYR	2.8
34	1c	76	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
3	2D	276	LYS	2.8
34	2c	160	ALA	2.8
38	1g	83	ALA	2.8
45	2n	15	LYS	2.8
51	2t	97	ALA	2.8
1	1A	1089	G	2.8
1	2A	2106	G	2.8
1	2A	2168	G	2.8
35	1d	162	LEU	2.8
33	1b	223	ILE	2.8
41	1j	5	ARG	2.8
41	2j	23	ILE	2.8
44	1m	93	ARG	2.8
51	1t	100	ILE	2.8
44	2m	41	PRO	2.8
50	1s	68	GLY	2.8
32	1a	991	U	2.8
50	1s	4	SER	2.8
34	2c	48	TYR	2.8
35	1d	170	VAL	2.8
50	2s	18	LYS	2.8
21	2Z	93	ASP	2.8
39	2h	7	ALA	2.8
40	1i	15	ALA	2.8
33	1b	37	ASN	2.8
41	2j	43	ARG	2.8
50	2s	3	ARG	2.8
1	2A	2184	G	2.8
32	2a	1124	G	2.8
33	1b	63	MET	2.8
34	2c	14	ILE	2.8
41	2j	91	PRO	2.8
6	2G	48	GLU	2.8
50	2s	10	PHE	2.8
1	1A	1175	U	2.8
32	1a	1020	U	2.8
41	1j	33	GLN	2.8
42	1k	25	TYR	2.8
6	2G	159	VAL	2.8
8	1I	136	VAL	2.8
37	2f	91	VAL	2.8
39	1h	93	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
44	2m	54	VAL	2.8
50	2s	67	VAL	2.8
29	17	45	ALA	2.8
29	27	45	ALA	2.8
32	1a	1030	C	2.8
32	2a	1218	C	2.8
41	2j	17	ASP	2.8
44	2m	72	ALA	2.8
45	1n	20	ALA	2.8
35	1d	120	LEU	2.8
50	2s	71	LEU	2.8
35	1d	89	THR	2.8
47	1p	44	THR	2.8
47	2p	48	TRP	2.8
45	2n	57	ARG	2.8
33	1b	201	ILE	2.8
33	2b	185	ILE	2.8
47	1p	16	HIS	2.8
17	2V	101	GLY	2.8
26	14	54	GLY	2.8
50	2s	26	GLY	2.8
41	1j	54	PHE	2.8
1	2A	11	G	2.8
1	2A	271(M)	G	2.8
32	1a	1023	G	2.8
32	1a	1030(C)	G	2.8
32	1a	1032	G	2.8
32	1a	1215	G	2.8
32	2a	1003	G	2.8
32	2a	1021	G	2.8
32	1a	1041	A	2.8
32	1a	1287	A	2.8
32	2a	1030(D)	A	2.8
37	1f	16	GLN	2.8
40	2i	95	LYS	2.8
44	2m	65	LYS	2.8
38	2g	85	TYR	2.8
33	1b	136	VAL	2.8
34	2c	120	VAL	2.8
35	1d	195	ALA	2.8
1	2A	2107	C	2.7
11	2P	15	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
22	20	11	ARG	2.7
32	1a	984	C	2.7
32	2a	1028	C	2.7
44	1m	49	THR	2.7
50	1s	77	THR	2.7
33	2b	24	TRP	2.7
21	2Z	32	HIS	2.7
38	2g	42	ILE	2.7
51	2t	100	ILE	2.7
33	2b	234	PRO	2.7
7	2H	100	GLY	2.7
52	2u	11	GLY	2.7
41	2j	14	LYS	2.7
50	1s	18	LYS	2.7
8	1I	91	SER	2.7
51	1t	70	SER	2.7
1	1A	1045	A	2.7
1	1A	2186	G	2.7
1	2A	1533	G	2.7
32	2a	1252	A	2.7
1	1A	271(K)	U	2.7
32	2a	1000	U	2.7
36	2e	100	VAL	2.7
38	1g	9	VAL	2.7
47	1p	62	VAL	2.7
6	2G	43	LEU	2.7
33	2b	121	LEU	2.7
34	2c	100	ALA	2.7
40	2i	122	ALA	2.7
44	1m	30	ALA	2.7
44	1m	96	LEU	2.7
44	1m	103	THR	2.7
50	2s	44	MET	2.7
6	1G	144	ILE	2.7
32	1a	985	C	2.7
32	1a	1018	C	2.7
32	2a	995	C	2.7
32	2a	1038	C	2.7
33	1b	42	ILE	2.7
44	1m	41	PRO	2.7
44	2m	9	ILE	2.7
3	2D	275	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
34	2c	171	GLY	2.7
35	1d	124	GLY	2.7
36	2e	45	PHE	2.7
38	2g	98	SER	2.7
5	2F	89	VAL	2.7
34	1c	184	TYR	2.7
35	1d	178	VAL	2.7
40	2i	17	VAL	2.7
44	2m	23	TYR	2.7
44	2m	98	VAL	2.7
46	2o	27	VAL	2.7
47	1p	79	VAL	2.7
1	2A	652(B)	A	2.7
7	2H	3	ARG	2.7
7	2H	97	ARG	2.7
7	2H	165	ALA	2.7
34	1c	100	ALA	2.7
35	1d	9	CYS	2.7
35	1d	174	LEU	2.7
36	1e	138	ALA	2.7
40	2i	56	LEU	2.7
40	2i	82	ALA	2.7
44	2m	66	LEU	2.7
50	2s	30	LEU	2.7
23	21	26	ARG	2.7
46	2o	68	ARG	2.7
53	2v	14	A	2.7
1	1A	275	G	2.7
46	2o	25	THR	2.7
50	1s	39	THR	2.7
41	2j	62	HIS	2.7
46	1o	3	ILE	2.7
50	1s	31	ILE	2.7
31	29	15	LYS	2.7
47	1p	12	LYS	2.7
8	2I	90	GLY	2.7
26	14	34	GLU	2.7
33	1b	18	GLY	2.7
34	1c	128	PHE	2.7
47	1p	80	PHE	2.7
33	2b	124	SER	2.7
26	24	35	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
26	24	50	VAL	2.7
34	2c	138	VAL	2.7
7	1H	3	ARG	2.7
15	2T	108	ARG	2.7
35	1d	153	ARG	2.7
50	2s	5	LEU	2.7
38	2g	2	ALA	2.7
40	2i	92	TYR	2.7
40	2i	114	TYR	2.7
41	1j	32	ALA	2.7
44	1m	76	ALA	2.7
40	1i	91	ASP	2.7
1	2A	896	A	2.7
7	2H	61	HIS	2.7
1	1A	2106	G	2.7
7	2H	8	PRO	2.7
26	14	14	ILE	2.7
34	2c	124	ILE	2.7
34	2c	157	ILE	2.7
35	1d	22	LYS	2.7
32	1a	1042	G	2.7
35	1d	158	ILE	2.7
19	2X	94	GLY	2.7
33	2b	66	GLY	2.7
47	1p	59	TRP	2.7
1	1A	2163	C	2.7
1	2A	2163	C	2.7
7	2H	19	VAL	2.6
7	2H	42	ARG	2.6
8	2I	50	ARG	2.6
8	2I	107	VAL	2.6
33	2b	164	VAL	2.6
33	2b	197	VAL	2.6
34	1c	138	VAL	2.6
40	1i	9	ARG	2.6
40	1i	66	ARG	2.6
46	2o	88	ARG	2.6
47	2p	28	ARG	2.6
54	1w	349	ALA	2.6
47	2p	16	HIS	2.6
41	1j	100	THR	2.6
41	2j	87	THR	2.6

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Mol	Chain	Res	Type	RSRZ
6	2G	77	ILE	2.6
48	1q	28	PRO	2.6
8	2I	85	GLU	2.6
32	2a	1130	A	2.6
50	1s	27	GLU	2.6
41	1j	93	GLY	2.6
1	2A	2805	G	2.6
32	1a	1009	G	2.6
33	1b	122	PHE	2.6
35	2d	3	ARG	2.6
45	2n	41	ARG	2.6
1	2A	2175	C	2.6
32	1a	1037	C	2.6
33	2b	196	LEU	2.6
34	1c	91	LEU	2.6
44	1m	34	LEU	2.6
45	1n	39	LEU	2.6
7	2H	99	VAL	2.6
50	1s	19	VAL	2.6
41	2j	27	ALA	2.6
44	2m	30	ALA	2.6
45	1n	59	ALA	2.6
49	1r	20	ALA	2.6
51	1t	74	LYS	2.6
34	1c	193	TYR	2.6
38	2g	151	TYR	2.6
40	2i	125	TYR	2.6
26	14	22	ILE	2.6
41	2j	6	ILE	2.6
41	2j	98	ILE	2.6
45	2n	42	ILE	2.6
1	2A	528	A	2.6
2	2B	120	A	2.6
1	2A	2101	G	2.6
1	2A	2104	G	2.6
34	1c	115	LEU	2.6
44	1m	66	LEU	2.6
34	1c	130	VAL	2.6
34	2c	173	VAL	2.6
36	1e	100	VAL	2.6
21	1Z	156	LYS	2.6
1	2A	277	C	2.6

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Mol	Chain	Res	Type	RSRZ
1	2A	645	C	2.6
1	2A	2161	C	2.6
1	2A	2188	C	2.6
34	1c	189	ALA	2.6
38	2g	153	HIS	2.6
19	2X	69	TYR	2.6
38	2g	112	PRO	2.6
38	1g	84	ASN	2.6
44	1m	40	ASN	2.6
32	2a	1150	U	2.6
34	2c	170	GLN	2.6
35	1d	87	GLY	2.6
45	2n	16	PHE	2.6
6	2G	96	ARG	2.6
24	12	69	ARG	2.6
34	2c	21	ARG	2.6
35	1d	159	ARG	2.6
38	1g	5	ARG	2.6
38	1g	79	ARG	2.6
40	2i	93	ARG	2.6
41	1j	28	ARG	2.6
1	1A	529	A	2.6
32	1a	389	A	2.6
32	2a	1151	A	2.6
50	2s	66	MET	2.6
34	1c	33	LEU	2.6
37	2f	48	LEU	2.6
38	1g	12	LEU	2.6
40	2i	99	LEU	2.6
45	2n	9	LYS	2.6
16	2U	90	VAL	2.6
34	2c	64	VAL	2.6
34	1c	129	ALA	2.6
36	1e	86	ALA	2.6
44	1m	5	ALA	2.6
44	1m	92	HIS	2.6
32	1a	998	G	2.6
32	2a	1001(A)	G	2.6
6	2G	20	ILE	2.6
8	1I	71	ILE	2.6
32	2a	979	C	2.6
33	2b	166	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
39	1h	100	ILE	2.6
41	2j	50	ILE	2.6
41	2j	58	ASP	2.6
38	2g	37	ASN	2.6
40	2i	80	GLY	2.6
41	2j	31	GLY	2.6
6	1G	141	PHE	2.6
32	1a	992	U	2.6
33	1b	28	PHE	2.6
41	1j	63	PHE	2.6
50	1s	29	ARG	2.6
20	2Y	94	LYS	2.5
46	1o	34	LEU	2.5
47	2p	43	LYS	2.5
32	1a	349	A	2.5
32	1a	1016	A	2.5
8	2I	144	VAL	2.5
34	2c	99	VAL	2.5
44	1m	45	VAL	2.5
44	2m	53	VAL	2.5
51	1t	73	HIS	2.5
33	2b	13	ALA	2.5
33	2b	29	ALA	2.5
40	2i	55	ALA	2.5
8	2I	10	GLU	2.5
26	14	31	ILE	2.5
36	2e	76	ILE	2.5
1	2A	2100	G	2.5
1	2A	2207	G	2.5
6	1G	145	THR	2.5
39	1h	99	GLU	2.5
44	2m	58	GLU	2.5
32	1a	1031	G	2.5
42	2k	25	TYR	2.5
1	1A	154(A)	C	2.5
1	1A	1076	C	2.5
32	2a	962	C	2.5
32	2a	1027	C	2.5
32	2a	1037	C	2.5
40	2i	69	GLY	2.5
40	2i	37	PHE	2.5
44	2m	110	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
45	1n	3	ARG	2.5
47	1p	1	MET	2.5
48	1q	91	ARG	2.5
49	1r	29	PHE	2.5
3	2D	38	LYS	2.5
32	1a	1446	U	2.5
32	2a	1126	U	2.5
24	22	35	LEU	2.5
33	1b	118	LEU	2.5
40	2i	47	LEU	2.5
48	2q	76	LEU	2.5
7	2H	50	VAL	2.5
26	14	33	VAL	2.5
33	2b	15	VAL	2.5
40	1i	41	VAL	2.5
41	2j	49	VAL	2.5
44	1m	98	VAL	2.5
40	1i	43	ALA	2.5
41	2j	18	ALA	2.5
44	1m	42	ALA	2.5
49	2r	24	ALA	2.5
6	1G	77	ILE	2.5
33	2b	211	ILE	2.5
35	1d	163	GLU	2.5
44	2m	73	GLU	2.5
45	2n	8	GLU	2.5
6	2G	138	GLN	2.5
6	2G	145	THR	2.5
33	2b	135	GLN	2.5
38	2g	33	ASP	2.5
46	2o	9	GLN	2.5
5	2F	16	GLY	2.5
40	1i	69	GLY	2.5
41	2j	52	GLY	2.5
23	11	26	ARG	2.5
33	2b	94	ASN	2.5
1	1A	614(B)	G	2.5
1	2A	2124	G	2.5
1	2A	2792	G	2.5
32	1a	350	G	2.5
32	1a	631	G	2.5
32	1a	993	G	2.5

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Mol	Chain	Res	Type	RSRZ
32	1a	1353	G	2.5
32	2a	1026	G	2.5
33	2b	57	PHE	2.5
45	1n	4	LYS	2.5
48	1q	27	PHE	2.5
1	1A	645	C	2.5
1	1A	1509	C	2.5
1	1A	2185	C	2.5
32	2a	1249	C	2.5
7	2H	64	LEU	2.5
36	2e	12	LEU	2.5
1	1A	12	U	2.5
32	2a	961	U	2.5
33	2b	40	HIS	2.5
44	2m	92	HIS	2.5
8	2I	136	VAL	2.5
35	2d	92	VAL	2.5
21	2Z	7	ALA	2.5
38	2g	77	SER	2.5
38	2g	152	ALA	2.5
40	2i	13	ALA	2.5
42	1k	15	ALA	2.5
26	24	53	GLU	2.5
45	1n	42	ILE	2.5
47	2p	36	ILE	2.5
32	1a	1044	A	2.5
32	2a	1250	A	2.5
21	2Z	170	THR	2.5
40	2i	103	THR	2.5
6	2G	49	ASP	2.5
7	2H	82	GLY	2.5
15	2T	129	ARG	2.5
35	2d	132	ARG	2.5
38	1g	34	GLY	2.5
38	2g	5	ARG	2.5
44	1m	114	ARG	2.5
50	1s	82	GLY	2.5
52	1u	22	ARG	2.5
54	2w	190	GLY	2.5
45	1n	34	TYR	2.5
47	1p	38	TYR	2.5
50	1s	23	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
45	1n	37	PHE	2.5
33	1b	98	LEU	2.5
35	1d	188	LEU	2.5
41	2j	88	LEU	2.5
44	2m	70	LEU	2.5
1	2A	886	C	2.5
1	2A	1178	C	2.5
1	2A	2103	C	2.5
1	2A	2181	G	2.5
1	2A	2803	C	2.5
32	1a	1017	G	2.5
32	1a	1220	G	2.5
32	1a	1312	G	2.5
32	2a	999	C	2.5
32	2a	1022	G	2.5
32	2a	1190	G	2.5
36	1e	115	VAL	2.5
38	1g	105	VAL	2.5
38	2g	87	VAL	2.5
34	1c	200	ALA	2.5
40	1i	21	PRO	2.5
42	2k	42	TRP	2.5
50	1s	76	PRO	2.5
50	2s	76	PRO	2.5
52	1u	14	TRP	2.5
7	2H	124	GLU	2.5
39	2h	70	GLN	2.5
44	1m	43	THR	2.5
49	2r	54	ARG	2.5
50	2s	63	THR	2.5
1	1A	1177	A	2.5
1	1A	2790	A	2.5
14	2S	60	GLY	2.5
32	1a	532	A	2.5
32	1a	983	A	2.5
32	2a	1286	A	2.5
34	2c	205	GLY	2.5
41	2j	10	GLY	2.5
50	1s	72	GLY	2.5
34	1c	175	LEU	2.4
41	2j	90	LEU	2.4
44	2m	56	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
45	2n	44	LEU	2.4
47	1p	74	LEU	2.4
48	2q	98	LEU	2.4
51	1t	62	LEU	2.4
45	2n	43	CYS	2.4
1	2A	2179	C	2.4
32	2a	990	C	2.4
49	1r	86	VAL	2.4
50	2s	19	VAL	2.4
1	1A	2153	G	2.4
32	1a	79	G	2.4
32	2a	630	G	2.4
32	2a	1017	G	2.4
32	2a	1253	G	2.4
50	2s	42	PRO	2.4
8	2I	83	ALA	2.4
34	1c	65	ALA	2.4
8	2I	91	SER	2.4
24	22	40	SER	2.4
35	2d	5	ILE	2.4
50	1s	35	SER	2.4
50	2s	34	TRP	2.4
51	1t	11	SER	2.4
9	2N	115	ARG	2.4
24	22	51	ARG	2.4
29	27	1	MET	2.4
35	1d	122	ARG	2.4
44	1m	27	LYS	2.4
45	1n	57	ARG	2.4
52	2u	6	ARG	2.4
52	1u	17	THR	2.4
38	2g	34	GLY	2.4
50	2s	68	GLY	2.4
33	1b	189	ASP	2.4
41	2j	73	ASP	2.4
32	1a	414	A	2.4
32	1a	946	A	2.4
32	2a	532	A	2.4
32	2a	1004	A	2.4
32	2a	1123	A	2.4
33	1b	196	LEU	2.4
34	2c	52	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
44	1m	59	TYR	2.4
50	1s	5	LEU	2.4
50	2s	22	LEU	2.4
50	2s	61	TYR	2.4
53	2v	13	A	2.4
54	2w	319	PHE	2.4
41	2j	56	HIS	2.4
7	2H	79	VAL	2.4
31	29	16	VAL	2.4
41	1j	34	VAL	2.4
32	1a	1307	U	2.4
32	2a	1020	U	2.4
45	2n	46	GLU	2.4
1	1A	2164	C	2.4
2	2B	88	C	2.4
33	2b	172	ILE	2.4
36	1e	10	MET	2.4
41	2j	80	LYS	2.4
44	1m	65	LYS	2.4
46	1o	87	ILE	2.4
33	1b	130	ARG	2.4
41	2j	5	ARG	2.4
47	2p	12	LYS	2.4
1	1A	2155	G	2.4
1	2A	2319	G	2.4
32	1a	111	G	2.4
32	1a	348	G	2.4
32	1a	1222	G	2.4
32	2a	988	G	2.4
32	2a	1216	G	2.4
32	2a	1221	G	2.4
6	1G	44	GLY	2.4
33	1b	38	GLY	2.4
34	2c	155	GLY	2.4
34	2c	194	GLY	2.4
35	1d	171	GLY	2.4
41	1j	67	THR	2.4
42	2k	31	THR	2.4
43	1l	63	GLY	2.4
51	1t	69	GLY	2.4
21	1Z	155	LEU	2.4
34	2c	188	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
4	1E	151	TYR	2.4
1	1A	548	A	2.4
1	1A	890	A	2.4
32	2a	978	A	2.4
32	2a	1180	A	2.4
44	1m	86	CYS	2.4
6	2G	160	VAL	2.4
9	2N	5	VAL	2.4
34	2c	7	PRO	2.4
38	1g	61	VAL	2.4
38	2g	21	VAL	2.4
39	1h	51	VAL	2.4
44	1m	117	VAL	2.4
45	2n	14	PRO	2.4
11	1P	149	GLU	2.4
34	1c	50	ALA	2.4
45	2n	50	LYS	2.4
15	2T	111	ARG	2.4
19	2X	68	ARG	2.4
33	2b	58	ILE	2.4
34	1c	39	ILE	2.4
34	2c	134	ILE	2.4
35	1d	3	ARG	2.4
38	1g	120	ILE	2.4
40	2i	128	ARG	2.4
44	1m	4	ILE	2.4
44	1m	94	ARG	2.4
44	2m	78	ILE	2.4
48	1q	26	GLN	2.4
1	2A	2189	U	2.4
33	2b	192	SER	2.4
1	2A	34	C	2.4
32	2a	985	C	2.4
32	2a	1043	C	2.4
18	2W	112	GLY	2.4
33	1b	190	THR	2.4
34	1c	51	GLY	2.4
1	1A	2101	G	2.4
1	1A	2184	G	2.4
1	2A	892	G	2.4
1	2A	2893	G	2.4
6	1G	3	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
7	2H	98	LEU	2.4
32	2a	951	G	2.4
44	1m	70	LEU	2.4
18	2W	60	ASN	2.4
21	2Z	121	HIS	2.4
50	1s	53	ASN	2.4
40	1i	4	TYR	2.4
1	1A	2310	A	2.4
1	2A	1847	A	2.4
26	14	16	CYS	2.4
8	2I	37	VAL	2.4
26	14	69	LYS	2.4
32	1a	959	A	2.4
32	1a	1004	A	2.4
32	2a	983	A	2.4
33	1b	91	PRO	2.4
34	2c	116	VAL	2.4
35	1d	112	VAL	2.4
36	2e	10	MET	2.4
37	2f	54	LYS	2.4
41	2j	41	PRO	2.4
53	2v	15	A	2.4
40	1i	17	VAL	2.4
46	1o	27	VAL	2.4
46	2o	60	VAL	2.4
7	2H	51	ARG	2.4
8	2I	70	GLU	2.4
46	1o	65	ARG	2.4
50	1s	3	ARG	2.4
6	2G	151	ALA	2.4
21	2Z	173	ALA	2.4
36	1e	80	ILE	2.4
36	2e	86	ALA	2.4
37	2f	53	ALA	2.4
44	1m	72	ALA	2.4
49	2r	63	GLN	2.4
54	2w	329	SER	2.4
6	1G	119	GLY	2.4
26	24	45	GLY	2.4
40	2i	115	GLY	2.4
1	1A	2794	C	2.3
8	1I	75	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
32	1a	433	C	2.3
32	1a	1006	C	2.3
33	2b	155	LEU	2.3
34	1c	43	LEU	2.3
34	1c	101	LEU	2.3
35	2d	162	LEU	2.3
39	1h	4	ASP	2.3
47	1p	47	ASP	2.3
34	2c	3	ASN	2.3
50	1s	65	ASN	2.3
51	2t	9	ASN	2.3
1	2A	2186	G	2.3
32	2a	1030(C)	G	2.3
37	2f	59	TYR	2.3
50	1s	52	TYR	2.3
50	2s	80	TYR	2.3
34	2c	4	LYS	2.3
35	1d	166	LYS	2.3
40	1i	11	LYS	2.3
45	2n	58	LYS	2.3
44	1m	82	MET	2.3
51	2t	98	PRO	2.3
54	1w	102	MET	2.3
14	2S	20	ARG	2.3
34	2c	75	VAL	2.3
39	1h	129	VAL	2.3
40	1i	14	VAL	2.3
40	1i	107	ARG	2.3
40	2i	53	VAL	2.3
44	1m	7	VAL	2.3
46	1o	88	ARG	2.3
7	2H	4	ILE	2.3
32	2a	1005	A	2.3
33	1b	39	ILE	2.3
33	2b	34	ALA	2.3
40	2i	84	ALA	2.3
42	1k	48	ILE	2.3
47	1p	7	ALA	2.3
49	1r	60	ALA	2.3
34	1c	20	SER	2.3
41	1j	30	SER	2.3
1	1A	2897	U	2.3

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Mol	Chain	Res	Type	RSRZ
26	14	64	GLY	2.3
32	1a	960	U	2.3
33	1b	89	GLY	2.3
52	2u	2	GLY	2.3
39	1h	24	THR	2.3
50	2s	77	THR	2.3
36	1e	142	LEU	2.3
41	2j	68	HIS	2.3
45	1n	53	LEU	2.3
54	2w	328	LEU	2.3
32	1a	948	C	2.3
43	2l	13	LYS	2.3
6	1G	148	MET	2.3
7	2H	128	PRO	2.3
34	2c	131	ARG	2.3
39	2h	67	PRO	2.3
42	2k	59	TYR	2.3
40	2i	20	ARG	2.3
41	1j	46	ARG	2.3
45	2n	26	ARG	2.3
1	1A	1176	G	2.3
7	2H	52	VAL	2.3
44	2m	60	VAL	2.3
47	1p	53	VAL	2.3
50	2s	41	VAL	2.3
31	29	26	ILE	2.3
34	1c	160	ALA	2.3
34	1c	187	ALA	2.3
41	2j	82	ILE	2.3
42	2k	119	CYS	2.3
54	1w	350	ALA	2.3
54	2w	349	ALA	2.3
56	2z	5	ALA	2.3
32	2a	974	A	2.3
32	2a	1015	A	2.3
32	2a	1092	A	2.3
32	2a	1357	A	2.3
4	2E	10	GLY	2.3
33	1b	151	GLY	2.3
33	2b	227	GLY	2.3
39	2h	71	GLY	2.3
40	2i	71	SER	2.3

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Mol	Chain	Res	Type	RSRZ
46	2o	20	GLY	2.3
51	1t	101	GLY	2.3
21	2Z	33	LEU	2.3
28	26	11	LEU	2.3
35	1d	176	LEU	2.3
35	1d	202	LEU	2.3
39	1h	3	THR	2.3
40	2i	79	LEU	2.3
40	2i	85	LEU	2.3
44	1m	48	LEU	2.3
44	2m	105	THR	2.3
32	2a	950	U	2.3
37	2f	97	PHE	2.3
40	2i	101	PHE	2.3
42	2k	125	PHE	2.3
50	1s	10	PHE	2.3
6	1G	49	ASP	2.3
20	2Y	81	LYS	2.3
34	2c	181	ASN	2.3
35	2d	151	LYS	2.3
38	2g	36	LYS	2.3
1	1A	34	C	2.3
12	1Q	5	ARG	2.3
26	14	48	ARG	2.3
26	24	61	ARG	2.3
32	1a	1019	C	2.3
21	2Z	168	GLU	2.3
26	14	43	TYR	2.3
32	2a	1116	C	2.3
32	2a	1260	C	2.3
35	1d	29	PRO	2.3
35	2d	40	PRO	2.3
41	1j	43	ARG	2.3
44	1m	113	PRO	2.3
48	1q	63	ARG	2.3
51	1t	80	ARG	2.3
35	2d	24	GLU	2.3
48	1q	96	GLU	2.3
34	1c	202	ILE	2.3
15	2T	131	ALA	2.3
33	1b	171	ALA	2.3
34	1c	113	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
45	1n	30	ALA	2.3
1	1A	1173	G	2.3
1	2A	2206	G	2.3
45	1n	27	CYS	2.3
35	1d	44	GLY	2.3
35	1d	123	HIS	2.3
35	2d	167	GLY	2.3
40	2i	39	GLY	2.3
41	2j	85	LEU	2.3
54	2w	152	LEU	2.3
32	1a	994	A	2.3
32	1a	1046	A	2.3
32	1a	1236	A	2.3
32	2a	977	A	2.3
32	2a	1503	A	2.3
14	2S	19	LYS	2.3
1	1A	1065	U	2.3
32	2a	202	U	2.3
32	2a	1025	U	2.3
33	1b	70	PHE	2.3
34	2c	147	LYS	2.3
45	2n	17	LYS	2.3
46	1o	15	PHE	2.3
44	1m	106	ASN	2.3
37	2f	47	ARG	2.3
41	1j	66	ARG	2.3
41	2j	46	ARG	2.3
44	1m	3	ARG	2.3
50	1s	78	ARG	2.3
50	1s	81	ARG	2.3
21	2Z	68	PRO	2.3
41	2j	53	PRO	2.3
50	2s	59	PRO	2.3
4	1E	73	GLU	2.3
8	2I	135	GLU	2.3
26	24	57	GLU	2.3
1	1A	2183	C	2.3
31	29	7	VAL	2.3
32	1a	840	C	2.3
32	1a	1223	C	2.3
32	2a	1132	C	2.3
35	2d	146	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
20	1Y	78	ALA	2.3
33	1b	29	ALA	2.3
33	2b	225	ALA	2.3
35	2d	32	ALA	2.3
38	2g	7	ALA	2.3
38	2g	128	ALA	2.3
44	2m	76	ALA	2.3
51	2t	95	ALA	2.3
8	2I	77	LEU	2.2
8	2I	116	LEU	2.2
8	2I	124	GLY	2.2
8	2I	133	HIS	2.2
12	1Q	15	GLY	2.2
23	21	84	GLY	2.2
24	22	24	LEU	2.2
33	2b	19	HIS	2.2
45	1n	38	GLY	2.2
47	2p	73	LEU	2.2
21	2Z	16	SER	2.2
32	1a	388	G	2.2
40	1i	70	LYS	2.2
42	2k	41	THR	2.2
44	1m	63	THR	2.2
12	2Q	65	PHE	2.2
34	2c	128	PHE	2.2
32	2a	969	A	2.2
32	2a	1285	A	2.2
29	27	47	ARG	2.2
32	1a	65	U	2.2
35	2d	118	ARG	2.2
38	2g	76	ARG	2.2
9	2N	10	GLU	2.2
35	2d	160	GLN	2.2
46	1o	9	GLN	2.2
5	1F	89	VAL	2.2
6	2G	15	VAL	2.2
14	2S	35	ILE	2.2
33	1b	15	VAL	2.2
33	2b	112	VAL	2.2
34	1c	66	VAL	2.2
35	1d	148	VAL	2.2
40	2i	108	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
8	1I	146	ALA	2.2
33	1b	62	ALA	2.2
34	2c	60	ALA	2.2
34	2c	168	ALA	2.2
35	1d	32	ALA	2.2
32	2a	1118	C	2.2
32	2a	1145	C	2.2
32	2a	1282	C	2.2
50	2s	14	HIS	2.2
50	2s	47	HIS	2.2
34	1c	97	LYS	2.2
35	1d	41	GLY	2.2
40	2i	118	LYS	2.2
41	2j	22	LYS	2.2
51	1t	47	GLY	2.2
51	1t	68	LYS	2.2
51	2t	74	LYS	2.2
52	1u	16	GLY	2.2
40	1i	103	THR	2.2
41	2j	92	THR	2.2
50	1s	38	SER	2.2
12	2Q	10	ARG	2.2
29	17	47	ARG	2.2
34	2c	127	ARG	2.2
36	1e	25	ARG	2.2
45	1n	23	ARG	2.2
47	1p	5	ARG	2.2
1	2A	614(B)	G	2.2
32	2a	993	G	2.2
32	2a	1023	G	2.2
32	2a	1224	G	2.2
8	2I	8	PRO	2.2
1	2A	2180	U	2.2
1	2A	2808	U	2.2
32	1a	59	A	2.2
32	2a	1122	U	2.2
32	2a	1256	A	2.2
32	2a	1324	A	2.2
43	2l	94	PRO	2.2
33	2b	231	GLU	2.2
50	2s	17	GLU	2.2
36	2e	20	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
41	1j	84	GLN	2.2
50	1s	56	GLN	2.2
8	2I	79	ILE	2.2
33	2b	42	ILE	2.2
46	2o	3	ILE	2.2
48	2q	35	VAL	2.2
54	2w	312	VAL	2.2
7	2H	94	TYR	2.2
6	1G	182	LYS	2.2
33	1b	40	HIS	2.2
35	1d	125	HIS	2.2
33	1b	44	LEU	2.2
35	2d	157	LEU	2.2
37	2f	45	LEU	2.2
41	1j	80	LYS	2.2
44	2m	46	LYS	2.2
47	1p	31	LYS	2.2
9	2N	64	GLY	2.2
36	1e	85	GLY	2.2
43	1l	14	GLY	2.2
46	1o	86	GLY	2.2
1	1A	1079	C	2.2
1	1A	1080	C	2.2
32	1a	1452	C	2.2
35	2d	165	MET	2.2
34	2c	15	THR	2.2
22	10	11	ARG	2.2
40	1i	33	PHE	2.2
45	1n	16	PHE	2.2
50	2s	78	ARG	2.2
51	2t	8	ARG	2.2
33	2b	131	PRO	2.2
54	2w	151	ASP	2.2
25	13	60	GLU	2.2
33	1b	12	GLU	2.2
34	2c	167	TRP	2.2
40	2i	87	GLN	2.2
1	2A	271(L)	U	2.2
1	2A	2102	U	2.2
1	1A	1174	A	2.2
2	2B	25	A	2.2
32	1a	55	A	2.2

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Mol	Chain	Res	Type	RSRZ
32	1a	102	G	2.2
29	17	46	VAL	2.2
29	27	46	VAL	2.2
35	2d	121	VAL	2.2
39	1h	95	VAL	2.2
50	2s	51	VAL	2.2
34	1c	71	ALA	2.2
38	1g	117	ALA	2.2
40	2i	46	ALA	2.2
44	1m	118	ALA	2.2
51	1t	65	LYS	2.2
6	2G	82	LEU	2.2
17	2V	94	LEU	2.2
45	2n	47	LEU	2.2
46	2o	31	LEU	2.2
48	1q	74	LEU	2.2
54	2w	332	LEU	2.2
21	2Z	147	GLY	2.2
35	1d	2	GLY	2.2
52	2u	4	GLY	2.2
6	1G	113	ARG	2.2
34	1c	192	THR	2.2
35	1d	168	ARG	2.2
38	2g	32	ARG	2.2
39	2h	18	ARG	2.2
47	1p	75	ARG	2.2
1	1A	2105	C	2.2
20	2Y	89	PHE	2.2
45	1n	36	PHE	2.2
45	1n	60	SER	2.2
32	2a	1054	C	2.2
46	2o	15	PHE	2.2
34	1c	162	GLN	2.2
44	1m	16	ASP	2.2
6	2G	100	TRP	2.2
1	2A	2172	U	2.2
7	2H	148	ILE	2.2
36	2e	109	ILE	2.2
41	2j	96	ILE	2.2
44	1m	39	ILE	2.2
51	1t	55	ILE	2.2
7	2H	113	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
12	2Q	22	LYS	2.2
34	1c	147	LYS	2.2
36	1e	82	VAL	2.2
38	1g	118	VAL	2.2
46	1o	8	LYS	2.2
1	1A	2187	G	2.2
1	2A	2208	A	2.2
19	2X	91	ALA	2.2
32	1a	383	A	2.2
32	1a	949	A	2.2
32	1a	1216	G	2.2
32	1a	1288	A	2.2
34	2c	31	HIS	2.2
36	2e	48	ALA	2.2
47	1p	13	HIS	2.2
32	2a	973	G	2.2
6	1G	43	LEU	2.1
34	2c	101	LEU	2.1
34	2c	204	LEU	2.1
35	1d	101	LEU	2.1
35	2d	68	TYR	2.1
37	2f	63	TYR	2.1
41	2j	71	LEU	2.1
44	2m	59	TYR	2.1
17	2V	1	MET	2.1
11	2P	116	GLY	2.1
33	2b	18	GLY	2.1
52	2u	16	GLY	2.1
6	2G	22	ARG	2.1
12	2Q	59	ARG	2.1
21	2Z	131	ARG	2.1
34	1c	79	ARG	2.1
35	2d	141	ARG	2.1
39	1h	84	ARG	2.1
40	1i	42	ARG	2.1
43	1l	19	ARG	2.1
46	1o	17	ARG	2.1
22	10	10	THR	2.1
33	2b	54	THR	2.1
14	2S	29	PHE	2.1
33	1b	57	PHE	2.1
40	2i	33	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
43	1l	62	SER	2.1
34	2c	114	PRO	2.1
46	1o	19	PRO	2.1
32	1a	1325	C	2.1
33	1b	20	GLU	2.1
47	1p	68	ASP	2.1
8	2I	88	ILE	2.1
24	22	8	LYS	2.1
35	2d	70	ILE	2.1
35	1d	173	TRP	2.1
35	2d	112	VAL	2.1
37	1f	90	VAL	2.1
44	1m	15	VAL	2.1
50	1s	57	HIS	2.1
50	2s	11	VAL	2.1
1	1A	1083	U	2.1
4	1E	28	ALA	2.1
32	2a	1040	U	2.1
32	2a	1121	U	2.1
7	2H	87	LEU	2.1
35	2d	19	LEU	2.1
38	2g	150	ALA	2.1
40	2i	19	LEU	2.1
42	1k	89	ALA	2.1
48	1q	31	LEU	2.1
48	1q	98	LEU	2.1
32	1a	162	A	2.1
32	2a	975	A	2.1
32	2a	986	A	2.1
32	2a	1191	A	2.1
34	1c	201	TYR	2.1
35	2d	4	TYR	2.1
7	2H	59	ARG	2.1
40	2i	16	ARG	2.1
1	2A	883	G	2.1
32	1a	644	G	2.1
32	1a	1221	G	2.1
32	1a	1274	G	2.1
32	1a	1368	G	2.1
32	2a	963	G	2.1
32	2a	1220	G	2.1
32	2a	1370	G	2.1

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Mol	Chain	Res	Type	RSRZ
39	2h	72	PRO	2.1
33	2b	129	GLU	2.1
36	1e	72	GLN	2.1
37	2f	94	GLN	2.1
38	1g	8	GLU	2.1
41	2j	83	GLU	2.1
6	1G	116	ASP	2.1
40	1i	23	ASN	2.1
48	1q	14	LYS	2.1
48	1q	67	LYS	2.1
50	1s	70	LYS	2.1
1	2A	2164	C	2.1
7	2H	92	ILE	2.1
32	1a	1320	C	2.1
33	1b	222	ILE	2.1
38	1g	42	ILE	2.1
39	2h	134	ILE	2.1
41	1j	98	ILE	2.1
49	2r	75	ILE	2.1
9	1N	9	VAL	2.1
33	1b	71	VAL	2.1
41	2j	94	VAL	2.1
34	1c	178	LEU	2.1
34	2c	22	TRP	2.1
35	1d	147	ALA	2.1
35	2d	155	LEU	2.1
43	2l	51	ALA	2.1
44	2m	90	LEU	2.1
50	1s	34	TRP	2.1
4	1E	204	ALA	2.1
37	1f	53	ALA	2.1
40	2i	94	ALA	2.1
1	2A	12	U	2.1
32	1a	841	U	2.1
36	1e	18	ARG	2.1
36	2e	107	ARG	2.1
38	2g	155	ARG	2.1
39	1h	102	ARG	2.1
43	1l	89	ARG	2.1
51	1t	8	ARG	2.1
30	28	45	GLY	2.1
31	29	37	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
33	1b	14	GLY	2.1
40	1i	57	GLY	2.1
40	2i	68	GLY	2.1
51	2t	96	GLY	2.1
52	1u	2	GLY	2.1
44	2m	87	TYR	2.1
32	2a	1289	A	2.1
33	2b	73	THR	2.1
49	2r	69	THR	2.1
6	2G	125	PHE	2.1
21	1Z	159	PRO	2.1
21	2Z	134	PRO	2.1
36	2e	84	PHE	2.1
44	1m	10	PRO	2.1
49	2r	43	PHE	2.1
50	1s	59	PRO	2.1
21	2Z	149	SER	2.1
32	1a	70	G	2.1
32	1a	78	G	2.1
32	1a	220	G	2.1
32	2a	1009	G	2.1
32	2a	1156	G	2.1
8	1I	139	GLN	2.1
26	14	53	GLU	2.1
47	2p	76	GLN	2.1
50	2s	64	GLU	2.1
26	14	18	CYS	2.1
35	1d	30	LYS	2.1
39	1h	116	LYS	2.1
39	2h	116	LYS	2.1
43	1l	91	LYS	2.1
26	14	15	ILE	2.1
34	2c	39	ILE	2.1
34	2c	202	ILE	2.1
41	2j	38	ILE	2.1
44	2m	84	ILE	2.1
4	2E	195	LEU	2.1
7	2H	11	VAL	2.1
7	2H	43	VAL	2.1
21	2Z	42	VAL	2.1
44	2m	15	VAL	2.1
1	2A	885	C	2.1

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Mol	Chain	Res	Type	RSRZ
32	1a	1262	C	2.1
32	2a	1217	C	2.1
33	1b	137	ARG	2.1
38	2g	107	ALA	2.1
47	1p	77	ALA	2.1
50	1s	75	ALA	2.1
32	1a	340	U	2.1
32	1a	723	U	2.1
32	2a	839	U	2.1
32	2a	1196	U	2.1
33	2b	65	GLY	2.1
33	2b	72	GLY	2.1
34	2c	145	GLY	2.1
38	2g	19	GLY	2.1
41	1j	52	GLY	2.1
33	1b	31	TYR	2.1
34	1c	29	TYR	2.1
35	2d	138	TYR	2.1
38	2g	18	TYR	2.1
46	1o	78	TYR	2.1
33	2b	122	PHE	2.1
35	2d	75	PHE	2.1
35	2d	206	PHE	2.1
41	1j	47	PHE	2.1
50	1s	42	PRO	2.1
50	1s	79	THR	2.1
1	2A	2171	A	2.1
32	1a	614	A	2.1
32	1a	1183	A	2.1
32	2a	1183	A	2.1
33	2b	170	GLU	2.1
34	2c	122	GLU	2.1
44	1m	31	LYS	2.1
48	1q	100	LYS	2.1
50	1s	43	GLU	2.1
35	2d	71	SER	2.1
45	2n	40	CYS	2.1
1	1A	2805	G	2.1
32	1a	423	G	2.1
32	2a	998	G	2.1
32	2a	1042	G	2.1
32	2a	1276	G	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1283	G	2.1
6	1G	140	ILE	2.1
6	2G	123	ASN	2.1
7	2H	9	ILE	2.1
12	2Q	123	HIS	2.1
34	1c	57	ILE	2.1
34	1c	134	ILE	2.1
37	2f	7	ASN	2.1
38	2g	27	ILE	2.1
41	1j	76	ASN	2.1
42	1k	36	ASP	2.1
43	2l	7	ILE	2.1
8	1I	92	VAL	2.0
14	2S	54	LEU	2.0
14	2S	80	LEU	2.0
19	2X	70	LEU	2.0
33	1b	174	VAL	2.0
33	2b	184	VAL	2.0
34	2c	196	LEU	2.0
41	1j	90	LEU	2.0
47	1p	49	LEU	2.0
47	2p	6	LEU	2.0
48	1q	43	LEU	2.0
6	2G	181	ARG	2.0
12	1Q	59	ARG	2.0
26	24	55	ARG	2.0
26	24	62	ARG	2.0
33	1b	226	ARG	2.0
51	2t	80	ARG	2.0
20	2Y	105	ALA	2.0
38	1g	7	ALA	2.0
38	1g	39	ALA	2.0
42	2k	15	ALA	2.0
1	2A	889	C	2.0
14	1S	60	GLY	2.0
32	1a	201	C	2.0
32	1a	221	C	2.0
32	1a	1051	C	2.0
32	1a	1218	C	2.0
33	2b	228	GLY	2.0
1	2A	271(N)	U	2.0
32	1a	223	U	2.0

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Mol	Chain	Res	Type	RSRZ
6	2G	2	PRO	2.0
7	2H	39	PRO	2.0
14	2S	92	TYR	2.0
8	1I	141	LYS	2.0
26	14	41	PRO	2.0
33	2b	199	TYR	2.0
34	2c	73	PRO	2.0
35	2d	29	PRO	2.0
36	1e	92	LYS	2.0
41	1j	37	PRO	2.0
41	2j	48	THR	2.0
41	2j	54	PHE	2.0
42	2k	124	LYS	2.0
46	1o	48	LYS	2.0
49	1r	25	THR	2.0
51	2t	48	LYS	2.0
52	2u	17	THR	2.0
54	2w	307	PHE	2.0
7	2H	32	GLU	2.0
33	2b	35	GLU	2.0
41	2j	33	GLN	2.0
5	2F	13	SER	2.0
50	2s	35	SER	2.0
1	2A	229	A	2.0
1	2A	2310	A	2.0
32	1a	609	A	2.0
32	1a	1227	A	2.0
32	2a	1213	A	2.0
6	2G	144	ILE	2.0
20	2Y	5	MET	2.0
21	1Z	1	MET	2.0
26	24	15	ILE	2.0
36	1e	11	ILE	2.0
41	2j	69	ASN	2.0
8	1I	12	LEU	2.0
22	20	84	LEU	2.0
7	2H	35	VAL	2.0
26	24	33	VAL	2.0
33	1b	36	ARG	2.0
37	1f	21	LEU	2.0
38	2g	41	ARG	2.0
39	2h	84	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
44	1m	56	LEU	2.0
47	1p	6	LEU	2.0
44	2m	74	VAL	2.0
44	2m	99	ARG	2.0
50	2s	20	LEU	2.0
48	1q	77	VAL	2.0
50	1s	67	VAL	2.0
1	2A	530	G	2.0
32	1a	66	G	2.0
32	1a	1283	G	2.0
32	2a	1323	G	2.0
34	2c	149	ALA	2.0
34	2c	13	GLY	2.0
38	1g	130	GLY	2.0
46	2o	23	GLY	2.0
34	2c	27	LYS	2.0
6	2G	87	PRO	2.0
21	1Z	136	PHE	2.0
21	2Z	9	TYR	2.0
32	1a	202	U	2.0
32	2a	1147	C	2.0
34	1c	114	PRO	2.0
33	1b	67	THR	2.0
34	1c	161	GLU	2.0
35	1d	156	GLU	2.0
38	1g	43	PHE	2.0
40	1i	7	THR	2.0
40	2i	62	TYR	2.0
44	2m	103	THR	2.0
54	1w	207	GLU	2.0
7	2H	38	SER	2.0
45	2n	32	SER	2.0
50	2s	38	SER	2.0
7	2H	89	ILE	2.0
7	2H	121	ILE	2.0
41	1j	50	ILE	2.0
7	1H	59	ARG	2.0
40	2i	107	ARG	2.0
44	1m	108	ARG	2.0
44	2m	94	ARG	2.0
48	1q	75	ARG	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
55	H2U	1x	21	20/21	0.66	0.16	75,86,98,108	0
55	H2U	2x	21	20/21	0.73	0.15	84,92,97,105	0
55	H2U	2x	20	20/21	0.76	0.13	73,86,95,98	0
32	2MG	1a	1207	24/25	0.81	0.16	76,86,93,95	0
55	PSU	2x	55	20/21	0.84	0.11	74,77,87,91	0
55	5MU	2x	54	21/22	0.85	0.12	72,77,85,95	0
32	2MG	2a	1207	24/25	0.85	0.13	74,81,85,87	0
55	PSU	1x	55	20/21	0.86	0.12	69,75,80,85	0
43	0TD	1l	92	10/11	0.86	0.14	51,60,64,72	0
55	5MU	1x	54	21/22	0.87	0.12	69,76,83,86	0
55	H2U	1x	20	20/21	0.87	0.11	67,79,86,91	0
32	M2G	2a	966	25/26	0.90	0.15	50,63,77,85	0
32	PSU	2a	516	20/21	0.90	0.12	54,69,77,77	0
32	M2G	1a	966	25/26	0.91	0.12	51,57,71,83	0
43	0TD	2l	92	10/11	0.91	0.12	53,57,60,78	0
1	5MU	2A	1915	21/22	0.91	0.11	59,63,71,76	0
55	PSU	2x	32	20/21	0.91	0.11	61,68,73,78	0
32	G7M	2a	527	24/25	0.92	0.13	56,62,66,71	0
55	MIA	2x	37	22/30	0.92	0.10	55,65,69,72	0
55	PSU	1x	32	20/21	0.93	0.10	56,61,65,75	0
55	PSU	2x	39	20/21	0.93	0.10	57,67,70,74	0
32	PSU	1a	516	20/21	0.93	0.12	57,67,71,72	0
1	PSU	2A	1911	20/21	0.94	0.09	51,58,61,71	0
32	5MC	2a	1400	21/22	0.94	0.12	62,66,70,74	0
55	MIA	1x	37	22/30	0.94	0.10	50,57,60,60	0
32	5MC	2a	1404	21/22	0.94	0.11	45,52,56,61	0
1	5MU	1A	1915	21/22	0.94	0.10	46,52,58,60	0
32	5MC	1a	967	21/22	0.94	0.11	54,58,66,68	0
1	PSU	1A	1911	20/21	0.94	0.11	43,49,56,61	0
32	G7M	1a	527	24/25	0.94	0.12	53,58,62,65	0
32	5MC	2a	967	21/22	0.94	0.12	59,66,74,82	0
32	MA6	2a	1518	24/25	0.95	0.11	45,56,61,62	0
1	PSU	2A	1917	20/21	0.95	0.09	53,60,67,67	0
55	4SU	2x	8	20/21	0.95	0.08	66,71,76,77	0
32	5MC	1a	1400	21/22	0.95	0.10	45,51,55,57	0
32	4OC	1a	1402	22/23	0.95	0.11	42,47,55,57	0
32	4OC	2a	1402	22/23	0.95	0.10	47,56,61,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	5MC	1a	1404	21/22	0.95	0.11	36,42,46,52	0
32	UR3	2a	1498	21/22	0.95	0.09	47,55,60,62	0
32	MA6	1a	1518	24/25	0.96	0.13	35,42,44,50	0
55	4SU	1x	8	20/21	0.96	0.09	46,55,62,69	0
32	MA6	1a	1519	24/25	0.96	0.11	35,40,44,60	0
55	PSU	1x	39	20/21	0.96	0.08	46,50,56,56	0
1	PSU	1A	1917	20/21	0.96	0.08	43,49,56,56	0
32	5MC	2a	1407	21/22	0.96	0.10	39,49,52,55	0
1	OMC	2A	1920	21/22	0.96	0.10	48,55,59,64	0
1	5MC	2A	1962	21/22	0.96	0.08	37,43,48,54	0
32	MA6	2a	1519	24/25	0.96	0.10	48,58,63,64	0
1	OMG	2A	2251	24/25	0.97	0.08	33,36,42,43	0
1	2MA	2A	2503	23/24	0.97	0.07	28,34,38,40	0
1	PSU	2A	2605	20/21	0.97	0.07	30,34,39,40	0
1	5MC	1A	1962	21/22	0.97	0.07	27,33,37,39	0
1	OMC	1A	1920	21/22	0.97	0.08	34,43,46,47	0
1	5MC	1A	1942	21/22	0.97	0.07	25,32,36,39	0
1	5MC	2A	1942	21/22	0.97	0.08	34,45,50,52	0
32	UR3	1a	1498	21/22	0.97	0.08	38,43,45,46	0
55	8AN	2x	76	22/23	0.97	0.08	30,40,44,46	0
1	OMU	2A	2552	21/22	0.98	0.07	31,36,41,42	0
1	OMU	1A	2552	21/22	0.98	0.07	24,28,33,35	0
1	PSU	1A	2605	20/21	0.98	0.07	22,25,31,33	0
1	5MU	2A	1939	21/22	0.98	0.08	27,34,37,39	0
1	5MU	1A	1939	21/22	0.98	0.06	21,26,29,32	0
1	OMG	1A	2251	24/25	0.98	0.07	22,26,30,39	0
1	2MA	1A	2503	23/24	0.98	0.06	18,21,23,25	0
55	8AN	1x	76	22/23	0.98	0.06	21,25,29,30	0
32	5MC	1a	1407	21/22	0.98	0.07	31,41,44,45	0

6.3 Carbohydrates (i)

There are no monosaccharides 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, 95th 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	3961	1/1	-0.04	0.37	87,87,87,87	0
57	MG	2j	201	1/1	0.19	0.26	88,88,88,88	0
57	MG	1l	201	1/1	0.38	0.16	75,75,75,75	0
57	MG	1a	1819	1/1	0.48	0.29	74,74,74,74	0
57	MG	2A	3650	1/1	0.50	0.35	76,76,76,76	0
57	MG	2A	3259	1/1	0.52	0.40	77,77,77,77	0
57	MG	1A	3981	1/1	0.52	0.22	70,70,70,70	0
57	MG	1a	1786	1/1	0.52	0.18	86,86,86,86	0
57	MG	1a	1783	1/1	0.53	0.27	91,91,91,91	0
57	MG	2A	3699	1/1	0.54	0.26	70,70,70,70	0
57	MG	1a	1667	1/1	0.54	0.19	82,82,82,82	0
57	MG	2A	3435	1/1	0.55	0.44	84,84,84,84	0
57	MG	1a	1778	1/1	0.55	0.28	88,88,88,88	0
57	MG	2a	1729	1/1	0.58	0.30	83,83,83,83	0
57	MG	1A	3966	1/1	0.59	0.23	71,71,71,71	0
57	MG	1A	3400	1/1	0.59	0.19	63,63,63,63	0
57	MG	2A	3714	1/1	0.61	0.23	46,46,46,46	0
57	MG	2A	3845	1/1	0.61	0.30	63,63,63,63	0
57	MG	1A	3930	1/1	0.61	0.24	71,71,71,71	0
57	MG	1A	3928	1/1	0.61	0.32	38,38,38,38	0
57	MG	2a	1760	1/1	0.62	0.21	74,74,74,74	0
57	MG	2B	205	1/1	0.65	0.33	76,76,76,76	0
57	MG	1A	3996	1/1	0.65	0.13	77,77,77,77	0
57	MG	2A	3050	1/1	0.66	0.31	76,76,76,76	0
57	MG	1a	1677	1/1	0.67	0.18	71,71,71,71	0
57	MG	2A	3532	1/1	0.67	0.23	46,46,46,46	0
57	MG	2a	1731	1/1	0.67	0.28	70,70,70,70	0
57	MG	2A	3757	1/1	0.67	0.19	79,79,79,79	0
57	MG	1B	231	1/1	0.67	0.26	69,69,69,69	0
57	MG	2A	3682	1/1	0.68	0.21	55,55,55,55	0
57	MG	2A	3193	1/1	0.68	0.35	78,78,78,78	0
57	MG	2a	1759	1/1	0.68	0.23	71,71,71,71	0
57	MG	2A	3239	1/1	0.68	0.44	81,81,81,81	0
57	MG	2a	1656	1/1	0.68	0.26	83,83,83,83	0
57	MG	1A	3963	1/1	0.69	0.17	69,69,69,69	0
57	MG	2a	1722	1/1	0.69	0.21	86,86,86,86	0
57	MG	2A	3316	1/1	0.69	0.16	71,71,71,71	0
57	MG	1a	1665	1/1	0.69	0.19	78,78,78,78	0
57	MG	1A	4018	1/1	0.69	0.14	67,67,67,67	0
57	MG	1A	4025	1/1	0.69	0.19	49,49,49,49	0
57	MG	2A	3674	1/1	0.69	0.26	77,77,77,77	0
57	MG	1A	4034	1/1	0.70	0.21	62,62,62,62	0
57	MG	2A	3372	1/1	0.70	0.25	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3430	1/1	0.70	0.38	70,70,70,70	0
57	MG	1A	3793	1/1	0.70	0.30	66,66,66,66	0
57	MG	2A	3687	1/1	0.70	0.17	79,79,79,79	0
57	MG	2A	3693	1/1	0.70	0.18	65,65,65,65	0
57	MG	1a	1758	1/1	0.71	0.21	82,82,82,82	0
57	MG	1a	1763	1/1	0.71	0.24	66,66,66,66	0
57	MG	2A	3761	1/1	0.71	0.15	81,81,81,81	0
57	MG	2x	110	1/1	0.71	0.30	76,76,76,76	0
57	MG	2A	3364	1/1	0.72	0.27	61,61,61,61	0
57	MG	2A	3085	1/1	0.72	0.38	78,78,78,78	0
57	MG	1A	4068	1/1	0.72	0.23	50,50,50,50	0
57	MG	1A	3820	1/1	0.72	0.22	74,74,74,74	0
57	MG	1a	1625	1/1	0.72	0.31	70,70,70,70	0
57	MG	2A	3560	1/1	0.72	0.25	73,73,73,73	0
57	MG	2A	3590	1/1	0.72	0.23	73,73,73,73	0
57	MG	1a	1732	1/1	0.72	0.29	82,82,82,82	0
57	MG	2A	3669	1/1	0.72	0.14	64,64,64,64	0
57	MG	2A	3227	1/1	0.73	0.21	79,79,79,79	0
57	MG	2a	1732	1/1	0.73	0.17	84,84,84,84	0
57	MG	2A	3244	1/1	0.73	0.12	69,69,69,69	0
57	MG	1B	230	1/1	0.74	0.17	76,76,76,76	0
57	MG	2A	3755	1/1	0.74	0.25	73,73,73,73	0
57	MG	1A	3985	1/1	0.74	0.18	52,52,52,52	0
57	MG	2a	1769	1/1	0.74	0.34	73,73,73,73	0
57	MG	2A	3242	1/1	0.74	0.27	74,74,74,74	0
57	MG	1W	206	1/1	0.74	0.19	58,58,58,58	0
57	MG	2A	3087	1/1	0.75	0.19	80,80,80,80	0
57	MG	2B	203	1/1	0.75	0.20	69,69,69,69	0
57	MG	2A	3274	1/1	0.75	0.29	64,64,64,64	0
57	MG	2A	3169	1/1	0.75	0.26	72,72,72,72	0
57	MG	1A	3225	1/1	0.75	0.20	52,52,52,52	0
57	MG	2A	3200	1/1	0.75	0.20	74,74,74,74	0
57	MG	2A	3373	1/1	0.75	0.20	67,67,67,67	0
57	MG	1A	3232	1/1	0.75	0.33	68,68,68,68	0
57	MG	1A	3330	1/1	0.75	0.19	63,63,63,63	0
57	MG	2A	3727	1/1	0.75	0.17	62,62,62,62	0
57	MG	1A	3074	1/1	0.75	0.27	65,65,65,65	0
57	MG	2A	3243	1/1	0.75	0.23	78,78,78,78	0
57	MG	1G	203	1/1	0.75	0.14	58,58,58,58	0
57	MG	1A	3816	1/1	0.76	0.17	58,58,58,58	0
57	MG	1A	4054	1/1	0.76	0.15	71,71,71,71	0
57	MG	2A	3235	1/1	0.76	0.27	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1755	1/1	0.76	0.26	73,73,73,73	0
57	MG	1A	3734	1/1	0.76	0.20	62,62,62,62	0
57	MG	1a	1706	1/1	0.76	0.25	67,67,67,67	0
57	MG	2R	202	1/1	0.76	0.22	62,62,62,62	0
57	MG	1a	1709	1/1	0.76	0.17	70,70,70,70	0
57	MG	1A	3699	1/1	0.76	0.28	68,68,68,68	0
57	MG	1a	1654	1/1	0.77	0.27	76,76,76,76	0
57	MG	2B	212	1/1	0.77	0.25	74,74,74,74	0
57	MG	2B	220	1/1	0.77	0.18	75,75,75,75	0
57	MG	1A	3865	1/1	0.77	0.17	27,27,27,27	0
57	MG	1A	3882	1/1	0.77	0.12	58,58,58,58	0
57	MG	1G	204	1/1	0.77	0.16	67,67,67,67	0
57	MG	1A	3785	1/1	0.77	0.14	58,58,58,58	0
57	MG	1a	1805	1/1	0.77	0.24	63,63,63,63	0
57	MG	2A	3586	1/1	0.77	0.16	49,49,49,49	0
57	MG	2A	3749	1/1	0.77	0.13	73,73,73,73	0
57	MG	1a	1620	1/1	0.77	0.17	74,74,74,74	0
57	MG	2A	3632	1/1	0.77	0.14	74,74,74,74	0
57	MG	2A	3330	1/1	0.77	0.23	66,66,66,66	0
57	MG	2a	1771	1/1	0.77	0.21	79,79,79,79	0
57	MG	2A	3661	1/1	0.77	0.27	52,52,52,52	0
57	MG	1A	3821	1/1	0.77	0.18	50,50,50,50	0
57	MG	1A	3603	1/1	0.78	0.15	53,53,53,53	0
57	MG	1A	3364	1/1	0.78	0.15	49,49,49,49	0
57	MG	1T	201	1/1	0.78	0.25	60,60,60,60	0
57	MG	1a	1810	1/1	0.78	0.15	76,76,76,76	0
57	MG	2B	214	1/1	0.78	0.18	69,69,69,69	0
57	MG	1a	1699	1/1	0.78	0.32	69,69,69,69	0
57	MG	2E	305	1/1	0.78	0.25	70,70,70,70	0
57	MG	1A	3708	1/1	0.78	0.16	58,58,58,58	0
57	MG	2a	1648	1/1	0.78	0.29	63,63,63,63	0
57	MG	1A	3405	1/1	0.78	0.14	69,69,69,69	0
57	MG	2a	1711	1/1	0.78	0.19	68,68,68,68	0
57	MG	1a	1726	1/1	0.78	0.33	75,75,75,75	0
57	MG	1A	4001	1/1	0.78	0.15	36,36,36,36	0
57	MG	2A	3341	1/1	0.78	0.32	79,79,79,79	0
57	MG	2A	3167	1/1	0.78	0.19	74,74,74,74	0
57	MG	2a	1745	1/1	0.78	0.23	73,73,73,73	0
57	MG	1a	1753	1/1	0.78	0.18	81,81,81,81	0
57	MG	2A	3179	1/1	0.78	0.27	60,60,60,60	0
57	MG	2A	3421	1/1	0.78	0.22	65,65,65,65	0
57	MG	1a	1628	1/1	0.78	0.35	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1640	1/1	0.78	0.21	76,76,76,76	0
57	MG	2A	3480	1/1	0.78	0.19	57,57,57,57	0
57	MG	2x	109	1/1	0.78	0.27	70,70,70,70	0
57	MG	1A	3593	1/1	0.78	0.14	30,30,30,30	0
57	MG	2A	3371	1/1	0.79	0.30	60,60,60,60	0
57	MG	2A	3164	1/1	0.79	0.21	67,67,67,67	0
57	MG	2A	3662	1/1	0.79	0.18	69,69,69,69	0
57	MG	1a	1749	1/1	0.79	0.21	69,69,69,69	0
57	MG	2A	3382	1/1	0.79	0.17	50,50,50,50	0
57	MG	2a	1617	1/1	0.79	0.22	62,62,62,62	0
57	MG	2a	1645	1/1	0.79	0.40	66,66,66,66	0
57	MG	2A	3390	1/1	0.79	0.20	73,73,73,73	0
57	MG	1A	3035	1/1	0.79	0.20	51,51,51,51	0
57	MG	2A	3249	1/1	0.79	0.14	57,57,57,57	0
57	MG	2a	1720	1/1	0.79	0.20	54,54,54,54	0
57	MG	1a	1636	1/1	0.79	0.21	69,69,69,69	0
57	MG	2A	3704	1/1	0.79	0.15	56,56,56,56	0
57	MG	2A	3273	1/1	0.79	0.29	63,63,63,63	0
57	MG	1A	3940	1/1	0.79	0.35	70,70,70,70	0
57	MG	2A	3539	1/1	0.79	0.12	40,40,40,40	0
57	MG	19	101	1/1	0.79	0.23	59,59,59,59	0
57	MG	1A	3809	1/1	0.79	0.15	39,39,39,39	0
57	MG	1R	205	1/1	0.79	0.17	45,45,45,45	0
57	MG	2A	3611	1/1	0.79	0.18	41,41,41,41	0
57	MG	2A	3847	1/1	0.79	0.22	69,69,69,69	0
57	MG	2A	3848	1/1	0.79	0.20	58,58,58,58	0
57	MG	2A	3094	1/1	0.79	0.18	77,77,77,77	0
57	MG	2A	3633	1/1	0.79	0.21	66,66,66,66	0
57	MG	1A	3706	1/1	0.80	0.14	50,50,50,50	0
57	MG	2A	3290	1/1	0.80	0.21	76,76,76,76	0
57	MG	2A	3299	1/1	0.80	0.26	65,65,65,65	0
57	MG	2B	215	1/1	0.80	0.17	77,77,77,77	0
57	MG	2A	3301	1/1	0.80	0.21	57,57,57,57	0
57	MG	1a	1647	1/1	0.80	0.38	77,77,77,77	0
57	MG	1A	3982	1/1	0.80	0.18	72,72,72,72	0
57	MG	2A	3667	1/1	0.80	0.27	71,71,71,71	0
57	MG	1A	3948	1/1	0.80	0.14	64,64,64,64	0
57	MG	1A	4055	1/1	0.80	0.17	56,56,56,56	0
57	MG	2A	3180	1/1	0.80	0.16	58,58,58,58	0
57	MG	2a	1672	1/1	0.80	0.19	75,75,75,75	0
57	MG	1A	3592	1/1	0.80	0.14	56,56,56,56	0
57	MG	1a	1682	1/1	0.80	0.24	70,70,70,70	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	0.80	0.20	61,61,61,61	0
57	MG	1a	1796	1/1	0.80	0.20	74,74,74,74	0
57	MG	1a	1690	1/1	0.80	0.14	63,63,63,63	0
57	MG	1a	1610	1/1	0.80	0.38	83,83,83,83	0
57	MG	1B	220	1/1	0.80	0.14	65,65,65,65	0
57	MG	1A	3496	1/1	0.80	0.12	63,63,63,63	0
57	MG	2A	3004	1/1	0.80	0.28	71,71,71,71	0
57	MG	2A	3246	1/1	0.80	0.16	60,60,60,60	0
57	MG	1A	4005	1/1	0.80	0.11	39,39,39,39	0
57	MG	2A	3575	1/1	0.80	0.25	63,63,63,63	0
57	MG	1A	3854	1/1	0.80	0.27	41,41,41,41	0
57	MG	2A	3853	1/1	0.80	0.41	74,74,74,74	0
57	MG	1a	1734	1/1	0.80	0.28	70,70,70,70	0
57	MG	1A	3984	1/1	0.81	0.14	58,58,58,58	0
57	MG	1A	4037	1/1	0.81	0.21	48,48,48,48	0
57	MG	2A	3321	1/1	0.81	0.17	69,69,69,69	0
57	MG	1a	1817	1/1	0.81	0.18	64,64,64,64	0
57	MG	1a	1818	1/1	0.81	0.18	70,70,70,70	0
57	MG	1A	3777	1/1	0.81	0.22	57,57,57,57	0
57	MG	1a	1757	1/1	0.81	0.37	79,79,79,79	0
57	MG	1n	101	1/1	0.81	0.11	69,69,69,69	0
57	MG	1a	1697	1/1	0.81	0.34	62,62,62,62	0
57	MG	2a	1616	1/1	0.81	0.19	56,56,56,56	0
57	MG	2A	3030	1/1	0.81	0.16	72,72,72,72	0
57	MG	1A	3516	1/1	0.81	0.17	67,67,67,67	0
57	MG	1A	3918	1/1	0.81	0.15	61,61,61,61	0
57	MG	1a	1781	1/1	0.81	0.21	69,69,69,69	0
57	MG	2A	3090	1/1	0.81	0.26	53,53,53,53	0
57	MG	2a	1676	1/1	0.81	0.13	72,72,72,72	0
57	MG	1a	1782	1/1	0.81	0.18	79,79,79,79	0
57	MG	2a	1718	1/1	0.81	0.20	68,68,68,68	0
57	MG	2A	3529	1/1	0.81	0.16	40,40,40,40	0
57	MG	2A	3734	1/1	0.81	0.25	77,77,77,77	0
57	MG	2A	3262	1/1	0.81	0.14	68,68,68,68	0
57	MG	2A	3119	1/1	0.81	0.23	63,63,63,63	0
57	MG	1A	3349	1/1	0.81	0.20	56,56,56,56	0
57	MG	2A	3275	1/1	0.81	0.18	59,59,59,59	0
57	MG	2A	3772	1/1	0.81	0.12	72,72,72,72	0
57	MG	2A	3813	1/1	0.81	0.14	45,45,45,45	0
57	MG	2A	3815	1/1	0.81	0.23	58,58,58,58	0
57	MG	2a	1766	1/1	0.81	0.27	71,71,71,71	0
57	MG	2A	3826	1/1	0.81	0.14	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	3828	1/1	0.81	0.26	63,63,63,63	0
57	MG	2A	3587	1/1	0.81	0.15	51,51,51,51	0
57	MG	2x	104	1/1	0.81	0.42	87,87,87,87	0
57	MG	1A	3756	1/1	0.81	0.09	20,20,20,20	0
57	MG	2A	3850	1/1	0.81	0.18	53,53,53,53	0
57	MG	1A	3698	1/1	0.82	0.11	68,68,68,68	0
57	MG	1a	1808	1/1	0.82	0.25	77,77,77,77	0
57	MG	1A	3421	1/1	0.82	0.19	61,61,61,61	0
57	MG	1a	1708	1/1	0.82	0.16	82,82,82,82	0
57	MG	1A	3986	1/1	0.82	0.11	36,36,36,36	0
57	MG	2A	3380	1/1	0.82	0.27	60,60,60,60	0
57	MG	2a	1637	1/1	0.82	0.24	61,61,61,61	0
57	MG	1A	3424	1/1	0.82	0.15	53,53,53,53	0
57	MG	1A	3450	1/1	0.82	0.25	71,71,71,71	0
57	MG	1A	3210	1/1	0.82	0.16	72,72,72,72	0
57	MG	2A	3725	1/1	0.82	0.16	63,63,63,63	0
57	MG	1a	1648	1/1	0.82	0.13	68,68,68,68	0
57	MG	2a	1679	1/1	0.82	0.31	63,63,63,63	0
57	MG	2a	1706	1/1	0.82	0.18	57,57,57,57	0
57	MG	2A	3022	1/1	0.82	0.31	71,71,71,71	0
57	MG	1A	4015	1/1	0.82	0.14	64,64,64,64	0
57	MG	1A	4017	1/1	0.82	0.15	69,69,69,69	0
57	MG	1A	3361	1/1	0.82	0.24	57,57,57,57	0
57	MG	1A	3328	1/1	0.82	0.24	56,56,56,56	0
57	MG	2A	3542	1/1	0.82	0.11	78,78,78,78	0
57	MG	2A	3265	1/1	0.82	0.21	71,71,71,71	0
57	MG	2a	1742	1/1	0.82	0.23	71,71,71,71	0
57	MG	2A	3088	1/1	0.82	0.16	63,63,63,63	0
57	MG	2a	1746	1/1	0.82	0.22	76,76,76,76	0
57	MG	1a	1775	1/1	0.82	0.19	69,69,69,69	0
57	MG	1a	1678	1/1	0.82	0.16	67,67,67,67	0
57	MG	2A	3278	1/1	0.82	0.15	68,68,68,68	0
57	MG	1a	1680	1/1	0.82	0.20	69,69,69,69	0
57	MG	2A	3136	1/1	0.82	0.25	71,71,71,71	0
57	MG	2a	1770	1/1	0.82	0.26	80,80,80,80	0
57	MG	1A	3329	1/1	0.82	0.19	43,43,43,43	0
57	MG	2a	1773	1/1	0.82	0.15	64,64,64,64	0
57	MG	2A	3639	1/1	0.82	0.14	68,68,68,68	0
57	MG	1a	1688	1/1	0.82	0.32	70,70,70,70	0
57	MG	1A	3145	1/1	0.82	0.11	52,52,52,52	0
57	MG	1A	4038	1/1	0.82	0.11	54,54,54,54	0
57	MG	1A	3627	1/1	0.83	0.12	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3842	1/1	0.83	0.12	30,30,30,30	0
57	MG	2A	3843	1/1	0.83	0.21	60,60,60,60	0
57	MG	1A	3648	1/1	0.83	0.15	57,57,57,57	0
57	MG	2A	3442	1/1	0.83	0.10	61,61,61,61	0
57	MG	2A	3460	1/1	0.83	0.18	72,72,72,72	0
57	MG	1a	1705	1/1	0.83	0.24	74,74,74,74	0
57	MG	1A	3671	1/1	0.83	0.15	58,58,58,58	0
57	MG	1A	3515	1/1	0.83	0.26	45,45,45,45	0
57	MG	1A	3350	1/1	0.83	0.22	66,66,66,66	0
57	MG	1A	3580	1/1	0.83	0.12	40,40,40,40	0
57	MG	2A	3252	1/1	0.83	0.18	58,58,58,58	0
57	MG	1A	3971	1/1	0.83	0.14	64,64,64,64	0
57	MG	2B	219	1/1	0.83	0.17	71,71,71,71	0
57	MG	1A	3972	1/1	0.83	0.12	48,48,48,48	0
57	MG	1A	3006	1/1	0.83	0.23	58,58,58,58	0
57	MG	1a	1642	1/1	0.83	0.28	70,70,70,70	0
57	MG	23	101	1/1	0.83	0.22	64,64,64,64	0
57	MG	1a	1646	1/1	0.83	0.13	87,87,87,87	0
57	MG	2A	3620	1/1	0.83	0.13	48,48,48,48	0
57	MG	2a	1633	1/1	0.83	0.40	70,70,70,70	0
57	MG	1A	4065	1/1	0.83	0.20	65,65,65,65	0
57	MG	2a	1643	1/1	0.83	0.20	77,77,77,77	0
57	MG	1A	3263	1/1	0.83	0.24	80,80,80,80	0
57	MG	2A	3638	1/1	0.83	0.23	73,73,73,73	0
57	MG	2A	3288	1/1	0.83	0.09	72,72,72,72	0
57	MG	2a	1669	1/1	0.83	0.34	63,63,63,63	0
57	MG	2A	3111	1/1	0.83	0.38	60,60,60,60	0
57	MG	2A	3653	1/1	0.83	0.14	66,66,66,66	0
57	MG	2A	3658	1/1	0.83	0.12	54,54,54,54	0
57	MG	2a	1681	1/1	0.83	0.21	61,61,61,61	0
57	MG	2A	3296	1/1	0.83	0.15	56,56,56,56	0
57	MG	1A	4070	1/1	0.83	0.15	61,61,61,61	0
57	MG	2A	3300	1/1	0.83	0.43	45,45,45,45	0
57	MG	1B	208	1/1	0.83	0.17	63,63,63,63	0
57	MG	2A	3305	1/1	0.83	0.16	70,70,70,70	0
57	MG	2A	3314	1/1	0.83	0.27	68,68,68,68	0
57	MG	1A	3737	1/1	0.83	0.11	49,49,49,49	0
57	MG	2A	3165	1/1	0.83	0.26	68,68,68,68	0
57	MG	2a	1738	1/1	0.83	0.31	68,68,68,68	0
57	MG	2a	1740	1/1	0.83	0.19	75,75,75,75	0
57	MG	2A	3329	1/1	0.83	0.30	69,69,69,69	0
57	MG	1A	3751	1/1	0.83	0.11	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	1A	3915	1/1	0.83	0.14	46,46,46,46	0
57	MG	2a	1747	1/1	0.83	0.15	74,74,74,74	0
57	MG	2A	3355	1/1	0.83	0.25	67,67,67,67	0
57	MG	1D	310	1/1	0.83	0.19	48,48,48,48	0
57	MG	1a	1794	1/1	0.83	0.17	45,45,45,45	0
57	MG	1A	3505	1/1	0.83	0.31	69,69,69,69	0
57	MG	1a	1687	1/1	0.83	0.23	66,66,66,66	0
57	MG	1A	3623	1/1	0.83	0.18	53,53,53,53	0
57	MG	2A	3216	1/1	0.83	0.20	69,69,69,69	0
57	MG	2A	3223	1/1	0.83	0.35	50,50,50,50	0
57	MG	2A	3777	1/1	0.83	0.16	63,63,63,63	0
57	MG	2q	203	1/1	0.83	0.30	75,75,75,75	0
57	MG	2A	3792	1/1	0.83	0.18	54,54,54,54	0
57	MG	1A	3929	1/1	0.83	0.17	31,31,31,31	0
57	MG	2A	3426	1/1	0.83	0.26	65,65,65,65	0
57	MG	1E	312	1/1	0.84	0.16	59,59,59,59	0
57	MG	2B	213	1/1	0.84	0.26	70,70,70,70	0
57	MG	1a	1674	1/1	0.84	0.19	77,77,77,77	0
57	MG	1F	304	1/1	0.84	0.11	60,60,60,60	0
57	MG	1A	3864	1/1	0.84	0.32	66,66,66,66	0
57	MG	2A	3174	1/1	0.84	0.14	73,73,73,73	0
57	MG	2D	308	1/1	0.84	0.13	62,62,62,62	0
57	MG	2A	3307	1/1	0.84	0.33	50,50,50,50	0
57	MG	1A	4019	1/1	0.84	0.13	53,53,53,53	0
57	MG	2A	3315	1/1	0.84	0.12	64,64,64,64	0
57	MG	2a	1607	1/1	0.84	0.16	53,53,53,53	0
57	MG	2A	3651	1/1	0.84	0.23	61,61,61,61	0
57	MG	1A	3385	1/1	0.84	0.15	63,63,63,63	0
57	MG	2a	1632	1/1	0.84	0.14	65,65,65,65	0
57	MG	2A	3191	1/1	0.84	0.22	66,66,66,66	0
57	MG	1A	3876	1/1	0.84	0.14	23,23,23,23	0
57	MG	1a	1804	1/1	0.84	0.24	77,77,77,77	0
57	MG	2A	3332	1/1	0.84	0.16	55,55,55,55	0
57	MG	2A	3203	1/1	0.84	0.24	61,61,61,61	0
57	MG	2A	3353	1/1	0.84	0.12	71,71,71,71	0
57	MG	2a	1662	1/1	0.84	0.17	73,73,73,73	0
57	MG	1A	3026	1/1	0.84	0.19	59,59,59,59	0
57	MG	2A	3686	1/1	0.84	0.09	64,64,64,64	0
57	MG	2a	1675	1/1	0.84	0.29	67,67,67,67	0
57	MG	2A	3357	1/1	0.84	0.11	69,69,69,69	0
57	MG	1A	3894	1/1	0.84	0.15	32,32,32,32	0
57	MG	2A	3696	1/1	0.84	0.18	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	1a	1691	1/1	0.84	0.47	64,64,64,64	0
57	MG	1a	1606	1/1	0.84	0.12	63,63,63,63	0
57	MG	1A	3899	1/1	0.84	0.21	48,48,48,48	0
57	MG	1a	1612	1/1	0.84	0.30	67,67,67,67	0
57	MG	1A	3901	1/1	0.84	0.23	53,53,53,53	0
57	MG	1A	4057	1/1	0.84	0.13	41,41,41,41	0
57	MG	2A	3411	1/1	0.84	0.23	57,57,57,57	0
57	MG	2A	3752	1/1	0.84	0.11	58,58,58,58	0
57	MG	2a	1737	1/1	0.84	0.19	77,77,77,77	0
57	MG	1A	3568	1/1	0.84	0.22	48,48,48,48	0
57	MG	1A	3487	1/1	0.84	0.22	67,67,67,67	0
57	MG	1a	1730	1/1	0.84	0.38	68,68,68,68	0
57	MG	1A	3669	1/1	0.84	0.10	48,48,48,48	0
57	MG	2A	3255	1/1	0.84	0.42	64,64,64,64	0
57	MG	2A	3790	1/1	0.84	0.17	51,51,51,51	0
57	MG	2A	3449	1/1	0.84	0.12	69,69,69,69	0
57	MG	1A	4085	1/1	0.84	0.19	54,54,54,54	0
57	MG	2A	3470	1/1	0.84	0.29	66,66,66,66	0
57	MG	2a	1765	1/1	0.84	0.21	80,80,80,80	0
57	MG	1A	3343	1/1	0.84	0.15	69,69,69,69	0
57	MG	1a	1752	1/1	0.84	0.17	68,68,68,68	0
57	MG	1A	3694	1/1	0.84	0.12	47,47,47,47	0
57	MG	1A	3837	1/1	0.84	0.13	64,64,64,64	0
57	MG	1A	3947	1/1	0.84	0.10	28,28,28,28	0
57	MG	2d	302	1/1	0.84	0.12	69,69,69,69	0
57	MG	2f	203	1/1	0.84	0.31	74,74,74,74	0
57	MG	2A	3552	1/1	0.84	0.17	70,70,70,70	0
57	MG	1a	1662	1/1	0.84	0.24	78,78,78,78	0
57	MG	2A	3280	1/1	0.84	0.10	59,59,59,59	0
57	MG	1A	3264	1/1	0.84	0.15	61,61,61,61	0
57	MG	2A	3146	1/1	0.84	0.24	65,65,65,65	0
57	MG	1A	3819	1/1	0.85	0.13	56,56,56,56	0
57	MG	1A	3967	1/1	0.85	0.16	61,61,61,61	0
57	MG	1A	3970	1/1	0.85	0.20	64,64,64,64	0
57	MG	1A	3422	1/1	0.85	0.15	48,48,48,48	0
57	MG	1Y	202	1/1	0.85	0.29	51,51,51,51	0
57	MG	2A	3622	1/1	0.85	0.34	63,63,63,63	0
57	MG	1a	1686	1/1	0.85	0.33	74,74,74,74	0
57	MG	1A	3254	1/1	0.85	0.14	57,57,57,57	0
57	MG	1A	3973	1/1	0.85	0.14	29,29,29,29	0
57	MG	2A	3322	1/1	0.85	0.37	73,73,73,73	0
57	MG	25	102	1/1	0.85	0.17	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	1605	1/1	0.85	0.31	67,67,67,67	0
57	MG	2A	3643	1/1	0.85	0.18	64,64,64,64	0
57	MG	2a	1609	1/1	0.85	0.15	67,67,67,67	0
57	MG	1A	3974	1/1	0.85	0.12	39,39,39,39	0
57	MG	2A	3205	1/1	0.85	0.11	75,75,75,75	0
57	MG	2A	3331	1/1	0.85	0.21	73,73,73,73	0
57	MG	2A	3207	1/1	0.85	0.19	69,69,69,69	0
57	MG	2a	1636	1/1	0.85	0.20	63,63,63,63	0
57	MG	1A	3912	1/1	0.85	0.12	47,47,47,47	0
57	MG	1a	1692	1/1	0.85	0.23	73,73,73,73	0
57	MG	1A	3822	1/1	0.85	0.13	46,46,46,46	0
57	MG	2a	1646	1/1	0.85	0.28	72,72,72,72	0
57	MG	1A	3170	1/1	0.85	0.29	58,58,58,58	0
57	MG	2a	1650	1/1	0.85	0.25	66,66,66,66	0
57	MG	1A	3578	1/1	0.85	0.21	55,55,55,55	0
57	MG	2a	1658	1/1	0.85	0.32	62,62,62,62	0
57	MG	2A	3370	1/1	0.85	0.27	66,66,66,66	0
57	MG	1A	3853	1/1	0.85	0.10	38,38,38,38	0
57	MG	1l	202	1/1	0.85	0.12	62,62,62,62	0
57	MG	1A	3460	1/1	0.85	0.20	67,67,67,67	0
57	MG	1x	106	1/1	0.85	0.15	57,57,57,57	0
57	MG	2a	1678	1/1	0.85	0.36	73,73,73,73	0
57	MG	1A	3858	1/1	0.85	0.27	46,46,46,46	0
57	MG	2A	3387	1/1	0.85	0.13	67,67,67,67	0
57	MG	2A	3712	1/1	0.85	0.12	64,64,64,64	0
57	MG	1a	1721	1/1	0.85	0.19	55,55,55,55	0
57	MG	2A	3721	1/1	0.85	0.10	61,61,61,61	0
57	MG	1A	3101	1/1	0.85	0.31	72,72,72,72	0
57	MG	2A	3415	1/1	0.85	0.34	60,60,60,60	0
57	MG	2A	3254	1/1	0.85	0.18	58,58,58,58	0
57	MG	2A	3424	1/1	0.85	0.18	72,72,72,72	0
57	MG	1A	3412	1/1	0.85	0.09	56,56,56,56	0
57	MG	1D	313	1/1	0.85	0.13	39,39,39,39	0
57	MG	1a	1733	1/1	0.85	0.15	76,76,76,76	0
57	MG	1a	1652	1/1	0.85	0.15	56,56,56,56	0
57	MG	2A	3763	1/1	0.85	0.10	73,73,73,73	0
57	MG	1a	1745	1/1	0.85	0.13	59,59,59,59	0
57	MG	1A	3957	1/1	0.85	0.23	66,66,66,66	0
57	MG	1a	1657	1/1	0.85	0.11	75,75,75,75	0
57	MG	2a	1751	1/1	0.85	0.14	59,59,59,59	0
57	MG	1a	1658	1/1	0.85	0.16	58,58,58,58	0
57	MG	2a	1758	1/1	0.85	0.16	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3809	1/1	0.85	0.13	42,42,42,42	0
57	MG	2A	3503	1/1	0.85	0.19	64,64,64,64	0
57	MG	2A	3510	1/1	0.85	0.14	64,64,64,64	0
57	MG	2A	3514	1/1	0.85	0.12	38,38,38,38	0
57	MG	2A	3840	1/1	0.85	0.11	40,40,40,40	0
57	MG	2A	3522	1/1	0.85	0.14	56,56,56,56	0
57	MG	2A	3123	1/1	0.85	0.10	53,53,53,53	0
57	MG	2A	3281	1/1	0.85	0.32	76,76,76,76	0
57	MG	1A	3295	1/1	0.85	0.34	74,74,74,74	0
57	MG	1F	315	1/1	0.85	0.22	54,54,54,54	0
57	MG	2i	201	1/1	0.85	0.32	76,76,76,76	0
57	MG	2A	3549	1/1	0.85	0.19	51,51,51,51	0
57	MG	2A	3295	1/1	0.85	0.09	52,52,52,52	0
57	MG	1A	3507	1/1	0.85	0.15	61,61,61,61	0
57	MG	1a	1672	1/1	0.85	0.14	63,63,63,63	0
57	MG	2B	207	1/1	0.85	0.20	64,64,64,64	0
57	MG	1V	206	1/1	0.86	0.08	59,59,59,59	0
57	MG	1A	3812	1/1	0.86	0.12	43,43,43,43	0
57	MG	2A	3456	1/1	0.86	0.38	60,60,60,60	0
57	MG	1A	3626	1/1	0.86	0.19	60,60,60,60	0
57	MG	17	105	1/1	0.86	0.33	70,70,70,70	0
57	MG	2A	3471	1/1	0.86	0.14	63,63,63,63	0
57	MG	1a	1823	1/1	0.86	0.23	74,74,74,74	0
57	MG	2A	3486	1/1	0.86	0.19	52,52,52,52	0
57	MG	1e	202	1/1	0.86	0.13	64,64,64,64	0
57	MG	1A	3185	1/1	0.86	0.17	61,61,61,61	0
57	MG	1a	1601	1/1	0.86	0.21	59,59,59,59	0
57	MG	1A	3631	1/1	0.86	0.08	27,27,27,27	0
57	MG	2B	204	1/1	0.86	0.18	72,72,72,72	0
57	MG	2A	3526	1/1	0.86	0.12	67,67,67,67	0
57	MG	1A	3300	1/1	0.86	0.25	63,63,63,63	0
57	MG	1x	110	1/1	0.86	0.14	67,67,67,67	0
57	MG	1A	3366	1/1	0.86	0.33	63,63,63,63	0
57	MG	2A	3269	1/1	0.86	0.39	62,62,62,62	0
57	MG	2A	3544	1/1	0.86	0.21	69,69,69,69	0
57	MG	2A	3545	1/1	0.86	0.12	40,40,40,40	0
57	MG	2A	3007	1/1	0.86	0.24	58,58,58,58	0
57	MG	1A	3378	1/1	0.86	0.20	55,55,55,55	0
57	MG	2A	3023	1/1	0.86	0.27	68,68,68,68	0
57	MG	1A	3233	1/1	0.86	0.16	55,55,55,55	0
57	MG	2A	3585	1/1	0.86	0.13	31,31,31,31	0
57	MG	1a	1627	1/1	0.86	0.14	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	27	102	1/1	0.86	0.30	68,68,68,68	0
57	MG	1A	3204	1/1	0.86	0.11	47,47,47,47	0
57	MG	1A	3968	1/1	0.86	0.13	60,60,60,60	0
57	MG	2A	3601	1/1	0.86	0.14	38,38,38,38	0
57	MG	2a	1613	1/1	0.86	0.26	62,62,62,62	0
57	MG	1A	3262	1/1	0.86	0.28	62,62,62,62	0
57	MG	2A	3613	1/1	0.86	0.20	62,62,62,62	0
57	MG	2a	1626	1/1	0.86	0.32	69,69,69,69	0
57	MG	2A	3293	1/1	0.86	0.21	59,59,59,59	0
57	MG	1A	3533	1/1	0.86	0.20	67,67,67,67	0
57	MG	1A	4079	1/1	0.86	0.20	55,55,55,55	0
57	MG	2A	3097	1/1	0.86	0.25	72,72,72,72	0
57	MG	2A	3099	1/1	0.86	0.29	66,66,66,66	0
57	MG	1a	1737	1/1	0.86	0.17	67,67,67,67	0
57	MG	2A	3642	1/1	0.86	0.15	52,52,52,52	0
57	MG	1A	3566	1/1	0.86	0.15	61,61,61,61	0
57	MG	2A	3646	1/1	0.86	0.11	55,55,55,55	0
57	MG	2a	1654	1/1	0.86	0.33	58,58,58,58	0
57	MG	1A	3728	1/1	0.86	0.10	22,22,22,22	0
57	MG	2A	3133	1/1	0.86	0.11	53,53,53,53	0
57	MG	1A	3335	1/1	0.86	0.32	57,57,57,57	0
57	MG	1B	221	1/1	0.86	0.13	56,56,56,56	0
57	MG	1A	3050	1/1	0.86	0.29	58,58,58,58	0
57	MG	1A	3183	1/1	0.86	0.26	51,51,51,51	0
57	MG	1A	3267	1/1	0.86	0.17	46,46,46,46	0
57	MG	1a	1766	1/1	0.86	0.20	70,70,70,70	0
57	MG	2A	3172	1/1	0.86	0.16	53,53,53,53	0
57	MG	2A	3677	1/1	0.86	0.13	54,54,54,54	0
57	MG	2A	3681	1/1	0.86	0.16	59,59,59,59	0
57	MG	1A	3900	1/1	0.86	0.27	38,38,38,38	0
57	MG	1A	3445	1/1	0.86	0.17	60,60,60,60	0
57	MG	2A	3352	1/1	0.86	0.21	68,68,68,68	0
57	MG	2A	3690	1/1	0.86	0.16	69,69,69,69	0
57	MG	2A	3692	1/1	0.86	0.13	56,56,56,56	0
57	MG	1a	1668	1/1	0.86	0.10	62,62,62,62	0
57	MG	2A	3185	1/1	0.86	0.24	70,70,70,70	0
57	MG	2A	3186	1/1	0.86	0.48	70,70,70,70	0
57	MG	2A	3701	1/1	0.86	0.12	56,56,56,56	0
57	MG	2A	3189	1/1	0.86	0.16	61,61,61,61	0
57	MG	2A	3707	1/1	0.86	0.10	38,38,38,38	0
57	MG	2a	1743	1/1	0.86	0.29	54,54,54,54	0
57	MG	2A	3708	1/1	0.86	0.20	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	2A	3711	1/1	0.86	0.15	73,73,73,73	0
57	MG	1A	3782	1/1	0.86	0.11	20,20,20,20	0
57	MG	2A	3192	1/1	0.86	0.21	55,55,55,55	0
57	MG	2a	1753	1/1	0.86	0.34	68,68,68,68	0
57	MG	1a	1673	1/1	0.86	0.30	69,69,69,69	0
57	MG	2A	3197	1/1	0.86	0.15	63,63,63,63	0
57	MG	1A	3360	1/1	0.86	0.18	62,62,62,62	0
57	MG	1a	1790	1/1	0.86	0.18	61,61,61,61	0
57	MG	1a	1793	1/1	0.86	0.15	69,69,69,69	0
57	MG	2A	3389	1/1	0.86	0.25	78,78,78,78	0
57	MG	1A	3609	1/1	0.86	0.09	45,45,45,45	0
57	MG	2A	3402	1/1	0.86	0.19	42,42,42,42	0
57	MG	1A	4010	1/1	0.86	0.14	66,66,66,66	0
57	MG	2a	1772	1/1	0.86	0.14	76,76,76,76	0
57	MG	2A	3213	1/1	0.86	0.13	58,58,58,58	0
57	MG	2A	3764	1/1	0.86	0.15	51,51,51,51	0
57	MG	2f	202	1/1	0.86	0.17	75,75,75,75	0
57	MG	2A	3770	1/1	0.86	0.16	49,49,49,49	0
57	MG	1a	1797	1/1	0.86	0.17	56,56,56,56	0
57	MG	1A	3457	1/1	0.86	0.14	63,63,63,63	0
57	MG	2l	201	1/1	0.86	0.15	62,62,62,62	0
57	MG	1A	3811	1/1	0.86	0.19	55,55,55,55	0
57	MG	1U	210	1/1	0.86	0.25	47,47,47,47	0
57	MG	2A	3795	1/1	0.86	0.13	57,57,57,57	0
57	MG	2A	3238	1/1	0.86	0.22	71,71,71,71	0
57	MG	2A	3824	1/1	0.87	0.12	73,73,73,73	0
57	MG	1A	3683	1/1	0.87	0.12	39,39,39,39	0
57	MG	2A	3836	1/1	0.87	0.21	70,70,70,70	0
57	MG	2A	3263	1/1	0.87	0.20	62,62,62,62	0
57	MG	1a	1603	1/1	0.87	0.18	58,58,58,58	0
57	MG	1a	1605	1/1	0.87	0.15	74,74,74,74	0
57	MG	2A	3043	1/1	0.87	0.13	71,71,71,71	0
57	MG	1A	3442	1/1	0.87	0.20	59,59,59,59	0
57	MG	1a	1714	1/1	0.87	0.11	73,73,73,73	0
57	MG	1A	3339	1/1	0.87	0.22	70,70,70,70	0
57	MG	2A	3852	1/1	0.87	0.14	53,53,53,53	0
57	MG	1A	3373	1/1	0.87	0.17	61,61,61,61	0
57	MG	1a	1613	1/1	0.87	0.11	68,68,68,68	0
57	MG	2A	3286	1/1	0.87	0.22	61,61,61,61	0
57	MG	1A	3835	1/1	0.87	0.19	55,55,55,55	0
57	MG	1A	3296	1/1	0.87	0.35	65,65,65,65	0
57	MG	1A	3849	1/1	0.87	0.14	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	3562	1/1	0.87	0.21	60,60,60,60	0
57	MG	2A	3104	1/1	0.87	0.32	57,57,57,57	0
57	MG	2A	3581	1/1	0.87	0.19	61,61,61,61	0
57	MG	2B	216	1/1	0.87	0.20	67,67,67,67	0
57	MG	1a	1736	1/1	0.87	0.38	72,72,72,72	0
57	MG	1A	3046	1/1	0.87	0.09	28,28,28,28	0
57	MG	1A	3392	1/1	0.87	0.20	36,36,36,36	0
57	MG	1A	4073	1/1	0.87	0.14	73,73,73,73	0
57	MG	2A	3598	1/1	0.87	0.18	66,66,66,66	0
57	MG	2W	201	1/1	0.87	0.23	65,65,65,65	0
57	MG	1a	1750	1/1	0.87	0.13	64,64,64,64	0
57	MG	2A	3602	1/1	0.87	0.13	59,59,59,59	0
57	MG	25	104	1/1	0.87	0.17	53,53,53,53	0
57	MG	1A	3489	1/1	0.87	0.10	51,51,51,51	0
57	MG	28	102	1/1	0.87	0.21	57,57,57,57	0
57	MG	29	101	1/1	0.87	0.22	65,65,65,65	0
57	MG	1A	3615	1/1	0.87	0.10	29,29,29,29	0
57	MG	2A	3615	1/1	0.87	0.15	70,70,70,70	0
57	MG	1B	202	1/1	0.87	0.25	59,59,59,59	0
57	MG	1B	205	1/1	0.87	0.29	70,70,70,70	0
57	MG	2A	3630	1/1	0.87	0.17	60,60,60,60	0
57	MG	1a	1649	1/1	0.87	0.26	63,63,63,63	0
57	MG	2a	1619	1/1	0.87	0.14	63,63,63,63	0
57	MG	1a	1650	1/1	0.87	0.18	72,72,72,72	0
57	MG	2A	3634	1/1	0.87	0.20	64,64,64,64	0
57	MG	2A	3323	1/1	0.87	0.18	59,59,59,59	0
57	MG	2A	3326	1/1	0.87	0.17	75,75,75,75	0
57	MG	2A	3327	1/1	0.87	0.11	73,73,73,73	0
57	MG	2A	3328	1/1	0.87	0.17	70,70,70,70	0
57	MG	2A	3644	1/1	0.87	0.20	66,66,66,66	0
57	MG	1a	1651	1/1	0.87	0.29	67,67,67,67	0
57	MG	1A	3616	1/1	0.87	0.09	26,26,26,26	0
57	MG	1a	1653	1/1	0.87	0.23	69,69,69,69	0
57	MG	2a	1651	1/1	0.87	0.20	68,68,68,68	0
57	MG	1A	3393	1/1	0.87	0.15	53,53,53,53	0
57	MG	2A	3339	1/1	0.87	0.14	64,64,64,64	0
57	MG	1A	3980	1/1	0.87	0.13	62,62,62,62	0
57	MG	1A	3877	1/1	0.87	0.13	71,71,71,71	0
57	MG	2a	1667	1/1	0.87	0.27	66,66,66,66	0
57	MG	2A	3190	1/1	0.87	0.34	68,68,68,68	0
57	MG	2a	1671	1/1	0.87	0.21	67,67,67,67	0
57	MG	1a	1787	1/1	0.87	0.19	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1788	1/1	0.87	0.22	68,68,68,68	0
57	MG	2A	3676	1/1	0.87	0.12	59,59,59,59	0
57	MG	2A	3359	1/1	0.87	0.21	75,75,75,75	0
57	MG	1A	3189	1/1	0.87	0.14	38,38,38,38	0
57	MG	2A	3369	1/1	0.87	0.29	61,61,61,61	0
57	MG	2a	1693	1/1	0.87	0.27	78,78,78,78	0
57	MG	1a	1792	1/1	0.87	0.14	65,65,65,65	0
57	MG	2A	3199	1/1	0.87	0.13	58,58,58,58	0
57	MG	1D	302	1/1	0.87	0.19	64,64,64,64	0
57	MG	1A	3351	1/1	0.87	0.22	66,66,66,66	0
57	MG	2A	3379	1/1	0.87	0.25	46,46,46,46	0
57	MG	1A	3359	1/1	0.87	0.10	49,49,49,49	0
57	MG	1E	308	1/1	0.87	0.21	60,60,60,60	0
57	MG	2A	3383	1/1	0.87	0.15	64,64,64,64	0
57	MG	2a	1733	1/1	0.87	0.12	55,55,55,55	0
57	MG	2A	3209	1/1	0.87	0.09	53,53,53,53	0
57	MG	2A	3705	1/1	0.87	0.15	49,49,49,49	0
57	MG	1A	3256	1/1	0.87	0.19	59,59,59,59	0
57	MG	1A	3989	1/1	0.87	0.14	46,46,46,46	0
57	MG	2A	3392	1/1	0.87	0.19	61,61,61,61	0
57	MG	2a	1744	1/1	0.87	0.23	74,74,74,74	0
57	MG	1A	3991	1/1	0.87	0.29	36,36,36,36	0
57	MG	1A	3794	1/1	0.87	0.18	56,56,56,56	0
57	MG	2A	3715	1/1	0.87	0.13	62,62,62,62	0
57	MG	1a	1679	1/1	0.87	0.13	66,66,66,66	0
57	MG	2A	3420	1/1	0.87	0.20	53,53,53,53	0
57	MG	1A	3911	1/1	0.87	0.13	29,29,29,29	0
57	MG	2a	1757	1/1	0.87	0.27	72,72,72,72	0
57	MG	1A	3795	1/1	0.87	0.13	45,45,45,45	0
57	MG	2A	3736	1/1	0.87	0.22	63,63,63,63	0
57	MG	2A	3745	1/1	0.87	0.11	68,68,68,68	0
57	MG	1A	3808	1/1	0.87	0.15	38,38,38,38	0
57	MG	1A	3655	1/1	0.87	0.11	40,40,40,40	0
57	MG	1A	3660	1/1	0.87	0.18	28,28,28,28	0
57	MG	1A	3294	1/1	0.87	0.16	56,56,56,56	0
57	MG	1A	3166	1/1	0.87	0.25	56,56,56,56	0
57	MG	2A	3453	1/1	0.87	0.14	69,69,69,69	0
57	MG	1x	104	1/1	0.87	0.17	65,65,65,65	0
57	MG	2A	3458	1/1	0.87	0.32	66,66,66,66	0
57	MG	1Y	203	1/1	0.87	0.14	62,62,62,62	0
57	MG	2A	3468	1/1	0.87	0.13	66,66,66,66	0
57	MG	2A	3779	1/1	0.87	0.08	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	3678	1/1	0.87	0.18	66,66,66,66	0
57	MG	1A	4033	1/1	0.87	0.14	59,59,59,59	0
57	MG	1a	1703	1/1	0.87	0.32	75,75,75,75	0
57	MG	2A	3482	1/1	0.87	0.26	55,55,55,55	0
57	MG	2A	3485	1/1	0.87	0.14	60,60,60,60	0
57	MG	2A	3261	1/1	0.87	0.10	68,68,68,68	0
57	MG	1A	3836	1/1	0.88	0.11	70,70,70,70	0
57	MG	2A	3294	1/1	0.88	0.23	64,64,64,64	0
57	MG	2A	3534	1/1	0.88	0.10	52,52,52,52	0
57	MG	2A	3124	1/1	0.88	0.10	66,66,66,66	0
57	MG	1A	4008	1/1	0.88	0.12	56,56,56,56	0
57	MG	2A	3298	1/1	0.88	0.20	60,60,60,60	0
57	MG	1D	312	1/1	0.88	0.24	41,41,41,41	0
57	MG	2A	3851	1/1	0.88	0.17	65,65,65,65	0
57	MG	1A	3427	1/1	0.88	0.12	61,61,61,61	0
57	MG	2A	3148	1/1	0.88	0.34	59,59,59,59	0
57	MG	2A	3303	1/1	0.88	0.14	60,60,60,60	0
57	MG	2A	3157	1/1	0.88	0.22	70,70,70,70	0
57	MG	2A	3563	1/1	0.88	0.20	58,58,58,58	0
57	MG	2B	206	1/1	0.88	0.29	67,67,67,67	0
57	MG	1a	1759	1/1	0.88	0.19	66,66,66,66	0
57	MG	2A	3310	1/1	0.88	0.17	56,56,56,56	0
57	MG	2A	3312	1/1	0.88	0.39	66,66,66,66	0
57	MG	1A	4013	1/1	0.88	0.08	59,59,59,59	0
57	MG	1A	3543	1/1	0.88	0.49	44,44,44,44	0
57	MG	1a	1774	1/1	0.88	0.11	61,61,61,61	0
57	MG	2B	218	1/1	0.88	0.21	70,70,70,70	0
57	MG	2A	3595	1/1	0.88	0.17	69,69,69,69	0
57	MG	2A	3319	1/1	0.88	0.20	55,55,55,55	0
57	MG	2B	222	1/1	0.88	0.21	73,73,73,73	0
57	MG	1A	3949	1/1	0.88	0.15	58,58,58,58	0
57	MG	2D	309	1/1	0.88	0.11	57,57,57,57	0
57	MG	1A	3612	1/1	0.88	0.09	32,32,32,32	0
57	MG	2E	306	1/1	0.88	0.10	30,30,30,30	0
57	MG	2O	201	1/1	0.88	0.10	60,60,60,60	0
57	MG	1A	3787	1/1	0.88	0.13	59,59,59,59	0
57	MG	2V	201	1/1	0.88	0.20	52,52,52,52	0
57	MG	2A	3612	1/1	0.88	0.12	46,46,46,46	0
57	MG	21	101	1/1	0.88	0.29	52,52,52,52	0
57	MG	1A	3962	1/1	0.88	0.12	39,39,39,39	0
57	MG	25	101	1/1	0.88	0.31	58,58,58,58	0
57	MG	1O	203	1/1	0.88	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	3619	1/1	0.88	0.34	47,47,47,47	0
57	MG	26	101	1/1	0.88	0.14	54,54,54,54	0
57	MG	1a	1671	1/1	0.88	0.18	65,65,65,65	0
57	MG	1O	204	1/1	0.88	0.11	60,60,60,60	0
57	MG	1A	3547	1/1	0.88	0.33	57,57,57,57	0
57	MG	2a	1603	1/1	0.88	0.12	63,63,63,63	0
57	MG	1A	3684	1/1	0.88	0.09	23,23,23,23	0
57	MG	1U	209	1/1	0.88	0.10	51,51,51,51	0
57	MG	1A	3548	1/1	0.88	0.27	51,51,51,51	0
57	MG	2A	3635	1/1	0.88	0.09	33,33,33,33	0
57	MG	2A	3340	1/1	0.88	0.12	58,58,58,58	0
57	MG	1A	3801	1/1	0.88	0.17	56,56,56,56	0
57	MG	2A	3641	1/1	0.88	0.26	68,68,68,68	0
57	MG	2a	1624	1/1	0.88	0.32	54,54,54,54	0
57	MG	2A	3348	1/1	0.88	0.18	65,65,65,65	0
57	MG	1A	4046	1/1	0.88	0.14	59,59,59,59	0
57	MG	1a	1681	1/1	0.88	0.17	68,68,68,68	0
57	MG	1A	4050	1/1	0.88	0.08	16,16,16,16	0
57	MG	2A	3649	1/1	0.88	0.14	53,53,53,53	0
57	MG	2A	3356	1/1	0.88	0.12	68,68,68,68	0
57	MG	1a	1684	1/1	0.88	0.26	60,60,60,60	0
57	MG	2A	3206	1/1	0.88	0.20	66,66,66,66	0
57	MG	2A	3363	1/1	0.88	0.26	62,62,62,62	0
57	MG	1A	4051	1/1	0.88	0.12	59,59,59,59	0
57	MG	1A	3695	1/1	0.88	0.13	62,62,62,62	0
57	MG	2A	3665	1/1	0.88	0.20	51,51,51,51	0
57	MG	1a	1815	1/1	0.88	0.09	68,68,68,68	0
57	MG	18	104	1/1	0.88	0.12	66,66,66,66	0
57	MG	2a	1660	1/1	0.88	0.50	71,71,71,71	0
57	MG	1A	3326	1/1	0.88	0.24	62,62,62,62	0
57	MG	2a	1666	1/1	0.88	0.13	66,66,66,66	0
57	MG	1A	3368	1/1	0.88	0.14	53,53,53,53	0
57	MG	2A	3225	1/1	0.88	0.20	59,59,59,59	0
57	MG	1a	1602	1/1	0.88	0.23	60,60,60,60	0
57	MG	2A	3232	1/1	0.88	0.25	61,61,61,61	0
57	MG	1A	4058	1/1	0.88	0.18	62,62,62,62	0
57	MG	1A	3898	1/1	0.88	0.12	25,25,25,25	0
57	MG	2a	1677	1/1	0.88	0.36	67,67,67,67	0
57	MG	1A	3577	1/1	0.88	0.19	56,56,56,56	0
57	MG	1A	3401	1/1	0.88	0.15	60,60,60,60	0
57	MG	1A	3720	1/1	0.88	0.11	49,49,49,49	0
57	MG	2a	1688	1/1	0.88	0.21	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	1A	3903	1/1	0.88	0.12	40,40,40,40	0
57	MG	2A	3409	1/1	0.88	0.30	57,57,57,57	0
57	MG	2a	1709	1/1	0.88	0.20	63,63,63,63	0
57	MG	1A	4080	1/1	0.88	0.22	70,70,70,70	0
57	MG	1A	3633	1/1	0.88	0.16	50,50,50,50	0
57	MG	2A	3250	1/1	0.88	0.20	62,62,62,62	0
57	MG	1a	1718	1/1	0.88	0.24	73,73,73,73	0
57	MG	1a	1720	1/1	0.88	0.42	68,68,68,68	0
57	MG	1A	3456	1/1	0.88	0.10	56,56,56,56	0
57	MG	2A	3028	1/1	0.88	0.14	64,64,64,64	0
57	MG	2A	3431	1/1	0.88	0.38	70,70,70,70	0
57	MG	1a	1723	1/1	0.88	0.38	56,56,56,56	0
57	MG	2A	3437	1/1	0.88	0.28	65,65,65,65	0
57	MG	2A	3722	1/1	0.88	0.16	64,64,64,64	0
57	MG	2A	3438	1/1	0.88	0.20	65,65,65,65	0
57	MG	2A	3726	1/1	0.88	0.15	64,64,64,64	0
57	MG	1A	3423	1/1	0.88	0.17	58,58,58,58	0
57	MG	2A	3733	1/1	0.88	0.19	46,46,46,46	0
57	MG	2A	3446	1/1	0.88	0.29	65,65,65,65	0
57	MG	1a	1729	1/1	0.88	0.32	73,73,73,73	0
57	MG	2a	1750	1/1	0.88	0.14	62,62,62,62	0
57	MG	2A	3264	1/1	0.88	0.12	70,70,70,70	0
57	MG	2A	3084	1/1	0.88	0.14	49,49,49,49	0
57	MG	2A	3267	1/1	0.88	0.12	60,60,60,60	0
57	MG	1a	1635	1/1	0.88	0.27	68,68,68,68	0
57	MG	2A	3271	1/1	0.88	0.17	66,66,66,66	0
57	MG	2A	3758	1/1	0.88	0.13	68,68,68,68	0
57	MG	1A	3320	1/1	0.88	0.30	35,35,35,35	0
57	MG	1B	209	1/1	0.88	0.27	58,58,58,58	0
57	MG	2A	3479	1/1	0.88	0.18	52,52,52,52	0
57	MG	2a	1768	1/1	0.88	0.26	61,61,61,61	0
57	MG	1A	3831	1/1	0.88	0.18	56,56,56,56	0
57	MG	2A	3276	1/1	0.88	0.14	66,66,66,66	0
57	MG	1a	1643	1/1	0.88	0.32	64,64,64,64	0
57	MG	1A	3832	1/1	0.88	0.16	63,63,63,63	0
57	MG	2A	3780	1/1	0.88	0.09	75,75,75,75	0
57	MG	2a	1776	1/1	0.88	0.14	68,68,68,68	0
57	MG	2A	3494	1/1	0.88	0.17	63,63,63,63	0
57	MG	2e	201	1/1	0.88	0.12	71,71,71,71	0
57	MG	2A	3500	1/1	0.88	0.14	44,44,44,44	0
57	MG	1a	1739	1/1	0.88	0.24	60,60,60,60	0
57	MG	2A	3800	1/1	0.88	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	3506	1/1	0.88	0.26	59,59,59,59	0
57	MG	2A	3282	1/1	0.88	0.29	69,69,69,69	0
57	MG	1B	223	1/1	0.88	0.13	53,53,53,53	0
57	MG	2v	101	1/1	0.88	0.33	63,63,63,63	0
57	MG	2A	3516	1/1	0.88	0.12	42,42,42,42	0
57	MG	1A	3664	1/1	0.88	0.19	56,56,56,56	0
57	MG	1A	4004	1/1	0.88	0.12	42,42,42,42	0
57	MG	2A	3617	1/1	0.89	0.10	59,59,59,59	0
57	MG	1A	3250	1/1	0.89	0.23	57,57,57,57	0
57	MG	1N	202	1/1	0.89	0.10	47,47,47,47	0
57	MG	1N	206	1/1	0.89	0.14	54,54,54,54	0
57	MG	1A	3024	1/1	0.89	0.30	56,56,56,56	0
57	MG	1A	3514	1/1	0.89	0.39	44,44,44,44	0
57	MG	1A	3091	1/1	0.89	0.12	48,48,48,48	0
57	MG	2A	3214	1/1	0.89	0.12	60,60,60,60	0
57	MG	2E	303	1/1	0.89	0.22	62,62,62,62	0
57	MG	2A	3215	1/1	0.89	0.10	59,59,59,59	0
57	MG	1a	1811	1/1	0.89	0.15	72,72,72,72	0
57	MG	2F	302	1/1	0.89	0.19	49,49,49,49	0
57	MG	2F	303	1/1	0.89	0.14	44,44,44,44	0
57	MG	1A	3645	1/1	0.89	0.08	23,23,23,23	0
57	MG	1A	3096	1/1	0.89	0.26	54,54,54,54	0
57	MG	1A	4022	1/1	0.89	0.18	63,63,63,63	0
57	MG	1A	3518	1/1	0.89	0.26	49,49,49,49	0
57	MG	2X	101	1/1	0.89	0.09	50,50,50,50	0
57	MG	1a	1820	1/1	0.89	0.17	66,66,66,66	0
57	MG	1A	3798	1/1	0.89	0.18	55,55,55,55	0
57	MG	1A	3923	1/1	0.89	0.13	61,61,61,61	0
57	MG	1a	1694	1/1	0.89	0.16	62,62,62,62	0
57	MG	1A	4035	1/1	0.89	0.09	39,39,39,39	0
57	MG	2A	3652	1/1	0.89	0.13	49,49,49,49	0
57	MG	1A	3306	1/1	0.89	0.20	45,45,45,45	0
57	MG	2A	3656	1/1	0.89	0.23	62,62,62,62	0
57	MG	1v	101	1/1	0.89	0.10	75,75,75,75	0
57	MG	2A	3391	1/1	0.89	0.30	71,71,71,71	0
57	MG	1A	3430	1/1	0.89	0.28	59,59,59,59	0
57	MG	2A	3663	1/1	0.89	0.10	68,68,68,68	0
57	MG	2a	1608	1/1	0.89	0.24	52,52,52,52	0
57	MG	1a	1704	1/1	0.89	0.16	62,62,62,62	0
57	MG	1A	4040	1/1	0.89	0.12	33,33,33,33	0
57	MG	2a	1615	1/1	0.89	0.14	58,58,58,58	0
57	MG	2A	3410	1/1	0.89	0.36	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3431	1/1	0.89	0.24	47,47,47,47	0
57	MG	1A	3810	1/1	0.89	0.09	36,36,36,36	0
57	MG	2a	1620	1/1	0.89	0.19	47,47,47,47	0
57	MG	2a	1621	1/1	0.89	0.38	66,66,66,66	0
57	MG	2A	3416	1/1	0.89	0.23	60,60,60,60	0
57	MG	2A	3680	1/1	0.89	0.19	48,48,48,48	0
57	MG	1A	3441	1/1	0.89	0.13	58,58,58,58	0
57	MG	1A	3675	1/1	0.89	0.13	28,28,28,28	0
57	MG	1a	1716	1/1	0.89	0.23	67,67,67,67	0
57	MG	1A	3551	1/1	0.89	0.28	62,62,62,62	0
57	MG	2a	1642	1/1	0.89	0.23	56,56,56,56	0
57	MG	1a	1609	1/1	0.89	0.20	71,71,71,71	0
57	MG	2A	3045	1/1	0.89	0.29	59,59,59,59	0
57	MG	1A	3682	1/1	0.89	0.12	30,30,30,30	0
57	MG	2A	3268	1/1	0.89	0.13	61,61,61,61	0
57	MG	2A	3078	1/1	0.89	0.16	54,54,54,54	0
57	MG	1A	3959	1/1	0.89	0.11	76,76,76,76	0
57	MG	1A	3386	1/1	0.89	0.46	48,48,48,48	0
57	MG	1A	3309	1/1	0.89	0.30	55,55,55,55	0
57	MG	2a	1657	1/1	0.89	0.26	59,59,59,59	0
57	MG	1A	3690	1/1	0.89	0.10	31,31,31,31	0
57	MG	2a	1659	1/1	0.89	0.28	62,62,62,62	0
57	MG	2A	3454	1/1	0.89	0.19	63,63,63,63	0
57	MG	1a	1731	1/1	0.89	0.30	64,64,64,64	0
57	MG	2A	3093	1/1	0.89	0.14	69,69,69,69	0
57	MG	1A	3311	1/1	0.89	0.12	59,59,59,59	0
57	MG	1A	3451	1/1	0.89	0.18	62,62,62,62	0
57	MG	1A	3453	1/1	0.89	0.09	59,59,59,59	0
57	MG	1A	4084	1/1	0.89	0.23	63,63,63,63	0
57	MG	2a	1674	1/1	0.89	0.17	75,75,75,75	0
57	MG	2A	3723	1/1	0.89	0.15	68,68,68,68	0
57	MG	2A	3724	1/1	0.89	0.11	62,62,62,62	0
57	MG	1A	3397	1/1	0.89	0.12	43,43,43,43	0
57	MG	2A	3116	1/1	0.89	0.13	62,62,62,62	0
57	MG	2A	3118	1/1	0.89	0.19	51,51,51,51	0
57	MG	2A	3730	1/1	0.89	0.18	46,46,46,46	0
57	MG	1A	4086	1/1	0.89	0.18	70,70,70,70	0
57	MG	1a	1740	1/1	0.89	0.23	71,71,71,71	0
57	MG	2a	1698	1/1	0.89	0.25	72,72,72,72	0
57	MG	2A	3492	1/1	0.89	0.21	57,57,57,57	0
57	MG	2A	3737	1/1	0.89	0.10	62,62,62,62	0
57	MG	1a	1742	1/1	0.89	0.15	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3747	1/1	0.89	0.12	50,50,50,50	0
57	MG	1A	3172	1/1	0.89	0.13	49,49,49,49	0
57	MG	2a	1721	1/1	0.89	0.16	59,59,59,59	0
57	MG	1A	3051	1/1	0.89	0.10	28,28,28,28	0
57	MG	2A	3140	1/1	0.89	0.12	46,46,46,46	0
57	MG	1A	3718	1/1	0.89	0.15	70,70,70,70	0
57	MG	1A	3851	1/1	0.89	0.14	42,42,42,42	0
57	MG	2A	3759	1/1	0.89	0.08	37,37,37,37	0
57	MG	1B	210	1/1	0.89	0.11	46,46,46,46	0
57	MG	2A	3162	1/1	0.89	0.28	57,57,57,57	0
57	MG	1A	3462	1/1	0.89	0.31	72,72,72,72	0
57	MG	2A	3311	1/1	0.89	0.20	57,57,57,57	0
57	MG	1A	3723	1/1	0.89	0.13	51,51,51,51	0
57	MG	2A	3773	1/1	0.89	0.09	62,62,62,62	0
57	MG	1A	3116	1/1	0.89	0.39	38,38,38,38	0
57	MG	1a	1762	1/1	0.89	0.14	70,70,70,70	0
57	MG	1A	3861	1/1	0.89	0.11	68,68,68,68	0
57	MG	2a	1748	1/1	0.89	0.15	65,65,65,65	0
57	MG	1A	3411	1/1	0.89	0.14	55,55,55,55	0
57	MG	1B	234	1/1	0.89	0.10	67,67,67,67	0
57	MG	1A	3736	1/1	0.89	0.11	43,43,43,43	0
57	MG	2A	3551	1/1	0.89	0.10	57,57,57,57	0
57	MG	1a	1661	1/1	0.89	0.32	62,62,62,62	0
57	MG	2A	3324	1/1	0.89	0.24	54,54,54,54	0
57	MG	1A	3495	1/1	0.89	0.18	57,57,57,57	0
57	MG	2A	3818	1/1	0.89	0.09	57,57,57,57	0
57	MG	2a	1762	1/1	0.89	0.10	71,71,71,71	0
57	MG	1A	3744	1/1	0.89	0.08	17,17,17,17	0
57	MG	2A	3566	1/1	0.89	0.10	65,65,65,65	0
57	MG	2A	3567	1/1	0.89	0.25	62,62,62,62	0
57	MG	1A	3995	1/1	0.89	0.09	64,64,64,64	0
57	MG	2A	3578	1/1	0.89	0.13	60,60,60,60	0
57	MG	1A	3879	1/1	0.89	0.14	35,35,35,35	0
57	MG	2A	3582	1/1	0.89	0.11	69,69,69,69	0
57	MG	1A	3617	1/1	0.89	0.12	54,54,54,54	0
57	MG	1A	3889	1/1	0.89	0.08	42,42,42,42	0
57	MG	1F	311	1/1	0.89	0.11	47,47,47,47	0
57	MG	2A	3333	1/1	0.89	0.09	64,64,64,64	0
57	MG	2A	3592	1/1	0.89	0.15	66,66,66,66	0
57	MG	2A	3335	1/1	0.89	0.12	61,61,61,61	0
57	MG	2g	3101	1/1	0.89	0.18	76,76,76,76	0
57	MG	2A	3337	1/1	0.89	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	3752	1/1	0.89	0.11	28,28,28,28	0
57	MG	1a	1676	1/1	0.89	0.19	72,72,72,72	0
57	MG	2A	3610	1/1	0.89	0.15	44,44,44,44	0
57	MG	1A	3270	1/1	0.89	0.28	53,53,53,53	0
57	MG	2x	101	1/1	0.89	0.15	77,77,77,77	0
57	MG	2A	3204	1/1	0.89	0.24	57,57,57,57	0
57	MG	2A	3349	1/1	0.89	0.18	67,67,67,67	0
57	MG	2A	3350	1/1	0.89	0.18	62,62,62,62	0
57	MG	2B	211	1/1	0.90	0.18	60,60,60,60	0
57	MG	2A	3194	1/1	0.90	0.16	51,51,51,51	0
57	MG	1A	3952	1/1	0.90	0.14	38,38,38,38	0
57	MG	1A	3052	1/1	0.90	0.16	32,32,32,32	0
57	MG	1A	3667	1/1	0.90	0.09	60,60,60,60	0
57	MG	1a	1789	1/1	0.90	0.20	71,71,71,71	0
57	MG	1A	3324	1/1	0.90	0.10	49,49,49,49	0
57	MG	2A	3618	1/1	0.90	0.23	71,71,71,71	0
57	MG	1A	3171	1/1	0.90	0.36	42,42,42,42	0
57	MG	1A	3054	1/1	0.90	0.12	52,52,52,52	0
57	MG	1A	3815	1/1	0.90	0.13	50,50,50,50	0
57	MG	2A	3623	1/1	0.90	0.28	54,54,54,54	0
57	MG	2A	3629	1/1	0.90	0.25	68,68,68,68	0
57	MG	2A	3361	1/1	0.90	0.12	75,75,75,75	0
57	MG	2A	3631	1/1	0.90	0.18	64,64,64,64	0
57	MG	1A	3550	1/1	0.90	0.21	43,43,43,43	0
57	MG	2A	3210	1/1	0.90	0.09	54,54,54,54	0
57	MG	2G	201	1/1	0.90	0.11	60,60,60,60	0
57	MG	2A	3366	1/1	0.90	0.23	59,59,59,59	0
57	MG	1B	212	1/1	0.90	0.10	46,46,46,46	0
57	MG	1A	3818	1/1	0.90	0.09	38,38,38,38	0
57	MG	1A	3448	1/1	0.90	0.44	46,46,46,46	0
57	MG	2W	202	1/1	0.90	0.13	54,54,54,54	0
57	MG	1A	3564	1/1	0.90	0.19	67,67,67,67	0
57	MG	1B	225	1/1	0.90	0.10	52,52,52,52	0
57	MG	1A	3103	1/1	0.90	0.12	32,32,32,32	0
57	MG	1a	1812	1/1	0.90	0.14	55,55,55,55	0
57	MG	2A	3645	1/1	0.90	0.33	40,40,40,40	0
57	MG	1A	3069	1/1	0.90	0.07	46,46,46,46	0
57	MG	25	106	1/1	0.90	0.12	51,51,51,51	0
57	MG	2A	3230	1/1	0.90	0.40	68,68,68,68	0
57	MG	1A	3333	1/1	0.90	0.12	46,46,46,46	0
57	MG	2A	3388	1/1	0.90	0.17	72,72,72,72	0
57	MG	2A	3233	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	3830	1/1	0.90	0.15	50,50,50,50	0
57	MG	1A	3265	1/1	0.90	0.26	46,46,46,46	0
57	MG	2A	3657	1/1	0.90	0.14	53,53,53,53	0
57	MG	1A	3118	1/1	0.90	0.27	35,35,35,35	0
57	MG	2A	3393	1/1	0.90	0.24	63,63,63,63	0
57	MG	2a	1612	1/1	0.90	0.18	62,62,62,62	0
57	MG	2A	3394	1/1	0.90	0.11	57,57,57,57	0
57	MG	1A	3983	1/1	0.90	0.09	47,47,47,47	0
57	MG	2A	3408	1/1	0.90	0.15	54,54,54,54	0
57	MG	1A	3833	1/1	0.90	0.22	47,47,47,47	0
57	MG	1A	3581	1/1	0.90	0.20	44,44,44,44	0
57	MG	2A	3672	1/1	0.90	0.12	33,33,33,33	0
57	MG	1A	3703	1/1	0.90	0.15	69,69,69,69	0
57	MG	2A	3412	1/1	0.90	0.37	58,58,58,58	0
57	MG	2a	1625	1/1	0.90	0.25	67,67,67,67	0
57	MG	1m	201	1/1	0.90	0.08	68,68,68,68	0
57	MG	1A	3583	1/1	0.90	0.09	47,47,47,47	0
57	MG	1A	3990	1/1	0.90	0.09	16,16,16,16	0
57	MG	1A	3848	1/1	0.90	0.07	22,22,22,22	0
57	MG	1A	3992	1/1	0.90	0.09	20,20,20,20	0
57	MG	2a	1640	1/1	0.90	0.22	49,49,49,49	0
57	MG	1N	201	1/1	0.90	0.38	43,43,43,43	0
57	MG	1a	1693	1/1	0.90	0.10	76,76,76,76	0
57	MG	1A	3124	1/1	0.90	0.16	43,43,43,43	0
57	MG	1N	205	1/1	0.90	0.18	56,56,56,56	0
57	MG	1A	3709	1/1	0.90	0.15	49,49,49,49	0
57	MG	2A	3697	1/1	0.90	0.10	46,46,46,46	0
57	MG	1A	3714	1/1	0.90	0.13	59,59,59,59	0
57	MG	1A	3272	1/1	0.90	0.14	46,46,46,46	0
57	MG	1Q	205	1/1	0.90	0.24	67,67,67,67	0
57	MG	1A	3719	1/1	0.90	0.14	58,58,58,58	0
57	MG	1A	3464	1/1	0.90	0.30	58,58,58,58	0
57	MG	2A	3061	1/1	0.90	0.08	66,66,66,66	0
57	MG	2A	3076	1/1	0.90	0.19	56,56,56,56	0
57	MG	1A	3408	1/1	0.90	0.18	50,50,50,50	0
57	MG	2a	1665	1/1	0.90	0.29	69,69,69,69	0
57	MG	2A	3082	1/1	0.90	0.16	62,62,62,62	0
57	MG	1A	3725	1/1	0.90	0.12	50,50,50,50	0
57	MG	1A	3727	1/1	0.90	0.18	48,48,48,48	0
57	MG	1a	1717	1/1	0.90	0.10	69,69,69,69	0
57	MG	1A	4016	1/1	0.90	0.11	61,61,61,61	0
57	MG	1A	3134	1/1	0.90	0.13	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3224	1/1	0.90	0.19	53,53,53,53	0
57	MG	2A	3483	1/1	0.90	0.15	74,74,74,74	0
57	MG	1A	3735	1/1	0.90	0.13	41,41,41,41	0
57	MG	1A	3417	1/1	0.90	0.17	62,62,62,62	0
57	MG	2A	3491	1/1	0.90	0.14	54,54,54,54	0
57	MG	1A	3893	1/1	0.90	0.10	49,49,49,49	0
57	MG	2A	3735	1/1	0.90	0.11	73,73,73,73	0
57	MG	2a	1692	1/1	0.90	0.17	53,53,53,53	0
57	MG	1A	4026	1/1	0.90	0.10	48,48,48,48	0
57	MG	2A	3107	1/1	0.90	0.27	56,56,56,56	0
57	MG	2a	1704	1/1	0.90	0.27	70,70,70,70	0
57	MG	1A	3504	1/1	0.90	0.12	57,57,57,57	0
57	MG	1A	3743	1/1	0.90	0.11	50,50,50,50	0
57	MG	1A	3355	1/1	0.90	0.10	49,49,49,49	0
57	MG	2a	1713	1/1	0.90	0.12	55,55,55,55	0
57	MG	1A	4036	1/1	0.90	0.08	32,32,32,32	0
57	MG	2A	3753	1/1	0.90	0.15	53,53,53,53	0
57	MG	1A	3745	1/1	0.90	0.13	47,47,47,47	0
57	MG	2A	3517	1/1	0.90	0.11	40,40,40,40	0
57	MG	2a	1725	1/1	0.90	0.34	70,70,70,70	0
57	MG	2a	1727	1/1	0.90	0.14	60,60,60,60	0
57	MG	1A	3625	1/1	0.90	0.08	15,15,15,15	0
57	MG	2a	1730	1/1	0.90	0.26	69,69,69,69	0
57	MG	2A	3525	1/1	0.90	0.21	51,51,51,51	0
57	MG	1a	1611	1/1	0.90	0.17	73,73,73,73	0
57	MG	2A	3308	1/1	0.90	0.28	62,62,62,62	0
57	MG	1A	3029	1/1	0.90	0.21	52,52,52,52	0
57	MG	2A	3769	1/1	0.90	0.20	63,63,63,63	0
57	MG	1A	3508	1/1	0.90	0.15	58,58,58,58	0
57	MG	2A	3771	1/1	0.90	0.10	56,56,56,56	0
57	MG	1a	1617	1/1	0.90	0.09	73,73,73,73	0
57	MG	2A	3313	1/1	0.90	0.29	68,68,68,68	0
57	MG	2A	3147	1/1	0.90	0.15	54,54,54,54	0
57	MG	1A	3630	1/1	0.90	0.07	32,32,32,32	0
57	MG	1A	3512	1/1	0.90	0.31	48,48,48,48	0
57	MG	2A	3787	1/1	0.90	0.10	57,57,57,57	0
57	MG	2A	3317	1/1	0.90	0.11	61,61,61,61	0
57	MG	2A	3160	1/1	0.90	0.12	45,45,45,45	0
57	MG	2A	3794	1/1	0.90	0.13	36,36,36,36	0
57	MG	1A	3783	1/1	0.90	0.11	35,35,35,35	0
57	MG	1A	3154	1/1	0.90	0.19	50,50,50,50	0
57	MG	1a	1630	1/1	0.90	0.21	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	3642	1/1	0.90	0.16	51,51,51,51	0
57	MG	1A	3165	1/1	0.90	0.09	41,41,41,41	0
57	MG	2A	3572	1/1	0.90	0.08	32,32,32,32	0
57	MG	2a	1764	1/1	0.90	0.24	75,75,75,75	0
57	MG	2A	3819	1/1	0.90	0.14	68,68,68,68	0
57	MG	1A	3247	1/1	0.90	0.12	63,63,63,63	0
57	MG	2A	3576	1/1	0.90	0.13	59,59,59,59	0
57	MG	2A	3827	1/1	0.90	0.11	64,64,64,64	0
57	MG	2A	3829	1/1	0.90	0.10	60,60,60,60	0
57	MG	2A	3173	1/1	0.90	0.17	72,72,72,72	0
57	MG	1A	3936	1/1	0.90	0.11	62,62,62,62	0
57	MG	1A	3049	1/1	0.90	0.07	20,20,20,20	0
57	MG	2a	1774	1/1	0.90	0.28	63,63,63,63	0
57	MG	2A	3584	1/1	0.90	0.07	34,34,34,34	0
57	MG	1a	1767	1/1	0.90	0.07	60,60,60,60	0
57	MG	1a	1769	1/1	0.90	0.11	78,78,78,78	0
57	MG	1A	3529	1/1	0.90	0.26	59,59,59,59	0
57	MG	1A	4074	1/1	0.90	0.17	38,38,38,38	0
57	MG	1A	4078	1/1	0.90	0.15	33,33,33,33	0
57	MG	2A	3338	1/1	0.90	0.26	60,60,60,60	0
57	MG	2A	3596	1/1	0.90	0.21	62,62,62,62	0
57	MG	2B	202	1/1	0.90	0.10	66,66,66,66	0
57	MG	1A	3662	1/1	0.90	0.09	29,29,29,29	0
57	MG	1A	3803	1/1	0.90	0.08	44,44,44,44	0
57	MG	1A	4083	1/1	0.90	0.16	48,48,48,48	0
57	MG	2x	103	1/1	0.90	0.15	35,35,35,35	0
57	MG	2A	3605	1/1	0.90	0.19	42,42,42,42	0
57	MG	2A	3608	1/1	0.90	0.13	41,41,41,41	0
57	MG	2B	208	1/1	0.90	0.18	57,57,57,57	0
57	MG	1A	3554	1/1	0.91	0.22	44,44,44,44	0
57	MG	2A	3226	1/1	0.91	0.27	62,62,62,62	0
57	MG	1A	4014	1/1	0.91	0.07	63,63,63,63	0
57	MG	1a	1773	1/1	0.91	0.10	58,58,58,58	0
57	MG	2A	3231	1/1	0.91	0.16	51,51,51,51	0
57	MG	1A	3063	1/1	0.91	0.16	52,52,52,52	0
57	MG	1A	3702	1/1	0.91	0.12	36,36,36,36	0
57	MG	1a	1776	1/1	0.91	0.22	71,71,71,71	0
57	MG	2A	3832	1/1	0.91	0.11	48,48,48,48	0
57	MG	2A	3834	1/1	0.91	0.13	46,46,46,46	0
57	MG	2A	3237	1/1	0.91	0.21	63,63,63,63	0
57	MG	1A	3317	1/1	0.91	0.13	55,55,55,55	0
57	MG	2A	3507	1/1	0.91	0.20	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	3705	1/1	0.91	0.15	53,53,53,53	0
57	MG	2A	3241	1/1	0.91	0.19	68,68,68,68	0
57	MG	1A	3227	1/1	0.91	0.11	48,48,48,48	0
57	MG	1A	3572	1/1	0.91	0.16	70,70,70,70	0
57	MG	1A	3575	1/1	0.91	0.17	55,55,55,55	0
57	MG	1A	3713	1/1	0.91	0.09	62,62,62,62	0
57	MG	1A	3321	1/1	0.91	0.10	56,56,56,56	0
57	MG	1A	3173	1/1	0.91	0.13	39,39,39,39	0
57	MG	2A	3530	1/1	0.91	0.10	48,48,48,48	0
57	MG	1A	3881	1/1	0.91	0.11	38,38,38,38	0
57	MG	2A	3533	1/1	0.91	0.18	65,65,65,65	0
57	MG	1a	1623	1/1	0.91	0.28	54,54,54,54	0
57	MG	2A	3536	1/1	0.91	0.15	55,55,55,55	0
57	MG	1A	3370	1/1	0.91	0.16	50,50,50,50	0
57	MG	1A	3886	1/1	0.91	0.10	39,39,39,39	0
57	MG	1A	3268	1/1	0.91	0.18	57,57,57,57	0
57	MG	1a	1629	1/1	0.91	0.23	60,60,60,60	0
57	MG	1a	1799	1/1	0.91	0.19	56,56,56,56	0
57	MG	1a	1800	1/1	0.91	0.11	66,66,66,66	0
57	MG	1A	4039	1/1	0.91	0.08	51,51,51,51	0
57	MG	1a	1634	1/1	0.91	0.27	65,65,65,65	0
57	MG	1A	3374	1/1	0.91	0.11	54,54,54,54	0
57	MG	1A	4043	1/1	0.91	0.30	54,54,54,54	0
57	MG	1a	1638	1/1	0.91	0.23	55,55,55,55	0
57	MG	1a	1639	1/1	0.91	0.22	81,81,81,81	0
57	MG	1A	3585	1/1	0.91	0.26	55,55,55,55	0
57	MG	1a	1641	1/1	0.91	0.12	59,59,59,59	0
57	MG	1A	3587	1/1	0.91	0.11	41,41,41,41	0
57	MG	1A	3589	1/1	0.91	0.12	26,26,26,26	0
57	MG	2A	3580	1/1	0.91	0.10	51,51,51,51	0
57	MG	2E	307	1/1	0.91	0.15	52,52,52,52	0
57	MG	1A	3269	1/1	0.91	0.14	55,55,55,55	0
57	MG	1A	3015	1/1	0.91	0.18	37,37,37,37	0
57	MG	2F	306	1/1	0.91	0.08	44,44,44,44	0
57	MG	1A	3597	1/1	0.91	0.12	56,56,56,56	0
57	MG	2A	3283	1/1	0.91	0.13	67,67,67,67	0
57	MG	2R	201	1/1	0.91	0.14	54,54,54,54	0
57	MG	1f	201	1/1	0.91	0.21	58,58,58,58	0
57	MG	2T	3502	1/1	0.91	0.15	64,64,64,64	0
57	MG	2U	201	1/1	0.91	0.38	62,62,62,62	0
57	MG	2U	202	1/1	0.91	0.15	54,54,54,54	0
57	MG	2A	3287	1/1	0.91	0.31	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3004	1/1	0.91	0.09	32,32,32,32	0
57	MG	1A	3742	1/1	0.91	0.14	46,46,46,46	0
57	MG	1A	3387	1/1	0.91	0.19	39,39,39,39	0
57	MG	2Z	301	1/1	0.91	0.12	60,60,60,60	0
57	MG	1A	4069	1/1	0.91	0.09	22,22,22,22	0
57	MG	1A	3470	1/1	0.91	0.15	49,49,49,49	0
57	MG	1A	3614	1/1	0.91	0.09	19,19,19,19	0
57	MG	1x	105	1/1	0.91	0.09	69,69,69,69	0
57	MG	1A	3747	1/1	0.91	0.13	22,22,22,22	0
57	MG	1A	4077	1/1	0.91	0.07	44,44,44,44	0
57	MG	1A	3474	1/1	0.91	0.10	57,57,57,57	0
57	MG	2A	3005	1/1	0.91	0.33	67,67,67,67	0
57	MG	2A	3304	1/1	0.91	0.14	66,66,66,66	0
57	MG	28	103	1/1	0.91	0.13	52,52,52,52	0
57	MG	1A	3331	1/1	0.91	0.18	55,55,55,55	0
57	MG	2A	3017	1/1	0.91	0.25	58,58,58,58	0
57	MG	2A	3019	1/1	0.91	0.13	59,59,59,59	0
57	MG	2A	3309	1/1	0.91	0.28	67,67,67,67	0
57	MG	1a	1663	1/1	0.91	0.15	66,66,66,66	0
57	MG	1A	3932	1/1	0.91	0.09	50,50,50,50	0
57	MG	1A	3332	1/1	0.91	0.17	56,56,56,56	0
57	MG	1A	3937	1/1	0.91	0.10	47,47,47,47	0
57	MG	2A	3626	1/1	0.91	0.15	55,55,55,55	0
57	MG	1A	3757	1/1	0.91	0.09	59,59,59,59	0
57	MG	2A	3044	1/1	0.91	0.09	45,45,45,45	0
57	MG	1A	3942	1/1	0.91	0.11	46,46,46,46	0
57	MG	1A	3762	1/1	0.91	0.07	45,45,45,45	0
57	MG	2A	3053	1/1	0.91	0.17	63,63,63,63	0
57	MG	2A	3057	1/1	0.91	0.15	63,63,63,63	0
57	MG	1A	3768	1/1	0.91	0.11	25,25,25,25	0
57	MG	2A	3064	1/1	0.91	0.40	55,55,55,55	0
57	MG	2a	1629	1/1	0.91	0.13	47,47,47,47	0
57	MG	2A	3069	1/1	0.91	0.18	49,49,49,49	0
57	MG	1a	1675	1/1	0.91	0.18	65,65,65,65	0
57	MG	1A	3619	1/1	0.91	0.08	29,29,29,29	0
57	MG	2A	3081	1/1	0.91	0.14	48,48,48,48	0
57	MG	1A	3950	1/1	0.91	0.10	35,35,35,35	0
57	MG	1A	3491	1/1	0.91	0.17	55,55,55,55	0
57	MG	1A	3953	1/1	0.91	0.08	41,41,41,41	0
57	MG	1B	218	1/1	0.91	0.21	51,51,51,51	0
57	MG	1A	3624	1/1	0.91	0.09	21,21,21,21	0
57	MG	1A	3494	1/1	0.91	0.21	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	2a	1649	1/1	0.91	0.39	60,60,60,60	0
57	MG	2A	3091	1/1	0.91	0.13	45,45,45,45	0
57	MG	1A	3394	1/1	0.91	0.17	45,45,45,45	0
57	MG	2a	1652	1/1	0.91	0.12	57,57,57,57	0
57	MG	2A	3654	1/1	0.91	0.15	49,49,49,49	0
57	MG	2a	1655	1/1	0.91	0.13	56,56,56,56	0
57	MG	1A	3395	1/1	0.91	0.21	51,51,51,51	0
57	MG	1A	3628	1/1	0.91	0.11	24,24,24,24	0
57	MG	2A	3098	1/1	0.91	0.21	68,68,68,68	0
57	MG	2A	3659	1/1	0.91	0.10	45,45,45,45	0
57	MG	2A	3347	1/1	0.91	0.10	64,64,64,64	0
57	MG	2a	1661	1/1	0.91	0.28	62,62,62,62	0
57	MG	1A	3964	1/1	0.91	0.10	62,62,62,62	0
57	MG	2a	1664	1/1	0.91	0.19	53,53,53,53	0
57	MG	2A	3102	1/1	0.91	0.24	71,71,71,71	0
57	MG	1a	1689	1/1	0.91	0.09	75,75,75,75	0
57	MG	2A	3106	1/1	0.91	0.19	63,63,63,63	0
57	MG	1A	3501	1/1	0.91	0.14	53,53,53,53	0
57	MG	1A	3089	1/1	0.91	0.11	54,54,54,54	0
57	MG	1D	309	1/1	0.91	0.18	49,49,49,49	0
57	MG	2A	3675	1/1	0.91	0.22	60,60,60,60	0
57	MG	1A	3168	1/1	0.91	0.11	33,33,33,33	0
57	MG	1A	3640	1/1	0.91	0.16	43,43,43,43	0
57	MG	2A	3122	1/1	0.91	0.14	56,56,56,56	0
57	MG	2A	3362	1/1	0.91	0.12	60,60,60,60	0
57	MG	1A	3336	1/1	0.91	0.23	61,61,61,61	0
57	MG	2A	3683	1/1	0.91	0.21	62,62,62,62	0
57	MG	2A	3684	1/1	0.91	0.13	60,60,60,60	0
57	MG	2a	1689	1/1	0.91	0.20	54,54,54,54	0
57	MG	1E	306	1/1	0.91	0.15	61,61,61,61	0
57	MG	2A	3125	1/1	0.91	0.31	64,64,64,64	0
57	MG	1A	3337	1/1	0.91	0.13	48,48,48,48	0
57	MG	1A	3647	1/1	0.91	0.07	24,24,24,24	0
57	MG	2A	3137	1/1	0.91	0.22	53,53,53,53	0
57	MG	2A	3695	1/1	0.91	0.14	54,54,54,54	0
57	MG	2a	1710	1/1	0.91	0.19	64,64,64,64	0
57	MG	1F	301	1/1	0.91	0.19	43,43,43,43	0
57	MG	1A	3001	1/1	0.91	0.11	38,38,38,38	0
57	MG	2A	3376	1/1	0.91	0.11	57,57,57,57	0
57	MG	2a	1719	1/1	0.91	0.17	68,68,68,68	0
57	MG	2A	3700	1/1	0.91	0.12	65,65,65,65	0
57	MG	1a	1707	1/1	0.91	0.23	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	3703	1/1	0.91	0.24	66,66,66,66	0
57	MG	2a	1723	1/1	0.91	0.16	62,62,62,62	0
57	MG	1A	3978	1/1	0.91	0.08	28,28,28,28	0
57	MG	2A	3149	1/1	0.91	0.11	60,60,60,60	0
57	MG	2A	3706	1/1	0.91	0.08	71,71,71,71	0
57	MG	1F	313	1/1	0.91	0.16	41,41,41,41	0
57	MG	2A	3385	1/1	0.91	0.13	57,57,57,57	0
57	MG	1a	1710	1/1	0.91	0.12	52,52,52,52	0
57	MG	2A	3161	1/1	0.91	0.36	64,64,64,64	0
57	MG	1a	1713	1/1	0.91	0.11	60,60,60,60	0
57	MG	1F	314	1/1	0.91	0.14	52,52,52,52	0
57	MG	1A	3297	1/1	0.91	0.13	51,51,51,51	0
57	MG	2a	1741	1/1	0.91	0.15	69,69,69,69	0
57	MG	1G	201	1/1	0.91	0.14	47,47,47,47	0
57	MG	2A	3168	1/1	0.91	0.11	53,53,53,53	0
57	MG	1A	3348	1/1	0.91	0.26	65,65,65,65	0
57	MG	2A	3396	1/1	0.91	0.20	52,52,52,52	0
57	MG	1A	3299	1/1	0.91	0.25	46,46,46,46	0
57	MG	2A	3403	1/1	0.91	0.18	53,53,53,53	0
57	MG	2A	3728	1/1	0.91	0.20	67,67,67,67	0
57	MG	1I	201	1/1	0.91	0.12	67,67,67,67	0
57	MG	1A	3259	1/1	0.91	0.09	36,36,36,36	0
57	MG	2a	1752	1/1	0.91	0.13	55,55,55,55	0
57	MG	1a	1724	1/1	0.91	0.10	52,52,52,52	0
57	MG	1A	3522	1/1	0.91	0.15	47,47,47,47	0
57	MG	1a	1728	1/1	0.91	0.15	53,53,53,53	0
57	MG	1A	3523	1/1	0.91	0.25	62,62,62,62	0
57	MG	2A	3738	1/1	0.91	0.08	59,59,59,59	0
57	MG	2A	3188	1/1	0.91	0.16	71,71,71,71	0
57	MG	1A	3526	1/1	0.91	0.24	49,49,49,49	0
57	MG	1O	201	1/1	0.91	0.15	59,59,59,59	0
57	MG	2A	3423	1/1	0.91	0.29	50,50,50,50	0
57	MG	1A	3988	1/1	0.91	0.09	41,41,41,41	0
57	MG	2a	1767	1/1	0.91	0.24	61,61,61,61	0
57	MG	1A	3214	1/1	0.91	0.09	42,42,42,42	0
57	MG	1A	3826	1/1	0.91	0.09	51,51,51,51	0
57	MG	1A	3352	1/1	0.91	0.27	43,43,43,43	0
57	MG	1S	203	1/1	0.91	0.09	65,65,65,65	0
57	MG	2A	3436	1/1	0.91	0.31	53,53,53,53	0
57	MG	1A	3681	1/1	0.91	0.09	35,35,35,35	0
57	MG	1A	3536	1/1	0.91	0.19	54,54,54,54	0
57	MG	2a	1775	1/1	0.91	0.13	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3353	1/1	0.91	0.11	59,59,59,59	0
57	MG	1V	202	1/1	0.91	0.38	38,38,38,38	0
57	MG	1A	3999	1/1	0.91	0.09	28,28,28,28	0
57	MG	1W	201	1/1	0.91	0.27	55,55,55,55	0
57	MG	1A	3308	1/1	0.91	0.14	51,51,51,51	0
57	MG	1A	3356	1/1	0.91	0.13	61,61,61,61	0
57	MG	1A	3691	1/1	0.91	0.16	31,31,31,31	0
57	MG	15	108	1/1	0.91	0.07	40,40,40,40	0
57	MG	2k	201	1/1	0.91	0.13	61,61,61,61	0
57	MG	2A	3467	1/1	0.91	0.13	47,47,47,47	0
57	MG	2A	3788	1/1	0.91	0.09	33,33,33,33	0
57	MG	2t	201	1/1	0.91	0.20	51,51,51,51	0
57	MG	1A	3027	1/1	0.91	0.21	69,69,69,69	0
57	MG	17	106	1/1	0.91	0.09	43,43,43,43	0
57	MG	18	102	1/1	0.91	0.17	49,49,49,49	0
57	MG	1a	1765	1/1	0.91	0.08	62,62,62,62	0
57	MG	2x	105	1/1	0.91	0.11	64,64,64,64	0
57	MG	1A	3432	1/1	0.91	0.14	43,43,43,43	0
57	MG	2A	3481	1/1	0.91	0.14	32,32,32,32	0
57	MG	2A	3285	1/1	0.92	0.15	51,51,51,51	0
57	MG	2A	3058	1/1	0.92	0.20	48,48,48,48	0
57	MG	1A	3420	1/1	0.92	0.12	55,55,55,55	0
57	MG	2A	3550	1/1	0.92	0.09	44,44,44,44	0
57	MG	1A	3251	1/1	0.92	0.29	40,40,40,40	0
57	MG	2A	3289	1/1	0.92	0.21	68,68,68,68	0
57	MG	2A	3558	1/1	0.92	0.22	53,53,53,53	0
57	MG	2A	3065	1/1	0.92	0.27	65,65,65,65	0
57	MG	2A	3068	1/1	0.92	0.25	50,50,50,50	0
57	MG	1A	4027	1/1	0.92	0.09	41,41,41,41	0
57	MG	2A	3070	1/1	0.92	0.07	41,41,41,41	0
57	MG	1A	3252	1/1	0.92	0.08	67,67,67,67	0
57	MG	2A	3570	1/1	0.92	0.12	49,49,49,49	0
57	MG	2A	3297	1/1	0.92	0.09	77,77,77,77	0
57	MG	1A	3519	1/1	0.92	0.26	57,57,57,57	0
57	MG	2A	3079	1/1	0.92	0.16	52,52,52,52	0
57	MG	1A	3521	1/1	0.92	0.27	47,47,47,47	0
57	MG	1A	3253	1/1	0.92	0.17	51,51,51,51	0
57	MG	2B	217	1/1	0.92	0.31	65,65,65,65	0
57	MG	1A	3354	1/1	0.92	0.12	58,58,58,58	0
57	MG	1A	3909	1/1	0.92	0.11	59,59,59,59	0
57	MG	2A	3086	1/1	0.92	0.14	61,61,61,61	0
57	MG	2B	221	1/1	0.92	0.26	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3637	1/1	0.92	0.11	53,53,53,53	0
57	MG	10	107	1/1	0.92	0.11	61,61,61,61	0
57	MG	11	104	1/1	0.92	0.14	63,63,63,63	0
57	MG	13	104	1/1	0.92	0.14	56,56,56,56	0
57	MG	15	104	1/1	0.92	0.33	43,43,43,43	0
57	MG	1A	3095	1/1	0.92	0.14	49,49,49,49	0
57	MG	1A	4041	1/1	0.92	0.08	29,29,29,29	0
57	MG	2E	309	1/1	0.92	0.14	61,61,61,61	0
57	MG	1A	3771	1/1	0.92	0.10	34,34,34,34	0
57	MG	1A	3773	1/1	0.92	0.07	39,39,39,39	0
57	MG	2F	305	1/1	0.92	0.10	56,56,56,56	0
57	MG	18	103	1/1	0.92	0.15	47,47,47,47	0
57	MG	1A	3527	1/1	0.92	0.06	60,60,60,60	0
57	MG	1A	3778	1/1	0.92	0.09	44,44,44,44	0
57	MG	1A	3781	1/1	0.92	0.09	19,19,19,19	0
57	MG	2A	3109	1/1	0.92	0.14	53,53,53,53	0
57	MG	2A	3110	1/1	0.92	0.16	57,57,57,57	0
57	MG	2T	3503	1/1	0.92	0.24	54,54,54,54	0
57	MG	1A	3209	1/1	0.92	0.12	53,53,53,53	0
57	MG	2A	3614	1/1	0.92	0.12	39,39,39,39	0
57	MG	2A	3112	1/1	0.92	0.34	62,62,62,62	0
57	MG	2A	3115	1/1	0.92	0.14	47,47,47,47	0
57	MG	1A	3532	1/1	0.92	0.22	58,58,58,58	0
57	MG	1A	3040	1/1	0.92	0.06	52,52,52,52	0
57	MG	1A	4059	1/1	0.92	0.07	40,40,40,40	0
57	MG	20	102	1/1	0.92	0.15	65,65,65,65	0
57	MG	2A	3120	1/1	0.92	0.10	47,47,47,47	0
57	MG	1A	4060	1/1	0.92	0.07	17,17,17,17	0
57	MG	1A	4063	1/1	0.92	0.12	52,52,52,52	0
57	MG	2A	3628	1/1	0.92	0.10	59,59,59,59	0
57	MG	1a	1743	1/1	0.92	0.11	59,59,59,59	0
57	MG	2A	3336	1/1	0.92	0.22	53,53,53,53	0
57	MG	25	107	1/1	0.92	0.11	49,49,49,49	0
57	MG	1A	3649	1/1	0.92	0.08	41,41,41,41	0
57	MG	2A	3126	1/1	0.92	0.10	56,56,56,56	0
57	MG	1A	3315	1/1	0.92	0.19	49,49,49,49	0
57	MG	1A	3436	1/1	0.92	0.13	60,60,60,60	0
57	MG	1A	3260	1/1	0.92	0.06	39,39,39,39	0
57	MG	2A	3636	1/1	0.92	0.09	59,59,59,59	0
57	MG	1A	3318	1/1	0.92	0.11	52,52,52,52	0
57	MG	2A	3141	1/1	0.92	0.26	66,66,66,66	0
57	MG	2A	3144	1/1	0.92	0.27	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	3444	1/1	0.92	0.11	57,57,57,57	0
57	MG	2a	1610	1/1	0.92	0.09	52,52,52,52	0
57	MG	1A	3365	1/1	0.92	0.19	59,59,59,59	0
57	MG	1a	1626	1/1	0.92	0.18	63,63,63,63	0
57	MG	1A	3807	1/1	0.92	0.12	35,35,35,35	0
57	MG	1A	3211	1/1	0.92	0.08	34,34,34,34	0
57	MG	2A	3158	1/1	0.92	0.23	55,55,55,55	0
57	MG	2A	3358	1/1	0.92	0.09	45,45,45,45	0
57	MG	1A	3449	1/1	0.92	0.26	58,58,58,58	0
57	MG	1A	3146	1/1	0.92	0.09	38,38,38,38	0
57	MG	1a	1632	1/1	0.92	0.21	50,50,50,50	0
57	MG	1a	1768	1/1	0.92	0.33	67,67,67,67	0
57	MG	1a	1633	1/1	0.92	0.25	72,72,72,72	0
57	MG	1A	3323	1/1	0.92	0.11	48,48,48,48	0
57	MG	2a	1631	1/1	0.92	0.20	61,61,61,61	0
57	MG	2A	3367	1/1	0.92	0.09	48,48,48,48	0
57	MG	2A	3368	1/1	0.92	0.24	52,52,52,52	0
57	MG	2a	1635	1/1	0.92	0.17	63,63,63,63	0
57	MG	2A	3660	1/1	0.92	0.17	51,51,51,51	0
57	MG	1A	3372	1/1	0.92	0.14	48,48,48,48	0
57	MG	1A	3814	1/1	0.92	0.21	58,58,58,58	0
57	MG	2a	1641	1/1	0.92	0.27	61,61,61,61	0
57	MG	1A	4087	1/1	0.92	0.15	40,40,40,40	0
57	MG	1A	4089	1/1	0.92	0.10	64,64,64,64	0
57	MG	1a	1779	1/1	0.92	0.14	71,71,71,71	0
57	MG	2A	3175	1/1	0.92	0.10	41,41,41,41	0
57	MG	2A	3671	1/1	0.92	0.09	60,60,60,60	0
57	MG	2A	3377	1/1	0.92	0.16	61,61,61,61	0
57	MG	1A	3573	1/1	0.92	0.09	39,39,39,39	0
57	MG	1A	3965	1/1	0.92	0.11	65,65,65,65	0
57	MG	1A	3219	1/1	0.92	0.17	56,56,56,56	0
57	MG	1A	3325	1/1	0.92	0.20	57,57,57,57	0
57	MG	1A	3106	1/1	0.92	0.09	33,33,33,33	0
57	MG	2A	3386	1/1	0.92	0.12	63,63,63,63	0
57	MG	1A	3693	1/1	0.92	0.10	37,37,37,37	0
57	MG	1A	3579	1/1	0.92	0.28	70,70,70,70	0
57	MG	1A	3159	1/1	0.92	0.10	35,35,35,35	0
57	MG	1A	3463	1/1	0.92	0.18	46,46,46,46	0
57	MG	1A	3582	1/1	0.92	0.24	65,65,65,65	0
57	MG	2A	3689	1/1	0.92	0.15	35,35,35,35	0
57	MG	1A	3976	1/1	0.92	0.12	20,20,20,20	0
57	MG	1a	1795	1/1	0.92	0.14	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	3829	1/1	0.92	0.10	55,55,55,55	0
57	MG	2A	3395	1/1	0.92	0.18	46,46,46,46	0
57	MG	2a	1668	1/1	0.92	0.09	72,72,72,72	0
57	MG	1A	3182	1/1	0.92	0.25	50,50,50,50	0
57	MG	2A	3401	1/1	0.92	0.27	41,41,41,41	0
57	MG	2A	3202	1/1	0.92	0.12	66,66,66,66	0
57	MG	1a	1798	1/1	0.92	0.08	53,53,53,53	0
57	MG	1A	3469	1/1	0.92	0.24	59,59,59,59	0
57	MG	1A	3230	1/1	0.92	0.25	34,34,34,34	0
57	MG	1a	1660	1/1	0.92	0.16	64,64,64,64	0
57	MG	1A	3160	1/1	0.92	0.07	55,55,55,55	0
57	MG	1A	3184	1/1	0.92	0.11	54,54,54,54	0
57	MG	1A	3277	1/1	0.92	0.21	38,38,38,38	0
57	MG	2a	1684	1/1	0.92	0.08	59,59,59,59	0
57	MG	2a	1685	1/1	0.92	0.12	60,60,60,60	0
57	MG	2a	1686	1/1	0.92	0.18	58,58,58,58	0
57	MG	2A	3211	1/1	0.92	0.15	67,67,67,67	0
57	MG	1A	3594	1/1	0.92	0.12	45,45,45,45	0
57	MG	1A	3847	1/1	0.92	0.15	55,55,55,55	0
57	MG	1A	3285	1/1	0.92	0.13	45,45,45,45	0
57	MG	2a	1694	1/1	0.92	0.14	63,63,63,63	0
57	MG	2a	1695	1/1	0.92	0.20	50,50,50,50	0
57	MG	1E	309	1/1	0.92	0.10	25,25,25,25	0
57	MG	2a	1700	1/1	0.92	0.15	58,58,58,58	0
57	MG	2a	1701	1/1	0.92	0.15	49,49,49,49	0
57	MG	2a	1702	1/1	0.92	0.15	50,50,50,50	0
57	MG	2A	3717	1/1	0.92	0.11	35,35,35,35	0
57	MG	2A	3718	1/1	0.92	0.19	48,48,48,48	0
57	MG	1E	310	1/1	0.92	0.18	50,50,50,50	0
57	MG	2A	3428	1/1	0.92	0.11	57,57,57,57	0
57	MG	2A	3218	1/1	0.92	0.17	59,59,59,59	0
57	MG	1A	3598	1/1	0.92	0.08	23,23,23,23	0
57	MG	1A	3288	1/1	0.92	0.16	43,43,43,43	0
57	MG	1a	1822	1/1	0.92	0.18	75,75,75,75	0
57	MG	1A	3289	1/1	0.92	0.16	54,54,54,54	0
57	MG	1e	201	1/1	0.92	0.08	67,67,67,67	0
57	MG	2A	3729	1/1	0.92	0.14	65,65,65,65	0
57	MG	2A	3440	1/1	0.92	0.21	38,38,38,38	0
57	MG	2A	3441	1/1	0.92	0.13	54,54,54,54	0
57	MG	1F	305	1/1	0.92	0.12	57,57,57,57	0
57	MG	1A	3290	1/1	0.92	0.21	52,52,52,52	0
57	MG	1A	3613	1/1	0.92	0.07	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3341	1/1	0.92	0.19	53,53,53,53	0
57	MG	2A	3236	1/1	0.92	0.12	60,60,60,60	0
57	MG	1A	3406	1/1	0.92	0.16	56,56,56,56	0
57	MG	1A	3732	1/1	0.92	0.13	64,64,64,64	0
57	MG	1p	101	1/1	0.92	0.12	63,63,63,63	0
57	MG	2A	3750	1/1	0.92	0.07	59,59,59,59	0
57	MG	2A	3461	1/1	0.92	0.07	43,43,43,43	0
57	MG	1r	101	1/1	0.92	0.29	60,60,60,60	0
57	MG	1G	202	1/1	0.92	0.17	57,57,57,57	0
57	MG	1A	3869	1/1	0.92	0.12	44,44,44,44	0
57	MG	1a	1685	1/1	0.92	0.09	53,53,53,53	0
57	MG	2A	3472	1/1	0.92	0.16	63,63,63,63	0
57	MG	2A	3476	1/1	0.92	0.12	54,54,54,54	0
57	MG	2A	3245	1/1	0.92	0.11	66,66,66,66	0
57	MG	1A	3872	1/1	0.92	0.10	24,24,24,24	0
57	MG	1A	3246	1/1	0.92	0.12	48,48,48,48	0
57	MG	1x	112	1/1	0.92	0.18	65,65,65,65	0
57	MG	2A	3001	1/1	0.92	0.30	55,55,55,55	0
57	MG	2a	1754	1/1	0.92	0.25	57,57,57,57	0
57	MG	1A	3130	1/1	0.92	0.16	51,51,51,51	0
57	MG	1A	3248	1/1	0.92	0.08	53,53,53,53	0
57	MG	2A	3257	1/1	0.92	0.10	65,65,65,65	0
57	MG	1A	3622	1/1	0.92	0.09	39,39,39,39	0
57	MG	1A	3741	1/1	0.92	0.15	51,51,51,51	0
57	MG	1A	3413	1/1	0.92	0.29	61,61,61,61	0
57	MG	1A	3888	1/1	0.92	0.14	55,55,55,55	0
57	MG	2A	3505	1/1	0.92	0.17	59,59,59,59	0
57	MG	1A	3132	1/1	0.92	0.06	60,60,60,60	0
57	MG	1a	1695	1/1	0.92	0.24	53,53,53,53	0
57	MG	2A	3508	1/1	0.92	0.15	45,45,45,45	0
57	MG	1a	1696	1/1	0.92	0.31	56,56,56,56	0
57	MG	2A	3807	1/1	0.92	0.14	66,66,66,66	0
57	MG	2A	3511	1/1	0.92	0.15	55,55,55,55	0
57	MG	2A	3033	1/1	0.92	0.07	42,42,42,42	0
57	MG	2A	3039	1/1	0.92	0.25	66,66,66,66	0
57	MG	2A	3817	1/1	0.92	0.08	62,62,62,62	0
57	MG	2A	3041	1/1	0.92	0.38	58,58,58,58	0
57	MG	2A	3519	1/1	0.92	0.07	33,33,33,33	0
57	MG	2d	301	1/1	0.92	0.29	57,57,57,57	0
57	MG	2A	3821	1/1	0.92	0.11	59,59,59,59	0
57	MG	2A	3272	1/1	0.92	0.16	54,54,54,54	0
57	MG	2f	201	1/1	0.92	0.15	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	1Q	201	1/1	0.92	0.27	48,48,48,48	0
57	MG	1A	3891	1/1	0.92	0.10	48,48,48,48	0
57	MG	2A	3828	1/1	0.92	0.11	30,30,30,30	0
57	MG	1a	1700	1/1	0.92	0.22	52,52,52,52	0
57	MG	2A	3830	1/1	0.92	0.26	65,65,65,65	0
57	MG	2A	3047	1/1	0.92	0.17	62,62,62,62	0
57	MG	2A	3048	1/1	0.92	0.15	48,48,48,48	0
57	MG	2A	3835	1/1	0.92	0.14	42,42,42,42	0
57	MG	1a	1701	1/1	0.92	0.33	57,57,57,57	0
57	MG	2A	3837	1/1	0.92	0.11	52,52,52,52	0
57	MG	1A	4023	1/1	0.92	0.12	39,39,39,39	0
57	MG	2A	3056	1/1	0.92	0.14	60,60,60,60	0
57	MG	1S	201	1/1	0.92	0.15	36,36,36,36	0
57	MG	2A	3541	1/1	0.92	0.14	48,48,48,48	0
57	MG	2x	107	1/1	0.92	0.12	74,74,74,74	0
57	MG	2A	3846	1/1	0.92	0.15	56,56,56,56	0
57	MG	2A	3284	1/1	0.92	0.33	55,55,55,55	0
57	MG	1A	3943	1/1	0.93	0.14	69,69,69,69	0
57	MG	2E	302	1/1	0.93	0.11	52,52,52,52	0
57	MG	2A	3624	1/1	0.93	0.16	64,64,64,64	0
57	MG	2A	3381	1/1	0.93	0.08	66,66,66,66	0
57	MG	2A	3627	1/1	0.93	0.12	51,51,51,51	0
57	MG	1a	1702	1/1	0.93	0.15	60,60,60,60	0
57	MG	2E	308	1/1	0.93	0.17	32,32,32,32	0
57	MG	1A	3946	1/1	0.93	0.07	52,52,52,52	0
57	MG	2A	3384	1/1	0.93	0.25	63,63,63,63	0
57	MG	1A	3092	1/1	0.93	0.20	55,55,55,55	0
57	MG	1A	3817	1/1	0.93	0.14	35,35,35,35	0
57	MG	10	103	1/1	0.93	0.12	52,52,52,52	0
57	MG	2F	307	1/1	0.93	0.15	58,58,58,58	0
57	MG	2A	3024	1/1	0.93	0.28	44,44,44,44	0
57	MG	1A	3314	1/1	0.93	0.25	53,53,53,53	0
57	MG	11	101	1/1	0.93	0.40	39,39,39,39	0
57	MG	2A	3637	1/1	0.93	0.12	62,62,62,62	0
57	MG	1A	4062	1/1	0.93	0.08	37,37,37,37	0
57	MG	12	101	1/1	0.93	0.09	49,49,49,49	0
57	MG	1A	3195	1/1	0.93	0.23	29,29,29,29	0
57	MG	1A	3534	1/1	0.93	0.08	61,61,61,61	0
57	MG	1a	1715	1/1	0.93	0.13	47,47,47,47	0
57	MG	2V	202	1/1	0.93	0.29	67,67,67,67	0
57	MG	1A	3316	1/1	0.93	0.09	45,45,45,45	0
57	MG	2A	3397	1/1	0.93	0.20	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	1A	3724	1/1	0.93	0.08	52,52,52,52	0
57	MG	1A	3415	1/1	0.93	0.11	48,48,48,48	0
57	MG	1A	3102	1/1	0.93	0.15	47,47,47,47	0
57	MG	2A	3405	1/1	0.93	0.25	57,57,57,57	0
57	MG	2A	3406	1/1	0.93	0.17	34,34,34,34	0
57	MG	2A	3052	1/1	0.93	0.17	60,60,60,60	0
57	MG	1A	3419	1/1	0.93	0.21	68,68,68,68	0
57	MG	25	103	1/1	0.93	0.18	62,62,62,62	0
57	MG	1a	1722	1/1	0.93	0.12	54,54,54,54	0
57	MG	1A	3729	1/1	0.93	0.12	33,33,33,33	0
57	MG	2A	3248	1/1	0.93	0.26	63,63,63,63	0
57	MG	2A	3413	1/1	0.93	0.13	48,48,48,48	0
57	MG	2A	3414	1/1	0.93	0.19	60,60,60,60	0
57	MG	28	101	1/1	0.93	0.12	60,60,60,60	0
57	MG	1A	3207	1/1	0.93	0.12	59,59,59,59	0
57	MG	1A	3480	1/1	0.93	0.13	58,58,58,58	0
57	MG	2A	3063	1/1	0.93	0.21	55,55,55,55	0
57	MG	2A	3253	1/1	0.93	0.26	60,60,60,60	0
57	MG	1a	1727	1/1	0.93	0.29	69,69,69,69	0
57	MG	1A	3553	1/1	0.93	0.07	22,22,22,22	0
57	MG	2A	3425	1/1	0.93	0.35	56,56,56,56	0
57	MG	2A	3256	1/1	0.93	0.21	61,61,61,61	0
57	MG	1A	3481	1/1	0.93	0.25	43,43,43,43	0
57	MG	1A	3377	1/1	0.93	0.08	57,57,57,57	0
57	MG	1A	3738	1/1	0.93	0.09	54,54,54,54	0
57	MG	2A	3433	1/1	0.93	0.28	58,58,58,58	0
57	MG	1a	1607	1/1	0.93	0.12	51,51,51,51	0
57	MG	1A	3841	1/1	0.93	0.10	55,55,55,55	0
57	MG	1A	3843	1/1	0.93	0.09	44,44,44,44	0
57	MG	1A	3846	1/1	0.93	0.15	59,59,59,59	0
57	MG	1B	201	1/1	0.93	0.10	57,57,57,57	0
57	MG	1A	3643	1/1	0.93	0.14	47,47,47,47	0
57	MG	1a	1615	1/1	0.93	0.09	68,68,68,68	0
57	MG	2A	3443	1/1	0.93	0.13	56,56,56,56	0
57	MG	2A	3444	1/1	0.93	0.27	59,59,59,59	0
57	MG	2A	3445	1/1	0.93	0.10	57,57,57,57	0
57	MG	1A	3975	1/1	0.93	0.11	39,39,39,39	0
57	MG	1a	1618	1/1	0.93	0.10	73,73,73,73	0
57	MG	2A	3450	1/1	0.93	0.14	61,61,61,61	0
57	MG	2A	3451	1/1	0.93	0.27	46,46,46,46	0
57	MG	2A	3698	1/1	0.93	0.18	72,72,72,72	0
57	MG	2a	1639	1/1	0.93	0.23	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	3093	1/1	0.93	0.15	55,55,55,55	0
57	MG	1A	3490	1/1	0.93	0.15	38,38,38,38	0
57	MG	1A	3850	1/1	0.93	0.10	48,48,48,48	0
57	MG	2A	3457	1/1	0.93	0.08	53,53,53,53	0
57	MG	2a	1644	1/1	0.93	0.18	57,57,57,57	0
57	MG	1a	1751	1/1	0.93	0.12	55,55,55,55	0
57	MG	2A	3277	1/1	0.93	0.10	65,65,65,65	0
57	MG	1B	211	1/1	0.93	0.11	53,53,53,53	0
57	MG	2A	3463	1/1	0.93	0.20	58,58,58,58	0
57	MG	2A	3465	1/1	0.93	0.23	61,61,61,61	0
57	MG	2A	3096	1/1	0.93	0.12	48,48,48,48	0
57	MG	1A	3380	1/1	0.93	0.12	47,47,47,47	0
57	MG	1B	213	1/1	0.93	0.20	59,59,59,59	0
57	MG	1B	214	1/1	0.93	0.07	50,50,50,50	0
57	MG	2A	3101	1/1	0.93	0.18	61,61,61,61	0
57	MG	2A	3473	1/1	0.93	0.09	53,53,53,53	0
57	MG	2A	3719	1/1	0.93	0.29	44,44,44,44	0
57	MG	1A	3492	1/1	0.93	0.10	38,38,38,38	0
57	MG	2A	3477	1/1	0.93	0.06	40,40,40,40	0
57	MG	1A	3383	1/1	0.93	0.29	29,29,29,29	0
57	MG	1A	3657	1/1	0.93	0.08	23,23,23,23	0
57	MG	1a	1764	1/1	0.93	0.17	52,52,52,52	0
57	MG	1B	222	1/1	0.93	0.10	64,64,64,64	0
57	MG	1A	3859	1/1	0.93	0.23	39,39,39,39	0
57	MG	2A	3484	1/1	0.93	0.06	29,29,29,29	0
57	MG	2A	3292	1/1	0.93	0.23	56,56,56,56	0
57	MG	1A	3425	1/1	0.93	0.23	50,50,50,50	0
57	MG	2a	1670	1/1	0.93	0.30	64,64,64,64	0
57	MG	2A	3488	1/1	0.93	0.10	40,40,40,40	0
57	MG	1A	3753	1/1	0.93	0.10	26,26,26,26	0
57	MG	1A	3234	1/1	0.93	0.23	48,48,48,48	0
57	MG	1B	232	1/1	0.93	0.08	60,60,60,60	0
57	MG	2A	3495	1/1	0.93	0.11	44,44,44,44	0
57	MG	1A	3244	1/1	0.93	0.22	44,44,44,44	0
57	MG	2A	3741	1/1	0.93	0.13	60,60,60,60	0
57	MG	2A	3502	1/1	0.93	0.14	53,53,53,53	0
57	MG	1A	3758	1/1	0.93	0.11	23,23,23,23	0
57	MG	2a	1682	1/1	0.93	0.25	55,55,55,55	0
57	MG	2A	3748	1/1	0.93	0.13	62,62,62,62	0
57	MG	1D	308	1/1	0.93	0.14	38,38,38,38	0
57	MG	1A	3873	1/1	0.93	0.06	28,28,28,28	0
57	MG	1A	3875	1/1	0.93	0.09	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	1a	1780	1/1	0.93	0.08	56,56,56,56	0
57	MG	2a	1691	1/1	0.93	0.20	56,56,56,56	0
57	MG	1A	3761	1/1	0.93	0.07	65,65,65,65	0
57	MG	2A	3756	1/1	0.93	0.07	62,62,62,62	0
57	MG	1A	3997	1/1	0.93	0.13	58,58,58,58	0
57	MG	1E	305	1/1	0.93	0.17	35,35,35,35	0
57	MG	1A	3665	1/1	0.93	0.11	53,53,53,53	0
57	MG	1A	3878	1/1	0.93	0.07	41,41,41,41	0
57	MG	2A	3518	1/1	0.93	0.08	45,45,45,45	0
57	MG	2A	3139	1/1	0.93	0.17	39,39,39,39	0
57	MG	2a	1703	1/1	0.93	0.16	41,41,41,41	0
57	MG	1A	3765	1/1	0.93	0.11	33,33,33,33	0
57	MG	1A	3503	1/1	0.93	0.11	50,50,50,50	0
57	MG	2a	1707	1/1	0.93	0.25	55,55,55,55	0
57	MG	2a	1708	1/1	0.93	0.21	56,56,56,56	0
57	MG	2A	3143	1/1	0.93	0.28	48,48,48,48	0
57	MG	2A	3527	1/1	0.93	0.08	45,45,45,45	0
57	MG	1a	1656	1/1	0.93	0.18	57,57,57,57	0
57	MG	2A	3774	1/1	0.93	0.13	77,77,77,77	0
57	MG	2a	1716	1/1	0.93	0.15	65,65,65,65	0
57	MG	1a	1791	1/1	0.93	0.10	52,52,52,52	0
57	MG	1A	3245	1/1	0.93	0.10	39,39,39,39	0
57	MG	1E	314	1/1	0.93	0.10	61,61,61,61	0
57	MG	1A	3389	1/1	0.93	0.11	62,62,62,62	0
57	MG	2A	3535	1/1	0.93	0.11	34,34,34,34	0
57	MG	2A	3151	1/1	0.93	0.08	40,40,40,40	0
57	MG	1A	3775	1/1	0.93	0.20	63,63,63,63	0
57	MG	1A	3131	1/1	0.93	0.16	45,45,45,45	0
57	MG	1A	3437	1/1	0.93	0.08	42,42,42,42	0
57	MG	2A	3543	1/1	0.93	0.07	35,35,35,35	0
57	MG	2A	3325	1/1	0.93	0.15	54,54,54,54	0
57	MG	1A	3509	1/1	0.93	0.17	62,62,62,62	0
57	MG	2A	3810	1/1	0.93	0.06	41,41,41,41	0
57	MG	2A	3812	1/1	0.93	0.07	50,50,50,50	0
57	MG	1a	1666	1/1	0.93	0.21	61,61,61,61	0
57	MG	2a	1739	1/1	0.93	0.21	60,60,60,60	0
57	MG	2A	3163	1/1	0.93	0.13	41,41,41,41	0
57	MG	1A	3588	1/1	0.93	0.10	55,55,55,55	0
57	MG	1A	3510	1/1	0.93	0.08	62,62,62,62	0
57	MG	2A	3557	1/1	0.93	0.21	61,61,61,61	0
57	MG	2A	3820	1/1	0.93	0.08	70,70,70,70	0
57	MG	1a	1669	1/1	0.93	0.11	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3591	1/1	0.93	0.09	22,22,22,22	0
57	MG	1A	3511	1/1	0.93	0.18	52,52,52,52	0
57	MG	2A	3334	1/1	0.93	0.18	58,58,58,58	0
57	MG	1A	3792	1/1	0.93	0.31	31,31,31,31	0
57	MG	1A	3439	1/1	0.93	0.24	65,65,65,65	0
57	MG	1a	1813	1/1	0.93	0.10	53,53,53,53	0
57	MG	1A	3298	1/1	0.93	0.09	40,40,40,40	0
57	MG	2A	3833	1/1	0.93	0.09	43,43,43,43	0
57	MG	2A	3178	1/1	0.93	0.10	39,39,39,39	0
57	MG	1A	3020	1/1	0.93	0.11	42,42,42,42	0
57	MG	2A	3577	1/1	0.93	0.11	54,54,54,54	0
57	MG	1A	3109	1/1	0.93	0.27	31,31,31,31	0
57	MG	2A	3838	1/1	0.93	0.16	62,62,62,62	0
57	MG	2A	3183	1/1	0.93	0.06	57,57,57,57	0
57	MG	2A	3841	1/1	0.93	0.09	77,77,77,77	0
57	MG	1A	3914	1/1	0.93	0.08	48,48,48,48	0
57	MG	1A	3800	1/1	0.93	0.10	32,32,32,32	0
57	MG	1A	3396	1/1	0.93	0.16	46,46,46,46	0
57	MG	1A	3301	1/1	0.93	0.21	36,36,36,36	0
57	MG	1A	3520	1/1	0.93	0.20	40,40,40,40	0
57	MG	2A	3354	1/1	0.93	0.21	44,44,44,44	0
57	MG	2A	3849	1/1	0.93	0.13	63,63,63,63	0
57	MG	2A	3589	1/1	0.93	0.17	40,40,40,40	0
57	MG	1P	202	1/1	0.93	0.28	48,48,48,48	0
57	MG	2A	3591	1/1	0.93	0.10	48,48,48,48	0
57	MG	1e	203	1/1	0.93	0.14	77,77,77,77	0
57	MG	1A	3398	1/1	0.93	0.26	41,41,41,41	0
57	MG	1A	3167	1/1	0.93	0.17	41,41,41,41	0
57	MG	2A	3196	1/1	0.93	0.21	63,63,63,63	0
57	MG	2A	3599	1/1	0.93	0.12	50,50,50,50	0
57	MG	1R	204	1/1	0.93	0.20	38,38,38,38	0
57	MG	1A	3931	1/1	0.93	0.11	60,60,60,60	0
57	MG	1A	3220	1/1	0.93	0.14	39,39,39,39	0
57	MG	2B	209	1/1	0.93	0.16	57,57,57,57	0
57	MG	1S	202	1/1	0.93	0.12	53,53,53,53	0
57	MG	2A	3609	1/1	0.93	0.09	36,36,36,36	0
57	MG	1A	4045	1/1	0.93	0.10	35,35,35,35	0
57	MG	1A	3086	1/1	0.93	0.13	32,32,32,32	0
57	MG	2l	202	1/1	0.93	0.12	57,57,57,57	0
57	MG	2q	201	1/1	0.93	0.23	70,70,70,70	0
57	MG	1x	102	1/1	0.93	0.07	66,66,66,66	0
57	MG	1U	203	1/1	0.93	0.18	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	1U	205	1/1	0.93	0.18	40,40,40,40	0
57	MG	1U	206	1/1	0.93	0.22	40,40,40,40	0
57	MG	1A	4049	1/1	0.93	0.11	66,66,66,66	0
57	MG	1A	3310	1/1	0.93	0.10	58,58,58,58	0
57	MG	1A	3710	1/1	0.93	0.14	57,57,57,57	0
57	MG	2A	3002	1/1	0.93	0.25	48,48,48,48	0
57	MG	2x	108	1/1	0.93	0.09	84,84,84,84	0
57	MG	2D	307	1/1	0.93	0.12	47,47,47,47	0
57	MG	1A	3528	1/1	0.93	0.34	63,63,63,63	0
57	MG	2D	306	1/1	0.94	0.28	41,41,41,41	0
57	MG	1A	3238	1/1	0.94	0.11	47,47,47,47	0
57	MG	1A	3088	1/1	0.94	0.15	37,37,37,37	0
57	MG	1a	1655	1/1	0.94	0.17	52,52,52,52	0
57	MG	2E	301	1/1	0.94	0.16	56,56,56,56	0
57	MG	2A	3184	1/1	0.94	0.27	61,61,61,61	0
57	MG	1A	3595	1/1	0.94	0.07	35,35,35,35	0
57	MG	1E	301	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3187	1/1	0.94	0.09	60,60,60,60	0
57	MG	1A	3497	1/1	0.94	0.23	31,31,31,31	0
57	MG	1A	3057	1/1	0.94	0.17	43,43,43,43	0
57	MG	1A	3602	1/1	0.94	0.07	34,34,34,34	0
57	MG	1A	3416	1/1	0.94	0.09	45,45,45,45	0
57	MG	1A	3123	1/1	0.94	0.13	39,39,39,39	0
57	MG	1E	311	1/1	0.94	0.10	23,23,23,23	0
57	MG	1A	3852	1/1	0.94	0.08	39,39,39,39	0
57	MG	1A	3418	1/1	0.94	0.15	53,53,53,53	0
57	MG	2F	308	1/1	0.94	0.12	42,42,42,42	0
57	MG	1b	301	1/1	0.94	0.05	79,79,79,79	0
57	MG	2N	201	1/1	0.94	0.07	57,57,57,57	0
57	MG	2A	3198	1/1	0.94	0.18	62,62,62,62	0
57	MG	2P	201	1/1	0.94	0.24	48,48,48,48	0
57	MG	2Q	203	1/1	0.94	0.10	63,63,63,63	0
57	MG	1A	3506	1/1	0.94	0.10	51,51,51,51	0
57	MG	1F	303	1/1	0.94	0.21	35,35,35,35	0
57	MG	1a	1670	1/1	0.94	0.08	52,52,52,52	0
57	MG	1A	3855	1/1	0.94	0.20	42,42,42,42	0
57	MG	1A	4000	1/1	0.94	0.06	27,27,27,27	0
57	MG	1F	307	1/1	0.94	0.07	32,32,32,32	0
57	MG	1A	3060	1/1	0.94	0.55	64,64,64,64	0
57	MG	1A	3125	1/1	0.94	0.29	32,32,32,32	0
57	MG	1A	3357	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	4007	1/1	0.94	0.09	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3863	1/1	0.94	0.08	43,43,43,43	0
57	MG	1x	101	1/1	0.94	0.20	57,57,57,57	0
57	MG	2A	3404	1/1	0.94	0.34	54,54,54,54	0
57	MG	2A	3655	1/1	0.94	0.16	67,67,67,67	0
57	MG	1A	3129	1/1	0.94	0.28	35,35,35,35	0
57	MG	23	102	1/1	0.94	0.09	55,55,55,55	0
57	MG	1x	103	1/1	0.94	0.35	56,56,56,56	0
57	MG	2A	3407	1/1	0.94	0.14	46,46,46,46	0
57	MG	1A	3061	1/1	0.94	0.09	36,36,36,36	0
57	MG	1A	3062	1/1	0.94	0.14	44,44,44,44	0
57	MG	1A	3363	1/1	0.94	0.14	40,40,40,40	0
57	MG	2A	3219	1/1	0.94	0.15	47,47,47,47	0
57	MG	2A	3220	1/1	0.94	0.11	59,59,59,59	0
57	MG	1x	107	1/1	0.94	0.10	52,52,52,52	0
57	MG	1A	3426	1/1	0.94	0.09	51,51,51,51	0
57	MG	1A	3016	1/1	0.94	0.33	51,51,51,51	0
57	MG	1N	204	1/1	0.94	0.50	48,48,48,48	0
57	MG	28	104	1/1	0.94	0.19	52,52,52,52	0
57	MG	2A	3228	1/1	0.94	0.14	48,48,48,48	0
57	MG	2A	3673	1/1	0.94	0.08	65,65,65,65	0
57	MG	2A	3229	1/1	0.94	0.16	45,45,45,45	0
57	MG	2A	3422	1/1	0.94	0.13	59,59,59,59	0
57	MG	1A	3312	1/1	0.94	0.20	53,53,53,53	0
57	MG	1A	3053	1/1	0.94	0.15	50,50,50,50	0
57	MG	2A	3679	1/1	0.94	0.13	35,35,35,35	0
57	MG	2a	1611	1/1	0.94	0.28	66,66,66,66	0
57	MG	1A	4021	1/1	0.94	0.08	43,43,43,43	0
57	MG	1A	3748	1/1	0.94	0.10	35,35,35,35	0
57	MG	2A	3234	1/1	0.94	0.20	47,47,47,47	0
57	MG	2A	3011	1/1	0.94	0.07	40,40,40,40	0
57	MG	1A	3200	1/1	0.94	0.09	33,33,33,33	0
57	MG	1A	3369	1/1	0.94	0.16	48,48,48,48	0
57	MG	1A	3257	1/1	0.94	0.09	64,64,64,64	0
57	MG	1Q	202	1/1	0.94	0.43	50,50,50,50	0
57	MG	2A	3240	1/1	0.94	0.28	57,57,57,57	0
57	MG	1A	3884	1/1	0.94	0.18	46,46,46,46	0
57	MG	1R	201	1/1	0.94	0.10	44,44,44,44	0
57	MG	2a	1628	1/1	0.94	0.28	63,63,63,63	0
57	MG	1A	4030	1/1	0.94	0.10	66,66,66,66	0
57	MG	2A	3031	1/1	0.94	0.08	47,47,47,47	0
57	MG	1A	4032	1/1	0.94	0.08	58,58,58,58	0
57	MG	2A	3034	1/1	0.94	0.15	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	2A	3247	1/1	0.94	0.12	59,59,59,59	0
57	MG	2A	3036	1/1	0.94	0.09	55,55,55,55	0
57	MG	2A	3037	1/1	0.94	0.10	42,42,42,42	0
57	MG	2A	3702	1/1	0.94	0.12	53,53,53,53	0
57	MG	1A	3754	1/1	0.94	0.11	28,28,28,28	0
57	MG	1A	3887	1/1	0.94	0.24	26,26,26,26	0
57	MG	1A	3138	1/1	0.94	0.17	34,34,34,34	0
57	MG	1A	3634	1/1	0.94	0.11	40,40,40,40	0
57	MG	1A	3524	1/1	0.94	0.30	51,51,51,51	0
57	MG	2A	3046	1/1	0.94	0.09	55,55,55,55	0
57	MG	2A	3710	1/1	0.94	0.11	54,54,54,54	0
57	MG	1A	3638	1/1	0.94	0.10	65,65,65,65	0
57	MG	2A	3258	1/1	0.94	0.17	61,61,61,61	0
57	MG	1A	3639	1/1	0.94	0.10	30,30,30,30	0
57	MG	1A	3205	1/1	0.94	0.13	21,21,21,21	0
57	MG	1A	3261	1/1	0.94	0.10	51,51,51,51	0
57	MG	1A	3376	1/1	0.94	0.21	38,38,38,38	0
57	MG	2A	3055	1/1	0.94	0.08	48,48,48,48	0
57	MG	1A	4044	1/1	0.94	0.08	61,61,61,61	0
57	MG	1A	3772	1/1	0.94	0.07	42,42,42,42	0
57	MG	1A	3144	1/1	0.94	0.08	49,49,49,49	0
57	MG	1X	102	1/1	0.94	0.45	43,43,43,43	0
57	MG	2A	3475	1/1	0.94	0.10	45,45,45,45	0
57	MG	2A	3270	1/1	0.94	0.10	57,57,57,57	0
57	MG	2A	3062	1/1	0.94	0.09	67,67,67,67	0
57	MG	1Y	201	1/1	0.94	0.12	63,63,63,63	0
57	MG	1A	4047	1/1	0.94	0.09	48,48,48,48	0
57	MG	1A	3908	1/1	0.94	0.07	60,60,60,60	0
57	MG	2A	3731	1/1	0.94	0.11	40,40,40,40	0
57	MG	2A	3067	1/1	0.94	0.14	39,39,39,39	0
57	MG	1Z	302	1/1	0.94	0.20	54,54,54,54	0
57	MG	1A	3774	1/1	0.94	0.08	20,20,20,20	0
57	MG	10	104	1/1	0.94	0.35	43,43,43,43	0
57	MG	2A	3279	1/1	0.94	0.13	64,64,64,64	0
57	MG	2A	3072	1/1	0.94	0.09	53,53,53,53	0
57	MG	2A	3740	1/1	0.94	0.17	67,67,67,67	0
57	MG	10	105	1/1	0.94	0.27	68,68,68,68	0
57	MG	2A	3743	1/1	0.94	0.12	51,51,51,51	0
57	MG	10	106	1/1	0.94	0.07	59,59,59,59	0
57	MG	1A	3646	1/1	0.94	0.07	20,20,20,20	0
57	MG	2a	1680	1/1	0.94	0.13	57,57,57,57	0
57	MG	1A	4052	1/1	0.94	0.10	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	3497	1/1	0.94	0.09	35,35,35,35	0
57	MG	2A	3499	1/1	0.94	0.09	33,33,33,33	0
57	MG	2A	3751	1/1	0.94	0.08	32,32,32,32	0
57	MG	1A	3531	1/1	0.94	0.21	54,54,54,54	0
57	MG	2A	3083	1/1	0.94	0.09	57,57,57,57	0
57	MG	1A	3100	1/1	0.94	0.09	43,43,43,43	0
57	MG	13	103	1/1	0.94	0.09	45,45,45,45	0
57	MG	1A	3379	1/1	0.94	0.18	52,52,52,52	0
57	MG	1A	3653	1/1	0.94	0.07	23,23,23,23	0
57	MG	2A	3291	1/1	0.94	0.11	71,71,71,71	0
57	MG	15	106	1/1	0.94	0.12	33,33,33,33	0
57	MG	2a	1696	1/1	0.94	0.09	50,50,50,50	0
57	MG	1A	3043	1/1	0.94	0.24	37,37,37,37	0
57	MG	2a	1699	1/1	0.94	0.18	61,61,61,61	0
57	MG	1a	1735	1/1	0.94	0.26	58,58,58,58	0
57	MG	2A	3765	1/1	0.94	0.14	79,79,79,79	0
57	MG	2A	3766	1/1	0.94	0.12	54,54,54,54	0
57	MG	17	101	1/1	0.94	0.12	39,39,39,39	0
57	MG	1A	3149	1/1	0.94	0.10	39,39,39,39	0
57	MG	1A	3539	1/1	0.94	0.09	51,51,51,51	0
57	MG	1A	3788	1/1	0.94	0.07	22,22,22,22	0
57	MG	2A	3521	1/1	0.94	0.09	35,35,35,35	0
57	MG	1A	3150	1/1	0.94	0.29	42,42,42,42	0
57	MG	2A	3775	1/1	0.94	0.11	64,64,64,64	0
57	MG	2A	3776	1/1	0.94	0.09	56,56,56,56	0
57	MG	1A	3663	1/1	0.94	0.05	24,24,24,24	0
57	MG	2a	1714	1/1	0.94	0.15	59,59,59,59	0
57	MG	1a	1744	1/1	0.94	0.15	59,59,59,59	0
57	MG	2A	3302	1/1	0.94	0.13	63,63,63,63	0
57	MG	2A	3781	1/1	0.94	0.13	45,45,45,45	0
57	MG	2A	3784	1/1	0.94	0.16	63,63,63,63	0
57	MG	2A	3528	1/1	0.94	0.14	36,36,36,36	0
57	MG	1A	3546	1/1	0.94	0.17	27,27,27,27	0
57	MG	2A	3103	1/1	0.94	0.12	58,58,58,58	0
57	MG	1a	1747	1/1	0.94	0.14	38,38,38,38	0
57	MG	2a	1726	1/1	0.94	0.20	68,68,68,68	0
57	MG	2A	3306	1/1	0.94	0.10	65,65,65,65	0
57	MG	1A	3455	1/1	0.94	0.15	43,43,43,43	0
57	MG	2A	3796	1/1	0.94	0.08	75,75,75,75	0
57	MG	1A	3939	1/1	0.94	0.08	50,50,50,50	0
57	MG	2A	3805	1/1	0.94	0.09	55,55,55,55	0
57	MG	1A	3666	1/1	0.94	0.09	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	2a	1734	1/1	0.94	0.13	53,53,53,53	0
57	MG	1A	4075	1/1	0.94	0.15	55,55,55,55	0
57	MG	1A	3215	1/1	0.94	0.12	43,43,43,43	0
57	MG	1A	3216	1/1	0.94	0.10	47,47,47,47	0
57	MG	1A	3945	1/1	0.94	0.06	35,35,35,35	0
57	MG	1A	3458	1/1	0.94	0.13	59,59,59,59	0
57	MG	1A	3805	1/1	0.94	0.07	27,27,27,27	0
57	MG	2A	3548	1/1	0.94	0.06	27,27,27,27	0
57	MG	1A	3388	1/1	0.94	0.11	70,70,70,70	0
57	MG	1A	3676	1/1	0.94	0.10	24,24,24,24	0
57	MG	2A	3121	1/1	0.94	0.23	60,60,60,60	0
57	MG	1A	3461	1/1	0.94	0.24	73,73,73,73	0
57	MG	2A	3555	1/1	0.94	0.22	55,55,55,55	0
57	MG	1A	3151	1/1	0.94	0.19	32,32,32,32	0
57	MG	1A	3082	1/1	0.94	0.12	42,42,42,42	0
57	MG	1A	3275	1/1	0.94	0.07	41,41,41,41	0
57	MG	1a	1622	1/1	0.94	0.08	65,65,65,65	0
57	MG	2A	3130	1/1	0.94	0.08	44,44,44,44	0
57	MG	1a	1770	1/1	0.94	0.14	60,60,60,60	0
57	MG	1A	3958	1/1	0.94	0.13	46,46,46,46	0
57	MG	1A	3465	1/1	0.94	0.20	47,47,47,47	0
57	MG	2A	3571	1/1	0.94	0.16	55,55,55,55	0
57	MG	1A	3157	1/1	0.94	0.06	32,32,32,32	0
57	MG	1A	3334	1/1	0.94	0.20	49,49,49,49	0
57	MG	1a	1777	1/1	0.94	0.11	69,69,69,69	0
57	MG	1A	3473	1/1	0.94	0.26	64,64,64,64	0
57	MG	1A	3281	1/1	0.94	0.20	33,33,33,33	0
57	MG	1A	3475	1/1	0.94	0.11	45,45,45,45	0
57	MG	1A	3696	1/1	0.94	0.17	51,51,51,51	0
57	MG	1A	3477	1/1	0.94	0.13	47,47,47,47	0
57	MG	1B	217	1/1	0.94	0.09	49,49,49,49	0
57	MG	1a	1784	1/1	0.94	0.12	66,66,66,66	0
57	MG	2A	3152	1/1	0.94	0.12	56,56,56,56	0
57	MG	2A	3155	1/1	0.94	0.07	53,53,53,53	0
57	MG	2A	3345	1/1	0.94	0.13	58,58,58,58	0
57	MG	2A	3346	1/1	0.94	0.08	64,64,64,64	0
57	MG	2A	3156	1/1	0.94	0.14	52,52,52,52	0
57	MG	2B	201	1/1	0.94	0.12	67,67,67,67	0
57	MG	1A	3478	1/1	0.94	0.20	59,59,59,59	0
57	MG	1A	3823	1/1	0.94	0.07	38,38,38,38	0
57	MG	1A	3825	1/1	0.94	0.09	45,45,45,45	0
57	MG	1A	3701	1/1	0.94	0.12	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	1A	3083	1/1	0.94	0.17	36,36,36,36	0
57	MG	1A	3226	1/1	0.94	0.19	50,50,50,50	0
57	MG	1B	229	1/1	0.94	0.08	64,64,64,64	0
57	MG	1A	3584	1/1	0.94	0.09	37,37,37,37	0
57	MG	2A	3607	1/1	0.94	0.08	28,28,28,28	0
57	MG	1a	1645	1/1	0.94	0.39	64,64,64,64	0
57	MG	1A	3104	1/1	0.94	0.22	35,35,35,35	0
57	MG	1A	3084	1/1	0.94	0.15	40,40,40,40	0
57	MG	2A	3360	1/1	0.94	0.08	48,48,48,48	0
57	MG	2A	3170	1/1	0.94	0.09	60,60,60,60	0
57	MG	1A	3291	1/1	0.94	0.19	55,55,55,55	0
57	MG	2v	102	1/1	0.94	0.13	45,45,45,45	0
57	MG	1B	235	1/1	0.94	0.09	39,39,39,39	0
57	MG	1A	3055	1/1	0.94	0.07	44,44,44,44	0
57	MG	1A	3111	1/1	0.94	0.10	41,41,41,41	0
57	MG	2A	3176	1/1	0.94	0.14	57,57,57,57	0
57	MG	1A	3115	1/1	0.94	0.08	38,38,38,38	0
57	MG	2D	301	1/1	0.94	0.23	44,44,44,44	0
57	MG	2D	303	1/1	0.94	0.24	46,46,46,46	0
57	MG	2D	304	1/1	0.94	0.08	51,51,51,51	0
57	MG	1A	3338	1/1	0.95	0.07	52,52,52,52	0
57	MG	1A	3384	1/1	0.95	0.25	30,30,30,30	0
57	MG	2T	3501	1/1	0.95	0.07	51,51,51,51	0
57	MG	1A	3567	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3222	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3569	1/1	0.95	0.21	52,52,52,52	0
57	MG	2A	3455	1/1	0.95	0.14	40,40,40,40	0
57	MG	1A	3979	1/1	0.95	0.06	49,49,49,49	0
57	MG	1A	3493	1/1	0.95	0.07	46,46,46,46	0
57	MG	1a	1631	1/1	0.95	0.23	64,64,64,64	0
57	MG	1a	1772	1/1	0.95	0.12	62,62,62,62	0
57	MG	1B	233	1/1	0.95	0.08	46,46,46,46	0
57	MG	2X	102	1/1	0.95	0.11	49,49,49,49	0
57	MG	1A	3749	1/1	0.95	0.06	25,25,25,25	0
57	MG	1A	3651	1/1	0.95	0.07	27,27,27,27	0
57	MG	2A	3688	1/1	0.95	0.08	38,38,38,38	0
57	MG	2A	3466	1/1	0.95	0.13	40,40,40,40	0
57	MG	1D	301	1/1	0.95	0.07	30,30,30,30	0
57	MG	1A	3433	1/1	0.95	0.20	54,54,54,54	0
57	MG	1A	3574	1/1	0.95	0.15	53,53,53,53	0
57	MG	1A	3857	1/1	0.95	0.29	36,36,36,36	0
57	MG	1A	3304	1/1	0.95	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	1A	3342	1/1	0.95	0.28	51,51,51,51	0
57	MG	1A	3860	1/1	0.95	0.11	28,28,28,28	0
57	MG	1A	3438	1/1	0.95	0.08	49,49,49,49	0
57	MG	1A	3498	1/1	0.95	0.29	29,29,29,29	0
57	MG	2A	3478	1/1	0.95	0.14	55,55,55,55	0
57	MG	1a	1785	1/1	0.95	0.06	66,66,66,66	0
57	MG	1A	3181	1/1	0.95	0.08	32,32,32,32	0
57	MG	1A	3307	1/1	0.95	0.10	47,47,47,47	0
57	MG	1A	3868	1/1	0.95	0.12	24,24,24,24	0
57	MG	2a	1601	1/1	0.95	0.07	54,54,54,54	0
57	MG	2a	1602	1/1	0.95	0.18	53,53,53,53	0
57	MG	1A	3073	1/1	0.95	0.11	13,13,13,13	0
57	MG	2a	1604	1/1	0.95	0.13	57,57,57,57	0
57	MG	1A	3766	1/1	0.95	0.15	56,56,56,56	0
57	MG	2a	1606	1/1	0.95	0.18	60,60,60,60	0
57	MG	1A	3767	1/1	0.95	0.11	54,54,54,54	0
57	MG	1E	313	1/1	0.95	0.25	43,43,43,43	0
57	MG	2A	3487	1/1	0.95	0.14	39,39,39,39	0
57	MG	1A	3034	1/1	0.95	0.24	33,33,33,33	0
57	MG	2A	3489	1/1	0.95	0.15	59,59,59,59	0
57	MG	1A	3769	1/1	0.95	0.08	64,64,64,64	0
57	MG	2A	3716	1/1	0.95	0.11	62,62,62,62	0
57	MG	2a	1614	1/1	0.95	0.15	55,55,55,55	0
57	MG	2A	3135	1/1	0.95	0.10	43,43,43,43	0
57	MG	2A	3493	1/1	0.95	0.07	39,39,39,39	0
57	MG	1A	3153	1/1	0.95	0.11	36,36,36,36	0
57	MG	2a	1618	1/1	0.95	0.19	59,59,59,59	0
57	MG	2A	3720	1/1	0.95	0.10	50,50,50,50	0
57	MG	1A	3446	1/1	0.95	0.14	51,51,51,51	0
57	MG	2A	3496	1/1	0.95	0.07	52,52,52,52	0
57	MG	1A	3674	1/1	0.95	0.09	37,37,37,37	0
57	MG	1A	3880	1/1	0.95	0.10	51,51,51,51	0
57	MG	1a	1659	1/1	0.95	0.11	46,46,46,46	0
57	MG	1A	4011	1/1	0.95	0.09	67,67,67,67	0
57	MG	1F	312	1/1	0.95	0.09	41,41,41,41	0
57	MG	1A	3127	1/1	0.95	0.31	41,41,41,41	0
57	MG	1a	1806	1/1	0.95	0.07	60,60,60,60	0
57	MG	1A	3231	1/1	0.95	0.12	57,57,57,57	0
57	MG	2a	1634	1/1	0.95	0.15	63,63,63,63	0
57	MG	1a	1809	1/1	0.95	0.07	69,69,69,69	0
57	MG	2A	3732	1/1	0.95	0.11	34,34,34,34	0
57	MG	2A	3509	1/1	0.95	0.15	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	3883	1/1	0.95	0.07	47,47,47,47	0
57	MG	1A	3677	1/1	0.95	0.09	24,24,24,24	0
57	MG	2A	3513	1/1	0.95	0.15	56,56,56,56	0
57	MG	2A	3318	1/1	0.95	0.20	52,52,52,52	0
57	MG	2A	3515	1/1	0.95	0.10	55,55,55,55	0
57	MG	2A	3153	1/1	0.95	0.12	38,38,38,38	0
57	MG	1A	3313	1/1	0.95	0.15	42,42,42,42	0
57	MG	1A	3590	1/1	0.95	0.09	39,39,39,39	0
57	MG	1A	3156	1/1	0.95	0.20	37,37,37,37	0
57	MG	2A	3746	1/1	0.95	0.09	62,62,62,62	0
57	MG	1A	3190	1/1	0.95	0.20	35,35,35,35	0
57	MG	1A	3108	1/1	0.95	0.24	39,39,39,39	0
57	MG	1A	3892	1/1	0.95	0.10	44,44,44,44	0
57	MG	1A	3786	1/1	0.95	0.06	41,41,41,41	0
57	MG	1a	1821	1/1	0.95	0.14	60,60,60,60	0
57	MG	1A	3686	1/1	0.95	0.10	29,29,29,29	0
57	MG	1A	3895	1/1	0.95	0.25	36,36,36,36	0
57	MG	1A	3897	1/1	0.95	0.05	29,29,29,29	0
57	MG	2A	3531	1/1	0.95	0.09	33,33,33,33	0
57	MG	1A	3689	1/1	0.95	0.09	53,53,53,53	0
57	MG	1A	3199	1/1	0.95	0.20	42,42,42,42	0
57	MG	1A	3097	1/1	0.95	0.15	34,34,34,34	0
57	MG	2A	3171	1/1	0.95	0.16	39,39,39,39	0
57	MG	1A	3407	1/1	0.95	0.37	49,49,49,49	0
57	MG	1A	3459	1/1	0.95	0.08	71,71,71,71	0
57	MG	1A	3904	1/1	0.95	0.05	77,77,77,77	0
57	MG	1a	1683	1/1	0.95	0.19	60,60,60,60	0
57	MG	1A	3905	1/1	0.95	0.10	67,67,67,67	0
57	MG	1A	3276	1/1	0.95	0.11	45,45,45,45	0
57	MG	2A	3343	1/1	0.95	0.15	69,69,69,69	0
57	MG	2A	3344	1/1	0.95	0.09	58,58,58,58	0
57	MG	1A	3799	1/1	0.95	0.18	65,65,65,65	0
57	MG	1A	3910	1/1	0.95	0.09	63,63,63,63	0
57	MG	1A	3098	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3697	1/1	0.95	0.15	55,55,55,55	0
57	MG	2A	3554	1/1	0.95	0.06	55,55,55,55	0
57	MG	1A	3802	1/1	0.95	0.40	30,30,30,30	0
57	MG	1A	3606	1/1	0.95	0.11	26,26,26,26	0
57	MG	1U	204	1/1	0.95	0.11	34,34,34,34	0
57	MG	2A	3782	1/1	0.95	0.11	75,75,75,75	0
57	MG	2a	1683	1/1	0.95	0.13	59,59,59,59	0
57	MG	1A	3916	1/1	0.95	0.10	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3607	1/1	0.95	0.08	36,36,36,36	0
57	MG	1A	3919	1/1	0.95	0.12	54,54,54,54	0
57	MG	1A	3806	1/1	0.95	0.08	32,32,32,32	0
57	MG	2A	3791	1/1	0.95	0.07	32,32,32,32	0
57	MG	1A	3926	1/1	0.95	0.07	51,51,51,51	0
57	MG	2A	3568	1/1	0.95	0.10	54,54,54,54	0
57	MG	2A	3569	1/1	0.95	0.12	60,60,60,60	0
57	MG	1a	1698	1/1	0.95	0.28	52,52,52,52	0
57	MG	2A	3797	1/1	0.95	0.17	30,30,30,30	0
57	MG	1A	3927	1/1	0.95	0.07	55,55,55,55	0
57	MG	2a	1697	1/1	0.95	0.17	63,63,63,63	0
57	MG	2A	3803	1/1	0.95	0.08	69,69,69,69	0
57	MG	2A	3195	1/1	0.95	0.12	65,65,65,65	0
57	MG	1A	3077	1/1	0.95	0.20	45,45,45,45	0
57	MG	1A	3065	1/1	0.95	0.10	36,36,36,36	0
57	MG	2A	3009	1/1	0.95	0.13	63,63,63,63	0
57	MG	2A	3811	1/1	0.95	0.09	33,33,33,33	0
57	MG	2A	3010	1/1	0.95	0.20	39,39,39,39	0
57	MG	1A	3117	1/1	0.95	0.24	42,42,42,42	0
57	MG	2A	3014	1/1	0.95	0.19	39,39,39,39	0
57	MG	2A	3015	1/1	0.95	0.17	64,64,64,64	0
57	MG	2A	3016	1/1	0.95	0.16	50,50,50,50	0
57	MG	1X	104	1/1	0.95	0.08	42,42,42,42	0
57	MG	1A	3367	1/1	0.95	0.26	57,57,57,57	0
57	MG	2a	1712	1/1	0.95	0.08	51,51,51,51	0
57	MG	2A	3021	1/1	0.95	0.31	42,42,42,42	0
57	MG	2A	3823	1/1	0.95	0.10	21,21,21,21	0
57	MG	1A	3140	1/1	0.95	0.10	37,37,37,37	0
57	MG	2a	1717	1/1	0.95	0.12	54,54,54,54	0
57	MG	2A	3374	1/1	0.95	0.11	67,67,67,67	0
57	MG	1A	3935	1/1	0.95	0.07	66,66,66,66	0
57	MG	1Z	301	1/1	0.95	0.07	60,60,60,60	0
57	MG	2A	3593	1/1	0.95	0.11	29,29,29,29	0
57	MG	2A	3378	1/1	0.95	0.07	50,50,50,50	0
57	MG	2A	3025	1/1	0.95	0.19	45,45,45,45	0
57	MG	2A	3597	1/1	0.95	0.08	40,40,40,40	0
57	MG	2A	3027	1/1	0.95	0.17	45,45,45,45	0
57	MG	1A	3066	1/1	0.95	0.08	50,50,50,50	0
57	MG	2A	3029	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3813	1/1	0.95	0.14	48,48,48,48	0
57	MG	2A	3603	1/1	0.95	0.21	58,58,58,58	0
57	MG	1A	4066	1/1	0.95	0.17	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	1A	3938	1/1	0.95	0.05	58,58,58,58	0
57	MG	1A	3471	1/1	0.95	0.24	37,37,37,37	0
57	MG	2a	1735	1/1	0.95	0.15	52,52,52,52	0
57	MG	2A	3221	1/1	0.95	0.08	39,39,39,39	0
57	MG	2A	3035	1/1	0.95	0.13	37,37,37,37	0
57	MG	2A	3224	1/1	0.95	0.26	42,42,42,42	0
57	MG	1A	3472	1/1	0.95	0.08	48,48,48,48	0
57	MG	1A	3711	1/1	0.95	0.20	61,61,61,61	0
57	MG	11	103	1/1	0.95	0.06	43,43,43,43	0
57	MG	1A	3120	1/1	0.95	0.13	47,47,47,47	0
57	MG	2A	3042	1/1	0.95	0.29	59,59,59,59	0
57	MG	1A	3944	1/1	0.95	0.06	45,45,45,45	0
57	MG	1A	3293	1/1	0.95	0.06	44,44,44,44	0
57	MG	1A	3121	1/1	0.95	0.13	38,38,38,38	0
57	MG	2A	3621	1/1	0.95	0.08	65,65,65,65	0
57	MG	2A	3400	1/1	0.95	0.23	52,52,52,52	0
57	MG	1A	3535	1/1	0.95	0.10	63,63,63,63	0
57	MG	1A	3009	1/1	0.95	0.06	22,22,22,22	0
57	MG	1A	4082	1/1	0.95	0.06	51,51,51,51	0
57	MG	2A	3049	1/1	0.95	0.10	33,33,33,33	0
57	MG	1A	3537	1/1	0.95	0.28	32,32,32,32	0
57	MG	2a	1756	1/1	0.95	0.24	62,62,62,62	0
57	MG	2A	3051	1/1	0.95	0.11	43,43,43,43	0
57	MG	2B	210	1/1	0.95	0.10	70,70,70,70	0
57	MG	17	103	1/1	0.95	0.14	55,55,55,55	0
57	MG	1A	3255	1/1	0.95	0.23	47,47,47,47	0
57	MG	2a	1761	1/1	0.95	0.07	53,53,53,53	0
57	MG	1A	3951	1/1	0.95	0.10	24,24,24,24	0
57	MG	2a	1763	1/1	0.95	0.16	52,52,52,52	0
57	MG	18	101	1/1	0.95	0.18	42,42,42,42	0
57	MG	1A	3824	1/1	0.95	0.14	52,52,52,52	0
57	MG	1A	3175	1/1	0.95	0.24	31,31,31,31	0
57	MG	2A	3059	1/1	0.95	0.09	49,49,49,49	0
57	MG	1A	4088	1/1	0.95	0.05	40,40,40,40	0
57	MG	1A	3954	1/1	0.95	0.14	51,51,51,51	0
57	MG	1A	3177	1/1	0.95	0.09	30,30,30,30	0
57	MG	2A	3417	1/1	0.95	0.19	56,56,56,56	0
57	MG	2A	3418	1/1	0.95	0.40	56,56,56,56	0
57	MG	1A	3632	1/1	0.95	0.04	24,24,24,24	0
57	MG	1B	203	1/1	0.95	0.24	68,68,68,68	0
57	MG	2A	3251	1/1	0.95	0.07	52,52,52,52	0
57	MG	2A	3066	1/1	0.95	0.20	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	1B	204	1/1	0.95	0.07	41,41,41,41	0
57	MG	1A	3484	1/1	0.95	0.10	44,44,44,44	0
57	MG	1A	3730	1/1	0.95	0.06	30,30,30,30	0
57	MG	1A	3485	1/1	0.95	0.23	32,32,32,32	0
57	MG	2A	3071	1/1	0.95	0.05	51,51,51,51	0
57	MG	1A	3733	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3636	1/1	0.95	0.07	39,39,39,39	0
57	MG	2A	3077	1/1	0.95	0.11	42,42,42,42	0
57	MG	1A	3834	1/1	0.95	0.08	19,19,19,19	0
57	MG	1A	3486	1/1	0.95	0.06	41,41,41,41	0
57	MG	1A	3258	1/1	0.95	0.13	27,27,27,27	0
57	MG	2A	3439	1/1	0.95	0.10	62,62,62,62	0
57	MG	1a	1616	1/1	0.95	0.08	73,73,73,73	0
57	MG	2q	202	1/1	0.95	0.06	72,72,72,72	0
57	MG	2F	304	1/1	0.95	0.07	53,53,53,53	0
57	MG	1A	3488	1/1	0.95	0.09	60,60,60,60	0
57	MG	1A	3838	1/1	0.95	0.09	20,20,20,20	0
57	MG	1a	1619	1/1	0.95	0.21	52,52,52,52	0
57	MG	1A	3221	1/1	0.95	0.17	42,42,42,42	0
57	MG	2A	3668	1/1	0.95	0.10	65,65,65,65	0
57	MG	1a	1760	1/1	0.95	0.06	46,46,46,46	0
57	MG	2A	3670	1/1	0.95	0.05	43,43,43,43	0
57	MG	1A	3560	1/1	0.95	0.12	52,52,52,52	0
57	MG	2Q	201	1/1	0.95	0.15	57,57,57,57	0
57	MG	2A	3448	1/1	0.95	0.11	55,55,55,55	0
57	MG	2Q	204	1/1	0.95	0.07	45,45,45,45	0
58	K	1A	3549	1/1	0.95	0.11	73,73,73,73	0
59	ZN	14	501	1/1	0.95	0.11	117,117,117,117	0
59	ZN	24	501	1/1	0.95	0.11	127,127,127,127	0
57	MG	15	102	1/1	0.96	0.24	33,33,33,33	0
57	MG	2A	3664	1/1	0.96	0.08	58,58,58,58	0
57	MG	15	103	1/1	0.96	0.23	35,35,35,35	0
57	MG	2A	3666	1/1	0.96	0.09	54,54,54,54	0
57	MG	1A	3763	1/1	0.96	0.10	31,31,31,31	0
57	MG	1A	3499	1/1	0.96	0.22	41,41,41,41	0
57	MG	2A	3054	1/1	0.96	0.07	49,49,49,49	0
57	MG	1A	3862	1/1	0.96	0.06	31,31,31,31	0
57	MG	16	101	1/1	0.96	0.08	57,57,57,57	0
57	MG	1A	3243	1/1	0.96	0.18	35,35,35,35	0
57	MG	1A	3502	1/1	0.96	0.18	38,38,38,38	0
57	MG	17	104	1/1	0.96	0.11	34,34,34,34	0
57	MG	1A	3381	1/1	0.96	0.14	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1738	1/1	0.96	0.06	50,50,50,50	0
57	MG	1A	3866	1/1	0.96	0.06	27,27,27,27	0
57	MG	1A	3440	1/1	0.96	0.25	41,41,41,41	0
57	MG	1a	1741	1/1	0.96	0.15	58,58,58,58	0
57	MG	1A	3197	1/1	0.96	0.09	48,48,48,48	0
57	MG	2A	3452	1/1	0.96	0.23	42,42,42,42	0
57	MG	1A	3871	1/1	0.96	0.08	44,44,44,44	0
57	MG	1A	3112	1/1	0.96	0.20	34,34,34,34	0
57	MG	1A	3443	1/1	0.96	0.13	56,56,56,56	0
57	MG	2A	3260	1/1	0.96	0.17	50,50,50,50	0
57	MG	1a	1746	1/1	0.96	0.06	36,36,36,36	0
57	MG	25	105	1/1	0.96	0.13	51,51,51,51	0
57	MG	1A	3114	1/1	0.96	0.08	34,34,34,34	0
57	MG	1A	3203	1/1	0.96	0.08	29,29,29,29	0
57	MG	2A	3074	1/1	0.96	0.06	43,43,43,43	0
57	MG	2A	3075	1/1	0.96	0.07	24,24,24,24	0
57	MG	2A	3694	1/1	0.96	0.05	38,38,38,38	0
57	MG	2A	3266	1/1	0.96	0.15	68,68,68,68	0
57	MG	1A	3776	1/1	0.96	0.14	59,59,59,59	0
57	MG	1A	3002	1/1	0.96	0.08	40,40,40,40	0
57	MG	1A	3680	1/1	0.96	0.08	43,43,43,43	0
57	MG	2A	3469	1/1	0.96	0.16	50,50,50,50	0
57	MG	1B	226	1/1	0.96	0.08	56,56,56,56	0
57	MG	2A	3080	1/1	0.96	0.12	51,51,51,51	0
57	MG	1a	1755	1/1	0.96	0.09	44,44,44,44	0
57	MG	1B	228	1/1	0.96	0.06	38,38,38,38	0
57	MG	1A	3779	1/1	0.96	0.05	24,24,24,24	0
57	MG	1A	3249	1/1	0.96	0.17	44,44,44,44	0
57	MG	1A	3994	1/1	0.96	0.06	67,67,67,67	0
57	MG	1A	3162	1/1	0.96	0.23	28,28,28,28	0
57	MG	1a	1614	1/1	0.96	0.11	30,30,30,30	0
57	MG	1A	3391	1/1	0.96	0.17	34,34,34,34	0
57	MG	2A	3089	1/1	0.96	0.15	38,38,38,38	0
57	MG	1A	3025	1/1	0.96	0.14	36,36,36,36	0
57	MG	1A	3685	1/1	0.96	0.06	56,56,56,56	0
57	MG	2A	3092	1/1	0.96	0.11	39,39,39,39	0
57	MG	1B	236	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3208	1/1	0.96	0.19	36,36,36,36	0
57	MG	2A	3095	1/1	0.96	0.11	43,43,43,43	0
57	MG	1A	3688	1/1	0.96	0.06	13,13,13,13	0
57	MG	1D	304	1/1	0.96	0.12	40,40,40,40	0
57	MG	2A	3490	1/1	0.96	0.08	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	1771	1/1	0.96	0.06	60,60,60,60	0
57	MG	1D	306	1/1	0.96	0.06	35,35,35,35	0
57	MG	1a	1624	1/1	0.96	0.10	57,57,57,57	0
57	MG	2a	1627	1/1	0.96	0.23	53,53,53,53	0
57	MG	1A	3517	1/1	0.96	0.26	48,48,48,48	0
57	MG	1A	3135	1/1	0.96	0.05	38,38,38,38	0
57	MG	1A	3344	1/1	0.96	0.26	56,56,56,56	0
57	MG	1A	3600	1/1	0.96	0.11	15,15,15,15	0
57	MG	1A	3796	1/1	0.96	0.16	43,43,43,43	0
57	MG	1A	3797	1/1	0.96	0.08	58,58,58,58	0
57	MG	2A	3501	1/1	0.96	0.08	27,27,27,27	0
57	MG	1E	302	1/1	0.96	0.09	39,39,39,39	0
57	MG	1A	3347	1/1	0.96	0.14	41,41,41,41	0
57	MG	2a	1638	1/1	0.96	0.17	53,53,53,53	0
57	MG	1A	3136	1/1	0.96	0.07	32,32,32,32	0
57	MG	2A	3113	1/1	0.96	0.19	51,51,51,51	0
57	MG	2A	3114	1/1	0.96	0.07	49,49,49,49	0
57	MG	1A	3604	1/1	0.96	0.08	36,36,36,36	0
57	MG	1A	3067	1/1	0.96	0.07	35,35,35,35	0
57	MG	2A	3739	1/1	0.96	0.13	57,57,57,57	0
57	MG	1A	3302	1/1	0.96	0.33	48,48,48,48	0
57	MG	1a	1637	1/1	0.96	0.15	28,28,28,28	0
57	MG	2A	3742	1/1	0.96	0.06	49,49,49,49	0
57	MG	2A	3512	1/1	0.96	0.07	49,49,49,49	0
57	MG	1A	3902	1/1	0.96	0.13	55,55,55,55	0
57	MG	1A	3303	1/1	0.96	0.18	50,50,50,50	0
57	MG	1A	4020	1/1	0.96	0.05	71,71,71,71	0
57	MG	2a	1653	1/1	0.96	0.11	48,48,48,48	0
57	MG	1A	3804	1/1	0.96	0.07	40,40,40,40	0
57	MG	1A	3525	1/1	0.96	0.13	26,26,26,26	0
57	MG	1F	302	1/1	0.96	0.13	36,36,36,36	0
57	MG	1a	1644	1/1	0.96	0.19	58,58,58,58	0
57	MG	2A	3520	1/1	0.96	0.10	36,36,36,36	0
57	MG	2A	3127	1/1	0.96	0.05	46,46,46,46	0
57	MG	2A	3754	1/1	0.96	0.06	60,60,60,60	0
57	MG	2A	3129	1/1	0.96	0.07	61,61,61,61	0
57	MG	1A	3402	1/1	0.96	0.10	53,53,53,53	0
57	MG	2A	3131	1/1	0.96	0.15	41,41,41,41	0
57	MG	2A	3132	1/1	0.96	0.08	41,41,41,41	0
57	MG	1A	4024	1/1	0.96	0.05	48,48,48,48	0
57	MG	2A	3134	1/1	0.96	0.14	34,34,34,34	0
57	MG	1A	3139	1/1	0.96	0.29	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3059	1/1	0.96	0.07	44,44,44,44	0
57	MG	1F	308	1/1	0.96	0.07	36,36,36,36	0
57	MG	2A	3138	1/1	0.96	0.21	49,49,49,49	0
57	MG	2A	3767	1/1	0.96	0.06	52,52,52,52	0
57	MG	2a	1673	1/1	0.96	0.14	47,47,47,47	0
57	MG	1F	309	1/1	0.96	0.16	22,22,22,22	0
57	MG	1F	310	1/1	0.96	0.12	27,27,27,27	0
57	MG	1a	1802	1/1	0.96	0.14	58,58,58,58	0
57	MG	2A	3537	1/1	0.96	0.07	33,33,33,33	0
57	MG	2A	3142	1/1	0.96	0.20	56,56,56,56	0
57	MG	1a	1803	1/1	0.96	0.07	50,50,50,50	0
57	MG	1A	3141	1/1	0.96	0.16	37,37,37,37	0
57	MG	1A	3530	1/1	0.96	0.12	55,55,55,55	0
57	MG	1A	4031	1/1	0.96	0.09	51,51,51,51	0
57	MG	1A	3466	1/1	0.96	0.08	42,42,42,42	0
57	MG	2A	3546	1/1	0.96	0.09	40,40,40,40	0
57	MG	1A	3620	1/1	0.96	0.06	46,46,46,46	0
57	MG	2A	3150	1/1	0.96	0.08	55,55,55,55	0
57	MG	2a	1687	1/1	0.96	0.08	53,53,53,53	0
57	MG	1A	3218	1/1	0.96	0.21	38,38,38,38	0
57	MG	2A	3785	1/1	0.96	0.06	48,48,48,48	0
57	MG	2a	1690	1/1	0.96	0.17	58,58,58,58	0
57	MG	1A	3410	1/1	0.96	0.10	53,53,53,53	0
57	MG	1A	3143	1/1	0.96	0.06	16,16,16,16	0
57	MG	1A	3715	1/1	0.96	0.08	38,38,38,38	0
57	MG	1A	3019	1/1	0.96	0.16	52,52,52,52	0
57	MG	2A	3342	1/1	0.96	0.08	66,66,66,66	0
57	MG	2A	3793	1/1	0.96	0.11	48,48,48,48	0
57	MG	1A	3041	1/1	0.96	0.07	28,28,28,28	0
57	MG	1A	3122	1/1	0.96	0.14	42,42,42,42	0
57	MG	2A	3159	1/1	0.96	0.16	54,54,54,54	0
57	MG	1a	1664	1/1	0.96	0.08	57,57,57,57	0
57	MG	2A	3798	1/1	0.96	0.11	29,29,29,29	0
57	MG	2A	3799	1/1	0.96	0.06	48,48,48,48	0
57	MG	1A	3538	1/1	0.96	0.21	34,34,34,34	0
57	MG	2A	3801	1/1	0.96	0.10	37,37,37,37	0
57	MG	2a	1705	1/1	0.96	0.08	52,52,52,52	0
57	MG	1A	3105	1/1	0.96	0.08	49,49,49,49	0
57	MG	1A	3362	1/1	0.96	0.24	41,41,41,41	0
57	MG	1A	3007	1/1	0.96	0.12	36,36,36,36	0
57	MG	2A	3808	1/1	0.96	0.08	54,54,54,54	0
57	MG	2A	3351	1/1	0.96	0.16	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3080	1/1	0.96	0.07	62,62,62,62	0
57	MG	2A	3166	1/1	0.96	0.19	66,66,66,66	0
57	MG	2A	3574	1/1	0.96	0.09	47,47,47,47	0
57	MG	1A	3152	1/1	0.96	0.17	36,36,36,36	0
57	MG	2a	1715	1/1	0.96	0.15	49,49,49,49	0
57	MG	1A	4048	1/1	0.96	0.08	21,21,21,21	0
57	MG	2A	3816	1/1	0.96	0.10	69,69,69,69	0
57	MG	1P	203	1/1	0.96	0.28	31,31,31,31	0
57	MG	1A	3635	1/1	0.96	0.09	37,37,37,37	0
57	MG	2A	3579	1/1	0.96	0.06	57,57,57,57	0
57	MG	1A	3186	1/1	0.96	0.08	36,36,36,36	0
57	MG	1Q	203	1/1	0.96	0.08	31,31,31,31	0
57	MG	1A	3022	1/1	0.96	0.07	44,44,44,44	0
57	MG	1Q	206	1/1	0.96	0.10	47,47,47,47	0
57	MG	1Q	207	1/1	0.96	0.08	47,47,47,47	0
57	MG	1Q	208	1/1	0.96	0.13	35,35,35,35	0
57	MG	2a	1728	1/1	0.96	0.12	60,60,60,60	0
57	MG	1t	201	1/1	0.96	0.11	58,58,58,58	0
57	MG	2A	3588	1/1	0.96	0.12	38,38,38,38	0
57	MG	1A	3271	1/1	0.96	0.08	32,32,32,32	0
57	MG	1w	402	1/1	0.96	0.07	49,49,49,49	0
57	MG	2A	3181	1/1	0.96	0.12	57,57,57,57	0
57	MG	2A	3182	1/1	0.96	0.08	56,56,56,56	0
57	MG	1A	4053	1/1	0.96	0.06	40,40,40,40	0
57	MG	2a	1736	1/1	0.96	0.15	56,56,56,56	0
57	MG	2A	3594	1/1	0.96	0.05	32,32,32,32	0
57	MG	1A	3941	1/1	0.96	0.09	56,56,56,56	0
57	MG	1A	3128	1/1	0.96	0.17	28,28,28,28	0
57	MG	1A	3556	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	3558	1/1	0.96	0.21	37,37,37,37	0
57	MG	1A	3274	1/1	0.96	0.20	33,33,33,33	0
57	MG	2A	3600	1/1	0.96	0.15	57,57,57,57	0
57	MG	1A	3739	1/1	0.96	0.11	46,46,46,46	0
57	MG	1x	108	1/1	0.96	0.12	55,55,55,55	0
57	MG	1A	4061	1/1	0.96	0.07	52,52,52,52	0
57	MG	1A	3644	1/1	0.96	0.07	29,29,29,29	0
57	MG	1x	113	1/1	0.96	0.12	50,50,50,50	0
57	MG	1A	3371	1/1	0.96	0.20	47,47,47,47	0
57	MG	1U	207	1/1	0.96	0.25	33,33,33,33	0
57	MG	1A	4064	1/1	0.96	0.08	50,50,50,50	0
57	MG	1A	3194	1/1	0.96	0.39	34,34,34,34	0
57	MG	2A	3006	1/1	0.96	0.15	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	3839	1/1	0.96	0.10	26,26,26,26	0
57	MG	1V	204	1/1	0.96	0.18	54,54,54,54	0
57	MG	2A	3201	1/1	0.96	0.12	53,53,53,53	0
57	MG	2A	3616	1/1	0.96	0.07	35,35,35,35	0
57	MG	1A	3840	1/1	0.96	0.14	33,33,33,33	0
57	MG	1A	3429	1/1	0.96	0.24	40,40,40,40	0
57	MG	2A	3013	1/1	0.96	0.07	40,40,40,40	0
57	MG	1W	205	1/1	0.96	0.13	35,35,35,35	0
57	MG	1A	3842	1/1	0.96	0.26	37,37,37,37	0
57	MG	1X	101	1/1	0.96	0.04	29,29,29,29	0
57	MG	2A	3208	1/1	0.96	0.13	51,51,51,51	0
57	MG	1A	3064	1/1	0.96	0.15	38,38,38,38	0
57	MG	2A	3398	1/1	0.96	0.19	42,42,42,42	0
57	MG	2A	3399	1/1	0.96	0.22	45,45,45,45	0
57	MG	1A	3955	1/1	0.96	0.13	47,47,47,47	0
57	MG	1X	105	1/1	0.96	0.18	37,37,37,37	0
57	MG	1A	3236	1/1	0.96	0.22	30,30,30,30	0
57	MG	1A	3570	1/1	0.96	0.09	41,41,41,41	0
57	MG	1A	3652	1/1	0.96	0.07	28,28,28,28	0
57	MG	1Y	204	1/1	0.96	0.23	43,43,43,43	0
57	MG	1A	3960	1/1	0.96	0.11	49,49,49,49	0
57	MG	1A	3279	1/1	0.96	0.18	35,35,35,35	0
57	MG	1A	4081	1/1	0.96	0.17	46,46,46,46	0
57	MG	1a	1711	1/1	0.96	0.06	51,51,51,51	0
57	MG	2D	305	1/1	0.96	0.09	29,29,29,29	0
57	MG	1a	1712	1/1	0.96	0.09	52,52,52,52	0
57	MG	2A	3222	1/1	0.96	0.14	46,46,46,46	0
57	MG	2A	3640	1/1	0.96	0.06	35,35,35,35	0
57	MG	2A	3032	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3196	1/1	0.96	0.23	29,29,29,29	0
57	MG	1A	3656	1/1	0.96	0.12	42,42,42,42	0
57	MG	1A	3435	1/1	0.96	0.16	33,33,33,33	0
57	MG	1A	3659	1/1	0.96	0.05	20,20,20,20	0
57	MG	10	108	1/1	0.96	0.10	45,45,45,45	0
57	MG	2A	3647	1/1	0.96	0.07	51,51,51,51	0
57	MG	2A	3038	1/1	0.96	0.11	23,23,23,23	0
57	MG	1A	3242	1/1	0.96	0.36	35,35,35,35	0
57	MG	2F	301	1/1	0.96	0.13	48,48,48,48	0
57	MG	2A	3040	1/1	0.96	0.10	52,52,52,52	0
57	MG	1a	1719	1/1	0.96	0.12	60,60,60,60	0
57	MG	2w	401	1/1	0.96	0.06	44,44,44,44	0
57	MG	11	102	1/1	0.96	0.07	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2x	102	1/1	0.96	0.17	65,65,65,65	0
57	MG	1A	3661	1/1	0.96	0.06	22,22,22,22	0
57	MG	1A	3759	1/1	0.96	0.08	22,22,22,22	0
57	MG	1A	3969	1/1	0.96	0.16	57,57,57,57	0
57	MG	2x	106	1/1	0.96	0.12	57,57,57,57	0
57	MG	13	102	1/1	0.96	0.06	41,41,41,41	0
57	MG	2F	309	1/1	0.96	0.18	38,38,38,38	0
57	MG	1a	1725	1/1	0.96	0.08	53,53,53,53	0
57	MG	1A	3576	1/1	0.96	0.17	32,32,32,32	0
57	MG	2A	3432	1/1	0.96	0.27	53,53,53,53	0
57	MG	1A	3286	1/1	0.96	0.10	32,32,32,32	0
59	ZN	1n	102	1/1	0.96	0.05	85,85,85,85	0
57	MG	2A	3434	1/1	0.96	0.37	65,65,65,65	0
57	MG	1A	3404	1/1	0.97	0.13	41,41,41,41	0
57	MG	1A	3178	1/1	0.97	0.15	29,29,29,29	0
57	MG	1A	3028	1/1	0.97	0.14	26,26,26,26	0
57	MG	2a	1647	1/1	0.97	0.17	32,32,32,32	0
57	MG	1A	3217	1/1	0.97	0.19	36,36,36,36	0
57	MG	2A	3060	1/1	0.97	0.05	38,38,38,38	0
57	MG	1A	4071	1/1	0.97	0.06	46,46,46,46	0
57	MG	1A	3467	1/1	0.97	0.09	51,51,51,51	0
57	MG	1A	3113	1/1	0.97	0.10	37,37,37,37	0
57	MG	1A	3081	1/1	0.97	0.15	32,32,32,32	0
57	MG	1A	4076	1/1	0.97	0.04	36,36,36,36	0
57	MG	1A	3038	1/1	0.97	0.18	32,32,32,32	0
57	MG	1A	3305	1/1	0.97	0.08	19,19,19,19	0
57	MG	1R	203	1/1	0.97	0.12	39,39,39,39	0
57	MG	1A	3780	1/1	0.97	0.05	21,21,21,21	0
57	MG	1A	3692	1/1	0.97	0.06	54,54,54,54	0
57	MG	1A	3133	1/1	0.97	0.07	38,38,38,38	0
57	MG	1A	3874	1/1	0.97	0.11	26,26,26,26	0
57	MG	2A	3839	1/1	0.97	0.04	58,58,58,58	0
57	MG	2a	1663	1/1	0.97	0.17	55,55,55,55	0
57	MG	2A	3504	1/1	0.97	0.04	30,30,30,30	0
57	MG	2A	3073	1/1	0.97	0.16	52,52,52,52	0
57	MG	1A	3358	1/1	0.97	0.09	53,53,53,53	0
57	MG	2A	3217	1/1	0.97	0.27	35,35,35,35	0
57	MG	1A	3784	1/1	0.97	0.07	35,35,35,35	0
57	MG	1T	202	1/1	0.97	0.07	54,54,54,54	0
57	MG	1U	201	1/1	0.97	0.20	37,37,37,37	0
57	MG	1A	3012	1/1	0.97	0.04	26,26,26,26	0
57	MG	1A	3618	1/1	0.97	0.10	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	3187	1/1	0.97	0.07	43,43,43,43	0
57	MG	1A	3188	1/1	0.97	0.07	37,37,37,37	0
57	MG	1A	3789	1/1	0.97	0.07	16,16,16,16	0
57	MG	1U	208	1/1	0.97	0.17	32,32,32,32	0
57	MG	1A	3479	1/1	0.97	0.12	39,39,39,39	0
57	MG	1A	3700	1/1	0.97	0.04	16,16,16,16	0
57	MG	1V	201	1/1	0.97	0.33	29,29,29,29	0
57	MG	1A	3541	1/1	0.97	0.20	32,32,32,32	0
57	MG	1A	3068	1/1	0.97	0.04	33,33,33,33	0
57	MG	1A	3987	1/1	0.97	0.05	50,50,50,50	0
57	MG	1a	1801	1/1	0.97	0.06	52,52,52,52	0
57	MG	1B	206	1/1	0.97	0.08	39,39,39,39	0
57	MG	2A	3375	1/1	0.97	0.21	57,57,57,57	0
57	MG	1W	202	1/1	0.97	0.16	52,52,52,52	0
57	MG	1W	203	1/1	0.97	0.13	37,37,37,37	0
57	MG	1W	204	1/1	0.97	0.21	37,37,37,37	0
57	MG	1B	207	1/1	0.97	0.16	40,40,40,40	0
57	MG	1A	3030	1/1	0.97	0.13	33,33,33,33	0
57	MG	1A	3704	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3483	1/1	0.97	0.22	30,30,30,30	0
57	MG	1X	103	1/1	0.97	0.10	42,42,42,42	0
57	MG	2A	3100	1/1	0.97	0.08	25,25,25,25	0
57	MG	1A	3228	1/1	0.97	0.19	29,29,29,29	0
57	MG	1A	3266	1/1	0.97	0.14	38,38,38,38	0
57	MG	2A	3540	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3629	1/1	0.97	0.07	31,31,31,31	0
57	MG	1A	3229	1/1	0.97	0.12	29,29,29,29	0
57	MG	1B	215	1/1	0.97	0.06	50,50,50,50	0
57	MG	1A	3193	1/1	0.97	0.04	38,38,38,38	0
57	MG	2A	3709	1/1	0.97	0.14	33,33,33,33	0
57	MG	1A	3137	1/1	0.97	0.12	36,36,36,36	0
57	MG	1B	219	1/1	0.97	0.10	36,36,36,36	0
57	MG	2A	3547	1/1	0.97	0.05	30,30,30,30	0
57	MG	2A	3713	1/1	0.97	0.07	50,50,50,50	0
57	MG	10	101	1/1	0.97	0.06	47,47,47,47	0
57	MG	10	102	1/1	0.97	0.20	45,45,45,45	0
57	MG	1A	3161	1/1	0.97	0.26	30,30,30,30	0
57	MG	1d	301	1/1	0.97	0.28	48,48,48,48	0
57	MG	1A	3557	1/1	0.97	0.20	38,38,38,38	0
57	MG	1A	3087	1/1	0.97	0.26	36,36,36,36	0
57	MG	1A	4002	1/1	0.97	0.10	22,22,22,22	0
57	MG	1A	3428	1/1	0.97	0.16	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	3561	1/1	0.97	0.20	34,34,34,34	0
57	MG	1B	227	1/1	0.97	0.05	41,41,41,41	0
57	MG	1A	3721	1/1	0.97	0.06	46,46,46,46	0
57	MG	1A	3722	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	4009	1/1	0.97	0.04	41,41,41,41	0
57	MG	1A	3562	1/1	0.97	0.15	38,38,38,38	0
57	MG	1A	3907	1/1	0.97	0.05	40,40,40,40	0
57	MG	1A	3319	1/1	0.97	0.13	32,32,32,32	0
57	MG	2A	3128	1/1	0.97	0.15	47,47,47,47	0
57	MG	2a	1724	1/1	0.97	0.14	47,47,47,47	0
57	MG	1A	3163	1/1	0.97	0.10	26,26,26,26	0
57	MG	15	101	1/1	0.97	0.07	37,37,37,37	0
57	MG	2A	3573	1/1	0.97	0.13	64,64,64,64	0
57	MG	1A	3726	1/1	0.97	0.06	48,48,48,48	0
57	MG	1A	3641	1/1	0.97	0.11	37,37,37,37	0
57	MG	2Q	202	1/1	0.97	0.23	50,50,50,50	0
57	MG	1A	3235	1/1	0.97	0.09	62,62,62,62	0
57	MG	1A	3198	1/1	0.97	0.08	40,40,40,40	0
57	MG	1D	303	1/1	0.97	0.11	49,49,49,49	0
57	MG	1A	3237	1/1	0.97	0.07	24,24,24,24	0
57	MG	1A	3434	1/1	0.97	0.16	26,26,26,26	0
57	MG	2A	3419	1/1	0.97	0.24	49,49,49,49	0
57	MG	1x	109	1/1	0.97	0.13	58,58,58,58	0
57	MG	17	102	1/1	0.97	0.12	28,28,28,28	0
57	MG	1A	3917	1/1	0.97	0.05	12,12,12,12	0
57	MG	1A	3072	1/1	0.97	0.21	30,30,30,30	0
57	MG	1A	3278	1/1	0.97	0.14	26,26,26,26	0
57	MG	1D	311	1/1	0.97	0.14	31,31,31,31	0
57	MG	2A	3003	1/1	0.97	0.30	52,52,52,52	0
57	MG	2A	3427	1/1	0.97	0.08	30,30,30,30	0
57	MG	1A	3239	1/1	0.97	0.13	34,34,34,34	0
57	MG	2A	3429	1/1	0.97	0.17	38,38,38,38	0
57	MG	20	101	1/1	0.97	0.05	57,57,57,57	0
57	MG	1A	3924	1/1	0.97	0.09	42,42,42,42	0
57	MG	2a	1749	1/1	0.97	0.18	68,68,68,68	0
57	MG	1A	3925	1/1	0.97	0.05	57,57,57,57	0
57	MG	1A	3280	1/1	0.97	0.39	39,39,39,39	0
57	MG	1E	303	1/1	0.97	0.07	28,28,28,28	0
57	MG	23	103	1/1	0.97	0.05	41,41,41,41	0
57	MG	1A	3240	1/1	0.97	0.06	30,30,30,30	0
57	MG	1A	3283	1/1	0.97	0.26	35,35,35,35	0
57	MG	2A	3012	1/1	0.97	0.08	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	2A	3154	1/1	0.97	0.08	50,50,50,50	0
57	MG	2A	3762	1/1	0.97	0.06	57,57,57,57	0
57	MG	1E	307	1/1	0.97	0.09	23,23,23,23	0
57	MG	1A	3284	1/1	0.97	0.08	38,38,38,38	0
57	MG	1A	3740	1/1	0.97	0.06	25,25,25,25	0
57	MG	1A	3241	1/1	0.97	0.26	37,37,37,37	0
57	MG	1a	1608	1/1	0.97	0.06	74,74,74,74	0
57	MG	2A	3018	1/1	0.97	0.07	38,38,38,38	0
57	MG	1A	3032	1/1	0.97	0.16	24,24,24,24	0
57	MG	2A	3020	1/1	0.97	0.04	25,25,25,25	0
57	MG	1A	3933	1/1	0.97	0.04	45,45,45,45	0
57	MG	1A	3287	1/1	0.97	0.20	45,45,45,45	0
57	MG	1A	3658	1/1	0.97	0.09	24,24,24,24	0
57	MG	1A	3090	1/1	0.97	0.15	41,41,41,41	0
57	MG	1A	3142	1/1	0.97	0.07	33,33,33,33	0
57	MG	1A	3390	1/1	0.97	0.17	30,30,30,30	0
57	MG	2A	3778	1/1	0.97	0.07	61,61,61,61	0
57	MG	1A	4042	1/1	0.97	0.09	21,21,21,21	0
57	MG	1A	3169	1/1	0.97	0.25	42,42,42,42	0
57	MG	1A	3513	1/1	0.97	0.10	32,32,32,32	0
57	MG	1A	3008	1/1	0.97	0.15	22,22,22,22	0
57	MG	1A	3340	1/1	0.97	0.07	29,29,29,29	0
57	MG	1a	1621	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3459	1/1	0.97	0.11	23,23,23,23	0
57	MG	1A	3292	1/1	0.97	0.17	31,31,31,31	0
57	MG	1A	3755	1/1	0.97	0.09	32,32,32,32	0
57	MG	1A	3075	1/1	0.97	0.10	31,31,31,31	0
57	MG	2A	3464	1/1	0.97	0.07	28,28,28,28	0
57	MG	1a	1748	1/1	0.97	0.12	36,36,36,36	0
57	MG	1A	3845	1/1	0.97	0.10	49,49,49,49	0
57	MG	1A	3668	1/1	0.97	0.05	19,19,19,19	0
57	MG	2A	3320	1/1	0.97	0.09	60,60,60,60	0
57	MG	2a	1623	1/1	0.97	0.10	59,59,59,59	0
57	MG	1A	3126	1/1	0.97	0.19	35,35,35,35	0
57	MG	1A	3047	1/1	0.97	0.04	34,34,34,34	0
57	MG	1A	3673	1/1	0.97	0.06	25,25,25,25	0
57	MG	1A	3346	1/1	0.97	0.11	39,39,39,39	0
57	MG	1A	3148	1/1	0.97	0.20	32,32,32,32	0
57	MG	2A	3474	1/1	0.97	0.06	58,58,58,58	0
57	MG	2a	1630	1/1	0.97	0.12	55,55,55,55	0
57	MG	2A	3804	1/1	0.97	0.05	48,48,48,48	0
57	MG	1A	3764	1/1	0.97	0.10	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3596	1/1	0.97	0.12	50,50,50,50	0
57	MG	1A	3956	1/1	0.97	0.10	53,53,53,53	0
57	MG	1a	1761	1/1	0.97	0.09	66,66,66,66	0
57	MG	1N	203	1/1	0.97	0.08	35,35,35,35	0
57	MG	1A	3212	1/1	0.97	0.14	38,38,38,38	0
57	MG	1A	3094	1/1	0.97	0.15	22,22,22,22	0
57	MG	1A	3599	1/1	0.97	0.07	36,36,36,36	0
57	MG	1A	3403	1/1	0.97	0.23	40,40,40,40	0
57	MG	2A	3648	1/1	0.97	0.09	71,71,71,71	0
57	MG	1O	202	1/1	0.97	0.10	42,42,42,42	0
57	MG	1A	3770	1/1	0.97	0.08	41,41,41,41	0
59	ZN	2n	501	1/1	0.97	0.05	87,87,87,87	0
60	SF4	1d	302	8/8	0.97	0.06	68,73,83,92	0
60	SF4	2d	303	8/8	0.97	0.06	60,71,82,89	0
57	MG	1A	3670	1/1	0.98	0.03	27,27,27,27	0
57	MG	1A	3544	1/1	0.98	0.10	33,33,33,33	0
57	MG	1A	3672	1/1	0.98	0.05	24,24,24,24	0
57	MG	1A	3545	1/1	0.98	0.19	40,40,40,40	0
57	MG	1A	3608	1/1	0.98	0.07	56,56,56,56	0
57	MG	1A	3079	1/1	0.98	0.05	26,26,26,26	0
57	MG	1A	3610	1/1	0.98	0.07	20,20,20,20	0
57	MG	2E	304	1/1	0.98	0.13	30,30,30,30	0
57	MG	1A	3750	1/1	0.98	0.06	35,35,35,35	0
57	MG	1A	3147	1/1	0.98	0.15	31,31,31,31	0
57	MG	2A	3498	1/1	0.98	0.10	44,44,44,44	0
57	MG	1A	3282	1/1	0.98	0.19	32,32,32,32	0
57	MG	2A	3625	1/1	0.98	0.17	55,55,55,55	0
57	MG	1A	3906	1/1	0.98	0.10	43,43,43,43	0
57	MG	1a	1604	1/1	0.98	0.08	57,57,57,57	0
57	MG	1A	3679	1/1	0.98	0.11	24,24,24,24	0
57	MG	1A	3827	1/1	0.98	0.04	56,56,56,56	0
57	MG	1A	3174	1/1	0.98	0.07	34,34,34,34	0
57	MG	1A	3993	1/1	0.98	0.04	40,40,40,40	0
57	MG	1A	3322	1/1	0.98	0.12	42,42,42,42	0
57	MG	1A	3552	1/1	0.98	0.17	36,36,36,36	0
57	MG	1A	3023	1/1	0.98	0.06	16,16,16,16	0
57	MG	2A	3177	1/1	0.98	0.06	48,48,48,48	0
57	MG	1P	201	1/1	0.98	0.21	28,28,28,28	0
57	MG	1A	3913	1/1	0.98	0.11	43,43,43,43	0
57	MG	2O	202	1/1	0.98	0.10	43,43,43,43	0
57	MG	1a	1816	1/1	0.98	0.04	58,58,58,58	0
57	MG	2A	3768	1/1	0.98	0.07	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	3998	1/1	0.98	0.04	32,32,32,32	0
57	MG	1P	204	1/1	0.98	0.23	25,25,25,25	0
57	MG	1A	3500	1/1	0.98	0.20	32,32,32,32	0
57	MG	1A	3555	1/1	0.98	0.23	45,45,45,45	0
57	MG	1A	3760	1/1	0.98	0.05	31,31,31,31	0
57	MG	1Q	204	1/1	0.98	0.06	43,43,43,43	0
57	MG	1A	3452	1/1	0.98	0.08	38,38,38,38	0
57	MG	1A	4003	1/1	0.98	0.03	28,28,28,28	0
57	MG	1A	3687	1/1	0.98	0.03	20,20,20,20	0
57	MG	1A	3621	1/1	0.98	0.10	45,45,45,45	0
57	MG	2A	3523	1/1	0.98	0.09	29,29,29,29	0
57	MG	1A	4006	1/1	0.98	0.10	36,36,36,36	0
57	MG	1A	3921	1/1	0.98	0.05	30,30,30,30	0
57	MG	1A	3922	1/1	0.98	0.05	33,33,33,33	0
57	MG	2A	3783	1/1	0.98	0.06	50,50,50,50	0
57	MG	1A	3176	1/1	0.98	0.09	33,33,33,33	0
57	MG	1A	3454	1/1	0.98	0.15	38,38,38,38	0
57	MG	2A	3786	1/1	0.98	0.09	44,44,44,44	0
57	MG	1A	3409	1/1	0.98	0.16	45,45,45,45	0
57	MG	1A	4012	1/1	0.98	0.04	40,40,40,40	0
57	MG	2A	3789	1/1	0.98	0.03	36,36,36,36	0
57	MG	1B	216	1/1	0.98	0.12	48,48,48,48	0
57	MG	1A	3044	1/1	0.98	0.06	33,33,33,33	0
57	MG	1A	3213	1/1	0.98	0.18	33,33,33,33	0
57	MG	1U	202	1/1	0.98	0.21	25,25,25,25	0
57	MG	1w	401	1/1	0.98	0.05	38,38,38,38	0
57	MG	1A	3327	1/1	0.98	0.29	50,50,50,50	0
57	MG	2A	3538	1/1	0.98	0.07	38,38,38,38	0
57	MG	1A	3844	1/1	0.98	0.07	46,46,46,46	0
57	MG	1A	3565	1/1	0.98	0.15	34,34,34,34	0
57	MG	1A	3045	1/1	0.98	0.09	40,40,40,40	0
57	MG	27	101	1/1	0.98	0.17	35,35,35,35	0
57	MG	1A	3414	1/1	0.98	0.30	42,42,42,42	0
57	MG	1A	3179	1/1	0.98	0.12	19,19,19,19	0
57	MG	1A	3934	1/1	0.98	0.04	61,61,61,61	0
57	MG	1A	3180	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3031	1/1	0.98	0.14	31,31,31,31	0
57	MG	1A	3571	1/1	0.98	0.08	33,33,33,33	0
57	MG	1A	3011	1/1	0.98	0.08	40,40,40,40	0
57	MG	1V	205	1/1	0.98	0.09	39,39,39,39	0
57	MG	2A	3105	1/1	0.98	0.07	49,49,49,49	0
57	MG	1A	3107	1/1	0.98	0.09	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3048	1/1	0.98	0.10	30,30,30,30	0
57	MG	2A	3553	1/1	0.98	0.09	23,23,23,23	0
57	MG	2A	3108	1/1	0.98	0.17	40,40,40,40	0
57	MG	1A	3155	1/1	0.98	0.09	35,35,35,35	0
57	MG	2A	3556	1/1	0.98	0.10	59,59,59,59	0
57	MG	1A	3856	1/1	0.98	0.21	36,36,36,36	0
57	MG	1A	3468	1/1	0.98	0.08	44,44,44,44	0
57	MG	2A	3685	1/1	0.98	0.08	44,44,44,44	0
57	MG	2A	3559	1/1	0.98	0.06	34,34,34,34	0
57	MG	2A	3822	1/1	0.98	0.04	52,52,52,52	0
57	MG	1A	3707	1/1	0.98	0.05	21,21,21,21	0
57	MG	2A	3561	1/1	0.98	0.08	53,53,53,53	0
57	MG	2A	3825	1/1	0.98	0.04	48,48,48,48	0
57	MG	1A	3033	1/1	0.98	0.27	33,33,33,33	0
57	MG	1A	3223	1/1	0.98	0.16	30,30,30,30	0
57	MG	2A	3691	1/1	0.98	0.08	34,34,34,34	0
57	MG	2A	3564	1/1	0.98	0.07	30,30,30,30	0
57	MG	2a	1622	1/1	0.98	0.04	56,56,56,56	0
57	MG	2A	3565	1/1	0.98	0.04	31,31,31,31	0
57	MG	2A	3831	1/1	0.98	0.08	28,28,28,28	0
57	MG	2A	3008	1/1	0.98	0.04	35,35,35,35	0
57	MG	1a	1754	1/1	0.98	0.10	58,58,58,58	0
57	MG	2A	3117	1/1	0.98	0.08	29,29,29,29	0
57	MG	2A	3447	1/1	0.98	0.12	23,23,23,23	0
57	MG	1A	3017	1/1	0.98	0.07	57,57,57,57	0
57	MG	1a	1756	1/1	0.98	0.06	37,37,37,37	0
57	MG	1A	3158	1/1	0.98	0.21	39,39,39,39	0
57	MG	1D	305	1/1	0.98	0.07	16,16,16,16	0
57	MG	1A	3712	1/1	0.98	0.08	52,52,52,52	0
57	MG	1D	307	1/1	0.98	0.11	36,36,36,36	0
57	MG	1A	3018	1/1	0.98	0.05	16,16,16,16	0
57	MG	1A	3003	1/1	0.98	0.04	25,25,25,25	0
57	MG	2A	3844	1/1	0.98	0.03	49,49,49,49	0
57	MG	1A	3790	1/1	0.98	0.04	43,43,43,43	0
57	MG	1A	3191	1/1	0.98	0.14	27,27,27,27	0
57	MG	1A	3192	1/1	0.98	0.19	31,31,31,31	0
57	MG	1A	3039	1/1	0.98	0.14	34,34,34,34	0
57	MG	1A	3586	1/1	0.98	0.07	22,22,22,22	0
57	MG	2A	3583	1/1	0.98	0.05	53,53,53,53	0
57	MG	1A	3650	1/1	0.98	0.07	36,36,36,36	0
57	MG	2A	3462	1/1	0.98	0.17	49,49,49,49	0
57	MG	1A	3070	1/1	0.98	0.10	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3013	1/1	0.98	0.09	29,29,29,29	0
57	MG	2A	3026	1/1	0.98	0.07	40,40,40,40	0
57	MG	1A	3164	1/1	0.98	0.16	29,29,29,29	0
57	MG	1A	3654	1/1	0.98	0.08	29,29,29,29	0
57	MG	1A	3482	1/1	0.98	0.19	36,36,36,36	0
57	MG	1A	3005	1/1	0.98	0.06	40,40,40,40	0
57	MG	1A	3056	1/1	0.98	0.13	32,32,32,32	0
57	MG	1A	3119	1/1	0.98	0.10	35,35,35,35	0
57	MG	1A	3273	1/1	0.98	0.09	38,38,38,38	0
57	MG	1A	4056	1/1	0.98	0.08	23,23,23,23	0
57	MG	12	102	1/1	0.98	0.13	41,41,41,41	0
57	MG	1A	3042	1/1	0.98	0.10	28,28,28,28	0
57	MG	1A	3202	1/1	0.98	0.07	40,40,40,40	0
57	MG	2A	3365	1/1	0.98	0.05	41,41,41,41	0
57	MG	1A	3885	1/1	0.98	0.09	33,33,33,33	0
57	MG	1A	3076	1/1	0.98	0.07	23,23,23,23	0
57	MG	1A	3058	1/1	0.98	0.06	33,33,33,33	0
57	MG	2A	3604	1/1	0.98	0.08	36,36,36,36	0
57	MG	1A	3399	1/1	0.98	0.31	56,56,56,56	0
57	MG	1F	306	1/1	0.98	0.12	30,30,30,30	0
57	MG	1A	3540	1/1	0.98	0.07	28,28,28,28	0
57	MG	1A	3078	1/1	0.98	0.06	30,30,30,30	0
57	MG	1A	3542	1/1	0.98	0.15	30,30,30,30	0
57	MG	2D	302	1/1	0.98	0.21	39,39,39,39	0
59	ZN	26	102	1/1	0.98	0.03	53,53,53,53	0
57	MG	1A	3206	1/1	0.98	0.09	36,36,36,36	0
57	MG	1A	3977	1/1	0.98	0.07	27,27,27,27	0
57	MG	1A	3605	1/1	0.98	0.07	41,41,41,41	0
57	MG	2A	3678	1/1	0.99	0.05	29,29,29,29	0
57	MG	1A	3085	1/1	0.99	0.10	24,24,24,24	0
57	MG	1A	3037	1/1	0.99	0.04	20,20,20,20	0
57	MG	1A	3746	1/1	0.99	0.08	40,40,40,40	0
57	MG	1A	3791	1/1	0.99	0.03	20,20,20,20	0
57	MG	1A	3110	1/1	0.99	0.20	30,30,30,30	0
57	MG	1E	304	1/1	0.99	0.17	31,31,31,31	0
57	MG	2A	3145	1/1	0.99	0.10	29,29,29,29	0
57	MG	1A	3201	1/1	0.99	0.09	21,21,21,21	0
57	MG	1A	3611	1/1	0.99	0.05	52,52,52,52	0
57	MG	1B	224	1/1	0.99	0.04	43,43,43,43	0
57	MG	1A	3559	1/1	0.99	0.20	29,29,29,29	0
57	MG	1A	3890	1/1	0.99	0.05	41,41,41,41	0
57	MG	1A	3375	1/1	0.99	0.09	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	1A	3021	1/1	0.99	0.04	22,22,22,22	0
57	MG	2A	3606	1/1	0.99	0.04	42,42,42,42	0
57	MG	1A	4029	1/1	0.99	0.04	49,49,49,49	0
57	MG	13	101	1/1	0.99	0.11	28,28,28,28	0
57	MG	2A	3524	1/1	0.99	0.08	29,29,29,29	0
57	MG	1V	203	1/1	0.99	0.16	28,28,28,28	0
57	MG	1a	1807	1/1	0.99	0.04	48,48,48,48	0
57	MG	1A	3920	1/1	0.99	0.08	26,26,26,26	0
57	MG	2A	3744	1/1	0.99	0.06	50,50,50,50	0
57	MG	1A	3867	1/1	0.99	0.09	30,30,30,30	0
57	MG	1x	111	1/1	0.99	0.05	49,49,49,49	0
57	MG	1E	315	1/1	0.99	0.06	40,40,40,40	0
57	MG	1A	3731	1/1	0.99	0.03	13,13,13,13	0
57	MG	1A	3010	1/1	0.99	0.08	35,35,35,35	0
57	MG	1A	3870	1/1	0.99	0.09	48,48,48,48	0
57	MG	15	105	1/1	0.99	0.17	28,28,28,28	0
57	MG	1A	3563	1/1	0.99	0.15	32,32,32,32	0
57	MG	15	107	1/1	0.99	0.05	40,40,40,40	0
57	MG	1A	3014	1/1	0.99	0.05	28,28,28,28	0
57	MG	1A	3345	1/1	0.99	0.18	33,33,33,33	0
57	MG	2A	3802	1/1	0.99	0.04	35,35,35,35	0
57	MG	1A	3071	1/1	0.99	0.04	15,15,15,15	0
57	MG	1A	4067	1/1	0.99	0.09	29,29,29,29	0
57	MG	1A	3601	1/1	0.99	0.11	34,34,34,34	0
57	MG	2A	3806	1/1	0.99	0.03	40,40,40,40	0
57	MG	1A	3716	1/1	0.99	0.07	26,26,26,26	0
57	MG	2A	3760	1/1	0.99	0.03	49,49,49,49	0
57	MG	1R	202	1/1	0.99	0.20	35,35,35,35	0
59	ZN	1Y	205	1/1	0.99	0.03	60,60,60,60	0
57	MG	1A	3036	1/1	0.99	0.12	28,28,28,28	0
59	ZN	15	109	1/1	0.99	0.03	44,44,44,44	0
59	ZN	16	102	1/1	0.99	0.05	44,44,44,44	0
59	ZN	19	102	1/1	0.99	0.06	44,44,44,44	0
57	MG	1A	3447	1/1	0.99	0.15	47,47,47,47	0
59	ZN	2Y	501	1/1	0.99	0.03	82,82,82,82	0
57	MG	1A	4072	1/1	0.99	0.07	37,37,37,37	0
59	ZN	25	108	1/1	0.99	0.02	56,56,56,56	0
57	MG	1A	3476	1/1	0.99	0.18	33,33,33,33	0
59	ZN	29	102	1/1	0.99	0.05	65,65,65,65	0
57	MG	2A	3814	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3382	1/1	0.99	0.31	27,27,27,27	0
57	MG	1A	3099	1/1	0.99	0.08	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	4028	1/1	1.00	0.05	24,24,24,24	0
57	MG	1A	3896	1/1	1.00	0.04	27,27,27,27	0
57	MG	1A	3717	1/1	1.00	0.07	20,20,20,20	0
57	MG	1a	1814	1/1	1.00	0.08	53,53,53,53	0

6.5 Other polymers (i)

There are no such residues in this entry.