Full wwPDB X-ray Structure Validation Report ⓘ

Mar 16, 2026 – 11:35 PM UTC

PDB ID	:	8VTX / pdb_00008vtx
Title	:	Crystal structure of the A2058-N6-dimethylated Thermus thermophilus 70S ribosome in complex with macrolone MCX-128, mRNA, aminoacylated A-site Phe-tRNAphe, aminoacylated P-site fMet-tRNAmet, and deacylated E-site tRNAphe at 2.40A resolution
Authors	:	Aleksandrova, E.V.; Ma, C.-X.; Klepacki, D.; Alizadeh, F.; Vazquez-Laslop, N.; Liang, J.-H.; Polikanov, Y.S.; Mankin, A.S.
Deposited on	:	2024-01-27
Resolution	:	2.40 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 ⓘ 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 ⓘ) were used in the production of this report:

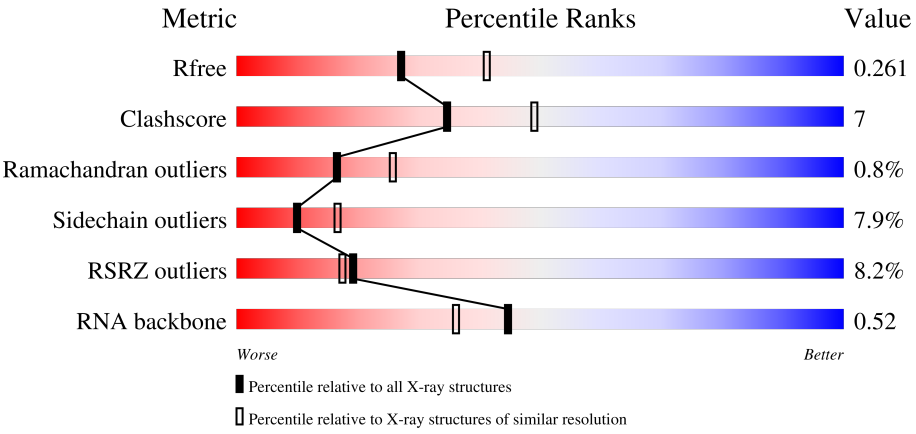
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

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 2.40 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	4642 (2.40-2.40)
Clashscore	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)
RNA backbone	3690	1084 (2.70-2.10)

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	7% 68% 25% 6% ·
1	2A	2915	6% 61% 29% 6% ·

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.48.1

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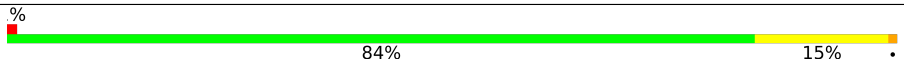
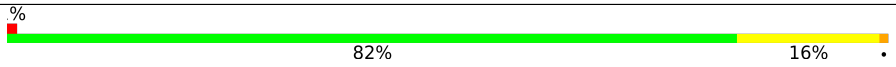
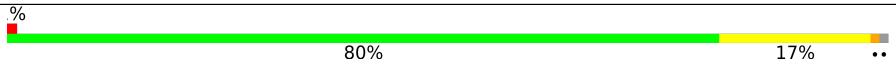
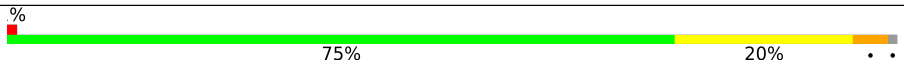
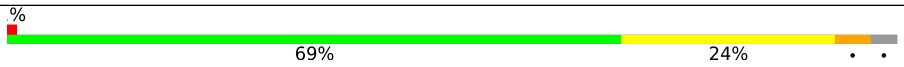
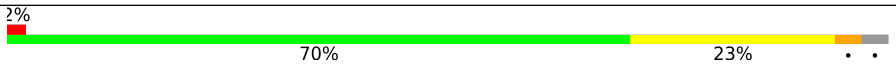
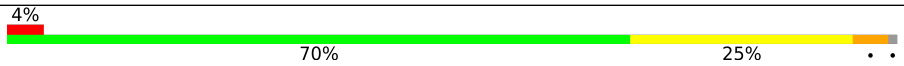
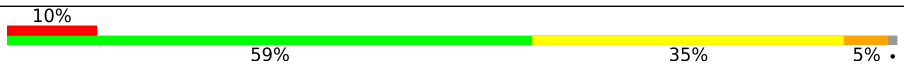
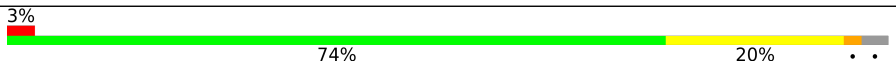
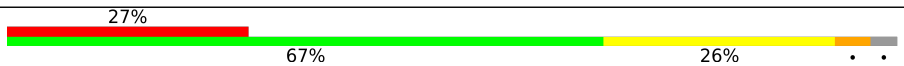
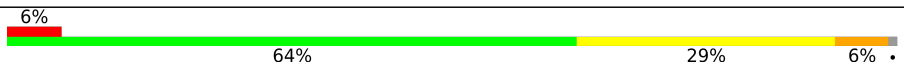
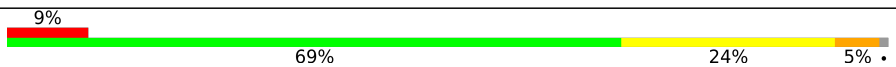
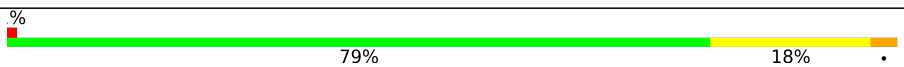
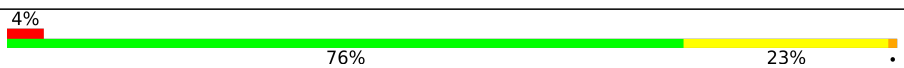
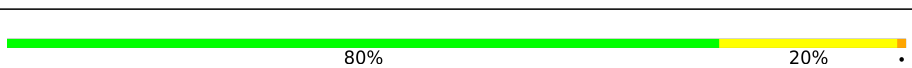
2	2B	121	
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
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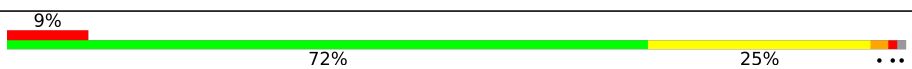
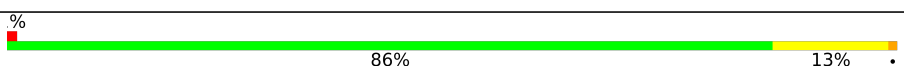
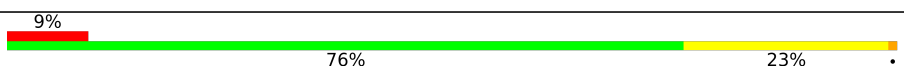
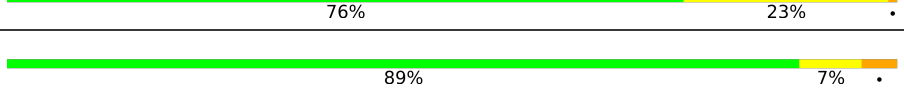
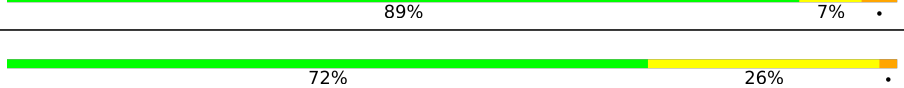
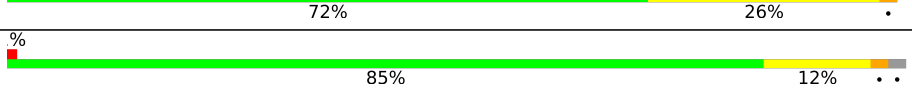
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	

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Mol	Chain	Length	Quality of chain
14	2S	112	12% 62% 30% 5%
15	1T	146	% 74% 15% 10%
15	2T	146	3% 67% 22% 10%
16	1U	118	79% 19%
16	2U	118	% 78% 19%
17	1V	101	% 83% 15%
17	2V	101	2% 85% 14%
18	1W	113	% 85% 14%
18	2W	113	2% 81% 17%
19	1X	96	3% 90% 8%
19	2X	96	2% 76% 19%
20	1Y	110	4% 76% 19%
20	2Y	110	13% 73% 21%
21	1Z	206	12% 50% 21% 25%
21	2Z	206	24% 45% 30% 22%
22	10	85	% 85% 12%
22	20	85	5% 84% 14%
23	11	98	2% 84% 13%
23	21	98	3% 82% 15%
24	12	72	4% 89% 7%
24	22	72	4% 67% 31%
25	13	60	2% 78% 18%
25	23	60	7% 72% 23%
26	14	71	23% 44% 32% 18%
26	24	71	31% 49% 41% 6%

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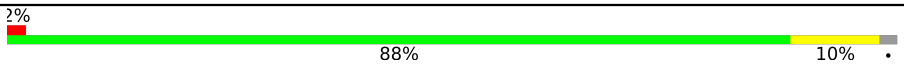
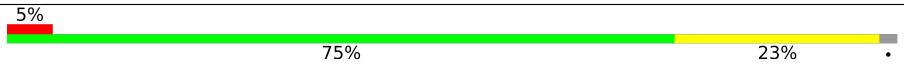
Mol	Chain	Length	Quality of chain
27	15	60	
27	25	60	
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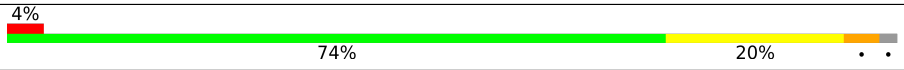
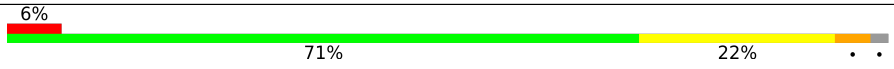
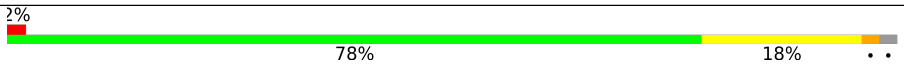
28	26	54	
29	17	49	
29	27	49	
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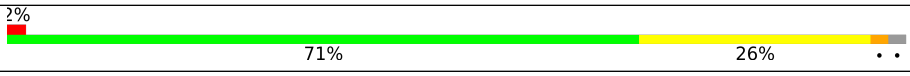
30	28	65	
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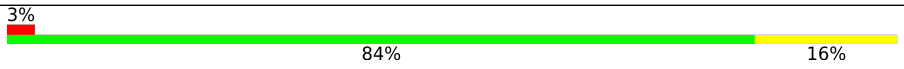
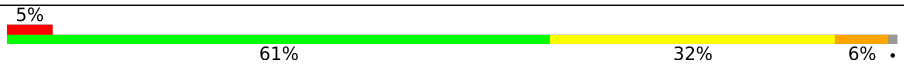
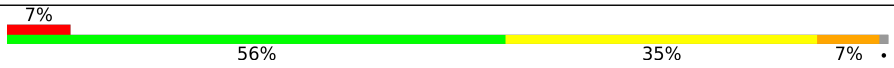
31	29	37	
32	1a	1521	
32	2a	1521	
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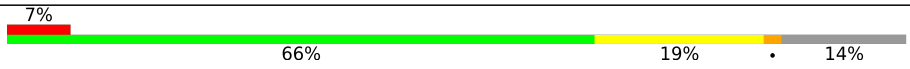
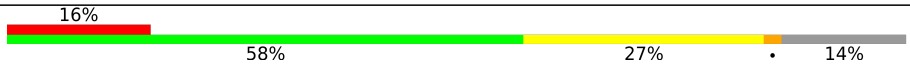
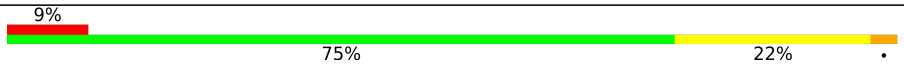
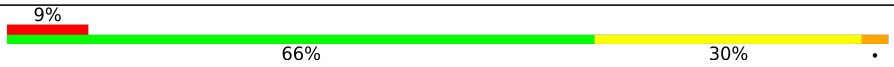
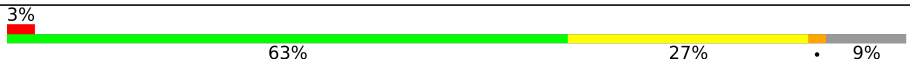
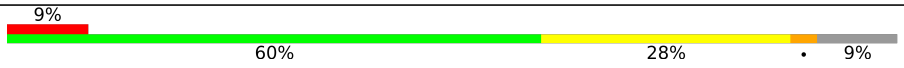
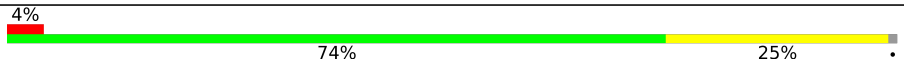
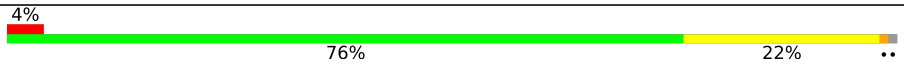
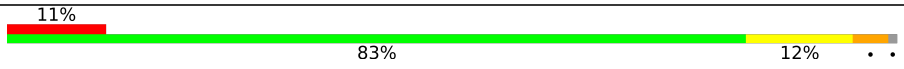
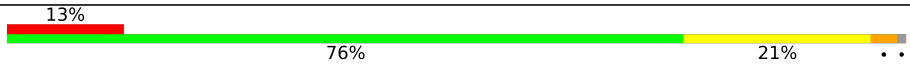
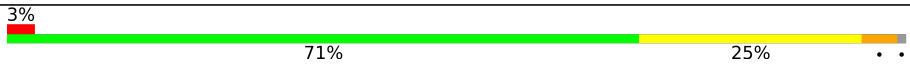
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	

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Mol	Chain	Length	Quality of chain
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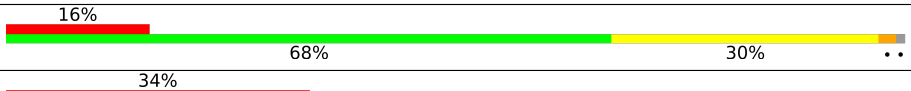
40	1i	128	
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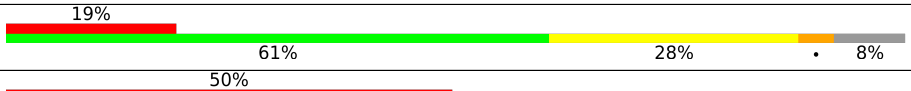
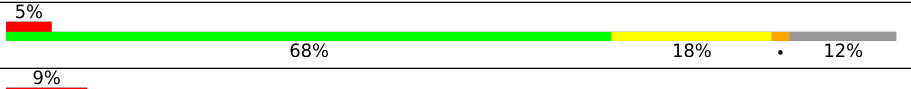
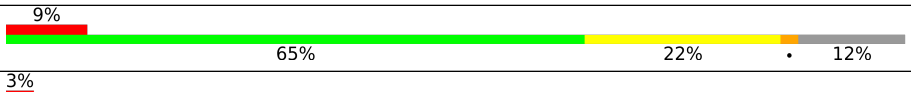
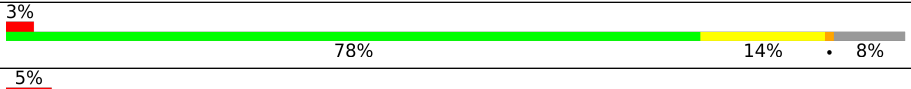
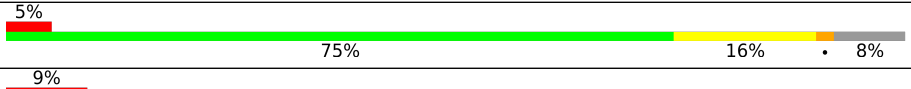
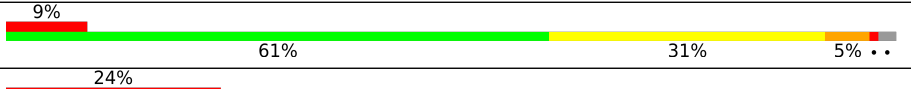
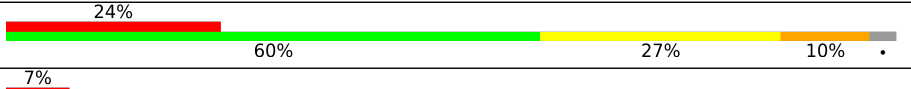
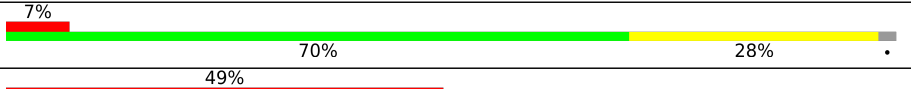
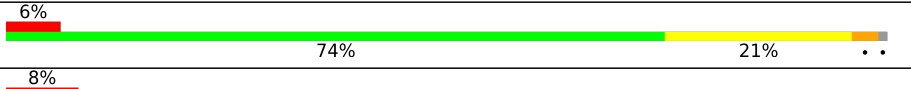
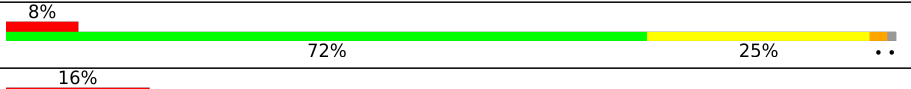
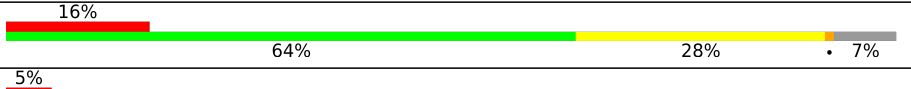
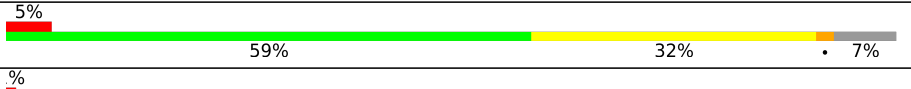
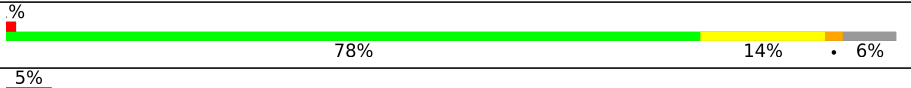
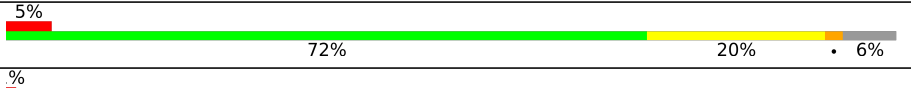
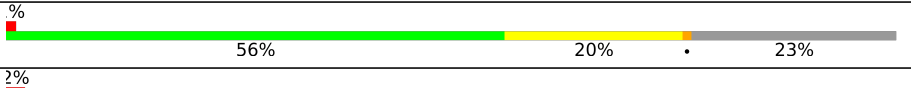
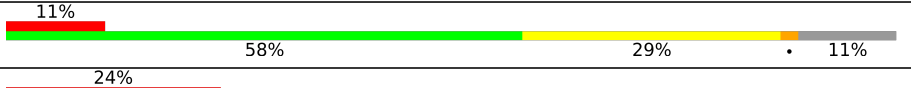
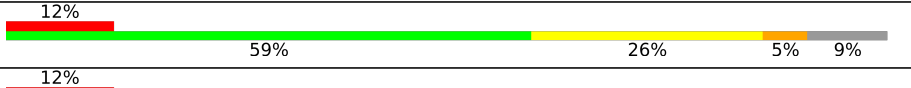
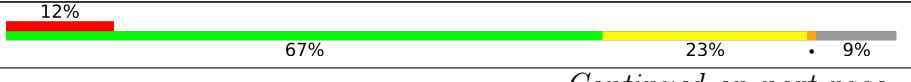
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	

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Mol	Chain	Length	Quality of chain
52	1u	27	11% 59% 22% 15%
52	2u	27	52% 56% 30% 15%
53	1v	24	8% 42% 12% 46%
53	2v	24	12% 38% 12% 46%
54	1w	76	33% 38% 43% 13%
54	2w	76	24% 30% 47% 17% 5%
55	1x	77	3% 79% 18%
55	2x	77	3% 57% 35% 8%
56	1y	76	45% 29% 36% 30%
56	2y	76	59% 32% 41% 22%

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	10	108	-	-	-	X
57	MG	1A	3507	-	-	-	X
57	MG	1U	209	-	-	-	X
57	MG	2A	3149	-	-	-	X
57	MG	2A	3277	-	-	-	X
57	MG	2A	3364	-	-	-	X
57	MG	2A	3400	-	-	-	X
57	MG	2a	1761	-	-	-	X
61	SF4	2d	303	-	-	X	-

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 300319 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
			61854	27533	11572	19878	2871			
1	2A	2800	Total	C	N	O	P	0	0	0
			60324	26850	11284	19390	2800			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 53 is a RNA chain called MF-mRNA.

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

- Molecule 54 is a RNA chain called Aminoacylated Phe-tRNAphe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1592	713	286	517	74	2			
54	2w	72	Total	C	N	O	P	S	0	0	0
			1544	690	279	501	72	2			

- Molecule 55 is a RNA chain called Aminoacylated fMet-tRNAmet.

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

- Molecule 56 is a RNA chain called Deacylated tRNAphe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
56	1y	74	Total	C	N	O	P	S	0	0	0
			1585	707	285	518	74	1			
56	2y	73	Total	C	N	O	P	S	0	0	0
			1565	698	283	510	73	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1093	Total	Mg	0	0
			1093	1093		
57	1B	36	Total	Mg	0	0
			36	36		
57	1D	14	Total	Mg	0	0
			14	14		
57	1E	16	Total	Mg	0	0
			16	16		
57	1F	14	Total	Mg	0	0
			14	14		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1G	4	Total Mg 4 4	0	0
57	1H	1	Total Mg 1 1	0	0
57	1I	1	Total Mg 1 1	0	0
57	1N	7	Total Mg 7 7	0	0
57	1O	6	Total Mg 6 6	0	0
57	1P	6	Total Mg 6 6	0	0
57	1Q	8	Total Mg 8 8	0	0
57	1R	3	Total Mg 3 3	0	0
57	1S	3	Total Mg 3 3	0	0
57	1T	4	Total Mg 4 4	0	0
57	1U	9	Total Mg 9 9	0	0
57	1V	8	Total Mg 8 8	0	0
57	1W	6	Total Mg 6 6	0	0
57	1X	7	Total Mg 7 7	0	0
57	1Y	2	Total Mg 2 2	0	0
57	1Z	3	Total Mg 3 3	0	0
57	10	11	Total Mg 11 11	0	0
57	11	6	Total Mg 6 6	0	0
57	12	2	Total Mg 2 2	0	0
57	13	4	Total Mg 4 4	0	0
57	14	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	15	7	Total Mg 7 7	0	0
57	16	1	Total Mg 1 1	0	0
57	17	7	Total Mg 7 7	0	0
57	18	6	Total Mg 6 6	0	0
57	19	1	Total Mg 1 1	0	0
57	1a	214	Total Mg 214 214	0	0
57	1b	1	Total Mg 1 1	0	0
57	1d	1	Total Mg 1 1	0	0
57	1e	2	Total Mg 2 2	0	0
57	1f	1	Total Mg 1 1	0	0
57	1h	1	Total Mg 1 1	0	0
57	1k	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	2	Total Mg 2 2	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	8	Total Mg 8 8	0	0
57	1x	14	Total Mg 14 14	0	0
57	2A	854	Total Mg 854 854	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2B	18	Total Mg 18 18	0	0
57	2D	8	Total Mg 8 8	0	0
57	2E	11	Total Mg 11 11	0	0
57	2F	5	Total Mg 5 5	0	0
57	2G	1	Total Mg 1 1	0	0
57	2N	1	Total Mg 1 1	0	0
57	2O	1	Total Mg 1 1	0	0
57	2P	2	Total Mg 2 2	0	0
57	2Q	2	Total Mg 2 2	0	0
57	2R	2	Total Mg 2 2	0	0
57	2T	3	Total Mg 3 3	0	0
57	2U	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	2	Total Mg 2 2	0	0
57	2Y	1	Total Mg 1 1	0	0
57	2Z	1	Total Mg 1 1	0	0
57	20	4	Total Mg 4 4	0	0
57	21	1	Total Mg 1 1	0	0
57	23	3	Total Mg 3 3	0	0
57	25	5	Total Mg 5 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	26	1	Total Mg 1 1	0	0
57	27	3	Total Mg 3 3	0	0
57	28	3	Total Mg 3 3	0	0
57	29	1	Total Mg 1 1	0	0
57	2a	210	Total Mg 210 210	0	0
57	2d	2	Total Mg 2 2	0	0
57	2e	1	Total Mg 1 1	0	0
57	2f	2	Total Mg 2 2	0	0
57	2g	1	Total Mg 1 1	0	0
57	2j	1	Total Mg 1 1	0	0
57	2l	5	Total Mg 5 5	0	0
57	2q	2	Total Mg 2 2	0	0
57	2r	1	Total Mg 1 1	0	0
57	2t	1	Total Mg 1 1	0	0
57	2v	3	Total Mg 3 3	0	0
57	2w	7	Total Mg 7 7	0	0
57	2x	7	Total Mg 7 7	0	0
57	2y	5	Total Mg 5 5	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

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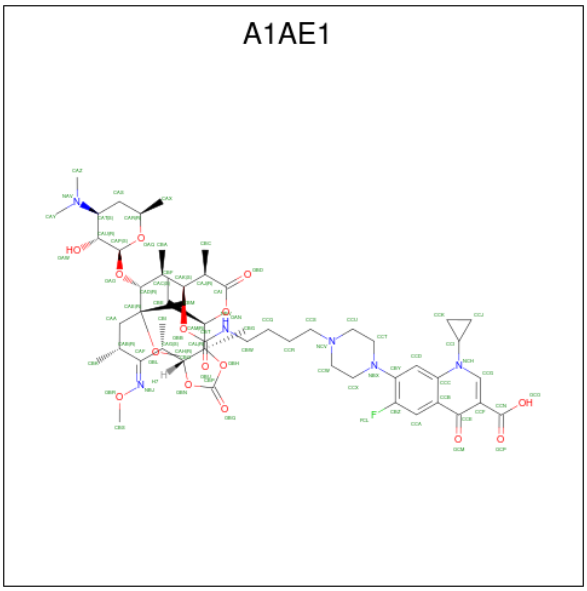
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	2A	1	Total K 1 1	0	0

- Molecule 59 is 1-cyclopropyl-7-(4-{4-[({[(3aR,4R,7R,8S,9S,10R,11R,13R,14E,15S,15aR)-10-{[(2S,3R,4S,6R)-4-(dimethylamino)-3-hydroxy-6-methyloxan-2-yl]oxy}-4-ethyl-11-methoxy-14-(methoxyimino)-3a,7,9,11,13,15-hexamethyl-2,6-dioxododecahydro-2H,4H-[1,3]dioxolo[4,5-c]oxacyclotetradecin-8-yl]oxy}carbonyl)amino]butyl}piperazin-1-yl)-6-fluoro-4-oxo-1,4-dihydroquinoline-3-carboxylic acid (non-preferred name) (CCD ID: A1AE1) (formula: $C_{54}H_{81}FN_6O_{15}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	1	Total C F N O 76 54 1 6 15	0	0
59	2A	1	Total C F N O 76 54 1 6 15	0	0

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

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

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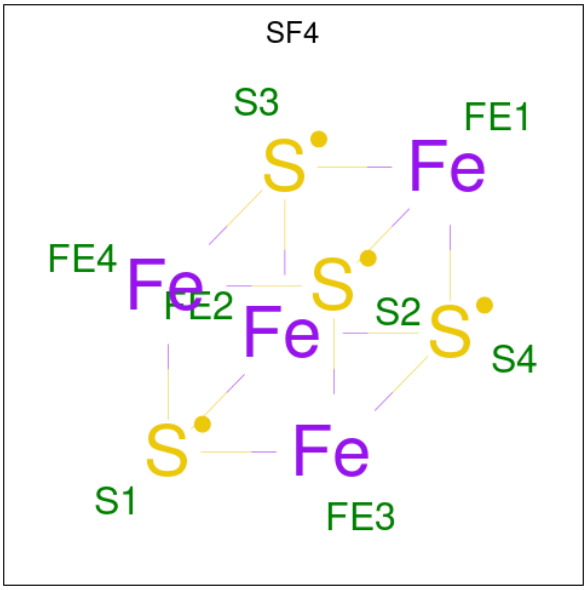
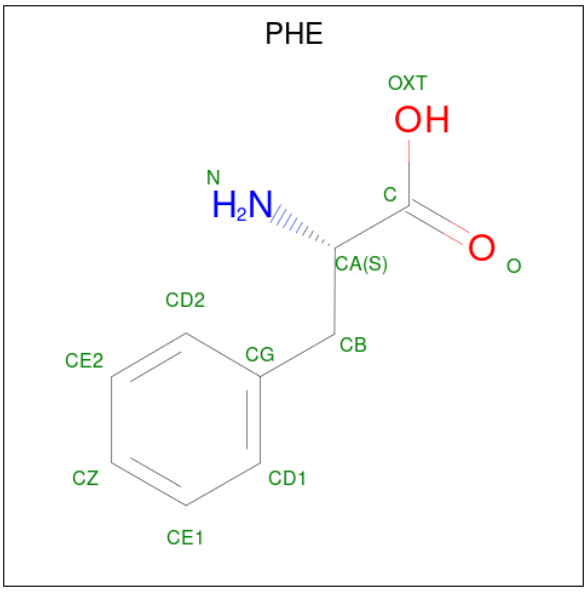
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	19	1	Total Zn 1 1	0	0
60	1n	1	Total Zn 1 1	0	0
60	2Y	1	Total Zn 1 1	0	0
60	24	1	Total Zn 1 1	0	0
60	25	1	Total Zn 1 1	0	0
60	26	1	Total Zn 1 1	0	0
60	29	1	Total Zn 1 1	0	0
60	2n	1	Total Zn 1 1	0	0

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



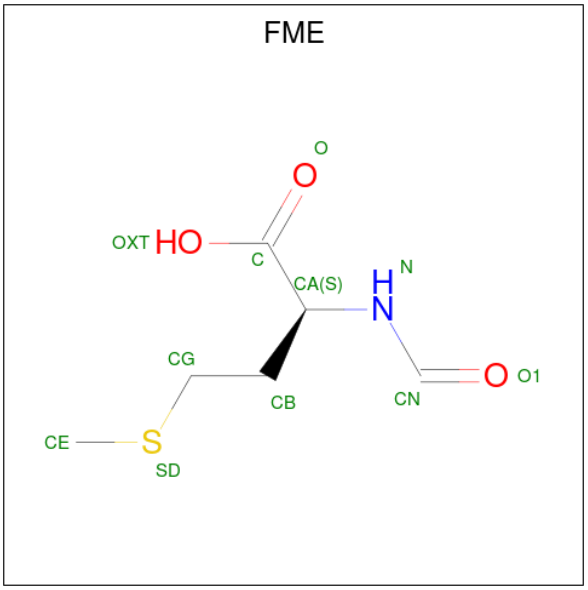
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1d	1	Total Fe S 8 4 4	0	0
61	2d	1	Total Fe S 8 4 4	0	0

- Molecule 62 is PHENYLALANINE (CCD ID: PHE) (formula: $C_9H_{11}NO_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1w	1	Total C N O 11 9 1 1	0	0
62	2w	1	Total C N O 11 9 1 1	0	0

- Molecule 63 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1x	1	Total C N O S 10 6 1 2 1	0	0
63	2x	1	Total C N O S 10 6 1 2 1	0	0

- Molecule 64 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	1A	2061	Total O 2061 2061	0	0
64	1B	60	Total O 60 60	0	0
64	1D	29	Total O 29 29	0	0
64	1E	27	Total O 27 27	0	0
64	1F	16	Total O 16 16	0	0
64	1G	1	Total O 1 1	0	0
64	1H	1	Total O 1 1	0	0
64	1N	5	Total O 5 5	0	0
64	1O	6	Total O 6 6	0	0
64	1P	22	Total O 22 22	0	0
64	1Q	9	Total O 9 9	0	0
64	1R	10	Total O 10 10	0	0
64	1S	4	Total O 4 4	0	0
64	1T	8	Total O 8 8	0	0
64	1U	10	Total O 10 10	0	0
64	1V	8	Total O 8 8	0	0
64	1W	9	Total O 9 9	0	0
64	1X	6	Total O 6 6	0	0
64	1Y	3	Total O 3 3	0	0
64	1Z	1	Total O 1 1	0	0
64	10	12	Total O 12 12	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	11	11	Total O 11 11	0	0
64	12	3	Total O 3 3	0	0
64	13	5	Total O 5 5	0	0
64	14	1	Total O 1 1	0	0
64	15	9	Total O 9 9	0	0
64	16	1	Total O 1 1	0	0
64	17	11	Total O 11 11	0	0
64	18	11	Total O 11 11	0	0
64	1a	388	Total O 388 388	0	0
64	1b	1	Total O 1 1	0	0
64	1c	2	Total O 2 2	0	0
64	1d	2	Total O 2 2	0	0
64	1e	3	Total O 3 3	0	0
64	1f	1	Total O 1 1	0	0
64	1g	1	Total O 1 1	0	0
64	1i	1	Total O 1 1	0	0
64	1j	2	Total O 2 2	0	0
64	1l	7	Total O 7 7	0	0
64	1m	1	Total O 1 1	0	0
64	1n	2	Total O 2 2	0	0
64	1o	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	1p	1	Total O 1 1	0	0
64	1q	2	Total O 2 2	0	0
64	1u	1	Total O 1 1	0	0
64	1v	5	Total O 5 5	0	0
64	1w	14	Total O 14 14	0	0
64	1x	15	Total O 15 15	0	0
64	1y	1	Total O 1 1	0	0
64	2A	1142	Total O 1142 1142	0	0
64	2B	19	Total O 19 19	0	0
64	2D	23	Total O 23 23	0	0
64	2E	12	Total O 12 12	0	0
64	2F	12	Total O 12 12	0	0
64	2I	2	Total O 2 2	0	0
64	2O	2	Total O 2 2	0	0
64	2P	11	Total O 11 11	0	0
64	2Q	2	Total O 2 2	0	0
64	2R	3	Total O 3 3	0	0
64	2T	5	Total O 5 5	0	0
64	2U	3	Total O 3 3	0	0
64	2V	1	Total O 1 1	0	0
64	2X	3	Total O 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	2Y	1	Total O 1 1	0	0
64	2Z	1	Total O 1 1	0	0
64	20	3	Total O 3 3	0	0
64	21	11	Total O 11 11	0	0
64	23	2	Total O 2 2	0	0
64	25	2	Total O 2 2	0	0
64	27	5	Total O 5 5	0	0
64	28	3	Total O 3 3	0	0
64	29	1	Total O 1 1	0	0
64	2a	221	Total O 221 221	0	0
64	2c	1	Total O 1 1	0	0
64	2d	2	Total O 2 2	0	0
64	2g	1	Total O 1 1	0	0
64	2j	3	Total O 3 3	0	0
64	2l	4	Total O 4 4	0	0
64	2p	2	Total O 2 2	0	0
64	2q	1	Total O 1 1	0	0
64	2r	1	Total O 1 1	0	0
64	2t	1	Total O 1 1	0	0
64	2v	2	Total O 2 2	0	0
64	2w	3	Total O 3 3	0	0

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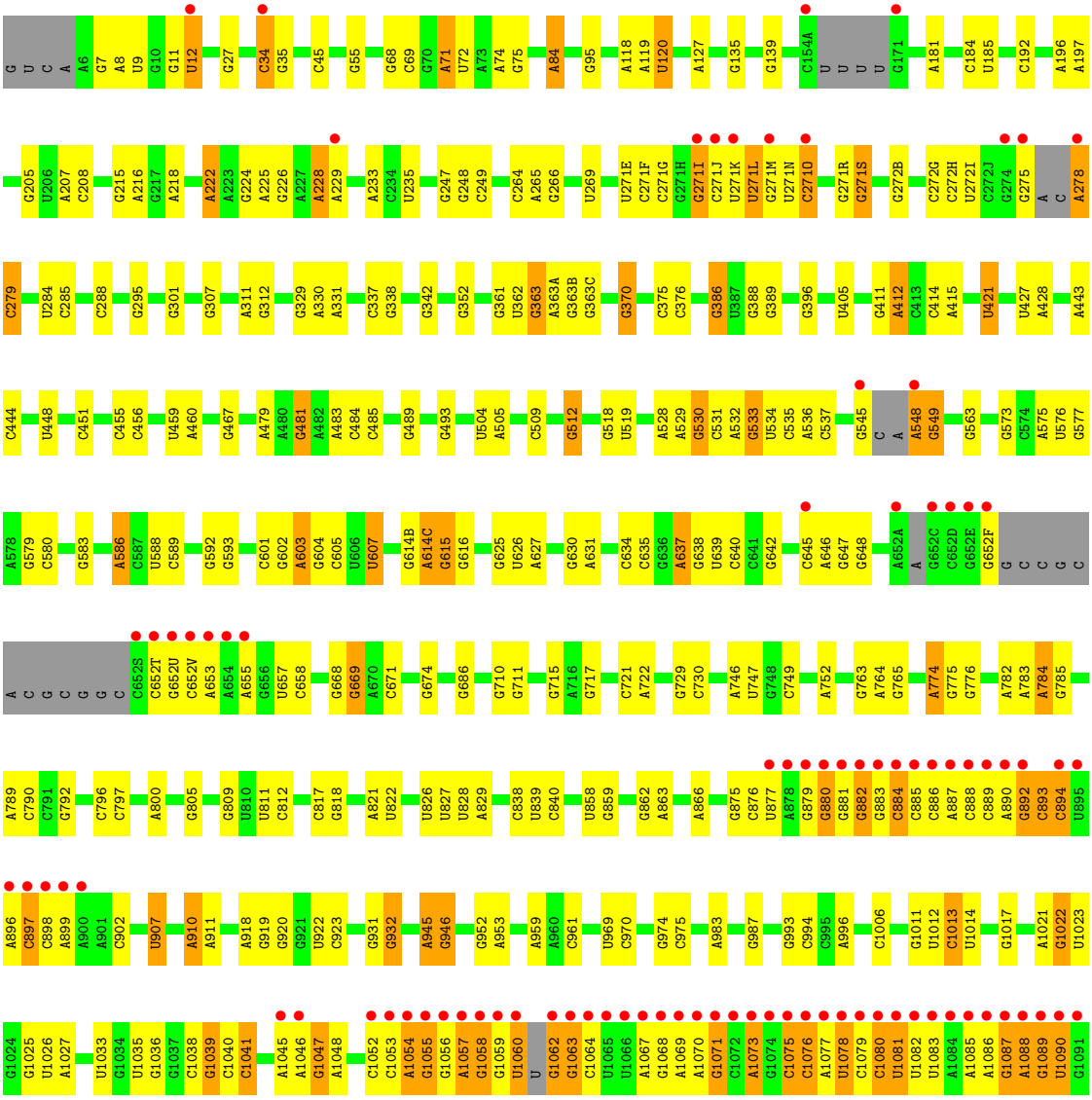
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
64	2x	7	Total O 7 7	0	0
64	2y	2	Total O 2 2	0	0

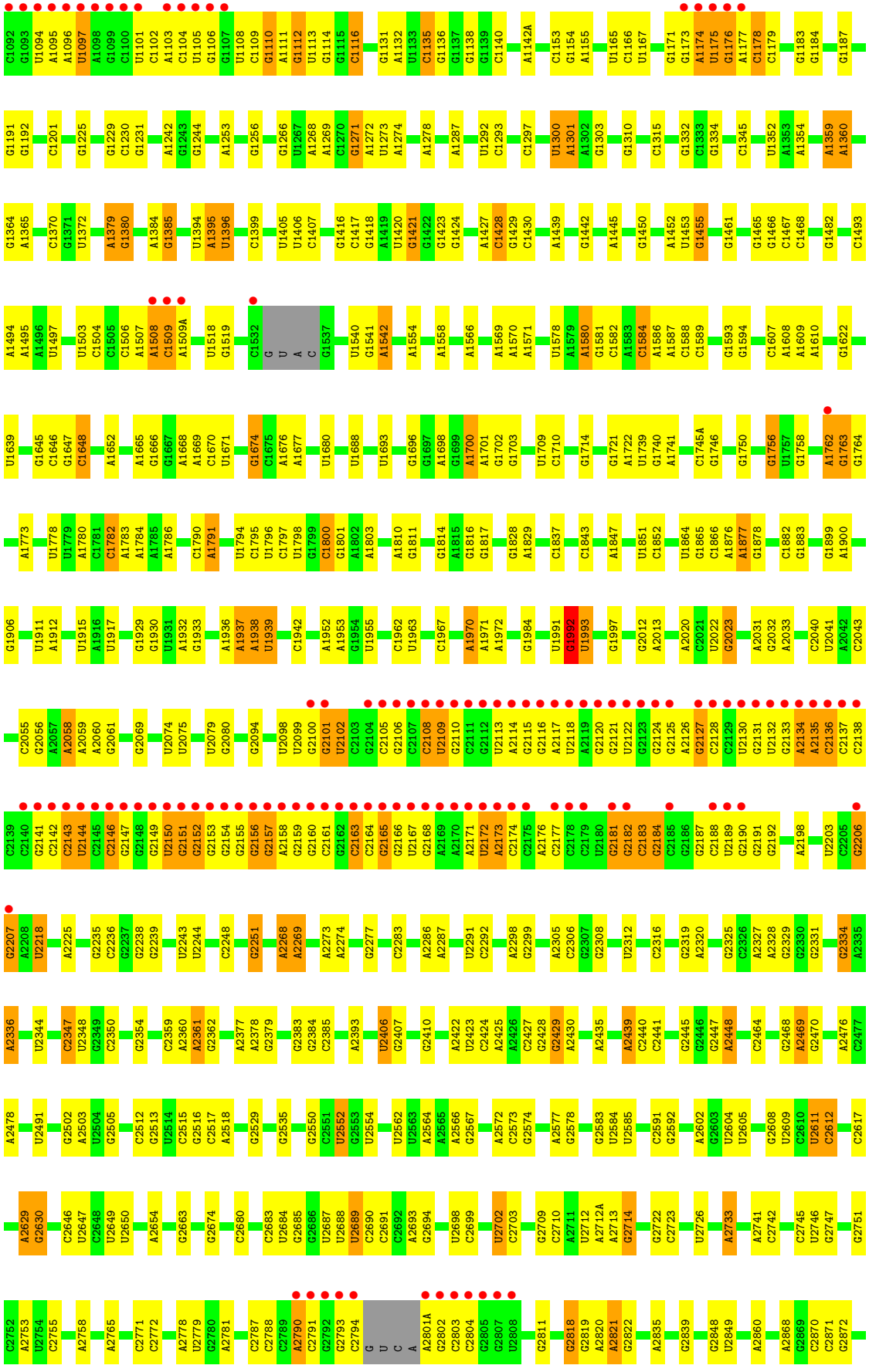
3 Residue-property plots (i)

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:




C1092 G1093 U1094 A1095 A1096 U1097 A1098 G1099 C1100 U1101 C1102 A1103 C1104 U1105 G1106 G1107 U1108 C1109 G1110 A1111 G1112 U1113 G1114 G1115 C1116 G1131 A1132 U1133 C1135 G1136 G1137 G1138 G1139 C1140 A1142A C1153 G1154 A1155 U1165 C1166 U1167 G1171 G1173 A1174 U1175 G1176 A1177 C1178 C1179 G1183 G1184 G1187
G1191 G1192 C1201 G1225 G1229 C1230 G1231 A1242 G1243 G1244 A1253 G1256 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1274 A1278 A1287 U1292 C1293 C1297 U1300 A1301 A1302 G1303 G1310 C1315 G1332 C1333 G1334 C1345 U1352 A1353 A1354 A1359 A1360
G1364 A1365 C1370 G1371 U1372 A1379 G1380 A1384 G1385 U1394 A1395 U1396 C1399 U1405 U1406 C1407 G1416 C1417 G1418 A1419 U1420 G1421 G1422 G1423 G1424 A1427 C1428 G1429 C1430 A1439 G1442 A1445 G1450 A1452 U1453 G1455 G1461 G1465 G1466 C1467 C1468 G1482 C1493
A1494 A1495 A1496 U1497 U1503 C1504 C1505 C1506 A1507 A1508 C1509 A1509A U1518 G1519 C1522 G U A C G1537 U1540 G1541 A1542 A1554 A1558 A1566 A1569 A1570 A1571 U1578 A1579 A1580 G1581 C1582 A1583 C1584 A1586 A1587 C1588 C1589 G1593 G1594 C1607 A1608 A1609 A1610 G1622
U1639 G1645 C1646 G1647 C1648 A1652 A1665 G1666 G1667 A1668 A1669 C1670 U1671 C1674 C1675 A1676 A1677 U1680 U1688 U1693 G1696 C1697 A1698 G1699 A1700 A1701 G1702 G1703 U1709 C1710 G1714 G1721 A1722 U1739 G1740 A1741 C1745A G1746 G1750 G1756 U1757 G1758 A1762 G1763 G1764
A1773 U1778 U1779 A1780 C1781 C1782 A1783 A1784 A1785 A1786 C1790 A1791 U1794 C1795 U1796 C1797 U1798 G1799 C1800 G1801 A1802 A1803 A1810 G1811 G1814 A1815 G1816 G1817 G1828 A1829 C1837 C1843 A1847 U1851 C1852 U1864 G1865 C1866 A1876 A1877 G1878 C1882 G1883 G1899 A1900
G1906 U1911 A1912 U1915 A1916 U1917 G1929 G1930 U1931 A1932 G1933 A1936 A1937 A1938 U1939 C1942 A1952 A1953 G1954 U1955 C1962 U1963 C1967 A1970 A1971 A1972 G1984 U1991 G1992 U1993 G1997 G2012 A2013 A2020 C2021 U2022 G2023 A2031 G2032 A2033 C2040 U2041 A2042 C2043
C2055 G2056 A2057 A2058 A2059 A2060 G2061 G2069 U2074 U2075 U2079 G2080 G2094 U2098 U2099 G2100 G2101 U2102 C2103 G2104 C2105 G2106 C2107 C2108 U2109 G2110 C2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 C2128 C2129 U2130 G2131 A2032 U2133 A2134 A2135 C2136 C2137 C2138
C2139 C2140 G2141 C2142 C2143 U2144 C2145 C2146 C2147 G2148 G2149 U2150 G2151 G2152 G2153 G2154 G2155 G2156 G2157 A2158 G2159 G2160 C2161 C2162 C2163 G2164 G2165 G2166 U2167 C2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 C2179 U2180 G2181 G2182 C2183 G2184 C2185 G2186 G2187 C2188 U2189 G2190 G2191 G2192 A2198 U2203 C2205 G2206
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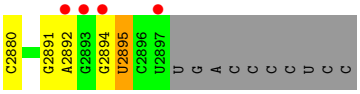
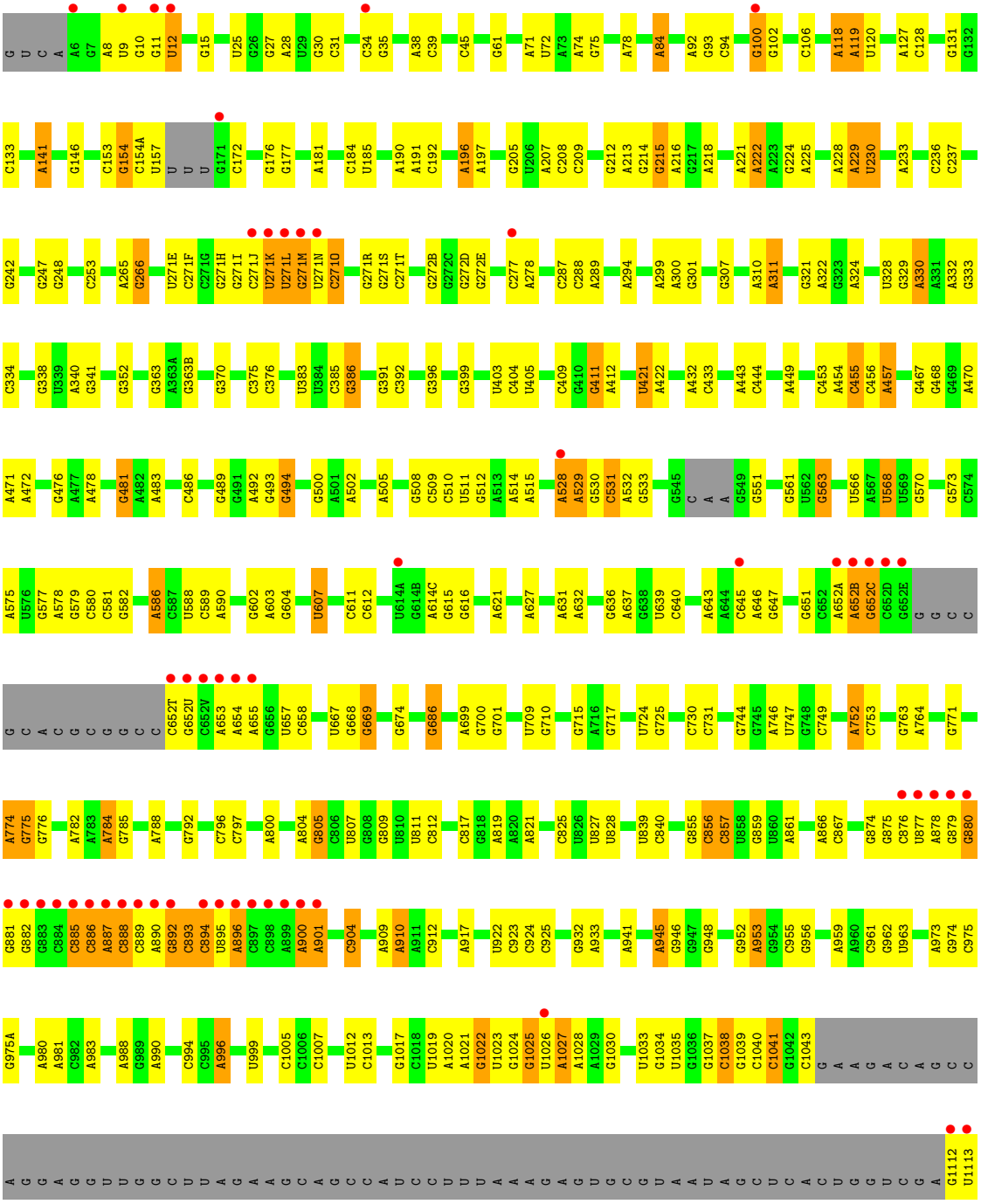
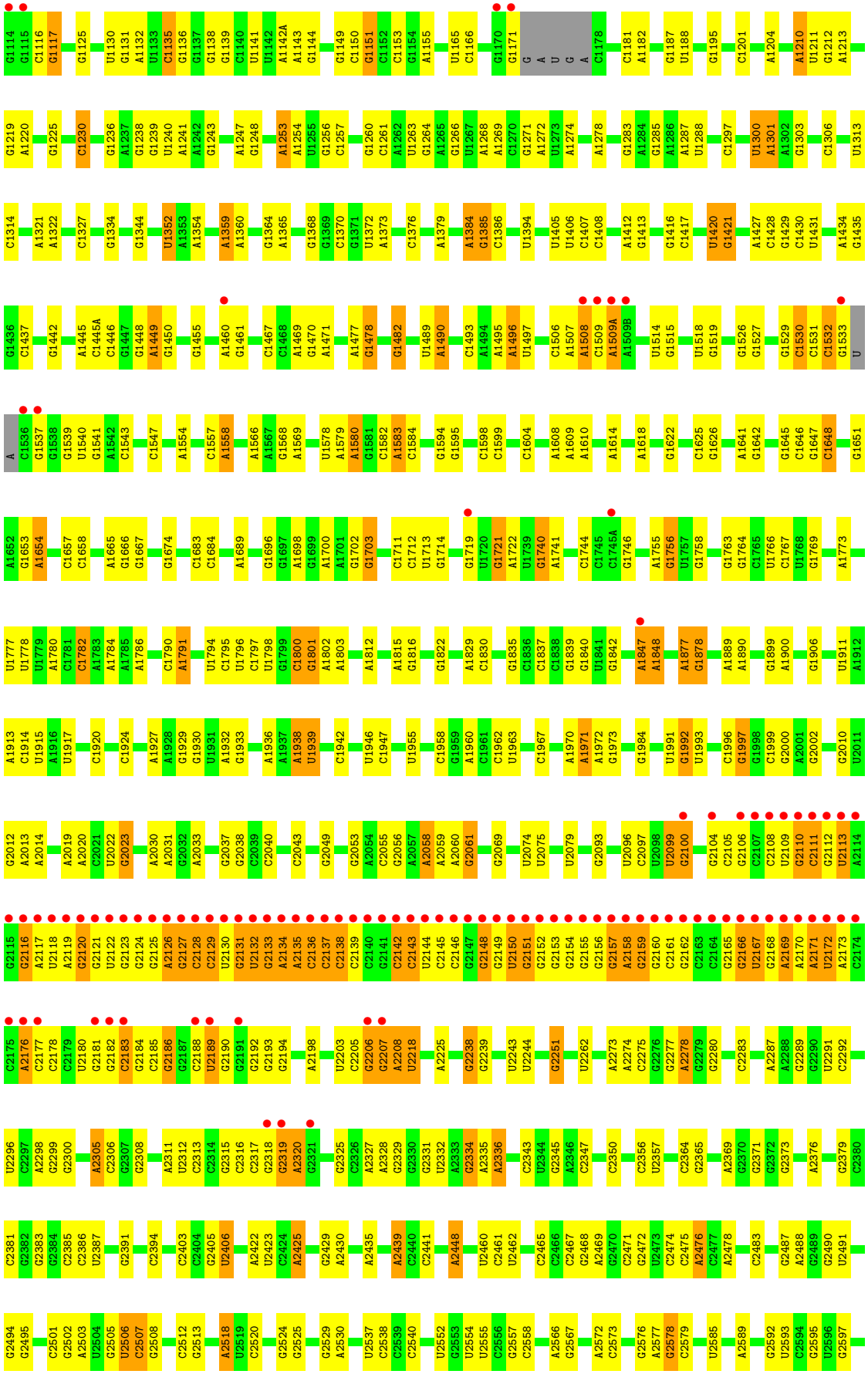
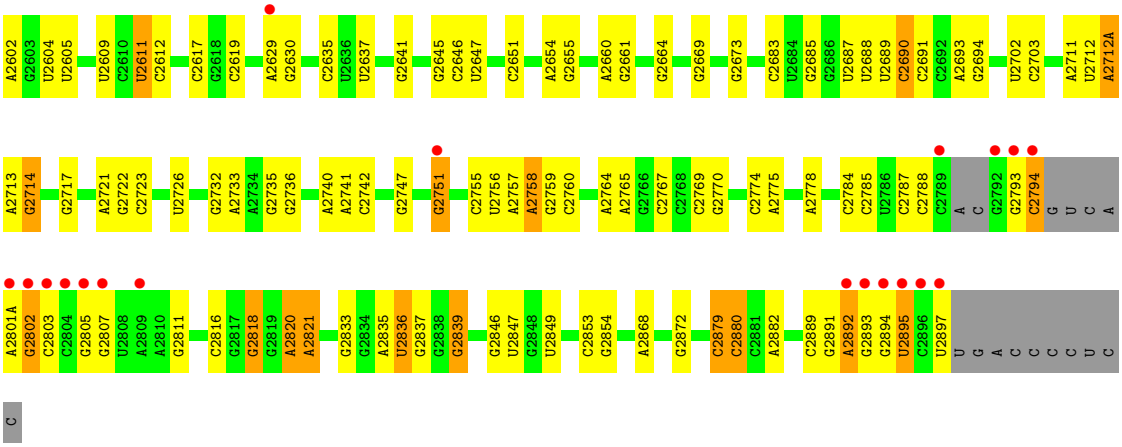


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

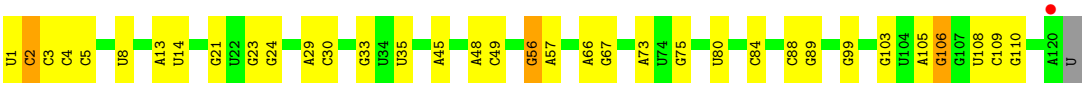






• Molecule 2: 5S Ribosomal RNA

Chain 1B:

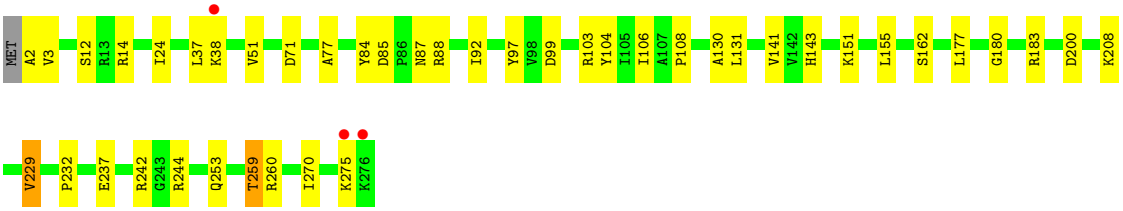


• Molecule 2: 5S Ribosomal RNA

Chain 2B:

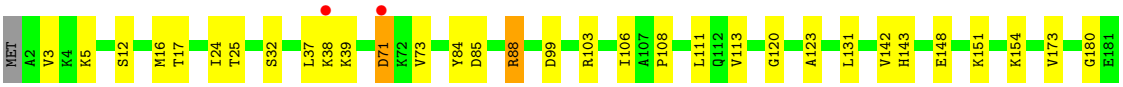
• Molecule 3: 50S ribosomal protein L2

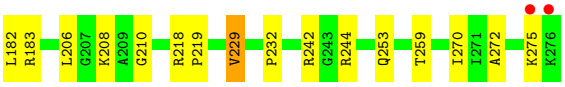
Chain 1D:



• Molecule 3: 50S ribosomal protein L2

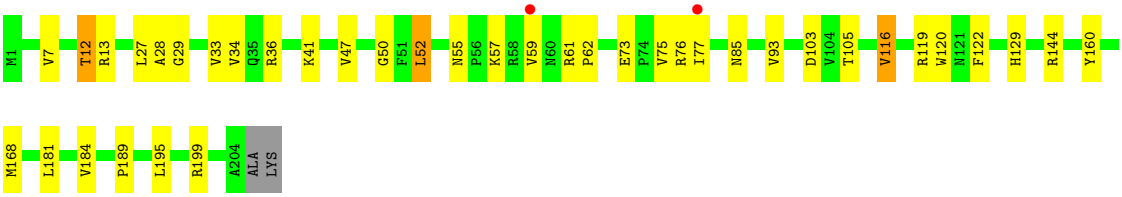
Chain 2D:





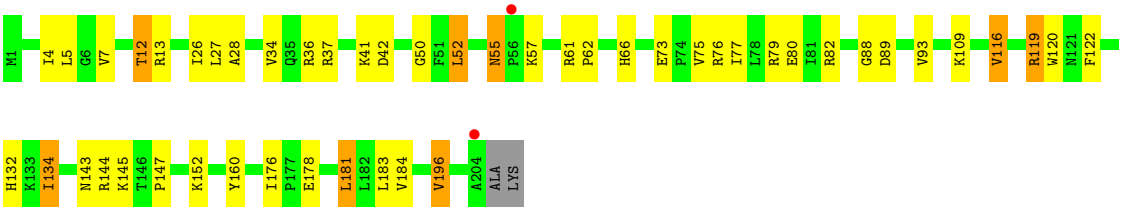
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



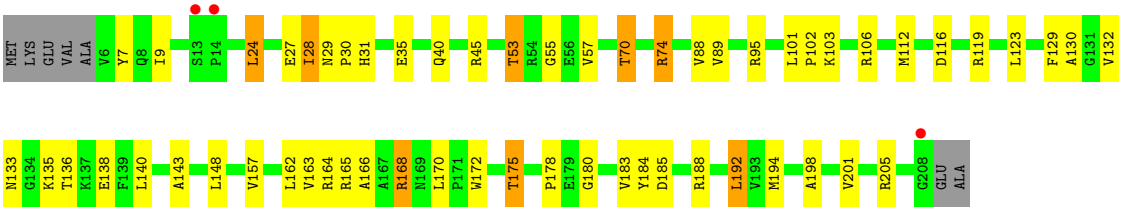
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



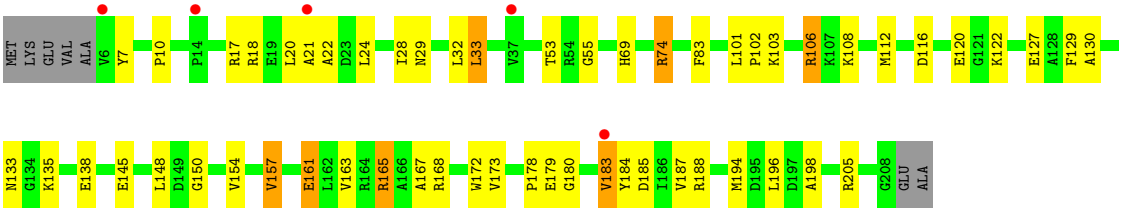
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



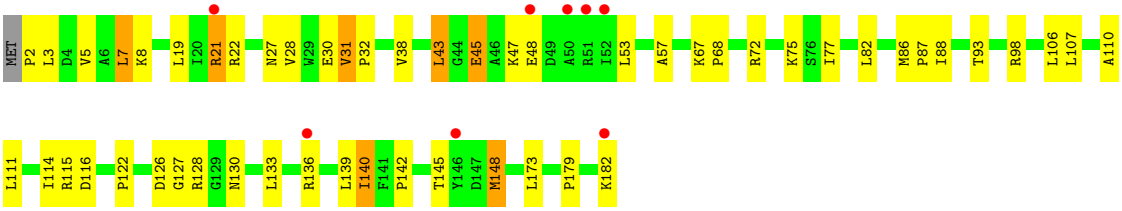
• Molecule 5: 50S ribosomal protein L4

Chain 2F:

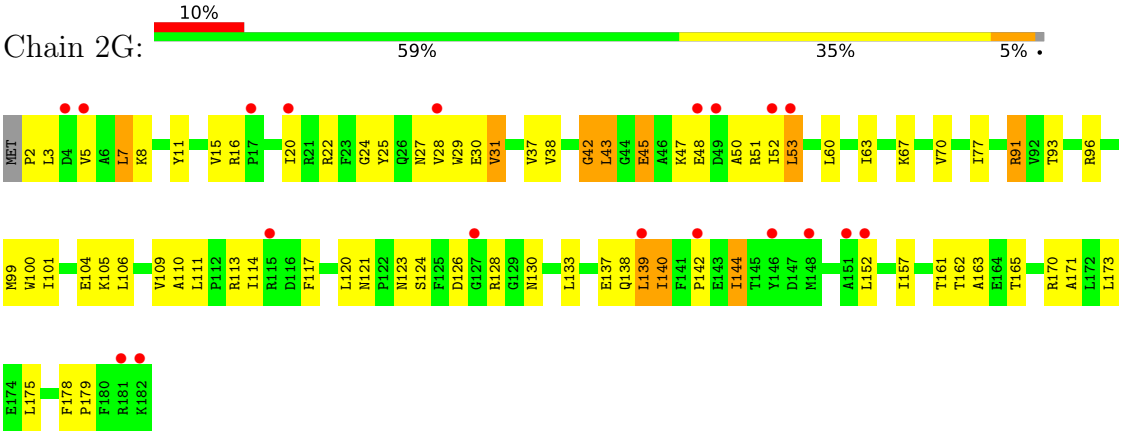


• Molecule 6: 50S ribosomal protein L5

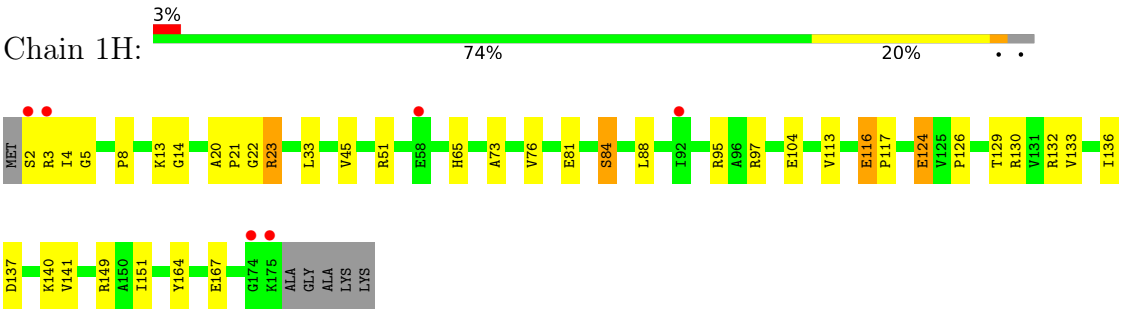
Chain 1G:



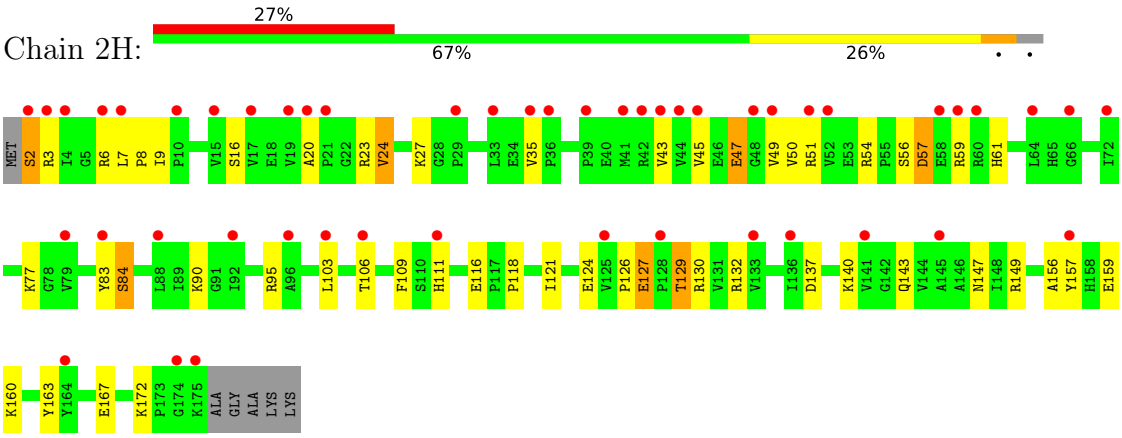
• Molecule 6: 50S ribosomal protein L5



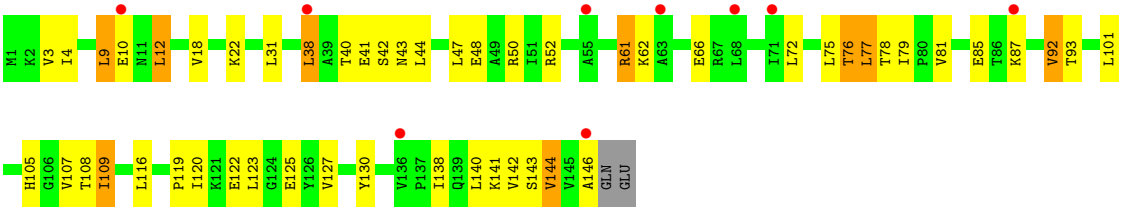
• Molecule 7: 50S ribosomal protein L6



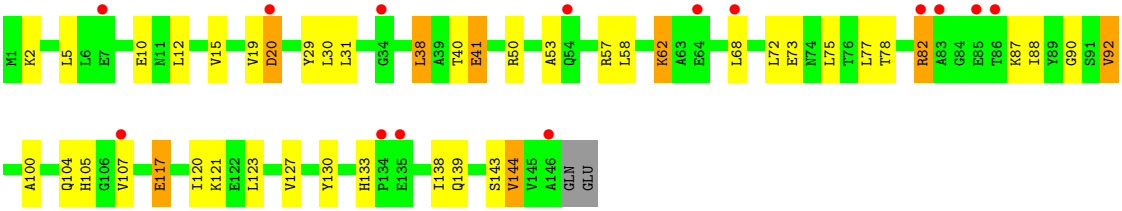
• Molecule 7: 50S ribosomal protein L6



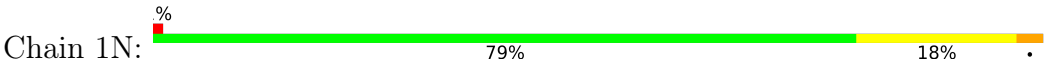
• Molecule 8: 50S ribosomal protein L9

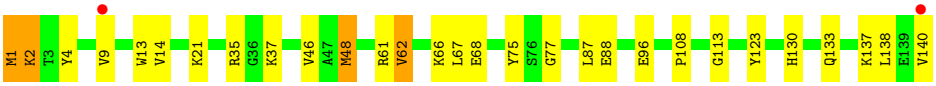


• Molecule 8: 50S ribosomal protein L9

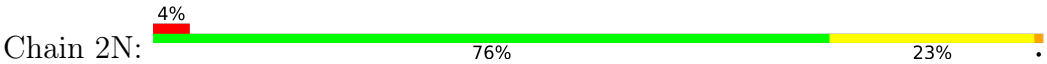


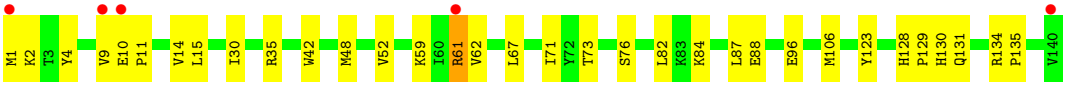
• Molecule 9: 50S ribosomal protein L13



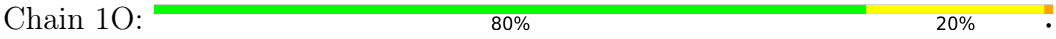


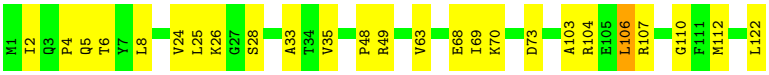
• Molecule 9: 50S ribosomal protein L13



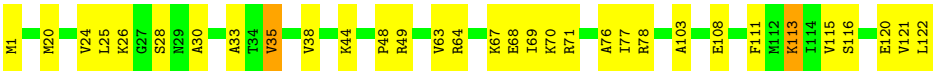


• Molecule 10: 50S ribosomal protein L14

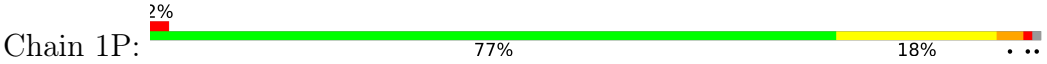


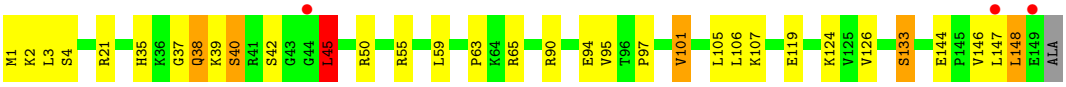


• Molecule 10: 50S ribosomal protein L14

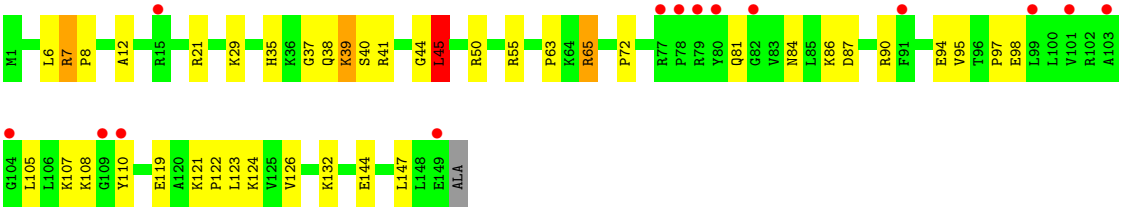


• Molecule 11: 50S ribosomal protein L15

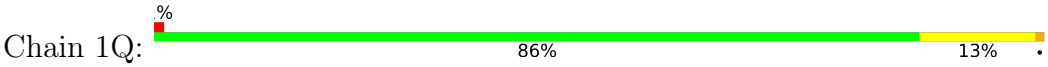


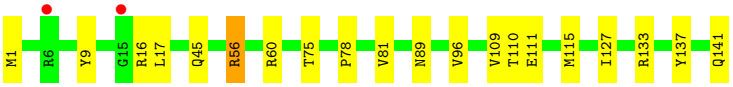


• Molecule 11: 50S ribosomal protein L15

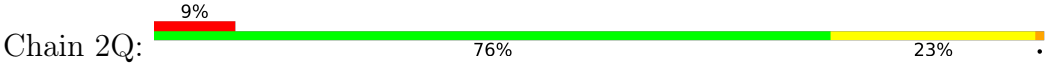


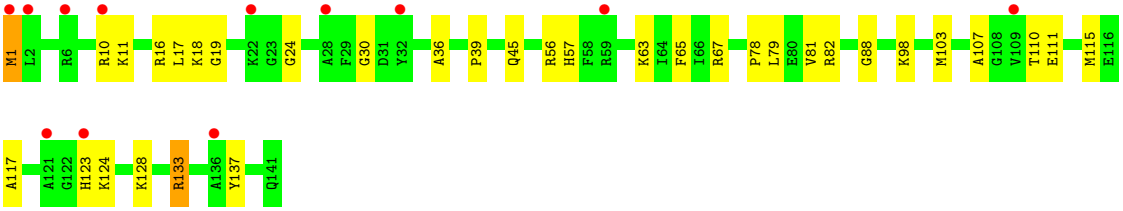
• Molecule 12: 50S ribosomal protein L16



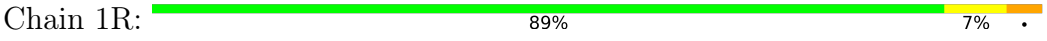


• Molecule 12: 50S ribosomal protein L16

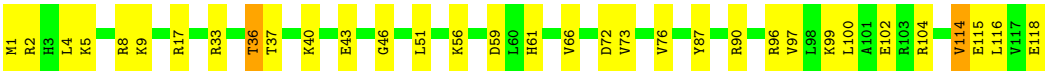




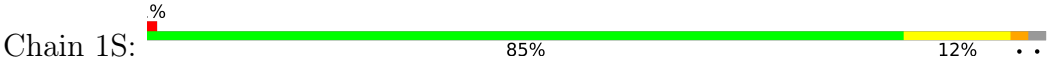
• Molecule 13: 50S ribosomal protein L17



• Molecule 13: 50S ribosomal protein L17

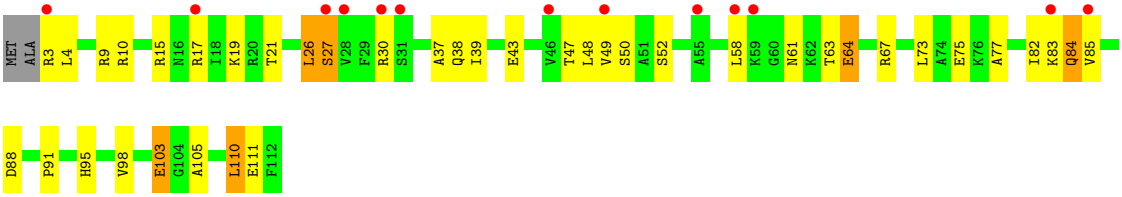


• Molecule 14: 50S ribosomal protein L18



• Molecule 14: 50S ribosomal protein L18

Chain 2S:

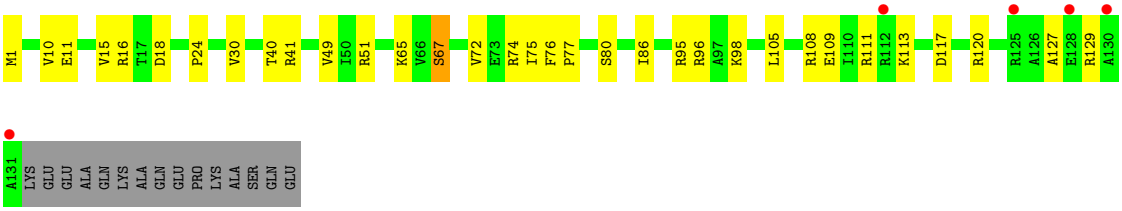


• Molecule 15: 50S ribosomal protein L19

Chain 1T:

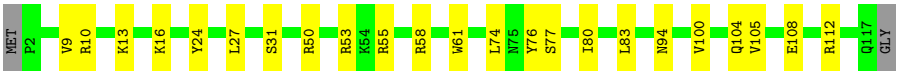
• Molecule 15: 50S ribosomal protein L19

Chain 2T:



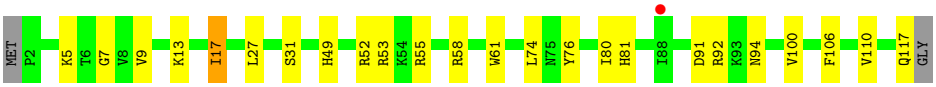
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



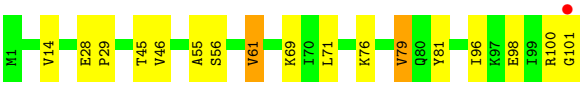
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



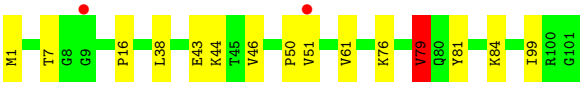
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



• Molecule 17: 50S ribosomal protein L21

Chain 2V:

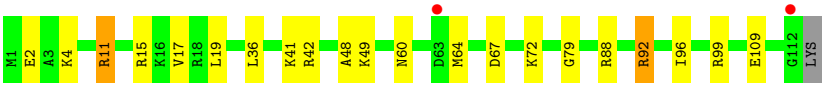


• Molecule 18: 50S ribosomal protein L22

Chain 1W:

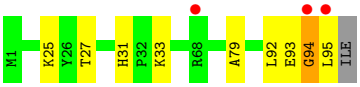
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



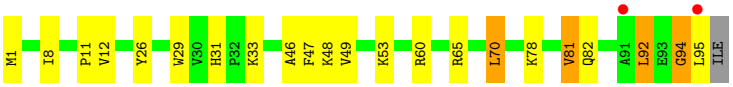
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



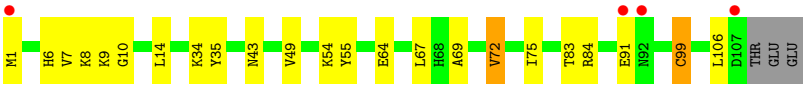
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



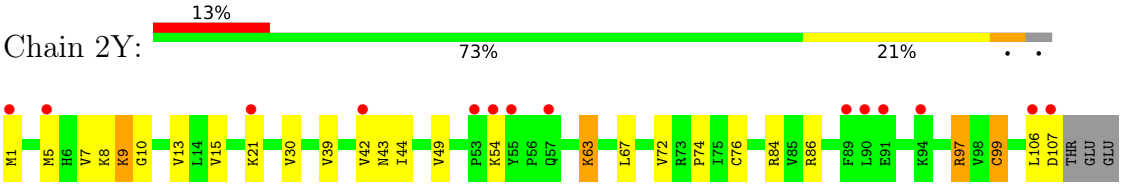
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



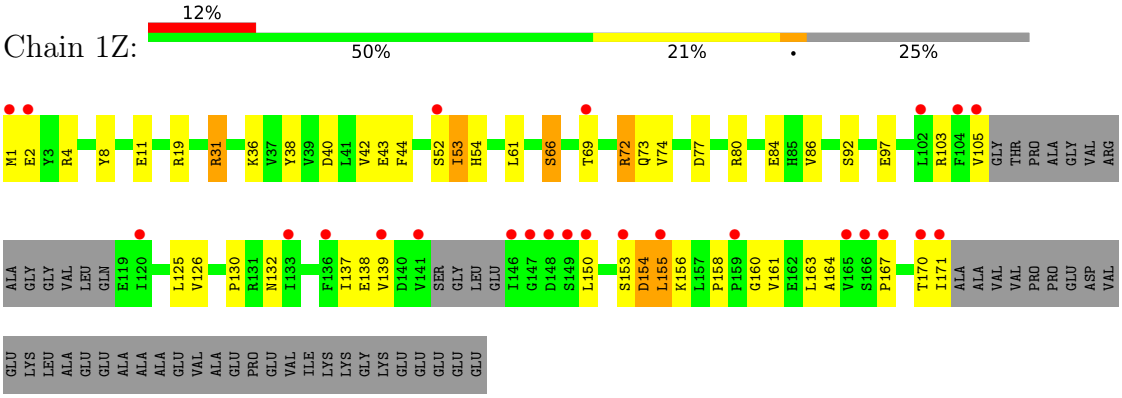
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



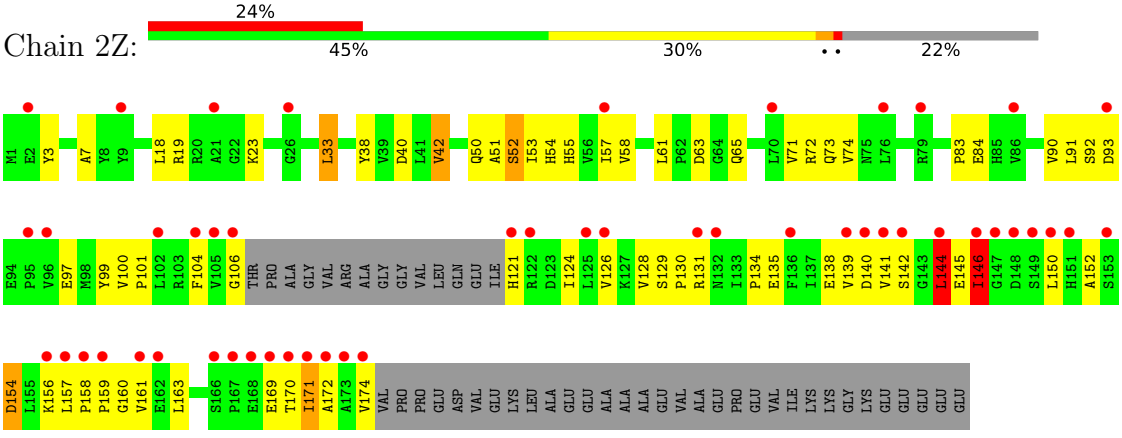
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



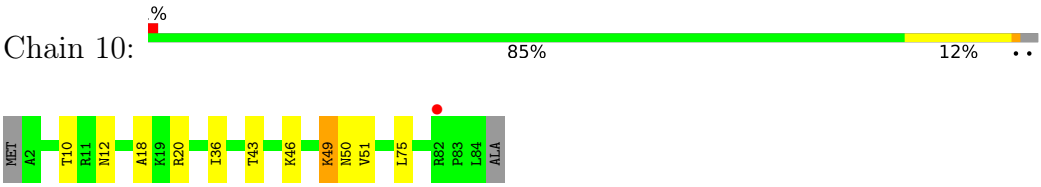
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



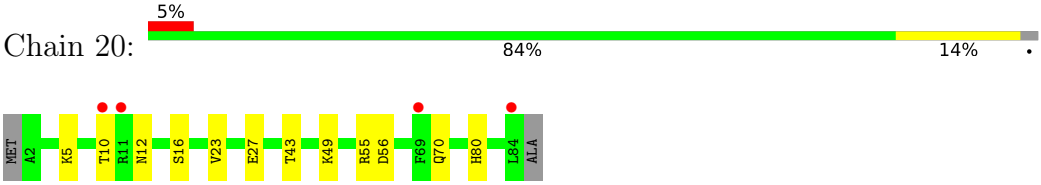
• Molecule 22: 50S ribosomal protein L27

Chain 10:



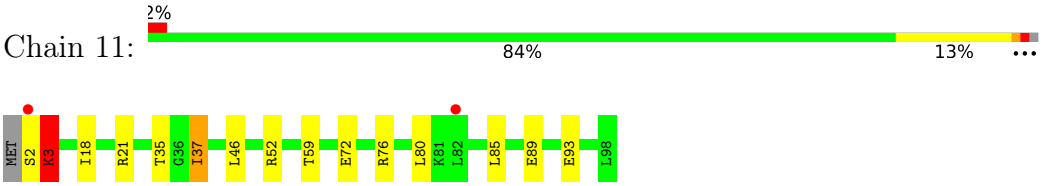
• Molecule 22: 50S ribosomal protein L27

Chain 20:



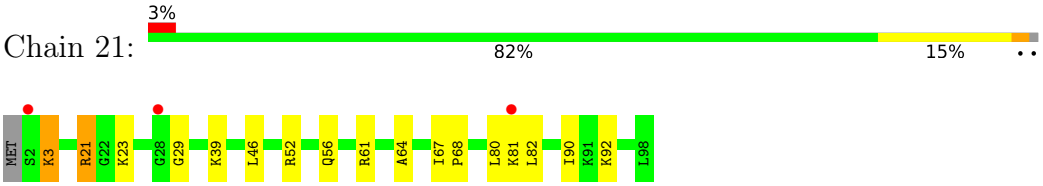
• Molecule 23: 50S ribosomal protein L28

Chain 11:



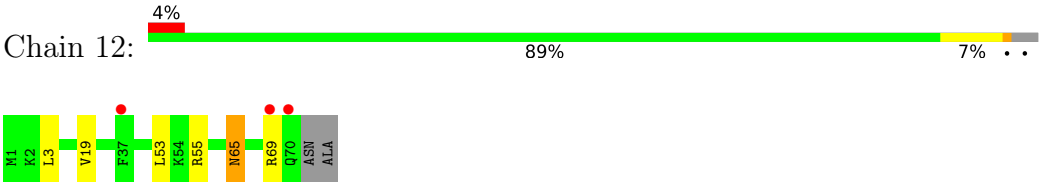
• Molecule 23: 50S ribosomal protein L28

Chain 21:



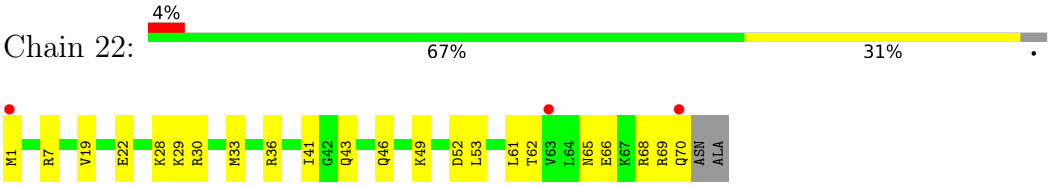
• Molecule 24: 50S ribosomal protein L29

Chain 12:



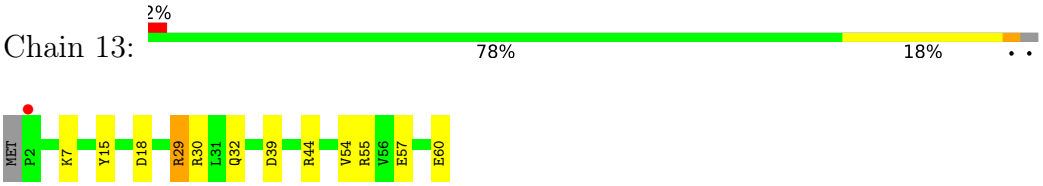
• Molecule 24: 50S ribosomal protein L29

Chain 22:



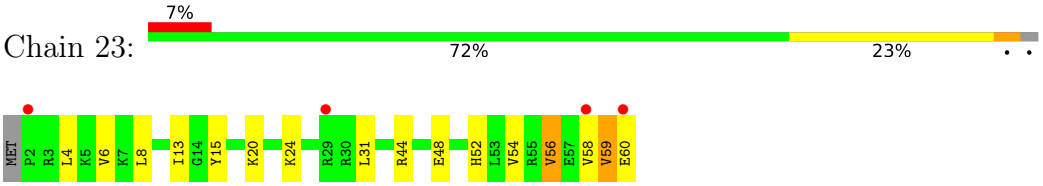
• Molecule 25: 50S ribosomal protein L30

Chain 13:



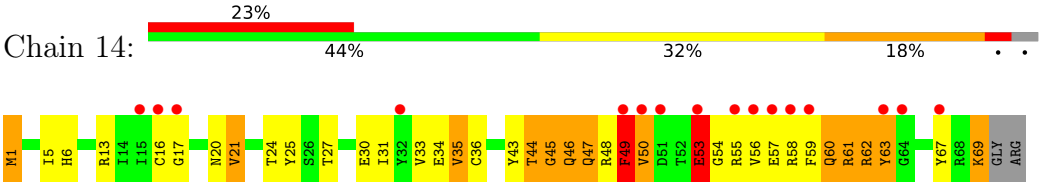
• Molecule 25: 50S ribosomal protein L30

Chain 23:



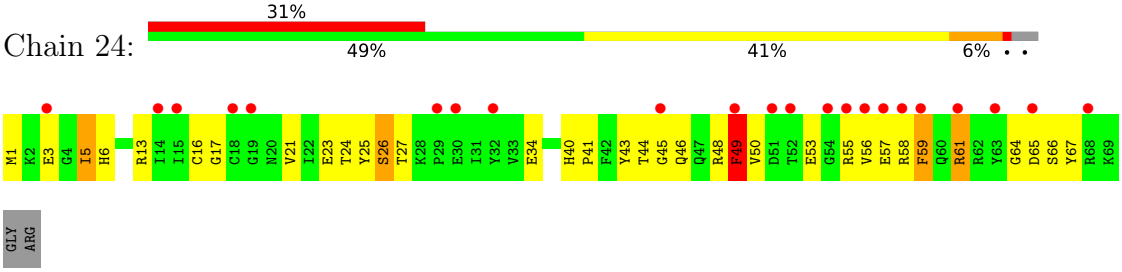
• Molecule 26: 50S ribosomal protein L31

Chain 14:



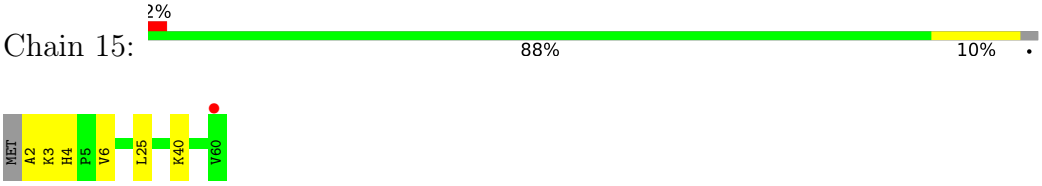
• Molecule 26: 50S ribosomal protein L31

Chain 24:



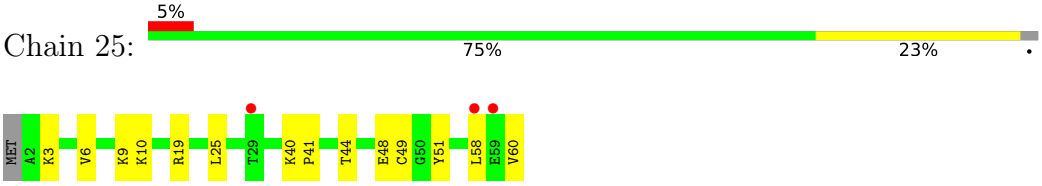
• Molecule 27: 50S ribosomal protein L32

Chain 15:



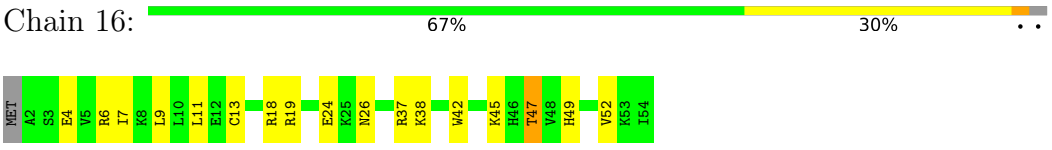
• Molecule 27: 50S ribosomal protein L32

Chain 25:



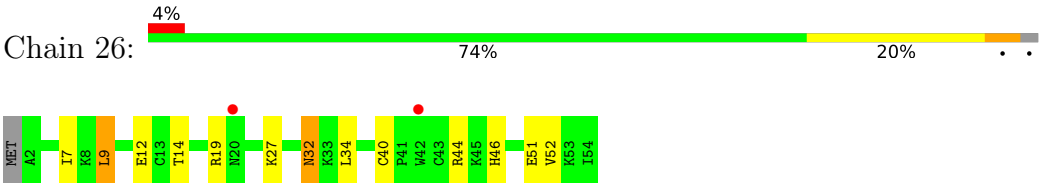
• Molecule 28: 50S ribosomal protein L33

Chain 16:



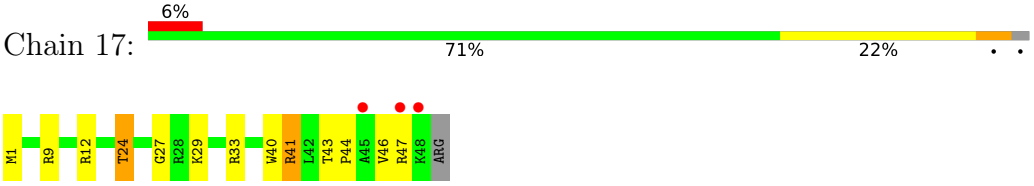
• Molecule 28: 50S ribosomal protein L33

Chain 26:



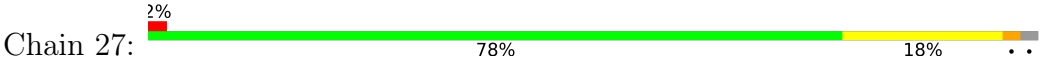
• Molecule 29: 50S ribosomal protein L34

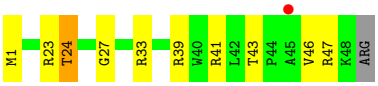
Chain 17:



• Molecule 29: 50S ribosomal protein L34

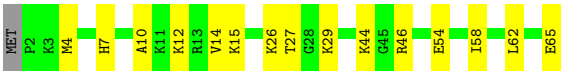
Chain 27:





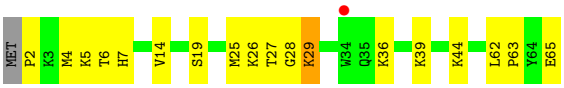
• Molecule 30: 50S ribosomal protein L35

Chain 18:



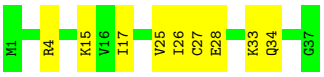
• Molecule 30: 50S ribosomal protein L35

Chain 28:



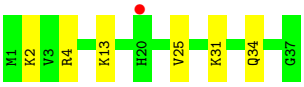
• Molecule 31: 50S ribosomal protein L36

Chain 19:



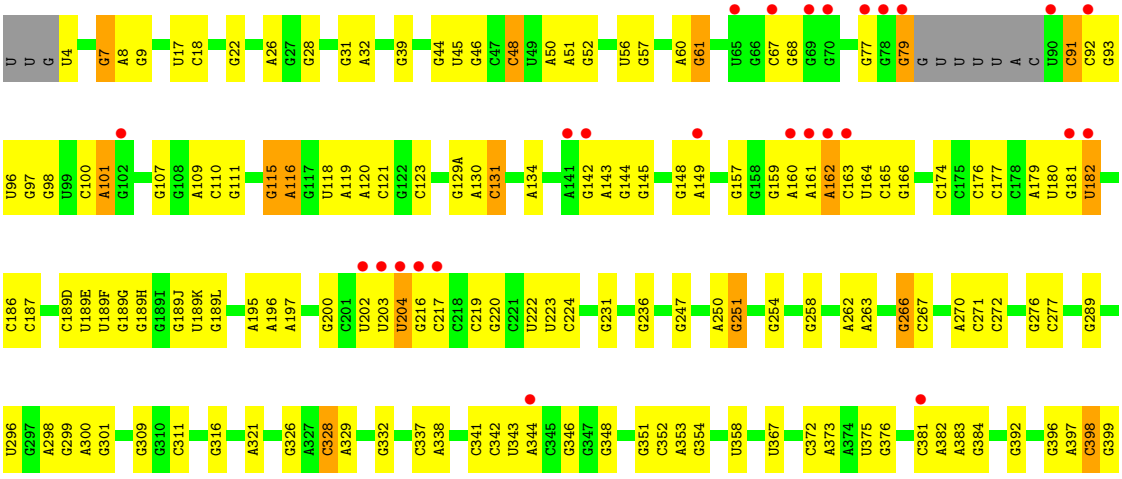
• Molecule 31: 50S ribosomal protein L36

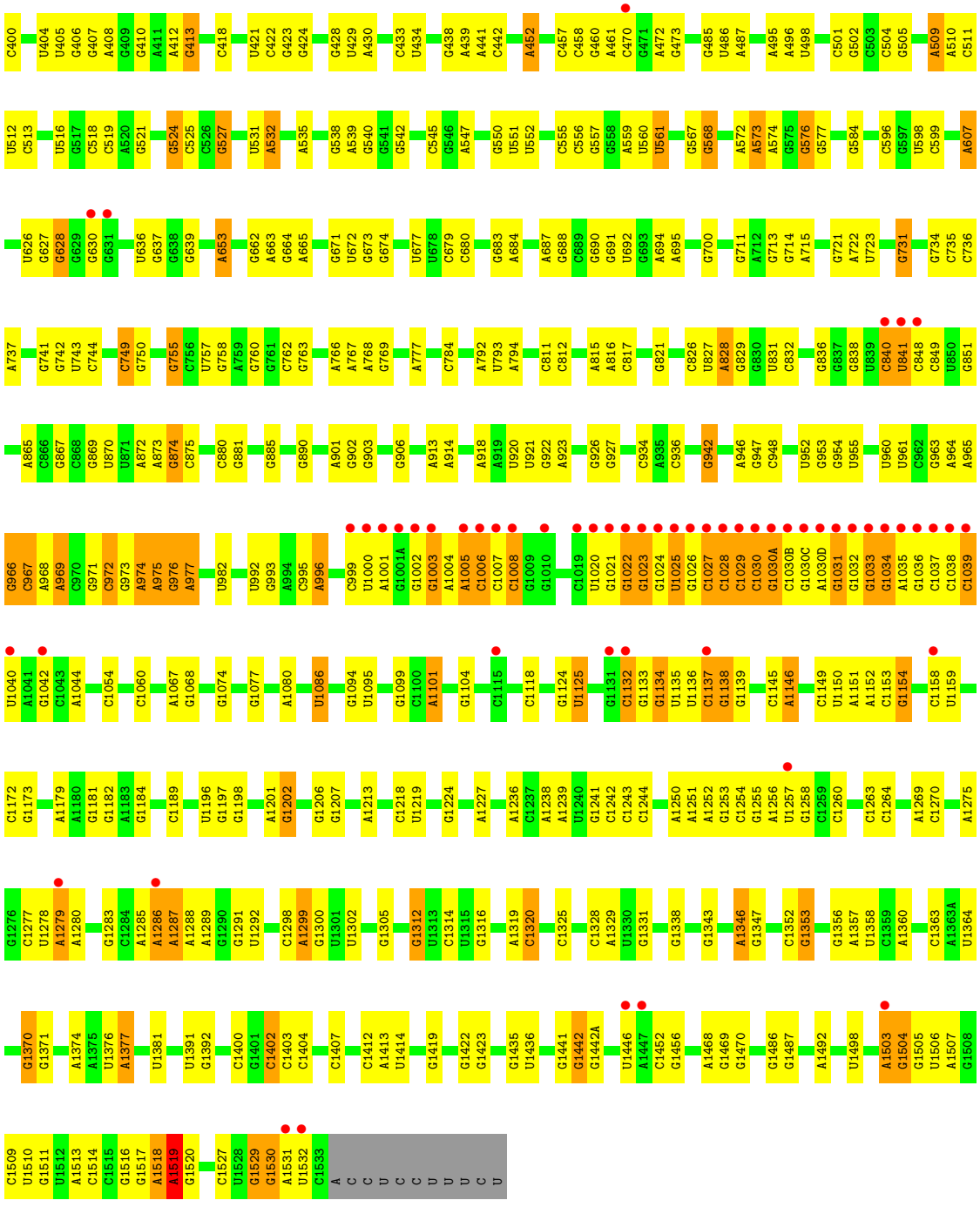
Chain 29:



• Molecule 32: 16S Ribosomal RNA

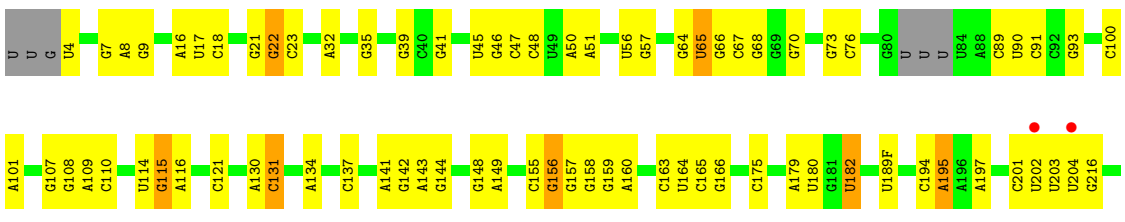
Chain 1a:

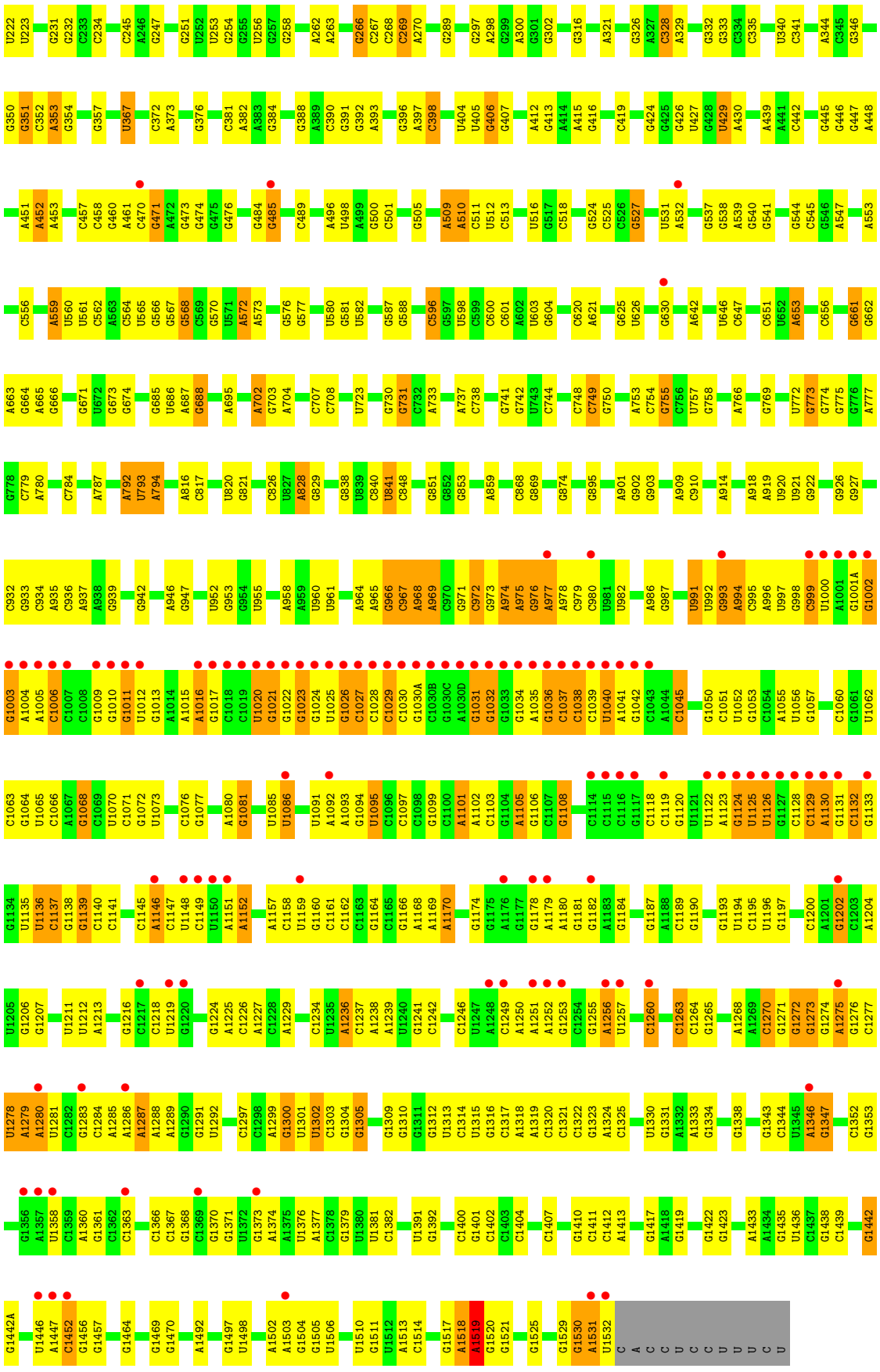




• Molecule 32: 16S Ribosomal RNA

Chain 2a:

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G350 G351 C352 A353 G354 G357 U367 C372 A373 G376 C381 A382 A383 G384 G388 A389 C390 G391 G392 A393 G396 A397 C398 U404 U405 G406 G407 A412 G413 A414 A415 G416 C419 G424 G425 G426 U427 G428 U429 A430 A439 A441 C442 G445 G446 G447 A448
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C556 A559 U560 U561 C562 A563 C564 U565 G566 G567 G568 C569 G570 U571 A572 A573 G576 G577 U580 G581 U582 G587 G588 C596 G597 U598 G599 C600 C601 A602 U603 G604 C620 A621 G625 U626 G630 A642 U646 C647 C651 U652 A653 C656 G661 G662
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G778 C779 A780 C784 A787 A792 U793 A794 A816 C817 U820 G821 C826 U827 A828 G829 G838 U839 C840 U841 C848 G851 G852 G853 A859 C868 G869 G874 G895 A901 G902 G903 A909 C910 A914 A918 A919 U920 U921 G922 G926 G927
C932 G933 C934 A935 C936 A937 A938 G939 G942 A946 G947 U952 G953 G954 U955 A958 A959 U960 U961 A964 A965 G966 C967 A968 A969 C970 G971 G972 G973 A974 A975 G976 A977 A978 C979 C980 U981 U982 A986 G987 U991 U992 G993 A994 C995 A996 U997 G998 C999 U1000 A1001 G1001A G1002
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C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 C1071 G1072 U1073 C1076 G1077 A1080 G1081 U1085 U1086 U1091 A1092 A1093 G1094 U1096 C1096 C1097 C1098 G1099 C1100 A1101 A1102 C1103 G1104 A1105 G1106 C1107 G1108 C1114 C1115 C1116 G1117 C1118 C1119 G1120 U1121 U1122 A1123 G1124 U1125 U1126 G1127 C1128 C1129 A1130 G1131 C1132 G1133
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U1278 A1279 A1280 U1281 C1282 G1283 C1284 A1285 A1286 A1287 A1288 A1289 G1290 G1291 U1292 C1297 C1298 A1299 G1300 U1301 U1302 C1303 G1304 G1305 G1309 G1310 G1311 G1312 U1313 C1314 U1315 G1316 C1317 A1318 A1319 C1320 C1321 C1322 G1323 A1324 C1325 U1330 G1331 A1332 A1333 G1334 G1338 G1343 C1344 U1345 A1346 G1347 C1352 G1353
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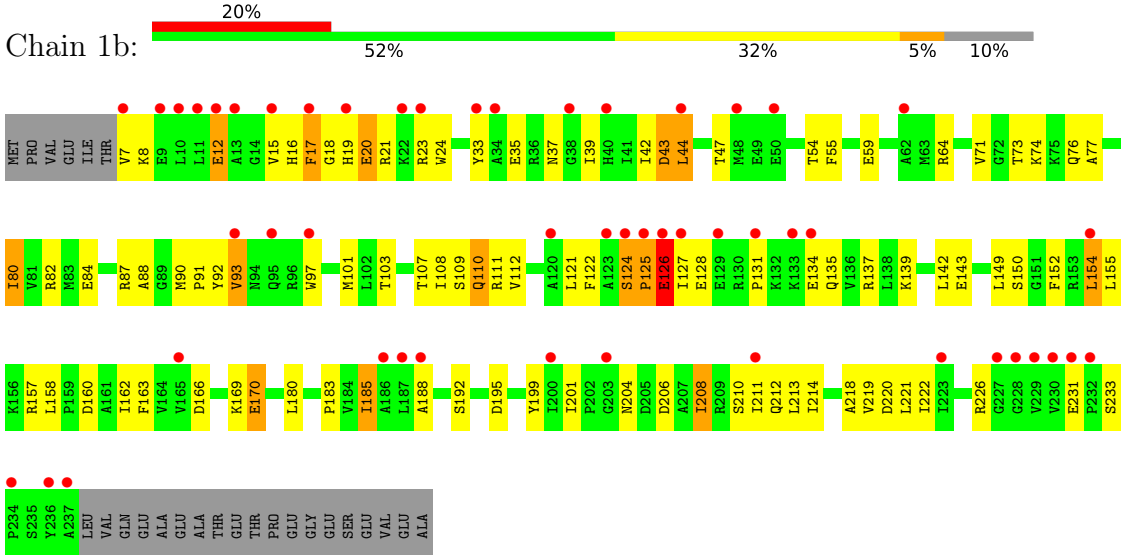
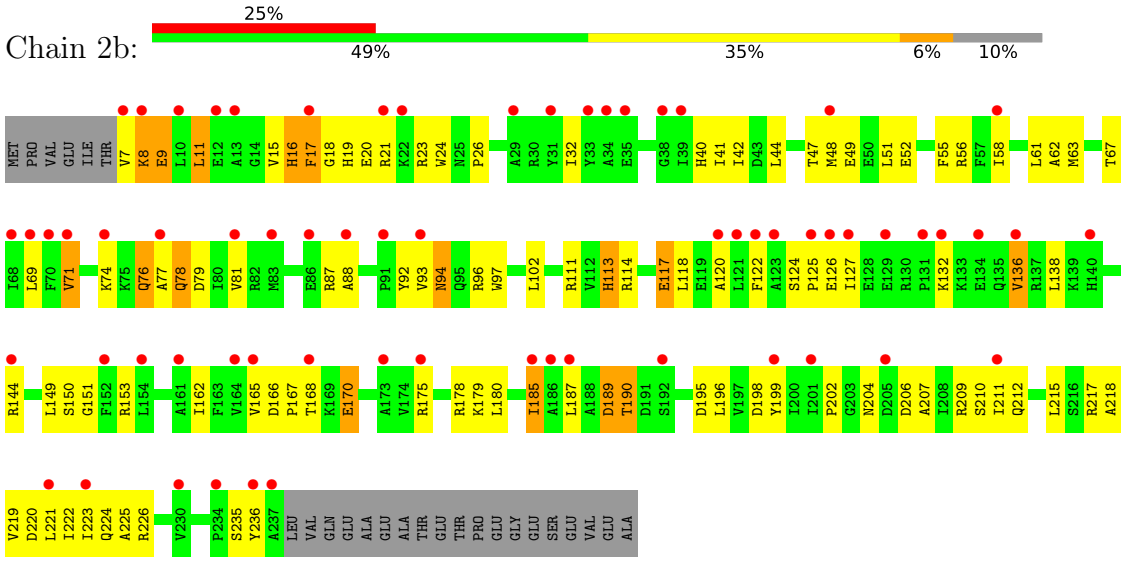
• Molecule 33: 30S ribosomal protein S2

Chain 1b:



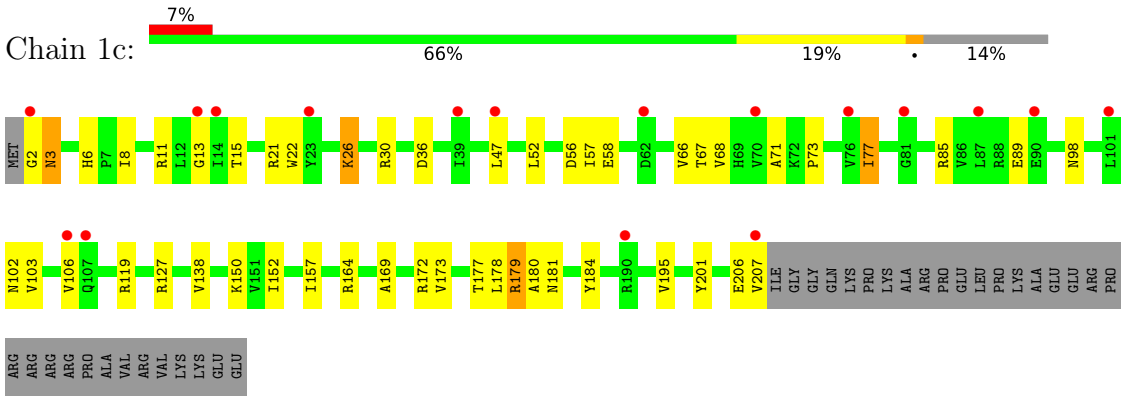
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



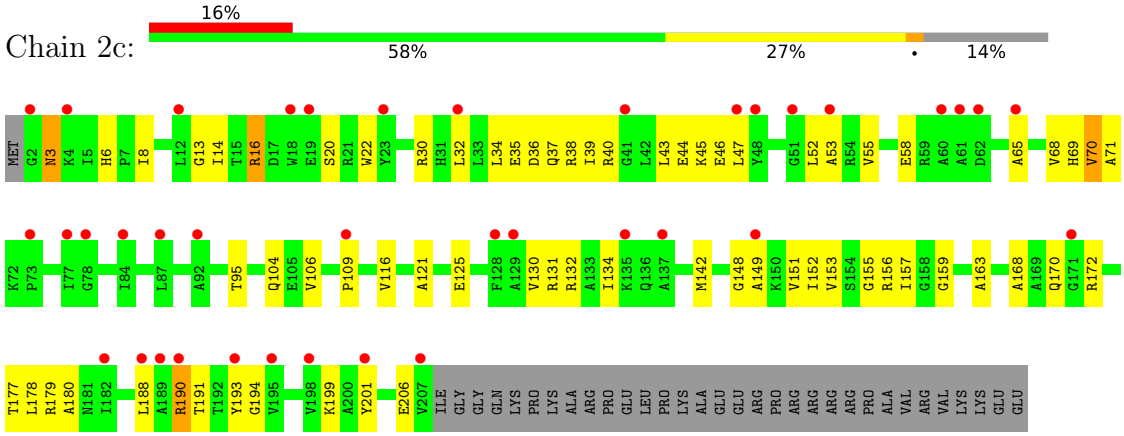
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



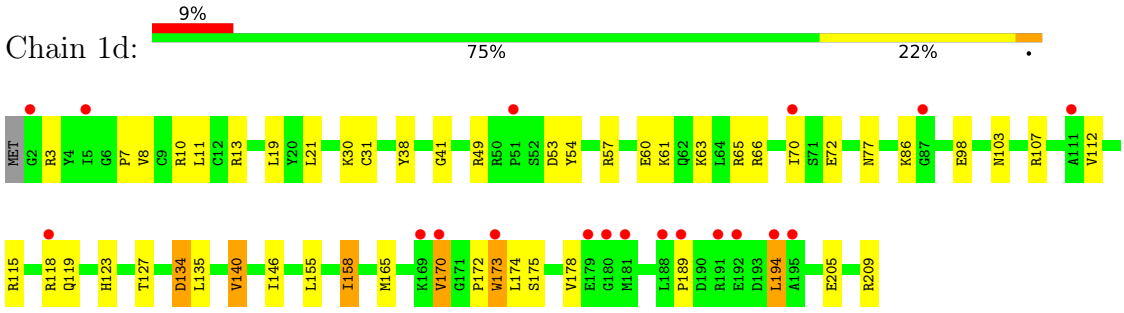
• Molecule 34: 30S ribosomal protein S3

Chain 2c:



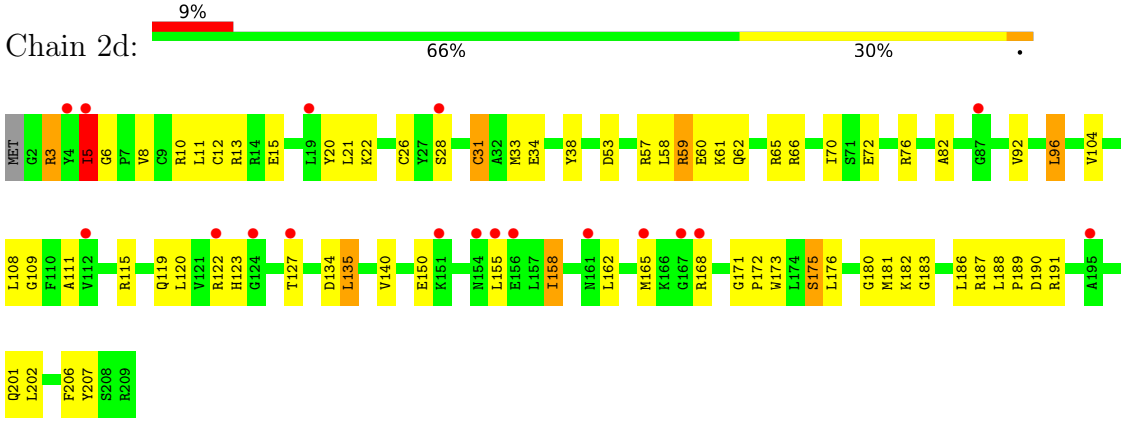
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



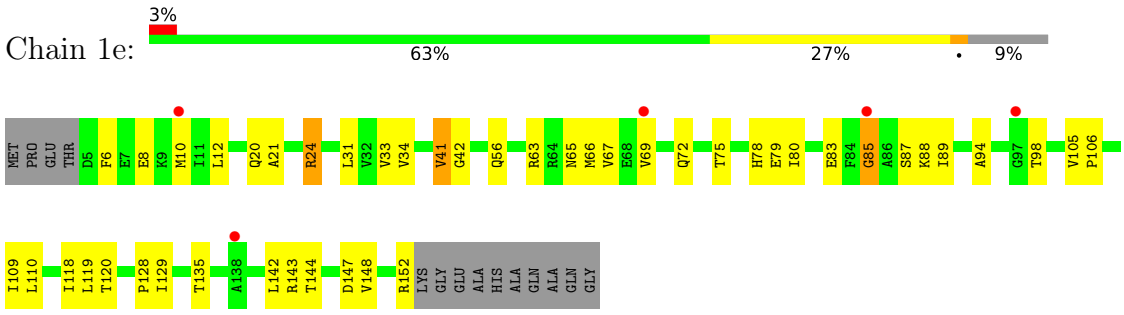
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



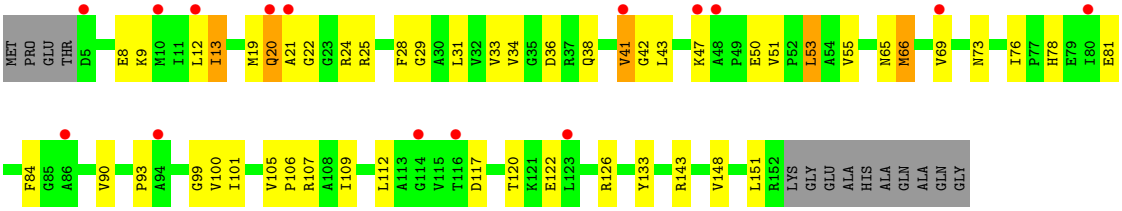
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



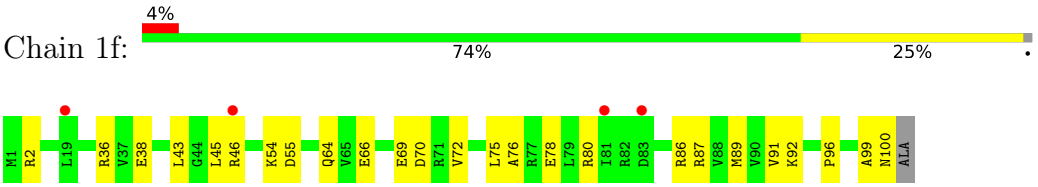
• Molecule 36: 30S ribosomal protein S5

Chain 2e:



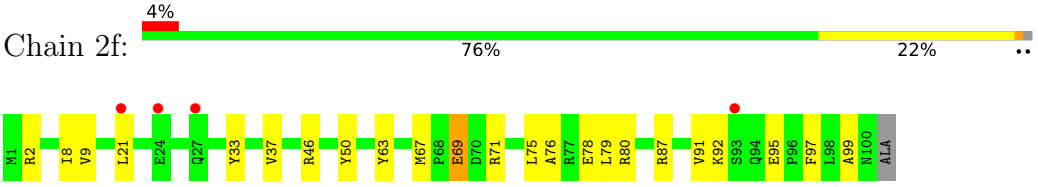
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



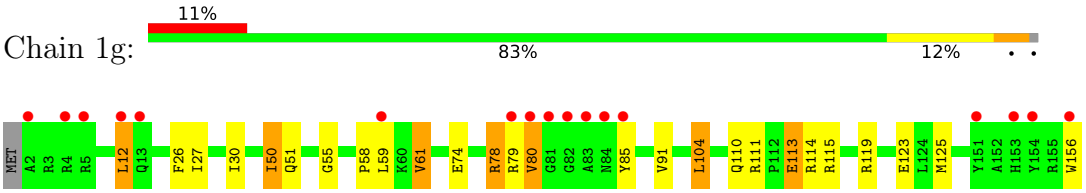
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



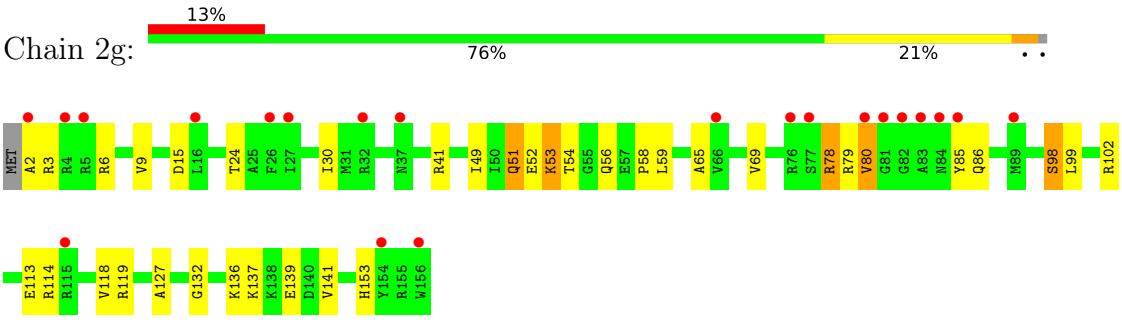
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



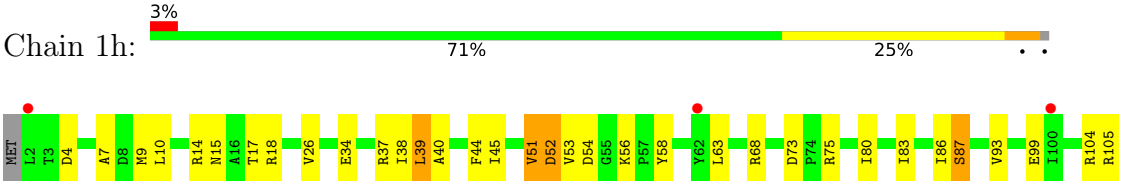
• Molecule 38: 30S ribosomal protein S7

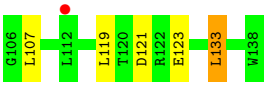
Chain 2g:



• Molecule 39: 30S ribosomal protein S8

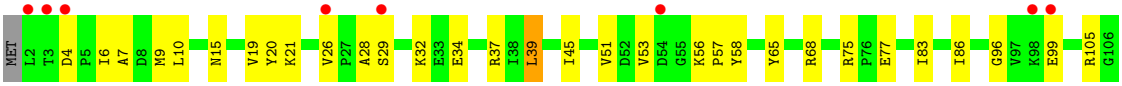
Chain 1h:

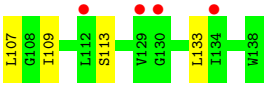




• Molecule 39: 30S ribosomal protein S8

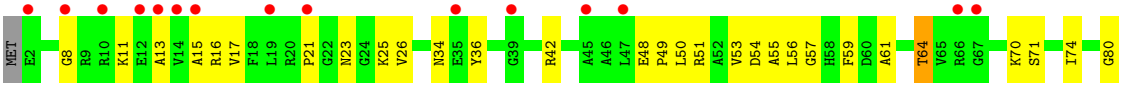
Chain 2h:

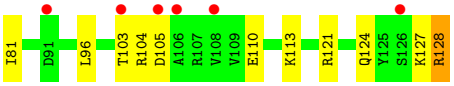




• Molecule 40: 30S ribosomal protein S9

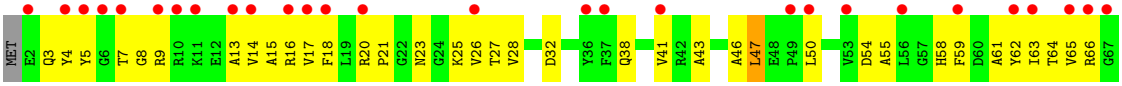
Chain 1i:

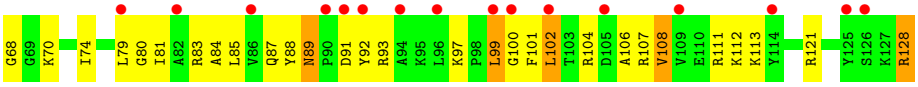




• Molecule 40: 30S ribosomal protein S9

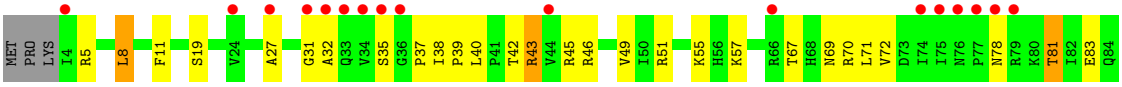
Chain 2i:

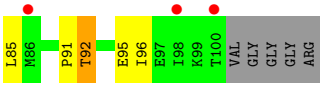




• Molecule 41: 30S ribosomal protein S10

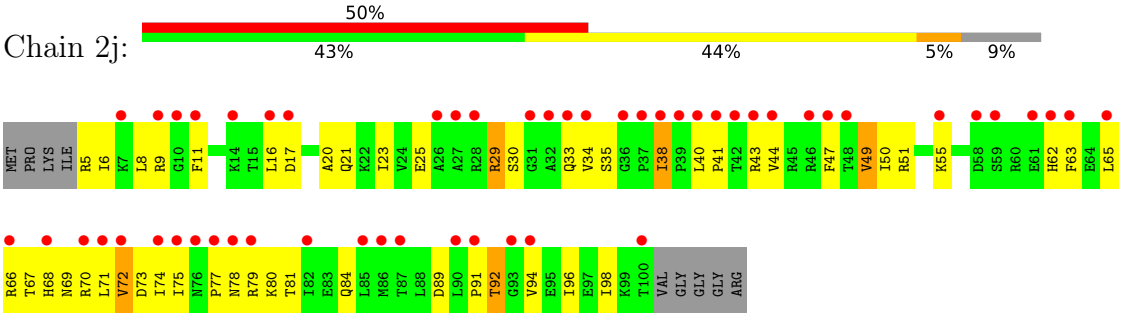
Chain 1j:





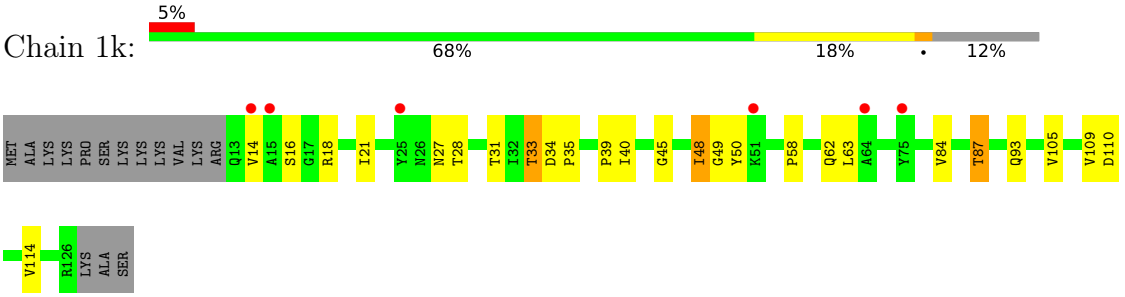
• Molecule 41: 30S ribosomal protein S10

Chain 2j:



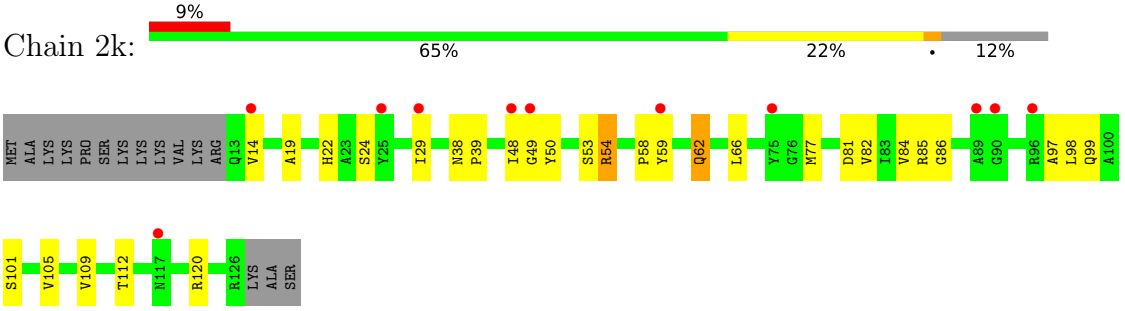
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



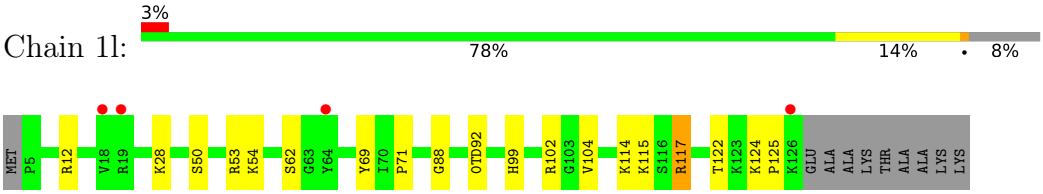
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



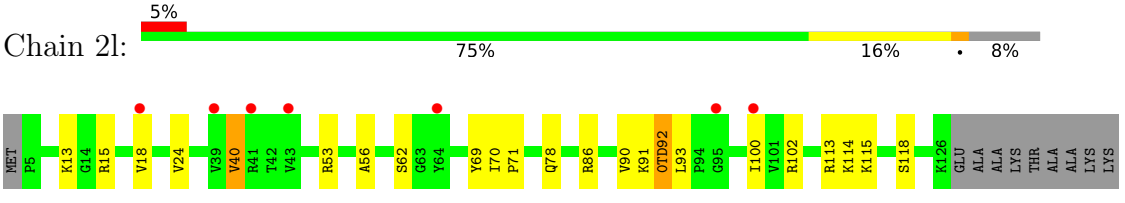
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



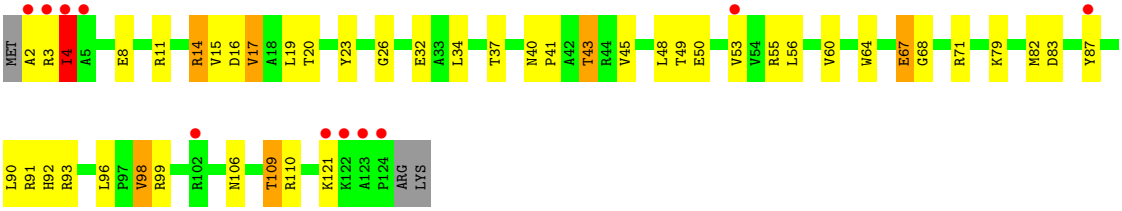
• Molecule 43: 30S ribosomal protein S12

Chain 2l:

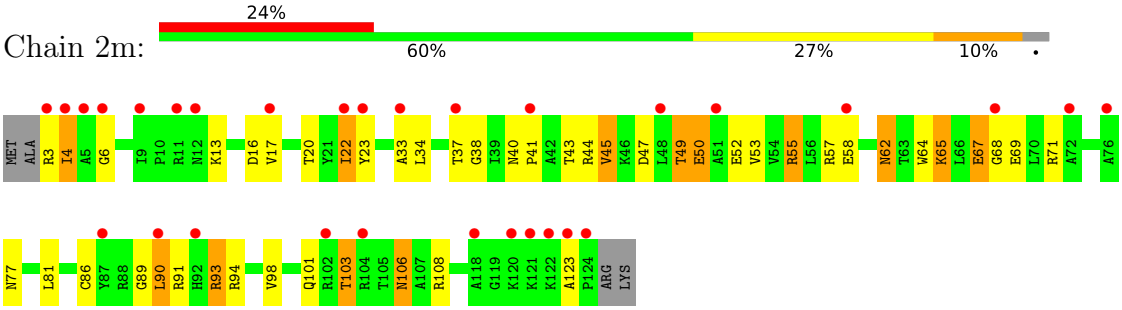


• Molecule 44: 30S ribosomal protein S13

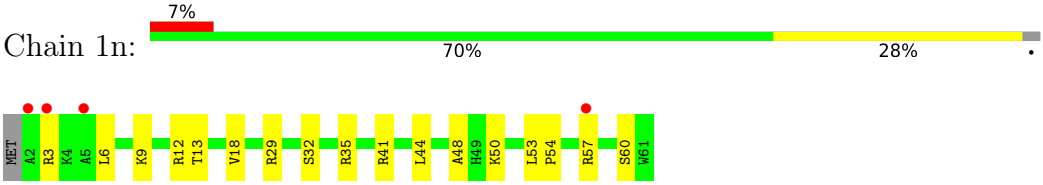
Chain 1m:



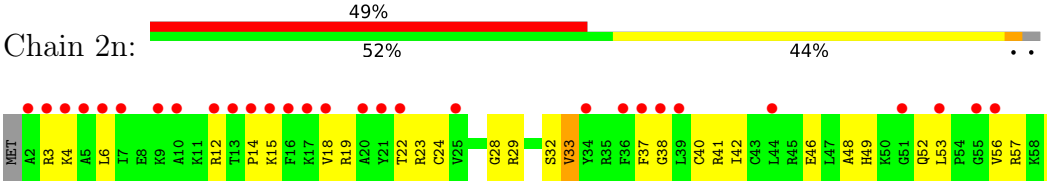
• Molecule 44: 30S ribosomal protein S13



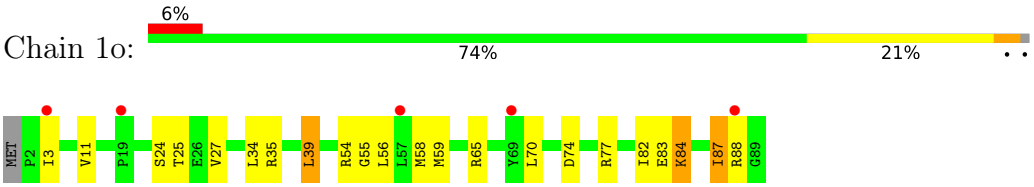
• Molecule 45: 30S ribosomal protein S14 type Z



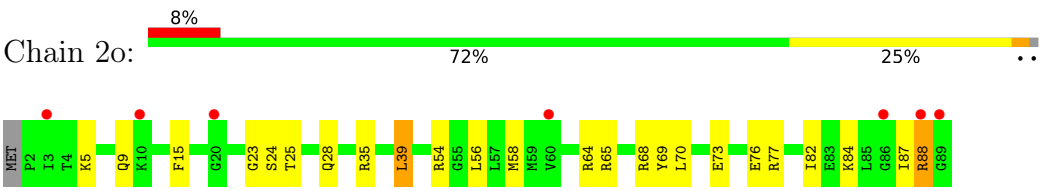
• Molecule 45: 30S ribosomal protein S14 type Z



• Molecule 46: 30S ribosomal protein S15

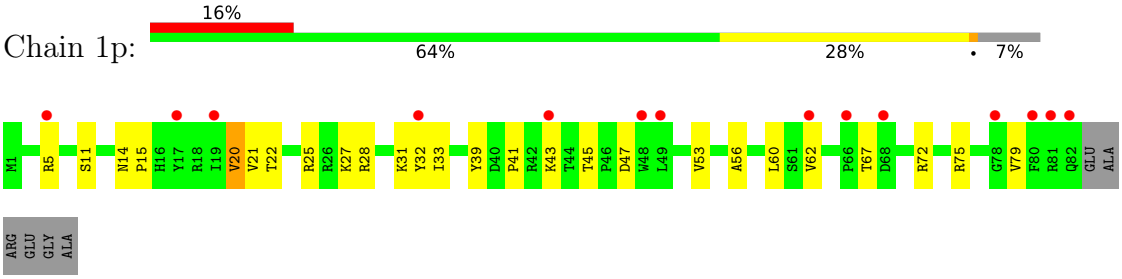


• Molecule 46: 30S ribosomal protein S15



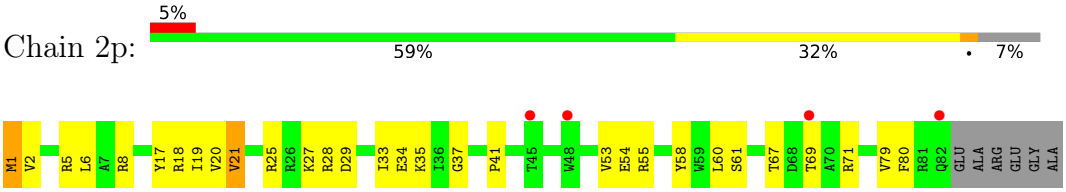
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



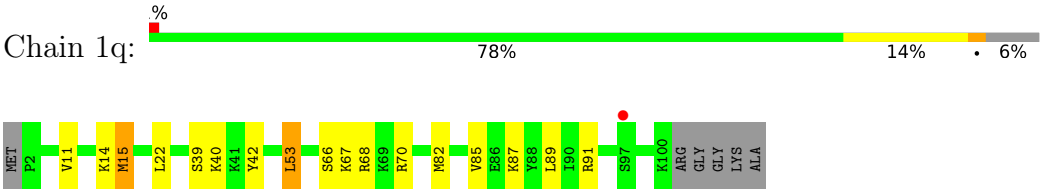
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



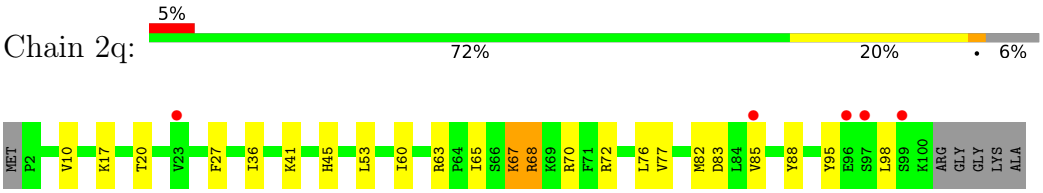
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



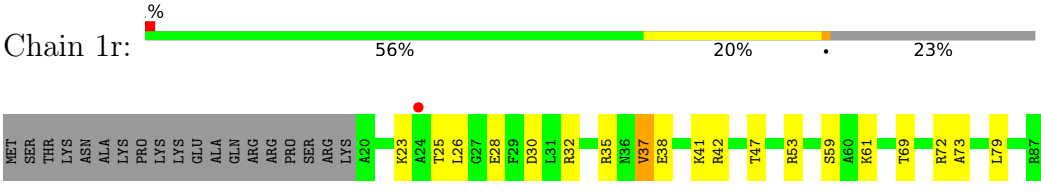
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



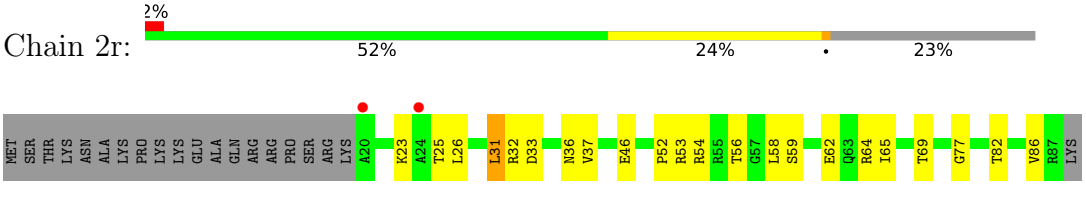
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



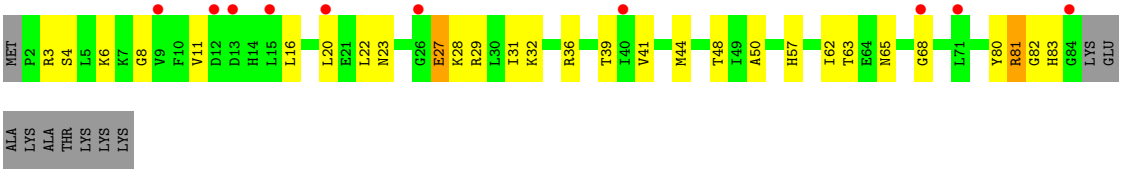
• Molecule 49: 30S ribosomal protein S18

Chain 2r:

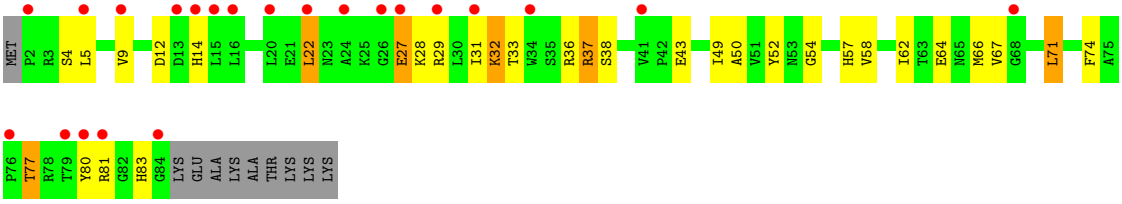


• Molecule 50: 30S ribosomal protein S19

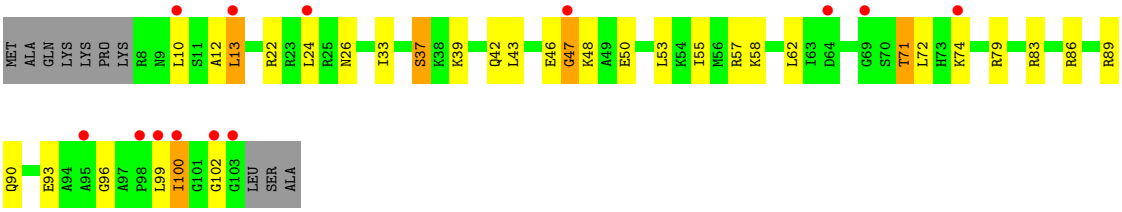
Chain 1s:



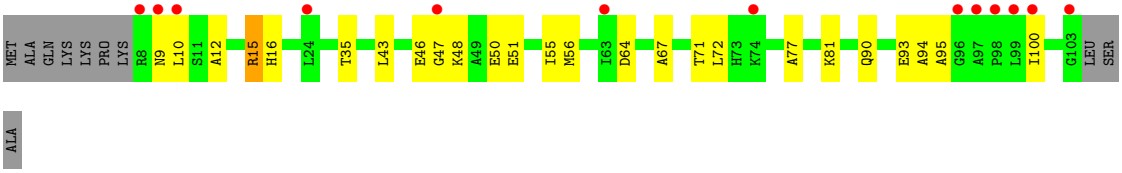
• Molecule 50: 30S ribosomal protein S19



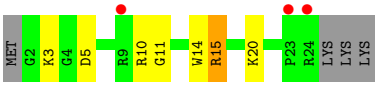
• Molecule 51: 30S ribosomal protein S20



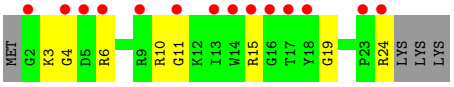
• Molecule 51: 30S ribosomal protein S20



• Molecule 52: 30S ribosomal protein Thx

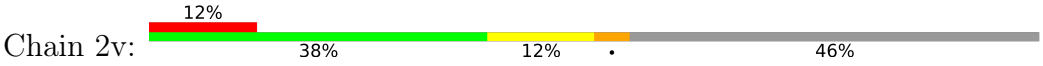


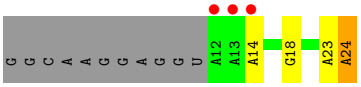
• Molecule 52: 30S ribosomal protein Thx



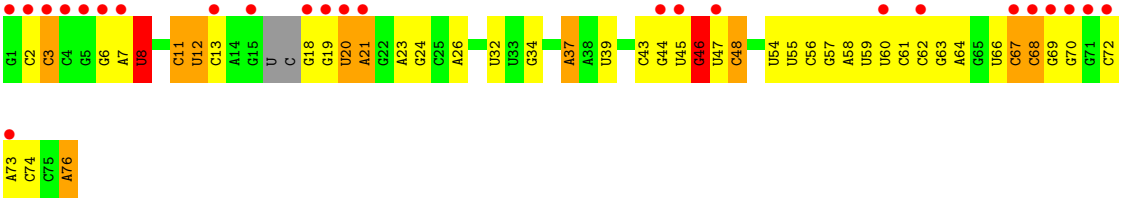
• Molecule 53: MF-mRNA

• Molecule 53: MF-mRNA

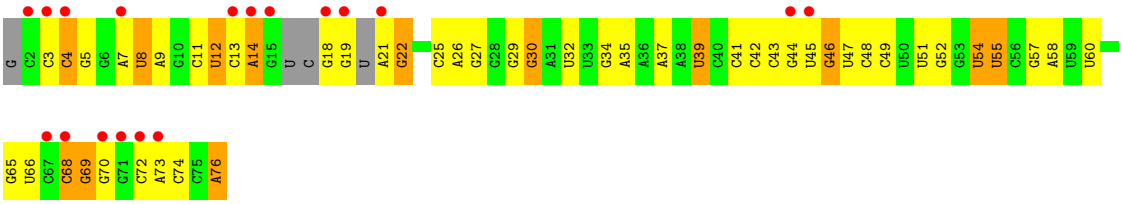




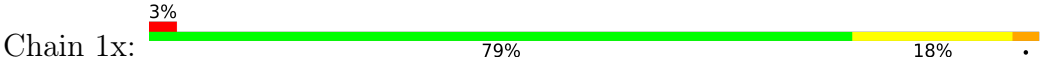
• Molecule 54: Aminoacylated Phe-tRNAphe

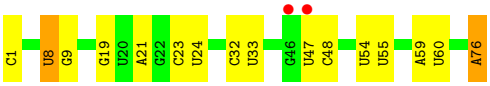


• Molecule 54: Aminoacylated Phe-tRNAphe

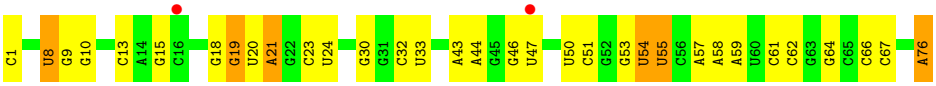


• Molecule 55: Aminoacylated fMet-tRNAmet



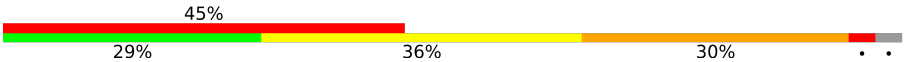


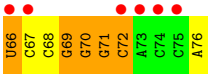
• Molecule 55: Aminoacylated fMet-tRNAmet



• Molecule 56: Deacylated tRNAphe

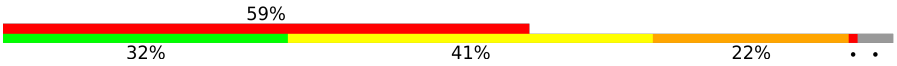
Chain 1y:

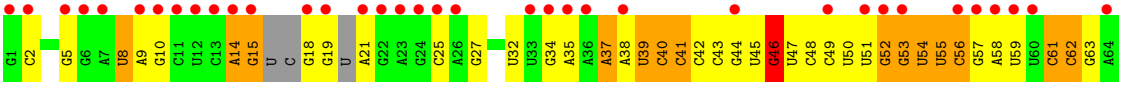


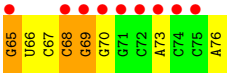


• Molecule 56: Deacylated tRNAphe

Chain 2y:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.54Å 448.51Å 620.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	147.20 – 2.40 147.20 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (147.20-2.40) 99.3 (147.20-2.40)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.22 (at 2.40Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.220 , 0.260 0.221 , 0.261	Depositor DCC
R_{free} test set	111821 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	47.8	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 49.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	300319	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.54% 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: 2MG, OMU, PSU, A1AE1, G7M, OMG, 5MC, 0TD, K, SF4, OMC, 4SU, M2G, FME, 5MU, MA6, 8AN, 4OC, MG, MIA, UR3, ZN, 2MA

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	0.31	0/68985	0.51	5/107677 (0.0%)
1	2A	0.24	0/67269	0.43	2/104999 (0.0%)
2	1B	0.25	0/2882	0.43	0/4494
2	2B	0.20	0/2879	0.39	0/4487
3	1D	0.29	0/2186	0.50	0/2944
3	2D	0.25	0/2186	0.48	0/2944
4	1E	0.30	0/1592	0.53	0/2149
4	2E	0.22	0/1592	0.45	0/2149
5	1F	0.29	0/1619	0.54	0/2193
5	2F	0.22	0/1615	0.47	0/2188
6	1G	0.24	0/1448	0.52	1/1957 (0.1%)
6	2G	0.19	0/1453	0.44	0/1963
7	1H	0.23	0/1356	0.44	0/1834
7	2H	0.20	0/1356	0.37	0/1834
8	1I	0.21	0/1112	0.43	0/1514
8	2I	0.22	0/1079	0.41	0/1475
9	1N	0.28	0/1144	0.49	0/1543
9	2N	0.20	0/1144	0.42	0/1543
10	1O	0.29	0/943	0.48	0/1269
10	2O	0.22	0/943	0.41	0/1269
11	1P	0.27	0/1152	0.60	0/1533
11	2P	0.23	0/1152	0.52	0/1533
12	1Q	0.29	0/1143	0.52	0/1527
12	2Q	0.21	0/1143	0.43	0/1527
13	1R	0.32	0/982	0.51	0/1312
13	2R	0.24	0/982	0.47	0/1312
14	1S	0.23	0/883	0.49	0/1176
14	2S	0.22	0/880	0.47	0/1172
15	1T	0.27	0/1105	0.51	0/1477
15	2T	0.22	0/1097	0.42	0/1468
16	1U	0.31	0/977	0.52	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.22	0/977	0.43	0/1301
17	1V	0.28	0/782	0.51	0/1049
17	2V	0.21	0/782	0.40	0/1049
18	1W	0.32	0/897	0.49	0/1205
18	2W	0.23	0/897	0.41	0/1205
19	1X	0.28	0/764	0.54	2/1025 (0.2%)
19	2X	0.22	0/764	0.49	2/1025 (0.2%)
20	1Y	0.25	0/819	0.50	0/1095
20	2Y	0.21	0/819	0.44	0/1095
21	1Z	0.24	0/1267	0.46	0/1717
21	2Z	0.22	0/1299	0.44	0/1763
22	10	0.30	0/662	0.50	0/881
22	20	0.22	0/662	0.45	0/881
23	11	0.27	0/762	0.46	0/1014
23	21	0.27	0/762	0.41	0/1014
24	12	0.26	0/590	0.47	0/781
24	22	0.20	0/590	0.38	0/781
25	13	0.27	0/474	0.52	0/635
25	23	0.20	0/469	0.43	0/630
26	14	0.26	0/565	0.58	0/761
26	24	0.25	0/545	0.51	0/737
27	15	0.30	0/469	0.54	0/635
27	25	0.23	0/469	0.43	0/635
28	16	0.30	0/460	0.50	0/613
28	26	0.25	0/456	0.47	0/608
29	17	0.32	0/426	0.54	0/561
29	27	0.28	0/426	0.53	0/561
30	18	0.27	0/525	0.50	0/691
30	28	0.21	0/525	0.44	0/691
31	19	0.30	0/310	0.56	0/407
31	29	0.20	0/310	0.46	0/407
32	1a	0.22	0/35795	0.41	2/55864 (0.0%)
32	2a	0.21	0/35886	0.39	3/56005 (0.0%)
33	1b	0.23	0/1881	0.48	0/2542
33	2b	0.22	0/1860	0.47	0/2518
34	1c	0.21	0/1572	0.41	0/2126
34	2c	0.22	0/1566	0.43	0/2119
35	1d	0.22	0/1685	0.45	0/2262
35	2d	0.22	0/1704	0.45	0/2284
36	1e	0.21	0/1145	0.45	0/1543
36	2e	0.23	0/1149	0.50	0/1548
37	1f	0.21	0/823	0.41	0/1115
37	2f	0.22	0/829	0.39	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.20	0/1250	0.40	0/1679
38	2g	0.20	0/1254	0.42	0/1683
39	1h	0.20	0/1108	0.40	0/1494
39	2h	0.18	0/1108	0.40	0/1494
40	1i	0.22	0/1002	0.49	0/1346
40	2i	0.23	0/997	0.51	0/1343
41	1j	0.22	0/722	0.45	0/982
41	2j	0.23	0/727	0.47	0/988
42	1k	0.20	0/844	0.41	0/1145
42	2k	0.19	0/848	0.38	0/1149
43	1l	0.24	0/937	0.44	0/1260
43	2l	0.20	0/937	0.42	0/1260
44	1m	0.21	0/969	0.50	1/1302 (0.1%)
44	2m	0.21	0/961	0.48	0/1291
45	1n	0.21	0/501	0.44	0/664
45	2n	0.22	0/501	0.49	0/664
46	1o	0.22	0/739	0.39	0/985
46	2o	0.20	0/739	0.41	0/985
47	1p	0.22	0/697	0.47	0/939
47	2p	0.21	0/693	0.47	0/935
48	1q	0.21	0/836	0.43	0/1117
48	2q	0.20	0/836	0.46	1/1117 (0.1%)
49	1r	0.21	0/560	0.40	0/746
49	2r	0.19	0/560	0.40	0/746
50	1s	0.22	0/667	0.49	0/900
50	2s	0.23	0/661	0.54	0/893
51	1t	0.22	0/730	0.48	0/965
51	2t	0.23	0/729	0.48	1/965 (0.1%)
52	1u	0.21	0/203	0.49	0/266
52	2u	0.29	0/203	0.48	0/266
53	1v	0.22	0/310	0.35	0/480
53	2v	0.20	0/310	0.38	0/480
54	1w	0.31	1/1581 (0.1%)	0.44	0/2458
54	2w	0.31	2/1531 (0.1%)	0.42	0/2379
55	1x	0.31	1/1723 (0.1%)	0.45	0/2684
55	2x	0.27	0/1723	0.41	0/2684
56	1y	0.35	2/1606 (0.1%)	0.45	0/2497
56	2y	0.34	2/1583 (0.1%)	0.44	0/2459
All	All	0.25	8/316584 (0.0%)	0.45	20/473955 (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
26	24	0	1
33	1b	0	1
51	1t	0	1
All	All	0	5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	2y	8	4SU	O3'-P	5.61	1.61	1.56
56	1y	46	G7M	O3'-P	5.49	1.61	1.56
54	2w	46	G7M	O3'-P	5.47	1.61	1.56
56	2y	46	G7M	O3'-P	5.39	1.61	1.56
55	1x	8	4SU	O3'-P	5.31	1.61	1.56
56	1y	8	4SU	O3'-P	5.27	1.61	1.56
54	2w	8	4SU	O3'-P	5.18	1.61	1.56
54	1w	46	G7M	O3'-P	5.04	1.61	1.56

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1992	G	C2'-C3'-O3'	7.62	120.93	109.50
6	1G	127	GLY	N-CA-C	-6.19	105.94	114.67
1	2A	1992	G	C2'-C3'-O3'	6.13	118.70	109.50
32	2a	1272	G	N1-C2-N2	-5.79	98.82	116.20
1	1A	512	G	O4'-C1'-N9	5.72	116.79	108.20
32	1a	266	G	C2'-C3'-O3'	5.56	117.84	109.50
19	2X	94	GLY	CA-C-N	5.52	131.64	121.70
19	2X	94	GLY	C-N-CA	5.52	131.64	121.70
19	1X	94	GLY	CA-C-N	5.36	131.34	121.70
19	1X	94	GLY	C-N-CA	5.36	131.34	121.70
32	1a	1067	A	P-O3'-C3'	5.29	128.14	120.20
32	2a	1263	C	N1-C2-O2	5.29	134.77	118.90
44	1m	106	ASN	CB-CA-C	-5.24	110.51	116.54
51	2t	94	ALA	N-CA-C	-5.18	107.48	112.97
1	1A	2689	U	C4'-C3'-O3'	5.16	117.14	109.40
48	2q	65	ILE	N-CA-C	-5.13	107.83	112.96
1	1A	2689	U	P-O3'-C3'	5.12	127.88	120.20
1	2A	271(M)	G	P-O3'-C3'	5.11	125.83	119.70
32	2a	1272	G	N3-C2-N2	5.09	135.19	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1992	G	P-O3'-C3'	5.05	127.78	120.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	1P	35	HIS	Peptide
33	1b	126	GLU	Peptide
51	1t	99	LEU	Peptide
26	24	59	PHE	Peptide
11	2P	35	HIS	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	61854	0	31201	523	0
1	2A	60324	0	30433	607	0
2	1B	2577	0	1305	23	0
2	2B	2575	0	1303	31	0
3	1D	2136	0	2218	31	0
3	2D	2136	0	2218	33	0
4	1E	1559	0	1618	23	0
4	2E	1559	0	1618	36	0
5	1F	1584	0	1625	35	0
5	2F	1580	0	1619	37	0
6	1G	1423	0	1436	39	0
6	2G	1428	0	1438	41	0
7	1H	1330	0	1407	23	0
7	2H	1330	0	1407	27	0
8	1I	1097	0	1140	37	0
8	2I	1064	0	1082	22	1
9	1N	1117	0	1184	18	0
9	2N	1117	0	1184	21	0
10	1O	933	0	996	20	0
10	2O	933	0	996	22	0
11	1P	1135	0	1212	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	2P	1135	0	1212	29	0
12	1Q	1122	0	1179	14	0
12	2Q	1122	0	1179	24	0
13	1R	968	0	1033	11	0
13	2R	968	0	1033	24	0
14	1S	873	0	927	12	0
14	2S	870	0	923	30	0
15	1T	1091	0	1151	17	0
15	2T	1083	0	1136	25	0
16	1U	959	0	1019	15	0
16	2U	959	0	1019	15	0
17	1V	771	0	830	9	0
17	2V	771	0	830	9	0
18	1W	886	0	940	9	0
18	2W	886	0	940	12	0
19	1X	750	0	814	7	0
19	2X	750	0	814	16	0
20	1Y	806	0	881	13	0
20	2Y	806	0	881	15	0
21	1Z	1240	0	1240	33	0
21	2Z	1271	0	1273	44	0
22	10	653	0	674	10	0
22	20	653	0	674	13	0
23	11	755	0	826	10	0
23	21	755	0	826	11	0
24	12	588	0	643	2	0
24	22	588	0	643	12	0
25	13	469	0	518	8	0
25	23	464	0	514	9	0
26	14	552	0	533	34	0
26	24	532	0	503	19	0
27	15	455	0	465	4	0
27	25	455	0	465	10	0
28	16	453	0	473	9	0
28	26	449	0	469	8	0
29	17	418	0	467	8	0
29	27	418	0	467	6	0
30	18	517	0	582	12	0
30	28	517	0	582	13	0
31	19	307	0	335	4	0
31	29	307	0	335	4	0
32	1a	32246	0	16295	334	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	2a	32327	0	16338	425	0
33	1b	1846	0	1867	59	0
33	2b	1825	0	1828	76	0
34	1c	1548	0	1535	30	0
34	2c	1542	0	1517	53	0
35	1d	1655	0	1672	31	0
35	2d	1674	0	1714	48	0
36	1e	1129	0	1185	28	0
36	2e	1133	0	1191	38	0
37	1f	810	0	804	13	0
37	2f	816	0	808	14	0
38	1g	1231	0	1238	15	0
38	2g	1235	0	1249	24	0
39	1h	1088	0	1126	24	0
39	2h	1088	0	1126	23	0
40	1i	983	0	986	20	0
40	2i	978	0	966	49	0
41	1j	709	0	650	25	0
41	2j	714	0	672	38	0
42	1k	829	0	825	13	0
42	2k	833	0	836	13	0
43	1l	932	0	981	11	0
43	2l	932	0	980	15	0
44	1m	958	0	1002	27	0
44	2m	950	0	988	38	0
45	1n	492	0	529	11	0
45	2n	492	0	529	22	0
46	1o	728	0	760	13	0
46	2o	728	0	760	20	0
47	1p	681	0	697	12	0
47	2p	677	0	686	18	0
48	1q	823	0	891	12	0
48	2q	823	0	891	12	0
49	1r	555	0	618	12	0
49	2r	555	0	618	15	0
50	1s	652	0	662	18	0
50	2s	646	0	644	24	0
51	1t	728	0	798	18	0
51	2t	727	0	796	13	0
52	1u	199	0	208	6	0
52	2u	199	0	208	7	0
53	1v	277	0	140	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	2v	277	0	140	4	0
54	1w	1592	0	817	24	0
54	2w	1544	0	783	21	0
55	1x	1646	0	838	10	0
55	2x	1646	0	838	22	0
56	1y	1585	0	803	39	0
56	2y	1565	0	794	33	0
57	10	11	0	0	0	0
57	11	6	0	0	0	0
57	12	2	0	0	0	0
57	13	4	0	0	0	0
57	14	1	0	0	0	0
57	15	7	0	0	0	0
57	16	1	0	0	0	0
57	17	7	0	0	0	0
57	18	6	0	0	0	0
57	19	1	0	0	0	0
57	1A	1093	0	0	0	0
57	1B	36	0	0	0	0
57	1D	14	0	0	0	0
57	1E	16	0	0	0	0
57	1F	14	0	0	0	0
57	1G	4	0	0	0	0
57	1H	1	0	0	0	0
57	1I	1	0	0	0	0
57	1N	7	0	0	0	0
57	1O	6	0	0	0	0
57	1P	6	0	0	0	0
57	1Q	8	0	0	0	0
57	1R	3	0	0	0	0
57	1S	3	0	0	0	0
57	1T	4	0	0	0	0
57	1U	9	0	0	0	0
57	1V	8	0	0	0	0
57	1W	6	0	0	0	0
57	1X	7	0	0	0	0
57	1Y	2	0	0	0	0
57	1Z	3	0	0	0	0
57	1a	214	0	0	0	0
57	1b	1	0	0	0	0
57	1d	1	0	0	0	0
57	1e	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1f	1	0	0	0	0
57	1h	1	0	0	0	0
57	1k	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	2	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
57	1w	8	0	0	0	0
57	1x	14	0	0	0	0
57	20	4	0	0	0	0
57	21	1	0	0	0	0
57	23	3	0	0	0	0
57	25	5	0	0	0	0
57	26	1	0	0	0	0
57	27	3	0	0	0	0
57	28	3	0	0	0	0
57	29	1	0	0	0	0
57	2A	854	0	0	0	0
57	2B	18	0	0	0	0
57	2D	8	0	0	0	0
57	2E	11	0	0	0	0
57	2F	5	0	0	0	0
57	2G	1	0	0	0	0
57	2N	1	0	0	0	0
57	2O	1	0	0	0	0
57	2P	2	0	0	0	0
57	2Q	2	0	0	0	0
57	2R	2	0	0	0	0
57	2T	3	0	0	0	0
57	2U	1	0	0	0	0
57	2V	2	0	0	0	0
57	2W	1	0	0	0	0
57	2X	2	0	0	0	0
57	2Y	1	0	0	0	0
57	2Z	1	0	0	0	0
57	2a	210	0	0	0	0
57	2d	2	0	0	0	0
57	2e	1	0	0	0	0
57	2f	2	0	0	0	0
57	2g	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2j	1	0	0	0	0
57	2l	5	0	0	0	0
57	2q	2	0	0	0	0
57	2r	1	0	0	0	0
57	2t	1	0	0	0	0
57	2v	3	0	0	0	0
57	2w	7	0	0	0	0
57	2x	7	0	0	0	0
57	2y	5	0	0	0	0
58	1A	1	0	0	0	0
58	2A	1	0	0	0	0
59	1A	76	0	0	0	0
59	2A	76	0	0	1	0
60	14	1	0	0	0	0
60	15	1	0	0	0	0
60	16	1	0	0	0	0
60	19	1	0	0	0	0
60	1Y	1	0	0	0	0
60	1n	1	0	0	0	0
60	24	1	0	0	0	0
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	29	1	0	0	0	0
60	2Y	1	0	0	0	0
60	2n	1	0	0	0	0
61	1d	8	0	0	0	0
61	2d	8	0	0	4	0
62	1w	11	0	8	1	0
62	2w	11	0	8	1	0
63	1x	10	0	10	0	0
63	2x	10	0	10	0	0
64	10	12	0	0	0	0
64	11	11	0	0	0	0
64	12	3	0	0	0	0
64	13	5	0	0	1	0
64	14	1	0	0	0	0
64	15	9	0	0	0	0
64	16	1	0	0	0	0
64	17	11	0	0	0	0
64	18	11	0	0	0	0
64	1A	2061	0	0	63	0
64	1B	60	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	1D	29	0	0	1	0
64	1E	27	0	0	1	0
64	1F	16	0	0	1	0
64	1G	1	0	0	0	0
64	1H	1	0	0	0	0
64	1N	5	0	0	0	0
64	1O	6	0	0	0	0
64	1P	22	0	0	1	0
64	1Q	9	0	0	0	0
64	1R	10	0	0	1	0
64	1S	4	0	0	0	0
64	1T	8	0	0	1	0
64	1U	10	0	0	0	0
64	1V	8	0	0	0	0
64	1W	9	0	0	1	0
64	1X	6	0	0	0	0
64	1Y	3	0	0	1	0
64	1Z	1	0	0	0	0
64	1a	388	0	0	22	0
64	1b	1	0	0	0	0
64	1c	2	0	0	0	0
64	1d	2	0	0	1	0
64	1e	3	0	0	0	0
64	1f	1	0	0	0	0
64	1g	1	0	0	0	0
64	1i	1	0	0	0	0
64	1j	2	0	0	0	0
64	1l	7	0	0	0	0
64	1m	1	0	0	0	0
64	1n	2	0	0	0	0
64	1o	1	0	0	0	0
64	1p	1	0	0	0	0
64	1q	2	0	0	0	0
64	1u	1	0	0	1	0
64	1v	5	0	0	0	0
64	1w	14	0	0	2	0
64	1x	15	0	0	1	0
64	1y	1	0	0	0	0
64	20	3	0	0	0	0
64	21	11	0	0	0	0
64	23	2	0	0	1	0
64	25	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	27	5	0	0	0	0
64	28	3	0	0	0	0
64	29	1	0	0	0	0
64	2A	1142	0	0	70	0
64	2B	19	0	0	0	0
64	2D	23	0	0	0	0
64	2E	12	0	0	0	0
64	2F	12	0	0	0	0
64	2I	2	0	0	0	0
64	2O	2	0	0	0	0
64	2P	11	0	0	0	0
64	2Q	2	0	0	0	0
64	2R	3	0	0	0	0
64	2T	5	0	0	0	0
64	2U	3	0	0	0	0
64	2V	1	0	0	0	0
64	2X	3	0	0	0	0
64	2Y	1	0	0	0	0
64	2Z	1	0	0	0	0
64	2a	221	0	0	12	0
64	2c	1	0	0	0	0
64	2d	2	0	0	0	0
64	2g	1	0	0	0	0
64	2j	3	0	0	2	0
64	2l	4	0	0	1	0
64	2p	2	0	0	0	0
64	2q	1	0	0	0	0
64	2r	1	0	0	0	0
64	2t	1	0	0	0	0
64	2v	2	0	0	0	0
64	2w	3	0	0	0	0
64	2x	7	0	0	0	0
64	2y	2	0	0	0	0
All	All	300319	0	196751	3569	1

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 7.

All (3569) 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	1.13	1.41
1:1A:1082:U:N3	1:1A:1086:A:N6	1.99	1.09
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.42	1.01
1:1A:1082:U:O4	1:1A:1086:A:N1	1.95	1.00
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.30	0.93
54:2w:4:C:H42	54:2w:69:G:H1	1.02	0.93
1:1A:2733:A:OP1	64:1A:4102:HOH:O	1.86	0.92
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.54	0.90
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.13	0.90
33:2b:8:LYS:HD2	33:2b:9:GLU:H	1.37	0.90
1:1A:1054:A:H61	1:1A:1105:U:H3	1.20	0.89
29:17:24:THR:HG22	29:17:27:GLY:H	1.33	0.89
22:10:10:THR:HG22	22:10:12:ASN:H	1.36	0.88
1:1A:2427:C:OP1	64:1A:4103:HOH:O	1.91	0.88
1:2A:1204:A:H2	1:2A:1241:A:H62	1.21	0.87
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.22	0.87
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.08	0.86
32:2a:1224:G:OP1	64:2a:1901:HOH:O	1.94	0.85
1:2A:2137:C:H42	1:2A:2154:G:H1	1.23	0.85
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.40	0.84
1:1A:826:U:OP1	64:1A:4103:HOH:O	1.95	0.84
6:1G:21:ARG:HG2	6:1G:21:ARG:HH11	1.42	0.84
54:2w:4:C:N4	54:2w:69:G:H1	1.74	0.84
1:1A:271(L):U:H4'	8:1I:50:ARG:HH12	1.41	0.83
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.60	0.83
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.59	0.83
21:2Z:171:ILE:HD12	21:2Z:172:ALA:H	1.43	0.83
1:1A:1865:G:OP1	64:1A:4104:HOH:O	1.96	0.83
32:2a:1029:C:C4	32:2a:1032:G:N1	2.47	0.82
26:24:53:GLU:HG2	26:24:55:ARG:H	1.44	0.82
1:2A:2134:A:H62	1:2A:2157:G:H4'	1.42	0.82
32:1a:1027:C:C2	32:1a:1034:G:N2	2.48	0.82
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.12	0.82
1:1A:2136:C:N3	1:1A:2155:G:N2	2.28	0.81
32:2a:1272:G:N2	32:2a:1273:G:N7	2.28	0.81
20:1Y:34:LYS:NZ	64:1Y:301:HOH:O	2.13	0.81
1:1A:1271:G:OP2	64:1A:4105:HOH:O	1.98	0.80
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.14	0.80
1:1A:1023:U:OP2	64:1A:4106:HOH:O	1.99	0.80
1:2A:2100:G:H1	1:2A:2189:U:H3	1.26	0.80
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.47	0.80
1:2A:2137:C:N4	1:2A:2154:G:H1	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:16:13:CYS:SG	28:16:47:THR:HG21	2.21	0.79
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.64	0.79
32:1a:116:A:OP1	64:1a:1902:HOH:O	2.00	0.79
1:2A:2099:U:H3	1:2A:2190:G:H1	1.31	0.79
32:2a:1029:C:N3	32:2a:1032:G:N2	2.31	0.79
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.64	0.78
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.15	0.78
32:2a:1310:G:H5'	44:2m:77:ASN:HD21	1.48	0.78
32:1a:1035:A:H2'	32:1a:1036:G:H21	1.48	0.78
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.66	0.78
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.15	0.78
32:1a:875:C:H1'	39:1h:15:ASN:HD21	1.47	0.78
1:1A:1039:G:H1	1:1A:1116:C:H42	1.31	0.78
1:2A:805:G:OP1	64:2A:3906:HOH:O	2.02	0.78
1:2A:1648:C:OP1	64:2A:3903:HOH:O	2.00	0.78
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.16	0.78
1:1A:2136:C:N4	1:1A:2155:G:N1	2.31	0.78
1:2A:2238:G:OP2	64:2A:3905:HOH:O	2.02	0.78
32:2a:1002:G:H1	32:2a:1038:C:H42	1.31	0.78
1:1A:1332:G:OP1	64:1A:4107:HOH:O	2.01	0.77
1:2A:2218:U:O2	23:21:52:ARG:NH1	2.16	0.77
33:2b:189:ASP:N	33:2b:189:ASP:OD1	2.15	0.77
1:1A:1669:A:OP2	64:1A:4108:HOH:O	2.02	0.77
1:2A:963:U:OP2	64:2A:3904:HOH:O	2.01	0.77
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.17	0.77
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.66	0.77
36:1e:78:HIS:HE1	36:1e:143:ARG:H	1.31	0.77
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.18	0.76
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.18	0.76
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.65	0.76
32:1a:664:G:H22	32:1a:741:G:H1	1.30	0.76
21:2Z:146:ILE:HG12	21:2Z:174:VAL:HG23	1.66	0.76
2:1B:21:G:N7	64:1B:303:HOH:O	2.17	0.76
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.18	0.76
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.67	0.76
17:2V:1:MET:HE2	17:2V:43:GLU:HB2	1.67	0.76
32:2a:975:A:H4'	32:2a:976:G:H5"	1.67	0.76
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.51	0.76
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.68	0.76
51:2t:10:LEU:HB3	51:2t:12:ALA:H	1.50	0.75
1:2A:2577:A:OP1	64:2A:3909:HOH:O	2.04	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.68	0.75
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.69	0.75
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.04	0.75
1:2A:1890:A:OP2	64:2A:3908:HOH:O	2.04	0.75
1:2A:2125:G:N3	1:2A:2173:A:N6	2.35	0.75
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.68	0.75
54:2w:18:G:O2'	54:2w:57:G:N2	2.20	0.75
1:1A:1648:C:OP1	64:1A:4105:HOH:O	2.04	0.75
11:2P:121:LYS:HE2	11:2P:123:LEU:HD11	1.67	0.75
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.18	0.75
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.33	0.74
32:2a:1029:C:N4	32:2a:1032:G:N1	2.35	0.74
1:1A:2384:G:N7	64:1A:4130:HOH:O	2.19	0.74
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.51	0.74
33:1b:33:TYR:HB2	33:1b:43:ASP:HB2	1.68	0.74
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.52	0.74
1:1A:2702:U:OP2	64:1A:4109:HOH:O	2.05	0.74
21:1Z:132:ASN:HD22	21:1Z:160:GLY:HA3	1.51	0.74
1:2A:1973:G:OP1	64:2A:3907:HOH:O	2.04	0.74
32:2a:1521:G:N3	64:2a:1910:HOH:O	2.21	0.74
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.69	0.74
32:1a:1086:U:H3	32:1a:1099:G:H22	1.35	0.74
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	1.70	0.74
1:2A:2712(A):A:OP2	64:2A:3911:HOH:O	2.05	0.73
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.70	0.73
1:2A:570:G:O6	64:2A:3910:HOH:O	2.05	0.73
10:1O:110:GLY:HA2	10:1O:112:MET:HE2	1.71	0.73
21:2Z:150:LEU:HB2	21:2Z:171:ILE:HD11	1.68	0.73
41:2j:21:GLN:HE22	41:2j:25:GLU:HG2	1.52	0.73
1:1A:192:C:OP1	64:1A:4112:HOH:O	2.07	0.73
1:1A:1054:A:N6	1:1A:1105:U:H3	1.86	0.73
1:2A:1021:A:H62	1:2A:1141:U:H3	1.36	0.73
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.53	0.73
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.71	0.73
37:1f:46:ARG:HH22	49:1r:37:VAL:HG11	1.52	0.73
1:1A:1014:U:OP2	64:1A:4110:HOH:O	2.05	0.73
32:1a:1505:G:OP2	64:1a:1903:HOH:O	2.07	0.73
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.21	0.73
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.70	0.73
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.70	0.73
48:2q:41:LYS:NZ	48:2q:88:TYR:OH	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:467:G:OP1	29:17:33:ARG:NH1	2.21	0.73
32:1a:700:G:N7	64:1a:1917:HOH:O	2.22	0.73
1:1A:376:C:OP1	64:1A:4111:HOH:O	2.06	0.73
44:1m:19:LEU:HD11	44:1m:56:LEU:HD21	1.69	0.72
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.22	0.72
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.54	0.72
59:2A:3855:A1AE1:OCM	64:2A:3912:HOH:O	2.06	0.72
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.20	0.72
32:2a:1126:U:H3	41:2j:40:LEU:HD11	1.54	0.72
50:1s:20:LEU:HD23	50:1s:23:ASN:HD22	1.53	0.72
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.25	0.72
2:1B:23:G:O6	64:1B:301:HOH:O	2.07	0.72
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.71	0.72
32:2a:953:G:H5'	32:2a:965:A:H61	1.53	0.72
1:1A:1055:G:H1	1:1A:1104:C:H42	1.38	0.72
1:2A:2592:G:OP1	64:2A:3914:HOH:O	2.08	0.72
32:2a:972:C:O2'	41:2j:55:LYS:O	2.08	0.72
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.23	0.72
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.22	0.72
9:2N:128:HIS:O	9:2N:131:GLN:NE2	2.23	0.72
32:1a:134:A:H61	47:1p:25:ARG:HH12	1.38	0.72
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.72	0.72
52:1u:5:ASP:OD2	64:1u:101:HOH:O	2.08	0.72
34:2c:34:LEU:HD11	34:2c:38:ARG:HH21	1.53	0.72
1:2A:1253:A:OP1	64:2A:3915:HOH:O	2.08	0.72
46:1o:87:ILE:HG22	46:1o:88:ARG:H	1.54	0.71
1:2A:1568:G:N7	64:2A:3954:HOH:O	2.23	0.71
51:1t:33:ILE:O	51:1t:37:SER:OG	2.08	0.71
32:2a:596:C:OP2	64:2a:1902:HOH:O	2.07	0.71
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.23	0.71
32:1a:677:U:H3	32:1a:713:G:H22	1.36	0.71
32:1a:975:A:H4'	32:1a:976:G:H5"	1.72	0.71
3:1D:180:GLY:HA3	3:1D:275:LYS:HG2	1.73	0.71
32:1a:574:A:OP2	64:1a:1905:HOH:O	2.08	0.71
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.22	0.71
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.23	0.71
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.38	0.71
7:2H:84:SER:OG	7:2H:132:ARG:NH1	2.23	0.71
1:1A:1315:C:OP2	64:1A:4107:HOH:O	2.09	0.71
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.56	0.71
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:903:G:OP1	64:1a:1904:HOH:O	2.07	0.71
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.72	0.70
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.24	0.70
1:1A:2235:G:N7	64:1A:4149:HOH:O	2.24	0.70
32:1a:224:C:OP1	51:1t:74:LYS:NZ	2.18	0.70
11:1P:39:LYS:HB2	11:1P:45:LEU:HD13	1.72	0.70
32:1a:1352:C:OP1	52:1u:3:LYS:NZ	2.25	0.70
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.72	0.70
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.72	0.70
32:1a:711:G:OP1	37:1f:54:LYS:NZ	2.24	0.70
1:2A:100:G:O2'	24:22:7:ARG:NH2	2.25	0.70
1:2A:981:A:OP1	64:2A:3916:HOH:O	2.09	0.70
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.23	0.70
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.26	0.70
1:2A:2448:A:OP1	64:2A:3910:HOH:O	2.09	0.70
1:2A:1023:U:OP2	64:2A:3913:HOH:O	2.07	0.70
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.74	0.70
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.25	0.70
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.74	0.70
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.24	0.70
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.40	0.70
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.74	0.70
1:1A:2306:C:O2	64:1A:4113:HOH:O	2.08	0.69
50:1s:27:GLU:HB2	50:1s:28:LYS:HA	1.72	0.69
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.09	0.69
32:1a:1224:G:OP1	64:1a:1906:HOH:O	2.10	0.69
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.24	0.69
1:2A:2576:G:OP1	64:2A:3909:HOH:O	2.09	0.69
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.25	0.69
1:1A:1082:U:H3	1:1A:1086:A:H61	0.71	0.69
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.58	0.69
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.24	0.69
4:1E:29:GLY:HA3	64:1E:408:HOH:O	1.93	0.69
1:2A:449:A:OP2	64:2A:3918:HOH:O	2.09	0.69
1:2A:2022:U:O2'	1:2A:2617:C:H5'	1.92	0.69
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.28	0.69
1:1A:2428:G:OP1	64:1A:4103:HOH:O	2.11	0.69
1:2A:1647:G:OP1	64:2A:3903:HOH:O	2.09	0.69
1:1A:2550:G:OP1	64:1A:4108:HOH:O	2.10	0.69
25:13:55:ARG:HH22	25:13:57:GLU:HB2	1.57	0.69
1:2A:467:G:OP1	29:27:33:ARG:NH1	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1647:G:OP1	64:1A:4105:HOH:O	2.10	0.69
1:1A:2350:C:OP2	64:1A:4114:HOH:O	2.09	0.69
1:1A:2849:U:OP2	15:1T:95:ARG:NH1	2.26	0.69
1:2A:72:U:OP1	64:2A:3917:HOH:O	2.09	0.69
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.75	0.69
1:2A:1254:A:OP2	64:2A:3922:HOH:O	2.11	0.69
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.73	0.69
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.75	0.69
1:1A:2136:C:N4	1:1A:2155:G:H1	1.89	0.68
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.23	0.68
4:2E:7:VAL:HG12	4:2E:27:LEU:HB3	1.75	0.68
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.17	0.68
1:1A:2136:C:N3	1:1A:2155:G:C2	2.61	0.68
1:2A:2759:G:OP2	64:2A:3920:HOH:O	2.11	0.68
32:2a:598:U:O4	64:2a:1902:HOH:O	2.10	0.68
32:2a:1194:U:H4'	36:2e:22:GLY:HA2	1.76	0.68
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.23	0.68
1:1A:307:G:N7	64:1A:4166:HOH:O	2.26	0.68
1:2A:1313:U:OP1	64:2A:3923:HOH:O	2.11	0.68
32:2a:588:G:OP2	64:2a:1903:HOH:O	2.12	0.68
36:2e:53:LEU:HD12	36:2e:53:LEU:H	1.59	0.68
1:1A:2517:C:OP1	64:1A:4115:HOH:O	2.10	0.68
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.74	0.68
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	1.75	0.68
37:2f:46:ARG:HH22	49:2r:37:VAL:HG11	1.58	0.68
40:2i:128:ARG:NH2	55:2x:33:U:OP2	2.26	0.68
1:2A:804:A:OP1	64:2A:3906:HOH:O	2.11	0.68
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.26	0.68
15:1T:125:ARG:HG2	15:1T:129:ARG:HH21	1.58	0.68
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.76	0.68
32:2a:266:G:H5"	32:2a:268:C:H41	1.57	0.68
1:1A:1993:U:OP2	64:1A:4118:HOH:O	2.11	0.68
56:1y:19:G:N2	56:1y:56:C:N3	2.41	0.68
1:2A:1352:U:OP2	64:2A:3919:HOH:O	2.11	0.68
1:1A:1062:G:H1	1:1A:1077:A:H61	1.42	0.68
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.75	0.68
1:1A:2822:G:OP2	64:1A:4116:HOH:O	2.13	0.67
7:1H:3:ARG:NH1	7:1H:5:GLY:H	1.93	0.67
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.27	0.67
1:2A:481:G:N7	64:2A:3966:HOH:O	2.27	0.67
1:2A:1376:C:OP1	64:2A:3924:HOH:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:89:MET:HE1	49:1r:72:ARG:HB3	1.77	0.67
54:1w:67:C:OP1	64:1w:201:HOH:O	2.12	0.67
56:1y:51:U:H3	56:1y:63:G:H1	1.40	0.67
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.26	0.67
34:1c:8:ILE:HD13	34:1c:184:TYR:HB3	1.75	0.67
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.76	0.67
32:2a:1002:G:H1	32:2a:1038:C:N4	1.92	0.67
42:2k:54:ARG:NH2	56:2y:39:PSU:O2'	2.27	0.67
1:1A:2821:A:OP2	64:1A:4116:HOH:O	2.10	0.67
1:2A:1689:A:H62	1:2A:1698:A:H2	1.41	0.67
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.77	0.67
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.28	0.67
1:2A:948:G:OP1	64:2A:3904:HOH:O	2.12	0.67
42:1k:48:ILE:O	42:1k:50:TYR:N	2.23	0.67
1:2A:568:U:O4	64:2A:3921:HOH:O	2.11	0.66
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.13	0.66
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.77	0.66
35:2d:175:SER:HB3	35:2d:186:LEU:HD11	1.77	0.66
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.76	0.66
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.60	0.66
39:1h:4:ASP:OD2	39:1h:7:ALA:N	2.21	0.66
6:2G:114:ILE:HA	6:2G:140:ILE:HD11	1.77	0.66
12:2Q:78:PRO:HG2	12:2Q:81:VAL:HG11	1.76	0.66
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.28	0.66
25:23:13:ILE:O	64:23:201:HOH:O	2.13	0.66
32:2a:1086:U:H3	32:2a:1099:G:H22	1.43	0.66
50:2s:38:SER:HB2	50:2s:71:LEU:HD22	1.78	0.66
1:1A:2753:A:N3	31:19:15:LYS:NZ	2.44	0.66
1:1A:120:U:OP2	64:1A:4120:HOH:O	2.13	0.66
1:1A:2099:U:H3	1:1A:2190:G:H1	1.43	0.66
44:1m:40:ASN:O	44:1m:43:THR:OG1	2.13	0.66
1:1A:1938:A:OP2	64:1A:4119:HOH:O	2.12	0.66
36:1e:78:HIS:HD2	39:1h:104:ARG:HD2	1.61	0.66
41:2j:78:ASN:O	41:2j:80:LYS:N	2.28	0.66
33:1b:134:GLU:HA	33:1b:137:ARG:HE	1.59	0.66
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.29	0.66
21:2Z:100:VAL:HG21	21:2Z:134:PRO:HG2	1.78	0.66
1:2A:2207:G:H3'	1:2A:2208:A:H5"	1.78	0.66
1:2A:2794:C:N4	1:2A:2802:G:O6	2.29	0.66
32:2a:76:C:H42	32:2a:93:G:H1	1.42	0.66
54:1w:57:G:OP2	64:1w:202:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2524:G:N7	64:2A:3979:HOH:O	2.29	0.65
36:2e:20:GLN:NE2	36:2e:21:ALA:O	2.29	0.65
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.24	0.65
51:1t:43:LEU:O	51:1t:47:GLY:N	2.24	0.65
1:1A:602:G:O2'	1:1A:655:A:N6	2.29	0.65
32:1a:505:G:N7	64:1a:1924:HOH:O	2.28	0.65
1:2A:962:G:OP1	64:2A:3904:HOH:O	2.15	0.65
37:2f:95:GLU:O	49:2r:32:ARG:NH1	2.29	0.65
1:2A:1394:U:OP1	64:2A:3927:HOH:O	2.15	0.65
26:24:44:THR:O	26:24:46:GLN:N	2.29	0.65
56:2y:43:C:H2'	56:2y:44:G:H8	1.62	0.65
1:1A:2316:C:O2'	6:1G:128:ARG:NH2	2.30	0.65
32:1a:573:A:OP2	64:1a:1905:HOH:O	2.14	0.65
33:1b:12:GLU:HB2	33:1b:213:LEU:HD21	1.78	0.65
32:2a:838:G:H1	32:2a:848:C:H42	1.44	0.65
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.77	0.65
2:1B:99:G:OP2	64:1B:302:HOH:O	2.14	0.65
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.79	0.65
64:1A:4116:HOH:O	13:1R:3:HIS:NE2	2.28	0.65
32:1a:560:U:O2'	32:1a:561:U:OP2	2.14	0.65
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.29	0.65
34:2c:20:SER:HB3	34:2c:22:TRP:HE1	1.62	0.65
1:1A:1607:C:O2	64:1A:4117:HOH:O	2.11	0.65
32:1a:263:A:OP1	51:1t:79:ARG:NH1	2.30	0.65
32:1a:1035:A:N3	32:1a:1036:G:N2	2.45	0.65
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.78	0.65
44:1m:2:ALA:N	44:1m:8:GLU:OE1	2.30	0.65
49:2r:31:LEU:HD23	49:2r:31:LEU:H	1.62	0.64
55:2x:55:PSU:O2'	55:2x:57:A:N7	2.30	0.64
1:2A:271(R):G:O6	64:2A:3925:HOH:O	2.14	0.64
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.32	0.64
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.78	0.64
40:1i:110:GLU:OE2	40:1i:113:LYS:NZ	2.31	0.64
44:1m:98:VAL:HG12	44:1m:99:ARG:HG3	1.78	0.64
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	1.80	0.64
32:1a:812:C:N3	64:1a:1927:HOH:O	2.29	0.64
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.13	0.64
1:2A:2049:G:N7	64:2A:3986:HOH:O	2.30	0.64
43:2l:40:VAL:HG21	43:2l:78:GLN:HA	1.80	0.64
32:1a:953:G:H5'	32:1a:965:A:H61	1.63	0.64
33:1b:80:ILE:HG13	33:1b:212:GLN:HG2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:106:C:H1'	20:2Y:1:MET:HE2	1.78	0.64
11:2P:81:GLN:NE2	11:2P:105:LEU:O	2.28	0.64
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.79	0.64
1:1A:674:G:O2'	5:1F:74:ARG:HD3	1.98	0.64
5:1F:31:HIS:NE2	5:1F:35:GLU:OE2	2.30	0.64
55:1x:76:8AN:O2P	64:1x:201:HOH:O	2.14	0.64
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.78	0.64
1:1A:1399:C:OP1	19:1X:25:LYS:NZ	2.31	0.64
1:2A:1300:U:H4'	1:2A:1301:A:H5"	1.80	0.64
21:2Z:144:LEU:HD23	21:2Z:145:GLU:H	1.63	0.64
56:1y:20:U:H1'	56:1y:21:A:H4'	1.78	0.64
1:2A:2131:G:OP2	1:2A:2131:G:N2	2.31	0.64
1:2A:2318:G:H21	14:2S:3:ARG:HD3	1.61	0.64
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.78	0.64
1:1A:1041:C:H42	1:1A:1114:G:H1	1.44	0.64
1:1A:1452:A:OP2	64:1A:4122:HOH:O	2.15	0.64
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.80	0.64
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.46	0.64
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	1.80	0.64
32:2a:1004:A:N6	32:2a:1037:C:H1'	2.13	0.64
32:2a:1099:G:OP2	33:2b:144:ARG:NH2	2.30	0.64
41:2j:44:VAL:HG13	41:2j:66:ARG:HB3	1.80	0.63
17:1V:55:ALA:HA	17:1V:101:GLY:HA2	1.80	0.63
32:1a:159:G:N2	32:1a:162:A:OP2	2.31	0.63
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.25	0.63
34:2c:191:THR:OG1	34:2c:194:GLY:O	2.16	0.63
1:1A:1418:G:OP2	64:1A:4121:HOH:O	2.15	0.63
32:1a:550:G:OP1	64:1a:1909:HOH:O	2.16	0.63
1:2A:752:A:H3'	29:27:1:MET:HE1	1.80	0.63
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.25	0.63
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.64	0.63
1:2A:399:G:OP2	64:2A:3928:HOH:O	2.15	0.63
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.80	0.63
26:24:13:ARG:HG2	26:24:23:GLU:HG2	1.81	0.63
32:2a:407:G:H5"	35:2d:115:ARG:HB3	1.81	0.63
32:2a:1026:G:N2	32:2a:1027:C:O4'	2.31	0.63
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.32	0.63
32:1a:472:A:OP1	47:1p:75:ARG:NH2	2.25	0.63
1:2A:2847:U:OP1	15:2T:98:LYS:NZ	2.32	0.63
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	1.81	0.63
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:2y:5:G:H1	56:2y:68:C:H42	1.43	0.63
56:2y:14:A:H61	56:2y:21:A:H2	1.45	0.63
1:1A:2218:U:O4'	23:11:52:ARG:NH2	2.32	0.63
13:2R:51:LEU:HD22	13:2R:66:VAL:HG13	1.80	0.63
21:2Z:154:ASP:N	21:2Z:154:ASP:OD1	2.32	0.63
1:1A:1506:C:H2'	1:1A:1507:A:H8	1.63	0.63
28:16:47:THR:HG22	28:16:49:HIS:CE1	2.32	0.63
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.16	0.63
41:2j:38:ILE:HD12	41:2j:71:LEU:HD23	1.79	0.63
44:2m:37:THR:O	44:2m:55:ARG:NH1	2.31	0.63
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.34	0.63
5:1F:133:ASN:N	5:1F:138:GLU:OE1	2.26	0.63
35:1d:119:GLN:HG2	35:1d:123:HIS:CD2	2.33	0.63
41:1j:38:ILE:HD11	41:1j:71:LEU:HD23	1.80	0.63
1:2A:422:A:OP2	64:2A:3930:HOH:O	2.16	0.63
32:2a:396:G:O2'	32:2a:398:C:OP1	2.09	0.63
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.34	0.63
32:2a:1132:C:H2'	32:2a:1133:G:H8	1.64	0.63
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.15	0.63
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.80	0.63
32:2a:973:G:H3'	32:2a:974:A:H5"	1.80	0.63
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.64	0.62
44:1m:82:MET:O	44:1m:93:ARG:NH2	2.32	0.62
33:2b:74:LYS:HD2	33:2b:166:ASP:HB2	1.80	0.62
42:2k:48:ILE:O	42:2k:50:TYR:N	2.25	0.62
21:1Z:105:VAL:N	21:1Z:139:VAL:O	2.31	0.62
36:1e:78:HIS:CE1	36:1e:143:ARG:H	2.17	0.62
1:2A:2711:A:OP2	64:2A:3911:HOH:O	2.16	0.62
34:2c:125:GLU:HB2	34:2c:190:ARG:HH21	1.63	0.62
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.80	0.62
21:1Z:74:VAL:HG22	21:1Z:86:VAL:HG12	1.81	0.62
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.31	0.62
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.99	0.62
1:2A:1721:G:H8	1:2A:1741:A:H62	1.46	0.62
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.80	0.62
38:2g:99:LEU:HD23	38:2g:102:ARG:HH12	1.64	0.62
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.33	0.62
26:14:46:GLN:O	26:14:48:ARG:N	2.32	0.62
34:1c:172:ARG:NH2	34:1c:206:GLU:OE2	2.32	0.62
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.82	0.62
35:2d:8:VAL:HG22	35:2d:21:LEU:HD13	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:187:ARG:NH1	35:2d:190:ASP:OD1	2.33	0.62
1:1A:2134:A:O2'	1:1A:2135:A:OP1	2.17	0.62
5:1F:89:VAL:O	64:1F:401:HOH:O	2.16	0.62
19:2X:94:GLY:H	19:2X:95:LEU:HB2	1.63	0.62
28:26:9:LEU:HD13	28:26:51:GLU:HG3	1.80	0.62
43:2l:56:ALA:HB2	43:2l:70:ILE:HD11	1.81	0.62
11:2P:94:GLU:HG3	11:2P:124:LYS:HE2	1.81	0.62
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.33	0.62
1:1A:588:U:H2'	1:1A:589:C:C6	2.35	0.62
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.32	0.62
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.26	0.62
54:1w:26:A:H61	54:1w:44:G:H1	1.48	0.62
1:2A:882:G:H22	1:2A:894:C:H42	1.47	0.62
17:2V:1:MET:HB3	17:2V:99:ILE:HD12	1.81	0.62
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.80	0.62
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.35	0.62
9:1N:123:TYR:OH	9:1N:130:HIS:NE2	2.23	0.62
1:1A:11:G:H2'	1:1A:12:U:H5"	1.82	0.61
1:1A:1183:G:O3'	25:13:29:ARG:NH1	2.30	0.61
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.00	0.61
32:1a:276:G:O3'	48:1q:68:ARG:NH1	2.33	0.61
40:1i:53:VAL:O	40:1i:55:ALA:N	2.32	0.61
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.17	0.61
12:1Q:1:MET:HE1	12:1Q:45:GLN:HG3	1.82	0.61
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.82	0.61
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.16	0.61
33:1b:37:ASN:C	33:1b:39:ILE:H	2.09	0.61
1:2A:885:C:O2	1:2A:890:A:N6	2.31	0.61
21:2Z:93:ASP:HA	21:2Z:131:ARG:HH12	1.65	0.61
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.81	0.61
1:1A:639:U:H2'	1:1A:640:C:C6	2.35	0.61
1:1A:2108:C:H2'	1:1A:2109:U:H6	1.65	0.61
8:1I:40:THR:O	8:1I:44:LEU:HB2	1.99	0.61
9:1N:123:TYR:HH	9:1N:130:HIS:HE2	1.30	0.61
32:1a:1531:A:H8	32:1a:1531:A:O5'	1.82	0.61
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.15	0.61
1:2A:2394:C:N3	56:2y:76:A:O2'	2.31	0.61
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.34	0.61
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.47	0.61
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.36	0.61
1:2A:131:G:OP1	64:2A:3932:HOH:O	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:8:LEU:HG	41:2j:96:ILE:HG12	1.83	0.61
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.35	0.61
8:1I:38:LEU:HD23	8:1I:38:LEU:H	1.65	0.61
51:1t:50:GLU:HA	51:1t:100:ILE:HG12	1.82	0.61
27:25:40:LYS:NZ	27:25:44:THR:O	2.32	0.61
28:26:34:LEU:HB2	28:26:51:GLU:HB2	1.82	0.61
50:2s:27:GLU:HB2	50:2s:28:LYS:HD3	1.81	0.61
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.66	0.61
1:2A:2332:U:O4	64:2A:3926:HOH:O	2.15	0.61
14:2S:37:ALA:HB1	14:2S:73:LEU:HD22	1.82	0.61
14:2S:48:LEU:HD23	14:2S:82:ILE:HD11	1.82	0.61
1:2A:2183:C:H2'	1:2A:2184:G:C8	2.36	0.61
35:2d:10:ARG:HG3	35:2d:11:LEU:HD12	1.83	0.61
41:2j:6:ILE:HB	41:2j:72:VAL:HG13	1.83	0.61
26:14:55:ARG:N	26:14:56:VAL:HA	2.15	0.60
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.35	0.60
6:2G:63:ILE:HD11	6:2G:144:ILE:HD11	1.81	0.60
35:2d:6:GLY:H	35:2d:115:ARG:HH12	1.47	0.60
44:2m:13:LYS:O	44:2m:45:VAL:N	2.33	0.60
56:2y:10:G:H1	56:2y:25:C:H42	1.47	0.60
1:2A:563:G:OP2	64:2A:3929:HOH:O	2.16	0.60
32:2a:995:C:O2	45:2n:4:LYS:NZ	2.34	0.60
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.25	0.60
4:1E:52:LEU:O	4:1E:76:ARG:N	2.34	0.60
32:1a:504:C:OP1	64:1a:1908:HOH:O	2.16	0.60
32:1a:535:A:OP1	64:1a:1912:HOH:O	2.16	0.60
42:1k:21:ILE:HB	42:1k:84:VAL:HG12	1.83	0.60
1:2A:2002:G:OP2	13:2R:9:LYS:NZ	2.34	0.60
33:2b:71:VAL:HG12	33:2b:170:GLU:HG2	1.82	0.60
51:1t:39:LYS:HG2	51:1t:55:ILE:HG21	1.82	0.60
3:2D:180:GLY:HA3	3:2D:275:LYS:HG2	1.82	0.60
1:1A:2344:U:OP1	28:16:37:ARG:NH1	2.33	0.60
1:2A:744:G:OP1	64:2A:3931:HOH:O	2.16	0.60
1:2A:2156:G:H2'	1:2A:2157:G:C2	2.36	0.60
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.83	0.60
30:28:4:MET:HE3	30:28:63:PRO:HG3	1.82	0.60
46:2o:87:ILE:HG22	46:2o:88:ARG:H	1.67	0.60
42:1k:62:GLN:OE1	42:1k:93:GLN:NE2	2.35	0.60
1:2A:1651:G:OP1	13:2R:40:LYS:NZ	2.35	0.60
3:2D:183:ARG:HG3	3:2D:270:ILE:HD13	1.83	0.60
1:2A:1024:G:OP2	64:2A:3913:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:48:A:OP1	14:2S:30:ARG:NH2	2.33	0.60
22:20:10:THR:HG22	22:20:12:ASN:H	1.66	0.60
1:1A:897:C:N3	1:1A:898:C:N4	2.50	0.60
8:1I:101:LEU:HG	8:1I:107:VAL:HB	1.82	0.60
32:1a:118:U:O4	64:1a:1907:HOH:O	2.15	0.60
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.84	0.60
4:2E:50:GLY:HA3	4:2E:75:VAL:HG21	1.83	0.60
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.15	0.60
1:1A:1762:A:H2'	64:1A:5864:HOH:O	2.01	0.60
6:1G:98:ARG:CZ	26:14:1:MET:HE3	2.31	0.60
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.83	0.60
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.34	0.60
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.82	0.60
41:2j:16:LEU:HD23	41:2j:70:ARG:HG2	1.82	0.60
5:1F:164:ARG:HD2	5:1F:175:THR:HG23	1.83	0.60
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.83	0.60
26:14:58:ARG:HE	50:1s:68:GLY:H	1.50	0.59
32:1a:1036:G:H3'	32:1a:1037:C:C6	2.37	0.59
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.02	0.59
11:2P:124:LYS:HG3	11:2P:144:GLU:HB3	1.83	0.59
14:2S:26:LEU:HD13	14:2S:85:VAL:HG11	1.83	0.59
32:2a:1010:G:N2	32:2a:1020:U:O2'	2.35	0.59
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.02	0.59
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.17	0.59
1:1A:2274:A:N7	64:1A:4190:HOH:O	2.31	0.59
7:1H:116:GLU:HG3	7:1H:117:PRO:HD2	1.82	0.59
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.83	0.59
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.84	0.59
1:1A:1359:A:H2	1:1A:1372:U:O4	1.83	0.59
29:27:24:THR:HG23	29:27:27:GLY:H	1.65	0.59
32:1a:557:G:OP1	64:1a:1913:HOH:O	2.16	0.59
36:1e:105:VAL:HG21	36:1e:128:PRO:HB3	1.84	0.59
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.49	0.59
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.68	0.59
16:2U:5:LYS:HG3	16:2U:7:GLY:H	1.68	0.59
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.84	0.59
32:1a:473:G:OP2	47:1p:75:ARG:NH1	2.35	0.59
32:2a:1102:A:O3'	33:2b:96:ARG:NH2	2.34	0.59
1:1A:952:G:OP1	12:1Q:16:ARG:NH2	2.35	0.59
7:1H:3:ARG:HH22	7:1H:65:HIS:HB3	1.66	0.59
31:19:17:ILE:HD13	31:19:26:ILE:HD13	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:24:PRO:HA	15:2T:49:VAL:HG12	1.85	0.59
32:2a:45:U:H2'	32:2a:46:G:C8	2.38	0.59
32:2a:572:A:OP1	64:2a:1906:HOH:O	2.16	0.59
32:2a:1274:G:N2	32:2a:1275:A:N7	2.50	0.59
1:1A:278:A:O2'	1:1A:279:C:OP1	2.17	0.59
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.85	0.59
26:14:16:CYS:SG	26:14:17:GLY:N	2.75	0.59
32:1a:683:G:N7	64:1a:1935:HOH:O	2.31	0.59
32:1a:1132:C:H2'	32:1a:1133:G:H8	1.67	0.59
32:2a:838:G:H1	32:2a:848:C:N4	2.01	0.59
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.83	0.59
41:2j:30:SER:O	41:2j:81:THR:OG1	2.14	0.59
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.85	0.59
10:1O:104:ARG:CZ	15:1T:34:VAL:HG11	2.32	0.59
56:1y:8:4SU:H4'	56:1y:48:C:H4'	1.85	0.59
56:1y:68:C:H2'	56:1y:69:G:H8	1.67	0.59
5:2F:7:TYR:O	5:2F:22:ALA:N	2.34	0.59
32:2a:1136:U:OP2	32:2a:1137:C:N4	2.35	0.59
1:1A:2128:C:N4	1:1A:2160:G:H1	2.00	0.59
26:14:55:ARG:H	26:14:56:VAL:HA	1.68	0.59
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.85	0.59
32:2a:664:G:H22	32:2a:741:G:H1	1.50	0.59
32:2a:1457:G:H5"	51:2t:35:THR:HG21	1.84	0.59
35:2d:119:GLN:HG2	35:2d:123:HIS:CD2	2.37	0.59
1:1A:2125:G:N1	1:1A:2172:U:OP1	2.36	0.59
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.84	0.59
41:1j:81:THR:HG22	41:1j:85:LEU:HG	1.84	0.59
32:2a:673:G:H2'	32:2a:674:G:C8	2.38	0.59
38:2g:79:ARG:NH2	38:2g:80:VAL:HA	2.18	0.59
1:1A:1912:A:OP1	64:1A:4123:HOH:O	2.16	0.58
10:1O:49:ARG:HH12	32:1a:1423:G:P	2.26	0.58
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.38	0.58
1:2A:2135:A:C5	1:2A:2136:C:H5	2.21	0.58
6:2G:121:ASN:HD21	6:2G:123:ASN:HB2	1.68	0.58
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.36	0.58
32:2a:1202:G:N2	45:2n:46:GLU:OE2	2.32	0.58
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.38	0.58
41:2j:33:GLN:HG2	41:2j:34:VAL:H	1.68	0.58
55:2x:50:U:H3	55:2x:64:G:H1	1.48	0.58
8:1I:87:LYS:HA	8:1I:122:GLU:HA	1.85	0.58
40:1i:21:PRO:HA	40:1i:59:PHE:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2130:U:O2'	1:2A:2133:G:H4'	2.03	0.58
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.85	0.58
32:2a:1132:C:H2'	32:2a:1133:G:C8	2.39	0.58
1:1A:9:U:H3	1:1A:2629:A:H2	1.49	0.58
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.04	0.58
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.84	0.58
1:2A:582:G:OP2	64:2A:3933:HOH:O	2.17	0.58
1:2A:1434:A:H61	1:2A:1558:A:H62	1.49	0.58
32:2a:56:U:H2'	32:2a:57:G:C8	2.38	0.58
26:14:58:ARG:HH21	50:1s:68:GLY:HA3	1.68	0.58
1:2A:2151:G:H2'	1:2A:2152:G:C8	2.38	0.58
1:1A:668:G:H5'	1:1A:669:G:OP2	2.04	0.58
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.37	0.58
1:2A:1604:C:OP1	64:2A:3927:HOH:O	2.17	0.58
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.36	0.58
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.35	0.58
32:2a:562:C:H1'	43:2l:15:ARG:HB3	1.86	0.58
32:2a:921:U:O2	36:2e:19:MET:HB2	2.03	0.58
33:2b:165:VAL:HG23	33:2b:187:LEU:HD23	1.84	0.58
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.85	0.58
38:1g:78:ARG:HG3	38:1g:156:TRP:CZ3	2.37	0.58
43:1l:117:ARG:HB3	43:1l:122:THR:HB	1.84	0.58
1:2A:1713:U:H2'	1:2A:1714:G:H8	1.69	0.58
32:2a:620:C:C2	35:2d:135:LEU:HG	2.38	0.58
1:1A:784:A:N6	3:1D:229:VAL:HG11	2.18	0.58
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.03	0.58
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.37	0.58
32:1a:1414:U:O4	64:1a:1911:HOH:O	2.16	0.58
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.86	0.58
1:2A:2277:G:OP2	22:20:10:THR:HG21	2.04	0.58
32:2a:661:G:H1	32:2a:744:C:H42	1.51	0.58
32:2a:1225:A:OP1	44:2m:103:THR:OG1	2.22	0.58
33:1b:20:GLU:HG2	33:1b:23:ARG:NH1	2.19	0.58
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.38	0.58
1:2A:330:A:H2	1:2A:1210:A:HO2'	1.50	0.58
12:2Q:78:PRO:HD3	55:2x:1:C:N3	2.19	0.58
16:2U:49:HIS:HA	16:2U:52:ARG:HB2	1.86	0.58
26:24:26:SER:OG	26:24:27:THR:N	2.34	0.58
32:2a:1135:U:H4'	32:2a:1136:U:H5	1.69	0.58
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.86	0.58
1:1A:603:A:O4'	1:1A:655:A:N6	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:1n:9:LYS:HG2	45:1n:12:ARG:HH21	1.68	0.58
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.39	0.58
32:2a:1226:C:H2'	44:2m:103:THR:HB	1.84	0.58
32:2a:1271:G:C2	32:2a:1272:G:N7	2.72	0.58
32:2a:1417:G:O6	64:2a:1904:HOH:O	2.14	0.58
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.04	0.58
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.12	0.58
1:2A:2278:A:OP2	22:20:12:ASN:ND2	2.36	0.58
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.84	0.58
32:2a:1004:A:C6	32:2a:1037:C:H1'	2.39	0.58
32:2a:1239:A:H62	32:2a:1299:A:N6	2.01	0.58
32:2a:1310:G:H5'	44:2m:77:ASN:ND2	2.17	0.58
56:2y:34:G:H2'	56:2y:35:A:C8	2.39	0.58
1:1A:630:G:OP2	30:18:15:LYS:NZ	2.30	0.57
29:17:9:ARG:HD3	29:17:47:ARG:HB2	1.86	0.57
56:1y:37:MIA:H8	56:1y:37:MIA:H5"	1.85	0.57
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.69	0.57
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.39	0.57
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.69	0.57
39:2h:39:LEU:HB3	39:2h:45:ILE:HG12	1.86	0.57
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.86	0.57
1:2A:375:C:H2'	1:2A:376:C:C6	2.39	0.57
1:2A:1035:U:H5"	7:2H:59:ARG:HD3	1.86	0.57
1:2A:1131:G:HO2'	1:2A:1132:A:H8	1.52	0.57
41:2j:47:PHE:N	41:2j:63:PHE:O	2.33	0.57
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.87	0.57
1:1A:184:C:H2'	1:1A:185:U:C6	2.37	0.57
1:1A:1300:U:H4'	1:1A:1301:A:H5"	1.85	0.57
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.39	0.57
7:1H:88:LEU:HD23	7:1H:130:ARG:HG3	1.84	0.57
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.03	0.57
1:2A:2892:A:H2'	1:2A:2893:G:H5'	1.86	0.57
6:2G:152:LEU:H	6:2G:152:LEU:HD12	1.68	0.57
14:2S:105:ALA:HB1	14:2S:110:LEU:HD23	1.86	0.57
32:2a:142:G:H2'	32:2a:143:A:H8	1.68	0.57
32:2a:447:G:O6	32:2a:485:G:O2'	2.15	0.57
32:2a:1133:G:H1	32:2a:1141:C:H42	1.49	0.57
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.37	0.57
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.21	0.57
32:2a:376:G:H5"	47:2p:5:ARG:HB2	1.86	0.57
32:2a:1347:G:H5"	40:2i:107:ARG:HB3	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.29	0.57
39:1h:9:MET:HG3	39:1h:26:VAL:HG21	1.87	0.57
46:1o:84:LYS:HD2	46:1o:84:LYS:O	2.04	0.57
54:1w:58:A:O2'	54:1w:60:U:OP2	2.21	0.57
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.37	0.57
32:2a:142:G:H2'	32:2a:143:A:C8	2.40	0.57
47:2p:34:GLU:OE1	47:2p:55:ARG:NH2	2.37	0.57
56:2y:66:U:H2'	56:2y:67:C:O4'	2.04	0.57
1:2A:763:G:OP1	64:2A:3935:HOH:O	2.18	0.57
1:2A:1376:C:OP2	64:2A:3919:HOH:O	2.18	0.57
32:2a:165:C:H2'	32:2a:166:G:H8	1.67	0.57
1:1A:615:G:OP1	5:1F:40:GLN:NE2	2.30	0.57
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.37	0.57
21:2Z:106:GLY:HA3	21:2Z:141:VAL:HB	1.85	0.57
1:1A:880:G:H2'	1:1A:881:G:C8	2.40	0.57
1:2A:568:U:H5'	1:2A:945:A:N1	2.20	0.57
1:2A:855:G:O2'	22:20:27:GLU:OE2	2.20	0.57
32:2a:1289:A:OP1	52:2u:10:ARG:NH2	2.37	0.57
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.02	0.57
32:1a:1239:A:H62	32:1a:1299:A:N6	2.03	0.57
2:2B:24:G:N7	2:2B:56:G:H2'	2.20	0.57
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.40	0.57
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.86	0.57
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.39	0.57
28:26:7:ILE:HD13	28:26:27:LYS:HD3	1.86	0.57
32:2a:134:A:H61	47:2p:25:ARG:NH1	2.02	0.57
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.35	0.57
32:2a:1193:G:O2'	36:2e:25:ARG:NH2	2.37	0.57
34:2c:69:HIS:CD2	34:2c:104:GLN:HG2	2.40	0.57
54:1w:2:C:H2'	54:1w:3:C:C6	2.39	0.56
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.70	0.56
32:2a:1263:C:N3	32:2a:1272:G:O6	2.38	0.56
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.19	0.56
46:2o:82:ILE:HD12	46:2o:88:ARG:HG3	1.86	0.56
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.69	0.56
32:1a:838:G:H1	32:1a:848:C:H42	1.53	0.56
1:2A:2143:C:H2'	1:2A:2144:U:O4'	2.04	0.56
32:2a:986:A:N3	50:2s:52:TYR:OH	2.30	0.56
35:2d:65:ARG:NH1	35:2d:70:ILE:O	2.37	0.56
35:2d:111:ALA:HB2	35:2d:120:LEU:HD12	1.86	0.56
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:7:G:H2'	36:1e:119:LEU:HD22	1.87	0.56
32:1a:815:A:N7	32:1a:1509:C:O2'	2.37	0.56
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.88	0.56
56:1y:38:A:H2'	56:1y:39:PSU:O4'	2.05	0.56
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.05	0.56
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.88	0.56
32:2a:651:C:N4	32:2a:753:A:OP2	2.38	0.56
36:2e:78:HIS:CE1	36:2e:143:ARG:H	2.23	0.56
39:2h:4:ASP:OD2	39:2h:7:ALA:N	2.22	0.56
50:1s:80:TYR:O	50:1s:81:ARG:HG2	2.06	0.56
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.53	0.56
2:2B:41:U:H5	6:2G:70:VAL:H	1.53	0.56
26:24:64:GLY:C	26:24:66:SER:H	2.12	0.56
32:2a:7:G:O2'	36:2e:120:THR:O	2.23	0.56
45:2n:12:ARG:HH12	45:2n:14:PRO:HA	1.69	0.56
1:1A:2182:G:H2'	1:1A:2183:C:C6	2.40	0.56
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.36	0.56
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.23	0.56
1:2A:300:A:P	20:2Y:86:ARG:HH12	2.29	0.56
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.71	0.56
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.06	0.56
32:1a:1030:C:N4	32:1a:1030(A):G:N3	2.54	0.56
1:2A:2379:G:HO2'	14:2S:17:ARG:HH12	1.46	0.56
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.88	0.56
41:2j:69:ASN:O	41:2j:70:ARG:NH1	2.33	0.56
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.21	0.56
32:1a:881:G:P	43:1l:12:ARG:HH22	2.29	0.56
25:23:6:VAL:HG22	25:23:56:VAL:HG12	1.88	0.56
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.41	0.56
32:1a:1030(A):G:H3'	32:1a:1030(B):C:H5"	1.87	0.56
32:1a:1036:G:H5"	32:1a:1037:C:C5	2.41	0.56
44:1m:14:ARG:NH2	44:1m:16:ASP:OD2	2.37	0.56
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.37	0.56
1:2A:1711:C:H2'	1:2A:1712:C:C6	2.41	0.56
1:2A:2136:C:N4	1:2A:2155:G:H1	2.03	0.56
3:2D:85:ASP:OD2	3:2D:88:ARG:HD2	2.06	0.56
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.39	0.56
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.21	0.56
12:2Q:111:GLU:OE1	12:2Q:133:ARG:NH2	2.39	0.56
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.21	0.56
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:18:G:H4'	54:2w:60:U:C5	2.41	0.56
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.88	0.56
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.87	0.56
1:2A:1532:C:H42	1:2A:1537:G:H1	1.54	0.56
14:2S:67:ARG:HH12	14:2S:103:GLU:HB3	1.71	0.56
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.88	0.56
1:1A:2612:C:OP2	27:15:2:ALA:N	2.39	0.56
26:14:50:VAL:HG21	44:1m:64:TRP:C	2.31	0.56
32:1a:200:G:H1	32:1a:217:C:H42	1.54	0.56
38:1g:74:GLU:HG2	38:1g:91:VAL:HG22	1.87	0.56
41:1j:49:VAL:HG13	45:1n:41:ARG:HB2	1.87	0.56
1:2A:1508:A:H4'	1:2A:1509(A):A:C5	2.39	0.56
1:1A:2079:U:OP1	23:11:21:ARG:NH2	2.29	0.55
32:1a:96:U:H2'	32:1a:97:G:C8	2.41	0.55
36:1e:142:LEU:O	36:1e:143:ARG:NH1	2.39	0.55
1:1A:1055:G:H3'	1:1A:1056:G:H8	1.69	0.55
21:1Z:163:LEU:HD23	21:1Z:167:PRO:HG3	1.88	0.55
32:1a:545:C:OP1	35:1d:61:LYS:NZ	2.38	0.55
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.70	0.55
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.22	0.55
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.70	0.55
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.41	0.55
32:2a:406:G:H5'	35:2d:5:ILE:HD11	1.89	0.55
36:2e:36:ASP:O	36:2e:38:GLN:N	2.35	0.55
36:2e:148:VAL:HG21	39:2h:107:LEU:HD22	1.87	0.55
32:2a:134:A:H61	47:2p:25:ARG:HH12	1.54	0.55
32:2a:222:U:H2'	32:2a:223:U:C6	2.41	0.55
40:2i:4:TYR:HD1	40:2i:87:GLN:HG2	1.71	0.55
40:2i:23:ASN:HD21	40:2i:25:LYS:HE2	1.70	0.55
56:2y:65:G:H2'	56:2y:66:U:C6	2.41	0.55
56:2y:68:C:H2'	56:2y:69:G:O4'	2.06	0.55
1:1A:579:G:H2'	1:1A:580:C:C6	2.41	0.55
32:1a:405:U:H5"	32:1a:495:A:H2	1.70	0.55
32:1a:757:U:H2'	32:1a:758:G:O4'	2.06	0.55
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.22	0.55
10:2O:63:VAL:HG23	10:2O:64:ARG:HG3	1.87	0.55
11:2P:39:LYS:HB2	11:2P:45:LEU:HD22	1.89	0.55
32:2a:1202:G:O4'	45:2n:29:ARG:NH1	2.39	0.55
36:2e:143:ARG:NE	39:2h:77:GLU:OE2	2.34	0.55
1:1A:278:A:H2'	1:1A:279:C:C6	2.42	0.55
1:1A:1991:U:H2'	1:1A:1992:G:H5"	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:98:LYS:NZ	64:1T:301:HOH:O	2.29	0.55
18:1W:23:LEU:HD21	27:15:25:LEU:HB2	1.88	0.55
21:1Z:150:LEU:HD12	21:1Z:154:ASP:HB2	1.87	0.55
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.21	0.55
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	1.90	0.55
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.12	0.55
32:2a:1076:C:OP1	33:2b:179:LYS:NZ	2.39	0.55
32:2a:1317:C:O2	50:2s:37:ARG:NH2	2.39	0.55
1:1A:1702:G:N7	64:1A:4186:HOH:O	2.33	0.55
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.41	0.55
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.16	0.55
1:1A:1580:A:OP2	1:1A:1580:A:H8	1.90	0.55
32:1a:714:G:H2'	32:1a:715:A:C8	2.42	0.55
33:1b:128:GLU:HG3	33:1b:135:GLN:HE22	1.71	0.55
51:1t:22:ARG:O	51:1t:26:ASN:ND2	2.40	0.55
1:2A:370:G:OP2	64:2A:3930:HOH:O	2.18	0.55
1:2A:775:G:O2'	64:2A:3934:HOH:O	2.18	0.55
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.42	0.55
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.36	0.55
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.41	0.55
33:2b:223:ILE:HA	33:2b:226:ARG:HD3	1.89	0.55
1:1A:614(C):A:C4	5:1F:180:GLY:HA2	2.41	0.55
10:1O:2:ILE:HG13	10:1O:8:LEU:HD21	1.89	0.55
32:1a:396:G:O2'	32:1a:398:C:OP1	2.17	0.55
1:2A:668:G:H5'	1:2A:669:G:OP2	2.06	0.55
32:2a:393:A:OP1	64:2a:1907:HOH:O	2.18	0.55
33:2b:118:LEU:O	33:2b:122:PHE:HB3	2.07	0.55
26:14:33:VAL:HG12	26:14:35:VAL:H	1.72	0.55
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.89	0.55
35:1d:134:ASP:N	35:1d:134:ASP:OD1	2.40	0.55
40:1i:49:PRO:HG2	40:1i:81:ILE:HG23	1.89	0.55
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.07	0.55
1:2A:1489:U:HO2'	1:2A:1490:A:H8	1.55	0.55
34:2c:130:VAL:HG11	34:2c:153:VAL:HG11	1.89	0.55
35:2d:165:MET:HE2	35:2d:168:ARG:CZ	2.37	0.55
38:2g:51:GLN:HG3	38:2g:58:PRO:HD3	1.89	0.55
40:2i:3:GLN:HE21	40:2i:20:ARG:HE	1.55	0.55
1:1A:1439:A:OP1	64:1A:4125:HOH:O	2.18	0.55
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.88	0.55
1:2A:1508:A:H4'	1:2A:1509(A):A:N7	2.22	0.55
25:23:44:ARG:O	25:23:48:GLU:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.89	0.55
32:2a:165:C:H2'	32:2a:166:G:C8	2.41	0.55
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.72	0.55
32:2a:1316:G:H22	32:2a:1319:A:H5"	1.72	0.55
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.42	0.54
18:2W:88:ARG:HB2	18:2W:92:ARG:HB3	1.88	0.54
32:2a:1239:A:H62	32:2a:1299:A:H62	1.54	0.54
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.43	0.54
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.89	0.54
46:2o:64:ARG:HH11	46:2o:68:ARG:HH21	1.56	0.54
50:2s:49:ILE:HG22	50:2s:62:ILE:HD11	1.88	0.54
32:1a:28:G:O2'	32:1a:296:U:OP1	2.22	0.54
33:1b:163:PHE:CD1	33:1b:185:ILE:HG13	2.42	0.54
1:2A:652(B):A:N6	1:2A:655:A:O2'	2.32	0.54
1:2A:2166:G:H3'	1:2A:2167:U:H5"	1.89	0.54
7:2H:90:LYS:HD3	7:2H:159:GLU:HG2	1.88	0.54
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.41	0.54
32:2a:1279:A:OP2	41:2j:9:ARG:NH2	2.24	0.54
34:2c:39:ILE:O	34:2c:43:LEU:HG	2.08	0.54
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.89	0.54
48:2q:82:MET:HA	48:2q:85:VAL:HG22	1.90	0.54
50:2s:27:GLU:HB2	50:2s:28:LYS:HA	1.89	0.54
1:1A:2136:C:C2	1:1A:2155:G:N2	2.75	0.54
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.23	0.54
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.25	0.54
11:1P:59:LEU:HD11	30:18:10:ALA:HA	1.89	0.54
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.07	0.54
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.41	0.54
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.89	0.54
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.42	0.54
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	1.89	0.54
41:2j:49:VAL:CG2	45:2n:41:ARG:HB2	2.38	0.54
32:1a:1006:C:H2'	32:1a:1007:C:C6	2.41	0.54
1:2A:2136:C:N3	1:2A:2155:G:N2	2.52	0.54
32:2a:920:U:H2'	32:2a:921:U:C6	2.43	0.54
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.41	0.54
4:1E:77:ILE:HD13	4:1E:195:LEU:HD13	1.90	0.54
32:1a:1320:C:O2	50:1s:36:ARG:NH2	2.41	0.54
1:2A:2104:G:H1	1:2A:2185:C:H42	1.55	0.54
27:25:41:PRO:O	27:25:44:THR:OG1	2.25	0.54
32:2a:1135:U:O2'	32:2a:1138:G:O6	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:92:VAL:O	35:2d:96:LEU:HD22	2.07	0.54
36:2e:8:GLU:HG2	36:2e:34:VAL:HG23	1.89	0.54
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.89	0.54
56:2y:14:A:O2'	56:2y:15:G:OP1	2.23	0.54
12:1Q:78:PRO:HG2	12:1Q:81:VAL:HG11	1.88	0.54
32:1a:532:A:N6	32:1a:1206:G:O2'	2.40	0.54
32:1a:1414:U:H3	32:1a:1486:G:H1	1.55	0.54
1:2A:84:A:H5"	20:2Y:8:LYS:HE3	1.90	0.54
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.22	0.54
34:2c:37:GLN:NE2	45:2n:52:GLN:OE1	2.32	0.54
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.88	0.54
45:2n:23:ARG:NH1	45:2n:28:GLY:O	2.39	0.54
45:2n:24:CYS:HB2	45:2n:40:CYS:HB3	1.89	0.54
1:1A:1077:A:H2'	1:1A:1078:U:H4'	1.89	0.54
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.08	0.54
15:1T:127:ALA:C	15:1T:129:ARG:H	2.15	0.54
26:14:54:GLY:N	26:14:55:ARG:HA	2.23	0.54
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.07	0.54
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.73	0.54
8:2I:40:THR:OG1	8:2I:41:GLU:N	2.34	0.54
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.08	0.54
9:2N:73:THR:HB	9:2N:82:LEU:HD11	1.90	0.54
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.71	0.54
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	1.90	0.54
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.07	0.54
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.42	0.54
32:2a:1272:G:N2	32:2a:1273:G:C5	2.75	0.54
11:1P:38:GLN:O	11:1P:40:SER:N	2.40	0.54
32:1a:17:U:H2'	32:1a:18:C:C6	2.43	0.54
32:1a:56:U:H2'	32:1a:57:G:C8	2.42	0.54
26:24:24:THR:OG1	26:24:25:TYR:N	2.39	0.54
32:2a:448:A:P	32:2a:485:G:H22	2.30	0.54
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.73	0.54
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.89	0.54
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.87	0.54
50:2s:12:ASP:HB3	50:2s:14:HIS:CD2	2.43	0.54
1:1A:1069:A:H1'	1:1A:1096:A:H4'	1.89	0.54
32:1a:1004:A:N6	32:1a:1037:C:H42	2.05	0.54
32:2a:1029:C:N4	32:2a:1032:G:C6	2.76	0.54
33:2b:114:ARG:NH1	33:2b:117:GLU:OE1	2.41	0.54
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.43	0.54
32:1a:673:G:H2'	32:1a:674:G:C8	2.42	0.54
32:1a:1030(A):G:O2'	32:1a:1031:G:N2	2.41	0.54
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.56	0.54
40:1i:8:GLY:O	40:1i:15:ALA:N	2.41	0.54
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.41	0.54
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.23	0.54
1:2A:2577:A:H5"	1:2A:2578:G:H5'	1.90	0.54
1:2A:2816:C:O3'	13:2R:99:LYS:NZ	2.40	0.54
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.91	0.54
1:1A:459:U:H5"	29:17:40:TRP:CD2	2.42	0.53
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.23	0.53
62:1w:109:PHE:N	55:1x:76:8AN:HO2'	2.07	0.53
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.71	0.53
32:2a:996:A:N1	32:2a:1045:C:O2'	2.39	0.53
1:1A:1056:G:H1'	1:1A:1103:A:H61	1.73	0.53
1:1A:2156:G:OP2	1:1A:2156:G:H8	1.90	0.53
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.41	0.53
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.90	0.53
8:1I:38:LEU:HG	8:1I:40:THR:HG23	1.89	0.53
8:1I:109:ILE:HG23	8:1I:130:TYR:CZ	2.43	0.53
32:1a:67:C:H2'	32:1a:68:G:C8	2.43	0.53
32:1a:731:G:H5'	32:1a:766:A:H4'	1.89	0.53
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.38	0.53
40:1i:48:GLU:HA	40:1i:51:ARG:HD3	1.90	0.53
56:1y:35:A:OP2	56:1y:35:A:H8	1.91	0.53
56:1y:55:PSU:C4	56:1y:57:G:H5'	2.44	0.53
1:2A:800:A:H8	1:2A:800:A:OP1	1.90	0.53
6:2G:27:ASN:HB3	6:2G:30:GLU:HB2	1.89	0.53
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.43	0.53
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.91	0.53
1:1A:626:U:O4	11:1P:107:LYS:HE2	2.09	0.53
1:1A:1075:C:H2'	1:1A:1076:C:H2'	1.90	0.53
8:1I:93:THR:HG22	8:1I:119:PRO:HB3	1.90	0.53
32:1a:1025:U:O2	32:1a:1036:G:O6	2.26	0.53
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.44	0.53
1:2A:333:G:N7	64:2A:3998:HOH:O	2.34	0.53
1:2A:892:G:H5'	1:2A:893:C:OP2	2.08	0.53
1:2A:2506:U:O2'	54:2w:76:8AN:H4'	2.08	0.53
15:2T:127:ALA:C	15:2T:129:ARG:H	2.16	0.53
33:2b:48:MET:SD	33:2b:49:GLU:N	2.81	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:6:ILE:HG12	41:2j:98:ILE:HG12	1.90	0.53
1:1A:1057:A:N6	1:1A:1087:G:OP1	2.41	0.53
1:1A:2361:A:OP1	30:18:27:THR:OG1	2.21	0.53
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.42	0.53
56:1y:9:A:O3'	56:1y:45:U:O2'	2.26	0.53
56:1y:37:MIA:H2'	56:1y:38:A:C8	2.43	0.53
1:2A:30:G:H2'	1:2A:31:C:C6	2.43	0.53
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.43	0.53
1:2A:340:A:H2'	1:2A:341:G:O4'	2.08	0.53
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.41	0.53
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.89	0.53
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.91	0.53
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.08	0.53
36:2e:24:ARG:NH1	53:2v:24:A:OP2	2.41	0.53
1:1A:796:C:H2'	1:1A:797:C:C6	2.42	0.53
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.44	0.53
21:1Z:77:ASP:OD2	21:1Z:80:ARG:NH1	2.42	0.53
32:1a:309:G:O2'	32:1a:607:A:N1	2.40	0.53
34:2c:44:GLU:HA	34:2c:52:LEU:HD23	1.91	0.53
50:2s:28:LYS:HB3	50:2s:29:ARG:CB	2.39	0.53
1:1A:1671:U:O4	64:1A:4108:HOH:O	2.18	0.53
1:1A:2156:G:H2'	1:1A:2157:G:C2	2.44	0.53
1:1A:2206:G:H5"	1:1A:2207:G:C5	2.44	0.53
3:1D:71:ASP:HB2	3:1D:103:ARG:HH12	1.72	0.53
32:1a:1381:U:H1'	38:1g:79:ARG:HG2	1.89	0.53
35:1d:119:GLN:HG2	35:1d:123:HIS:HD2	1.74	0.53
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	1.90	0.53
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.90	0.53
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.42	0.53
49:2r:53:ARG:HH21	49:2r:59:SER:HA	1.73	0.53
50:2s:33:THR:HG21	50:2s:49:ILE:HD11	1.91	0.53
1:1A:880:G:H2'	1:1A:881:G:H8	1.74	0.53
1:1A:2102:U:H3	1:1A:2187:G:H1	1.57	0.53
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.08	0.53
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.23	0.53
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.09	0.53
32:1a:963:G:H5'	64:1a:2063:HOH:O	2.08	0.53
12:2Q:81:VAL:HG12	22:20:5:LYS:HD3	1.91	0.53
22:20:70:GLN:OE1	22:20:80:HIS:NE2	2.41	0.53
32:2a:64:G:H4'	32:2a:65:U:H3'	1.91	0.53
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1242:A:N1	11:1P:4:SER:OG	2.38	0.53
8:1I:76:THR:HG23	8:1I:141:LYS:HE2	1.91	0.53
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.44	0.53
1:2A:10:G:O2'	1:2A:2801(A):A:N7	2.35	0.53
1:2A:247:G:H4'	1:2A:386:G:C5	2.44	0.53
1:2A:288:C:H2'	1:2A:289:A:H8	1.73	0.53
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.44	0.53
1:2A:882:G:H22	1:2A:894:C:N4	2.06	0.53
1:2A:2125:G:H1'	1:2A:2173:A:N6	2.23	0.53
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.42	0.53
32:2a:737:A:H2'	32:2a:738:C:C6	2.44	0.53
35:2d:59:ARG:HH12	35:2d:62:GLN:HG3	1.73	0.53
55:2x:8:4SU:O5'	55:2x:8:4SU:H6	2.08	0.53
1:1A:637:A:OP1	11:1P:133:SER:OG	2.21	0.53
11:1P:42:SER:O	64:1P:301:HOH:O	2.18	0.53
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.44	0.53
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.36	0.53
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.44	0.53
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.09	0.53
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.44	0.53
32:2a:460:G:N2	32:2a:471:G:N7	2.57	0.53
1:1A:583:G:OP2	16:1U:10:ARG:HD2	2.10	0.53
1:1A:2429:G:OP1	64:1A:4103:HOH:O	2.19	0.53
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.24	0.53
32:1a:222:U:H2'	32:1a:223:U:C6	2.44	0.53
44:1m:92:HIS:CE1	44:1m:98:VAL:HG21	2.44	0.53
1:2A:271(K):U:O2	8:2I:50:ARG:NH2	2.42	0.53
1:2A:1711:C:H2'	1:2A:1712:C:H6	1.74	0.53
1:2A:2134:A:H1'	1:2A:2158:A:C6	2.45	0.53
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.26	0.53
5:2F:10:PRO:HB3	5:2F:17:ARG:NH1	2.24	0.53
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.26	0.53
32:2a:1280:A:O2'	32:2a:1281:U:H5'	2.08	0.53
1:1A:536:A:H2'	1:1A:537:C:C6	2.44	0.52
1:1A:1079:C:H2'	1:1A:1080:C:O4'	2.09	0.52
23:11:2:SER:HB3	23:11:46:LEU:HD12	1.89	0.52
28:16:19:ARG:NH1	28:16:52:VAL:HG21	2.24	0.52
36:1e:83:GLU:HG2	36:1e:88:LYS:HG3	1.91	0.52
1:2A:643:A:N1	1:2A:2369:A:O2'	2.40	0.52
1:2A:731:C:H5"	64:2A:4078:HOH:O	2.09	0.52
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:40:ARG:O	34:2c:44:GLU:HG2	2.09	0.52
5:1F:178:PRO:HB3	5:1F:198:ALA:HA	1.92	0.52
26:14:44:THR:OG1	26:14:47:GLN:HB2	2.09	0.52
32:1a:920:U:H2'	32:1a:921:U:C6	2.44	0.52
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.44	0.52
56:1y:19:G:N1	56:1y:56:C:N4	2.56	0.52
1:2A:1219:G:H1	1:2A:1230:C:H42	1.58	0.52
7:2H:3:ARG:HG2	7:2H:6:ARG:HB2	1.90	0.52
15:2T:111:ARG:NH2	32:2a:1464:G:OP2	2.42	0.52
30:28:28:GLY:O	30:28:36:LYS:NZ	2.33	0.52
32:2a:446:G:O6	64:2a:1908:HOH:O	2.18	0.52
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.23	0.52
33:2b:16:HIS:O	33:2b:18:GLY:N	2.43	0.52
42:2k:86:GLY:H	42:2k:112:THR:HG23	1.74	0.52
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.92	0.52
56:1y:71:G:H2'	56:1y:72:C:C6	2.43	0.52
1:2A:1334:G:O6	64:2A:3940:HOH:O	2.19	0.52
32:2a:826:C:O2	39:2h:15:ASN:ND2	2.42	0.52
32:2a:921:U:O2'	36:2e:19:MET:O	2.20	0.52
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.44	0.52
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.75	0.52
1:1A:1230:C:H2'	1:1A:1231:G:C8	2.45	0.52
1:1A:2629:A:H1'	1:1A:2630:G:H5"	1.91	0.52
3:1D:24:ILE:HD13	3:1D:84:TYR:HB2	1.91	0.52
11:1P:38:GLN:O	11:1P:39:LYS:HB3	2.10	0.52
32:1a:1036:G:H5"	32:1a:1037:C:H5	1.75	0.52
33:1b:20:GLU:HG2	33:1b:23:ARG:HH11	1.74	0.52
56:1y:71:G:H2'	56:1y:72:C:H6	1.73	0.52
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.40	0.52
23:21:80:LEU:HD23	23:21:82:LEU:HD21	1.91	0.52
32:2a:1236:A:O2'	32:2a:1304:G:H4'	2.09	0.52
44:2m:13:LYS:HA	44:2m:44:ARG:NH1	2.23	0.52
46:2o:87:ILE:O	46:2o:88:ARG:HB2	2.09	0.52
1:1A:414:C:H2'	1:1A:415:A:C8	2.44	0.52
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.45	0.52
6:1G:115:ARG:HG2	6:1G:136:ARG:HH22	1.75	0.52
32:1a:399:G:H2'	32:1a:400:C:C6	2.44	0.52
32:1a:1028:C:H2'	32:1a:1029:C:O4'	2.09	0.52
56:1y:68:C:C2	56:1y:69:G:C8	2.97	0.52
1:2A:222:A:H5"	1:2A:421:U:OP1	2.09	0.52
1:2A:253:C:O2'	64:2A:3937:HOH:O	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1038:C:H42	1:2A:1117:G:H1	1.55	0.52
1:2A:1359:A:H2	1:2A:1372:U:O4	1.93	0.52
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.91	0.52
25:23:15:TYR:O	25:23:20:LYS:NZ	2.42	0.52
26:24:61:ARG:HA	26:24:61:ARG:HH11	1.74	0.52
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.45	0.52
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.75	0.52
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.10	0.52
32:2a:1318:A:H1'	50:2s:37:ARG:HH21	1.73	0.52
34:2c:3:ASN:N	34:2c:3:ASN:OD1	2.41	0.52
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	1.90	0.52
36:2e:41:VAL:O	36:2e:66:MET:HA	2.10	0.52
1:1A:899:A:H2'	1:1A:899:A:N3	2.24	0.52
1:1A:1025:G:O2'	64:1A:4106:HOH:O	2.14	0.52
1:1A:2141:G:H8	1:1A:2141:G:O5'	1.93	0.52
1:1A:2147:G:H3'	1:1A:2147:G:N3	2.25	0.52
33:1b:19:HIS:HA	33:1b:39:ILE:HG23	1.92	0.52
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.09	0.52
32:2a:524:G:H2'	32:2a:525:C:C6	2.45	0.52
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.24	0.52
1:1A:1055:G:H1	1:1A:1104:C:N4	2.04	0.52
20:1Y:14:LEU:HB2	20:1Y:75:ILE:HD11	1.91	0.52
32:1a:7:G:H5'	32:1a:298:A:O4'	2.08	0.52
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.45	0.52
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.91	0.52
1:2A:493:G:H2'	1:2A:494:G:O4'	2.10	0.52
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.45	0.52
1:2A:2136:C:N4	1:2A:2155:G:N1	2.57	0.52
1:2A:2439:A:N6	55:2x:76:8AN:O1P	2.42	0.52
1:2A:2818:G:OP1	1:2A:2837:G:O2'	2.17	0.52
9:2N:67:LEU:C	9:2N:88:GLU:HG3	2.34	0.52
32:2a:792:A:H4'	32:2a:793:U:H5"	1.91	0.52
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.92	0.52
1:1A:2128:C:N3	1:1A:2160:G:N2	2.51	0.52
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.10	0.52
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.45	0.52
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.90	0.52
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.10	0.52
5:2F:32:LEU:HD22	5:2F:112:MET:HE2	1.90	0.52
14:2S:26:LEU:HD12	14:2S:39:ILE:HG12	1.92	0.52
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1275:A:H2'	32:2a:1276:G:O4'	2.10	0.52
33:2b:92:TYR:CE2	33:2b:151:GLY:HA3	2.45	0.52
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.91	0.52
41:2j:65:LEU:HB2	45:2n:56:VAL:HG22	1.91	0.52
50:2s:66:MET:HB2	50:2s:74:PHE:CZ	2.44	0.52
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.10	0.52
1:1A:1421:G:N2	1:1A:1495:A:N1	2.56	0.52
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.91	0.52
32:1a:1027:C:H5	32:1a:1028:C:C4	2.28	0.52
44:1m:79:LYS:NZ	44:1m:83:ASP:OD2	2.40	0.52
56:1y:55:PSU:N3	56:1y:57:G:H5'	2.24	0.52
1:2A:212:G:H2'	1:2A:213:A:O4'	2.10	0.52
1:2A:1830:C:OP2	64:2A:3939:HOH:O	2.19	0.52
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.75	0.52
32:2a:155:C:H2'	32:2a:156:G:O4'	2.10	0.52
32:2a:157:G:N2	32:2a:164:U:O2	2.37	0.52
40:2i:97:LYS:HA	40:2i:102:LEU:HG	1.91	0.52
1:1A:2629:A:H1'	1:1A:2630:G:C5'	2.40	0.52
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.91	0.52
15:1T:1:MET:HE2	15:1T:3:ARG:HG3	1.91	0.52
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.38	0.52
32:1a:1029:C:N4	32:1a:1031:G:O6	2.43	0.52
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.92	0.52
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.58	0.52
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.75	0.52
6:2G:15:VAL:HG13	6:2G:175:LEU:HB2	1.91	0.52
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.43	0.52
18:2W:11:ARG:NH1	18:2W:99:ARG:O	2.43	0.52
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.93	0.52
33:2b:120:ALA:O	33:2b:125:PRO:HD2	2.09	0.52
1:1A:1506:C:H2'	1:1A:1507:A:C8	2.43	0.51
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.43	0.51
6:1G:115:ARG:HG2	6:1G:136:ARG:NH2	2.26	0.51
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.91	0.51
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.28	0.51
1:2A:764:A:H5"	3:2D:210:GLY:CA	2.40	0.51
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.25	0.51
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.40	0.51
32:2a:328:C:H4'	32:2a:329:A:H5'	1.92	0.51
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.41	0.51
33:2b:15:VAL:HG12	33:2b:209:ARG:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:7:G:H2'	1:1A:8:A:O4'	2.09	0.51
1:1A:135:G:N7	64:1A:4204:HOH:O	2.34	0.51
32:1a:692:U:O2'	32:1a:694:A:N7	2.35	0.51
33:1b:107:THR:O	33:1b:110:GLN:HB2	2.10	0.51
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.90	0.51
56:1y:9:A:H4'	56:1y:46:G7M:OP2	2.10	0.51
1:2A:686:G:N2	1:2A:788:A:H61	2.07	0.51
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.45	0.51
1:2A:2589:A:OP1	64:2A:3936:HOH:O	2.18	0.51
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.25	0.51
7:2H:20:ALA:HB3	7:2H:23:ARG:HB2	1.92	0.51
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.43	0.51
34:2c:52:LEU:HD12	34:2c:53:ALA:H	1.75	0.51
37:2f:8:ILE:HD11	37:2f:79:LEU:HD13	1.92	0.51
1:1A:493:G:O6	64:1A:4129:HOH:O	2.19	0.51
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.46	0.51
1:1A:2124:G:H1	1:1A:2174:C:H42	1.56	0.51
7:1H:113:VAL:HG11	7:1H:151:ILE:HD13	1.92	0.51
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.92	0.51
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.39	0.51
1:2A:1181:C:H2'	1:2A:1182:A:C8	2.45	0.51
12:2Q:1:MET:HE1	12:2Q:45:GLN:HA	1.91	0.51
14:2S:10:ARG:HG2	14:2S:91:PRO:HA	1.91	0.51
24:22:41:ILE:HG13	24:22:43:GLN:HG2	1.91	0.51
32:2a:109:A:H5'	32:2a:110:C:C5	2.45	0.51
32:2a:157:G:H2'	32:2a:158:G:H8	1.75	0.51
32:2a:512:U:H2'	32:2a:513:C:C6	2.44	0.51
32:2a:1291:G:O2'	40:2i:38:GLN:O	2.20	0.51
32:2a:1518:MA6:H93	32:2a:1519:MA6:C9	2.41	0.51
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.93	0.51
32:1a:501:C:H2'	32:1a:502:G:C8	2.46	0.51
38:1g:78:ARG:HG3	38:1g:156:TRP:HZ3	1.76	0.51
1:2A:1283:G:O2'	1:2A:1285:G:N7	2.42	0.51
1:2A:2136:C:H1'	1:2A:2137:C:H5'	1.93	0.51
1:2A:2518:A:OP2	64:2A:3941:HOH:O	2.19	0.51
8:2I:130:TYR:HD2	8:2I:138:ILE:HD12	1.76	0.51
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.91	0.51
21:2Z:158:PRO:O	21:2Z:161:VAL:HG12	2.10	0.51
23:21:64:ALA:HA	23:21:67:ILE:HG13	1.92	0.51
32:2a:473:G:H2'	32:2a:474:G:H8	1.74	0.51
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.26	0.51
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.45	0.51
6:1G:122:PRO:HG3	6:1G:182:LYS:H	1.75	0.51
9:1N:35:ARG:HD3	9:1N:37:LYS:HD2	1.93	0.51
32:1a:79:G:H1'	32:1a:91:C:O2	2.10	0.51
32:1a:110:C:H2'	32:1a:111:G:O4'	2.11	0.51
1:2A:307:G:N1	1:2A:310:A:OP2	2.43	0.51
1:2A:1713:U:H2'	1:2A:1714:G:C8	2.45	0.51
1:2A:2572:A:C8	4:2E:144:ARG:HD3	2.45	0.51
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.92	0.51
11:2P:87:ASP:O	11:2P:90:ARG:NH1	2.44	0.51
32:2a:157:G:H2'	32:2a:158:G:C8	2.45	0.51
32:2a:991:U:C5	32:2a:1212:U:H1'	2.46	0.51
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.46	0.51
33:2b:52:GLU:O	33:2b:56:ARG:NH1	2.44	0.51
1:1A:271(I):G:N7	1:1A:271(J):C:N4	2.58	0.51
1:1A:1174:A:H1'	1:1A:1175:U:H5"	1.93	0.51
5:1F:116:ASP:OD2	11:1P:1:MET:N	2.36	0.51
5:1F:123:LEU:HD13	5:1F:192:LEU:HD13	1.93	0.51
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.44	0.51
32:1a:975:A:H5'	32:1a:975:A:H8	1.76	0.51
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	1.93	0.51
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.35	0.51
1:2A:952:G:OP1	12:2Q:16:ARG:NH2	2.43	0.51
1:2A:2120:G:H2'	1:2A:2121:G:C8	2.46	0.51
1:2A:2131:G:H4'	1:2A:2132:U:H3'	1.93	0.51
5:2F:133:ASN:N	5:2F:138:GLU:OE1	2.43	0.51
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.76	0.51
56:2y:15:G:N2	56:2y:48:C:H42	2.08	0.51
1:1A:412:A:OP1	64:1A:4126:HOH:O	2.18	0.51
1:1A:884:C:H42	1:1A:892:G:H1	1.56	0.51
1:1A:1062:G:H2'	1:1A:1063:G:C8	2.45	0.51
1:1A:2137:C:H2'	1:1A:2138:C:C6	2.45	0.51
1:2A:886:C:H2'	1:2A:887:A:O4'	2.11	0.51
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.46	0.51
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.26	0.51
32:2a:977:A:O3'	32:2a:980:C:N4	2.44	0.51
32:2a:1272:G:N2	32:2a:1273:G:C8	2.78	0.51
34:2c:20:SER:HB3	34:2c:22:TRP:NE1	2.25	0.51
36:2e:28:PHE:O	36:2e:47:LYS:HA	2.11	0.51
51:2t:67:ALA:HA	51:2t:72:LEU:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:264:C:O2'	1:1A:265:A:H2'	2.11	0.51
21:1Z:103:ARG:O	21:1Z:139:VAL:N	2.42	0.51
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.93	0.51
1:2A:2171:A:N3	1:2A:2172:U:N3	2.59	0.51
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	1.92	0.51
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	1.93	0.51
25:23:8:LEU:HG	25:23:31:LEU:HD23	1.92	0.51
32:2a:748:C:H4'	32:2a:749:C:O5'	2.11	0.51
1:1A:249:C:O2	30:18:12:LYS:NZ	2.38	0.51
1:1A:2155:G:H5"	1:1A:2156:G:C8	2.46	0.51
26:14:56:VAL:HB	26:14:60:GLN:HG3	1.93	0.51
28:16:6:ARG:HD3	28:16:24:GLU:OE2	2.11	0.51
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.46	0.51
32:1a:674:G:OP1	37:1f:87:ARG:NH2	2.43	0.51
39:1h:73:ASP:OD1	39:1h:75:ARG:NE	2.43	0.51
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.74	0.51
1:2A:287:C:H2'	1:2A:288:C:H6	1.74	0.51
14:2S:77:ALA:HB1	14:2S:82:ILE:HB	1.93	0.51
33:2b:102:LEU:HB3	33:2b:180:LEU:HD12	1.92	0.51
1:1A:34:C:H5"	1:1A:35:G:OP2	2.11	0.51
1:1A:1095:A:N6	1:1A:1097:U:O2	2.43	0.51
1:1A:2277:G:OP2	22:10:10:THR:HG21	2.11	0.51
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.39	0.51
26:14:57:GLU:HB3	26:14:58:ARG:HG2	1.93	0.51
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.26	0.51
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.42	0.51
32:2a:67:C:H2'	32:2a:68:G:C8	2.46	0.51
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.46	0.51
1:1A:1057:A:H61	1:1A:1081:U:H3	1.58	0.50
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.44	0.50
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.43	0.50
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.46	0.50
1:2A:184:C:H2'	1:2A:185:U:C6	2.46	0.50
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.27	0.50
8:2I:88:ILE:HD11	8:2I:144:VAL:HG11	1.93	0.50
32:2a:1002:G:N3	32:2a:1003:G:H1'	2.26	0.50
32:2a:1002:G:N2	32:2a:1038:C:N3	2.54	0.50
32:2a:1124:G:N7	32:2a:1145:C:O2'	2.44	0.50
32:2a:1178:G:N2	32:2a:1181:G:OP2	2.34	0.50
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.46	0.50
44:2m:86:CYS:O	44:2m:89:GLY:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:43:LEU:HD13	51:2t:51:GLU:HB3	1.92	0.50
1:1A:1055:G:H3'	1:1A:1056:G:C8	2.45	0.50
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.92	0.50
12:1Q:78:PRO:HD3	55:1x:1:C:N3	2.26	0.50
21:1Z:158:PRO:O	21:1Z:161:VAL:HG22	2.11	0.50
32:1a:382:A:H2'	32:1a:383:A:C8	2.46	0.50
56:1y:5:G:H1'	56:1y:69:G:N2	2.26	0.50
1:2A:403:U:H4'	1:2A:404:C:H5'	1.93	0.50
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.76	0.50
4:2E:119:ARG:CD	4:2E:160:TYR:HB2	2.40	0.50
5:2F:10:PRO:HB3	5:2F:17:ARG:HH11	1.76	0.50
21:2Z:3:TYR:HB2	21:2Z:57:ILE:HD13	1.92	0.50
32:2a:1101:A:H62	33:2b:175:ARG:HH21	1.58	0.50
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.10	0.50
34:2c:30:ARG:HH21	45:2n:38:GLY:HA2	1.75	0.50
35:2d:173:TRP:CD2	35:2d:189:PRO:HB3	2.47	0.50
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.46	0.50
54:2w:34:G:H2'	54:2w:35:A:C8	2.46	0.50
54:2w:68:C:H2'	54:2w:69:G:H8	1.76	0.50
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.75	0.50
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.19	0.50
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	1.92	0.50
1:2A:892:G:H2'	1:2A:892:G:N3	2.27	0.50
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.28	0.50
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	1.93	0.50
7:2H:56:SER:HB3	7:2H:61:HIS:ND1	2.27	0.50
32:2a:76:C:N4	32:2a:93:G:H1	2.09	0.50
32:2a:1178:G:N2	32:2a:1180:A:H3'	2.27	0.50
33:2b:48:MET:HA	33:2b:51:LEU:HB2	1.93	0.50
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.93	0.50
56:2y:61:C:H2'	56:2y:62:C:C6	2.46	0.50
1:1A:1851:U:H2'	1:1A:1852:C:O4'	2.12	0.50
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.47	0.50
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.10	0.50
31:19:25:VAL:HB	31:19:34:GLN:HB2	1.93	0.50
32:1a:767:A:H2'	32:1a:768:A:O4'	2.11	0.50
34:1c:71:ALA:O	34:1c:73:PRO:HD3	2.11	0.50
38:1g:78:ARG:HH12	38:1g:156:TRP:HB3	1.76	0.50
46:1o:82:ILE:HD12	46:1o:88:ARG:HG3	1.94	0.50
1:2A:190:A:OP2	23:21:39:LYS:HE3	2.11	0.50
1:2A:307:G:H21	1:2A:330:A:H62	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.45	0.50
2:2B:94:C:H2'	2:2B:95:C:C6	2.47	0.50
9:2N:42:TRP:HA	9:2N:48:MET:SD	2.51	0.50
21:2Z:104:PHE:HA	21:2Z:139:VAL:HG22	1.92	0.50
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.47	0.50
56:2y:51:U:H3	56:2y:63:G:H1	1.60	0.50
1:1A:1059:G:H2'	1:1A:1060:U:C5	2.47	0.50
1:1A:1508:A:O2'	1:1A:1509:C:OP1	2.23	0.50
5:1F:103:LYS:HA	5:1F:106:ARG:HD3	1.92	0.50
7:1H:97:ARG:NE	7:1H:104:GLU:OE1	2.35	0.50
32:1a:328:C:H4'	32:1a:329:A:H5'	1.93	0.50
32:1a:1033:G:H3'	32:1a:1034:G:H8	1.76	0.50
32:1a:1060:C:H5"	41:1j:51:ARG:HG2	1.92	0.50
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.47	0.50
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.59	0.50
32:2a:1056:U:OP1	34:2c:163:ALA:N	2.38	0.50
1:1A:222:A:H5"	1:1A:421:U:OP1	2.11	0.50
1:1A:295:G:H4'	20:1Y:1:MET:HE3	1.93	0.50
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.47	0.50
6:1G:126:ASP:HB2	6:1G:130:ASN:O	2.11	0.50
26:14:63:TYR:N	26:14:63:TYR:CD1	2.79	0.50
32:1a:539:A:OP2	43:1l:115:LYS:NZ	2.35	0.50
33:1b:139:LYS:O	33:1b:143:GLU:HG3	2.12	0.50
34:1c:150:LYS:HG3	34:1c:169:ALA:HB2	1.94	0.50
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.77	0.50
1:2A:636:G:OP1	11:2P:132:LYS:HE2	2.12	0.50
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.10	0.50
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.26	0.50
1:2A:2619:C:OP1	4:2E:152:LYS:NZ	2.39	0.50
32:2a:1446:U:O4	64:2a:1905:HOH:O	2.15	0.50
1:1A:1013:C:OP2	64:1A:4110:HOH:O	2.19	0.50
6:1G:145:THR:OG1	6:1G:148:MET:SD	2.66	0.50
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.11	0.50
17:1V:98:GLU:CD	17:1V:100:ARG:HH11	2.19	0.50
26:14:43:TYR:O	26:14:45:GLY:N	2.43	0.50
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.75	0.50
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.44	0.50
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.28	0.50
1:2A:1645:G:H5"	1:2A:1646:C:H5'	1.93	0.50
1:2A:2331:G:O2'	22:20:43:THR:HG22	2.12	0.50
10:2O:77:ILE:HB	15:2T:74:ARG:HD2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.57	0.50
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.93	0.50
1:1A:576:U:H2'	1:1A:577:G:C8	2.46	0.50
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.46	0.50
35:1d:7:PRO:HB2	35:1d:10:ARG:HD2	1.93	0.50
46:1o:11:VAL:HG21	46:1o:34:LEU:HD22	1.94	0.50
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.94	0.50
1:2A:299:A:N1	1:2A:322:A:O2'	2.39	0.50
1:2A:332:A:O2'	1:2A:334:C:OP2	2.29	0.50
1:2A:2635:C:O2'	4:2E:80:GLU:OE2	2.19	0.50
7:2H:24:VAL:HG23	7:2H:35:VAL:HB	1.93	0.50
32:2a:419:C:OP1	32:2a:513:C:O2'	2.26	0.50
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.44	0.50
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.44	0.50
32:2a:1226:C:P	44:2m:91:ARG:HH12	2.35	0.50
34:2c:6:HIS:HB3	45:2n:49:HIS:CD2	2.47	0.50
34:2c:47:LEU:CD2	34:2c:68:VAL:HG11	2.42	0.50
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.46	0.50
41:2j:5:ARG:N	64:2j:302:HOH:O	2.45	0.50
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.27	0.50
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	1.93	0.50
8:1I:4:ILE:HG12	8:1I:18:VAL:HG12	1.94	0.50
32:1a:161:A:H2'	32:1a:162:A:C8	2.47	0.50
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	1.93	0.50
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.45	0.50
39:1h:17:THR:HG22	39:1h:63:LEU:HD13	1.93	0.50
1:2A:271(K):U:H4'	1:2A:271(L):U:OP1	2.12	0.50
3:2D:25:THR:HG21	3:2D:113:VAL:HG21	1.93	0.50
25:23:59:VAL:HG12	25:23:60:GLU:H	1.77	0.50
32:2a:1040:U:H2'	32:2a:1041:A:H8	1.77	0.50
32:2a:1265:G:C2	32:2a:1271:G:C2	3.00	0.50
34:2c:179:ARG:HH12	34:2c:206:GLU:CD	2.19	0.50
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	1.94	0.50
37:2f:97:PHE:HE2	49:2r:62:GLU:HG2	1.76	0.50
38:2g:78:ARG:HD3	38:2g:79:ARG:HG3	1.94	0.50
1:1A:55:G:O2'	1:1A:127:A:N1	2.38	0.49
1:1A:602:G:N1	1:1A:655:A:OP2	2.41	0.49
1:1A:2108:C:H2'	1:1A:2109:U:C6	2.45	0.49
1:1A:2243:U:OP1	64:1A:4112:HOH:O	2.19	0.49
7:1H:124:GLU:HG3	7:1H:132:ARG:HB3	1.94	0.49
1:2A:1287:A:H8	13:2R:104:ARG:HD3	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.27	0.49
1:2A:1840:G:OP2	64:2A:3938:HOH:O	2.19	0.49
1:2A:2365:G:OP1	22:20:55:ARG:N	2.43	0.49
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.92	0.49
32:2a:553:A:H5"	43:2l:24:VAL:HG21	1.93	0.49
32:2a:975:A:H5'	32:2a:975:A:H8	1.77	0.49
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.47	0.49
33:2b:126:GLU:CD	33:2b:126:GLU:H	2.19	0.49
34:2c:155:GLY:O	34:2c:157:ILE:N	2.45	0.49
54:2w:68:C:H2'	54:2w:69:G:C8	2.47	0.49
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.94	0.49
32:1a:219:C:H2'	32:1a:220:G:O4'	2.12	0.49
32:1a:486:U:H2'	32:1a:487:A:C8	2.47	0.49
32:1a:811:C:O2'	32:1a:901:A:N1	2.42	0.49
40:1i:70:LYS:O	40:1i:74:ILE:HG13	2.13	0.49
1:2A:224:G:H2'	1:2A:225:A:O4'	2.12	0.49
1:2A:764:A:H5"	3:2D:210:GLY:HA2	1.93	0.49
1:2A:2053:G:OP2	64:2A:3944:HOH:O	2.20	0.49
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	1.93	0.49
32:2a:445:G:H1	32:2a:489:C:H42	1.59	0.49
34:2c:39:ILE:HG22	34:2c:43:LEU:HD11	1.93	0.49
1:1A:593:G:H4'	30:18:4:MET:HE2	1.93	0.49
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.27	0.49
1:1A:1782:C:H1'	1:1A:2609:U:H5"	1.93	0.49
32:1a:100:C:H2'	32:1a:101:A:C8	2.47	0.49
32:1a:1003:G:C4	32:1a:1004:A:H2	2.30	0.49
33:1b:91:PRO:HG3	33:1b:154:LEU:HB3	1.94	0.49
1:2A:1622:G:OP2	64:2A:3943:HOH:O	2.19	0.49
1:2A:2129:C:N4	1:2A:2159:G:H1	2.10	0.49
2:2B:72:G:O2'	2:2B:105:A:N6	2.45	0.49
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.93	0.49
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.95	0.49
49:2r:25:THR:HB	49:2r:26:LEU:HD12	1.94	0.49
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.47	0.49
32:1a:421:U:O4	34:1c:127:ARG:NH2	2.41	0.49
32:1a:626:U:H2'	32:1a:627:G:H8	1.77	0.49
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.28	0.49
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.47	0.49
1:2A:236:C:H2'	1:2A:237:C:H6	1.76	0.49
1:2A:922:U:H2'	1:2A:923:C:C6	2.47	0.49
1:2A:1037:G:H2'	1:2A:1038:C:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2336:A:H61	22:20:43:THR:CG2	2.26	0.49
3:2D:71:ASP:CB	3:2D:103:ARG:HH12	2.26	0.49
9:2N:67:LEU:HA	9:2N:87:LEU:HD23	1.93	0.49
26:24:41:PRO:HG3	26:24:49:PHE:CE1	2.48	0.49
32:2a:560:U:H5'	32:2a:566:G:N2	2.27	0.49
32:2a:688:G:O2'	32:2a:704:A:N1	2.44	0.49
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.95	0.49
1:1A:1166:C:H2'	1:1A:1167:U:C6	2.48	0.49
1:1A:1851:U:H4'	56:1y:71:G:H4'	1.94	0.49
33:1b:93:VAL:HG11	33:1b:97:TRP:CD1	2.47	0.49
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.45	0.49
1:2A:2722:G:H5'	13:2R:4:LEU:HD12	1.93	0.49
6:2G:138:GLN:OE1	6:2G:138:GLN:N	2.45	0.49
11:2P:121:LYS:HB3	11:2P:123:LEU:HD12	1.94	0.49
15:2T:108:ARG:NH1	32:2a:1464:G:OP1	2.46	0.49
32:2a:1133:G:H1	32:2a:1141:C:N4	2.09	0.49
32:2a:1271:G:N2	32:2a:1272:G:N7	2.60	0.49
32:2a:1313:U:OP2	50:2s:5:LEU:HD13	2.13	0.49
34:2c:152:ILE:HG13	34:2c:199:LYS:HB2	1.94	0.49
1:1A:642:G:OP1	64:1A:4127:HOH:O	2.19	0.49
1:1A:918:A:N3	2:1B:80:U:O2'	2.39	0.49
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.45	0.49
4:2E:89:ASP:OD2	4:2E:89:ASP:N	2.44	0.49
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.29	0.49
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.95	0.49
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.94	0.49
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	1.95	0.49
1:1A:1468:C:OP1	64:1A:4125:HOH:O	2.20	0.49
1:1A:2680:C:H5'	4:1E:189:PRO:HA	1.95	0.49
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.47	0.49
32:1a:458:C:H2'	32:1a:460:G:O4'	2.13	0.49
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.38	0.49
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.13	0.49
2:2B:8:U:H6	2:2B:8:U:H5"	1.78	0.49
9:2N:71:ILE:HG21	9:2N:84:LYS:HB3	1.95	0.49
32:2a:56:U:H2'	32:2a:57:G:H8	1.78	0.49
32:2a:1146:A:H2'	32:2a:1147:C:O4'	2.13	0.49
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.13	0.49
54:2w:4:C:N3	54:2w:69:G:N2	2.48	0.49
1:1A:271(I):G:H1	1:1A:271(O):C:H42	1.61	0.49
1:1A:969:U:H2'	1:1A:970:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.28	0.49
8:1I:42:SER:OG	8:1I:43:ASN:N	2.46	0.49
32:1a:7:G:O2'	36:1e:120:THR:O	2.31	0.49
32:1a:890:G:O2'	32:1a:906:G:O6	2.29	0.49
32:1a:977:A:H1'	32:1a:982:U:O4	2.13	0.49
32:1a:1151:A:O4'	41:1j:39:PRO:HB2	2.13	0.49
33:1b:76:GLN:NE2	33:1b:206:ASP:OD1	2.46	0.49
42:1k:16:SER:O	42:1k:35:PRO:HD3	2.12	0.49
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.47	0.49
1:2A:2135:A:H2'	1:2A:2136:C:H5"	1.95	0.49
1:2A:2735:G:H2'	1:2A:2736:G:H8	1.77	0.49
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.78	0.49
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.77	0.49
54:2w:29:G:H1	54:2w:41:C:H42	1.61	0.49
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.13	0.49
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.94	0.49
32:1a:92:C:H2'	32:1a:93:G:C8	2.48	0.49
12:2Q:1:MET:HE1	12:2Q:45:GLN:HG3	1.94	0.49
36:2e:81:GLU:HG2	36:2e:90:VAL:HG22	1.94	0.49
40:2i:9:ARG:HA	40:2i:13:ALA:O	2.13	0.49
54:2w:14:A:H61	54:2w:21:A:H2	1.61	0.49
55:2x:19:G:H4'	55:2x:20:U:OP2	2.13	0.49
1:1A:443:A:C5	5:1F:45:ARG:HD2	2.48	0.49
2:1B:84:C:OP1	25:13:15:TYR:OH	2.27	0.49
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.61	0.49
32:1a:626:U:H2'	32:1a:627:G:C8	2.48	0.49
32:1a:684:A:N6	64:1a:1966:HOH:O	2.43	0.49
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.94	0.49
36:1e:41:VAL:HG23	36:1e:67:VAL:HG13	1.95	0.49
56:1y:66:U:H2'	56:1y:67:C:C6	2.48	0.49
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.27	0.49
5:2F:33:LEU:HD22	5:2F:112:MET:HE3	1.95	0.49
32:2a:179:A:H2'	32:2a:180:U:C6	2.48	0.49
32:2a:936:C:H2'	32:2a:937:A:O4'	2.13	0.49
32:2a:1026:G:O6	32:2a:1036:G:N2	2.46	0.49
32:2a:1161:C:H2'	32:2a:1162:C:C6	2.47	0.49
47:2p:18:ARG:HD3	47:2p:35:LYS:HD3	1.94	0.49
1:1A:616:G:H5'	5:1F:205:ARG:HD3	1.95	0.48
1:1A:1062:G:H8	1:1A:1070:A:H4'	1.78	0.48
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.78	0.48
2:1B:24:G:N7	2:1B:56:G:H2'	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:21:ARG:HH11	6:1G:21:ARG:CG	2.19	0.48
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	1.95	0.48
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.13	0.48
32:1a:31:G:O2'	32:1a:48:C:N4	2.46	0.48
32:1a:1030(A):G:H5'	32:1a:1030(B):C:OP2	2.13	0.48
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.94	0.48
54:1w:18:G:O2'	54:1w:57:G:N2	2.27	0.48
1:2A:2126:A:N3	1:2A:2127:G:H1'	2.28	0.48
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.13	0.48
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.47	0.48
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.48	0.48
33:2b:78:GLN:O	33:2b:94:ASN:ND2	2.37	0.48
54:2w:43:C:H2'	54:2w:44:G:C8	2.48	0.48
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.61	0.48
1:1A:1041:C:N4	1:1A:1114:G:H1	2.09	0.48
1:1A:1541:G:H3'	1:1A:1542:A:H2'	1.94	0.48
1:1A:2206:G:H8	1:1A:2207:G:N7	2.11	0.48
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.39	0.48
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.12	0.48
1:2A:652(C):G:N2	1:2A:653:A:H1'	2.28	0.48
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.48	0.48
1:2A:1038:C:N4	1:2A:1117:G:H1	2.11	0.48
1:2A:1243:G:O2'	11:2P:7:ARG:NH2	2.46	0.48
38:2g:78:ARG:HD3	38:2g:79:ARG:H	1.79	0.48
1:1A:1071:G:O2'	1:1A:1089:G:H2'	2.13	0.48
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.47	0.48
32:1a:109:A:H2'	32:1a:326:G:N2	2.28	0.48
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.95	0.48
56:1y:1:G:H1	56:1y:72:C:H42	1.59	0.48
1:2A:586:A:N1	1:2A:809:G:O2'	2.42	0.48
1:2A:653:A:H2'	1:2A:654:A:C8	2.49	0.48
1:2A:910:A:N1	1:2A:2277:G:H1'	2.28	0.48
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.94	0.48
8:2I:73:GLU:HG3	8:2I:138:ILE:HG23	1.95	0.48
12:2Q:16:ARG:HG3	12:2Q:18:LYS:HG3	1.95	0.48
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.94	0.48
32:2a:600:C:H2'	32:2a:601:C:C6	2.48	0.48
34:2c:131:ARG:NH2	36:2e:50:GLU:HG3	2.27	0.48
1:1A:1680:U:O2'	1:1A:1763:G:N7	2.37	0.48
1:1A:2153:G:H2'	1:1A:2154:G:C8	2.49	0.48
1:1A:2674:G:H5"	10:1O:26:LYS:HE3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2790:A:H3'	1:1A:2790:A:N3	2.28	0.48
6:1G:116:ASP:OD2	44:1m:68:GLY:HA3	2.12	0.48
26:14:20:ASN:OD1	26:14:21:VAL:N	2.46	0.48
32:1a:841:U:C4	32:1a:848:C:H1'	2.49	0.48
32:1a:1153:C:H2'	32:1a:1154:G:O4'	2.14	0.48
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.49	0.48
1:2A:2116:G:N1	1:2A:2162:G:OP1	2.46	0.48
1:2A:2299:G:H2'	1:2A:2300:G:H8	1.77	0.48
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.48	0.48
32:2a:316:G:OP2	32:2a:351:G:O2'	2.29	0.48
32:2a:841:U:C5	32:2a:848:C:H1'	2.48	0.48
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.46	0.48
1:1A:881:G:C2	1:1A:882:G:H1'	2.49	0.48
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	1.96	0.48
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.41	0.48
13:1R:12:ARG:O	13:1R:17:ARG:NH1	2.46	0.48
22:10:10:THR:HG22	22:10:12:ASN:N	2.16	0.48
32:1a:1027:C:C4	32:1a:1034:G:N1	2.81	0.48
32:1a:1137:C:H4'	32:1a:1138:G:C2	2.47	0.48
35:1d:13:ARG:HB3	35:1d:38:TYR:O	2.14	0.48
56:1y:5:G:N3	56:1y:69:G:C2	2.82	0.48
1:2A:699:A:H2'	1:2A:700:G:O4'	2.14	0.48
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.47	0.48
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.48	0.48
3:2D:123:ALA:HB3	3:2D:131:LEU:HG	1.94	0.48
7:2H:160:LYS:N	7:2H:163:TYR:OH	2.46	0.48
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.14	0.48
33:2b:48:MET:O	33:2b:52:GLU:N	2.44	0.48
52:2u:6:ARG:HA	52:2u:11:GLY:HA3	1.95	0.48
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.13	0.48
25:13:30:ARG:NH2	64:13:201:HOH:O	2.37	0.48
32:1a:1002:G:C5	32:1a:1003:G:H1'	2.49	0.48
1:2A:236:C:H2'	1:2A:237:C:C6	2.48	0.48
1:2A:324:A:N6	1:2A:338:G:O2'	2.45	0.48
1:2A:1187:G:H5"	17:2V:81:TYR:CE1	2.48	0.48
1:2A:1539:G:H2'	1:2A:1540:U:O4'	2.14	0.48
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.79	0.48
1:2A:2712:U:OP1	1:2A:2714:G:H4'	2.14	0.48
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.95	0.48
6:2G:50:ALA:O	6:2G:52:ILE:N	2.47	0.48
9:2N:59:LYS:O	9:2N:61:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:41:ARG:NH1	32:2a:346:G:OP1	2.41	0.48
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.14	0.48
33:2b:58:ILE:O	33:2b:62:ALA:N	2.39	0.48
1:1A:284:U:H2'	1:1A:285:C:C6	2.48	0.48
6:1G:107:LEU:HA	6:1G:111:LEU:HD12	1.96	0.48
8:1I:77:LEU:HB2	8:1I:142:VAL:HG12	1.94	0.48
32:1a:486:U:H2'	32:1a:487:A:H8	1.79	0.48
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.49	0.48
39:1h:39:LEU:HB3	39:1h:45:ILE:HG12	1.96	0.48
54:1w:66:U:O4	54:1w:67:C:N4	2.47	0.48
55:1x:23:C:H2'	55:1x:24:U:C6	2.49	0.48
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.48	0.48
32:2a:1194:U:H2'	32:2a:1195:C:C6	2.49	0.48
38:2g:137:LYS:O	38:2g:141:VAL:HG23	2.14	0.48
40:2i:23:ASN:ND2	40:2i:25:LYS:HE2	2.29	0.48
56:2y:52:G:H5'	56:2y:53:G:OP2	2.14	0.48
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.95	0.48
1:1A:2188:C:H2'	1:1A:2189:U:O4'	2.13	0.48
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.13	0.48
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.95	0.48
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.95	0.48
1:2A:2540:C:O2'	1:2A:2740:A:N3	2.44	0.48
32:2a:642:A:N3	39:2h:113:SER:OG	2.37	0.48
32:2a:977:A:O2'	32:2a:979:C:OP2	2.26	0.48
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.95	0.48
40:2i:17:VAL:HG11	40:2i:81:ILE:HA	1.96	0.48
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.79	0.48
1:1A:8:A:H2'	1:1A:9:U:C6	2.49	0.48
1:1A:2128:C:N4	1:1A:2160:G:N1	2.60	0.48
32:1a:382:A:H2'	32:1a:383:A:H8	1.79	0.48
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.49	0.48
32:1a:1198:G:N7	64:1a:1945:HOH:O	2.35	0.48
1:2A:141:A:H8	1:2A:1408:C:O2'	1.96	0.48
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.25	0.48
1:2A:2125:G:H1'	1:2A:2173:A:H61	1.78	0.48
3:2D:275:LYS:NZ	32:2a:775:G:OP1	2.46	0.48
12:2Q:24:GLY:HA2	12:2Q:67:ARG:NH2	2.29	0.48
26:24:16:CYS:SG	26:24:17:GLY:N	2.87	0.48
28:26:12:GLU:OE1	28:26:52:VAL:HG11	2.13	0.48
32:2a:109:A:C6	32:2a:326:G:C6	3.02	0.48
32:2a:662:G:H2'	32:2a:663:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:664:G:N2	32:2a:741:G:H1	2.10	0.48
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	1.94	0.48
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.79	0.48
54:2w:11:C:H2'	54:2w:12:U:C6	2.49	0.48
55:2x:53:G:H2'	55:2x:54:5MU:C6	2.48	0.48
1:1A:1062:G:H22	1:1A:1077:A:H61	1.62	0.48
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.48	0.48
10:1O:107:ARG:NH2	32:1a:346:G:OP2	2.47	0.48
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.96	0.48
32:1a:458:C:H42	32:1a:473:G:H1	1.60	0.48
32:1a:1503:A:N1	53:1v:12:A:H2	2.11	0.48
34:1c:85:ARG:O	34:1c:89:GLU:HG2	2.12	0.48
37:1f:99:ALA:HB1	49:1r:23:LYS:NZ	2.29	0.48
1:2A:774:A:H2'	1:2A:774:A:N3	2.29	0.48
1:2A:1287:A:C8	13:2R:104:ARG:HD3	2.49	0.48
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.49	0.48
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD21	1.94	0.48
32:2a:952:U:H2'	32:2a:953:G:H8	1.78	0.48
32:2a:1119:C:OP2	40:2i:9:ARG:NH2	2.47	0.48
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.49	0.48
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.47	0.48
1:1A:881:G:H3'	1:1A:882:G:H8	1.79	0.47
1:1A:907:U:OP2	64:1A:4134:HOH:O	2.20	0.47
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.50	0.47
1:1A:2359:C:H2'	1:1A:2360:A:O4'	2.14	0.47
33:1b:55:PHE:HD1	33:1b:221:LEU:HD13	1.78	0.47
1:2A:602:G:O2'	1:2A:655:A:N6	2.47	0.47
1:2A:856:C:H2'	1:2A:857:C:C6	2.49	0.47
1:2A:933:A:OP1	25:23:24:LYS:NZ	2.46	0.47
20:2Y:5:MET:HG2	20:2Y:30:VAL:HG11	1.95	0.47
32:2a:895:G:N7	64:2a:1922:HOH:O	2.36	0.47
47:2p:17:TYR:HE2	47:2p:41:PRO:HG3	1.79	0.47
56:2y:9:A:H5'	56:2y:46:G7M:O4'	2.13	0.47
1:1A:919:G:N2	1:1A:2269:A:OP2	2.44	0.47
1:1A:1693:U:H1'	3:1D:14:ARG:NH1	2.30	0.47
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.12	0.47
35:1d:165:MET:HE1	35:1d:170:VAL:HG12	1.96	0.47
50:1s:22:LEU:HD13	50:1s:29:ARG:H	1.79	0.47
32:2a:999:C:H42	32:2a:1042:G:H1	1.61	0.47
34:2c:40:ARG:HA	34:2c:43:LEU:HD12	1.96	0.47
34:2c:47:LEU:HD23	34:2c:70:VAL:HG11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:18:PHE:HD2	40:2i:62:TYR:HD2	1.61	0.47
42:2k:19:ALA:HB3	42:2k:82:VAL:HG22	1.96	0.47
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.79	0.47
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.64	0.47
32:1a:865:A:H2	32:1a:918:A:H4'	1.77	0.47
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.50	0.47
1:2A:2557:G:H2'	1:2A:2558:C:H6	1.79	0.47
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.43	0.47
4:2E:4:ILE:HD13	4:2E:28:ALA:HB1	1.95	0.47
9:2N:131:GLN:O	9:2N:134:ARG:HG3	2.15	0.47
14:2S:84:GLN:H	14:2S:111:GLU:HB2	1.79	0.47
32:2a:357:G:OP1	32:2a:367:U:H5"	2.12	0.47
32:2a:946:A:H2'	32:2a:947:G:C8	2.50	0.47
32:2a:986:A:H2'	32:2a:987:G:O4'	2.15	0.47
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.14	0.47
32:2a:1325:C:OP1	52:2u:15:ARG:NH1	2.47	0.47
32:2a:1376:U:OP1	38:2g:98:SER:OG	2.32	0.47
41:2j:89:ASP:O	41:2j:91:PRO:HD3	2.14	0.47
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.14	0.47
1:1A:1698:A:C8	1:1A:1700:A:O4'	2.67	0.47
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.49	0.47
2:1B:2:C:H2'	2:1B:3:C:C6	2.49	0.47
32:1a:576:G:O6	32:1a:880:C:O2'	2.28	0.47
34:1c:179:ARG:HG3	34:1c:206:GLU:HB3	1.96	0.47
50:1s:3:ARG:NE	50:1s:8:GLY:O	2.41	0.47
1:2A:616:G:H4'	5:2F:205:ARG:HE	1.79	0.47
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.29	0.47
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.49	0.47
4:2E:178:GLU:H	4:2E:178:GLU:CD	2.22	0.47
21:2Z:140:ASP:OD1	21:2Z:141:VAL:N	2.47	0.47
24:22:1:MET:N	24:22:52:ASP:OD2	2.44	0.47
32:2a:17:U:H2'	32:2a:18:C:C6	2.50	0.47
32:2a:544:G:P	35:2d:59:ARG:HH22	2.37	0.47
33:2b:58:ILE:HA	33:2b:61:LEU:HB3	1.97	0.47
34:2c:35:GLU:O	34:2c:39:ILE:HG13	2.14	0.47
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.47	0.47
55:2x:53:G:H2'	55:2x:54:5MU:H6	1.78	0.47
56:2y:8:4SU:O4'	56:2y:48:C:O2'	2.31	0.47
56:2y:15:G:H22	56:2y:48:C:H42	1.61	0.47
6:1G:47:LYS:C	6:1G:86:MET:HE2	2.39	0.47
8:1I:77:LEU:HD13	8:1I:79:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:45:U:H2'	32:1a:46:G:C8	2.49	0.47
32:1a:1005:A:O2'	32:1a:1037:C:O2	2.30	0.47
32:1a:1329:A:H5"	44:1m:26:GLY:H	1.78	0.47
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.15	0.47
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.94	0.47
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.50	0.47
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.50	0.47
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.40	0.47
21:2Z:54:HIS:HB3	21:2Z:101:PRO:HD3	1.96	0.47
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.47	0.47
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.78	0.47
1:1A:84:A:H5"	20:1Y:8:LYS:HE3	1.97	0.47
1:1A:1075:C:C2'	1:1A:1076:C:H5'	2.44	0.47
32:1a:271:C:H2'	32:1a:272:C:C6	2.49	0.47
32:1a:973:G:H3'	32:1a:974:A:H5"	1.97	0.47
32:1a:1007:C:H2'	32:1a:1008:C:C6	2.50	0.47
34:1c:73:PRO:O	34:1c:77:ILE:HG12	2.15	0.47
35:1d:49:ARG:NH1	64:1d:401:HOH:O	2.47	0.47
1:2A:881:G:H3'	1:2A:882:G:H8	1.79	0.47
1:2A:2723:C:OP2	4:2E:109:LYS:NZ	2.48	0.47
19:2X:48:LYS:HE2	24:22:30:ARG:HH22	1.79	0.47
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.79	0.47
32:2a:107:G:H2'	32:2a:108:G:O4'	2.15	0.47
32:2a:1272:G:H5'	32:2a:1273:G:OP2	2.14	0.47
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.97	0.47
40:2i:80:GLY:O	40:2i:84:ALA:N	2.42	0.47
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.96	0.47
44:2m:34:LEU:O	44:2m:38:GLY:N	2.47	0.47
48:2q:95:TYR:HA	48:2q:98:LEU:HG	1.96	0.47
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.50	0.47
1:1A:657:U:H2'	1:1A:658:C:C6	2.50	0.47
1:1A:763:G:OP1	64:1A:4133:HOH:O	2.20	0.47
1:1A:839:U:H2'	1:1A:840:C:C6	2.49	0.47
1:1A:1268:A:C2	1:1A:2013:A:C4	3.03	0.47
1:1A:2203:U:O4'	3:1D:151:LYS:HE2	2.14	0.47
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.48	0.47
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.49	0.47
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.96	0.47
8:1I:109:ILE:HD12	8:1I:130:TYR:CE2	2.50	0.47
15:1T:127:ALA:O	15:1T:128:GLU:HB3	2.14	0.47
32:1a:129(A):G:C6	32:1a:189(E):U:H4'	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:538:G:H5”	43:1l:114:LYS:HB2	1.97	0.47
32:1a:743:U:H2’	32:1a:744:C:C6	2.50	0.47
32:1a:1277:C:O2’	32:1a:1279:A:H8	1.98	0.47
35:1d:60:GLU:OE2	35:1d:63:LYS:NZ	2.37	0.47
44:1m:15:VAL:HG13	44:1m:43:THR:O	2.15	0.47
1:2A:411:G:C5	11:2P:72:PRO:HB3	2.50	0.47
1:2A:579:G:H2’	1:2A:580:C:C6	2.49	0.47
1:2A:1971:A:OP1	64:2A:3946:HOH:O	2.20	0.47
1:2A:2010:G:H5”	18:2W:42:ARG:HB2	1.96	0.47
1:2A:2836:U:H2’	1:2A:2837:G:C8	2.50	0.47
5:2F:20:LEU:HG	5:2F:21:ALA:H	1.80	0.47
8:2I:72:LEU:HA	8:2I:75:LEU:HD12	1.96	0.47
16:2U:9:VAL:O	16:2U:13:LYS:HG3	2.14	0.47
20:2Y:15:VAL:HG21	20:2Y:42:VAL:HG11	1.97	0.47
28:26:12:GLU:OE1	28:26:19:ARG:NH1	2.48	0.47
32:2a:109:A:H2’	32:2a:326:G:N2	2.30	0.47
32:2a:974:A:P	45:2n:29:ARG:HH21	2.37	0.47
32:2a:1128:C:O2’	32:2a:1129:C:OP1	2.32	0.47
36:2e:20:GLN:HE21	36:2e:21:ALA:N	2.13	0.47
47:2p:6:LEU:HD23	47:2p:17:TYR:CG	2.49	0.47
51:2t:64:ASP:CG	51:2t:81:LYS:HZ2	2.23	0.47
1:1A:800:A:H8	1:1A:800:A:OP1	1.97	0.47
19:1X:92:LEU:O	19:1X:94:GLY:N	2.47	0.47
23:11:89:GLU:O	23:11:93:GLU:HG2	2.14	0.47
26:14:34:GLU:HG2	26:14:35:VAL:HG12	1.97	0.47
32:1a:160:A:H2’	32:1a:161:A:O4’	2.15	0.47
32:1a:838:G:H1	32:1a:848:C:N4	2.12	0.47
32:1a:869:G:OP2	64:1a:1915:HOH:O	2.20	0.47
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.13	0.47
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.30	0.47
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.97	0.47
1:2A:1364:G:P	23:21:3:LYS:HG3	2.54	0.47
1:2A:2774:C:H2’	1:2A:2775:A:O4’	2.15	0.47
6:2G:67:LYS:HD3	26:24:5:ILE:HD12	1.97	0.47
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.96	0.47
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HG23	1.97	0.47
32:2a:646:U:H2’	32:2a:647:C:H6	1.80	0.47
33:2b:8:LYS:O	33:2b:11:LEU:HD22	2.14	0.47
36:2e:76:ILE:O	36:2e:93:PRO:HB3	2.15	0.47
1:1A:774:A:N3	1:1A:774:A:H2’	2.29	0.47
1:1A:862:G:H2’	1:1A:863:A:O4’	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1230:C:H2'	1:1A:1231:G:H8	1.79	0.47
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.50	0.47
33:1b:134:GLU:HA	33:1b:137:ARG:NE	2.27	0.47
1:2A:176:G:O2'	1:2A:177:G:H5'	2.15	0.47
1:2A:667:U:O2	30:28:2:PRO:HD2	2.15	0.47
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.32	0.47
1:2A:1766:U:H2'	1:2A:1767:C:H6	1.80	0.47
5:2F:148:LEU:HD13	5:2F:154:VAL:HG21	1.97	0.47
21:2Z:171:ILE:CD1	21:2Z:172:ALA:H	2.21	0.47
32:2a:429:U:O3'	35:2d:22:LYS:NZ	2.38	0.47
32:2a:757:U:H2'	32:2a:758:G:O4'	2.14	0.47
32:2a:947:G:H1	32:2a:1234:C:H42	1.61	0.47
32:2a:1130:A:H5"	40:2i:18:PHE:CE2	2.49	0.47
33:2b:8:LYS:HB3	33:2b:217:ARG:HG3	1.97	0.47
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.83	0.47
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.15	0.47
44:2m:20:THR:C	44:2m:22:ILE:H	2.22	0.47
1:1A:586:A:N1	1:1A:809:G:O2'	2.40	0.47
1:1A:1062:G:O5'	1:1A:1070:A:O2'	2.33	0.47
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.30	0.47
1:1A:2079:U:O3'	23:11:35:THR:OG1	2.33	0.47
1:1A:2470:G:P	12:1Q:56:ARG:HH12	2.37	0.47
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.49	0.47
1:1A:2751:G:C4	7:1H:2:SER:HA	2.49	0.47
5:1F:165:ARG:HA	5:1F:168:ARG:HD2	1.97	0.47
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.97	0.47
11:1P:37:GLY:C	11:1P:38:GLN:O	2.58	0.47
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.50	0.47
50:1s:44:MET:HB3	50:1s:62:ILE:HD13	1.97	0.47
1:2A:478:A:N1	1:2A:500:G:H4'	2.30	0.47
1:2A:1790:C:H5"	1:2A:1791:A:OP1	2.14	0.47
1:2A:2853:C:H2'	1:2A:2854:G:H8	1.79	0.47
2:2B:54:G:H21	6:2G:29:TRP:HE1	1.61	0.47
13:2R:87:TYR:OH	13:2R:116:LEU:HB3	2.14	0.47
21:2Z:138:GLU:HG2	21:2Z:156:LYS:HE2	1.96	0.47
24:22:62:THR:O	24:22:66:GLU:HG3	2.13	0.47
32:2a:939:G:H1	32:2a:1344:C:H42	1.63	0.47
32:2a:955:U:O2'	50:2s:83:HIS:HD2	1.98	0.47
55:2x:50:U:H2'	55:2x:51:C:C6	2.50	0.47
56:2y:37:MIA:H2'	56:2y:38:A:O4'	2.15	0.47
1:1A:370:G:H8	1:1A:370:G:OP2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.50	0.46
1:1A:2583:G:O2'	54:1w:76:8AN:N1	2.47	0.46
1:1A:2685:G:H5'	10:1O:68:GLU:OE2	2.15	0.46
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	1.96	0.46
11:1P:2:LYS:HG2	11:1P:3:LEU:N	2.29	0.46
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.50	0.46
1:2A:651:G:OP1	30:28:19:SER:OG	2.32	0.46
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.15	0.46
1:2A:1257:C:H4'	5:2F:83:PHE:CD1	2.51	0.46
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.14	0.46
12:2Q:1:MET:HB3	12:2Q:1:MET:HE2	1.55	0.46
13:2R:8:ARG:HE	13:2R:43:GLU:HG2	1.80	0.46
14:2S:61:ASN:O	14:2S:64:GLU:HG3	2.15	0.46
19:2X:94:GLY:N	19:2X:95:LEU:HB2	2.28	0.46
33:2b:113:HIS:O	33:2b:117:GLU:HB2	2.15	0.46
38:2g:65:ALA:O	38:2g:69:VAL:HG23	2.15	0.46
47:2p:28:ARG:HG2	47:2p:29:ASP:OD1	2.15	0.46
47:2p:71:ARG:HG3	47:2p:80:PHE:HE2	1.80	0.46
1:1A:1108:U:H2'	1:1A:1109:C:O4'	2.15	0.46
21:1Z:72:ARG:HA	21:1Z:72:ARG:HD3	1.67	0.46
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.40	0.46
32:1a:1029:C:H41	32:1a:1030(A):G:H21	1.63	0.46
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.50	0.46
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.63	0.46
51:1t:90:GLN:HA	51:1t:93:GLU:HG2	1.96	0.46
1:2A:287:C:H2'	1:2A:288:C:C6	2.50	0.46
1:2A:839:U:H2'	1:2A:840:C:C6	2.49	0.46
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.98	0.46
1:1A:625:G:N7	11:1P:107:LYS:NZ	2.62	0.46
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.15	0.46
13:1R:104:ARG:HB2	13:1R:111:LEU:HD21	1.97	0.46
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.50	0.46
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.23	0.46
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.48	0.46
33:1b:152:PHE:CE1	33:1b:155:LEU:HD23	2.50	0.46
34:1c:177:THR:HG22	34:1c:180:ALA:H	1.81	0.46
54:1w:26:A:N6	54:1w:44:G:H1	2.12	0.46
1:2A:93:G:H2'	1:2A:94:C:C6	2.50	0.46
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.50	0.46
1:2A:2597:G:OP1	64:2A:3945:HOH:O	2.20	0.46
2:2B:3:C:H2'	2:2B:4:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.97	0.46
31:29:2:LYS:HE2	31:29:31:LYS:O	2.15	0.46
32:2a:653:A:OP1	39:2h:56:LYS:NZ	2.49	0.46
32:2a:1131:G:H2'	32:2a:1132:C:C6	2.50	0.46
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.16	0.46
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.97	0.46
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.47	0.46
1:1A:1104:C:H2'	1:1A:1105:U:C6	2.50	0.46
1:1A:1113:U:H2'	1:1A:1114:G:H8	1.79	0.46
1:1A:1174:A:H1'	1:1A:1175:U:C5'	2.45	0.46
1:1A:1876:A:H2'	1:1A:1877:A:C8	2.49	0.46
32:1a:165:C:H2'	32:1a:166:G:H8	1.80	0.46
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.29	0.46
32:1a:999:C:H42	32:1a:1042:G:H1	1.63	0.46
44:1m:67:GLU:HG3	44:1m:71:ARG:NH2	2.29	0.46
1:2A:38:A:H2'	1:2A:39:C:C6	2.50	0.46
1:2A:141:A:C8	1:2A:1408:C:O2'	2.67	0.46
1:2A:2371:G:O2'	28:26:46:HIS:ND1	2.40	0.46
1:2A:2747:G:O6	1:2A:2755:C:H5"	2.15	0.46
2:2B:51:G:OP2	14:2S:61:ASN:HA	2.16	0.46
11:2P:121:LYS:HB3	11:2P:123:LEU:CD1	2.46	0.46
32:2a:7:G:H5'	32:2a:298:A:O4'	2.15	0.46
32:2a:457:C:H2'	32:2a:458:C:C6	2.49	0.46
32:2a:1055:A:N7	32:2a:1200:C:N4	2.58	0.46
40:2i:3:GLN:NE2	40:2i:20:ARG:HE	2.14	0.46
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	1.96	0.46
44:2m:23:TYR:CE2	44:2m:71:ARG:HG3	2.50	0.46
44:2m:90:LEU:HG	44:2m:93:ARG:HE	1.80	0.46
1:1A:363:G:H2'	1:1A:363(A):A:H8	1.79	0.46
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.50	0.46
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.50	0.46
4:1E:33:VAL:HG13	4:1E:47:VAL:HG23	1.97	0.46
32:1a:713:G:H2'	32:1a:714:G:C8	2.50	0.46
32:1a:828:A:H2'	32:1a:829:G:O4'	2.14	0.46
32:1a:1104:G:O5'	33:1b:111:ARG:HD2	2.16	0.46
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.15	0.46
36:1e:24:ARG:H	36:1e:24:ARG:HG2	1.53	0.46
1:2A:796:C:H2'	1:2A:797:C:C6	2.51	0.46
1:2A:1582:C:H2'	1:2A:1583:A:H8	1.81	0.46
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.50	0.46
1:2A:2096:U:H2'	1:2A:2097:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2334:G:H5'	14:2S:9:ARG:HG2	1.98	0.46
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.41	0.46
9:2N:123:TYR:CZ	9:2N:129:PRO:HD2	2.51	0.46
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.49	0.46
31:29:2:LYS:HD3	31:29:4:ARG:NH2	2.30	0.46
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.30	0.46
33:2b:93:VAL:HG11	33:2b:97:TRP:HE3	1.80	0.46
35:2d:12:CYS:HB2	61:2d:303:SF4:S2	2.55	0.46
35:2d:122:ARG:HD2	35:2d:122:ARG:HA	1.64	0.46
35:2d:176:LEU:HD12	35:2d:182:LYS:O	2.15	0.46
37:2f:33:TYR:HE2	37:2f:78:GLU:HG2	1.81	0.46
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.51	0.46
1:1A:11:G:H2'	1:1A:12:U:C5'	2.46	0.46
1:1A:875:G:H1	1:1A:902:C:H42	1.63	0.46
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.15	0.46
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.15	0.46
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.51	0.46
3:1D:183:ARG:HG3	3:1D:270:ILE:HD13	1.97	0.46
17:1V:71:LEU:HD23	17:1V:71:LEU:HA	1.83	0.46
26:14:57:GLU:HA	26:14:58:ARG:HA	1.58	0.46
32:1a:123:C:OP1	32:1a:311:C:O2'	2.30	0.46
32:1a:438:G:H4'	35:1d:123:HIS:ND1	2.30	0.46
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.40	0.46
32:1a:1288:A:H2'	32:1a:1289:A:C8	2.50	0.46
33:1b:160:ASP:O	33:1b:183:PRO:HD2	2.16	0.46
1:2A:492:A:H2'	1:2A:493:G:O4'	2.15	0.46
1:2A:876:C:H2'	1:2A:877:U:O4'	2.15	0.46
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.16	0.46
4:2E:176:ILE:HD12	4:2E:181:LEU:HB3	1.98	0.46
8:2I:88:ILE:HG22	8:2I:90:GLY:H	1.81	0.46
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.96	0.46
13:2R:72:ASP:O	13:2R:76:VAL:HG23	2.16	0.46
32:2a:646:U:H2'	32:2a:647:C:C6	2.50	0.46
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.51	0.46
1:1A:272(G):C:H42	1:1A:363(C):G:H1	1.63	0.46
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.96	0.46
6:1G:57:ALA:HA	6:1G:68:PRO:HG2	1.98	0.46
26:14:49:PHE:HB3	26:14:50:VAL:H	1.55	0.46
32:1a:250:A:H4'	32:1a:251:G:O5'	2.14	0.46
56:1y:66:U:C4	56:1y:67:C:C4	3.04	0.46
1:2A:1034:G:O6	64:2A:3947:HOH:O	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.97	0.46
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.16	0.46
5:2F:116:ASP:O	5:2F:120:GLU:HG2	2.15	0.46
6:2G:7:LEU:HD23	6:2G:100:TRP:CE3	2.50	0.46
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.49	0.46
16:2U:27:LEU:HB3	16:2U:31:SER:HB3	1.97	0.46
18:2W:2:GLU:OE2	18:2W:72:LYS:NZ	2.26	0.46
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.96	0.46
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.15	0.46
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.50	0.46
1:1A:821:A:H2'	1:1A:946:G:H5"	1.98	0.46
1:1A:1740:G:H2'	1:1A:1741:A:C8	2.51	0.46
12:1Q:89:ASN:HB2	55:1x:1:C:N3	2.30	0.46
21:1Z:40:ASP:HB3	21:1Z:43:GLU:HB2	1.96	0.46
21:1Z:156:LYS:HG3	21:1Z:158:PRO:HD3	1.97	0.46
28:16:11:LEU:HB3	28:16:49:HIS:HB3	1.97	0.46
32:1a:26:A:O2'	35:1d:209:ARG:NH2	2.49	0.46
37:1f:86:ARG:O	37:1f:87:ARG:HG2	2.15	0.46
47:1p:22:THR:HA	47:1p:33:ILE:HD12	1.98	0.46
1:2A:153:C:H2'	1:2A:154:G:O4'	2.15	0.46
1:2A:2129:C:N4	1:2A:2159:G:N1	2.64	0.46
6:2G:5:VAL:HG23	6:2G:8:LYS:H	1.80	0.46
15:2T:74:ARG:HG2	15:2T:76:PHE:CZ	2.51	0.46
32:2a:130:A:O2'	32:2a:131:C:O5'	2.28	0.46
32:2a:160:A:H1'	32:2a:344:A:C5	2.51	0.46
32:2a:779:C:H2'	32:2a:780:A:O4'	2.15	0.46
32:2a:1469:G:H2'	32:2a:1470:G:C8	2.51	0.46
33:2b:74:LYS:NZ	33:2b:206:ASP:OD1	2.49	0.46
33:2b:167:PRO:HD3	33:2b:187:LEU:O	2.16	0.46
34:2c:121:ALA:HB1	34:2c:188:LEU:O	2.15	0.46
42:2k:98:LEU:O	42:2k:101:SER:OG	2.20	0.46
55:2x:21:A:N6	55:2x:46:G:H2'	2.30	0.46
1:1A:363(A):A:H2'	1:1A:363(B):G:H8	1.80	0.46
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.51	0.46
32:1a:299:G:C6	32:1a:300:A:C6	3.04	0.46
32:1a:948:C:OP1	44:1m:109:THR:OG1	2.34	0.46
32:1a:1181:G:O2'	32:1a:1182:G:N7	2.47	0.46
33:1b:166:ASP:O	33:1b:170:GLU:N	2.49	0.46
38:1g:51:GLN:O	38:1g:55:GLY:HA2	2.16	0.46
48:1q:87:LYS:HA	48:1q:87:LYS:HD3	1.66	0.46
1:2A:1155:A:OP1	16:2U:55:ARG:HD3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2127:G:H22	1:2A:2160:G:H1	1.64	0.46
2:2B:9:G:H1	2:2B:112:U:H3	1.64	0.46
2:2B:83:G:H5"	25:23:52:HIS:CD2	2.51	0.46
12:2Q:30:GLY:HA2	12:2Q:107:ALA:HB2	1.98	0.46
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	1.97	0.46
32:2a:1502:A:C8	32:2a:1505:G:N2	2.84	0.46
38:2g:49:ILE:O	38:2g:53:LYS:HG3	2.15	0.46
44:2m:33:ALA:HB2	44:2m:64:TRP:CH2	2.51	0.46
56:2y:15:G:H22	56:2y:48:C:N4	2.14	0.46
1:1A:818:G:H4'	1:1A:838:C:O3'	2.15	0.46
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	1.98	0.46
40:1i:11:LYS:C	40:1i:13:ALA:H	2.24	0.46
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.16	0.46
1:2A:646:A:H2'	1:2A:647:G:O4'	2.16	0.46
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.25	0.46
1:2A:2150:U:H2'	1:2A:2151:G:H8	1.80	0.46
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.80	0.46
4:2E:12:THR:HG22	4:2E:13:ARG:H	1.79	0.46
4:2E:55:ASN:HD22	4:2E:57:LYS:H	1.64	0.46
12:2Q:63:LYS:HG2	12:2Q:65:PHE:CE2	2.51	0.46
26:24:57:GLU:CB	26:24:58:ARG:HD3	2.45	0.46
32:2a:23:C:H5	32:2a:561:U:O4	1.98	0.46
32:2a:986:A:H1'	50:2s:54:GLY:O	2.16	0.46
37:2f:76:ALA:HB1	37:2f:80:ARG:HH22	1.80	0.46
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.16	0.46
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.50	0.46
47:2p:21:VAL:HG22	47:2p:33:ILE:HB	1.98	0.46
1:1A:247:G:H4'	1:1A:386:G:C5	2.50	0.45
1:1A:1225:G:OP1	17:1V:69:LYS:NZ	2.41	0.45
8:1I:78:THR:HA	8:1I:143:SER:OG	2.16	0.45
11:1P:90:ARG:NH1	11:1P:105:LEU:HD11	2.30	0.45
23:11:85:LEU:HD23	23:11:89:GLU:HB3	1.98	0.45
32:1a:341:C:H2'	32:1a:342:C:H6	1.81	0.45
32:1a:1006:C:H42	32:1a:1023:G:H1	1.63	0.45
32:1a:1054:C:C5	54:1w:34:G:H1'	2.51	0.45
54:1w:18:G:HO2'	54:1w:57:G:H22	1.57	0.45
1:2A:214:G:O2'	1:2A:215:G:O4'	2.30	0.45
1:2A:2508:G:O3'	1:2A:2555:U:H5'	2.16	0.45
2:2B:88:C:H2'	2:2B:89:G:O4'	2.16	0.45
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.98	0.45
32:2a:1130:A:H5"	40:2i:18:PHE:HE2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.16	0.45
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.51	0.45
1:1A:858:U:O2	1:1A:2268:A:H2'	2.15	0.45
1:1A:1062:G:P	1:1A:1070:A:H1'	2.56	0.45
1:1A:1721:G:H1'	1:1A:1741:A:H61	1.80	0.45
1:1A:1837:C:OP1	32:1a:784:C:H4'	2.16	0.45
1:1A:2151:G:H2'	1:1A:2152:G:C8	2.52	0.45
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.49	0.45
4:1E:119:ARG:HD2	4:1E:160:TYR:HB2	1.98	0.45
8:1I:61:ARG:HD3	8:1I:61:ARG:HA	1.66	0.45
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.97	0.45
32:1a:236:G:H5"	48:1q:42:TYR:OH	2.16	0.45
32:1a:952:U:H2'	32:1a:953:G:H8	1.80	0.45
34:1c:47:LEU:HD13	34:1c:68:VAL:HG11	1.98	0.45
35:1d:155:LEU:H	35:1d:158:ILE:HD11	1.81	0.45
1:2A:1478:G:O2'	1:2A:1558:A:N1	2.45	0.45
1:2A:2137:C:N3	1:2A:2154:G:N2	2.50	0.45
14:2S:3:ARG:HD2	14:2S:3:ARG:HA	1.68	0.45
32:2a:109:A:H5'	32:2a:110:C:H5	1.81	0.45
32:2a:302:G:N3	32:2a:556:C:H4'	2.32	0.45
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.48	0.45
32:2a:707:C:OP1	42:2k:85:ARG:NH1	2.49	0.45
32:2a:1401:G:OP1	53:2v:18:G:O2'	2.28	0.45
32:2a:1452:C:H5'	32:2a:1457:G:H1'	1.98	0.45
33:2b:16:HIS:C	33:2b:18:GLY:H	2.24	0.45
33:2b:76:GLN:NE2	33:2b:76:GLN:H	2.14	0.45
1:1A:185:U:H4'	1:1A:218:A:H4'	1.98	0.45
1:1A:710:G:H2'	1:1A:711:G:H8	1.82	0.45
1:1A:749:C:H4'	1:1A:1271:G:N3	2.31	0.45
1:1A:920:G:O6	64:1A:4132:HOH:O	2.20	0.45
1:1A:1274:A:N3	1:1A:1297:C:H1'	2.31	0.45
1:1A:2235:G:H2'	1:1A:2236:C:C6	2.51	0.45
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.51	0.45
2:1B:75:G:H22	21:1Z:73:GLN:NE2	2.14	0.45
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.98	0.45
8:1I:77:LEU:HA	8:1I:77:LEU:HD23	1.69	0.45
13:1R:97:VAL:CG2	13:1R:114:VAL:HG13	2.45	0.45
25:13:39:ASP:OD1	25:13:44:ARG:HD2	2.16	0.45
34:1c:30:ARG:NH1	45:1n:35:ARG:O	2.47	0.45
1:2A:749:C:O2	1:2A:1618:A:H2'	2.16	0.45
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.16	0.45
2:2B:105:A:P	21:2Z:72:ARG:HE	2.38	0.45
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.79	0.45
32:2a:157:G:H1	32:2a:164:U:H3	1.64	0.45
32:2a:222:U:H2'	32:2a:223:U:H6	1.80	0.45
32:2a:373:A:O2'	32:2a:451:A:N7	2.49	0.45
32:2a:1178:G:OP1	40:2i:93:ARG:NH1	2.48	0.45
32:2a:1285:A:H5'	32:2a:1286:A:C2	2.52	0.45
34:2c:47:LEU:HD22	34:2c:68:VAL:HG11	1.98	0.45
50:2s:64:GLU:CD	50:2s:64:GLU:H	2.23	0.45
1:1A:388:G:O2'	1:1A:389:G:N7	2.46	0.45
1:1A:2058:MA6:H92	64:1A:5373:HOH:O	2.17	0.45
1:1A:2167:U:O2	1:1A:2167:U:H2'	2.16	0.45
26:14:58:ARG:O	26:14:61:ARG:HB3	2.17	0.45
32:1a:148:G:H2'	32:1a:149:A:C8	2.51	0.45
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.50	0.45
32:1a:1004:A:H5"	32:1a:1025:U:C5	2.51	0.45
33:1b:19:HIS:HA	33:1b:39:ILE:CG2	2.46	0.45
33:1b:71:VAL:HG13	33:1b:93:VAL:HG13	1.99	0.45
33:1b:157:ARG:HB3	33:1b:157:ARG:NH1	2.32	0.45
1:2A:1301:A:H2	1:2A:1626:G:N3	2.14	0.45
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	1.98	0.45
1:2A:2058:MA6:H101	64:2A:3956:HOH:O	2.15	0.45
1:2A:2751:G:H8	7:2H:2:SER:HA	1.81	0.45
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.16	0.45
7:2H:7:LEU:HD12	7:2H:8:PRO:HD2	1.99	0.45
32:2a:333:G:H4'	51:2t:16:HIS:CE1	2.51	0.45
32:2a:427:U:OP1	35:2d:13:ARG:NH1	2.48	0.45
32:2a:1040:U:H2'	32:2a:1041:A:C8	2.51	0.45
32:2a:1381:U:O2'	38:2g:79:ARG:HD3	2.16	0.45
33:2b:97:TRP:HH2	33:2b:102:LEU:HD13	1.79	0.45
36:2e:105:VAL:HB	36:2e:106:PRO:HD3	1.99	0.45
44:2m:16:ASP:OD1	44:2m:17:VAL:N	2.50	0.45
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.51	0.45
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.81	0.45
21:1Z:137:ILE:HA	21:1Z:156:LYS:HE2	1.98	0.45
32:1a:96:U:H2'	32:1a:97:G:H8	1.80	0.45
32:1a:1037:C:H2'	32:1a:1038:C:H6	1.81	0.45
33:1b:169:LYS:O	33:1b:169:LYS:HD3	2.17	0.45
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.98	0.45
1:2A:747:U:O2	1:2A:2014:A:H1'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:49:ARG:NH2	32:2a:1423:G:OP1	2.41	0.45
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.35	0.45
32:2a:16:A:N3	32:2a:1080:A:O2'	2.44	0.45
40:2i:8:GLY:O	40:2i:15:ALA:N	2.48	0.45
40:2i:47:LEU:H	40:2i:47:LEU:HG	1.64	0.45
40:2i:55:ALA:HA	40:2i:58:HIS:CD2	2.50	0.45
40:2i:85:LEU:HB3	40:2i:92:TYR:HD2	1.82	0.45
43:2l:90:VAL:O	43:2l:92:0TD:N	2.50	0.45
51:2t:77:ALA:O	51:2t:81:LYS:HG3	2.17	0.45
1:1A:829:A:N7	1:1A:2248:C:H5'	2.31	0.45
1:1A:2094:G:OP1	8:1I:22:LYS:HD2	2.16	0.45
1:1A:2849:U:P	15:1T:95:ARG:HH12	2.39	0.45
5:1F:170:LEU:HD13	5:1F:172:TRP:CZ2	2.52	0.45
6:1G:179:PRO:HG3	26:14:43:TYR:CZ	2.51	0.45
8:1I:87:LYS:HE3	8:1I:87:LYS:HB2	1.86	0.45
10:1O:63:VAL:HG12	10:1O:106:LEU:HD21	1.99	0.45
26:14:13:ARG:HB3	26:14:30:GLU:HG2	1.97	0.45
32:1a:115:G:H4'	32:1a:116:A:O5'	2.16	0.45
32:1a:270:A:H2'	32:1a:271:C:O4'	2.16	0.45
32:1a:381:C:H2'	32:1a:382:A:O4'	2.16	0.45
32:1a:404:U:OP1	35:1d:118:ARG:NH1	2.49	0.45
32:1a:952:U:H2'	32:1a:953:G:C8	2.52	0.45
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.98	0.45
40:1i:128:ARG:NH2	55:1x:33:U:OP2	2.46	0.45
50:1s:81:ARG:HE	50:1s:81:ARG:HB3	1.56	0.45
1:2A:639:U:H2'	1:2A:640:C:C6	2.52	0.45
1:2A:904:C:H4'	21:2Z:169:GLU:OE2	2.16	0.45
1:2A:909:A:C6	1:2A:912:C:C2	3.05	0.45
1:2A:988:A:N7	64:2A:4005:HOH:O	2.36	0.45
1:2A:1490:A:O2'	3:2D:99:ASP:OD1	2.34	0.45
1:2A:2128:C:H6	1:2A:2128:C:O5'	1.99	0.45
11:2P:8:PRO:HB2	11:2P:12:ALA:HB3	1.98	0.45
32:2a:114:U:O2'	32:2a:115:G:H5'	2.16	0.45
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.32	0.45
32:2a:952:U:H2'	32:2a:953:G:C8	2.52	0.45
45:2n:53:LEU:HD23	45:2n:53:LEU:HA	1.70	0.45
1:1A:375:C:H2'	1:1A:376:C:C6	2.52	0.45
1:1A:652(U):G:H2'	1:1A:652(V):C:C6	2.52	0.45
1:1A:1184:G:P	25:13:29:ARG:HH12	2.40	0.45
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.32	0.45
1:1A:2298:A:H2'	1:1A:2299:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:14:U:O2	2:1B:108:U:H4'	2.16	0.45
32:1a:1370:G:C2	32:1a:1371:G:C8	3.05	0.45
32:1a:1532:U:O5'	32:1a:1532:U:H6	1.99	0.45
36:1e:85:GLY:C	36:1e:87:SER:H	2.25	0.45
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.99	0.45
1:2A:980:A:N3	1:2A:2037:G:O2'	2.49	0.45
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.51	0.45
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.82	0.45
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.32	0.45
18:2W:41:LYS:HE3	27:25:25:LEU:HD11	1.98	0.45
21:2Z:23:LYS:HB3	21:2Z:38:TYR:CD1	2.52	0.45
32:2a:603:U:H2'	32:2a:604:G:H8	1.82	0.45
32:2a:741:G:H2'	32:2a:742:G:O4'	2.17	0.45
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.99	0.45
35:2d:108:LEU:HD13	35:2d:183:GLY:HA3	1.99	0.45
41:2j:17:ASP:O	41:2j:21:GLN:HB2	2.16	0.45
55:2x:23:C:H2'	55:2x:24:U:C6	2.52	0.45
1:1A:548:A:H1'	1:1A:549:G:OP1	2.17	0.45
1:1A:1071:G:OP1	1:1A:1071:G:H3'	2.17	0.45
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.98	0.45
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.50	0.45
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.44	0.45
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.69	0.45
35:1d:53:ASP:O	35:1d:57:ARG:HG3	2.17	0.45
42:1k:45:GLY:O	42:1k:50:TYR:HB2	2.17	0.45
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.43	0.45
56:1y:40:C:H2'	56:1y:41:C:C6	2.51	0.45
1:2A:821:A:N1	64:2A:4003:HOH:O	2.35	0.45
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.31	0.45
1:2A:2129:C:N3	1:2A:2159:G:N2	2.61	0.45
1:2A:2471:C:N4	1:2A:2476:A:O2'	2.46	0.45
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.50	0.45
5:2F:29:ASN:HB3	5:2F:112:MET:HE1	1.99	0.45
13:2R:118:GLU:CD	13:2R:118:GLU:H	2.23	0.45
14:2S:49:VAL:HG12	14:2S:73:LEU:HD12	1.99	0.45
21:2Z:92:SER:O	21:2Z:130:PRO:HG3	2.17	0.45
32:2a:130:A:H1'	32:2a:263:A:O2'	2.16	0.45
32:2a:256:U:P	48:2q:17:LYS:HZ2	2.39	0.45
32:2a:731:G:OP1	32:2a:766:A:H1'	2.16	0.45
32:2a:738:C:OP1	37:2f:2:ARG:NH1	2.49	0.45
32:2a:1147:C:O2	40:2i:16:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:33:MET:HB2	61:2d:303:SF4:S2	2.57	0.45
35:2d:158:ILE:H	35:2d:158:ILE:HG12	1.36	0.45
40:2i:5:TYR:OH	40:2i:16:ARG:HG2	2.17	0.45
44:2m:49:THR:HG23	44:2m:52:GLU:OE2	2.17	0.45
1:1A:184:C:H2'	1:1A:185:U:H6	1.79	0.45
1:1A:1069:A:H2'	1:1A:1073:A:N7	2.32	0.45
8:1I:62:LYS:O	8:1I:66:GLU:HG2	2.17	0.45
22:10:43:THR:O	22:10:43:THR:HG23	2.17	0.45
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.82	0.45
32:1a:1254:C:H42	32:1a:1283:G:H1	1.65	0.45
37:1f:2:ARG:HD2	37:1f:69:GLU:HB3	1.99	0.45
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.98	0.45
8:2I:62:LYS:HG3	8:2I:133:HIS:CE1	2.52	0.45
32:2a:509:A:O2'	32:2a:510:A:OP1	2.28	0.45
35:2d:171:GLY:HA2	35:2d:172:PRO:HD3	1.81	0.45
38:2g:15:ASP:HB3	38:2g:24:THR:HG23	1.99	0.45
46:2o:15:PHE:HZ	46:2o:84:LYS:HD2	1.82	0.45
1:1A:2040:C:H2'	1:1A:2041:U:O4'	2.17	0.45
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.98	0.45
6:1G:7:LEU:HD23	6:1G:7:LEU:HA	1.82	0.45
7:1H:126:PRO:HB2	7:1H:130:ARG:HH21	1.82	0.45
10:1O:49:ARG:NH1	32:1a:1422:G:O3'	2.48	0.45
13:1R:2:ARG:HD2	64:1R:307:HOH:O	2.16	0.45
21:1Z:8:TYR:HB2	21:1Z:38:TYR:CE2	2.52	0.45
35:1d:8:VAL:HG21	35:1d:21:LEU:HB2	1.98	0.45
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.43	0.45
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.48	0.45
47:1p:53:VAL:HG13	47:1p:79:VAL:HG13	1.99	0.45
54:1w:48:C:C2	54:1w:59:U:H1'	2.52	0.45
56:1y:6:G:C6	56:1y:7:A:C6	3.05	0.45
1:2A:570:G:H2'	1:2A:2030:A:C5	2.51	0.45
1:2A:2193:G:H2'	1:2A:2194:G:C8	2.52	0.45
2:2B:14:U:OP2	2:2B:70:C:O2'	2.30	0.45
13:2R:33:ARG:NH2	13:2R:115:GLU:OE1	2.41	0.45
32:2a:297:G:N2	32:2a:300:A:OP2	2.49	0.45
34:2c:178:LEU:C	34:2c:180:ALA:H	2.25	0.45
41:2j:50:ILE:HB	45:2n:41:ARG:NH1	2.32	0.45
44:2m:49:THR:OG1	44:2m:52:GLU:HG3	2.17	0.45
55:2x:15:G:H2'	55:2x:59:A:N1	2.32	0.45
56:2y:5:G:H1	56:2y:68:C:N4	2.10	0.45
1:1A:671:C:N4	64:1A:4344:HOH:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.52	0.44
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.18	0.44
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.50	0.44
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.44	0.44
21:1Z:155:LEU:HD12	21:1Z:156:LYS:H	1.82	0.44
32:1a:840:C:H4'	32:1a:841:U:OP1	2.17	0.44
32:1a:922:G:H4'	36:1e:20:GLN:HA	2.00	0.44
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.52	0.44
38:1g:50:ILE:HD11	38:1g:125:MET:HG2	1.98	0.44
42:1k:34:ASP:HB2	42:1k:35:PRO:HD2	1.98	0.44
54:1w:37:MIA:H8	54:1w:37:MIA:O5'	2.16	0.44
1:2A:288:C:H2'	1:2A:289:A:C8	2.50	0.44
1:2A:586:A:OP2	64:2A:3942:HOH:O	2.19	0.44
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.52	0.44
1:2A:1999:C:H2'	1:2A:2000:G:O4'	2.16	0.44
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.53	0.44
1:2A:2118:U:OP1	1:2A:2148:G:H4'	2.17	0.44
1:2A:2651:C:H42	1:2A:2669:G:H1	1.65	0.44
14:2S:3:ARG:NH2	14:2S:4:LEU:O	2.50	0.44
21:2Z:128:VAL:HG12	21:2Z:161:VAL:HA	1.99	0.44
28:26:32:ASN:OD1	28:26:32:ASN:N	2.39	0.44
32:2a:707:C:H2'	32:2a:708:C:C6	2.52	0.44
32:2a:1321:C:O2'	50:2s:77:THR:HG21	2.17	0.44
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.98	0.44
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	1.99	0.44
42:2k:59:TYR:O	42:2k:62:GLN:HB3	2.17	0.44
56:2y:53:G:H2'	56:2y:54:5MU:C6	2.51	0.44
1:1A:922:U:H2'	1:1A:923:C:C6	2.52	0.44
1:1A:1670:C:O2	4:1E:129:HIS:NE2	2.48	0.44
1:1A:2080:G:OP1	23:11:35:THR:HG21	2.16	0.44
64:1A:4797:HOH:O	5:1F:70:THR:HG23	2.17	0.44
8:1I:107:VAL:HG12	8:1I:109:ILE:HG12	1.98	0.44
32:1a:130:A:O2'	32:1a:131:C:O5'	2.35	0.44
32:1a:145:G:H1	32:1a:177:C:H42	1.65	0.44
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.49	0.44
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.99	0.44
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.50	0.44
47:1p:56:ALA:O	47:1p:60:LEU:HB2	2.18	0.44
54:1w:12:U:H2'	54:1w:13:C:O4'	2.16	0.44
1:2A:880:G:H2'	1:2A:881:G:H8	1.83	0.44
1:2A:973:A:OP2	64:2A:3948:HOH:O	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.52	0.44
1:2A:1526:G:C6	1:2A:1527:G:C2	3.06	0.44
1:2A:1755:A:OP2	15:2T:113:LYS:NZ	2.37	0.44
1:2A:2019:A:N7	27:25:9:LYS:HE2	2.31	0.44
2:2B:34:U:OP1	6:2G:2:PRO:HG3	2.17	0.44
2:2B:48:A:P	14:2S:30:ARG:HH22	2.40	0.44
4:2E:7:VAL:HG11	15:2T:1:MET:HE1	1.99	0.44
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.81	0.44
6:2G:106:LEU:HG	6:2G:111:LEU:HD13	1.99	0.44
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.17	0.44
32:2a:148:G:H2'	32:2a:149:A:H8	1.83	0.44
33:2b:63:MET:HG3	33:2b:225:ALA:HB1	1.99	0.44
35:2d:201:GLN:HE22	36:2e:99:GLY:CA	2.31	0.44
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	2.00	0.44
38:2g:113:GLU:HG3	38:2g:118:VAL:HG12	1.99	0.44
47:2p:1:MET:HE2	47:2p:1:MET:HB3	1.76	0.44
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.82	0.44
1:1A:2115:G:C2	1:1A:2117:A:N7	2.86	0.44
1:1A:2181:G:O2'	1:1A:2182:G:OP1	2.29	0.44
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.50	0.44
2:1B:75:G:H22	21:1Z:73:GLN:HE21	1.65	0.44
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.99	0.44
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.16	0.44
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.99	0.44
42:1k:33:THR:HA	42:1k:39:PRO:HA	1.99	0.44
56:1y:37:MIA:H8	56:1y:37:MIA:C5'	2.47	0.44
56:1y:51:U:H2'	56:1y:52:G:C8	2.52	0.44
1:2A:486:C:H4'	18:2W:60:ASN:ND2	2.32	0.44
1:2A:657:U:H2'	1:2A:658:C:C6	2.52	0.44
1:2A:709:U:H2'	1:2A:710:G:C8	2.52	0.44
1:2A:724:U:H2'	1:2A:725:G:O4'	2.17	0.44
1:2A:1344:G:O2'	1:2A:1385:G:H2'	2.18	0.44
6:2G:22:ARG:NH1	6:2G:175:LEU:HD21	2.32	0.44
32:2a:901:A:O2'	32:2a:1513:A:OP1	2.30	0.44
33:2b:16:HIS:HB2	33:2b:204:ASN:HD22	1.82	0.44
33:2b:16:HIS:CB	33:2b:204:ASN:HB3	2.43	0.44
35:2d:31:CYS:HB2	61:2d:303:SF4:S3	2.57	0.44
44:2m:108:ARG:HD3	44:2m:108:ARG:HA	1.71	0.44
56:2y:8:4SU:H6	56:2y:8:4SU:O5'	2.18	0.44
1:1A:1297:C:OP1	64:1A:4136:HOH:O	2.21	0.44
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.17	0.44
1:1A:2336:A:H61	22:10:43:THR:HG22	1.83	0.44
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.17	0.44
4:1E:55:ASN:C	4:1E:55:ASN:HD22	2.25	0.44
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.53	0.44
7:1H:73:ALA:O	7:1H:76:VAL:HG12	2.17	0.44
11:1P:1:MET:HE3	11:1P:1:MET:HB2	1.77	0.44
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.50	0.44
32:1a:262:A:C6	32:1a:263:A:C6	3.04	0.44
32:1a:509:A:H5'	35:1d:54:TYR:HD2	1.82	0.44
32:1a:519:C:OP2	43:1l:50:SER:OG	2.28	0.44
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.99	0.44
32:1a:1179:A:H4'	40:1i:103:THR:HA	1.99	0.44
38:1g:58:PRO:O	38:1g:61:VAL:N	2.50	0.44
41:1j:49:VAL:HG21	45:1n:44:LEU:HD22	1.98	0.44
1:2A:1151:G:H5'	16:2U:81:HIS:CE1	2.52	0.44
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.53	0.44
1:2A:1815:A:H8	1:2A:1815:A:OP1	1.99	0.44
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.53	0.44
1:2A:2298:A:H62	1:2A:2318:G:H8	1.62	0.44
1:2A:2506:U:H1'	62:2w:108:PHE:HD2	1.82	0.44
2:2B:22:U:H2'	2:2B:23:G:C8	2.53	0.44
15:2T:16:ARG:NH2	15:2T:18:ASP:OD2	2.49	0.44
21:2Z:7:ALA:HB3	21:2Z:61:LEU:HD12	2.00	0.44
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.98	0.44
32:2a:269:C:H2'	32:2a:270:A:C8	2.52	0.44
32:2a:335:C:O2'	32:2a:1433:A:N3	2.46	0.44
32:2a:1264:C:C4	32:2a:1272:G:O6	2.70	0.44
33:2b:118:LEU:HD12	33:2b:122:PHE:HB2	2.00	0.44
47:2p:71:ARG:HG3	47:2p:80:PHE:CE2	2.52	0.44
1:1A:222:A:H3'	1:1A:421:U:H5'	2.00	0.44
1:1A:301:G:OP2	20:1Y:84:ARG:NH2	2.33	0.44
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.82	0.44
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.52	0.44
1:1A:2362:G:OP1	30:18:44:LYS:NZ	2.50	0.44
7:1H:22:GLY:C	7:1H:23:ARG:HG3	2.41	0.44
9:1N:61:ARG:HA	9:1N:61:ARG:HD3	1.81	0.44
64:1W:306:HOH:O	27:15:4:HIS:HE1	2.00	0.44
32:1a:60:A:N1	32:1a:107:G:O2'	2.45	0.44
35:1d:107:ARG:HH22	35:1d:194:LEU:HG	1.82	0.44
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.52	0.44
1:2A:1582:C:H2'	1:2A:1583:A:C8	2.53	0.44
1:2A:1654:A:OP1	13:2R:1:MET:N	2.31	0.44
1:2A:1719:G:N2	1:2A:1744:C:H1'	2.32	0.44
5:2F:178:PRO:HG2	5:2F:179:GLU:OE2	2.17	0.44
11:2P:84:ASN:HB3	11:2P:86:LYS:HG2	1.98	0.44
15:2T:51:ARG:HG3	15:2T:98:LYS:HD2	2.00	0.44
32:2a:90:U:H2'	32:2a:91:C:C6	2.52	0.44
32:2a:404:U:H2'	32:2a:405:U:C6	2.52	0.44
36:2e:13:ILE:HA	36:2e:29:GLY:O	2.18	0.44
43:2l:86:ARG:NH1	64:2l:301:HOH:O	2.49	0.44
43:2l:113:ARG:NE	43:2l:115:LYS:O	2.41	0.44
44:2m:89:GLY:O	44:2m:93:ARG:HG3	2.18	0.44
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.32	0.44
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.53	0.44
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.53	0.44
6:1G:114:ILE:HA	6:1G:140:ILE:HD11	1.99	0.44
11:1P:94:GLU:HG3	11:1P:124:LYS:HD3	2.00	0.44
15:1T:122:ASP:O	15:1T:126:ALA:N	2.41	0.44
16:1U:16:LYS:HB3	16:1U:16:LYS:HE2	1.72	0.44
32:1a:964:A:N3	32:1a:969:A:O2'	2.43	0.44
34:1c:77:ILE:HG12	34:1c:77:ILE:H	1.57	0.44
43:1l:28:LYS:HG3	43:1l:62:SER:HB2	2.00	0.44
44:1m:3:ARG:HG3	44:1m:4:ILE:HG22	2.00	0.44
1:2A:265:A:H1'	1:2A:266:G:O4'	2.18	0.44
1:2A:652(A):A:H3'	1:2A:652(B):A:H5"	2.00	0.44
1:2A:674:G:H1'	5:2F:74:ARG:HD3	2.00	0.44
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.18	0.44
10:2O:25:LEU:HD12	10:2O:38:VAL:HG12	1.99	0.44
19:2X:1:MET:N	24:22:29:LYS:HE3	2.33	0.44
32:2a:953:G:H5'	32:2a:965:A:N6	2.27	0.44
32:2a:1219:U:P	45:2n:19:ARG:HH12	2.41	0.44
32:2a:1292:U:P	38:2g:41:ARG:HH22	2.41	0.44
32:2a:1360:A:H2'	32:2a:1361:G:O4'	2.18	0.44
34:2c:6:HIS:CD2	34:2c:8:ILE:H	2.35	0.44
50:2s:32:LYS:HA	50:2s:50:ALA:HB3	2.00	0.44
54:2w:27:G:H1	54:2w:43:C:H42	1.66	0.44
1:1A:752:A:H3'	29:17:1:MET:HE1	2.00	0.44
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.18	0.44
1:1A:1970:A:OP1	64:1A:4135:HOH:O	2.21	0.44
1:1A:2206:G:H3'	1:1A:2207:G:N7	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2562:U:H4'	10:1O:25:LEU:HD21	2.00	0.44
6:1G:47:LYS:CG	6:1G:48:GLU:H	2.31	0.44
8:1I:31:LEU:HD21	8:1I:38:LEU:HD22	1.98	0.44
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	2.00	0.44
18:1W:45:TYR:CZ	18:1W:49:LYS:HE3	2.52	0.44
32:1a:501:C:H2'	32:1a:502:G:H8	1.82	0.44
32:1a:512:U:H2'	32:1a:513:C:C6	2.53	0.44
32:1a:736:C:H2'	32:1a:737:A:C8	2.53	0.44
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.18	0.44
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.51	0.44
32:2a:1080:A:H5"	32:2a:1081:G:OP2	2.18	0.44
32:2a:1268:A:H4'	52:2u:19:GLY:HA2	2.00	0.44
39:2h:34:GLU:OE1	39:2h:37:ARG:NH1	2.51	0.44
40:2i:9:ARG:HD3	40:2i:14:VAL:HG12	1.98	0.44
46:2o:15:PHE:CZ	46:2o:84:LYS:HD2	2.53	0.44
1:1A:301:G:P	20:1Y:84:ARG:HH22	2.40	0.44
1:1A:1652:A:OP1	13:1R:8:ARG:HD3	2.18	0.44
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.53	0.44
3:1D:141:VAL:HG13	3:1D:162:SER:HB2	1.99	0.44
8:1I:9:LEU:HD12	8:1I:12:LEU:HD12	2.00	0.44
20:1Y:6:HIS:HE1	20:1Y:72:VAL:O	2.01	0.44
22:10:49:LYS:HD3	22:10:50:ASN:ND2	2.33	0.44
32:1a:524:G:H2'	32:1a:525:C:C6	2.53	0.44
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.53	0.44
33:1b:188:ALA:HB1	33:1b:192:SER:OG	2.18	0.44
42:1k:18:ARG:HG3	42:1k:33:THR:OG1	2.18	0.44
1:2A:531:C:OP1	1:2A:561:G:N1	2.49	0.44
1:2A:1683:C:H2'	1:2A:1684:C:C6	2.53	0.44
1:2A:2111:C:N4	1:2A:2144:U:O2'	2.51	0.44
1:2A:2169:A:H2'	1:2A:2170:A:C8	2.53	0.44
1:2A:2572:A:N7	4:2E:145:LYS:HB2	2.32	0.44
1:2A:2595:G:N7	64:2A:4012:HOH:O	2.36	0.44
1:2A:2801(A):A:H1'	1:2A:2895:U:O2'	2.18	0.44
5:2F:108:LYS:O	5:2F:112:MET:HG3	2.18	0.44
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	2.00	0.44
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.99	0.44
7:2H:126:PRO:HG2	7:2H:130:ARG:HH21	1.82	0.44
9:2N:10:GLU:OE1	9:2N:11:PRO:HD2	2.17	0.44
12:2Q:19:GLY:O	12:2Q:98:LYS:HD2	2.16	0.44
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.18	0.44
32:2a:415:A:H2'	32:2a:416:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:473:G:H2'	32:2a:474:G:C8	2.52	0.44
32:2a:966:M2G:HM23	32:2a:967:5MC:H1'	1.98	0.44
32:2a:976:G:OP2	32:2a:1358:U:O2'	2.31	0.44
36:2e:84:PHE:CE2	36:2e:133:TYR:HD2	2.36	0.44
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.99	0.44
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	2.00	0.44
54:2w:54:5MU:H2'	54:2w:55:PSU:O4'	2.18	0.44
1:1A:265:A:N1	1:1A:427:U:O2'	2.47	0.44
1:1A:1676:A:H2'	1:1A:1677:A:O4'	2.18	0.44
6:1G:75:LYS:HE3	6:1G:77:ILE:HD11	2.00	0.44
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.83	0.44
32:1a:186:C:H2'	32:1a:187:C:C6	2.53	0.44
32:1a:812:C:OP1	32:1a:903:G:H1'	2.18	0.44
32:1a:955:U:O2'	50:1s:83:HIS:HD2	2.01	0.44
32:1a:1004:A:H5'	32:1a:1024:G:H22	1.82	0.44
32:1a:1325:C:OP1	52:1u:15:ARG:NH1	2.50	0.44
33:1b:90:MET:HE2	33:1b:90:MET:HA	2.00	0.44
37:1f:36:ARG:HH21	37:1f:66:GLU:CD	2.26	0.44
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.18	0.44
38:1g:12:LEU:HD12	38:1g:12:LEU:H	1.82	0.44
56:1y:53:G:H1	56:1y:61:C:H42	1.66	0.44
1:2A:127:A:H5"	1:2A:128:C:C6	2.52	0.44
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.53	0.44
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.18	0.44
1:2A:2123:G:H2'	1:2A:2124:G:C8	2.53	0.44
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.53	0.44
4:2E:26:ILE:HD13	4:2E:196:VAL:HG21	1.99	0.44
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.18	0.44
17:2V:50:PRO:HG2	17:2V:51:VAL:HG23	2.00	0.44
32:2a:340:U:H2'	32:2a:341:C:C6	2.53	0.44
32:2a:500:G:H2'	32:2a:501:C:C6	2.51	0.44
33:2b:41:ILE:HD13	33:2b:41:ILE:HA	1.87	0.44
33:2b:124:SER:HB3	33:2b:125:PRO:HD3	1.99	0.44
34:2c:121:ALA:O	34:2c:125:GLU:HG2	2.18	0.44
1:1A:271(F):C:H2'	1:1A:271(G):C:C6	2.53	0.43
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.50	0.43
1:1A:1709:U:H2'	1:1A:1710:C:C6	2.53	0.43
32:1a:636:U:H2'	32:1a:637:G:H8	1.82	0.43
32:1a:721:G:H4'	32:1a:722:A:O4'	2.18	0.43
32:1a:1298:C:H4'	32:1a:1299:A:C4	2.53	0.43
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:148:VAL:O	36:1e:152:ARG:HG3	2.18	0.43
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.43	0.43
49:1r:38:GLU:HA	49:1r:41:LYS:HE2	2.00	0.43
1:2A:589:C:H2'	1:2A:590:A:C8	2.53	0.43
1:2A:715:G:C2	46:2o:56:LEU:HD21	2.52	0.43
1:2A:1364:G:N7	23:21:3:LYS:HD2	2.33	0.43
2:2B:2:C:H2'	2:2B:3:C:C6	2.53	0.43
7:2H:156:ALA:O	7:2H:172:LYS:HG2	2.18	0.43
25:23:4:LEU:HD23	25:23:4:LEU:HA	1.78	0.43
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.53	0.43
32:2a:994:A:N7	32:2a:1216:G:H4'	2.33	0.43
32:2a:1016:A:H2'	32:2a:1017:G:O4'	2.17	0.43
33:2b:32:ILE:HD13	33:2b:40:HIS:CG	2.53	0.43
40:2i:106:ALA:O	40:2i:108:VAL:HG22	2.18	0.43
1:1A:1063:G:H2'	1:1A:1064:C:C5	2.53	0.43
1:1A:1354:A:H5"	3:1D:38:LYS:HD3	2.00	0.43
1:1A:2379:G:O2'	14:1S:17:ARG:NH2	2.51	0.43
1:1A:2709:G:H2'	1:1A:2710:C:C6	2.53	0.43
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.99	0.43
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.18	0.43
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	2.00	0.43
15:1T:127:ALA:C	15:1T:129:ARG:N	2.75	0.43
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.99	0.43
32:1a:254:G:OP1	48:1q:67:LYS:O	2.36	0.43
32:1a:966:M2G:HM13	32:1a:967:5MC:H1'	2.00	0.43
32:1a:1243:C:H2'	32:1a:1244:C:C6	2.53	0.43
41:1j:38:ILE:HD11	41:1j:71:LEU:HB3	2.00	0.43
56:1y:5:G:C2	56:1y:6:G:C8	3.07	0.43
1:2A:207:A:H2'	1:2A:208:C:O4'	2.18	0.43
1:2A:900:A:HO2'	1:2A:901:A:P	2.39	0.43
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.18	0.43
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH1	2.33	0.43
32:2a:1095:U:P	32:2a:1108:G:H1	2.41	0.43
35:2d:82:ALA:HB1	35:2d:92:VAL:HG13	2.00	0.43
37:2f:76:ALA:HB1	37:2f:80:ARG:NH2	2.32	0.43
39:2h:20:TYR:HE2	39:2h:75:ARG:HD2	1.83	0.43
47:2p:58:TYR:O	47:2p:61:SER:HB3	2.18	0.43
50:2s:80:TYR:O	50:2s:81:ARG:HG2	2.17	0.43
1:1A:721:C:H2'	1:1A:722:A:C8	2.53	0.43
1:1A:826:U:H4'	11:1P:55:ARG:HB3	1.99	0.43
1:1A:1090:U:C2	1:1A:1102:C:H1'	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1131:G:C2	1:1A:1132:A:C4	3.07	0.43
1:1A:1714:G:H1	1:1A:1745(A):C:H42	1.66	0.43
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	2.00	0.43
9:1N:1:MET:HE1	16:1U:94:ASN:ND2	2.34	0.43
19:1X:27:THR:HA	19:1X:79:ALA:O	2.18	0.43
32:1a:551:U:H2'	32:1a:552:U:C6	2.53	0.43
32:1a:555:C:H2'	32:1a:556:C:C6	2.53	0.43
32:1a:584:G:H5'	48:1q:91:ARG:NH2	2.34	0.43
33:1b:73:THR:OG1	33:1b:170:GLU:OE1	2.36	0.43
39:1h:40:ALA:HA	39:1h:45:ILE:HG13	2.00	0.43
49:1r:73:ALA:HB3	49:1r:79:LEU:HD12	2.00	0.43
55:1x:23:C:H2'	55:1x:24:U:H6	1.82	0.43
1:2A:577:G:C6	1:2A:578:A:C6	3.07	0.43
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.19	0.43
1:2A:1540:U:H2'	1:2A:1541:G:O4'	2.18	0.43
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.29	0.43
8:2I:82:ARG:NH2	8:2I:90:GLY:N	2.67	0.43
32:2a:381:C:H2'	32:2a:382:A:O4'	2.19	0.43
32:2a:512:U:H2'	32:2a:513:C:H6	1.83	0.43
33:2b:132:LYS:O	33:2b:136:VAL:N	2.46	0.43
35:2d:31:CYS:CB	61:2d:303:SF4:S3	3.06	0.43
40:2i:43:ALA:HA	40:2i:74:ILE:HD13	1.99	0.43
46:2o:70:LEU:HD11	46:2o:77:ARG:HB3	1.99	0.43
48:2q:76:LEU:HD12	48:2q:77:VAL:H	1.84	0.43
54:2w:21:A:O2'	54:2w:22:G:OP1	2.36	0.43
6:1G:53:LEU:HD11	6:1G:87:PRO:HB2	2.00	0.43
16:1U:104:GLN:NE2	16:1U:105:VAL:HG23	2.32	0.43
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.51	0.43
26:14:16:CYS:HB2	26:14:36:CYS:HB3	2.01	0.43
32:1a:316:G:H4'	64:1a:2109:HOH:O	2.18	0.43
32:1a:690:G:C6	32:1a:691:G:C6	3.06	0.43
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.18	0.43
54:1w:68:C:H3'	54:1w:69:G:H8	1.82	0.43
1:2A:811:U:H2'	11:2P:21:ARG:HA	2.01	0.43
1:2A:1354:A:O3'	3:2D:38:LYS:HE3	2.18	0.43
1:2A:1482:G:H1	1:2A:1506:C:H42	1.66	0.43
1:2A:2121:G:H1	1:2A:2177:C:H42	1.65	0.43
1:2A:2712:U:H2'	1:2A:2714:G:H5"	1.99	0.43
3:2D:38:LYS:HE2	3:2D:39:LYS:O	2.19	0.43
6:2G:121:ASN:HD22	6:2G:124:SER:N	2.16	0.43
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:232:G:H1'	32:2a:262:A:N1	2.33	0.43
32:2a:1330:U:H2'	32:2a:1331:G:H5'	2.00	0.43
34:2c:52:LEU:HD11	34:2c:55:VAL:HG22	1.99	0.43
49:2r:65:ILE:O	49:2r:69:THR:HG23	2.18	0.43
55:2x:43:A:H2'	55:2x:44:A:C8	2.54	0.43
1:1A:729:G:C5	3:1D:208:LYS:HB2	2.53	0.43
1:1A:1006:C:C2	1:1A:1138:G:N2	2.86	0.43
1:1A:2098:U:H3	1:1A:2191:G:H1	1.65	0.43
1:1A:2406:U:H6	1:1A:2406:U:H2'	1.66	0.43
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.17	0.43
5:1F:157:VAL:HB	5:1F:194:MET:HG2	2.00	0.43
6:1G:19:LEU:HD13	6:1G:32:PRO:HD2	1.98	0.43
11:1P:124:LYS:HA	11:1P:144:GLU:HB3	2.01	0.43
21:1Z:4:ARG:NH2	21:1Z:66:SER:OG	2.52	0.43
32:1a:44:G:C2	32:1a:45:U:H1'	2.54	0.43
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.53	0.43
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.86	0.43
47:1p:39:TYR:CE2	47:1p:41:PRO:HB3	2.53	0.43
51:1t:89:ARG:HA	51:1t:89:ARG:HD2	1.86	0.43
54:1w:18:G:H4'	54:1w:60:U:C5	2.53	0.43
1:2A:321:G:OP2	5:2F:135:LYS:HD3	2.18	0.43
1:2A:1260:G:C6	1:2A:1261:C:C4	3.07	0.43
1:2A:2131:G:H22	1:2A:2158:A:N6	2.16	0.43
7:2H:157:TYR:CE1	7:2H:172:LYS:HG3	2.53	0.43
8:2I:104:GLN:HG2	8:2I:105:HIS:CE1	2.54	0.43
32:2a:194:C:H2'	32:2a:195:A:H5"	1.99	0.43
32:2a:1255:G:N7	41:2j:43:ARG:NH2	2.65	0.43
33:2b:24:TRP:CZ2	33:2b:26:PRO:HG3	2.54	0.43
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	2.00	0.43
42:2k:38:ASN:HA	42:2k:39:PRO:HD3	1.92	0.43
51:2t:10:LEU:HD23	51:2t:12:ALA:HB2	2.01	0.43
56:2y:18:G:O6	56:2y:56:C:N4	2.52	0.43
1:1A:652(U):G:C2	1:1A:652(V):C:C2	3.07	0.43
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.46	0.43
4:1E:50:GLY:HA3	4:1E:75:VAL:HG21	2.00	0.43
17:1V:29:PRO:HA	17:1V:61:VAL:HG22	2.00	0.43
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.61	0.43
28:16:38:LYS:HE3	28:16:38:LYS:HB3	1.86	0.43
32:1a:60:A:H4'	32:1a:61:G:H5'	1.99	0.43
32:1a:179:A:H2'	32:1a:180:U:C6	2.53	0.43
32:1a:433:C:H2'	32:1a:434:U:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:598:U:H2'	32:1a:599:C:C6	2.53	0.43
38:1g:78:ARG:NH1	38:1g:156:TRP:HB3	2.34	0.43
41:1j:27:ALA:HB2	41:1j:81:THR:HG21	2.00	0.43
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.52	0.43
1:2A:1594:G:H2'	1:2A:1595:G:O4'	2.19	0.43
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.19	0.43
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.83	0.43
1:2A:2262:U:OP1	1:2A:2387:U:O2'	2.33	0.43
21:2Z:126:VAL:HB	21:2Z:161:VAL:HG23	2.01	0.43
32:2a:540:G:C6	32:2a:541:G:C5	3.06	0.43
32:2a:625:G:H2'	32:2a:626:U:C6	2.54	0.43
32:2a:792:A:O2'	32:2a:794:A:N7	2.50	0.43
32:2a:1263:C:H1'	32:2a:1273:G:N2	2.33	0.43
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.53	0.43
48:2q:10:VAL:HA	48:2q:20:THR:O	2.19	0.43
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	2.00	0.43
55:2x:20:U:H4'	55:2x:21:A:OP2	2.16	0.43
55:2x:21:A:H61	55:2x:46:G:H2'	1.84	0.43
1:1A:652(V):C:H2'	1:1A:653:A:O4'	2.17	0.43
1:1A:1843:C:H5'	3:1D:253:GLN:OE1	2.19	0.43
5:1F:135:LYS:HB2	5:1F:138:GLU:HG3	2.00	0.43
7:1H:8:PRO:HB3	7:1H:51:ARG:HG2	2.00	0.43
8:1I:125:GLU:OE2	8:1I:143:SER:HB2	2.18	0.43
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.53	0.43
32:1a:176:C:H2'	32:1a:177:C:H6	1.83	0.43
32:1a:749:C:H2'	32:1a:750:G:H8	1.84	0.43
33:1b:37:ASN:C	33:1b:39:ILE:N	2.76	0.43
34:1c:150:LYS:HD3	34:1c:152:ILE:HD11	2.00	0.43
44:1m:50:GLU:HA	44:1m:53:VAL:HG22	2.00	0.43
50:1s:31:ILE:O	50:1s:50:ALA:N	2.42	0.43
55:1x:8:4SU:O2	55:1x:21:A:H2	2.01	0.43
55:1x:59:A:H2'	55:1x:60:U:H5'	2.00	0.43
1:2A:27:G:O2'	1:2A:28:A:OP2	2.35	0.43
1:2A:568:U:H5'	1:2A:945:A:C6	2.53	0.43
1:2A:2741:A:H2'	1:2A:2742:C:O4'	2.18	0.43
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.18	0.43
7:2H:54:ARG:HH21	7:2H:57:ASP:CG	2.26	0.43
30:28:6:THR:HG23	30:28:62:LEU:HD23	2.00	0.43
30:28:26:LYS:HB2	30:28:44:LYS:O	2.19	0.43
32:2a:266:G:H2'	32:2a:266:G:N3	2.34	0.43
32:2a:673:G:O3'	37:2f:87:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:964:A:N3	32:2a:969:A:O2'	2.47	0.43
32:2a:1013:G:O2'	32:2a:1015:A:N7	2.47	0.43
32:2a:1368:G:H5"	40:2i:112:LYS:HB3	2.01	0.43
38:2g:153:HIS:ND1	42:2k:58:PRO:HD2	2.33	0.43
44:2m:4:ILE:HG23	44:2m:22:ILE:HD11	2.00	0.43
1:1A:207:A:H2'	1:1A:208:C:O4'	2.18	0.43
1:1A:647:G:H2'	1:1A:648:G:O4'	2.18	0.43
1:1A:1062:G:H22	1:1A:1077:A:N6	2.15	0.43
8:1I:9:LEU:HD23	8:1I:9:LEU:HA	1.79	0.43
8:1I:38:LEU:H	8:1I:38:LEU:CD2	2.31	0.43
32:1a:872:A:C8	32:1a:874:G:C8	3.07	0.43
32:1a:946:A:H2'	32:1a:947:G:C8	2.53	0.43
41:1j:5:ARG:HG3	41:1j:71:LEU:HD11	2.00	0.43
1:2A:817:C:O2'	1:2A:839:U:H5"	2.19	0.43
1:2A:2512:C:H2'	1:2A:2513:G:O4'	2.19	0.43
8:2I:2:LYS:HE3	8:2I:20:ASP:OD2	2.19	0.43
18:2W:64:MET:HE2	18:2W:109:GLU:HG3	2.01	0.43
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.58	0.43
21:2Z:63:ASP:OD2	21:2Z:65:GLN:NE2	2.52	0.43
32:2a:100:C:H2'	32:2a:101:A:C8	2.53	0.43
42:2k:62:GLN:HE21	42:2k:97:ALA:HB2	1.84	0.43
44:2m:67:GLU:HB3	44:2m:68:GLY:H	1.64	0.43
45:2n:33:VAL:HA	45:2n:40:CYS:HA	2.00	0.43
51:2t:51:GLU:O	51:2t:55:ILE:HG12	2.19	0.43
1:1A:218:A:C2	1:1A:235:U:H4'	2.53	0.43
1:1A:312:G:H5'	1:1A:331:A:O2'	2.19	0.43
1:1A:2059:A:OP2	64:1A:4137:HOH:O	2.21	0.43
1:1A:2251:OMG:HM23	1:1A:2251:OMG:H1'	1.86	0.43
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.54	0.43
6:1G:3:LEU:O	6:1G:8:LYS:NZ	2.26	0.43
26:14:24:THR:OG1	26:14:25:TYR:N	2.51	0.43
32:1a:735:C:H2'	32:1a:736:C:H6	1.84	0.43
32:1a:762:C:H2'	32:1a:763:G:H8	1.82	0.43
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.48	0.43
34:1c:157:ILE:HD12	34:1c:164:ARG:HB3	2.00	0.43
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.99	0.43
54:1w:43:C:H2'	54:1w:44:G:C8	2.54	0.43
56:1y:10:G:H2'	56:1y:10:G:N3	2.34	0.43
1:2A:1449:A:O2'	1:2A:1529:G:N2	2.45	0.43
1:2A:2262:U:OP2	22:20:16:SER:OG	2.35	0.43
1:2A:2305:A:H2'	1:2A:2306:C:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.51	0.43
1:2A:2685:G:P	15:2T:51:ARG:HH12	2.42	0.43
19:2X:47:PHE:O	19:2X:49:VAL:HG13	2.18	0.43
32:2a:841:U:H6	32:2a:841:U:P	2.42	0.43
32:2a:1057:G:C4	32:2a:1204:A:C2	3.07	0.43
32:2a:1085:U:H3'	32:2a:1086:U:C5	2.54	0.43
32:2a:1151:A:C5'	41:2j:41:PRO:HA	2.49	0.43
32:2a:1237:C:O2'	32:2a:1300:G:N1	2.41	0.43
32:2a:1263:C:C4	32:2a:1272:G:O6	2.72	0.43
48:2q:67:LYS:HA	48:2q:70:ARG:HH12	1.84	0.43
54:2w:25:C:H2'	54:2w:26:A:C8	2.53	0.43
1:1A:226:G:N2	1:1A:228:A:H62	2.15	0.43
1:1A:533:G:H5'	16:1U:24:TYR:CE1	2.54	0.43
1:1A:1750:G:O2'	1:1A:2860:A:N1	2.45	0.43
4:1E:119:ARG:HG2	4:1E:120:TRP:NE1	2.34	0.43
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	2.00	0.43
21:1Z:126:VAL:HG11	21:1Z:161:VAL:HB	2.01	0.43
32:1a:142:G:H2'	32:1a:143:A:H8	1.84	0.43
32:1a:1136:U:H5"	32:1a:1137:C:C4	2.53	0.43
42:1k:58:PRO:O	42:1k:93:GLN:HG2	2.19	0.43
1:2A:196:A:O2'	1:2A:805:G:O6	2.25	0.43
1:2A:310:A:OP2	20:2Y:21:LYS:NZ	2.40	0.43
1:2A:453:C:O2	1:2A:457:A:O2'	2.37	0.43
1:2A:455:C:N3	1:2A:472:A:H2'	2.34	0.43
1:2A:2109:U:H3	1:2A:2180:U:H3	1.67	0.43
1:2A:2386:C:H2'	1:2A:2387:U:C6	2.54	0.43
2:2B:87:G:N2	2:2B:90:A:OP2	2.44	0.43
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	2.01	0.43
6:2G:20:ILE:HA	6:2G:25:TYR:HD2	1.84	0.43
15:2T:105:LEU:HD22	15:2T:109:GLU:HB3	2.01	0.43
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.54	0.43
20:2Y:99:CYS:HB2	20:2Y:106:LEU:HD21	2.00	0.43
21:2Z:55:HIS:CE1	21:2Z:135:GLU:HB2	2.53	0.43
24:22:46:GLN:O	24:22:49:LYS:HG3	2.18	0.43
32:2a:587:G:N2	32:2a:754:C:OP2	2.44	0.43
32:2a:620:C:H2'	32:2a:621:A:O4'	2.19	0.43
32:2a:1004:A:N3	32:2a:1038:C:C2	2.87	0.43
32:2a:1060:C:C5'	41:2j:51:ARG:HB3	2.49	0.43
32:2a:1314:C:H2'	32:2a:1315:U:C6	2.54	0.43
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.52	0.43
1:1A:1039:G:H1	1:1A:1116:C:N4	2.09	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2100:G:H1	1:1A:2189:U:H3	1.67	0.42
1:1A:2788:C:P	4:1E:61:ARG:HH21	2.42	0.42
7:1H:133:VAL:HG12	7:1H:141:VAL:HG13	2.01	0.42
8:1I:72:LEU:HB2	8:1I:138:ILE:HG21	2.01	0.42
32:1a:157:G:H1	32:1a:164:U:H3	1.66	0.42
32:1a:922:G:C6	32:1a:923:A:C6	3.07	0.42
33:1b:103:THR:HA	33:1b:180:LEU:HD11	2.00	0.42
51:1t:83:ARG:HG2	51:1t:86:ARG:HH12	1.84	0.42
54:1w:11:C:H2'	54:1w:12:U:C6	2.54	0.42
1:2A:133:C:H42	1:2A:146:G:H1	1.66	0.42
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.83	0.42
1:2A:383:U:H2'	1:2A:385:C:H5	1.84	0.42
1:2A:476:G:H4'	1:2A:502:A:N1	2.34	0.42
1:2A:900:A:H2'	1:2A:901:A:H8	1.84	0.42
1:2A:945:A:C4	1:2A:2448:A:C2	3.06	0.42
1:2A:1756:G:H4'	1:2A:1758:G:O4'	2.19	0.42
1:2A:2365:G:O6	30:28:39:LYS:HE3	2.19	0.42
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.54	0.42
1:2A:2879:C:OP2	64:2A:3950:HOH:O	2.22	0.42
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.17	0.42
3:2D:5:LYS:HG2	3:2D:17:THR:HG22	2.01	0.42
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	2.01	0.42
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.59	0.42
15:2T:77:PRO:HB2	15:2T:80:SER:HB2	2.01	0.42
21:2Z:121:HIS:N	21:2Z:171:ILE:O	2.52	0.42
26:24:58:ARG:HB3	50:2s:67:VAL:HB	2.01	0.42
30:28:29:LYS:HD2	30:28:44:LYS:HB3	2.00	0.42
32:2a:538:G:H5"	43:2l:114:LYS:HB2	2.00	0.42
32:2a:1360:A:H8	32:2a:1360:A:OP1	2.03	0.42
35:2d:57:ARG:HB3	35:2d:206:PHE:HB2	2.00	0.42
35:2d:180:GLY:O	35:2d:182:LYS:HG3	2.17	0.42
40:2i:89:ASN:HD22	40:2i:91:ASP:H	1.66	0.42
1:1A:534:U:H2'	1:1A:535:C:C6	2.54	0.42
1:1A:893:C:H2'	1:1A:894:C:C6	2.53	0.42
1:1A:897:C:H5'	54:1w:56:C:OP1	2.18	0.42
1:1A:987:G:N7	64:1A:4222:HOH:O	2.37	0.42
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.38	0.42
1:1A:1068:G:O2'	1:1A:1096:A:N3	2.50	0.42
1:1A:2100:G:O2'	1:1A:2101:G:H5'	2.20	0.42
1:1A:2393:A:H5"	11:1P:63:PRO:HB3	2.01	0.42
4:1E:7:VAL:CG1	4:1E:27:LEU:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:7:TYR:CD2	5:1F:24:LEU:HB2	2.54	0.42
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	2.01	0.42
9:1N:14:VAL:HG11	9:1N:138:LEU:HD12	1.99	0.42
11:1P:63:PRO:HD3	30:18:27:THR:HG22	2.02	0.42
18:1W:27:LYS:HD2	18:1W:31:GLU:CD	2.44	0.42
21:1Z:19:ARG:NH2	21:1Z:84:GLU:O	2.45	0.42
32:1a:1003:G:H2'	32:1a:1004:A:N3	2.34	0.42
32:1a:1118:C:P	40:1i:104:ARG:HH11	2.42	0.42
34:1c:11:ARG:HB3	34:1c:15:THR:HB	2.02	0.42
37:1f:91:VAL:HG11	49:1r:72:ARG:NH1	2.35	0.42
51:1t:53:LEU:HD22	51:1t:102:GLY:HA3	2.02	0.42
1:2A:311:A:C6	1:2A:328:U:C4	3.08	0.42
1:2A:1040:C:H2'	1:2A:1041:C:C6	2.54	0.42
16:2U:17:ILE:HD12	16:2U:17:ILE:HA	1.76	0.42
32:2a:772:U:H2'	32:2a:773:G:O4'	2.19	0.42
35:2d:158:ILE:O	35:2d:162:LEU:HD12	2.18	0.42
37:2f:2:ARG:NE	37:2f:69:GLU:HG2	2.33	0.42
40:2i:70:LYS:O	40:2i:74:ILE:HG13	2.19	0.42
44:2m:101:GLN:OE1	44:2m:101:GLN:N	2.51	0.42
56:2y:14:A:N6	56:2y:21:A:H2	2.14	0.42
1:1A:271(L):U:OP1	8:1I:50:ARG:NH1	2.52	0.42
1:1A:362:U:H6	1:1A:362:U:H2'	1.68	0.42
1:1A:839:U:H1'	1:1A:1191:G:H1'	2.01	0.42
1:1A:1176:G:N2	1:1A:1178:C:OP2	2.52	0.42
1:1A:1310:G:OP2	29:17:9:ARG:NE	2.43	0.42
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.84	0.42
2:1B:29:A:C2	2:1B:30:C:C2	3.07	0.42
3:1D:37:LEU:HD13	3:1D:87:ASN:ND2	2.34	0.42
4:1E:55:ASN:HD22	4:1E:57:LYS:H	1.66	0.42
5:1F:28:ILE:O	5:1F:30:PRO:HD3	2.19	0.42
32:1a:92:C:H2'	32:1a:93:G:H8	1.83	0.42
32:1a:653:A:O5'	39:1h:56:LYS:NZ	2.52	0.42
32:1a:1030(D):A:H2'	32:1a:1031:G:H4'	2.01	0.42
39:1h:53:VAL:HB	39:1h:58:TYR:CD2	2.54	0.42
47:1p:14:ASN:N	47:1p:15:PRO:HD3	2.35	0.42
51:1t:42:GLN:HE21	51:1t:46:GLU:HG3	1.84	0.42
1:2A:191:A:H2'	1:2A:192:C:C6	2.53	0.42
1:2A:893:C:H5'	1:2A:894:C:C5	2.54	0.42
1:2A:1782:C:O2'	1:2A:2609:U:H5"	2.19	0.42
1:2A:2142:C:N4	1:2A:2148:G:O6	2.52	0.42
1:2A:2439:A:H5'	1:2A:2439:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	2.00	0.42
1:2A:2882:A:OP1	13:2R:96:ARG:NE	2.38	0.42
10:2O:120:GLU:HG2	10:2O:122:LEU:HG	2.00	0.42
18:2W:19:LEU:HB3	27:25:25:LEU:HG	2.01	0.42
19:2X:26:TYR:O	19:2X:81:VAL:HG23	2.19	0.42
32:2a:903:G:OP1	64:2a:1911:HOH:O	2.21	0.42
34:2c:179:ARG:NH1	34:2c:206:GLU:HB2	2.35	0.42
38:2g:99:LEU:HD23	38:2g:102:ARG:NH1	2.32	0.42
44:2m:52:GLU:HG2	44:2m:55:ARG:HH21	1.85	0.42
50:2s:22:LEU:HD13	50:2s:31:ILE:HD11	2.01	0.42
1:1A:1192:G:OP2	64:1A:4138:HOH:O	2.21	0.42
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.19	0.42
1:1A:1665:A:H2'	1:1A:1666:G:O4'	2.19	0.42
1:1A:2100:G:H2'	1:1A:2101:G:C8	2.54	0.42
1:1A:2101:G:H2'	1:1A:2102:U:C6	2.54	0.42
1:1A:2319:G:H22	14:1S:3:ARG:CD	2.31	0.42
9:1N:67:LEU:HA	9:1N:87:LEU:HD23	2.02	0.42
12:1Q:1:MET:HB3	12:1Q:1:MET:HE2	1.75	0.42
32:1a:277:C:P	48:1q:68:ARG:HH12	2.42	0.42
34:1c:6:HIS:CD2	34:1c:8:ILE:HB	2.55	0.42
38:1g:79:ARG:HD2	38:1g:80:VAL:HA	2.01	0.42
42:1k:84:VAL:HG23	42:1k:110:ASP:HA	2.02	0.42
46:1o:55:GLY:O	46:1o:59:MET:HG3	2.19	0.42
56:1y:51:U:H2'	56:1y:52:G:H8	1.84	0.42
1:2A:432:A:H2'	1:2A:433:C:O4'	2.19	0.42
1:2A:861:A:N3	2:2B:79:C:O2'	2.49	0.42
1:2A:1204:A:N6	1:2A:1240:U:H2'	2.34	0.42
1:2A:2721:A:H2'	1:2A:2722:G:O4'	2.19	0.42
7:2H:84:SER:HG	7:2H:132:ARG:NH1	2.16	0.42
19:2X:29:TRP:CZ3	19:2X:78:LYS:HG3	2.55	0.42
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.60	0.42
32:2a:730:G:C5	32:2a:731:G:H1'	2.54	0.42
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.48	0.42
33:2b:178:ARG:NH1	33:2b:198:ASP:OD1	2.48	0.42
37:2f:99:ALA:HB1	49:2r:23:LYS:NZ	2.33	0.42
44:2m:123:ALA:HB2	54:2w:39:PSU:H1'	2.02	0.42
1:1A:715:G:C2	46:1o:56:LEU:HD21	2.54	0.42
1:1A:1622:G:OP2	64:1A:4139:HOH:O	2.22	0.42
1:1A:2100:G:H2'	1:1A:2101:G:H8	1.83	0.42
32:1a:8:A:N6	35:1d:205:GLU:O	2.51	0.42
32:1a:430:A:OP2	35:1d:8:VAL:HG12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1269:A:H2	32:1a:1312:G:N3	2.17	0.42
33:1b:158:LEU:HD23	33:1b:158:LEU:HA	1.88	0.42
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.54	0.42
54:1w:20:U:OP2	54:1w:20:U:H4'	2.17	0.42
56:1y:70:G:H3'	56:1y:71:G:H8	1.84	0.42
1:2A:515:A:H1'	1:2A:581:C:H1'	2.02	0.42
1:2A:1532:C:N4	1:2A:1537:G:H1	2.16	0.42
1:2A:2061:G:H2'	1:2A:2501:C:O2'	2.20	0.42
2:2B:66:A:N6	2:2B:108:U:H3'	2.34	0.42
21:2Z:40:ASP:OD2	21:2Z:42:VAL:HG13	2.19	0.42
32:2a:570:G:H1'	32:2a:820:U:C4	2.54	0.42
32:2a:1103:C:P	33:2b:96:ARG:HH22	2.41	0.42
32:2a:1265:G:C4	32:2a:1271:G:N2	2.88	0.42
33:2b:16:HIS:CB	33:2b:210:SER:HB2	2.45	0.42
33:2b:185:ILE:HG22	33:2b:199:TYR:CD2	2.55	0.42
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	2.01	0.42
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.19	0.42
54:2w:29:G:H2'	54:2w:30:G:C8	2.54	0.42
1:1A:84:A:H5'	20:1Y:8:LYS:HG2	2.02	0.42
1:1A:479:A:N3	1:1A:481:G:H5"	2.34	0.42
1:1A:1060:U:O2	1:1A:1088:A:H8	2.03	0.42
1:1A:1287:A:N1	1:1A:1648:C:O2'	2.46	0.42
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.20	0.42
1:1A:2512:C:H2'	1:1A:2513:G:O4'	2.19	0.42
2:1B:48:A:H2'	2:1B:49:C:C6	2.54	0.42
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	2.01	0.42
23:11:18:ILE:HG12	23:11:37:ILE:HG23	2.01	0.42
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.55	0.42
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.20	0.42
44:1m:3:ARG:HG3	44:1m:4:ILE:N	2.33	0.42
49:1r:26:LEU:HD11	49:1r:42:ARG:HH21	1.84	0.42
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.20	0.42
1:2A:1213:A:N3	1:2A:1238:G:O2'	2.48	0.42
1:2A:2138:C:N4	1:2A:2153:G:H1	2.17	0.42
1:2A:2717:G:O2'	15:2T:96:ARG:HD3	2.19	0.42
4:2E:52:LEU:O	4:2E:76:ARG:N	2.47	0.42
8:2I:29:TYR:HD2	8:2I:30:LEU:HD23	1.84	0.42
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.19	0.42
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	2.00	0.42
21:2Z:72:ARG:HH22	21:2Z:97:GLU:HB2	1.85	0.42
32:2a:21:G:H2'	32:2a:22:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:625:G:H2'	32:2a:626:U:H6	1.85	0.42
32:2a:685:G:C2	32:2a:686:U:C4	3.07	0.42
32:2a:1272:G:C2	32:2a:1273:G:C8	3.07	0.42
32:2a:1330:U:O4	32:2a:1331:G:C6	2.72	0.42
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.55	0.42
34:2c:131:ARG:HH21	36:2e:50:GLU:HG3	1.84	0.42
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	2.01	0.42
48:2q:27:PHE:CE1	48:2q:36:ILE:HD11	2.54	0.42
51:2t:50:GLU:O	51:2t:100:ILE:HD11	2.19	0.42
53:2v:23:A:H4'	53:2v:24:A:H5'	2.02	0.42
54:2w:51:U:H2'	54:2w:52:G:C8	2.54	0.42
56:2y:42:C:H2'	56:2y:43:C:C6	2.54	0.42
1:1A:1153:C:H2'	1:1A:1154:G:O4'	2.19	0.42
1:1A:2137:C:H2'	1:1A:2138:C:H6	1.84	0.42
3:1D:237:GLU:OE2	64:1D:401:HOH:O	2.22	0.42
5:1F:29:ASN:H	5:1F:112:MET:CE	2.32	0.42
21:1Z:52:SER:O	21:1Z:52:SER:OG	2.37	0.42
26:14:69:LYS:HE3	26:14:69:LYS:HA	2.01	0.42
31:19:27:CYS:SG	31:19:28:GLU:N	2.93	0.42
32:1a:1291:G:C6	32:1a:1292:U:C4	3.08	0.42
32:1a:1468:A:H8	32:1a:1468:A:O5'	2.02	0.42
34:1c:13:GLY:HA3	45:1n:57:ARG:NH1	2.34	0.42
36:1e:10:MET:H	36:1e:10:MET:HG2	1.60	0.42
38:1g:104:LEU:HD13	38:1g:104:LEU:HA	1.81	0.42
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.19	0.42
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.20	0.42
1:2A:1448:G:H2'	1:2A:1449:A:C8	2.54	0.42
1:2A:1614:A:N7	64:2A:4015:HOH:O	2.37	0.42
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.20	0.42
1:2A:2356:C:H2'	1:2A:2357:U:O4'	2.20	0.42
3:2D:232:PRO:HB3	3:2D:244:ARG:CZ	2.49	0.42
6:2G:11:TYR:OH	6:2G:16:ARG:HD3	2.20	0.42
10:2O:70:LYS:HB3	10:2O:70:LYS:HE2	1.92	0.42
24:22:61:LEU:HA	24:22:61:LEU:HD23	1.88	0.42
32:2a:391:G:C6	32:2a:392:G:C5	3.08	0.42
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.54	0.42
32:2a:1053:G:N7	32:2a:1200:C:H5"	2.35	0.42
32:2a:1279:A:H5"	32:2a:1280:A:OP1	2.20	0.42
41:2j:68:HIS:CD2	41:2j:68:HIS:H	2.37	0.42
41:2j:74:ILE:HG22	64:2j:302:HOH:O	2.19	0.42
43:2l:53:ARG:HB3	43:2l:69:TYR:HE1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:23:TYR:CZ	44:2m:71:ARG:HG3	2.54	0.42
51:2t:9:ASN:O	51:2t:10:LEU:HB2	2.18	0.42
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.20	0.42
1:1A:945:A:C4	1:1A:2448:A:C2	3.08	0.42
1:1A:1087:G:H2'	1:1A:1089:G:C8	2.54	0.42
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.55	0.42
1:1A:2181:G:HO2'	1:1A:2182:G:P	2.42	0.42
1:1A:2464:C:H1'	64:1A:4475:HOH:O	2.20	0.42
6:1G:43:LEU:C	6:1G:45:GLU:H	2.26	0.42
10:1O:24:VAL:HG13	10:1O:33:ALA:HB2	2.02	0.42
11:1P:59:LEU:HD21	30:18:10:ALA:HB2	2.02	0.42
32:1a:262:A:H2'	32:1a:263:A:C8	2.55	0.42
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	2.01	0.42
35:1d:11:LEU:HG	35:1d:66:ARG:HD3	2.02	0.42
41:1j:38:ILE:CG1	41:1j:71:LEU:HB3	2.50	0.42
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.51	0.42
56:1y:53:G:H3'	56:1y:54:5MU:H71	2.02	0.42
1:2A:1268:A:C2	1:2A:2013:A:C4	3.08	0.42
1:2A:1598:C:H2'	1:2A:1599:C:H6	1.84	0.42
1:2A:2319:G:N2	14:2S:3:ARG:HA	2.34	0.42
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.35	0.42
6:2G:114:ILE:HB	6:2G:117:PHE:HD1	1.85	0.42
7:2H:127:GLU:C	7:2H:129:THR:H	2.28	0.42
13:2R:59:ASP:OD2	13:2R:61:HIS:HB3	2.20	0.42
19:2X:65:ARG:HH11	19:2X:70:LEU:HD21	1.84	0.42
32:2a:920:U:H2'	32:2a:921:U:H6	1.84	0.42
33:2b:185:ILE:O	33:2b:185:ILE:HG12	2.20	0.42
33:2b:195:ASP:O	39:2h:68:ARG:NH2	2.53	0.42
41:2j:20:ALA:HA	41:2j:23:ILE:HG22	2.00	0.42
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.54	0.42
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.54	0.42
1:1A:2745:C:H2'	1:1A:2746:U:O4'	2.20	0.42
9:1N:1:MET:O	9:1N:2:LYS:HB2	2.20	0.42
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.54	0.42
21:1Z:125:LEU:HG	21:1Z:164:ALA:HB3	2.02	0.42
22:10:46:LYS:NZ	22:10:75:LEU:O	2.38	0.42
32:1a:142:G:O2'	32:1a:196:A:N1	2.50	0.42
32:1a:271:C:H2'	32:1a:272:C:H6	1.84	0.42
32:1a:735:C:H2'	32:1a:736:C:C6	2.55	0.42
32:1a:742:G:P	46:1o:35:ARG:HH22	2.39	0.42
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:34:ASN:N	40:1i:34:ASN:HD22	2.18	0.42
51:1t:71:THR:O	51:1t:72:LEU:HD23	2.20	0.42
1:2A:11:G:C2'	1:2A:12:U:H5'	2.50	0.42
1:2A:857:C:H4'	22:20:23:VAL:HG21	2.02	0.42
1:2A:924:C:H2'	1:2A:925:C:C6	2.54	0.42
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.54	0.42
1:2A:2506:U:OP1	4:2E:144:ARG:NH1	2.40	0.42
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.85	0.42
6:2G:133:LEU:HG	6:2G:157:ILE:HB	2.02	0.42
10:2O:26:LYS:O	10:2O:30:ALA:HB2	2.20	0.42
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	2.02	0.42
26:24:57:GLU:CB	26:24:58:ARG:HA	2.50	0.42
28:26:40:CYS:O	28:26:44:ARG:N	2.51	0.42
32:2a:253:U:H2'	32:2a:254:G:H8	1.84	0.42
32:2a:1260:C:HO2'	32:2a:1283:G:HO2'	1.57	0.42
33:2b:19:HIS:ND1	33:2b:206:ASP:OD2	2.52	0.42
34:2c:71:ALA:CB	34:2c:109:PRO:HB3	2.50	0.42
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.55	0.42
56:2y:40:C:H2'	56:2y:41:C:C6	2.55	0.42
1:1A:910:A:N1	1:1A:2277:G:H1'	2.34	0.42
1:1A:1062:G:C8	1:1A:1070:A:H4'	2.55	0.42
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.26	0.42
1:1A:2155:G:H5"	1:1A:2156:G:N7	2.35	0.42
1:1A:2469:A:O3'	12:1Q:56:ARG:NH1	2.53	0.42
1:1A:2684:U:O2'	10:1O:68:GLU:OE2	2.30	0.42
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.27	0.42
10:1O:104:ARG:HE	15:1T:36:GLU:CD	2.28	0.42
11:1P:39:LYS:HB2	11:1P:45:LEU:CD1	2.43	0.42
11:1P:126:VAL:HG22	11:1P:146:VAL:HB	2.02	0.42
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.35	0.42
32:1a:160:A:H1'	32:1a:344:A:C5	2.55	0.42
32:1a:200:G:H1	32:1a:217:C:N4	2.16	0.42
32:1a:418:C:H1'	32:1a:540:G:O2'	2.19	0.42
32:1a:826:C:H2'	32:1a:827:U:C6	2.55	0.42
32:1a:831:U:H2'	32:1a:832:C:C6	2.55	0.42
32:1a:1518:MA6:O5'	32:1a:1518:MA6:H8	2.19	0.42
36:1e:89:ILE:HG21	36:1e:135:THR:HA	2.01	0.42
42:1k:87:THR:O	42:1k:87:THR:OG1	2.29	0.42
1:2A:242:G:C8	30:28:5:LYS:HG2	2.54	0.42
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.19	0.42
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2317:C:H2'	1:2A:2318:G:H5'	2.01	0.42
1:2A:2364:C:H4'	22:20:56:ASP:OD1	2.19	0.42
2:2B:105:A:OP1	21:2Z:72:ARG:NH2	2.46	0.42
4:2E:183:LEU:HD21	15:2T:10:VAL:HG11	2.02	0.42
8:2I:117:GLU:H	8:2I:117:GLU:HG3	1.52	0.42
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.83	0.42
32:2a:1250:A:H4'	40:2i:68:GLY:N	2.34	0.42
32:2a:1260:C:O2'	32:2a:1283:G:O2'	2.30	0.42
32:2a:1438:G:H2'	32:2a:1439:C:C6	2.55	0.42
56:2y:10:G:H1	56:2y:25:C:N4	2.14	0.42
1:1A:1022:G:C5	1:1A:1140:C:C4	3.08	0.41
11:1P:101:VAL:HA	11:1P:106:LEU:O	2.20	0.41
21:1Z:155:LEU:HD13	21:1Z:155:LEU:HA	1.82	0.41
32:1a:567:G:N3	64:1a:1948:HOH:O	2.37	0.41
32:1a:848:C:H2'	32:1a:849:C:C6	2.56	0.41
32:1a:995:C:O2'	32:1a:996:A:H5'	2.19	0.41
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	2.01	0.41
51:1t:13:LEU:H	51:1t:13:LEU:HG	1.73	0.41
56:1y:37:MIA:C6	56:1y:38:A:C6	3.03	0.41
1:2A:118:A:C8	1:2A:119:A:C8	3.08	0.41
1:2A:468:G:N7	29:27:39:ARG:NH2	2.58	0.41
1:2A:855:G:C6	1:2A:856:C:C4	3.07	0.41
1:2A:892:G:H3'	1:2A:893:C:C5'	2.50	0.41
1:2A:1204:A:H61	1:2A:1240:U:H2'	1.85	0.41
1:2A:1288:U:C2	1:2A:1327:C:O2	2.73	0.41
1:2A:1740:G:H2'	1:2A:1740:G:N3	2.34	0.41
1:2A:1777:U:O2'	1:2A:1778:U:H5'	2.19	0.41
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.20	0.41
1:2A:2128:C:H2'	1:2A:2129:C:O4'	2.20	0.41
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.55	0.41
1:2A:2769:C:H2'	1:2A:2770:G:O4'	2.19	0.41
1:2A:2802:G:H8	1:2A:2802:G:O5'	2.03	0.41
1:2A:2807:G:C2	1:2A:2893:G:O6	2.73	0.41
5:2F:18:ARG:NH2	5:2F:127:GLU:OE2	2.41	0.41
6:2G:16:ARG:NE	6:2G:31:VAL:HG11	2.35	0.41
7:2H:16:SER:HB3	7:2H:27:LYS:HB2	2.02	0.41
7:2H:95:ARG:HG3	7:2H:106:THR:HB	2.01	0.41
1:1A:1070:A:N6	1:1A:1097:U:H4'	2.35	0.41
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.20	0.41
23:11:72:GLU:O	23:11:76:ARG:HG2	2.20	0.41
32:1a:119:A:H4'	32:1a:120:A:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.48	0.41
36:1e:72:GLN:O	36:1e:75:THR:HG22	2.19	0.41
39:1h:87:SER:OG	39:1h:93:VAL:N	2.45	0.41
1:2A:184:C:H2'	1:2A:185:U:H6	1.84	0.41
1:2A:271(S):G:C6	1:2A:271(T):C:C4	3.08	0.41
1:2A:272(D):G:C2	1:2A:272(E):G:C8	3.08	0.41
1:2A:566:U:H5"	11:2P:29:LYS:HE3	2.02	0.41
1:2A:895:U:H5'	1:2A:896:A:OP1	2.20	0.41
1:2A:1755:A:P	15:2T:113:LYS:HZ1	2.41	0.41
1:2A:1946:U:H2'	1:2A:1947:C:C6	2.56	0.41
1:2A:2306:C:N4	6:2G:42:GLY:O	2.52	0.41
1:2A:2660:A:H2'	1:2A:2661:G:O4'	2.20	0.41
7:2H:109:PHE:C	7:2H:111:HIS:H	2.28	0.41
11:2P:107:LYS:O	11:2P:110:TYR:HB2	2.20	0.41
16:2U:58:ARG:HA	16:2U:61:TRP:CE3	2.56	0.41
26:24:64:GLY:C	26:24:66:SER:N	2.78	0.41
32:2a:565:U:OP2	32:2a:566:G:O2'	2.38	0.41
32:2a:1034:G:N3	32:2a:1034:G:H2'	2.36	0.41
33:2b:19:HIS:HB2	33:2b:204:ASN:HB2	2.01	0.41
33:2b:92:TYR:CE1	33:2b:94:ASN:HB2	2.54	0.41
34:2c:45:LYS:HE2	34:2c:45:LYS:HB3	1.78	0.41
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.82	0.41
47:2p:19:ILE:N	47:2p:37:GLY:O	2.54	0.41
55:2x:53:G:H3'	55:2x:54:5MU:H73	2.02	0.41
1:1A:224:G:H2'	1:1A:225:A:O4'	2.19	0.41
1:1A:530:G:N1	1:1A:2023:G:OP1	2.38	0.41
1:1A:875:G:H1	1:1A:902:C:N4	2.19	0.41
1:1A:1668:A:O2'	1:1A:1674:G:N7	2.46	0.41
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.81	0.41
26:14:50:VAL:H	26:14:50:VAL:HG23	1.58	0.41
30:18:26:LYS:HG2	30:18:46:ARG:O	2.20	0.41
32:1a:841:U:OP2	32:1a:841:U:H6	2.03	0.41
32:1a:976:G:OP1	45:1n:32:SER:N	2.51	0.41
32:1a:1518:MA6:H93	32:1a:1519:MA6:C9	2.49	0.41
35:1d:65:ARG:NH1	35:1d:72:GLU:HB2	2.35	0.41
37:1f:100:ASN:HB2	49:1r:28:GLU:HA	2.02	0.41
39:1h:119:LEU:HB3	39:1h:123:GLU:HB2	2.02	0.41
54:1w:21:A:C6	54:1w:46:G7M:C5	3.04	0.41
1:2A:330:A:H2	1:2A:1210:A:O2'	2.01	0.41
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.55	0.41
1:2A:1225:G:H4'	17:2V:84:LYS:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1842:G:O2'	3:2D:253:GLN:OE1	2.35	0.41
2:2B:94:C:H2'	2:2B:95:C:H6	1.84	0.41
10:2O:120:GLU:OE2	10:2O:122:LEU:HD21	2.21	0.41
11:2P:39:LYS:HE3	11:2P:45:LEU:HD22	2.01	0.41
19:2X:92:LEU:HA	19:2X:92:LEU:HD12	1.87	0.41
27:25:48:GLU:O	27:25:60:VAL:HG11	2.21	0.41
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.35	0.41
38:2g:54:THR:O	38:2g:56:GLN:N	2.47	0.41
39:2h:19:VAL:HG23	39:2h:21:LYS:HG3	2.02	0.41
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.53	0.41
56:2y:66:U:C4	56:2y:67:C:C4	3.08	0.41
1:1A:483:A:O2'	20:1Y:49:VAL:O	2.34	0.41
1:1A:603:A:C8	1:1A:655:A:C6	3.08	0.41
1:1A:1017:G:N7	64:1A:4221:HOH:O	2.37	0.41
1:1A:2149:G:C4	1:1A:2150:U:H1'	2.55	0.41
1:1A:2154:G:C2	1:1A:2155:G:H1'	2.55	0.41
21:1Z:44:PHE:CZ	21:1Z:86:VAL:HG11	2.55	0.41
32:1a:413:G:N2	32:1a:428:G:H1'	2.36	0.41
32:1a:1516:G:H2'	32:1a:1518:MA6:OP2	2.20	0.41
35:1d:140:VAL:HG21	35:1d:146:ILE:HD11	2.01	0.41
56:1y:63:G:H2'	56:1y:64:A:O4'	2.21	0.41
1:2A:881:G:C2	1:2A:882:G:H1'	2.56	0.41
1:2A:909:A:O2'	1:2A:910:A:H5'	2.20	0.41
1:2A:1445(A):C:H2'	1:2A:1446:C:H6	1.85	0.41
1:2A:1713:U:H3	1:2A:1746:G:H1	1.67	0.41
1:2A:2592:G:H2'	1:2A:2593:U:O4'	2.20	0.41
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.54	0.41
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.84	0.41
6:2G:171:ALA:O	6:2G:175:LEU:HG	2.20	0.41
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.52	0.41
8:2I:82:ARG:H	8:2I:82:ARG:HG3	1.65	0.41
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.55	0.41
31:29:13:LYS:HD3	31:29:13:LYS:HA	1.77	0.41
32:2a:452:A:HO2'	32:2a:453:A:H8	1.68	0.41
32:2a:1003:G:C6	32:2a:1004:A:C6	3.08	0.41
32:2a:1122:U:C4	32:2a:1123:A:N7	2.88	0.41
32:2a:1379:G:O6	38:2g:2:ALA:HB3	2.21	0.41
33:2b:212:GLN:OE1	33:2b:235:SER:HB3	2.20	0.41
35:2d:3:ARG:O	35:2d:5:ILE:HG22	2.20	0.41
35:2d:11:LEU:O	35:2d:15:GLU:HG2	2.20	0.41
1:1A:363:G:H2'	1:1A:363(A):A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:460:A:P	29:17:41:ARG:HH22	2.43	0.41
1:1A:817:C:H4'	1:1A:932:G:C5	2.56	0.41
1:1A:1052:C:H2'	1:1A:1053:C:H6	1.85	0.41
1:1A:1103:A:H2'	1:1A:1104:C:C6	2.56	0.41
1:1A:1364:G:P	23:11:3:LYS:HG3	2.61	0.41
1:1A:1465:G:C6	1:1A:1466:G:C5	3.09	0.41
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.81	0.41
1:1A:2094:G:P	8:1I:22:LYS:HD2	2.61	0.41
1:1A:2712:U:H2'	1:1A:2714:G:H5"	2.03	0.41
6:1G:98:ARG:NE	26:14:1:MET:HE3	2.34	0.41
7:1H:3:ARG:HD2	7:1H:3:ARG:HA	1.84	0.41
30:18:54:GLU:O	30:18:58:ILE:HG13	2.21	0.41
32:1a:22:G:H4'	32:1a:885:G:C8	2.56	0.41
32:1a:343:U:O2'	32:1a:346:G:O6	2.35	0.41
32:1a:1285:A:H4'	32:1a:1286:A:O5'	2.20	0.41
34:1c:22:TRP:CH2	45:1n:54:PRO:HG2	2.55	0.41
34:1c:52:LEU:HD13	34:1c:68:VAL:HG13	2.03	0.41
36:1e:41:VAL:O	36:1e:66:MET:HA	2.21	0.41
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.21	0.41
54:1w:8:4SU:H6	54:1w:8:4SU:O5'	2.20	0.41
1:2A:25:U:H5'	18:2W:79:GLY:HA2	2.03	0.41
1:2A:514:A:N3	1:2A:581:C:O2'	2.51	0.41
1:2A:975(A):G:C2	1:2A:990:A:C8	3.08	0.41
1:2A:1530:C:H6	1:2A:1530:C:H2'	1.60	0.41
4:2E:5:LEU:HD21	4:2E:79:ARG:HB2	2.03	0.41
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.20	0.41
6:2G:45:GLU:H	6:2G:45:GLU:HG2	1.41	0.41
6:2G:179:PRO:HG3	26:24:43:TYR:CZ	2.56	0.41
29:27:24:THR:CG2	29:27:27:GLY:H	2.31	0.41
32:2a:1027:C:C4	32:2a:1034:G:O6	2.73	0.41
32:2a:1410:G:H2'	32:2a:1411:C:C6	2.55	0.41
32:2a:1530:G:H2'	32:2a:1531:A:O4'	2.21	0.41
35:2d:191:ARG:HD2	35:2d:191:ARG:HA	1.88	0.41
38:2g:79:ARG:O	38:2g:80:VAL:C	2.63	0.41
39:2h:21:LYS:N	39:2h:65:TYR:OH	2.53	0.41
39:2h:53:VAL:HB	39:2h:58:TYR:CD2	2.56	0.41
41:2j:9:ARG:HH22	41:2j:69:ASN:ND2	2.19	0.41
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	2.03	0.41
55:2x:58:A:H4'	55:2x:59:A:OP1	2.20	0.41
56:2y:34:G:H2'	56:2y:35:A:H8	1.85	0.41
1:1A:226:G:H21	1:1A:228:A:H62	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1423:G:H2'	1:1A:1424:G:H8	1.85	0.41
1:1A:1584:C:O2'	1:1A:1586:A:H5'	2.20	0.41
1:1A:1647:G:H3'	1:1A:1647:G:OP2	2.20	0.41
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.20	0.41
1:1A:2149:G:C2	1:1A:2150:U:H1'	2.56	0.41
1:1A:2741:A:H2'	1:1A:2742:C:O4'	2.20	0.41
2:1B:66:A:H61	2:1B:108:U:H2'	1.84	0.41
2:1B:88:C:H2'	2:1B:89:G:O4'	2.20	0.41
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.67	0.41
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.63	0.41
8:1I:4:ILE:HD11	8:1I:44:LEU:HD12	2.02	0.41
8:1I:109:ILE:HD13	8:1I:109:ILE:HA	1.84	0.41
9:1N:13:TRP:CE2	9:1N:133:GLN:HG2	2.56	0.41
12:1Q:17:LEU:HD21	12:1Q:96:VAL:HG13	2.02	0.41
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.77	0.41
32:1a:627:G:O2'	32:1a:628:G:H5'	2.20	0.41
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.20	0.41
33:1b:122:PHE:HE2	33:1b:139:LYS:HB2	1.85	0.41
36:1e:31:LEU:HD11	36:1e:129:ILE:HA	2.02	0.41
36:1e:94:ALA:HB1	36:1e:98:THR:HG21	2.02	0.41
40:1i:16:ARG:HB2	40:1i:64:THR:HB	2.01	0.41
44:1m:96:LEU:O	44:1m:110:ARG:NE	2.51	0.41
49:1r:53:ARG:HH21	49:1r:59:SER:HA	1.86	0.41
51:1t:58:LYS:HE2	51:1t:62:LEU:HD21	2.02	0.41
1:2A:955:C:N4	1:2A:956:G:C6	2.88	0.41
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.48	0.41
1:2A:2298:A:N6	1:2A:2318:G:H8	2.17	0.41
1:2A:2853:C:H2'	1:2A:2854:G:C8	2.55	0.41
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	2.03	0.41
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.56	0.41
9:2N:96:GLU:H	9:2N:96:GLU:CD	2.29	0.41
10:2O:71:ARG:HH22	10:2O:122:LEU:C	2.28	0.41
12:2Q:79:LEU:HD23	12:2Q:79:LEU:HA	1.77	0.41
26:24:1:MET:HE2	26:24:6:HIS:CD2	2.55	0.41
32:2a:390:C:H4'	47:2p:28:ARG:HH21	1.86	0.41
32:2a:909:A:H2'	32:2a:910:C:O4'	2.20	0.41
32:2a:1070:U:H2'	32:2a:1071:C:H6	1.85	0.41
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.56	0.41
33:2b:111:ARG:HA	33:2b:111:ARG:HD3	1.89	0.41
33:2b:118:LEU:HD11	33:2b:138:LEU:HB3	2.03	0.41
40:2i:85:LEU:O	40:2i:89:ASN:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2o:69:TYR:CZ	46:2o:73:GLU:HG3	2.56	0.41
48:2q:53:LEU:HD12	48:2q:53:LEU:HA	1.92	0.41
1:1A:875:G:H2'	1:1A:876:C:C6	2.56	0.41
1:1A:1021:A:N3	1:1A:1021:A:H3'	2.36	0.41
1:1A:1334:G:OP2	64:1A:4141:HOH:O	2.22	0.41
1:1A:2143:C:H2'	1:1A:2144:U:C4'	2.51	0.41
1:1A:2336:A:H61	22:10:43:THR:CG2	2.34	0.41
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.56	0.41
1:1A:2848:G:H3'	15:1T:95:ARG:O	2.21	0.41
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.18	0.41
4:1E:103:ASP:OD2	4:1E:168:MET:HE3	2.20	0.41
5:1F:136:THR:HA	5:1F:166:ALA:O	2.19	0.41
8:1I:48:GLU:HB3	8:1I:52:ARG:HH12	1.85	0.41
32:1a:337:C:H2'	32:1a:338:A:C8	2.56	0.41
32:1a:691:G:H2'	32:1a:692:U:C6	2.56	0.41
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.20	0.41
35:1d:172:PRO:C	35:1d:174:LEU:H	2.28	0.41
42:1k:63:LEU:HD23	42:1k:63:LEU:HA	1.92	0.41
1:2A:1449:A:HO2'	1:2A:1529:G:H21	1.68	0.41
1:2A:2641:G:H5"	9:2N:76:SER:HB3	2.01	0.41
8:2I:78:THR:HA	8:2I:143:SER:HB2	2.02	0.41
18:2W:36:LEU:HD13	18:2W:48:ALA:HA	2.02	0.41
19:2X:60:ARG:HH22	29:27:47:ARG:NH1	2.19	0.41
21:2Z:157:LEU:HD12	21:2Z:161:VAL:O	2.20	0.41
21:2Z:163:LEU:HD12	21:2Z:163:LEU:HA	1.93	0.41
32:2a:580:U:H2'	32:2a:581:G:O4'	2.20	0.41
32:2a:976:G:OP1	45:2n:32:SER:N	2.52	0.41
32:2a:1016:A:N6	32:2a:1017:G:C2	2.89	0.41
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.53	0.41
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.21	0.41
33:2b:150:SER:O	33:2b:153:ARG:HG2	2.21	0.41
34:2c:159:GLY:HA2	34:2c:193:TYR:CZ	2.56	0.41
36:2e:42:GLY:HA2	36:2e:65:ASN:O	2.21	0.41
40:2i:80:GLY:HA2	40:2i:83:ARG:HB2	2.02	0.41
46:2o:87:ILE:HG22	46:2o:88:ARG:N	2.34	0.41
1:1A:484:C:H2'	1:1A:485:C:C6	2.56	0.41
1:1A:1035:U:H2'	1:1A:1036:G:C8	2.55	0.41
1:1A:1040:C:H2'	1:1A:1041:C:O4'	2.21	0.41
2:1B:108:U:H2'	2:1B:109:C:H5"	2.03	0.41
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.51	0.41
25:13:18:ASP:OD1	25:13:18:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:53:GLU:H	26:14:53:GLU:HG3	1.43	0.41
32:1a:4:U:C4	39:1h:105:ARG:HD3	2.56	0.41
32:1a:204:U:H4'	32:1a:216:G:H5"	2.01	0.41
32:1a:816:A:OP2	32:1a:1527:C:H5'	2.21	0.41
33:1b:88:ALA:O	33:1b:226:ARG:NH1	2.54	0.41
47:1p:5:ARG:NH2	47:1p:28:ARG:HA	2.36	0.41
1:2A:8:A:H2'	1:2A:9:U:C6	2.56	0.41
1:2A:1647:G:OP2	1:2A:1647:G:H3'	2.21	0.41
1:2A:2406:U:H6	1:2A:2406:U:H2'	1.72	0.41
10:2O:111:PHE:O	10:2O:115:VAL:HG23	2.20	0.41
14:2S:83:LYS:HD2	14:2S:111:GLU:CD	2.46	0.41
20:2Y:43:ASN:HB2	20:2Y:67:LEU:HD21	2.02	0.41
21:2Z:159:PRO:HA	21:2Z:160:GLY:HA2	1.67	0.41
32:2a:16:A:N1	32:2a:919:A:H2	2.19	0.41
32:2a:918:A:H2'	32:2a:919:A:O4'	2.21	0.41
32:2a:993:G:N3	32:2a:993:G:H2'	2.36	0.41
32:2a:1027:C:O2'	32:2a:1034:G:N2	2.46	0.41
33:2b:92:TYR:CZ	33:2b:151:GLY:HA3	2.55	0.41
35:2d:109:GLY:HA3	35:2d:165:MET:HE3	2.02	0.41
35:2d:201:GLN:HE22	36:2e:99:GLY:HA2	1.85	0.41
39:2h:9:MET:HB2	39:2h:26:VAL:HG11	2.03	0.41
44:2m:40:ASN:ND2	44:2m:43:THR:HG23	2.36	0.41
54:2w:58:A:O2'	54:2w:60:U:OP2	2.30	0.41
1:1A:271(R):G:H2'	1:1A:271(S):G:H5"	2.03	0.41
1:1A:337:C:H2'	1:1A:338:G:O4'	2.21	0.41
1:1A:811:U:H2'	11:1P:21:ARG:HA	2.03	0.41
1:1A:822:U:OP2	64:1A:4140:HOH:O	2.22	0.41
1:1A:897:C:C2	1:1A:898:C:C4	3.09	0.41
1:1A:1057:A:N7	1:1A:1086:A:H2'	2.36	0.41
1:1A:2552:OMU:O5'	1:1A:2552:OMU:H6	2.20	0.41
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.56	0.41
3:1D:130:ALA:C	3:1D:131:LEU:HD12	2.45	0.41
3:1D:155:LEU:HD23	3:1D:177:LEU:HD22	2.02	0.41
6:1G:67:LYS:HD3	26:14:5:ILE:HD12	2.03	0.41
7:1H:84:SER:HA	7:1H:133:VAL:O	2.21	0.41
13:1R:9:LYS:O	13:1R:17:ARG:HD3	2.20	0.41
16:1U:9:VAL:O	16:1U:13:LYS:HG3	2.21	0.41
26:14:53:GLU:HB2	26:14:55:ARG:O	2.20	0.41
32:1a:4:U:O4	39:1h:105:ARG:HD3	2.21	0.41
32:1a:341:C:H2'	32:1a:342:C:C6	2.55	0.41
32:1a:407:G:H2'	32:1a:408:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:433:C:H2'	32:1a:434:U:C6	2.56	0.41
32:1a:472:A:H2'	32:1a:473:G:O4'	2.21	0.41
32:1a:636:U:H2'	32:1a:637:G:C8	2.56	0.41
32:1a:662:G:H2'	32:1a:663:A:C8	2.55	0.41
32:1a:762:C:H2'	32:1a:763:G:C8	2.56	0.41
32:1a:1004:A:H5'	32:1a:1024:G:N2	2.35	0.41
32:1a:1251:A:H2'	32:1a:1252:A:O4'	2.21	0.41
33:1b:208:ILE:H	33:1b:208:ILE:HG12	1.71	0.41
40:1i:36:TYR:CZ	40:1i:70:LYS:HE2	2.56	0.41
41:1j:19:SER:OG	41:1j:91:PRO:HD2	2.21	0.41
41:1j:31:GLY:HA3	41:1j:32:ALA:HA	1.69	0.41
41:1j:81:THR:C	41:1j:83:GLU:N	2.79	0.41
44:1m:90:LEU:HD23	44:1m:93:ARG:NH1	2.35	0.41
56:1y:14:A:C6	56:1y:22:G:C2	3.09	0.41
56:1y:57:G:H2'	56:1y:58:A:H5'	2.02	0.41
56:1y:69:G:C4	56:1y:70:G:C8	3.09	0.41
1:2A:229:A:H5'	1:2A:230:U:OP1	2.21	0.41
1:2A:457:A:H61	1:2A:470:A:H5"	1.85	0.41
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.54	0.41
1:2A:1372:U:H2'	1:2A:1373:A:O4'	2.21	0.41
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.55	0.41
1:2A:1702:G:H2'	1:2A:1703:G:O4'	2.19	0.41
1:2A:1802:A:N1	1:2A:1822:G:H1'	2.36	0.41
1:2A:1848:A:C6	32:2a:702:A:C6	3.09	0.41
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.56	0.41
1:2A:2336:A:H61	22:20:43:THR:HG22	1.86	0.41
1:2A:2655:G:O2'	1:2A:2664:G:O6	2.33	0.41
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	2.03	0.41
7:2H:77:LYS:HD2	7:2H:83:TYR:CZ	2.56	0.41
9:2N:73:THR:HG22	9:2N:84:LYS:HG2	2.03	0.41
10:2O:113:LYS:HD3	10:2O:113:LYS:HA	1.79	0.41
23:21:56:GLN:HG3	23:21:90:ILE:HD12	2.03	0.41
23:21:67:ILE:N	23:21:68:PRO:HD2	2.36	0.41
26:24:64:GLY:O	26:24:66:SER:N	2.45	0.41
32:2a:90:U:H2'	32:2a:91:C:H6	1.86	0.41
32:2a:580:U:H5"	46:2o:58:MET:HG2	2.02	0.41
32:2a:868:C:H2'	32:2a:869:G:O4'	2.21	0.41
33:2b:32:ILE:HD11	33:2b:190:THR:HB	2.03	0.41
33:2b:81:VAL:HG22	33:2b:215:LEU:HD11	2.03	0.41
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.21	0.41
39:2h:96:GLY:H	39:2h:99:GLU:CD	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:4:TYR:CE1	40:2i:88:TYR:HA	2.55	0.41
41:2j:44:VAL:HA	41:2j:66:ARG:HA	2.03	0.41
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.21	0.41
53:2v:14:A:C2	56:2y:34:G:C2	3.08	0.41
1:1A:710:G:H2'	1:1A:711:G:C8	2.55	0.41
1:1A:2164:C:H2'	1:1A:2165:G:H5'	2.02	0.41
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.56	0.41
32:1a:148:G:H2'	32:1a:149:A:H8	1.86	0.41
32:1a:953:G:H2'	32:1a:954:G:O4'	2.21	0.41
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.36	0.41
32:1a:1441:G:H5"	32:1a:1442:G:O5'	2.21	0.41
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.90	0.41
1:2A:510:C:H2'	1:2A:511:U:O4'	2.21	0.41
1:2A:611:C:H2'	1:2A:612:C:C6	2.56	0.41
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.21	0.41
1:2A:1321:A:H2'	1:2A:1322:A:O4'	2.21	0.41
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	2.02	0.41
4:2E:36:ARG:NH2	4:2E:88:GLY:O	2.53	0.41
5:2F:120:GLU:HG3	5:2F:122:LYS:HG2	2.03	0.41
13:2R:36:THR:HG22	13:2R:37:THR:H	1.86	0.41
21:2Z:55:HIS:HE1	21:2Z:135:GLU:HB2	1.85	0.41
32:2a:1004:A:H61	32:2a:1037:C:H1'	1.83	0.41
32:2a:1225:A:H2'	32:2a:1226:C:C5	2.55	0.41
32:2a:1297:C:O2'	38:2g:114:ARG:NH1	2.54	0.41
34:2c:13:GLY:HA3	45:2n:57:ARG:HH12	1.86	0.41
34:2c:38:ARG:HE	34:2c:38:ARG:HB2	1.55	0.41
1:1A:279:C:H42	1:1A:361:G:H1	1.68	0.40
1:1A:637:A:H4'	1:1A:638:G:O5'	2.21	0.40
1:1A:1047:G:H2'	1:1A:1110:G:N1	2.36	0.40
6:1G:148:MET:HE2	6:1G:148:MET:HB2	1.98	0.40
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.21	0.40
24:12:3:LEU:HA	24:12:3:LEU:HD23	1.87	0.40
32:1a:375:U:C2	32:1a:376:G:C8	3.08	0.40
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	2.03	0.40
34:1c:71:ALA:HA	34:1c:106:VAL:CG2	2.51	0.40
40:1i:56:LEU:HD23	40:1i:57:GLY:H	1.86	0.40
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	2.03	0.40
1:2A:888:C:OP1	44:2m:93:ARG:HD3	2.20	0.40
1:2A:1384:A:N3	1:2A:1405:U:H1'	2.36	0.40
1:2A:2058:MA6:H92	64:2A:4416:HOH:O	2.21	0.40
1:2A:2113:U:H3	1:2A:2169:A:H62	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.56	0.40
1:2A:2319:G:H22	14:2S:3:ARG:HD2	1.82	0.40
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.53	0.40
2:2B:24:G:H4'	2:2B:25:A:C8	2.55	0.40
2:2B:78:A:C2	2:2B:100:A:C4	3.09	0.40
6:2G:53:LEU:HA	6:2G:53:LEU:HD22	1.85	0.40
7:2H:137:ASP:HB3	7:2H:140:LYS:HB2	2.03	0.40
8:2I:53:ALA:O	8:2I:57:ARG:HG2	2.21	0.40
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.20	0.40
32:2a:540:G:C4	32:2a:541:G:C8	3.09	0.40
32:2a:1320:C:N3	50:2s:36:ARG:NH2	2.69	0.40
34:2c:134:ILE:HG22	34:2c:168:ALA:HB3	2.03	0.40
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.46	0.40
1:1A:27:G:C2	1:1A:512:G:N3	2.89	0.40
1:1A:518:G:H2'	1:1A:519:U:C6	2.56	0.40
1:1A:518:G:H4'	18:1W:18:ARG:NE	2.36	0.40
1:1A:1394:U:H2'	1:1A:1395:A:O4'	2.22	0.40
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.21	0.40
1:1A:1952:A:C6	1:1A:1953:A:N1	2.90	0.40
1:1A:2577:A:OP2	27:15:3:LYS:NZ	2.41	0.40
2:1B:1:U:H2'	2:1B:2:C:C6	2.56	0.40
11:1P:3:LEU:HD23	11:1P:3:LEU:HA	1.90	0.40
26:14:61:ARG:O	26:14:62:ARG:C	2.64	0.40
32:1a:181:G:H4'	32:1a:182:U:H5'	2.03	0.40
32:1a:567:G:H2'	32:1a:568:G:O4'	2.22	0.40
32:1a:1039:C:H2'	32:1a:1040:U:H6	1.87	0.40
38:1g:111:ARG:HD2	38:1g:123:GLU:HB2	2.03	0.40
54:1w:63:G:H2'	54:1w:64:A:C8	2.57	0.40
56:1y:24:G:H2'	56:1y:25:C:O4'	2.21	0.40
1:2A:1263:U:H1'	27:25:10:LYS:HG3	2.03	0.40
1:2A:2104:G:C2	1:2A:2186:G:C2	3.09	0.40
1:2A:2788:C:C5'	4:2E:61:ARG:HH21	2.35	0.40
1:2A:2849:U:OP1	15:2T:95:ARG:NH1	2.53	0.40
4:2E:181:LEU:HA	4:2E:181:LEU:HD12	1.80	0.40
6:2G:109:VAL:HG21	6:2G:142:PRO:HG3	2.03	0.40
6:2G:173:LEU:HD22	6:2G:178:PHE:CE1	2.56	0.40
32:2a:4:U:O4	39:2h:105:ARG:HD3	2.21	0.40
32:2a:909:A:N3	32:2a:1413:A:O2'	2.49	0.40
32:2a:1001(A):G:C4	32:2a:1002:G:H1'	2.57	0.40
32:2a:1125:U:OP1	41:2j:35:SER:OG	2.37	0.40
32:2a:1229:A:O3'	55:2x:30:G:H5"	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1249:C:O4'	40:2i:70:LYS:NZ	2.54	0.40
33:2b:74:LYS:HD2	33:2b:166:ASP:CB	2.50	0.40
34:2c:16:ARG:HD3	34:2c:16:ARG:HA	1.77	0.40
34:2c:188:LEU:HA	34:2c:188:LEU:HD12	1.80	0.40
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.48	0.40
36:2e:99:GLY:O	36:2e:117:ASP:HA	2.21	0.40
40:2i:100:GLY:O	40:2i:102:LEU:N	2.54	0.40
44:2m:50:GLU:O	44:2m:53:VAL:HG22	2.21	0.40
49:2r:53:ARG:HA	49:2r:56:THR:OG1	2.21	0.40
56:2y:67:C:H2'	56:2y:68:C:C6	2.57	0.40
1:1A:1058:G:N2	1:1A:1080:C:N3	2.66	0.40
1:1A:1669:A:H5"	1:1A:2550:G:OP1	2.21	0.40
1:1A:2105:C:H2'	1:1A:2106:G:C8	2.57	0.40
1:1A:2515:C:O2'	1:1A:2516:G:H5'	2.21	0.40
2:1B:4:C:H2'	2:1B:5:C:O4'	2.22	0.40
22:10:18:ALA:HB3	22:10:20:ARG:NH1	2.36	0.40
28:16:6:ARG:NH2	28:16:26:ASN:HB2	2.36	0.40
32:1a:679:C:H2'	32:1a:680:C:C6	2.56	0.40
32:1a:865:A:C2	32:1a:918:A:H4'	2.56	0.40
32:1a:867:G:O2'	32:1a:873:A:N1	2.53	0.40
32:1a:972:C:O2'	41:1j:55:LYS:O	2.38	0.40
32:1a:1132:C:H2'	32:1a:1133:G:C8	2.53	0.40
32:1a:1172:C:H2'	32:1a:1173:G:H8	1.87	0.40
32:1a:1239:A:C4	32:1a:1298:C:N4	2.89	0.40
33:1b:44:LEU:HA	33:1b:47:THR:OG1	2.21	0.40
33:1b:74:LYS:HE3	33:1b:166:ASP:HB2	2.02	0.40
34:1c:26:LYS:HE2	34:1c:26:LYS:HB3	1.94	0.40
1:2A:185:U:H4'	1:2A:218:A:H4'	2.03	0.40
1:2A:208:C:H2'	1:2A:209:C:C6	2.57	0.40
1:2A:271(I):G:H1	1:2A:271(O):C:H42	1.70	0.40
1:2A:894:C:O2'	1:2A:895:U:H5"	2.22	0.40
1:2A:952:G:C6	1:2A:953:A:N7	2.89	0.40
1:2A:1138:G:N3	9:2N:106:MET:HE2	2.35	0.40
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.56	0.40
1:2A:2096:U:H3	1:2A:2193:G:H1	1.69	0.40
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.20	0.40
17:2V:1:MET:HE1	17:2V:44:LYS:H	1.86	0.40
26:24:50:VAL:HG21	44:2m:65:LYS:HA	2.04	0.40
32:2a:35:G:O2'	43:2l:118:SER:O	2.38	0.40
32:2a:141:A:H1'	32:2a:182:U:O2	2.21	0.40
32:2a:567:G:H2'	32:2a:568:G:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:16:HIS:C	33:2b:18:GLY:N	2.79	0.40
33:2b:55:PHE:CE1	33:2b:218:ALA:HA	2.57	0.40
35:2d:165:MET:HE2	35:2d:168:ARG:NE	2.36	0.40
1:1A:68:G:H2'	1:1A:69:C:O4'	2.21	0.40
1:1A:1645:G:H5"	1:1A:1646:C:H5'	2.04	0.40
1:1A:2105:C:H2'	1:1A:2106:G:H8	1.86	0.40
1:1A:2160:G:C6	1:1A:2161:C:N4	2.90	0.40
1:1A:2584:U:O2	1:1A:2585:U:C4	2.74	0.40
1:1A:2818:G:O2'	1:1A:2819:G:H5'	2.20	0.40
3:1D:92:ILE:HD12	3:1D:104:TYR:CD1	2.56	0.40
11:1P:126:VAL:HG12	11:1P:148:LEU:HD22	2.02	0.40
32:1a:1025:U:C2	32:1a:1036:G:O6	2.75	0.40
33:1b:131:PRO:O	33:1b:135:GLN:N	2.54	0.40
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	2.02	0.40
48:1q:14:LYS:H	48:1q:14:LYS:HG2	1.74	0.40
48:1q:15:MET:HB2	48:1q:15:MET:HE3	1.83	0.40
54:1w:11:C:O2'	54:1w:12:U:H5'	2.22	0.40
1:2A:27:G:C2	1:2A:512:G:N3	2.89	0.40
1:2A:392:C:H5"	1:2A:409:C:H5"	2.04	0.40
1:2A:528:A:O2'	1:2A:529:A:H5'	2.22	0.40
1:2A:631:A:H2'	1:2A:632:A:O4'	2.20	0.40
1:2A:686:G:H21	1:2A:788:A:H61	1.69	0.40
1:2A:1181:C:H2'	1:2A:1182:A:H8	1.85	0.40
1:2A:1625:C:H2'	1:2A:1626:G:O4'	2.21	0.40
1:2A:2391:G:O6	1:2A:2425:A:H8	2.05	0.40
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.55	0.40
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.55	0.40
32:2a:537:G:H5"	43:2l:113:ARG:NH1	2.37	0.40
32:2a:828:A:H2'	32:2a:829:G:O4'	2.22	0.40
32:2a:978:A:O2'	32:2a:1322:C:N3	2.40	0.40
32:2a:1006:C:H42	32:2a:1023:G:H1	1.68	0.40
32:2a:1072:G:H2'	32:2a:1073:U:C6	2.57	0.40
32:2a:1168:A:C6	32:2a:1169:A:C6	3.10	0.40
33:2b:207:ALA:O	33:2b:211:ILE:HG13	2.21	0.40
35:2d:20:TYR:HD1	35:2d:26:CYS:HB3	1.85	0.40
38:2g:53:LYS:HB3	38:2g:53:LYS:HE2	1.88	0.40
41:2j:47:PHE:CZ	45:2n:37:PHE:HE2	2.40	0.40
55:2x:61:C:H2'	55:2x:62:C:C6	2.56	0.40
55:2x:66:C:H2'	55:2x:67:C:C6	2.57	0.40
56:2y:42:C:H2'	56:2y:43:C:H6	1.85	0.40
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:601:C:O2'	1:1A:605:C:H5"	2.21	0.40
1:1A:634:C:H2'	1:1A:635:C:C6	2.56	0.40
1:1A:1756:G:H4'	1:1A:1758:G:O4'	2.21	0.40
1:1A:2127:G:N2	1:1A:2173:A:H1'	2.36	0.40
1:1A:2144:U:H3'	1:1A:2146:C:N4	2.37	0.40
1:1A:2779:U:H5'	1:1A:2781:A:O4'	2.22	0.40
3:1D:108:PRO:HB3	3:1D:143:HIS:HE1	1.84	0.40
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	2.04	0.40
9:1N:68:GLU:HG2	9:1N:88:GLU:OE2	2.21	0.40
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.22	0.40
12:1Q:17:LEU:HD23	12:1Q:17:LEU:HA	1.77	0.40
12:1Q:137:TYR:O	12:1Q:141:GLN:HG2	2.21	0.40
13:1R:100:LEU:HD12	13:1R:100:LEU:HA	1.95	0.40
20:1Y:83:THR:HG21	20:1Y:99:CYS:HB2	2.04	0.40
32:1a:1328:C:H2'	32:1a:1329:A:O4'	2.22	0.40
32:1a:1343:G:H1'	40:1i:121:ARG:NH1	2.35	0.40
34:1c:36:ASP:OD1	34:1c:57:ILE:HG21	2.21	0.40
36:1e:42:GLY:HA2	36:1e:65:ASN:O	2.22	0.40
39:1h:44:PHE:HB3	39:1h:80:ILE:CG1	2.51	0.40
1:2A:471:A:H2'	1:2A:472:A:O4'	2.21	0.40
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.85	0.40
1:2A:2193:G:H2'	1:2A:2194:G:H8	1.87	0.40
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.57	0.40
1:2A:2343:C:O2'	1:2A:2373:G:O2'	2.30	0.40
1:2A:2495:G:H5"	12:2Q:82:ARG:HG2	2.03	0.40
1:2A:2811:G:N2	1:2A:2891:G:H1'	2.36	0.40
1:2A:2839:G:H5'	13:2R:46:GLY:CA	2.47	0.40
11:2P:37:GLY:O	11:2P:40:SER:OG	2.34	0.40
12:2Q:137:TYR:CE1	21:2Z:83:PRO:HG3	2.56	0.40
20:2Y:43:ASN:HD22	20:2Y:43:ASN:HA	1.69	0.40
32:2a:353:A:H5'	32:2a:353:A:H8	1.87	0.40
32:2a:566:G:H4'	32:2a:567:G:OP1	2.22	0.40
32:2a:1147:C:H5'	32:2a:1148:U:OP2	2.22	0.40
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.54	0.40
32:2a:1206:G:O2'	34:2c:193:TYR:HA	2.22	0.40
32:2a:1270:C:OP2	52:2u:24:ARG:NH2	2.54	0.40
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.56	0.40
32:2a:1316:G:H22	32:2a:1319:A:C5'	2.32	0.40
34:2c:149:ALA:HA	34:2c:201:TYR:O	2.21	0.40
44:2m:53:VAL:HG23	44:2m:57:ARG:HH12	1.87	0.40
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:58:LEU:HD22	49:2r:62:GLU:HB3	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:358:U:OP1	8:2I:121:LYS:NZ[2_655]	2.17	0.03

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%)	260 (95%)	13 (5%)	0	100	100
3	2D	273/276 (99%)	259 (95%)	14 (5%)	0	100	100
4	1E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	25	38
4	2E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	25	38
5	1F	201/210 (96%)	197 (98%)	3 (2%)	1 (0%)	25	38
5	2F	201/210 (96%)	192 (96%)	8 (4%)	1 (0%)	25	38
6	1G	179/182 (98%)	168 (94%)	11 (6%)	0	100	100
6	2G	179/182 (98%)	156 (87%)	18 (10%)	5 (3%)	4	4
7	1H	172/180 (96%)	165 (96%)	7 (4%)	0	100	100
7	2H	172/180 (96%)	153 (89%)	18 (10%)	1 (1%)	22	33
8	1I	144/148 (97%)	134 (93%)	10 (7%)	0	100	100
8	2I	144/148 (97%)	123 (85%)	18 (12%)	3 (2%)	5	7
9	1N	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
9	2N	138/140 (99%)	129 (94%)	8 (6%)	1 (1%)	19	29
10	1O	120/122 (98%)	113 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
10	2O	120/122 (98%)	115 (96%)	5 (4%)	0	100 100
11	1P	147/150 (98%)	130 (88%)	15 (10%)	2 (1%)	9 13
11	2P	147/150 (98%)	132 (90%)	12 (8%)	3 (2%)	6 8
12	1Q	139/141 (99%)	134 (96%)	5 (4%)	0	100 100
12	2Q	139/141 (99%)	132 (95%)	7 (5%)	0	100 100
13	1R	116/118 (98%)	113 (97%)	3 (3%)	0	100 100
13	2R	116/118 (98%)	112 (97%)	4 (3%)	0	100 100
14	1S	108/112 (96%)	102 (94%)	6 (6%)	0	100 100
14	2S	108/112 (96%)	101 (94%)	6 (6%)	1 (1%)	14 22
15	1T	129/146 (88%)	124 (96%)	4 (3%)	1 (1%)	16 26
15	2T	129/146 (88%)	121 (94%)	8 (6%)	0	100 100
16	1U	114/118 (97%)	114 (100%)	0	0	100 100
16	2U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
17	1V	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	13 20
17	2V	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	13 20
18	1W	110/113 (97%)	110 (100%)	0	0	100 100
18	2W	110/113 (97%)	108 (98%)	2 (2%)	0	100 100
19	1X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	12 18
19	2X	93/96 (97%)	88 (95%)	5 (5%)	0	100 100
20	1Y	105/110 (96%)	98 (93%)	6 (6%)	1 (1%)	13 20
20	2Y	105/110 (96%)	97 (92%)	7 (7%)	1 (1%)	13 20
21	1Z	148/206 (72%)	136 (92%)	11 (7%)	1 (1%)	19 29
21	2Z	156/206 (76%)	131 (84%)	20 (13%)	5 (3%)	3 3
22	10	81/85 (95%)	80 (99%)	1 (1%)	0	100 100
22	20	81/85 (95%)	79 (98%)	2 (2%)	0	100 100
23	11	95/98 (97%)	94 (99%)	0	1 (1%)	12 18
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	12 18
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100 100
24	22	68/72 (94%)	68 (100%)	0	0	100 100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
25	23	57/60 (95%)	53 (93%)	4 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
26	14	67/71 (94%)	57 (85%)	4 (6%)	6 (9%)	0 0
26	24	67/71 (94%)	49 (73%)	14 (21%)	4 (6%)	1 0
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
27	25	57/60 (95%)	57 (100%)	0	0	100 100
28	16	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
28	26	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
29	17	46/49 (94%)	46 (100%)	0	0	100 100
29	27	46/49 (94%)	46 (100%)	0	0	100 100
30	18	62/65 (95%)	61 (98%)	1 (2%)	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%)	34 (97%)	1 (3%)	0	100 100
33	1b	229/256 (90%)	196 (86%)	26 (11%)	7 (3%)	3 3
33	2b	229/256 (90%)	194 (85%)	30 (13%)	5 (2%)	5 6
34	1c	204/239 (85%)	193 (95%)	11 (5%)	0	100 100
34	2c	204/239 (85%)	178 (87%)	23 (11%)	3 (2%)	8 12
35	1d	206/209 (99%)	195 (95%)	10 (5%)	1 (0%)	25 38
35	2d	206/209 (99%)	192 (93%)	12 (6%)	2 (1%)	13 20
36	1e	146/162 (90%)	137 (94%)	6 (4%)	3 (2%)	5 7
36	2e	146/162 (90%)	133 (91%)	12 (8%)	1 (1%)	19 29
37	1f	98/101 (97%)	93 (95%)	5 (5%)	0	100 100
37	2f	98/101 (97%)	95 (97%)	3 (3%)	0	100 100
38	1g	153/156 (98%)	142 (93%)	11 (7%)	0	100 100
38	2g	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	19 29
39	1h	135/138 (98%)	128 (95%)	7 (5%)	0	100 100
39	2h	135/138 (98%)	125 (93%)	10 (7%)	0	100 100
40	1i	125/128 (98%)	109 (87%)	14 (11%)	2 (2%)	8 11
40	2i	125/128 (98%)	109 (87%)	15 (12%)	1 (1%)	16 26
41	1j	95/105 (90%)	84 (88%)	10 (10%)	1 (1%)	12 18
41	2j	94/105 (90%)	77 (82%)	13 (14%)	4 (4%)	2 1
42	1k	112/129 (87%)	100 (89%)	10 (9%)	2 (2%)	7 9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
42	2k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	14 22
43	1l	119/132 (90%)	114 (96%)	5 (4%)	0	100 100
43	2l	119/132 (90%)	109 (92%)	9 (8%)	1 (1%)	16 26
44	1m	121/126 (96%)	110 (91%)	9 (7%)	2 (2%)	7 10
44	2m	120/126 (95%)	103 (86%)	14 (12%)	3 (2%)	4 5
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100 100
45	2n	58/61 (95%)	53 (91%)	5 (9%)	0	100 100
46	1o	86/89 (97%)	81 (94%)	5 (6%)	0	100 100
46	2o	86/89 (97%)	84 (98%)	1 (1%)	1 (1%)	11 16
47	1p	80/88 (91%)	73 (91%)	7 (9%)	0	100 100
47	2p	80/88 (91%)	73 (91%)	7 (9%)	0	100 100
48	1q	97/105 (92%)	91 (94%)	6 (6%)	0	100 100
48	2q	97/105 (92%)	91 (94%)	4 (4%)	2 (2%)	5 7
49	1r	66/88 (75%)	61 (92%)	5 (8%)	0	100 100
49	2r	66/88 (75%)	64 (97%)	2 (3%)	0	100 100
50	1s	81/93 (87%)	74 (91%)	6 (7%)	1 (1%)	11 16
50	2s	81/93 (87%)	66 (82%)	13 (16%)	2 (2%)	4 5
51	1t	94/106 (89%)	82 (87%)	10 (11%)	2 (2%)	5 7
51	2t	94/106 (89%)	84 (89%)	9 (10%)	1 (1%)	12 18
52	1u	21/27 (78%)	20 (95%)	1 (5%)	0	100 100
52	2u	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
All	All	11370/12128 (94%)	10564 (93%)	713 (6%)	93 (1%)	16 26

All (93) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	1P	45	LEU
40	1i	54	ASP
44	1m	67	GLU
5	2F	130	ALA
6	2G	51	ARG
11	2P	45	LEU
21	2Z	52	SER
33	2b	17	PHE
38	2g	80	VAL

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Mol	Chain	Res	Type
41	2j	79	ARG
43	2l	91	LYS
44	2m	67	GLU
5	1F	130	ALA
20	1Y	54	LYS
21	1Z	53	ILE
23	11	3	LYS
26	14	47	GLN
26	14	49	PHE
26	14	62	ARG
33	1b	8	LYS
33	1b	126	GLU
42	1k	49	GLY
42	1k	105	VAL
51	1t	47	GLY
51	1t	96	GLY
6	2G	42	GLY
6	2G	126	ASP
7	2H	47	GLU
11	2P	44	GLY
21	2Z	51	ALA
21	2Z	146	ILE
23	21	3	LYS
26	24	45	GLY
35	2d	5	ILE
42	2k	49	GLY
44	2m	106	ASN
48	2q	68	ARG
50	2s	27	GLU
11	1P	38	GLN
26	14	45	GLY
33	1b	17	PHE
6	2G	43	LEU
8	2I	41	GLU
14	2S	84	GLN
33	2b	20	GLU
33	2b	21	ARG
34	2c	95	THR
34	2c	156	ARG
40	2i	121	ARG
46	2o	88	ARG
48	2q	67	LYS

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Mol	Chain	Res	Type
50	2s	9	VAL
4	1E	52	LEU
19	1X	93	GLU
26	14	53	GLU
33	1b	20	GLU
36	1e	21	ALA
36	1e	85	GLY
40	1i	127	LYS
41	1j	78	ASN
50	1s	27	GLU
4	2E	52	LEU
8	2I	10	GLU
9	2N	2	LYS
21	2Z	142	SER
21	2Z	144	LEU
26	24	48	ARG
26	24	49	PHE
33	2b	78	GLN
34	2c	177	THR
41	2j	29	ARG
51	2t	95	ALA
17	1V	79	VAL
33	1b	124	SER
33	1b	231	GLU
35	1d	173	TRP
8	2I	100	ALA
20	2Y	54	LYS
26	24	65	ASP
33	2b	9	GLU
35	2d	3	ARG
26	14	44	THR
41	2j	75	ILE
36	1e	69	VAL
36	2e	69	VAL
41	2j	77	PRO
17	2V	79	VAL
44	2m	6	GLY
15	1T	37	GLY
44	1m	4	ILE
6	2G	24	GLY
11	2P	122	PRO
33	1b	125	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%)	209 (97%)	6 (3%)	38 59
3	2D	215/218 (99%)	205 (95%)	10 (5%)	22 38
4	1E	164/166 (99%)	156 (95%)	8 (5%)	21 36
4	2E	164/166 (99%)	152 (93%)	12 (7%)	11 20
5	1F	160/166 (96%)	142 (89%)	18 (11%)	4 7
5	2F	159/166 (96%)	147 (92%)	12 (8%)	11 18
6	1G	143/156 (92%)	130 (91%)	13 (9%)	7 12
6	2G	143/156 (92%)	123 (86%)	20 (14%)	3 3
7	1H	144/148 (97%)	136 (94%)	8 (6%)	17 30
7	2H	144/148 (97%)	132 (92%)	12 (8%)	9 15
8	1I	113/124 (91%)	95 (84%)	18 (16%)	2 2
8	2I	105/124 (85%)	90 (86%)	15 (14%)	2 3
9	1N	118/119 (99%)	112 (95%)	6 (5%)	20 35
9	2N	118/119 (99%)	114 (97%)	4 (3%)	32 52
10	1O	100/100 (100%)	97 (97%)	3 (3%)	36 57
10	2O	100/100 (100%)	93 (93%)	7 (7%)	12 21
11	1P	115/116 (99%)	107 (93%)	8 (7%)	12 21
11	2P	115/116 (99%)	107 (93%)	8 (7%)	12 21
12	1Q	111/111 (100%)	105 (95%)	6 (5%)	18 32
12	2Q	111/111 (100%)	106 (96%)	5 (4%)	23 40
13	1R	101/101 (100%)	96 (95%)	5 (5%)	20 36
13	2R	101/101 (100%)	96 (95%)	5 (5%)	20 36
14	1S	86/88 (98%)	79 (92%)	7 (8%)	9 15
14	2S	85/88 (97%)	72 (85%)	13 (15%)	2 3
15	1T	115/127 (91%)	112 (97%)	3 (3%)	41 62
15	2T	113/127 (89%)	110 (97%)	3 (3%)	40 60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
16	1U	93/94 (99%)	89 (96%)	4 (4%)	25 42
16	2U	93/94 (99%)	90 (97%)	3 (3%)	34 54
17	1V	80/82 (98%)	74 (92%)	6 (8%)	11 18
17	2V	80/82 (98%)	74 (92%)	6 (8%)	11 18
18	1W	90/92 (98%)	86 (96%)	4 (4%)	24 41
18	2W	90/92 (98%)	84 (93%)	6 (7%)	13 23
19	1X	77/78 (99%)	77 (100%)	0	100 100
19	2X	77/78 (99%)	74 (96%)	3 (4%)	27 46
20	1Y	85/91 (93%)	77 (91%)	8 (9%)	7 11
20	2Y	85/91 (93%)	76 (89%)	9 (11%)	5 8
21	1Z	135/179 (75%)	123 (91%)	12 (9%)	8 12
21	2Z	137/179 (76%)	124 (90%)	13 (10%)	7 11
22	10	65/67 (97%)	63 (97%)	2 (3%)	35 56
22	20	65/67 (97%)	64 (98%)	1 (2%)	60 77
23	11	80/83 (96%)	76 (95%)	4 (5%)	20 36
23	21	80/83 (96%)	76 (95%)	4 (5%)	20 36
24	12	65/67 (97%)	61 (94%)	4 (6%)	15 26
24	22	65/67 (97%)	61 (94%)	4 (6%)	15 26
25	13	51/52 (98%)	48 (94%)	3 (6%)	16 28
25	23	50/52 (96%)	46 (92%)	4 (8%)	10 16
26	14	59/63 (94%)	45 (76%)	14 (24%)	0 0
26	24	53/63 (84%)	43 (81%)	10 (19%)	1 1
27	15	50/52 (96%)	48 (96%)	2 (4%)	27 45
27	25	50/52 (96%)	48 (96%)	2 (4%)	27 45
28	16	51/52 (98%)	46 (90%)	5 (10%)	6 10
28	26	50/52 (96%)	47 (94%)	3 (6%)	16 27
29	17	41/42 (98%)	36 (88%)	5 (12%)	4 5
29	27	41/42 (98%)	36 (88%)	5 (12%)	4 5
30	18	54/55 (98%)	52 (96%)	2 (4%)	29 48
30	28	54/55 (98%)	52 (96%)	2 (4%)	29 48
31	19	34/34 (100%)	32 (94%)	2 (6%)	16 28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
31	29	34/34 (100%)	34 (100%)	0	100 100
33	1b	192/220 (87%)	168 (88%)	24 (12%)	3 5
33	2b	187/220 (85%)	162 (87%)	25 (13%)	3 4
34	1c	142/188 (76%)	126 (89%)	16 (11%)	4 7
34	2c	140/188 (74%)	132 (94%)	8 (6%)	17 29
35	1d	169/181 (93%)	153 (90%)	16 (10%)	7 11
35	2d	173/181 (96%)	156 (90%)	17 (10%)	6 10
36	1e	113/123 (92%)	106 (94%)	7 (6%)	15 26
36	2e	114/123 (93%)	104 (91%)	10 (9%)	8 13
37	1f	84/90 (93%)	76 (90%)	8 (10%)	7 11
37	2f	85/90 (94%)	78 (92%)	7 (8%)	9 15
38	1g	119/127 (94%)	106 (89%)	13 (11%)	5 7
38	2g	120/127 (94%)	108 (90%)	12 (10%)	6 9
39	1h	114/119 (96%)	106 (93%)	8 (7%)	12 21
39	2h	114/119 (96%)	111 (97%)	3 (3%)	41 62
40	1i	90/99 (91%)	83 (92%)	7 (8%)	10 17
40	2i	89/99 (90%)	75 (84%)	14 (16%)	2 2
41	1j	66/92 (72%)	57 (86%)	9 (14%)	3 3
41	2j	69/92 (75%)	62 (90%)	7 (10%)	6 9
42	1k	82/99 (83%)	74 (90%)	8 (10%)	6 10
42	2k	83/99 (84%)	73 (88%)	10 (12%)	4 5
43	1l	96/108 (89%)	94 (98%)	2 (2%)	48 69
43	2l	96/108 (89%)	92 (96%)	4 (4%)	25 43
44	1m	93/101 (92%)	83 (89%)	10 (11%)	5 7
44	2m	92/101 (91%)	74 (80%)	18 (20%)	1 1
45	1n	49/50 (98%)	43 (88%)	6 (12%)	4 5
45	2n	49/50 (98%)	42 (86%)	7 (14%)	2 3
46	1o	78/80 (98%)	71 (91%)	7 (9%)	8 12
46	2o	78/80 (98%)	75 (96%)	3 (4%)	28 47
47	1p	69/74 (93%)	60 (87%)	9 (13%)	3 4
47	2p	68/74 (92%)	58 (85%)	10 (15%)	2 3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
48	1q	94/97 (97%)	89 (95%)	5 (5%)	19 33
48	2q	94/97 (97%)	91 (97%)	3 (3%)	34 54
49	1r	59/77 (77%)	55 (93%)	4 (7%)	13 22
49	2r	59/77 (77%)	55 (93%)	4 (7%)	13 22
50	1s	69/80 (86%)	64 (93%)	5 (7%)	12 20
50	2s	67/80 (84%)	60 (90%)	7 (10%)	5 8
51	1t	70/82 (85%)	65 (93%)	5 (7%)	12 20
51	2t	70/82 (85%)	64 (91%)	6 (9%)	8 14
52	1u	18/22 (82%)	16 (89%)	2 (11%)	5 7
52	2u	18/22 (82%)	18 (100%)	0	100 100
All	All	9303/10064 (92%)	8570 (92%)	733 (8%)	10 16

All (733) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	99	ASP
3	1D	106	ILE
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	12	THR
4	1E	34	VAL
4	1E	41	LYS
4	1E	59	VAL
4	1E	73	GLU
4	1E	116	VAL
4	1E	181	LEU
4	1E	184	VAL
5	1F	9	ILE
5	1F	24	LEU
5	1F	27	GLU
5	1F	28	ILE
5	1F	53	THR
5	1F	57	VAL
5	1F	70	THR
5	1F	74	ARG
5	1F	88	VAL

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Mol	Chain	Res	Type
5	1F	95	ARG
5	1F	132	VAL
5	1F	140	LEU
5	1F	162	LEU
5	1F	168	ARG
5	1F	175	THR
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	5	VAL
6	1G	7	LEU
6	1G	21	ARG
6	1G	22	ARG
6	1G	31	VAL
6	1G	43	LEU
6	1G	45	GLU
6	1G	82	LEU
6	1G	133	LEU
6	1G	139	LEU
6	1G	140	ILE
6	1G	148	MET
6	1G	173	LEU
7	1H	23	ARG
7	1H	45	VAL
7	1H	81	GLU
7	1H	84	SER
7	1H	95	ARG
7	1H	116	GLU
7	1H	124	GLU
7	1H	129	THR
8	1I	9	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	38	LEU
8	1I	41	GLU
8	1I	47	LEU
8	1I	61	ARG
8	1I	76	THR
8	1I	77	LEU
8	1I	85	GLU
8	1I	92	VAL
8	1I	108	THR

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Mol	Chain	Res	Type
8	1I	109	ILE
8	1I	116	LEU
8	1I	123	LEU
8	1I	127	VAL
8	1I	140	LEU
8	1I	144	VAL
9	1N	1	MET
9	1N	2	LYS
9	1N	9	VAL
9	1N	48	MET
9	1N	62	VAL
9	1N	137	LYS
10	1O	28	SER
10	1O	69	ILE
10	1O	106	LEU
11	1P	40	SER
11	1P	45	LEU
11	1P	95	VAL
11	1P	101	VAL
11	1P	119	GLU
11	1P	133	SER
11	1P	147	LEU
11	1P	148	LEU
12	1Q	56	ARG
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	109	VAL
12	1Q	110	THR
12	1Q	127	ILE
13	1R	8	ARG
13	1R	36	THR
13	1R	100	LEU
13	1R	111	LEU
13	1R	114	VAL
14	1S	13	ARG
14	1S	14	VAL
14	1S	46	VAL
14	1S	49	VAL
14	1S	73	LEU
14	1S	85	VAL
14	1S	110	LEU
15	1T	28	VAL

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Mol	Chain	Res	Type
15	1T	49	VAL
15	1T	96	ARG
16	1U	27	LEU
16	1U	31	SER
16	1U	74	LEU
16	1U	83	LEU
17	1V	28	GLU
17	1V	45	THR
17	1V	46	VAL
17	1V	56	SER
17	1V	61	VAL
17	1V	79	VAL
18	1W	4	LYS
18	1W	11	ARG
18	1W	17	VAL
18	1W	67	ASP
20	1Y	7	VAL
20	1Y	43	ASN
20	1Y	55	TYR
20	1Y	64	GLU
20	1Y	67	LEU
20	1Y	72	VAL
20	1Y	91	GLU
20	1Y	99	CYS
21	1Z	31	ARG
21	1Z	42	VAL
21	1Z	53	ILE
21	1Z	61	LEU
21	1Z	66	SER
21	1Z	69	THR
21	1Z	72	ARG
21	1Z	138	GLU
21	1Z	154	ASP
21	1Z	155	LEU
21	1Z	170	THR
21	1Z	171	ILE
22	10	36	ILE
22	10	49	LYS
23	11	3	LYS
23	11	37	ILE
23	11	59	THR
23	11	80	LEU

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Mol	Chain	Res	Type
24	12	19	VAL
24	12	53	LEU
24	12	55	ARG
24	12	65	ASN
25	13	29	ARG
25	13	54	VAL
25	13	60	GLU
26	14	1	MET
26	14	21	VAL
26	14	27	THR
26	14	35	VAL
26	14	46	GLN
26	14	49	PHE
26	14	50	VAL
26	14	53	GLU
26	14	59	PHE
26	14	60	GLN
26	14	61	ARG
26	14	63	TYR
26	14	67	TYR
26	14	69	LYS
27	15	6	VAL
27	15	40	LYS
28	16	4	GLU
28	16	7	ILE
28	16	9	LEU
28	16	45	LYS
28	16	47	THR
29	17	24	THR
29	17	29	LYS
29	17	41	ARG
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	29	LYS
31	19	4	ARG
31	19	33	LYS
33	1b	7	VAL
33	1b	12	GLU
33	1b	15	VAL
33	1b	21	ARG
33	1b	35	GLU

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Mol	Chain	Res	Type
33	1b	43	ASP
33	1b	44	LEU
33	1b	54	THR
33	1b	64	ARG
33	1b	80	ILE
33	1b	93	VAL
33	1b	101	MET
33	1b	108	ILE
33	1b	110	GLN
33	1b	121	LEU
33	1b	126	GLU
33	1b	127	ILE
33	1b	142	LEU
33	1b	150	SER
33	1b	154	LEU
33	1b	170	GLU
33	1b	185	ILE
33	1b	208	ILE
33	1b	233	SER
34	1c	3	ASN
34	1c	21	ARG
34	1c	26	LYS
34	1c	66	VAL
34	1c	77	ILE
34	1c	98	ASN
34	1c	102	ASN
34	1c	103	VAL
34	1c	119	ARG
34	1c	138	VAL
34	1c	173	VAL
34	1c	178	LEU
34	1c	179	ARG
34	1c	195	VAL
34	1c	201	TYR
34	1c	207	VAL
35	1d	3	ARG
35	1d	19	LEU
35	1d	31	CYS
35	1d	70	ILE
35	1d	77	ASN
35	1d	86	LYS
35	1d	112	VAL

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Mol	Chain	Res	Type
35	1d	127	THR
35	1d	134	ASP
35	1d	135	LEU
35	1d	140	VAL
35	1d	158	ILE
35	1d	170	VAL
35	1d	175	SER
35	1d	178	VAL
35	1d	194	LEU
36	1e	8	GLU
36	1e	24	ARG
36	1e	41	VAL
36	1e	56	GLN
36	1e	63	ARG
36	1e	79	GLU
36	1e	80	ILE
37	1f	43	LEU
37	1f	45	LEU
37	1f	55	ASP
37	1f	70	ASP
37	1f	72	VAL
37	1f	75	LEU
37	1f	78	GLU
37	1f	92	LYS
38	1g	12	LEU
38	1g	27	ILE
38	1g	50	ILE
38	1g	59	LEU
38	1g	61	VAL
38	1g	78	ARG
38	1g	80	VAL
38	1g	85	TYR
38	1g	104	LEU
38	1g	110	GLN
38	1g	113	GLU
38	1g	114	ARG
38	1g	115	ARG
39	1h	38	ILE
39	1h	39	LEU
39	1h	51	VAL
39	1h	52	ASP
39	1h	54	ASP

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Mol	Chain	Res	Type
39	1h	87	SER
39	1h	99	GLU
39	1h	133	LEU
40	1i	23	ASN
40	1i	25	LYS
40	1i	50	LEU
40	1i	64	THR
40	1i	96	LEU
40	1i	105	ASP
40	1i	128	ARG
41	1j	8	LEU
41	1j	35	SER
41	1j	42	THR
41	1j	43	ARG
41	1j	45	ARG
41	1j	46	ARG
41	1j	81	THR
41	1j	92	THR
41	1j	95	GLU
42	1k	14	VAL
42	1k	31	THR
42	1k	33	THR
42	1k	40	ILE
42	1k	48	ILE
42	1k	87	THR
42	1k	109	VAL
42	1k	114	VAL
43	1l	104	VAL
43	1l	117	ARG
44	1m	4	ILE
44	1m	14	ARG
44	1m	17	VAL
44	1m	32	GLU
44	1m	43	THR
44	1m	49	THR
44	1m	60	VAL
44	1m	98	VAL
44	1m	109	THR
44	1m	121	LYS
45	1n	3	ARG
45	1n	6	LEU
45	1n	13	THR

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Mol	Chain	Res	Type
45	1n	18	VAL
45	1n	50	LYS
45	1n	60	SER
46	1o	3	ILE
46	1o	24	SER
46	1o	27	VAL
46	1o	39	LEU
46	1o	83	GLU
46	1o	84	LYS
46	1o	87	ILE
47	1p	11	SER
47	1p	20	VAL
47	1p	21	VAL
47	1p	27	LYS
47	1p	31	LYS
47	1p	43	LYS
47	1p	45	THR
47	1p	62	VAL
47	1p	67	THR
48	1q	11	VAL
48	1q	15	MET
48	1q	53	LEU
48	1q	85	VAL
48	1q	89	LEU
49	1r	25	THR
49	1r	35	ARG
49	1r	37	VAL
49	1r	47	THR
50	1s	6	LYS
50	1s	39	THR
50	1s	41	VAL
50	1s	48	THR
50	1s	81	ARG
51	1t	13	LEU
51	1t	24	LEU
51	1t	37	SER
51	1t	71	THR
51	1t	100	ILE
52	1u	15	ARG
52	1u	20	LYS
3	2D	3	VAL
3	2D	32	SER

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Mol	Chain	Res	Type
3	2D	37	LEU
3	2D	71	ASP
3	2D	88	ARG
3	2D	106	ILE
3	2D	142	VAL
3	2D	173	VAL
3	2D	229	VAL
3	2D	242	ARG
4	2E	12	THR
4	2E	34	VAL
4	2E	42	ASP
4	2E	55	ASN
4	2E	73	GLU
4	2E	77	ILE
4	2E	116	VAL
4	2E	119	ARG
4	2E	134	ILE
4	2E	181	LEU
4	2E	184	VAL
4	2E	196	VAL
5	2F	24	LEU
5	2F	28	ILE
5	2F	33	LEU
5	2F	74	ARG
5	2F	106	ARG
5	2F	145	GLU
5	2F	157	VAL
5	2F	161	GLU
5	2F	165	ARG
5	2F	168	ARG
5	2F	183	VAL
5	2F	196	LEU
6	2G	3	LEU
6	2G	7	LEU
6	2G	28	VAL
6	2G	31	VAL
6	2G	37	VAL
6	2G	43	LEU
6	2G	45	GLU
6	2G	53	LEU
6	2G	60	LEU
6	2G	77	ILE

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Mol	Chain	Res	Type
6	2G	91	ARG
6	2G	120	LEU
6	2G	130	ASN
6	2G	137	GLU
6	2G	139	LEU
6	2G	140	ILE
6	2G	144	ILE
6	2G	162	THR
6	2G	165	THR
6	2G	170	ARG
7	2H	2	SER
7	2H	24	VAL
7	2H	43	VAL
7	2H	45	VAL
7	2H	47	GLU
7	2H	49	VAL
7	2H	57	ASP
7	2H	84	SER
7	2H	103	LEU
7	2H	116	GLU
7	2H	127	GLU
7	2H	129	THR
8	2I	15	VAL
8	2I	20	ASP
8	2I	38	LEU
8	2I	58	LEU
8	2I	62	LYS
8	2I	68	LEU
8	2I	77	LEU
8	2I	82	ARG
8	2I	87	LYS
8	2I	92	VAL
8	2I	117	GLU
8	2I	123	LEU
8	2I	127	VAL
8	2I	139	GLN
8	2I	144	VAL
9	2N	9	VAL
9	2N	14	VAL
9	2N	61	ARG
9	2N	62	VAL
10	2O	1	MET

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Mol	Chain	Res	Type
10	2O	28	SER
10	2O	35	VAL
10	2O	69	ILE
10	2O	108	GLU
10	2O	113	LYS
10	2O	116	SER
11	2P	7	ARG
11	2P	39	LYS
11	2P	45	LEU
11	2P	65	ARG
11	2P	95	VAL
11	2P	98	GLU
11	2P	119	GLU
11	2P	147	LEU
12	2Q	1	MET
12	2Q	10	ARG
12	2Q	56	ARG
12	2Q	110	THR
12	2Q	133	ARG
13	2R	36	THR
13	2R	73	VAL
13	2R	100	LEU
13	2R	102	GLU
13	2R	114	VAL
14	2S	21	THR
14	2S	26	LEU
14	2S	27	SER
14	2S	43	GLU
14	2S	50	SER
14	2S	52	SER
14	2S	58	LEU
14	2S	63	THR
14	2S	64	GLU
14	2S	75	GLU
14	2S	98	VAL
14	2S	103	GLU
14	2S	110	LEU
15	2T	40	THR
15	2T	67	SER
15	2T	72	VAL
16	2U	17	ILE
16	2U	74	LEU

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Mol	Chain	Res	Type
16	2U	117	GLN
17	2V	7	THR
17	2V	38	LEU
17	2V	46	VAL
17	2V	61	VAL
17	2V	76	LYS
17	2V	79	VAL
18	2W	4	LYS
18	2W	11	ARG
18	2W	17	VAL
18	2W	67	ASP
18	2W	92	ARG
18	2W	96	ILE
19	2X	70	LEU
19	2X	81	VAL
19	2X	92	LEU
20	2Y	7	VAL
20	2Y	9	LYS
20	2Y	39	VAL
20	2Y	63	LYS
20	2Y	72	VAL
20	2Y	76	CYS
20	2Y	97	ARG
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	58	VAL
21	2Z	74	VAL
21	2Z	91	LEU
21	2Z	129	SER
21	2Z	144	LEU
21	2Z	146	ILE
21	2Z	154	ASP
21	2Z	170	THR
21	2Z	171	ILE
22	20	49	LYS
23	21	21	ARG
23	21	46	LEU
23	21	81	LYS

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Mol	Chain	Res	Type
23	21	92	LYS
24	22	19	VAL
24	22	28	LYS
24	22	53	LEU
24	22	70	GLN
25	23	54	VAL
25	23	56	VAL
25	23	58	VAL
25	23	59	VAL
26	24	3	GLU
26	24	5	ILE
26	24	21	VAL
26	24	26	SER
26	24	34	GLU
26	24	49	PHE
26	24	56	VAL
26	24	59	PHE
26	24	61	ARG
26	24	67	TYR
27	25	6	VAL
27	25	58	LEU
28	26	9	LEU
28	26	14	THR
28	26	32	ASN
29	27	23	ARG
29	27	24	THR
29	27	41	ARG
29	27	43	THR
29	27	46	VAL
30	28	14	VAL
30	28	29	LYS
33	2b	7	VAL
33	2b	8	LYS
33	2b	11	LEU
33	2b	16	HIS
33	2b	23	ARG
33	2b	44	LEU
33	2b	67	THR
33	2b	71	VAL
33	2b	76	GLN
33	2b	79	ASP
33	2b	94	ASN

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Mol	Chain	Res	Type
33	2b	113	HIS
33	2b	117	GLU
33	2b	127	ILE
33	2b	136	VAL
33	2b	149	LEU
33	2b	168	THR
33	2b	170	GLU
33	2b	185	ILE
33	2b	189	ASP
33	2b	190	THR
33	2b	196	LEU
33	2b	221	LEU
33	2b	224	GLN
33	2b	236	TYR
34	2c	3	ASN
34	2c	14	ILE
34	2c	16	ARG
34	2c	46	GLU
34	2c	70	VAL
34	2c	116	VAL
34	2c	132	ARG
34	2c	190	ARG
35	2d	5	ILE
35	2d	28	SER
35	2d	31	CYS
35	2d	34	GLU
35	2d	53	ASP
35	2d	58	LEU
35	2d	59	ARG
35	2d	76	ARG
35	2d	96	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	150	GLU
35	2d	155	LEU
35	2d	158	ILE
35	2d	175	SER
35	2d	181	MET
35	2d	188	LEU
36	2e	9	LYS
36	2e	13	ILE
36	2e	20	GLN

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Mol	Chain	Res	Type
36	2e	41	VAL
36	2e	51	VAL
36	2e	53	LEU
36	2e	55	VAL
36	2e	66	MET
36	2e	73	ASN
36	2e	151	LEU
37	2f	21	LEU
37	2f	37	VAL
37	2f	63	TYR
37	2f	69	GLU
37	2f	71	ARG
37	2f	91	VAL
37	2f	92	LYS
38	2g	6	ARG
38	2g	9	VAL
38	2g	30	ILE
38	2g	51	GLN
38	2g	52	GLU
38	2g	53	LYS
38	2g	59	LEU
38	2g	78	ARG
38	2g	85	TYR
38	2g	86	GLN
38	2g	98	SER
38	2g	139	GLU
39	2h	39	LEU
39	2h	51	VAL
39	2h	109	ILE
40	2i	7	THR
40	2i	27	THR
40	2i	32	ASP
40	2i	41	VAL
40	2i	47	LEU
40	2i	50	LEU
40	2i	54	ASP
40	2i	65	VAL
40	2i	66	ARG
40	2i	89	ASN
40	2i	99	LEU
40	2i	102	LEU
40	2i	108	VAL

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Mol	Chain	Res	Type
40	2i	128	ARG
41	2j	29	ARG
41	2j	38	ILE
41	2j	49	VAL
41	2j	72	VAL
41	2j	84	GLN
41	2j	92	THR
41	2j	94	VAL
42	2k	14	VAL
42	2k	24	SER
42	2k	53	SER
42	2k	54	ARG
42	2k	62	GLN
42	2k	66	LEU
42	2k	77	MET
42	2k	81	ASP
42	2k	84	VAL
42	2k	109	VAL
43	2l	13	LYS
43	2l	18	VAL
43	2l	40	VAL
43	2l	62	SER
44	2m	3	ARG
44	2m	4	ILE
44	2m	22	ILE
44	2m	45	VAL
44	2m	47	ASP
44	2m	49	THR
44	2m	50	GLU
44	2m	55	ARG
44	2m	62	ASN
44	2m	65	LYS
44	2m	69	GLU
44	2m	81	LEU
44	2m	90	LEU
44	2m	93	ARG
44	2m	94	ARG
44	2m	98	VAL
44	2m	103	THR
44	2m	106	ASN
45	2n	3	ARG
45	2n	6	LEU

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Mol	Chain	Res	Type
45	2n	15	LYS
45	2n	18	VAL
45	2n	22	THR
45	2n	33	VAL
45	2n	42	ILE
46	2o	24	SER
46	2o	39	LEU
46	2o	76	GLU
47	2p	1	MET
47	2p	2	VAL
47	2p	8	ARG
47	2p	20	VAL
47	2p	21	VAL
47	2p	27	LYS
47	2p	54	GLU
47	2p	60	LEU
47	2p	67	THR
47	2p	69	THR
48	2q	60	ILE
48	2q	63	ARG
48	2q	83	ASP
49	2r	31	LEU
49	2r	46	GLU
49	2r	82	THR
49	2r	86	VAL
50	2s	22	LEU
50	2s	32	LYS
50	2s	37	ARG
50	2s	43	GLU
50	2s	58	VAL
50	2s	71	LEU
50	2s	77	THR
51	2t	15	ARG
51	2t	46	GLU
51	2t	56	MET
51	2t	71	THR
51	2t	90	GLN
51	2t	93	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (145) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	126	GLN
4	1E	48	GLN
4	1E	55	ASN
4	1E	180	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
8	1I	105	HIS
9	1N	8	GLN
9	1N	94	HIS
12	1Q	57	HIS
13	1R	13	HIS
15	1T	84	GLN
15	1T	90	GLN
16	1U	81	HIS
16	1U	94	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
21	1Z	50	GLN
21	1Z	73	GLN
21	1Z	121	HIS
21	1Z	151	HIS
22	10	50	ASN
25	13	32	GLN
26	14	46	GLN
30	18	35	GLN
33	1b	135	GLN
34	1c	6	HIS
34	1c	98	ASN
34	1c	118	GLN
34	1c	162	GLN
34	1c	181	ASN
35	1d	77	ASN
35	1d	116	GLN
35	1d	123	HIS
35	1d	201	GLN
36	1e	20	GLN
36	1e	65	ASN
36	1e	73	ASN
36	1e	78	HIS
37	1f	13	ASN

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Mol	Chain	Res	Type
37	1f	100	ASN
38	1g	13	GLN
38	1g	28	ASN
38	1g	64	GLN
38	1g	86	GLN
39	1h	15	ASN
40	1i	31	GLN
40	1i	34	ASN
40	1i	124	GLN
41	1j	56	HIS
43	1l	99	HIS
44	1m	40	ASN
44	1m	92	HIS
46	1o	9	GLN
46	1o	62	GLN
47	1p	14	ASN
48	1q	26	GLN
49	1r	63	GLN
50	1s	23	ASN
50	1s	47	HIS
50	1s	83	HIS
51	1t	16	HIS
51	1t	42	GLN
51	1t	73	HIS
51	1t	90	GLN
3	2D	87	ASN
4	2E	48	GLN
4	2E	55	ASN
4	2E	143	ASN
5	2F	69	HIS
5	2F	75	HIS
6	2G	41	GLN
6	2G	108	ASN
6	2G	121	ASN
8	2I	104	GLN
9	2N	8	GLN
10	2O	5	GLN
10	2O	89	ASN
11	2P	27	HIS
12	2Q	123	HIS
13	2R	50	HIS
13	2R	71	GLN

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Mol	Chain	Res	Type
14	2S	38	GLN
15	2T	43	GLN
16	2U	94	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	6	HIS
20	2Y	43	ASN
21	2Z	34	ASN
21	2Z	55	HIS
21	2Z	65	GLN
21	2Z	73	GLN
21	2Z	151	HIS
25	23	32	GLN
26	24	46	GLN
33	2b	37	ASN
33	2b	40	HIS
33	2b	76	GLN
33	2b	78	GLN
33	2b	135	GLN
33	2b	140	HIS
33	2b	224	GLN
34	2c	6	HIS
34	2c	69	HIS
34	2c	162	GLN
35	2d	45	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	123	HIS
35	2d	201	GLN
36	2e	20	GLN
36	2e	73	ASN
37	2f	100	ASN
38	2g	28	ASN
38	2g	148	ASN
40	2i	3	GLN
40	2i	31	GLN
40	2i	58	HIS
40	2i	87	GLN
40	2i	89	ASN
40	2i	117	HIS
41	2j	13	HIS
41	2j	21	GLN

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Mol	Chain	Res	Type
41	2j	62	HIS
41	2j	68	HIS
42	2k	38	ASN
42	2k	62	GLN
42	2k	104	GLN
42	2k	117	ASN
43	2l	99	HIS
44	2m	12	ASN
44	2m	77	ASN
45	2n	49	HIS
46	2o	9	GLN
47	2p	16	HIS
49	2r	63	GLN
50	2s	14	HIS
50	2s	69	HIS
50	2s	83	HIS
51	2t	16	HIS
51	2t	90	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	423 (14%)	30 (1%)
1	2A	2791/2915 (95%)	450 (16%)	25 (0%)
2	1B	119/121 (98%)	10 (8%)	0
2	2B	118/121 (97%)	22 (18%)	0
32	1a	1497/1521 (98%)	231 (15%)	0
32	2a	1501/1521 (98%)	266 (17%)	0
53	1v	12/24 (50%)	2 (16%)	0
53	2v	12/24 (50%)	1 (8%)	0
54	1w	71/76 (93%)	23 (32%)	0
54	2w	68/76 (89%)	26 (38%)	0
55	1x	75/77 (97%)	4 (5%)	0
55	2x	75/77 (97%)	6 (8%)	0
56	1y	72/76 (94%)	31 (43%)	0
56	2y	70/76 (92%)	26 (37%)	0
All	All	9346/9620 (97%)	1521 (16%)	55 (0%)

All (1521) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	34	C
1	1A	45	C
1	1A	71	A
1	1A	72	U
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	139	G
1	1A	181	A
1	1A	196	A
1	1A	197	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	222	A
1	1A	228	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	269	U
1	1A	271(I)	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(B)	G
1	1A	272(H)	C
1	1A	272(I)	U
1	1A	275	G
1	1A	279	C
1	1A	288	C
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	342	G
1	1A	352	G

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Mol	Chain	Res	Type
1	1A	363	G
1	1A	370	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	428	A
1	1A	444	C
1	1A	448	U
1	1A	451	C
1	1A	455	C
1	1A	456	C
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	509	C
1	1A	528	A
1	1A	529	A
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	586	A
1	1A	592	G
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	614(C)	A
1	1A	615	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(F)	G

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Mol	Chain	Res	Type
1	1A	652(T)	C
1	1A	669	G
1	1A	686	G
1	1A	717	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	789	A
1	1A	790	C
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	877	U
1	1A	879	G
1	1A	880	G
1	1A	882	G
1	1A	883	G
1	1A	884	C
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	892	G
1	1A	893	C
1	1A	894	C
1	1A	896	A
1	1A	897	C
1	1A	907	U

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Mol	Chain	Res	Type
1	1A	910	A
1	1A	931	G
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1022	G
1	1A	1026	U
1	1A	1027	A
1	1A	1033	U
1	1A	1038	C
1	1A	1039	G
1	1A	1041	C
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1054	A
1	1A	1055	G
1	1A	1057	A
1	1A	1058	G
1	1A	1060	U
1	1A	1062	G
1	1A	1063	G
1	1A	1071	G
1	1A	1073	A
1	1A	1075	C
1	1A	1076	C
1	1A	1078	U
1	1A	1080	C
1	1A	1081	U
1	1A	1083	U
1	1A	1085	A
1	1A	1087	G
1	1A	1088	A

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Mol	Chain	Res	Type
1	1A	1089	G
1	1A	1090	U
1	1A	1094	U
1	1A	1097	U
1	1A	1101	U
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G
1	1A	1116	C
1	1A	1135	C
1	1A	1136	G
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1229	G
1	1A	1244	G
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1345	C
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	1395	A
1	1A	1396	U
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U

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Mol	Chain	Res	Type
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1450	G
1	1A	1455	G
1	1A	1461	G
1	1A	1467	C
1	1A	1482	G
1	1A	1493	C
1	1A	1494	A
1	1A	1497	U
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1540	U
1	1A	1542	A
1	1A	1554	A
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	1582	C
1	1A	1584	C
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1639	U
1	1A	1648	C
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1746	G
1	1A	1756	G
1	1A	1762	A
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A

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Mol	Chain	Res	Type
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	1877	A
1	1A	1878	G
1	1A	1900	A
1	1A	1906	G
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1984	G
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	2032	G
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	2101	G
1	1A	2102	U
1	1A	2108	C
1	1A	2109	U

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Mol	Chain	Res	Type
1	1A	2110	G
1	1A	2113	U
1	1A	2114	A
1	1A	2116	G
1	1A	2118	U
1	1A	2120	G
1	1A	2121	G
1	1A	2122	U
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	2150	U
1	1A	2151	G
1	1A	2152	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G
1	1A	2163	C
1	1A	2165	G
1	1A	2166	G
1	1A	2168	G
1	1A	2171	A
1	1A	2172	U
1	1A	2173	A
1	1A	2181	G
1	1A	2182	G
1	1A	2184	G
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G

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Mol	Chain	Res	Type
1	1A	2218	U
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2283	C
1	1A	2286	A
1	1A	2287	A
1	1A	2305	A
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	2354	G
1	1A	2361	A
1	1A	2383	G
1	1A	2385	C
1	1A	2406	U
1	1A	2407	G
1	1A	2422	A
1	1A	2423	U
1	1A	2424	C
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2435	A
1	1A	2439	A
1	1A	2440	C
1	1A	2441	C
1	1A	2447	G
1	1A	2448	A
1	1A	2468	G
1	1A	2469	A
1	1A	2476	A
1	1A	2478	A
1	1A	2491	U
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A

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Mol	Chain	Res	Type
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	2602	A
1	1A	2611	U
1	1A	2612	C
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	2691	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	2758	A
1	1A	2765	A
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2793	G
1	1A	2794	C
1	1A	2802	G
1	1A	2803	C
1	1A	2804	C
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2835	A
1	1A	2872	G
1	1A	2880	C
1	1A	2892	A

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Mol	Chain	Res	Type
1	1A	2894	G
1	1A	2895	U
2	1B	2	C
2	1B	13	A
2	1B	35	U
2	1B	45	A
2	1B	56	G
2	1B	57	A
2	1B	67	G
2	1B	73	A
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	52	G
32	1a	61	G
32	1a	77	G
32	1a	79	G
32	1a	91	C
32	1a	98	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	144	G
32	1a	162	A
32	1a	163	C
32	1a	174	C
32	1a	182	U
32	1a	189(D)	C
32	1a	189(F)	U
32	1a	189(G)	G
32	1a	189(H)	G
32	1a	189(J)	G
32	1a	195	A
32	1a	197	A

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Mol	Chain	Res	Type
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	231	G
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	348	G
32	1a	351	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	392	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	422	C
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	441	A
32	1a	442	C
32	1a	452	A
32	1a	457	C
32	1a	461	A
32	1a	470	C
32	1a	485	G
32	1a	496	A

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Mol	Chain	Res	Type
32	1a	498	U
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	524	G
32	1a	527	G7M
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	607	A
32	1a	628	G
32	1a	630	G
32	1a	639	G
32	1a	653	A
32	1a	665	A
32	1a	671	G
32	1a	672	U
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	723	U
32	1a	731	G
32	1a	734	G
32	1a	749	C
32	1a	755	G
32	1a	760	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	817	C
32	1a	821	G

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Mol	Chain	Res	Type
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	870	U
32	1a	874	G
32	1a	902	G
32	1a	913	A
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	936	C
32	1a	942	G
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	972	C
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	996	A
32	1a	1000	U
32	1a	1001	A
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1008	C
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C

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Mol	Chain	Res	Type
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1034	G
32	1a	1039	C
32	1a	1044	A
32	1a	1068	G
32	1a	1086	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1124	G
32	1a	1125	U
32	1a	1132	C
32	1a	1134	G
32	1a	1135	U
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1146	A
32	1a	1152	A
32	1a	1154	G
32	1a	1158	C
32	1a	1159	U
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1213	A
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1250	A
32	1a	1253	G
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C
32	1a	1275	A

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Mol	Chain	Res	Type
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1312	G
32	1a	1320	C
32	1a	1338	G
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1364	U
32	1a	1370	G
32	1a	1377	A
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1452	C
32	1a	1456	G
32	1a	1492	A
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1517	G
32	1a	1519	MA6
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
53	1v	13	A
53	1v	24	A
54	1w	3	C
54	1w	6	G
54	1w	7	A
54	1w	8	4SU
54	1w	11	C
54	1w	12	U
54	1w	19	G

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Mol	Chain	Res	Type
54	1w	20	U
54	1w	21	A
54	1w	23	A
54	1w	24	G
54	1w	45	U
54	1w	46	G7M
54	1w	47	U
54	1w	48	C
54	1w	61	C
54	1w	62	C
54	1w	67	C
54	1w	68	C
54	1w	70	G
54	1w	72	C
54	1w	73	A
54	1w	74	C
55	1x	9	G
55	1x	19	G
55	1x	47	U
55	1x	48	C
56	1y	9	A
56	1y	11	C
56	1y	13	C
56	1y	14	A
56	1y	19	G
56	1y	20	U
56	1y	21	A
56	1y	23	A
56	1y	28	G
56	1y	35	A
56	1y	36	A
56	1y	37	MIA
56	1y	40	C
56	1y	44	G
56	1y	45	U
56	1y	46	G7M
56	1y	47	U
56	1y	48	C
56	1y	51	U
56	1y	56	C
56	1y	57	G
56	1y	58	A

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Mol	Chain	Res	Type
56	1y	59	U
56	1y	61	C
56	1y	65	G
56	1y	66	U
56	1y	69	G
56	1y	70	G
56	1y	71	G
56	1y	72	C
56	1y	76	A
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	61	G
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	78	A
1	2A	84	A
1	2A	92	A
1	2A	100	G
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	141	A
1	2A	154	G
1	2A	154(A)	C
1	2A	157	U
1	2A	172	C
1	2A	181	A
1	2A	196	A
1	2A	197	A
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	228	A
1	2A	229	A
1	2A	230	U

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Mol	Chain	Res	Type
1	2A	233	A
1	2A	248	G
1	2A	271(J)	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	294	A
1	2A	311	A
1	2A	329	G
1	2A	330	A
1	2A	352	G
1	2A	363	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	421	U
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	481	G
1	2A	494	G
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	528	A
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	551	G

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Mol	Chain	Res	Type
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	588	U
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	615	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	669	G
1	2A	686	G
1	2A	701	G
1	2A	717	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	771	G
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	857	C
1	2A	859	G
1	2A	866	A
1	2A	867	C
1	2A	874	G
1	2A	875	G
1	2A	878	A
1	2A	879	G

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Mol	Chain	Res	Type
1	2A	880	G
1	2A	885	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	892	G
1	2A	893	C
1	2A	894	C
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	904	C
1	2A	910	A
1	2A	917	A
1	2A	932	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	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	999	U
1	2A	1005	C
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1027	A
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1041	C
1	2A	1043	C
1	2A	1117	G
1	2A	1130	U

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Mol	Chain	Res	Type
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1143	A
1	2A	1144	G
1	2A	1151	G
1	2A	1171	G
1	2A	1195	G
1	2A	1210	A
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1230	C
1	2A	1236	G
1	2A	1247	A
1	2A	1248	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1306	C
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1370	C
1	2A	1379	A
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1435	G
1	2A	1437	C

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Mol	Chain	Res	Type
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1461	G
1	2A	1467	C
1	2A	1471	A
1	2A	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
1	2A	1532	C
1	2A	1533	G
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	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1703	G
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G

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Mol	Chain	Res	Type
1	2A	1756	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	1829	A
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1938	A
1	2A	1955	U
1	2A	1960	A
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	2033	A
1	2A	2043	C
1	2A	2055	C

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Mol	Chain	Res	Type
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2093	G
1	2A	2099	U
1	2A	2100	G
1	2A	2108	C
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2113	U
1	2A	2116	G
1	2A	2117	A
1	2A	2120	G
1	2A	2122	U
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	2137	C
1	2A	2138	C
1	2A	2139	C
1	2A	2142	C
1	2A	2143	C
1	2A	2145	C
1	2A	2146	C
1	2A	2148	G
1	2A	2149	G
1	2A	2150	U
1	2A	2151	G
1	2A	2157	G
1	2A	2158	A
1	2A	2159	G
1	2A	2161	C
1	2A	2165	G

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Mol	Chain	Res	Type
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2171	A
1	2A	2172	U
1	2A	2176	A
1	2A	2178	C
1	2A	2181	G
1	2A	2182	G
1	2A	2183	C
1	2A	2186	G
1	2A	2188	C
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2275	C
1	2A	2278	A
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	2311	A
1	2A	2312	U
1	2A	2319	G
1	2A	2320	A
1	2A	2325	G
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C
1	2A	2376	A

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Mol	Chain	Res	Type
1	2A	2383	G
1	2A	2385	C
1	2A	2403	C
1	2A	2406	U
1	2A	2422	A
1	2A	2423	U
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2460	U
1	2A	2465	C
1	2A	2468	G
1	2A	2469	A
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2487	G
1	2A	2490	G
1	2A	2491	U
1	2A	2494	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2507	C
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2530	A
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2585	U
1	2A	2602	A
1	2A	2611	U
1	2A	2612	C

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Mol	Chain	Res	Type
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	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2751	G
1	2A	2757	A
1	2A	2758	A
1	2A	2760	C
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2793	G
1	2A	2794	C
1	2A	2802	G
1	2A	2803	C
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2836	U
1	2A	2839	G
1	2A	2872	G
1	2A	2879	C
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2895	U
1	2A	2897	U
2	2B	2	C
2	2B	3	C
2	2B	8	U

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Mol	Chain	Res	Type
2	2B	12	C
2	2B	13	A
2	2B	33	G
2	2B	34	U
2	2B	41	U
2	2B	45	A
2	2B	53	A
2	2B	56	G
2	2B	63	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	84	C
2	2B	105	A
2	2B	108	U
2	2B	110	G
2	2B	111	G
2	2B	117	G
2	2B	120	A
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	41	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	65	U
32	2a	66	G
32	2a	70	G
32	2a	73	G
32	2a	89	C
32	2a	115	G
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	137	C
32	2a	144	G
32	2a	156	G
32	2a	159	G
32	2a	163	C

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Mol	Chain	Res	Type
32	2a	175	C
32	2a	182	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	231	G
32	2a	234	C
32	2a	245	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	269	C
32	2a	289	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	350	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	384	G
32	2a	388	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C

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Mol	Chain	Res	Type
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	476	G
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	527	G7M
32	2a	531	U
32	2a	532	A
32	2a	547	A
32	2a	559	A
32	2a	564	C
32	2a	568	G
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	630	G
32	2a	653	A
32	2a	661	G
32	2a	665	A
32	2a	666	G
32	2a	671	G
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	702	A
32	2a	703	G
32	2a	723	U
32	2a	731	G
32	2a	733	A
32	2a	749	C
32	2a	755	G

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Mol	Chain	Res	Type
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	787	A
32	2a	792	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	840	C
32	2a	841	U
32	2a	851	G
32	2a	853	G
32	2a	859	A
32	2a	874	G
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	932	C
32	2a	934	C
32	2a	935	A
32	2a	942	G
32	2a	958	A
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	991	U
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	997	U

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Mol	Chain	Res	Type
32	2a	998	G
32	2a	999	C
32	2a	1000	U
32	2a	1002	G
32	2a	1003	G
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1011	G
32	2a	1016	A
32	2a	1020	U
32	2a	1021	G
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1035	A
32	2a	1036	G
32	2a	1037	C
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1045	C
32	2a	1050	G
32	2a	1064	G
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1081	G
32	2a	1086	U
32	2a	1091	U
32	2a	1092	A
32	2a	1093	A
32	2a	1094	G

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Mol	Chain	Res	Type
32	2a	1095	U
32	2a	1097	C
32	2a	1101	A
32	2a	1105	A
32	2a	1108	G
32	2a	1124	G
32	2a	1125	U
32	2a	1126	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1136	U
32	2a	1137	C
32	2a	1139	G
32	2a	1140	C
32	2a	1146	A
32	2a	1152	A
32	2a	1157	A
32	2a	1158	C
32	2a	1159	U
32	2a	1160	G
32	2a	1164	G
32	2a	1170	A
32	2a	1174	G
32	2a	1182	G
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1211	U
32	2a	1213	A
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
32	2a	1246	C
32	2a	1256	A
32	2a	1257	U
32	2a	1260	C
32	2a	1270	C
32	2a	1273	G
32	2a	1275	A
32	2a	1277	C

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Mol	Chain	Res	Type
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1287	A
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1312	G
32	2a	1338	G
32	2a	1346	A
32	2a	1347	G
32	2a	1363	C
32	2a	1370	G
32	2a	1382	C
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1492	A
32	2a	1497	G
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1519	MA6
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	24	A
54	2w	3	C
54	2w	4	C
54	2w	5	G
54	2w	7	A
54	2w	8	4SU
54	2w	9	A
54	2w	12	U
54	2w	13	C

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Mol	Chain	Res	Type
54	2w	14	A
54	2w	19	G
54	2w	22	G
54	2w	30	G
54	2w	42	C
54	2w	45	U
54	2w	46	G7M
54	2w	47	U
54	2w	48	C
54	2w	49	C
54	2w	65	G
54	2w	66	U
54	2w	68	C
54	2w	69	G
54	2w	70	G
54	2w	72	C
54	2w	73	A
54	2w	74	C
55	2x	9	G
55	2x	10	G
55	2x	18	G
55	2x	19	G
55	2x	21	A
55	2x	47	U
56	2y	2	C
56	2y	14	A
56	2y	15	G
56	2y	19	G
56	2y	27	G
56	2y	40	C
56	2y	41	C
56	2y	45	U
56	2y	46	G7M
56	2y	47	U
56	2y	49	C
56	2y	50	U
56	2y	52	G
56	2y	53	G
56	2y	55	PSU
56	2y	56	C
56	2y	57	G
56	2y	58	A

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Mol	Chain	Res	Type
56	2y	59	U
56	2y	61	C
56	2y	62	C
56	2y	65	G
56	2y	68	C
56	2y	69	G
56	2y	70	G
56	2y	73	A

All (55) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	266	G
1	1A	271(K)	U
1	1A	278	A
1	1A	548	A
1	1A	573	G
1	1A	746	A
1	1A	764	A
1	1A	774	A
1	1A	776	G
1	1A	827	U
1	1A	974	G
1	1A	1067	A
1	1A	1142(A)	A
1	1A	1174	A
1	1A	1176	G
1	1A	1379	A
1	1A	1442	G
1	1A	1508	A
1	1A	1608	A
1	1A	1992	G
1	1A	2134	A
1	1A	2181	G
1	1A	2183	C
1	1A	2406	U
1	1A	2422	A
1	1A	2439	A
1	1A	2611	U
1	1A	2629	A
1	1A	2689	U

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Mol	Chain	Res	Type
1	2A	196	A
1	2A	228	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	746	A
1	2A	752	A
1	2A	774	A
1	2A	827	U
1	2A	856	C
1	2A	900	A
1	2A	1026	U
1	2A	1210	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2119	A
1	2A	2126	A
1	2A	2439	A
1	2A	2689	U
1	2A	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	2A	1917	1	18,21,22	1.37	2 (11%)	21,30,33	1.96	4 (19%)
1	OMU	2A	2552	57,1	19,22,23	1.12	1 (5%)	25,31,34	1.81	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
54	PSU	1w	39	54	18,21,22	1.43	3 (16%)	21,30,33	1.63	3 (14%)
1	OMC	1A	1920	1	19,22,23	0.80	0	25,31,34	0.90	0
54	G7M	1w	46	54	20,26,27	1.22	2 (10%)	16,39,42	0.59	0
32	5MC	2a	1404	32	19,22,23	1.66	3 (15%)	26,32,35	1.18	3 (11%)
43	0TD	1l	92	43	8,9,10	4.43	3 (37%)	6,11,13	7.28	2 (33%)
1	MA6	2A	2058	1	19,26,27	1.00	2 (10%)	18,38,41	2.00	4 (22%)
1	PSU	2A	2605	1	18,21,22	1.25	1 (5%)	21,30,33	2.07	4 (19%)
54	G7M	2w	46	54	20,26,27	1.23	1 (5%)	16,39,42	0.68	0
54	PSU	1w	55	54	18,21,22	1.33	2 (11%)	21,30,33	2.00	3 (14%)
56	MIA	2y	37	56	17,24,32	1.02	1 (5%)	16,35,47	1.30	2 (12%)
1	MA6	1A	2058	57,1	19,26,27	1.01	1 (5%)	18,38,41	1.91	4 (22%)
1	2MA	1A	2503	57,1	18,25,26	0.74	0	20,37,40	1.96	4 (20%)
32	PSU	1a	516	32	18,21,22	1.34	2 (11%)	21,30,33	1.90	5 (23%)
56	PSU	1y	32	56	18,21,22	1.36	2 (11%)	21,30,33	1.93	4 (19%)
55	8AN	2x	76	57,55,63	17,24,25	1.15	2 (11%)	13,35,38	3.48	3 (23%)
54	5MU	1w	54	54	19,22,23	1.32	3 (15%)	27,32,35	2.17	6 (22%)
56	PSU	1y	39	56	18,21,22	1.45	2 (11%)	21,30,33	1.71	3 (14%)
1	5MC	2A	1962	57,1	19,22,23	1.89	3 (15%)	26,32,35	1.17	3 (11%)
32	5MC	1a	1404	32	19,22,23	1.72	3 (15%)	26,32,35	1.25	4 (15%)
55	PSU	2x	55	55	18,21,22	1.38	2 (11%)	21,30,33	2.14	5 (23%)
56	PSU	2y	55	56	18,21,22	1.42	2 (11%)	21,30,33	1.98	4 (19%)
32	UR3	2a	1498	32	19,22,23	1.09	1 (5%)	26,32,35	1.82	3 (11%)
32	5MC	1a	967	32	19,22,23	1.65	3 (15%)	26,32,35	1.04	2 (7%)
54	4SU	1w	8	54	18,21,22	1.72	4 (22%)	25,30,33	1.78	5 (20%)
32	5MC	2a	1400	32	19,22,23	1.65	3 (15%)	26,32,35	1.29	3 (11%)
32	G7M	1a	527	57,32	20,26,27	1.18	2 (10%)	16,39,42	0.66	0
56	G7M	2y	46	56	20,26,27	1.38	2 (10%)	16,39,42	0.65	0
55	5MC	1x	32	55	19,22,23	1.60	3 (15%)	26,32,35	1.28	3 (11%)
56	G7M	1y	46	56	20,26,27	1.37	1 (5%)	16,39,42	0.45	0
32	MA6	1a	1518	32	19,26,27	1.03	2 (10%)	18,38,41	2.07	3 (16%)
32	M2G	2a	966	32	20,27,28	1.32	3 (15%)	19,40,43	1.04	1 (5%)
1	5MU	2A	1939	1	19,22,23	1.44	6 (31%)	27,32,35	2.32	6 (22%)
54	8AN	2w	76	1,62,54	17,24,25	1.39	4 (23%)	13,35,38	1.94	1 (7%)
56	PSU	2y	32	56	18,21,22	1.35	2 (11%)	21,30,33	1.95	3 (14%)
1	5MC	1A	1942	1	19,22,23	1.85	3 (15%)	26,32,35	1.33	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
32	G7M	2a	527	57,32	20,26,27	1.27	2 (10%)	16,39,42	0.53	0
1	PSU	2A	1911	1	18,21,22	1.39	2 (11%)	21,30,33	1.96	4 (19%)
32	MA6	1a	1519	32	19,26,27	1.06	2 (10%)	18,38,41	1.95	3 (16%)
56	4SU	2y	8	56	18,21,22	1.76	4 (22%)	25,30,33	2.32	5 (20%)
1	PSU	1A	2605	57,1	18,21,22	1.52	3 (16%)	21,30,33	2.02	4 (19%)
1	5MU	1A	1915	1	19,22,23	1.44	6 (31%)	27,32,35	2.15	7 (25%)
32	5MC	2a	967	32	19,22,23	1.68	2 (10%)	26,32,35	1.04	2 (7%)
54	MIA	2w	37	54,53	19,27,32	1.88	3 (15%)	18,39,47	1.32	3 (16%)
1	5MC	1A	1962	57,1	19,22,23	1.79	3 (15%)	26,32,35	1.15	3 (11%)
1	OMG	2A	2251	55,1	19,26,27	0.90	1 (5%)	21,38,41	1.11	3 (14%)
55	5MU	2x	54	55	19,22,23	1.39	5 (26%)	27,32,35	2.18	6 (22%)
54	PSU	1w	32	57,54	18,21,22	1.34	2 (11%)	21,30,33	1.93	3 (14%)
32	M2G	1a	966	32	20,27,28	1.33	3 (15%)	19,40,43	1.02	2 (10%)
1	OMC	2A	1920	1	19,22,23	0.82	0	25,31,34	0.98	1 (4%)
56	PSU	1y	55	56	18,21,22	1.34	2 (11%)	21,30,33	2.08	4 (19%)
56	5MU	2y	54	56	19,22,23	1.46	5 (26%)	27,32,35	1.78	6 (22%)
1	OMG	1A	2251	57,1,55	19,26,27	0.95	1 (5%)	21,38,41	1.07	2 (9%)
32	2MG	1a	1207	32	18,26,27	0.97	1 (5%)	16,38,41	1.33	3 (18%)
54	8AN	1w	76	1,62,54	17,24,25	1.43	4 (23%)	13,35,38	2.05	2 (15%)
56	5MU	1y	54	56	19,22,23	1.46	5 (26%)	27,32,35	2.07	6 (22%)
32	4OC	1a	1402	32	20,23,24	0.75	0	25,32,35	1.08	2 (8%)
32	PSU	2a	516	32	18,21,22	1.34	2 (11%)	21,30,33	2.09	5 (23%)
43	0TD	2l	92	43	8,9,10	4.56	1 (12%)	6,11,13	4.85	2 (33%)
56	PSU	2y	39	56	18,21,22	1.38	2 (11%)	21,30,33	1.77	4 (19%)
55	5MU	1x	54	57,55	19,22,23	1.42	4 (21%)	27,32,35	2.17	6 (22%)
32	5MC	2a	1407	57,32	19,22,23	1.54	3 (15%)	26,32,35	1.13	2 (7%)
1	PSU	1A	1917	1	18,21,22	1.37	2 (11%)	21,30,33	2.08	3 (14%)
55	4SU	1x	8	55	18,21,22	2.32	5 (27%)	25,30,33	1.73	7 (28%)
1	5MU	1A	1939	57,1	19,22,23	1.54	6 (31%)	27,32,35	2.20	6 (22%)
55	5MC	2x	32	55	19,22,23	1.68	3 (15%)	26,32,35	1.24	2 (7%)
54	PSU	2w	55	54	18,21,22	1.39	2 (11%)	21,30,33	2.06	4 (19%)
32	2MG	2a	1207	32	18,26,27	0.91	1 (5%)	16,38,41	1.56	3 (18%)
55	8AN	1x	76	57,55,63	17,24,25	1.30	3 (17%)	13,35,38	4.12	4 (30%)
54	PSU	2w	39	54	18,21,22	1.35	2 (11%)	21,30,33	1.88	3 (14%)
32	5MC	1a	1400	32	19,22,23	1.64	3 (15%)	26,32,35	1.19	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
32	UR3	1a	1498	32	19,22,23	1.02	1 (5%)	26,32,35	1.86	5 (19%)
56	4SU	1y	8	56	18,21,22	1.80	6 (33%)	25,30,33	1.90	5 (20%)
32	5MC	1a	1407	32	19,22,23	1.69	2 (10%)	26,32,35	1.17	4 (15%)
1	5MC	2A	1942	1	19,22,23	1.66	2 (10%)	26,32,35	1.08	2 (7%)
1	5MU	2A	1915	1	19,22,23	1.44	5 (26%)	27,32,35	2.30	6 (22%)
54	4SU	2w	8	54	18,21,22	1.75	4 (22%)	25,30,33	2.75	5 (20%)
54	MIA	1w	37	54	24,31,32	2.18	3 (12%)	22,44,47	2.42	7 (31%)
1	2MA	2A	2503	57,1	18,25,26	0.72	0	20,37,40	1.97	4 (20%)
56	MIA	1y	37	56	17,24,32	0.98	1 (5%)	16,35,47	1.32	1 (6%)
54	PSU	2w	32	54	18,21,22	1.38	2 (11%)	21,30,33	1.93	3 (14%)
55	4SU	2x	8	57,55	18,21,22	2.16	5 (27%)	25,30,33	1.46	5 (20%)
1	OMU	1A	2552	57,1	19,22,23	1.20	2 (10%)	25,31,34	1.81	5 (20%)
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	1.08	3 (12%)
32	MA6	2a	1519	32	19,26,27	1.02	2 (10%)	18,38,41	1.95	3 (16%)
1	PSU	1A	1911	1	18,21,22	1.35	2 (11%)	21,30,33	2.13	4 (19%)
54	5MU	2w	54	54	19,22,23	1.34	3 (15%)	27,32,35	1.83	6 (22%)
32	MA6	2a	1518	32	19,26,27	1.01	2 (10%)	18,38,41	1.96	3 (16%)
55	PSU	1x	55	57,55	18,21,22	1.39	2 (11%)	21,30,33	2.01	3 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	57,1	-	0/9/27/28	0/2/2/2
54	PSU	1w	39	54	-	0/7/25/26	0/2/2/2
1	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2
54	G7M	1w	46	54	-	1/3/25/26	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	3/7/12/14	-
1	MA6	2A	2058	1	-	0/7/29/30	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
54	G7M	2w	46	54	-	1/3/25/26	0/3/3/3
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
56	MIA	2y	37	56	-	0/3/25/34	0/3/3/3
1	MA6	1A	2058	57,1	-	0/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MA	1A	2503	57,1	-	1/3/25/26	0/3/3/3
32	PSU	1a	516	32	-	0/7/25/26	0/2/2/2
56	PSU	1y	32	56	-	0/7/25/26	0/2/2/2
55	8AN	2x	76	57,55,63	-	3/3/25/26	0/3/3/3
54	5MU	1w	54	54	-	0/7/25/26	0/2/2/2
56	PSU	1y	39	56	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	57,1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
56	PSU	2y	55	56	-	2/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
54	4SU	1w	8	54	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	57,32	-	3/3/25/26	0/3/3/3
56	G7M	2y	46	56	-	2/3/25/26	0/3/3/3
55	5MC	1x	32	55	-	0/7/25/26	0/2/2/2
56	G7M	1y	46	56	-	1/3/25/26	0/3/3/3
32	MA6	1a	1518	32	-	0/7/29/30	0/3/3/3
32	M2G	2a	966	32	-	0/7/29/30	0/3/3/3
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
54	8AN	2w	76	1,62,54	-	0/3/25/26	0/3/3/3
56	PSU	2y	32	56	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	57,32	-	3/3/25/26	0/3/3/3
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/7/29/30	0/3/3/3
56	4SU	2y	8	56	-	1/7/25/26	0/2/2/2
1	PSU	1A	2605	57,1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
54	MIA	2w	37	54,53	-	4/7/29/34	0/3/3/3
1	5MC	1A	1962	57,1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	55,1	-	0/5/27/28	0/3/3/3
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
54	PSU	1w	32	57,54	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/7/29/30	0/3/3/3
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
56	PSU	1y	55	56	-	2/7/25/26	0/2/2/2
56	5MU	2y	54	56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	1A	2251	57,1,55	-	0/5/27/28	0/3/3/3
32	2MG	1a	1207	32	-	0/5/27/28	0/3/3/3
54	8AN	1w	76	1,62,54	-	0/3/25/26	0/3/3/3
56	5MU	1y	54	56	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	0/9/29/30	0/2/2/2
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
56	PSU	2y	39	56	-	0/7/25/26	0/2/2/2
55	5MU	1x	54	57,55	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	57,32	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	57,1	-	0/7/25/26	0/2/2/2
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
54	PSU	2w	55	54	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/5/27/28	0/3/3/3
55	8AN	1x	76	57,55,63	-	3/3/25/26	0/3/3/3
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
56	4SU	1y	8	56	-	1/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	0/7/25/26	0/2/2/2
54	4SU	2w	8	54	-	0/7/25/26	0/2/2/2
54	MIA	1w	37	54	-	2/11/33/34	0/3/3/3
1	2MA	2A	2503	57,1	-	1/3/25/26	0/3/3/3
56	MIA	1y	37	56	-	2/3/25/34	0/3/3/3
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	57,55	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	57,1	-	0/9/27/28	0/2/2/2
32	4OC	2a	1402	32	-	0/9/29/30	0/2/2/2
32	MA6	2a	1519	32	-	3/7/29/30	0/3/3/3
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
54	5MU	2w	54	54	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/7/29/30	0/3/3/3
55	PSU	1x	55	57,55	-	0/7/25/26	0/2/2/2

All (221) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.43	1.69	1.82
43	1l	92	0TD	CB-SB	-11.78	1.70	1.82
1	2A	1962	5MC	C5-C4	7.11	1.49	1.44
54	1w	37	MIA	C13-C14	6.96	1.53	1.32
1	1A	1942	5MC	C5-C4	6.85	1.49	1.44
54	2w	37	MIA	C2-S10	-6.82	1.70	1.75
1	1A	1962	5MC	C5-C4	6.82	1.49	1.44
54	1w	37	MIA	C2-S10	-6.80	1.70	1.75
32	1a	1407	5MC	C5-C4	6.44	1.49	1.44
32	2a	967	5MC	C5-C4	6.15	1.48	1.44
32	1a	1404	5MC	C5-C4	6.14	1.48	1.44
32	1a	967	5MC	C5-C4	6.13	1.48	1.44
1	2A	1942	5MC	C5-C4	6.12	1.48	1.44
55	2x	32	5MC	C5-C4	6.07	1.48	1.44
55	1x	8	4SU	C4-N3	-6.06	1.31	1.37
32	2a	1404	5MC	C5-C4	5.94	1.48	1.44
32	2a	1400	5MC	C5-C4	5.93	1.48	1.44
32	1a	1400	5MC	C5-C4	5.88	1.48	1.44
55	1x	32	5MC	C5-C4	5.58	1.48	1.44
32	2a	1407	5MC	C5-C4	5.35	1.48	1.44
55	2x	8	4SU	C4-N3	-5.32	1.32	1.37
54	2w	8	4SU	C4-S4	-5.08	1.59	1.68
56	2y	8	4SU	C4-S4	-4.96	1.59	1.68
56	1y	8	4SU	C4-S4	-4.51	1.60	1.68
54	1w	8	4SU	C4-S4	-4.42	1.60	1.68
55	2x	8	4SU	C4-S4	-4.35	1.61	1.68
55	1x	8	4SU	C4-S4	-4.30	1.61	1.68
56	1y	39	PSU	C6-C5	4.25	1.40	1.35
56	2y	46	G7M	C5-C4	4.23	1.47	1.39
55	1x	8	4SU	C2-N3	-4.20	1.30	1.38
56	1y	46	G7M	C5-C4	4.15	1.47	1.39
56	1y	32	PSU	C6-C5	4.02	1.39	1.35
32	2a	966	M2G	C2-N3	4.02	1.36	1.30
54	2w	32	PSU	C6-C5	4.01	1.39	1.35
56	2y	39	PSU	C6-C5	3.94	1.39	1.35
32	2a	527	G7M	C5-C4	3.93	1.46	1.39
54	2w	46	G7M	C5-C4	3.87	1.46	1.39
56	1y	55	PSU	C6-C5	3.82	1.39	1.35
55	1x	55	PSU	C6-C5	3.81	1.39	1.35
54	2w	39	PSU	C6-C5	3.80	1.39	1.35
56	2y	32	PSU	C6-C5	3.76	1.39	1.35
54	2w	55	PSU	C6-C5	3.75	1.39	1.35
32	1a	966	M2G	C2-N3	3.75	1.35	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	2y	55	PSU	C6-C5	3.71	1.39	1.35
1	2A	1911	PSU	C6-C5	3.68	1.39	1.35
1	1A	1917	PSU	C6-C5	3.67	1.39	1.35
54	1w	76	8AN	O4'-C1'	3.66	1.45	1.40
1	1A	1911	PSU	C6-C5	3.66	1.39	1.35
32	1a	527	G7M	C5-C4	3.64	1.46	1.39
54	1w	46	G7M	C5-C4	3.62	1.46	1.39
54	1w	39	PSU	C6-C5	3.57	1.39	1.35
55	2x	55	PSU	C6-C5	3.56	1.39	1.35
54	1w	55	PSU	C6-C5	3.55	1.39	1.35
1	2A	2605	PSU	C6-C5	3.54	1.39	1.35
32	2a	516	PSU	C6-C5	3.54	1.39	1.35
1	1A	2605	PSU	C4-N3	-3.54	1.32	1.38
54	1w	32	PSU	C6-C5	3.52	1.39	1.35
32	1a	516	PSU	C6-C5	3.52	1.39	1.35
1	2A	1917	PSU	C6-C5	3.52	1.39	1.35
54	1w	8	4SU	C4-N3	-3.48	1.34	1.37
55	2x	8	4SU	C2-N3	-3.43	1.32	1.38
56	1y	8	4SU	C4-N3	-3.41	1.34	1.37
54	2w	76	8AN	O4'-C1'	3.35	1.45	1.40
55	1x	8	4SU	C5-C4	-3.34	1.38	1.42
55	2x	8	4SU	C5-C4	-3.20	1.38	1.42
32	1a	966	M2G	C2-N2	3.12	1.40	1.35
1	1A	2605	PSU	C6-C5	3.10	1.38	1.35
54	1w	39	PSU	C4-N3	-3.06	1.33	1.38
54	2w	8	4SU	C4-N3	-3.03	1.34	1.37
55	1x	54	5MU	C6-C5	2.98	1.39	1.34
56	2y	54	5MU	C6-C5	2.97	1.39	1.34
1	1A	1942	5MC	C6-C5	2.96	1.39	1.34
1	2A	1915	5MU	C6-C5	2.96	1.39	1.34
1	2A	1942	5MC	C6-C5	2.94	1.39	1.34
1	1A	1939	5MU	C6-C5	2.90	1.39	1.34
54	2w	54	5MU	C6-C5	2.89	1.39	1.34
56	2y	37	MIA	C2-N3	2.88	1.36	1.32
56	1y	37	MIA	C2-N3	2.87	1.36	1.32
55	1x	76	8AN	C6-C5	-2.87	1.32	1.43
55	2x	54	5MU	C6-C5	2.85	1.39	1.34
32	2a	1404	5MC	C6-C5	2.85	1.39	1.34
56	1y	54	5MU	C4-C5	2.84	1.49	1.44
32	1a	1404	5MC	C6-C5	2.81	1.39	1.34
56	2y	8	4SU	C4-N3	-2.81	1.34	1.37
32	2a	1400	5MC	C6-C5	2.81	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	1939	5MU	C4-N3	-2.81	1.33	1.38
32	1a	1400	5MC	C6-C5	2.79	1.39	1.34
1	1A	1939	5MU	C2-N3	-2.78	1.33	1.38
56	1y	54	5MU	C6-C5	2.78	1.39	1.34
1	2A	1917	PSU	C4-N3	-2.77	1.33	1.38
32	2a	967	5MC	C6-C5	2.76	1.39	1.34
1	2A	1939	5MU	C6-C5	2.75	1.39	1.34
54	1w	54	5MU	C2-N1	2.71	1.42	1.38
55	2x	32	5MC	C6-C5	2.70	1.39	1.34
1	1A	1915	5MU	C4-N3	-2.69	1.33	1.38
54	2w	55	PSU	C4-N3	-2.69	1.33	1.38
1	2A	1962	5MC	C6-C5	2.68	1.39	1.34
55	1x	32	5MC	C6-C5	2.68	1.39	1.34
54	1w	54	5MU	C6-C5	2.66	1.39	1.34
55	2x	55	PSU	C4-N3	-2.65	1.33	1.38
56	2y	8	4SU	C5-C4	-2.65	1.39	1.42
32	1a	1207	2MG	C6-N1	-2.65	1.33	1.37
56	1y	54	5MU	C2-N1	2.64	1.42	1.38
32	2a	1407	5MC	C6-C5	2.64	1.38	1.34
1	1A	1915	5MU	C6-C5	2.63	1.38	1.34
1	1A	2605	PSU	C2-N3	-2.63	1.33	1.37
55	1x	32	5MC	C6-N1	-2.62	1.33	1.38
1	1A	1911	PSU	C4-N3	-2.61	1.34	1.38
55	1x	54	5MU	C4-N3	-2.61	1.34	1.38
32	2a	1498	UR3	C2-N1	2.61	1.42	1.38
32	1a	1407	5MC	C6-C5	2.59	1.38	1.34
1	1A	1915	5MU	C2-N1	2.58	1.42	1.38
56	2y	55	PSU	C4-N3	-2.58	1.34	1.38
1	2A	1915	5MU	C2-N1	2.58	1.42	1.38
1	1A	1942	5MC	C6-N1	-2.58	1.33	1.38
56	1y	8	4SU	C2-N1	2.57	1.42	1.38
54	1w	32	PSU	C4-N3	-2.57	1.34	1.38
56	2y	54	5MU	C4-N3	-2.56	1.34	1.38
1	2A	1911	PSU	C4-N3	-2.56	1.34	1.38
32	1a	967	5MC	C6-C5	2.56	1.38	1.34
54	1w	8	4SU	C2-N3	-2.55	1.33	1.38
1	1A	1917	PSU	C4-N3	-2.55	1.34	1.38
56	2y	39	PSU	C4-N3	-2.54	1.34	1.38
54	2w	76	8AN	C6-C5	-2.54	1.33	1.43
1	1A	1939	5MU	C4-C5	2.54	1.49	1.44
56	2y	54	5MU	C4-C5	2.54	1.49	1.44
1	1A	1939	5MU	C4-N3	-2.53	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	37	MIA	C6-C5	2.53	1.48	1.44
32	2a	966	M2G	C2-N2	2.52	1.39	1.35
54	2w	37	MIA	C2-N3	2.52	1.37	1.34
54	1w	76	8AN	C6-C5	-2.51	1.34	1.43
32	1a	516	PSU	C4-N3	-2.50	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.50	1.34	1.37
1	1A	1915	5MU	C4-C5	2.49	1.48	1.44
1	2A	1915	5MU	C4-C5	2.49	1.48	1.44
56	1y	39	PSU	C4-N3	-2.47	1.34	1.38
32	2a	516	PSU	C4-N3	-2.46	1.34	1.38
1	2A	2058	MA6	C6-C5	-2.45	1.41	1.44
1	2A	2251	OMG	C6-N1	-2.45	1.34	1.37
55	2x	54	5MU	C4-N3	-2.45	1.34	1.38
55	2x	54	5MU	C4-C5	2.45	1.48	1.44
32	1a	1498	UR3	C2-N1	2.44	1.41	1.38
1	2A	1939	5MU	C4-C5	2.43	1.48	1.44
1	1A	1939	5MU	C6-N1	-2.43	1.33	1.38
32	1a	1518	MA6	C6-C5	-2.43	1.41	1.44
56	2y	54	5MU	C2-N1	2.42	1.42	1.38
1	2A	1915	5MU	C4-N3	-2.42	1.34	1.38
55	1x	54	5MU	C4-C5	2.42	1.48	1.44
55	1x	76	8AN	O4'-C1'	2.41	1.44	1.40
1	1A	2058	MA6	C6-C5	-2.41	1.41	1.44
1	2A	1939	5MU	C6-N1	-2.41	1.33	1.38
56	1y	8	4SU	C5-C4	-2.39	1.39	1.42
1	1A	1939	5MU	C2-N1	2.37	1.42	1.38
1	1A	1962	5MC	C6-C5	2.37	1.38	1.34
54	2w	8	4SU	C5-C4	-2.37	1.39	1.42
54	2w	39	PSU	C4-N3	-2.37	1.34	1.38
32	1a	1519	MA6	C6-C5	-2.36	1.41	1.44
32	2a	1404	5MC	C6-N1	-2.35	1.34	1.38
54	1w	55	PSU	C4-N3	-2.33	1.34	1.38
54	1w	76	8AN	C2'-C3'	-2.33	1.50	1.53
32	2a	1518	MA6	C6-C5	-2.33	1.41	1.44
55	2x	8	4SU	O2-C2	2.33	1.27	1.23
54	2w	54	5MU	C4-N3	-2.33	1.34	1.38
1	1A	2552	OMU	C4-N3	-2.33	1.34	1.38
55	1x	54	5MU	C2-N1	2.33	1.42	1.38
55	2x	32	5MC	C6-N1	-2.32	1.34	1.38
32	1a	1400	5MC	C6-N1	-2.32	1.34	1.38
55	2x	76	8AN	C6-C5	-2.32	1.34	1.43
32	2a	1407	5MC	C6-N1	-2.30	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1404	5MC	C6-N1	-2.30	1.34	1.38
32	2a	1519	MA6	C6-C5	-2.29	1.41	1.44
43	1l	92	0TD	CSB-SB	-2.28	1.75	1.79
56	1y	55	PSU	C4-N3	-2.28	1.34	1.38
1	1A	2552	OMU	C5-C4	-2.28	1.38	1.43
55	2x	76	8AN	C5-N7	-2.28	1.31	1.39
1	2A	1962	5MC	C6-N1	-2.28	1.34	1.38
56	1y	32	PSU	C4-N3	-2.28	1.34	1.38
32	2a	527	G7M	C6-N1	-2.27	1.34	1.37
55	1x	55	PSU	C4-N3	-2.27	1.34	1.38
54	1w	37	MIA	C6-C5	2.26	1.48	1.44
55	1x	8	4SU	O2-C2	2.26	1.27	1.23
54	2w	54	5MU	C4-C5	2.25	1.48	1.44
55	2x	54	5MU	C2-N1	2.23	1.42	1.38
32	1a	966	M2G	C6-N1	-2.23	1.34	1.37
32	2a	1400	5MC	C6-N1	-2.23	1.34	1.38
54	2w	76	8AN	C5-N7	-2.23	1.31	1.39
56	1y	54	5MU	C4-N3	-2.22	1.34	1.38
1	2A	1939	5MU	C2-N1	2.21	1.41	1.38
1	1A	1962	5MC	C6-N1	-2.20	1.34	1.38
54	1w	76	8AN	C5-N7	-2.20	1.32	1.39
54	1w	54	5MU	C4-N3	-2.19	1.34	1.38
54	1w	8	4SU	C5-C4	-2.18	1.39	1.42
54	2w	76	8AN	C2'-C3'	-2.17	1.50	1.53
1	2A	2552	OMU	C4-N3	-2.17	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.17	1.34	1.38
56	2y	46	G7M	C6-N1	-2.16	1.34	1.37
56	2y	32	PSU	C4-N3	-2.16	1.34	1.38
1	2A	1915	5MU	C6-N1	-2.15	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.15	1.34	1.37
56	2y	8	4SU	C2-N1	2.12	1.41	1.38
56	2y	54	5MU	C2-N3	-2.12	1.34	1.38
32	2a	1518	MA6	C6-N1	2.12	1.35	1.32
1	1A	1915	5MU	C2-N3	-2.12	1.34	1.38
54	1w	39	PSU	C2-N3	-2.12	1.34	1.37
32	1a	527	G7M	C6-N1	-2.12	1.34	1.37
56	1y	54	5MU	C6-N1	-2.11	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.10	1.34	1.38
54	2w	32	PSU	C4-N3	-2.10	1.34	1.38
54	1w	46	G7M	C6-N1	-2.10	1.34	1.37
43	1l	92	0TD	CB-CG	2.09	1.55	1.52
32	2a	1519	MA6	C6-N1	2.09	1.35	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2x	54	5MU	C6-N1	-2.08	1.34	1.38
56	1y	8	4SU	C2-N3	-2.08	1.34	1.38
1	2A	2058	MA6	C6-N1	2.08	1.35	1.32
32	1a	1519	MA6	C6-N1	2.07	1.35	1.32
32	1a	1518	MA6	C6-N1	2.04	1.35	1.32
56	1y	8	4SU	C6-C5	2.02	1.39	1.35
32	2a	966	M2G	C6-N1	-2.02	1.34	1.37
32	1a	967	5MC	C6-N1	-2.01	1.34	1.38
55	1x	76	8AN	C5-N7	-2.01	1.32	1.39
54	2w	8	4SU	C2-N1	2.00	1.41	1.38

All (307) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	1l	92	0TD	CSB-SB-CB	-17.54	70.83	102.36
43	2l	92	0TD	CSB-SB-CB	-11.47	81.75	102.36
55	1x	76	8AN	O4'-C1'-N9	10.42	122.56	108.75
54	2w	8	4SU	C4-N3-C2	-8.85	118.83	127.31
55	2x	76	8AN	C4'-O4'-C1'	-8.47	102.16	109.92
54	1w	37	MIA	C12-C13-C14	-8.38	111.98	127.01
32	1a	1498	UR3	C4-N3-C2	-7.36	118.65	124.58
55	1x	76	8AN	C4'-O4'-C1'	-7.31	103.23	109.92
32	2a	1498	UR3	C4-N3-C2	-7.24	118.75	124.58
1	2A	2503	2MA	C2-N3-C4	7.17	121.25	115.46
1	1A	2503	2MA	C2-N3-C4	6.80	120.95	115.46
55	1x	76	8AN	N3-C2-N1	-6.72	119.55	128.67
56	2y	8	4SU	C4-N3-C2	-6.68	120.91	127.31
55	2x	55	PSU	N1-C2-N3	6.61	122.14	115.17
1	1A	2605	PSU	N1-C2-N3	6.52	122.05	115.17
56	1y	55	PSU	N1-C2-N3	6.51	122.03	115.17
32	2a	516	PSU	N1-C2-N3	6.50	122.02	115.17
54	2w	76	8AN	N3-C2-N1	-6.48	119.87	128.67
1	1A	1911	PSU	N1-C2-N3	6.47	121.99	115.17
54	1w	76	8AN	N3-C2-N1	-6.46	119.91	128.67
55	2x	76	8AN	O4'-C1'-N9	6.45	117.30	108.75
54	2w	8	4SU	C5-C4-N3	6.41	120.72	114.75
55	1x	55	PSU	N1-C2-N3	6.36	121.88	115.17
55	2x	76	8AN	N3-C2-N1	-6.36	120.04	128.67
1	1A	1917	PSU	N1-C2-N3	6.35	121.87	115.17
54	2w	55	PSU	N1-C2-N3	6.30	121.81	115.17
1	2A	1917	PSU	N1-C2-N3	6.13	121.64	115.17
1	2A	1911	PSU	N1-C2-N3	6.07	121.57	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2058	MA6	N3-C2-N1	-6.02	120.50	128.67
56	2y	32	PSU	N1-C2-N3	6.00	121.50	115.17
56	2y	55	PSU	N1-C2-N3	5.99	121.49	115.17
54	1w	55	PSU	N1-C2-N3	5.95	121.45	115.17
54	2w	32	PSU	N1-C2-N3	5.95	121.44	115.17
32	1a	1518	MA6	N3-C2-N1	-5.90	120.66	128.67
1	2A	2605	PSU	N1-C2-N3	5.88	121.37	115.17
54	1w	32	PSU	N1-C2-N3	5.84	121.32	115.17
54	1w	54	5MU	O4-C4-C5	-5.83	118.25	124.92
1	2A	1939	5MU	C4-N3-C2	-5.75	119.81	127.34
32	2a	1518	MA6	N3-C2-N1	-5.73	120.89	128.67
54	2w	39	PSU	N1-C2-N3	5.72	121.20	115.17
32	1a	516	PSU	N1-C2-N3	5.72	121.20	115.17
56	1y	32	PSU	N1-C2-N3	5.72	121.20	115.17
56	2y	8	4SU	C5-C4-N3	5.68	120.04	114.75
1	2A	1915	5MU	C4-N3-C2	-5.66	119.92	127.34
32	2a	1519	MA6	N3-C2-N1	-5.59	121.08	128.67
56	2y	39	PSU	N1-C2-N3	5.59	121.06	115.17
32	1a	1519	MA6	N3-C2-N1	-5.59	121.09	128.67
1	2A	1939	5MU	C5-C4-N3	5.55	120.15	115.32
32	1a	1518	MA6	C2-N1-C6	5.50	122.23	116.84
55	2x	54	5MU	N3-C2-N1	5.49	122.04	114.89
56	1y	39	PSU	N1-C2-N3	5.49	120.95	115.17
55	1x	54	5MU	N3-C2-N1	5.45	121.99	114.89
1	1A	2058	MA6	N3-C2-N1	-5.40	121.34	128.67
1	2A	1915	5MU	N3-C2-N1	5.38	121.89	114.89
54	2w	8	4SU	N3-C2-N1	5.34	121.85	114.89
55	2x	54	5MU	C4-N3-C2	-5.31	120.38	127.34
1	1A	1915	5MU	N3-C2-N1	5.31	121.80	114.89
55	1x	54	5MU	C4-N3-C2	-5.30	120.39	127.34
1	1A	1915	5MU	C4-N3-C2	-5.22	120.50	127.34
1	1A	1939	5MU	C4-N3-C2	-5.22	120.50	127.34
1	1A	1939	5MU	C5-C4-N3	5.20	119.84	115.32
54	1w	39	PSU	N1-C2-N3	5.18	120.63	115.17
54	1w	8	4SU	C4-N3-C2	-5.14	122.39	127.31
56	1y	54	5MU	C4-N3-C2	-5.11	120.64	127.34
56	1y	8	4SU	C4-N3-C2	-5.09	122.43	127.31
56	1y	54	5MU	N3-C2-N1	5.02	121.42	114.89
1	2A	1939	5MU	N3-C2-N1	4.97	121.36	114.89
54	1w	54	5MU	C4-N3-C2	-4.96	120.84	127.34
32	2a	1518	MA6	C2-N1-C6	4.92	121.66	116.84
1	2A	1915	5MU	O4-C4-C5	-4.86	119.35	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1915	5MU	C5-C4-N3	4.84	119.53	115.32
54	1w	54	5MU	N3-C2-N1	4.77	121.10	114.89
1	2A	2552	OMU	C4-N3-C2	-4.76	120.70	126.61
1	2A	2058	MA6	C2-N1-C6	4.72	121.47	116.84
1	1A	1939	5MU	C5-C6-N1	-4.71	118.19	123.31
54	1w	8	4SU	C5-C4-N3	4.69	119.12	114.75
1	1A	2058	MA6	C2-N1-C6	4.66	121.41	116.84
55	2x	55	PSU	C4-N3-C2	-4.66	119.95	126.37
54	1w	54	5MU	C5-C4-N3	4.59	119.31	115.32
56	1y	8	4SU	C5-C4-N3	4.56	119.00	114.75
1	1A	1915	5MU	C5-C4-N3	4.56	119.28	115.32
1	2A	1939	5MU	O4-C4-C5	-4.48	119.79	124.92
56	2y	8	4SU	C5-C4-S4	-4.48	119.19	124.31
1	1A	1911	PSU	C4-N3-C2	-4.44	120.26	126.37
1	1A	2552	OMU	C4-N3-C2	-4.42	121.13	126.61
32	2a	1519	MA6	C2-N1-C6	4.40	121.16	116.84
1	1A	1939	5MU	N3-C2-N1	4.38	120.59	114.89
32	1a	1519	MA6	C2-N1-C6	4.36	121.11	116.84
1	2A	2605	PSU	C4-N3-C2	-4.33	120.40	126.37
54	2w	8	4SU	C5-C4-S4	-4.30	119.39	124.31
54	2w	54	5MU	N3-C2-N1	4.25	120.42	114.89
56	2y	54	5MU	N3-C2-N1	4.22	120.38	114.89
55	1x	54	5MU	C5-C4-N3	4.21	118.99	115.32
54	2w	55	PSU	C4-N3-C2	-4.19	120.60	126.37
1	1A	1917	PSU	C4-N3-C2	-4.19	120.60	126.37
1	2A	2552	OMU	N3-C2-N1	4.17	120.32	114.89
56	1y	54	5MU	C5-C4-N3	4.15	118.93	115.32
56	2y	8	4SU	N3-C2-N1	4.12	120.26	114.89
1	1A	1911	PSU	O2-C2-N1	-4.12	118.54	122.79
55	2x	54	5MU	C5-C4-N3	4.11	118.90	115.32
32	2a	516	PSU	C4-N3-C2	-4.11	120.71	126.37
56	2y	32	PSU	O2-C2-N1	-4.10	118.56	122.79
54	2w	54	5MU	C4-N3-C2	-4.09	121.98	127.34
54	2w	54	5MU	O4-C4-C5	-4.09	120.24	124.92
56	2y	54	5MU	C4-N3-C2	-4.08	121.99	127.34
32	1a	516	PSU	C4-N3-C2	-4.08	120.75	126.37
56	2y	37	MIA	N3-C2-N1	-4.08	123.14	128.67
1	2A	1939	5MU	C5-C6-N1	-4.07	118.89	123.31
55	2x	54	5MU	O4-C4-C5	-4.06	120.27	124.92
1	1A	1942	5MC	C5-C6-N1	-4.05	118.92	123.31
56	2y	54	5MU	C5-C4-N3	4.04	118.83	115.32
54	1w	37	MIA	C15-C14-C13	-4.03	110.55	122.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1x	8	4SU	S4-C4-N3	-4.03	115.99	120.20
56	1y	55	PSU	O2-C2-N1	-4.03	118.64	122.79
1	1A	2552	OMU	N3-C2-N1	4.02	120.13	114.89
55	1x	54	5MU	O4-C4-C5	-4.00	120.34	124.92
54	1w	32	PSU	C4-N3-C2	-4.00	120.86	126.37
1	2A	1911	PSU	C4-N3-C2	-3.99	120.87	126.37
1	2A	1917	PSU	C4-N3-C2	-3.98	120.89	126.37
1	1A	1939	5MU	O4-C4-C5	-3.98	120.36	124.92
54	1w	55	PSU	O2-C2-N1	-3.96	118.70	122.79
1	1A	2605	PSU	C4-N3-C2	-3.96	120.91	126.37
54	1w	55	PSU	C4-N3-C2	-3.92	120.97	126.37
56	1y	55	PSU	C4-N3-C2	-3.91	120.98	126.37
54	2w	32	PSU	C4-N3-C2	-3.91	120.99	126.37
55	1x	32	5MC	C5-C6-N1	-3.90	119.07	123.31
55	1x	55	PSU	C4-N3-C2	-3.85	121.06	126.37
32	2a	516	PSU	O2-C2-N1	-3.84	118.83	122.79
55	1x	8	4SU	O2-C2-N1	3.81	127.75	122.80
54	2w	39	PSU	C4-N3-C2	-3.81	121.12	126.37
55	2x	32	5MC	C5-C6-N1	-3.78	119.21	123.31
56	1y	8	4SU	N3-C2-N1	3.75	119.78	114.89
1	2A	1915	5MU	C5-C6-N1	-3.74	119.25	123.31
32	2a	1404	5MC	C5-C6-N1	-3.74	119.25	123.31
1	2A	2605	PSU	O2-C2-N1	-3.73	118.94	122.79
55	1x	8	4SU	C6-C5-C4	-3.72	116.73	119.95
56	1y	32	PSU	C4-N3-C2	-3.72	121.25	126.37
54	1w	8	4SU	N3-C2-N1	3.69	119.70	114.89
56	2y	55	PSU	O2-C2-N1	-3.67	119.01	122.79
55	1x	54	5MU	C5-C6-N1	-3.67	119.33	123.31
32	1a	1404	5MC	C5-C4-N3	-3.67	118.00	121.75
1	1A	1917	PSU	O2-C2-N1	-3.65	119.02	122.79
32	1a	1400	5MC	C5-C6-N1	-3.64	119.36	123.31
1	2A	2552	OMU	C5-C4-N3	3.64	119.89	114.80
54	2w	54	5MU	C5-C4-N3	3.63	118.48	115.32
1	1A	1915	5MU	O4-C4-C5	-3.63	120.77	124.92
56	1y	37	MIA	N3-C2-N1	-3.63	123.75	128.67
56	1y	54	5MU	O4-C4-C5	-3.62	120.78	124.92
55	1x	55	PSU	O2-C2-N1	-3.59	119.08	122.79
56	2y	32	PSU	C4-N3-C2	-3.58	121.44	126.37
1	1A	2552	OMU	O4-C4-C5	-3.57	119.01	125.16
54	2w	8	4SU	O2-C2-N1	-3.54	118.19	122.80
32	2a	1207	2MG	N1-C2-N2	3.53	120.17	116.56
56	2y	55	PSU	C4-N3-C2	-3.53	121.51	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1w	37	MIA	C16-C14-C13	-3.52	112.09	122.66
56	1y	32	PSU	O2-C2-N1	-3.51	119.17	122.79
1	2A	1942	5MC	C5-C6-N1	-3.48	119.53	123.31
32	2a	1400	5MC	C5-C6-N1	-3.46	119.55	123.31
1	2A	2552	OMU	O2-C2-N1	-3.46	118.29	122.80
1	1A	1942	5MC	C5-C4-N3	-3.45	118.22	121.75
32	1a	967	5MC	C5-C6-N1	-3.44	119.57	123.31
56	1y	54	5MU	C5-C6-N1	-3.41	119.61	123.31
56	2y	39	PSU	C4-N3-C2	-3.39	121.70	126.37
55	2x	54	5MU	C5-C6-N1	-3.37	119.65	123.31
55	1x	54	5MU	O2-C2-N1	-3.32	118.47	122.80
1	1A	2552	OMU	C5-C4-N3	3.32	119.44	114.80
32	2a	1407	5MC	C5-C4-N3	-3.29	118.39	121.75
54	2w	55	PSU	O2-C2-N1	-3.28	119.41	122.79
56	2y	54	5MU	O4-C4-C5	-3.26	121.18	124.92
55	2x	8	4SU	C6-C5-C4	-3.26	117.13	119.95
1	2A	1911	PSU	O2-C2-N1	-3.21	119.48	122.79
56	1y	8	4SU	C1'-N1-C2	3.21	123.36	117.59
54	1w	32	PSU	O2-C2-N1	-3.21	119.48	122.79
1	2A	1917	PSU	O2-C2-N1	-3.20	119.49	122.79
54	2w	32	PSU	O2-C2-N1	-3.19	119.50	122.79
32	2a	1519	MA6	C4-C5-N7	-3.19	105.96	109.34
32	1a	1407	5MC	C5-C6-N1	-3.17	119.87	123.31
1	1A	2552	OMU	O2-C2-N1	-3.16	118.68	122.80
32	2a	1407	5MC	C5-C6-N1	-3.15	119.89	123.31
32	1a	1498	UR3	C5-C4-N3	3.15	119.18	115.04
55	2x	54	5MU	O2-C2-N1	-3.09	118.77	122.80
56	1y	39	PSU	C4-N3-C2	-3.08	122.13	126.37
32	1a	1207	2MG	C8-N7-C5	3.08	107.79	102.55
32	2a	1498	UR3	C5-C4-N3	3.05	119.06	115.04
32	2a	967	5MC	C5-C6-N1	-3.05	120.00	123.31
55	1x	32	5MC	C5-C4-N3	-3.03	118.64	121.75
32	2a	966	M2G	C8-N7-C5	3.03	107.70	102.55
55	2x	8	4SU	O2-C2-N1	3.02	126.73	122.80
32	1a	1402	4OC	C6-C5-C4	3.01	120.63	117.00
32	2a	1207	2MG	N2-C2-N3	-3.01	116.68	120.51
55	2x	55	PSU	O2-C2-N1	-3.01	119.69	122.79
1	2A	2552	OMU	O4-C4-C5	-3.00	119.98	125.16
1	1A	1915	5MU	C5-C6-N1	-3.00	120.05	123.31
1	2A	1962	5MC	C5-C6-N1	-2.99	120.06	123.31
32	1a	966	M2G	C8-N7-C5	2.98	107.63	102.55
1	1A	1962	5MC	C5-C4-N3	-2.97	118.71	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2w	39	PSU	O2-C2-N1	-2.96	119.73	122.79
32	1a	1404	5MC	C5-C6-N1	-2.96	120.10	123.31
1	1A	2605	PSU	O2-C2-N3	-2.95	116.62	121.86
55	2x	32	5MC	C5-C4-N3	-2.94	118.74	121.75
32	1a	1519	MA6	C4-C5-N7	-2.92	106.25	109.34
54	2w	54	5MU	C5-C6-N1	-2.91	120.15	123.31
56	2y	54	5MU	C5-C6-N1	-2.89	120.17	123.31
56	2y	55	PSU	C6-C5-C4	-2.89	116.22	118.17
1	2A	1962	5MC	C5-C4-N3	-2.89	118.80	121.75
54	1w	39	PSU	C4-N3-C2	-2.79	122.52	126.37
1	1A	2251	OMG	C8-N7-C5	2.79	107.29	102.55
32	2a	1207	2MG	C8-N7-C5	2.78	107.29	102.55
32	1a	1400	5MC	C5-C4-N3	-2.78	118.90	121.75
54	1w	54	5MU	C5-C6-N1	-2.77	120.30	123.31
1	2A	2251	OMG	C8-N7-C5	2.76	107.25	102.55
55	2x	8	4SU	C5-C4-N3	2.75	117.31	114.75
54	1w	37	MIA	C11-S10-C2	-2.73	100.20	102.25
32	2a	1400	5MC	C5-C4-N3	-2.69	119.00	121.75
32	2a	1400	5MC	O2-C2-N3	-2.67	118.12	122.33
1	1A	2605	PSU	C5-C6-N1	-2.67	118.44	122.14
1	2A	1915	5MU	O2-C2-N1	-2.66	119.33	122.80
32	2a	1518	MA6	C4-C5-N7	-2.61	106.57	109.34
56	1y	8	4SU	C5-C4-S4	-2.61	121.32	124.31
1	1A	2503	2MA	C4-C5-N7	-2.61	106.58	109.34
32	1a	1407	5MC	O2-C2-N3	-2.61	118.22	122.33
54	2w	37	MIA	C1'-N9-C4	2.59	131.20	126.64
55	2x	8	4SU	C1'-N1-C2	2.59	122.24	117.59
32	2a	1404	5MC	C5-C4-N3	-2.59	119.10	121.75
55	1x	76	8AN	C4-C5-N7	-2.58	106.61	109.34
1	1A	1962	5MC	C5-C6-N1	-2.57	120.52	123.31
55	1x	8	4SU	C5-C4-N3	2.57	117.14	114.75
1	1A	2058	MA6	C4-C5-N7	-2.57	106.63	109.34
54	1w	37	MIA	C2-N1-C6	2.56	121.97	117.42
32	2a	1402	4OC	C6-C5-C4	2.55	120.08	117.00
55	2x	8	4SU	S4-C4-N3	-2.55	117.54	120.20
32	1a	1407	5MC	C5-C4-N3	-2.54	119.15	121.75
1	1A	1915	5MU	C5M-C5-C4	2.51	121.46	118.78
1	2A	1939	5MU	O2-C2-N1	-2.49	119.55	122.80
1	1A	2503	2MA	C5-C6-N1	-2.49	117.89	120.84
1	1A	1962	5MC	CM5-C5-C6	-2.48	119.49	122.85
54	2w	54	5MU	O2-C2-N1	-2.48	119.57	122.80
55	1x	8	4SU	C4-N3-C2	2.48	129.69	127.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1942	5MC	C5-C4-N3	-2.47	119.22	121.75
56	1y	32	PSU	C6-C5-C4	-2.47	116.51	118.17
1	2A	2503	2MA	C4-C5-N7	-2.47	106.73	109.34
55	2x	55	PSU	C5-C6-N1	-2.46	118.73	122.14
43	1l	92	0TD	OD2-CG-CB	2.44	118.43	113.15
54	1w	37	MIA	C4-C5-N7	-2.44	106.76	109.34
1	1A	1942	5MC	CM5-C5-C6	-2.41	119.58	122.85
32	1a	516	PSU	O2-C2-N1	-2.41	120.31	122.79
32	2a	967	5MC	C5-C4-N3	-2.38	119.31	121.75
56	2y	8	4SU	O2-C2-N1	-2.37	119.71	122.80
1	2A	2058	MA6	C9-N6-C6	2.37	125.94	119.40
1	2A	2503	2MA	C2-N1-C6	2.36	121.72	118.10
56	2y	37	MIA	C4-C5-N7	-2.36	106.85	109.34
54	2w	37	MIA	C2-N1-C6	2.34	121.58	117.42
32	1a	1518	MA6	C4-C5-N7	-2.33	106.88	109.34
43	2l	92	0TD	OD2-CG-CB	2.32	118.16	113.15
1	2A	2251	OMG	C5-C6-N1	2.31	118.49	114.07
32	1a	1404	5MC	O2-C2-N3	-2.31	118.68	122.33
1	2A	1920	OMC	O2-C2-N3	-2.31	118.68	122.33
54	1w	54	5MU	O2-C2-N1	-2.30	119.80	122.80
55	1x	32	5MC	O2-C2-N3	-2.30	118.71	122.33
1	1A	2503	2MA	C2-N1-C6	2.29	121.62	118.10
54	1w	76	8AN	C4'-O4'-C1'	-2.27	107.84	109.92
55	1x	8	4SU	C5-C4-S4	2.25	126.87	124.31
1	2A	1962	5MC	CM5-C5-C6	-2.23	119.84	122.85
32	2a	1404	5MC	O2-C2-N3	-2.22	118.83	122.33
54	1w	39	PSU	O2-C2-N3	-2.21	117.93	121.86
1	1A	1911	PSU	C5-C6-N1	-2.20	119.08	122.14
32	1a	1207	2MG	N1-C2-N2	2.20	118.81	116.56
32	1a	1207	2MG	C5-C6-N1	2.19	118.26	114.07
32	1a	1498	UR3	C1'-N1-C2	2.19	120.62	117.04
1	1A	2251	OMG	C5-C6-N1	2.18	118.24	114.07
56	1y	54	5MU	O2-C2-N1	-2.17	119.97	122.80
32	1a	1498	UR3	C3U-N3-C4	2.16	120.87	117.87
32	2a	516	PSU	C5-C6-N1	-2.16	119.14	122.14
56	2y	54	5MU	C5M-C5-C4	2.16	121.08	118.78
32	1a	516	PSU	C5-C6-N1	-2.15	119.15	122.14
32	2a	1402	4OC	O2-C2-N3	-2.15	118.94	122.33
1	2A	2058	MA6	C4-C5-N7	-2.15	107.06	109.34
32	1a	966	M2G	C5-C6-N1	2.15	118.17	114.07
56	2y	39	PSU	O2-C2-N3	-2.14	118.06	121.86
32	2a	1402	4OC	CM4-N4-C4	-2.14	118.27	122.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2w	37	MIA	C12-N6-C6	-2.12	120.89	122.85
1	2A	2605	PSU	O4-C4-C5	-2.11	118.77	124.01
54	1w	37	MIA	N3-C2-N1	-2.11	123.17	127.03
32	1a	1498	UR3	C6-N1-C2	-2.09	120.09	121.80
54	1w	8	4SU	O2-C2-N1	-2.08	120.08	122.80
1	2A	1911	PSU	C5-C6-N1	-2.08	119.25	122.14
56	2y	39	PSU	C5-C6-N1	-2.08	119.25	122.14
55	2x	55	PSU	O2-C2-N3	-2.08	118.17	121.86
32	2a	1498	UR3	C1'-N1-C2	2.08	120.44	117.04
32	2a	516	PSU	O4'-C1'-C2'	2.08	108.03	105.15
32	1a	516	PSU	O4'-C1'-C2'	2.08	108.03	105.15
1	1A	1915	5MU	O2-C2-N3	-2.08	117.66	121.49
54	2w	55	PSU	C5-C6-N1	-2.07	119.26	122.14
32	1a	1404	5MC	CM5-C5-C6	-2.07	120.05	122.85
32	1a	967	5MC	C5-C4-N3	-2.07	119.64	121.75
55	1x	8	4SU	O2-C2-N3	-2.06	117.68	121.49
54	1w	8	4SU	C5-C4-S4	-2.06	121.95	124.31
1	1A	1939	5MU	C5M-C5-C4	2.06	120.98	118.78
1	1A	1942	5MC	N1-C2-N3	2.06	122.37	118.80
1	2A	2251	OMG	O6-C6-C5	-2.05	120.25	124.32
56	1y	55	PSU	O4'-C1'-C2'	2.04	107.98	105.15
1	2A	2503	2MA	C5-C6-N1	-2.03	118.44	120.84
32	1a	1407	5MC	N1-C2-N3	2.02	122.31	118.80
1	2A	1917	PSU	C5-C6-N1	-2.02	119.34	122.14
56	1y	39	PSU	O2-C2-N3	-2.01	118.29	121.86
1	1A	2058	MA6	C9-N6-C6	2.01	124.95	119.40
32	1a	1402	4OC	C5-C6-N1	-2.00	118.59	121.84

There are no chirality outliers.

All (45) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	O-C-CA-CB
43	1l	92	0TD	CG-CB-SB-CSB
54	1w	37	MIA	C12-C13-C14-C15
54	1w	37	MIA	C12-C13-C14-C16
56	1y	37	MIA	O4'-C4'-C5'-O5'
56	1y	46	G7M	C4'-C5'-O5'-P
32	2a	1519	MA6	O4'-C4'-C5'-O5'
54	2w	37	MIA	C5-C6-N6-C12
54	2w	37	MIA	N1-C6-N6-C12

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Mol	Chain	Res	Type	Atoms
54	2w	37	MIA	N1-C2-S10-C11
54	2w	37	MIA	N3-C2-S10-C11
55	2x	76	8AN	O4'-C4'-C5'-O5'
55	2x	76	8AN	C3'-C4'-C5'-O5'
55	1x	76	8AN	C3'-C4'-C5'-O5'
56	1y	37	MIA	C3'-C4'-C5'-O5'
54	1w	46	G7M	C4'-C5'-O5'-P
55	1x	76	8AN	O4'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
54	2w	46	G7M	C4'-C5'-O5'-P
32	2a	527	G7M	O4'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
56	2y	46	G7M	O4'-C4'-C5'-O5'
56	2y	55	PSU	C3'-C4'-C5'-O5'
55	2x	76	8AN	C4'-C5'-O5'-P
43	1l	92	0TD	SB-CB-CG-OD1
43	2l	92	0TD	SB-CB-CG-OD1
55	1x	76	8AN	C4'-C5'-O5'-P
56	1y	55	PSU	O4'-C1'-C5-C4
56	2y	55	PSU	O4'-C1'-C5-C4
56	2y	46	G7M	C3'-C4'-C5'-O5'
32	1a	527	G7M	C4'-C5'-O5'-P
32	1a	1519	MA6	C4'-C5'-O5'-P
32	2a	527	G7M	C4'-C5'-O5'-P
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C4'-C5'-O5'-P
56	1y	55	PSU	O4'-C1'-C5-C6
1	1A	2503	2MA	C4'-C5'-O5'-P
43	2l	92	0TD	CG-CB-SB-CSB
1	1A	1920	OMC	C2'-C1'-N1-C2
56	2y	8	4SU	C4'-C5'-O5'-P
56	1y	8	4SU	C2'-C1'-N1-C2
32	1a	527	G7M	O4'-C4'-C5'-O5'

There are no ring outliers.

42 monomers are involved in 52 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	1w	46	G7M	1	0
1	2A	2058	MA6	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	2y	37	MIA	1	0
1	1A	2058	MA6	1	0
55	2x	76	8AN	1	0
56	1y	39	PSU	1	0
55	2x	55	PSU	1	0
32	1a	967	5MC	1	0
54	1w	8	4SU	1	0
56	2y	46	G7M	1	0
56	1y	46	G7M	1	0
32	1a	1518	MA6	4	0
32	2a	966	M2G	1	0
1	2A	1939	5MU	1	0
54	2w	76	8AN	1	0
32	1a	1519	MA6	2	0
56	2y	8	4SU	2	0
32	2a	967	5MC	2	0
1	2A	2251	OMG	1	0
55	2x	54	5MU	3	0
32	1a	966	M2G	1	0
56	1y	55	PSU	2	0
56	2y	54	5MU	1	0
1	1A	2251	OMG	1	0
54	1w	76	8AN	1	0
56	1y	54	5MU	1	0
32	1a	1402	4OC	1	0
43	2l	92	0TD	1	0
56	2y	39	PSU	1	0
55	1x	8	4SU	2	0
1	1A	1939	5MU	1	0
54	2w	55	PSU	1	0
55	1x	76	8AN	2	0
54	2w	39	PSU	1	0
56	1y	8	4SU	1	0
54	1w	37	MIA	1	0
56	1y	37	MIA	4	0
55	2x	8	4SU	1	0
1	1A	2552	OMU	1	0
32	2a	1519	MA6	2	0
54	2w	54	5MU	1	0
32	2a	1518	MA6	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2755 ligands modelled in this entry, 2747 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
63	FME	2x	108	55	8,9,10	0.36	0	8,9,11	1.31	2 (25%)
59	A1AE1	1A	4094	57	82,82,82	2.30	12 (14%)	116,122,122	2.14	33 (28%)
59	A1AE1	2A	3855	57	82,82,82	2.21	13 (15%)	116,122,122	2.21	31 (26%)
62	PHE	2w	108	54	10,11,12	1.63	1 (10%)	8,13,15	0.55	0
63	FME	1x	115	55	8,9,10	0.42	0	8,9,11	1.62	2 (25%)
61	SF4	1d	302	35	0,12,12	-	-	-		
61	SF4	2d	303	35	0,12,12	-	-	-		
62	PHE	1w	109	54	10,11,12	1.55	1 (10%)	8,13,15	0.54	0

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
63	FME	2x	108	55	-	0/7/9/11	-
59	A1AE1	1A	4094	57	-	13/89/132/132	0/7/7/7
59	A1AE1	2A	3855	57	-	14/89/132/132	0/7/7/7
62	PHE	2w	108	54	-	3/5/6/8	0/1/1/1
63	FME	1x	115	55	-	1/7/9/11	-
61	SF4	1d	302	35	-	-	0/6/5/5
61	SF4	2d	303	35	-	-	0/6/5/5
62	PHE	1w	109	54	-	1/5/6/8	0/1/1/1

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1A	4094	A1AE1	CAG-CAF	-12.78	1.41	1.53
59	2A	3855	A1AE1	CAG-CAF	-11.71	1.42	1.53
59	2A	3855	A1AE1	CAB-CAF	-7.13	1.40	1.52
59	1A	4094	A1AE1	CAB-CAF	-6.88	1.40	1.52
59	1A	4094	A1AE1	OBR-NBJ	5.87	1.54	1.40
59	2A	3855	A1AE1	CAJ-CAI	-5.76	1.39	1.51
59	1A	4094	A1AE1	CAJ-CAI	-5.16	1.40	1.51
62	2w	108	PHE	CB-CG	-4.94	1.39	1.51
59	2A	3855	A1AE1	CCF-CCN	-4.84	1.41	1.48
62	1w	109	PHE	CB-CG	-4.67	1.40	1.51
59	1A	4094	A1AE1	CCF-CCN	-4.52	1.41	1.48
59	1A	4094	A1AE1	CCC-NCH	-4.46	1.34	1.40
59	1A	4094	A1AE1	CCB-CCE	-4.38	1.39	1.48
59	2A	3855	A1AE1	CCG-NCH	4.26	1.41	1.34
59	2A	3855	A1AE1	CCB-CCE	-4.13	1.40	1.48
59	2A	3855	A1AE1	OBR-NBJ	3.98	1.50	1.40
59	1A	4094	A1AE1	CCG-NCH	3.95	1.41	1.34
59	2A	3855	A1AE1	CCC-NCH	-3.90	1.35	1.40
59	1A	4094	A1AE1	CAF-NBJ	3.85	1.34	1.28
59	2A	3855	A1AE1	CAF-NBJ	3.80	1.33	1.28
59	2A	3855	A1AE1	CBY-NBX	-2.88	1.35	1.41
59	1A	4094	A1AE1	CAG-CAH	2.87	1.58	1.54
59	2A	3855	A1AE1	CAG-CAH	2.84	1.58	1.54
59	1A	4094	A1AE1	CBY-NBX	-2.56	1.35	1.41
59	2A	3855	A1AE1	OBH-CAL	-2.55	1.43	1.47
59	2A	3855	A1AE1	OBH-CBP	2.26	1.37	1.34
59	1A	4094	A1AE1	CAA-CAE	2.18	1.55	1.52

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	2A	3855	A1AE1	CAB-CAF-NBJ	-12.26	117.17	126.21
59	1A	4094	A1AE1	CAB-CAF-NBJ	-10.52	118.45	126.21
59	1A	4094	A1AE1	OBB-CBT-NBV	6.79	122.08	111.01
59	2A	3855	A1AE1	OBB-CBT-NBV	6.34	121.34	111.01
59	1A	4094	A1AE1	CAK-OBB-CBT	-5.76	108.58	117.04
59	2A	3855	A1AE1	CAK-OBB-CBT	-5.66	108.73	117.04
59	1A	4094	A1AE1	OBU-CBT-NBV	-4.68	117.88	124.93
59	2A	3855	A1AE1	CAB-CAF-CAG	4.59	124.24	119.34
59	2A	3855	A1AE1	CCA-CBZ-CBY	-4.31	119.54	123.35
59	2A	3855	A1AE1	CCX-NBX-CCT	4.30	121.24	111.57
59	1A	4094	A1AE1	OBH-CAL-CBG	4.29	114.37	106.80
59	2A	3855	A1AE1	OBU-CBT-NBV	-4.25	118.52	124.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	1A	4094	A1AE1	CBE-CAM-CAL	-4.20	109.43	115.23
59	1A	4094	A1AE1	CAB-CAF-CAG	3.96	123.57	119.34
59	2A	3855	A1AE1	CAG-CAF-NBJ	3.91	118.42	114.40
59	2A	3855	A1AE1	CBE-CAM-CAL	-3.71	110.12	115.23
59	1A	4094	A1AE1	CCK-CCI-NCH	-3.65	113.10	118.87
59	1A	4094	A1AE1	FCL-CBZ-CBY	3.59	121.79	118.37
59	1A	4094	A1AE1	CCA-CBZ-CBY	-3.49	120.27	123.35
59	2A	3855	A1AE1	CCB-CCE-CCF	3.47	120.02	115.64
59	2A	3855	A1AE1	OBH-CAL-CBG	3.39	112.77	106.80
63	1x	115	FME	CA-N-CN	-3.37	117.63	122.82
59	1A	4094	A1AE1	CCX-NBX-CCT	3.31	119.02	111.57
59	2A	3855	A1AE1	CCF-CCG-NCH	-3.28	120.49	124.42
59	1A	4094	A1AE1	CCG-CCF-CCE	-3.19	117.59	119.94
59	2A	3855	A1AE1	CAM-OAN-CAI	-3.15	112.70	118.20
59	2A	3855	A1AE1	CAE-CAD-CAC	-3.10	108.81	113.54
59	1A	4094	A1AE1	OBB-CBT-OBU	-3.07	120.04	124.55
59	1A	4094	A1AE1	CCD-CBY-NBX	-3.06	118.13	122.59
59	1A	4094	A1AE1	OBL-CAE-CAA	3.05	112.13	105.71
59	1A	4094	A1AE1	CCB-CCE-CCF	3.05	119.49	115.64
59	1A	4094	A1AE1	CAG-CAF-NBJ	3.03	117.53	114.40
59	2A	3855	A1AE1	OBB-CBT-OBU	-3.00	120.13	124.55
59	1A	4094	A1AE1	CBO-OBL-CAE	-2.91	111.59	117.51
59	2A	3855	A1AE1	CAX-CAR-CAS	-2.87	108.93	113.27
59	2A	3855	A1AE1	OAN-CAM-CBE	2.86	112.68	107.36
59	2A	3855	A1AE1	OBL-CAE-CAA	2.77	111.54	105.71
59	1A	4094	A1AE1	OAO-CAD-CAE	2.66	112.63	106.44
63	1x	115	FME	O1-CN-N	-2.63	118.52	125.32
59	1A	4094	A1AE1	OCO-CCN-OCP	-2.59	117.74	123.90
59	2A	3855	A1AE1	CCD-CBY-CBZ	2.56	119.20	116.53
59	2A	3855	A1AE1	FCL-CBZ-CBY	2.53	120.78	118.37
59	2A	3855	A1AE1	CCD-CBY-NBX	-2.53	118.91	122.59
59	1A	4094	A1AE1	OCM-CCE-CCB	-2.53	117.53	121.57
59	2A	3855	A1AE1	CBI-CAG-CAH	2.53	116.38	112.94
59	2A	3855	A1AE1	CBO-OBL-CAE	-2.52	112.38	117.51
59	1A	4094	A1AE1	CBI-CAG-CAH	2.50	116.34	112.94
59	1A	4094	A1AE1	CCN-CCF-CCE	2.49	125.31	121.61
59	1A	4094	A1AE1	CAA-CAB-CAF	-2.49	110.17	113.16
59	1A	4094	A1AE1	OBR-NBJ-CAF	2.48	118.31	111.25
59	1A	4094	A1AE1	CCF-CCG-NCH	-2.47	121.46	124.42
59	2A	3855	A1AE1	CAA-CAB-CAF	-2.44	110.23	113.16
59	2A	3855	A1AE1	CCG-CCF-CCE	-2.43	118.16	119.94
59	2A	3855	A1AE1	OAN-CAI-CAJ	2.36	116.58	111.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	1A	4094	A1AE1	CAX-CAR-CAS	-2.36	109.70	113.27
59	2A	3855	A1AE1	CBC-CAJ-CAK	-2.34	107.77	113.00
59	1A	4094	A1AE1	CAE-CAD-CAC	-2.30	110.03	113.54
59	1A	4094	A1AE1	CBG-CAL-CAM	-2.29	108.29	112.36
59	2A	3855	A1AE1	OCO-CCN-OCP	-2.24	118.56	123.90
59	1A	4094	A1AE1	CCD-CBY-CBZ	2.23	118.86	116.53
63	2x	108	FME	CA-N-CN	-2.23	119.40	122.82
59	1A	4094	A1AE1	CBZ-CBY-NBX	2.22	123.01	120.42
59	2A	3855	A1AE1	CAH-OBN-CBP	-2.22	105.72	109.45
59	2A	3855	A1AE1	OBR-NBJ-CAF	2.21	117.56	111.25
63	2x	108	FME	O1-CN-N	-2.18	119.67	125.32
59	1A	4094	A1AE1	CCT-NBX-CBY	2.10	121.16	116.19
59	2A	3855	A1AE1	OBH-CAL-CAM	2.06	110.20	105.63
59	1A	4094	A1AE1	OBH-CAL-CAM	2.04	110.15	105.63

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	1w	109	PHE	O-C-CA-CB
62	2w	108	PHE	O-C-CA-CB
59	1A	4094	A1AE1	CBZ-CBY-NBX-CCX
59	2A	3855	A1AE1	CBZ-CBY-NBX-CCX
59	1A	4094	A1AE1	CCJ-CCI-NCH-CCG
59	2A	3855	A1AE1	CCJ-CCI-NCH-CCG
63	1x	115	FME	CB-CG-SD-CE
59	1A	4094	A1AE1	CCJ-CCI-NCH-CCC
59	2A	3855	A1AE1	CCJ-CCI-NCH-CCC
59	2A	3855	A1AE1	CBW-CCQ-CCR-CCS
59	1A	4094	A1AE1	OBB-CBT-NBV-CBW
59	2A	3855	A1AE1	OBB-CBT-NBV-CBW
59	1A	4094	A1AE1	OBU-CBT-NBV-CBW
59	2A	3855	A1AE1	OBU-CBT-NBV-CBW
59	1A	4094	A1AE1	CCD-CBY-NBX-CCX
59	1A	4094	A1AE1	CBW-CCQ-CCR-CCS
59	2A	3855	A1AE1	CCK-CCI-NCH-CCG
59	1A	4094	A1AE1	CBK-CAB-CAF-NBJ
59	2A	3855	A1AE1	CBK-CAB-CAF-NBJ
59	2A	3855	A1AE1	CCD-CBY-NBX-CCX
59	1A	4094	A1AE1	CCK-CCI-NCH-CCG
59	1A	4094	A1AE1	NBV-CBW-CCQ-CCR
62	2w	108	PHE	N-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
62	2w	108	PHE	C-CA-CB-CG
59	2A	3855	A1AE1	OAN-CAM-CBE-CBF
59	1A	4094	A1AE1	CAU-CAP-OAO-CAD
59	1A	4094	A1AE1	OAQ-CAP-OAO-CAD
59	2A	3855	A1AE1	NBV-CBW-CCQ-CCR
59	2A	3855	A1AE1	CCK-CCI-NCH-CCC
59	2A	3855	A1AE1	CAL-CAM-CBE-CBF
59	1A	4094	A1AE1	CCK-CCI-NCH-CCC
59	2A	3855	A1AE1	CCQ-CCR-CCS-NCV

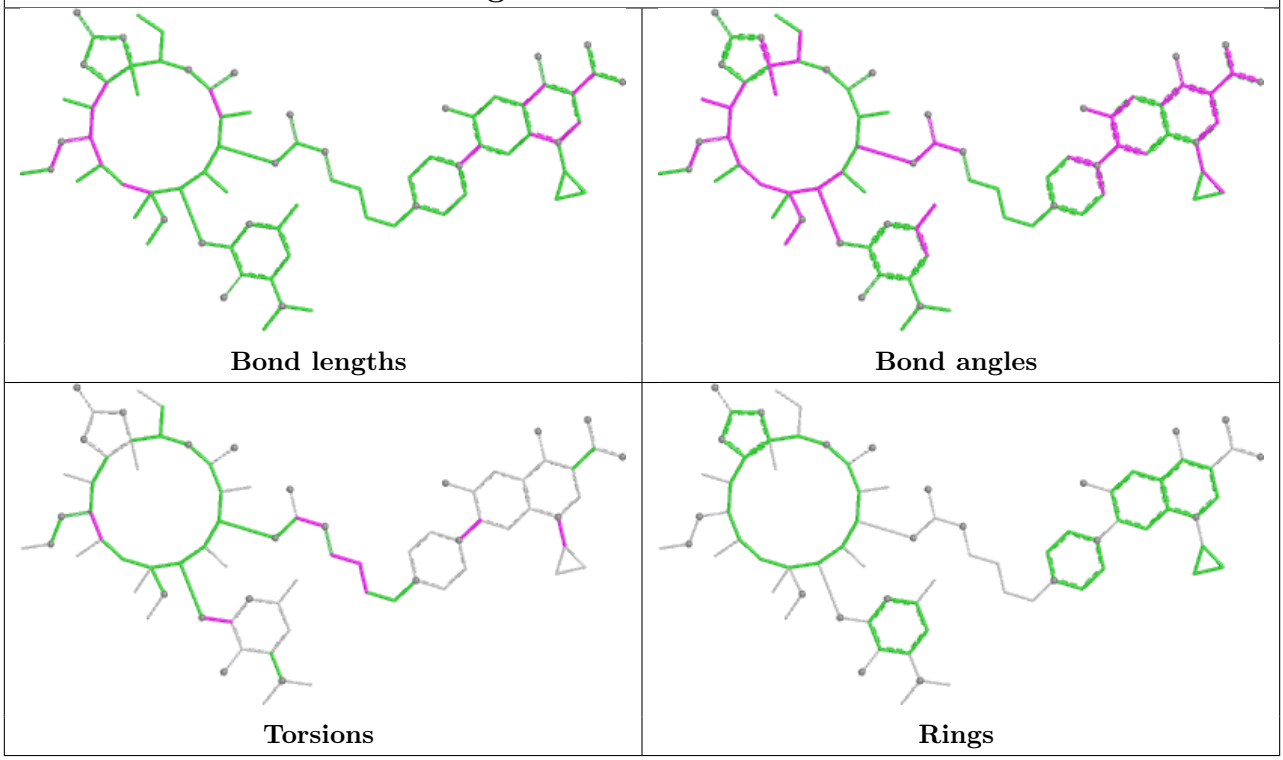
There are no ring outliers.

4 monomers are involved in 7 short contacts:

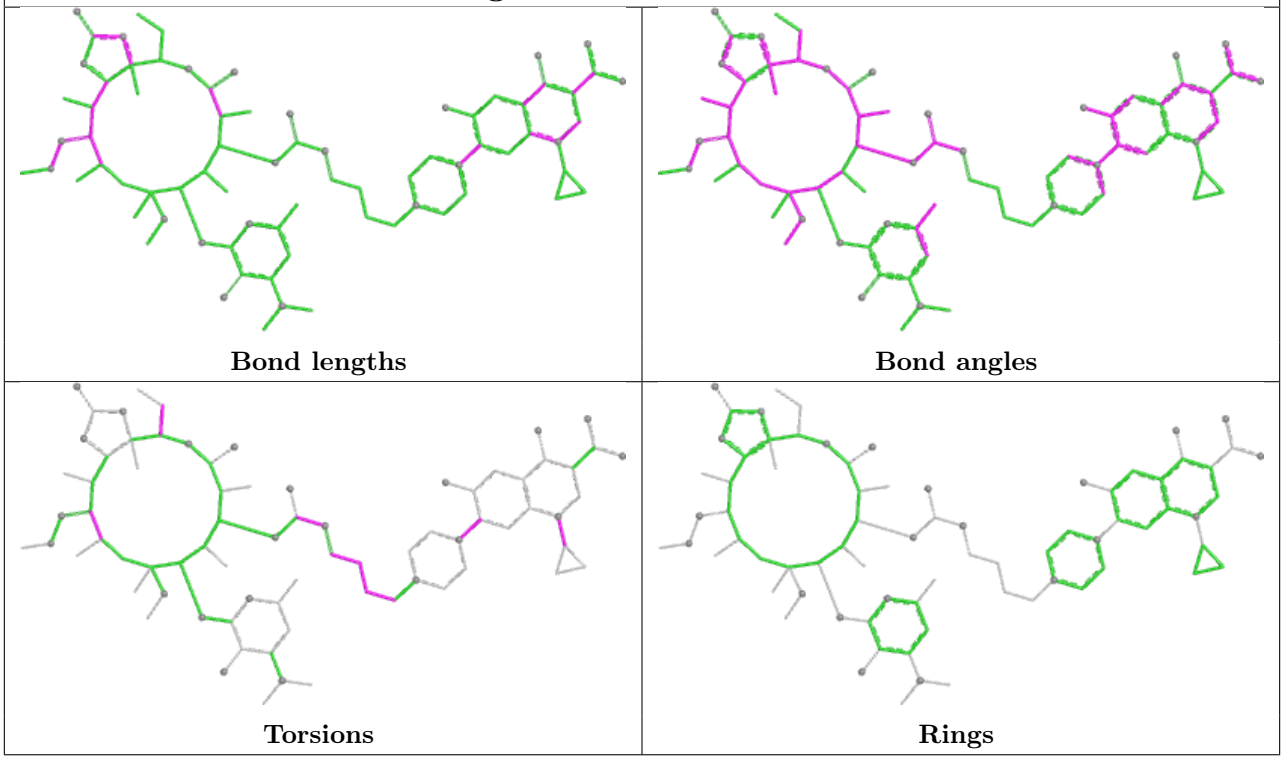
Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	2A	3855	A1AE1	1	0
62	2w	108	PHE	1	0
61	2d	303	SF4	4	0
62	1w	109	PHE	1	0

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

Ligand A1AE1 1A 4094



Ligand A1AE1 2A 3855



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	2859/2915 (98%)	-0.34	215 (7%) 22 20	20, 37, 89, 98	0
1	2A	2788/2915 (95%)	0.16	173 (6%) 28 25	33, 55, 87, 97	0
2	1B	120/121 (99%)	-0.12	1 (0%) 82 80	34, 50, 65, 81	0
2	2B	120/121 (99%)	0.79	0 100 100	58, 69, 77, 84	0
3	1D	275/276 (99%)	-0.19	3 (1%) 77 75	24, 38, 52, 72	0
3	2D	275/276 (99%)	0.11	4 (1%) 71 68	30, 48, 59, 81	0
4	1E	204/206 (99%)	-0.15	2 (0%) 79 76	21, 40, 58, 72	0
4	2E	204/206 (99%)	0.44	2 (0%) 79 76	36, 57, 68, 75	0
5	1F	203/210 (96%)	-0.06	3 (1%) 71 68	20, 43, 66, 77	0
5	2F	203/210 (96%)	0.49	5 (2%) 58 55	33, 62, 75, 79	0
6	1G	181/182 (99%)	0.54	8 (4%) 39 37	42, 56, 69, 78	0
6	2G	181/182 (99%)	1.17	19 (10%) 13 11	58, 71, 79, 84	0
7	1H	174/180 (96%)	0.40	6 (3%) 48 45	40, 52, 64, 72	0
7	2H	174/180 (96%)	1.58	49 (28%) 1 2	65, 77, 83, 88	0
8	1I	146/148 (98%)	0.94	9 (6%) 28 25	46, 67, 76, 80	0
8	2I	146/148 (98%)	1.15	14 (9%) 15 13	50, 68, 76, 80	0
9	1N	140/140 (100%)	-0.08	2 (1%) 73 70	26, 39, 60, 69	0
9	2N	140/140 (100%)	0.69	5 (3%) 46 43	46, 61, 73, 82	0
10	1O	122/122 (100%)	-0.24	0 100 100	29, 40, 58, 62	0
10	2O	122/122 (100%)	0.39	0 100 100	47, 57, 67, 72	0
11	1P	149/150 (99%)	0.08	3 (2%) 64 61	22, 49, 67, 71	0
11	2P	149/150 (99%)	0.85	14 (9%) 15 14	37, 63, 77, 80	0
12	1Q	141/141 (100%)	-0.14	2 (1%) 73 70	25, 41, 56, 69	0
12	2Q	141/141 (100%)	0.90	12 (8%) 18 17	44, 62, 71, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.43	0 100 100	26, 35, 48, 56	0
13	2R	118/118 (100%)	0.28	0 100 100	41, 52, 62, 68	0
14	1S	110/112 (98%)	0.34	1 (0%) 81 78	39, 50, 61, 65	0
14	2S	110/112 (98%)	1.04	13 (11%) 10 9	58, 65, 73, 78	0
15	1T	131/146 (89%)	0.10	2 (1%) 71 68	33, 45, 66, 74	0
15	2T	131/146 (89%)	0.63	5 (3%) 44 42	50, 60, 71, 77	0
16	1U	116/118 (98%)	-0.49	0 100 100	23, 31, 47, 62	0
16	2U	116/118 (98%)	0.53	1 (0%) 81 78	43, 58, 69, 74	0
17	1V	101/101 (100%)	-0.34	1 (0%) 79 76	25, 39, 55, 65	0
17	2V	101/101 (100%)	0.86	2 (1%) 64 61	42, 66, 73, 80	0
18	1W	112/113 (99%)	-0.36	1 (0%) 81 78	26, 33, 50, 77	0
18	2W	112/113 (99%)	0.20	2 (1%) 67 63	41, 49, 62, 82	0
19	1X	95/96 (98%)	-0.05	3 (3%) 50 47	30, 41, 63, 77	0
19	2X	95/96 (98%)	0.42	2 (2%) 63 60	45, 57, 71, 78	0
20	1Y	107/110 (97%)	0.38	4 (3%) 45 43	39, 51, 63, 73	0
20	2Y	107/110 (97%)	1.10	14 (13%) 8 7	54, 66, 76, 80	0
21	1Z	154/206 (74%)	0.91	25 (16%) 5 5	41, 62, 78, 82	0
21	2Z	160/206 (77%)	1.80	50 (31%) 1 1	63, 75, 82, 88	0
22	10	83/85 (97%)	-0.08	1 (1%) 76 73	28, 37, 51, 64	0
22	20	83/85 (97%)	0.79	4 (4%) 36 34	38, 58, 66, 75	0
23	11	97/98 (98%)	0.34	2 (2%) 63 60	30, 50, 69, 75	0
23	21	97/98 (98%)	0.46	3 (3%) 51 48	40, 54, 69, 75	0
24	12	70/72 (97%)	0.29	3 (4%) 40 38	35, 49, 59, 68	0
24	22	70/72 (97%)	0.81	3 (4%) 40 38	58, 66, 74, 75	0
25	13	59/60 (98%)	-0.19	1 (1%) 69 65	25, 36, 60, 72	0
25	23	59/60 (98%)	0.70	4 (6%) 25 22	51, 61, 71, 77	0
26	14	69/71 (97%)	1.30	16 (23%) 2 3	49, 71, 81, 85	0
26	24	69/71 (97%)	1.74	22 (31%) 1 1	70, 77, 84, 87	0
27	15	59/60 (98%)	-0.39	1 (1%) 69 65	22, 34, 53, 58	0
27	25	59/60 (98%)	0.25	3 (5%) 34 32	38, 49, 64, 75	0
28	16	53/54 (98%)	-0.14	0 100 100	33, 44, 56, 61	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.59	2 (3%) 44 42	47, 57, 63, 66	0
29	17	48/49 (97%)	-0.29	3 (6%) 27 25	21, 29, 55, 62	0
29	27	48/49 (97%)	0.06	1 (2%) 63 60	32, 41, 61, 69	0
30	18	64/65 (98%)	-0.42	0 100 100	28, 36, 43, 57	0
30	28	64/65 (98%)	0.34	1 (1%) 70 67	44, 51, 58, 63	0
31	19	37/37 (100%)	-0.15	0 100 100	31, 39, 51, 58	0
31	29	37/37 (100%)	0.93	1 (2%) 56 53	58, 64, 72, 77	0
32	1a	1488/1521 (97%)	0.46	83 (5%) 31 28	36, 62, 85, 97	0
32	2a	1491/1521 (98%)	0.73	112 (7%) 22 20	45, 69, 86, 97	0
33	1b	231/256 (90%)	1.42	50 (21%) 3 3	60, 73, 80, 84	0
33	2b	231/256 (90%)	1.59	65 (28%) 2 2	64, 76, 81, 86	0
34	1c	206/239 (86%)	1.03	17 (8%) 19 17	56, 67, 77, 81	0
34	2c	206/239 (86%)	1.43	38 (18%) 4 4	65, 74, 81, 86	0
35	1d	208/209 (99%)	1.03	19 (9%) 16 14	53, 65, 72, 80	0
35	2d	208/209 (99%)	0.96	18 (8%) 17 16	55, 65, 73, 79	0
36	1e	148/162 (91%)	0.71	5 (3%) 48 45	48, 61, 69, 73	0
36	2e	148/162 (91%)	1.21	15 (10%) 14 12	59, 68, 74, 80	0
37	1f	100/101 (99%)	0.87	4 (4%) 43 40	54, 64, 70, 73	0
37	2f	100/101 (99%)	0.86	4 (4%) 43 40	55, 63, 71, 75	0
38	1g	155/156 (99%)	0.90	17 (10%) 12 10	57, 66, 78, 81	0
38	2g	155/156 (99%)	1.26	21 (13%) 8 7	65, 72, 78, 82	0
39	1h	137/138 (99%)	0.66	4 (2%) 54 50	51, 63, 70, 73	0
39	2h	137/138 (99%)	1.07	12 (8%) 17 16	60, 69, 75, 78	0
40	1i	127/128 (99%)	1.34	21 (16%) 5 5	51, 71, 77, 80	0
40	2i	127/128 (99%)	1.77	44 (34%) 1 1	62, 75, 81, 83	0
41	1j	97/105 (92%)	1.49	20 (20%) 3 3	53, 71, 81, 85	0
41	2j	96/105 (91%)	2.14	53 (55%) 0 0	66, 77, 83, 85	0
42	1k	114/129 (88%)	0.63	6 (5%) 33 30	42, 63, 71, 78	0
42	2k	114/129 (88%)	0.95	11 (9%) 15 13	54, 67, 74, 76	0
43	1l	121/132 (91%)	0.38	4 (3%) 49 46	42, 50, 61, 69	0
43	2l	121/132 (91%)	0.75	7 (5%) 30 27	53, 60, 68, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	123/126 (97%)	1.06	11 (8%) 17 15	50, 65, 72, 84	0
44	2m	122/126 (96%)	1.62	30 (24%) 2 2	65, 74, 78, 82	0
45	1n	60/61 (98%)	1.02	4 (6%) 25 23	55, 62, 68, 71	0
45	2n	60/61 (98%)	2.17	30 (50%) 0 0	68, 75, 79, 83	0
46	1o	88/89 (98%)	0.76	5 (5%) 30 28	45, 62, 70, 74	0
46	2o	88/89 (98%)	0.92	7 (7%) 20 18	56, 66, 75, 80	0
47	1p	82/88 (93%)	1.37	14 (17%) 5 5	54, 66, 71, 79	0
47	2p	82/88 (93%)	1.04	4 (4%) 36 33	56, 65, 72, 75	0
48	1q	99/105 (94%)	0.83	1 (1%) 79 76	55, 63, 71, 74	0
48	2q	99/105 (94%)	0.85	5 (5%) 34 32	59, 67, 74, 78	0
49	1r	68/88 (77%)	0.53	1 (1%) 71 68	52, 63, 72, 74	0
49	2r	68/88 (77%)	0.67	2 (2%) 54 50	58, 65, 73, 77	0
50	1s	83/93 (89%)	1.19	10 (12%) 10 8	60, 67, 74, 78	0
50	2s	83/93 (89%)	1.65	22 (26%) 2 2	71, 77, 81, 88	0
51	1t	96/106 (90%)	1.01	13 (13%) 8 7	57, 65, 74, 78	0
51	2t	96/106 (90%)	1.04	13 (13%) 8 7	57, 65, 75, 78	0
52	1u	23/27 (85%)	1.15	3 (13%) 9 7	54, 62, 66, 68	0
52	2u	23/27 (85%)	2.19	14 (60%) 0 0	66, 72, 75, 78	0
53	1v	13/24 (54%)	0.62	2 (15%) 6 6	47, 52, 82, 85	0
53	2v	13/24 (54%)	1.25	3 (23%) 2 3	57, 66, 86, 93	0
54	1w	66/76 (86%)	1.78	25 (37%) 1 1	29, 80, 90, 92	0
54	2w	64/76 (84%)	1.67	18 (28%) 2 2	45, 85, 90, 94	0
55	1x	72/77 (93%)	0.23	2 (2%) 55 51	25, 56, 75, 83	0
55	2x	72/77 (93%)	0.65	2 (2%) 55 51	39, 69, 80, 89	0
56	1y	67/76 (88%)	2.10	34 (50%) 0 0	61, 90, 95, 97	0
56	2y	66/76 (86%)	2.26	45 (68%) 0 0	67, 91, 94, 96	0
All	All	20871/21748 (95%)	0.48	1718 (8%) 19 17	20, 60, 82, 98	0

All (1718) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	2A	652(U)	G	9.7
1	2A	652(V)	C	8.7

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Mol	Chain	Res	Type	RSRZ
1	1A	652(V)	C	8.5
1	1A	652(C)	G	8.4
1	1A	653	A	8.4
1	1A	654	A	8.3
1	2A	653	A	8.2
44	2m	124	PRO	8.1
44	2m	123	ALA	7.7
44	1m	123	ALA	7.3
1	1A	652(U)	G	7.3
21	1Z	141	VAL	7.2
1	2A	883	G	7.0
45	1n	2	ALA	6.8
32	2a	1033	G	6.7
1	2A	654	A	6.6
1	2A	652(C)	G	6.4
44	1m	2	ALA	6.3
45	2n	2	ALA	6.3
7	1H	2	SER	6.3
1	1A	652(S)	C	6.2
32	1a	1027	C	6.1
1	2A	2802	G	6.1
32	2a	1032	G	6.0
1	2A	652(T)	C	5.8
1	1A	2117	A	5.8
1	1A	884	C	5.7
1	2A	2111	C	5.7
32	1a	1035	A	5.6
1	2A	2147	G	5.5
1	1A	652(T)	C	5.5
1	2A	2146	C	5.5
1	1A	1094	U	5.5
1	1A	2119	A	5.5
1	2A	2803	C	5.5
46	2o	89	GLY	5.5
21	2Z	172	ALA	5.4
21	2Z	146	ILE	5.4
33	2b	165	VAL	5.4
1	2A	884	C	5.4
1	1A	1068	G	5.3
21	1Z	146	ILE	5.2
34	2c	2	GLY	5.2
41	2j	32	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
1	1A	1057	A	5.2
1	1A	652(E)	G	5.2
1	2A	882	G	5.2
1	1A	1087	G	5.1
44	1m	124	PRO	5.1
32	1a	1025	U	5.1
44	2m	102	ARG	5.1
32	1a	1257	U	5.0
20	2Y	1	MET	5.0
38	2g	83	ALA	5.0
44	2m	122	LYS	5.0
34	1c	2	GLY	5.0
1	2A	2145	C	5.0
54	1w	70	G	5.0
23	11	2	SER	4.9
1	2A	2112	G	4.9
1	2A	2149	G	4.9
32	2a	1002	G	4.9
1	1A	2111	C	4.9
1	1A	2145	C	4.9
3	1D	276	LYS	4.9
40	1i	8	GLY	4.9
32	1a	1447	A	4.8
54	1w	73	A	4.8
1	1A	879	G	4.8
32	2a	1031	G	4.8
1	1A	2108	C	4.8
33	2b	121	LEU	4.8
1	1A	2159	G	4.8
32	1a	1034	G	4.8
54	2w	71	G	4.8
1	1A	652(D)	C	4.8
1	1A	1095	A	4.8
1	1A	1081	U	4.8
26	14	56	VAL	4.7
1	1A	1073	A	4.7
1	2A	2155	G	4.7
1	2A	896	A	4.7
1	1A	652(F)	G	4.7
32	1a	1030(A)	G	4.7
1	1A	1064	C	4.6
1	1A	1078	U	4.6

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Mol	Chain	Res	Type	RSRZ
38	2g	84	ASN	4.6
1	2A	2159	G	4.6
1	1A	2130	U	4.6
32	2a	1018	C	4.6
1	1A	2793	G	4.6
1	2A	2144	U	4.6
1	1A	1509	C	4.6
1	2A	885	C	4.6
1	2A	2126	A	4.6
1	1A	885	C	4.6
1	1A	1096	A	4.5
11	2P	15	ARG	4.5
1	1A	2116	G	4.5
1	1A	2143	C	4.5
21	2Z	150	LEU	4.5
1	2A	2113	U	4.5
1	2A	2893	G	4.5
32	1a	630	G	4.5
32	1a	1003	G	4.5
32	1a	1033	G	4.5
32	1a	1036	G	4.5
54	1w	72	C	4.5
1	1A	1059	G	4.5
41	2j	78	ASN	4.4
33	2b	237	ALA	4.4
35	1d	195	ALA	4.4
1	1A	2115	G	4.4
1	1A	2114	A	4.4
1	1A	2790	A	4.4
41	2j	65	LEU	4.4
1	2A	2804	C	4.4
54	2w	72	C	4.4
1	1A	1176	G	4.4
1	1A	1098	A	4.4
32	2a	1035	A	4.4
1	1A	2792	G	4.4
1	2A	2125	G	4.4
21	2Z	149	SER	4.3
1	2A	1536	C	4.3
1	1A	1063	G	4.3
56	1y	15	G	4.3
7	2H	2	SER	4.3

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Mol	Chain	Res	Type	RSRZ
1	1A	2136	C	4.3
1	1A	2803	C	4.3
32	1a	1030	C	4.3
51	1t	103	GLY	4.3
1	2A	2158	A	4.3
54	1w	71	G	4.3
15	1T	131	ALA	4.3
32	2a	1004	A	4.3
38	2g	16	LEU	4.3
1	1A	2112	G	4.3
40	2i	102	LEU	4.2
41	2j	47	PHE	4.2
15	1T	130	ALA	4.2
32	2a	1001(A)	G	4.2
32	2a	1034	G	4.2
50	1s	13	ASP	4.2
32	1a	1030(D)	A	4.2
32	2a	1030(D)	A	4.2
1	2A	2115	G	4.2
1	2A	2127	G	4.2
32	2a	1026	G	4.2
1	1A	897	C	4.2
1	2A	1509	C	4.2
1	2A	652(B)	A	4.2
1	2A	2793	G	4.2
7	2H	128	PRO	4.2
33	1b	232	PRO	4.2
44	1m	122	LYS	4.2
1	1A	2166	G	4.1
1	2A	11	G	4.1
54	2w	70	G	4.1
40	2i	11	LYS	4.1
1	1A	1066	U	4.1
21	2Z	147	GLY	4.1
52	2u	16	GLY	4.1
1	1A	2146	C	4.1
32	2a	1149	C	4.1
1	1A	1058	G	4.1
1	1A	2131	G	4.1
32	1a	1032	G	4.1
6	1G	146	TYR	4.1
33	1b	188	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	1A	1088	A	4.1
1	1A	1508	A	4.1
26	24	63	TYR	4.1
1	1A	1093	G	4.1
32	1a	1030(C)	G	4.1
50	2s	2	PRO	4.1
44	2m	58	GLU	4.1
1	2A	2174	C	4.1
54	2w	73	A	4.1
56	1y	75	C	4.1
45	2n	55	GLY	4.0
41	2j	74	ILE	4.0
1	1A	2170	A	4.0
1	1A	2173	A	4.0
54	1w	4	C	4.0
40	2i	14	VAL	4.0
44	2m	4	ILE	4.0
1	1A	1089	G	4.0
1	1A	2110	G	4.0
54	2w	15	G	4.0
1	2A	878	A	4.0
21	2Z	171	ILE	4.0
1	2A	881	G	4.0
32	1a	1001(A)	G	4.0
56	2y	57	G	4.0
32	1a	1030(B)	C	4.0
33	1b	11	LEU	4.0
3	2D	276	LYS	4.0
50	1s	9	VAL	4.0
41	1j	32	ALA	3.9
45	2n	3	ARG	3.9
1	1A	882	G	3.9
1	1A	2142	C	3.9
32	2a	1030	C	3.9
32	1a	204	U	3.9
15	2T	128	GLU	3.9
1	2A	892	G	3.9
1	2A	2133	G	3.9
32	2a	1003	G	3.9
32	2a	1036	G	3.9
1	1A	2794	C	3.9
1	2A	2143	C	3.9

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Mol	Chain	Res	Type	RSRZ
32	2a	1027	C	3.9
33	1b	17	PHE	3.9
32	2a	1257	U	3.9
33	1b	133	LYS	3.9
39	2h	2	LEU	3.9
26	14	32	TYR	3.9
38	2g	5	ARG	3.9
33	1b	229	VAL	3.9
1	1A	1065	U	3.9
1	1A	1082	U	3.9
51	2t	103	GLY	3.9
35	1d	191	ARG	3.9
1	1A	1086	A	3.8
1	2A	2173	A	3.8
32	1a	1023	G	3.8
32	1a	1024	G	3.8
11	2P	101	VAL	3.8
32	1a	1029	C	3.8
32	2a	1039	C	3.8
33	1b	129	GLU	3.8
1	1A	896	A	3.8
21	2Z	121	HIS	3.8
1	1A	888	C	3.8
52	2u	2	GLY	3.8
40	2i	62	TYR	3.8
33	2b	122	PHE	3.8
51	2t	99	LEU	3.8
1	1A	887	A	3.8
1	1A	1054	A	3.8
1	1A	898	C	3.8
1	1A	2141	G	3.8
1	2A	2128	C	3.8
18	2W	112	GLY	3.8
1	1A	1069	A	3.8
1	1A	2135	A	3.8
54	1w	7	A	3.8
1	1A	1072	C	3.8
1	1A	2174	C	3.8
1	1A	1060	U	3.8
1	2A	2160	G	3.8
1	2A	2805	G	3.8
56	2y	19	G	3.8

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Mol	Chain	Res	Type	RSRZ
38	1g	156	TRP	3.7
6	1G	50	ALA	3.7
33	1b	237	ALA	3.7
56	2y	36	A	3.7
1	2A	898	C	3.7
1	2A	2136	C	3.7
54	1w	67	C	3.7
21	2Z	144	LEU	3.7
50	1s	71	LEU	3.7
26	24	56	VAL	3.7
33	1b	127	ILE	3.7
1	1A	655	A	3.7
1	2A	1509(A)	A	3.7
1	2A	2169	A	3.7
26	14	59	PHE	3.7
45	2n	25	VAL	3.7
32	2a	1030(A)	G	3.7
33	2b	123	ALA	3.7
36	1e	10	MET	3.7
1	1A	2118	U	3.7
33	2b	17	PHE	3.7
41	2j	77	PRO	3.7
41	2j	76	ASN	3.6
51	2t	98	PRO	3.6
32	2a	1150	U	3.6
35	1d	192	GLU	3.6
56	2y	35	A	3.6
1	1A	2137	C	3.6
1	2A	894	C	3.6
1	2A	1533	G	3.6
1	2A	2110	G	3.6
23	21	2	SER	3.6
33	1b	125	PRO	3.6
33	1b	9	GLU	3.6
1	1A	2109	U	3.6
11	2P	109	GLY	3.6
1	1A	1062	G	3.6
1	2A	2156	G	3.6
38	2g	80	VAL	3.6
50	2s	79	THR	3.6
1	2A	2130	U	3.6
54	1w	20	U	3.6

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Mol	Chain	Res	Type	RSRZ
33	2b	236	TYR	3.6
41	1j	74	ILE	3.6
1	1A	2169	A	3.6
1	1A	2171	A	3.6
32	1a	1005	A	3.6
7	2H	36	PRO	3.6
40	2i	9	ARG	3.6
1	1A	2133	G	3.6
1	1A	2162	G	3.6
1	2A	2168	G	3.6
32	2a	630	G	3.6
41	2j	34	VAL	3.6
1	1A	2113	U	3.6
38	1g	85	TYR	3.6
45	2n	34	TYR	3.6
1	1A	2158	A	3.5
1	2A	2801(A)	A	3.5
32	1a	1001	A	3.5
32	2a	1001	A	3.5
1	1A	1080	C	3.5
1	1A	2129	C	3.5
33	1b	131	PRO	3.5
6	1G	48	GLU	3.5
33	2b	21	ARG	3.5
34	1c	207	VAL	3.5
8	2I	146	ALA	3.5
1	1A	2148	G	3.5
1	1A	2151	G	3.5
1	1A	2160	G	3.5
1	1A	2168	G	3.5
1	2A	2751	G	3.5
32	2a	1021	G	3.5
1	1A	1175	U	3.5
1	2A	2109	U	3.5
50	2s	80	TYR	3.5
34	2c	62	ASP	3.5
1	2A	2137	C	3.5
1	2A	2794	C	3.5
32	2a	1043	C	3.5
33	1b	230	VAL	3.5
41	2j	44	VAL	3.5
15	2T	131	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1099	G	3.5
32	2a	1020	U	3.5
11	2P	79	ARG	3.5
21	2Z	159	PRO	3.5
52	2u	24	ARG	3.5
21	2Z	168	GLU	3.5
40	2i	126	SER	3.5
1	1A	889	C	3.5
1	1A	1100	C	3.5
32	2a	1030(B)	C	3.5
45	2n	6	LEU	3.5
1	1A	2172	U	3.5
38	2g	32	ARG	3.5
1	1A	2152	G	3.5
1	2A	2318	G	3.5
54	1w	1	G	3.5
33	1b	134	GLU	3.5
21	2Z	136	PHE	3.5
26	24	54	GLY	3.5
21	2Z	174	VAL	3.5
38	1g	80	VAL	3.5
32	1a	1286	A	3.5
33	2b	39	ILE	3.5
32	1a	1037	C	3.4
19	1X	95	LEU	3.4
33	1b	10	LEU	3.4
38	2g	156	TRP	3.4
1	1A	271(K)	U	3.4
1	1A	2167	U	3.4
32	1a	65	U	3.4
56	1y	47	U	3.4
3	2D	275	LYS	3.4
7	1H	174	GLY	3.4
32	1a	1026	G	3.4
32	1a	1031	G	3.4
33	1b	227	GLY	3.4
21	1Z	105	VAL	3.4
1	1A	2134	A	3.4
32	2a	1005	A	3.4
53	2v	13	A	3.4
1	1A	2138	C	3.4
6	2G	182	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
36	2e	114	GLY	3.4
1	1A	2190	G	3.4
1	2A	2154	G	3.4
1	2A	2807	G	3.4
1	1A	1084	A	3.4
53	2v	12	A	3.4
1	1A	886	C	3.4
56	1y	13	C	3.4
7	1H	175	LYS	3.4
1	2A	2167	U	3.4
50	2s	84	GLY	3.4
43	2l	18	VAL	3.4
1	1A	2120	G	3.4
1	2A	1170	G	3.4
1	2A	2116	G	3.4
1	2A	2148	G	3.4
1	2A	2792	G	3.4
1	2A	2894	G	3.4
1	2A	2119	A	3.4
1	2A	2135	A	3.4
26	24	51	ASP	3.4
44	1m	121	LYS	3.4
1	1A	2107	C	3.4
1	1A	2164	C	3.4
47	2p	82	GLN	3.4
1	1A	1097	U	3.4
33	1b	19	HIS	3.4
33	2b	185	ILE	3.4
7	2H	96	ALA	3.3
40	2i	20	ARG	3.3
41	1j	77	PRO	3.3
45	2n	14	PRO	3.3
1	1A	880	G	3.3
1	1A	2156	G	3.3
32	1a	1021	G	3.3
1	2A	2114	A	3.3
6	2G	146	TYR	3.3
32	2a	1447	A	3.3
38	2g	85	TYR	3.3
53	1v	13	A	3.3
26	24	45	GLY	3.3
45	2n	38	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	1A	2161	C	3.3
1	2A	888	C	3.3
32	2a	1038	C	3.3
9	2N	9	VAL	3.3
39	1h	2	LEU	3.3
21	1Z	148	ASP	3.3
26	14	63	TYR	3.3
1	1A	2165	G	3.3
1	2A	879	G	3.3
1	2A	880	G	3.3
1	2A	2117	A	3.3
1	2A	2170	A	3.3
38	1g	82	GLY	3.3
33	2b	81	VAL	3.3
41	1j	4	ILE	3.3
34	2c	190	ARG	3.3
21	1Z	149	SER	3.3
44	2m	121	LYS	3.3
41	2j	36	GLY	3.3
52	2u	4	GLY	3.3
7	2H	19	VAL	3.3
41	2j	46	ARG	3.3
1	2A	1171	G	3.3
1	2A	2120	G	3.3
32	1a	1531	A	3.3
56	1y	19	G	3.3
1	1A	1092	C	3.3
41	2j	41	PRO	3.3
56	2y	56	C	3.3
26	14	49	PHE	3.3
7	2H	7	LEU	3.2
7	2H	43	VAL	3.2
7	2H	52	VAL	3.2
33	1b	187	LEU	3.2
33	2b	71	VAL	3.2
44	2m	33	ALA	3.2
1	1A	1509(A)	A	3.2
41	2j	59	SER	3.2
1	1A	2132	U	3.2
1	2A	2100	G	3.2
32	2a	485	G	3.2
54	1w	5	G	3.2

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Mol	Chain	Res	Type	RSRZ
54	2w	19	G	3.2
32	2a	1037	C	3.2
26	24	19	GLY	3.2
35	1d	2	GLY	3.2
40	2i	67	GLY	3.2
50	2s	68	GLY	3.2
35	1d	194	LEU	3.2
12	2Q	121	ALA	3.2
33	2b	120	ALA	3.2
40	1i	106	ALA	3.2
41	2j	37	PRO	3.2
1	1A	2897	U	3.2
1	2A	1508	A	3.2
1	1A	1071	G	3.2
1	1A	2182	G	3.2
32	1a	1002	G	3.2
1	1A	2175	C	3.2
1	1A	2178	C	3.2
1	2A	652(D)	C	3.2
50	2s	13	ASP	3.2
23	21	28	GLY	3.2
38	1g	81	GLY	3.2
39	1h	112	LEU	3.2
32	1a	1532	U	3.2
32	2a	1532	U	3.2
54	2w	45	U	3.2
1	1A	1070	A	3.2
7	2H	175	LYS	3.2
47	1p	68	ASP	3.2
1	2A	2789	C	3.2
1	2A	2896	C	3.2
32	1a	1028	C	3.2
54	2w	2	C	3.2
20	2Y	90	LEU	3.2
33	2b	187	LEU	3.2
45	2n	5	ALA	3.2
45	2n	13	THR	3.2
1	1A	2150	U	3.2
1	2A	2118	U	3.2
1	1A	652(A)	A	3.2
1	1A	1067	A	3.2
44	2m	6	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
34	1c	47	LEU	3.1
1	1A	1091	G	3.1
1	1A	2127	G	3.1
1	2A	886	C	3.1
32	2a	1019	C	3.1
32	2a	1028	C	3.1
32	2a	1115	C	3.1
56	2y	5	G	3.1
56	2y	13	C	3.1
15	2T	130	ALA	3.1
21	2Z	95	PRO	3.1
29	27	45	ALA	3.1
44	2m	87	TYR	3.1
7	2H	6	ARG	3.1
20	2Y	54	LYS	3.1
26	24	55	ARG	3.1
11	2P	82	GLY	3.1
21	1Z	1	MET	3.1
1	2A	2134	A	3.1
7	2H	136	ILE	3.1
34	2c	87	LEU	3.1
21	2Z	105	VAL	3.1
33	2b	161	ALA	3.1
1	1A	271(I)	G	3.1
1	1A	2100	G	3.1
1	1A	2149	G	3.1
1	1A	2804	C	3.1
32	1a	79	G	3.1
32	2a	470	C	3.1
56	2y	49	C	3.1
35	1d	173	TRP	3.1
33	2b	127	ILE	3.1
1	1A	548	A	3.1
1	1A	899	A	3.1
33	2b	93	VAL	3.1
1	1A	2128	C	3.1
54	1w	3	C	3.1
56	1y	48	C	3.1
21	2Z	153	SER	3.1
33	2b	48	MET	3.1
19	1X	94	GLY	3.1
21	1Z	104	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
37	2f	21	LEU	3.1
21	2Z	139	VAL	3.1
33	2b	34	ALA	3.1
1	1A	1046	A	3.1
1	1A	2801(A)	A	3.1
32	2a	1286	A	3.1
26	14	67	TYR	3.1
32	1a	1137	C	3.1
33	1b	97	TRP	3.1
1	1A	2157	G	3.0
1	1A	2802	G	3.0
1	2A	2123	G	3.0
1	2A	2166	G	3.0
50	2s	16	LEU	3.0
41	2j	75	ILE	3.0
46	1o	19	PRO	3.0
33	2b	136	VAL	3.0
54	1w	47	U	3.0
21	2Z	173	ALA	3.0
32	2a	1123	A	3.0
32	2a	1531	A	3.0
56	2y	21	A	3.0
20	2Y	5	MET	3.0
34	1c	87	LEU	3.0
1	2A	2138	C	3.0
35	1d	5	ILE	3.0
1	1A	883	G	3.0
1	2A	2124	G	3.0
1	2A	2131	G	3.0
6	2G	49	ASP	3.0
25	23	2	PRO	3.0
32	1a	78	G	3.0
33	1b	234	PRO	3.0
33	2b	234	PRO	3.0
54	1w	15	G	3.0
33	2b	7	VAL	3.0
1	2A	2132	U	3.0
33	1b	236	TYR	3.0
56	2y	7	A	3.0
4	1E	77	ILE	3.0
34	1c	81	GLY	3.0
1	1A	1079	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2107	C	3.0
32	1a	1019	C	3.0
56	2y	68	C	3.0
9	1N	140	VAL	3.0
40	1i	2	GLU	3.0
40	2i	17	VAL	3.0
40	2i	109	VAL	3.0
1	1A	881	G	3.0
1	1A	2893	G	3.0
1	2A	271(M)	G	3.0
1	1A	2144	U	3.0
1	1A	878	A	3.0
1	1A	1045	A	3.0
38	2g	82	GLY	3.0
41	2j	63	PHE	3.0
21	2Z	148	ASP	3.0
19	1X	68	ARG	3.0
32	1a	1008	C	3.0
32	1a	1038	C	3.0
8	1I	146	ALA	3.0
1	1A	1083	U	3.0
32	1a	1446	U	3.0
1	1A	2106	G	3.0
1	1A	2805	G	3.0
1	2A	2165	G	3.0
26	24	32	TYR	2.9
37	2f	93	SER	2.9
20	2Y	89	PHE	2.9
1	2A	899	A	2.9
56	1y	35	A	2.9
7	2H	60	ARG	2.9
52	1u	24	ARG	2.9
40	1i	91	ASP	2.9
41	1j	24	VAL	2.9
43	1l	18	VAL	2.9
20	1Y	1	MET	2.9
34	2c	65	ALA	2.9
38	1g	83	ALA	2.9
1	2A	889	C	2.9
45	2n	22	THR	2.9
56	1y	49	C	2.9
1	2A	652(E)	G	2.9

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Mol	Chain	Res	Type	RSRZ
32	1a	70	G	2.9
32	2a	1024	G	2.9
38	1g	154	TYR	2.9
56	2y	15	G	2.9
56	2y	18	G	2.9
35	1d	87	GLY	2.9
44	2m	9	ILE	2.9
20	1Y	91	GLU	2.9
50	2s	14	HIS	2.9
7	2H	35	VAL	2.9
21	2Z	140	ASP	2.9
26	14	50	VAL	2.9
34	1c	107	GLN	2.9
1	2A	2129	C	2.9
1	2A	2140	C	2.9
1	2A	1026	U	2.9
3	1D	275	LYS	2.9
51	1t	13	LEU	2.9
56	2y	33	U	2.9
1	2A	2153	G	2.9
1	2A	2157	G	2.9
54	1w	69	G	2.9
7	2H	45	VAL	2.9
43	2l	39	VAL	2.9
20	1Y	92	ASN	2.9
3	2D	38	LYS	2.9
45	2n	4	LYS	2.9
22	20	84	LEU	2.9
35	2d	5	ILE	2.9
55	1x	47	U	2.9
56	1y	12	U	2.9
7	2H	59	ARG	2.9
34	2c	109	PRO	2.9
35	2d	168	ARG	2.9
38	1g	5	ARG	2.9
40	2i	16	ARG	2.9
41	2j	93	GLY	2.9
26	24	49	PHE	2.9
36	2e	41	VAL	2.9
1	1A	2155	G	2.9
32	2a	1131	G	2.9
56	1y	24	G	2.9

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Mol	Chain	Res	Type	RSRZ
56	2y	70	G	2.9
33	2b	132	LYS	2.9
1	1A	1085	A	2.8
12	1Q	15	GLY	2.8
21	2Z	26	GLY	2.8
41	2j	31	GLY	2.8
45	2n	12	ARG	2.8
26	24	59	PHE	2.8
32	2a	1025	U	2.8
1	2A	645	C	2.8
1	2A	2164	C	2.8
11	2P	110	TYR	2.8
20	2Y	91	GLU	2.8
33	2b	199	TYR	2.8
35	2d	156	GLU	2.8
47	1p	82	GLN	2.8
42	1k	14	VAL	2.8
45	2n	10	ALA	2.8
1	1A	1173	G	2.8
1	2A	100	G	2.8
1	2A	2141	G	2.8
32	2a	1117	G	2.8
35	2d	161	ASN	2.8
41	2j	42	THR	2.8
7	2H	64	LEU	2.8
21	2Z	125	LEU	2.8
50	2s	15	LEU	2.8
1	1A	1077	A	2.8
1	1A	1103	A	2.8
56	2y	9	A	2.8
41	2j	38	ILE	2.8
21	2Z	106	GLY	2.8
36	2e	10	MET	2.8
42	2k	49	GLY	2.8
26	24	57	GLU	2.8
32	1a	841	U	2.8
39	2h	99	GLU	2.8
40	2i	2	GLU	2.8
56	2y	12	U	2.8
33	2b	31	TYR	2.8
38	2g	154	TYR	2.8
56	1y	25	C	2.8

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Mol	Chain	Res	Type	RSRZ
21	1Z	139	VAL	2.8
41	2j	94	VAL	2.8
29	17	45	ALA	2.8
34	2c	129	ALA	2.8
38	2g	2	ALA	2.8
21	2Z	157	LEU	2.8
40	2i	99	LEU	2.8
38	2g	4	ARG	2.8
40	2i	66	ARG	2.8
56	1y	34	G	2.8
56	2y	71	G	2.8
40	2i	49	PRO	2.8
40	2i	90	PRO	2.8
1	1A	1174	A	2.8
1	2A	2892	A	2.8
40	1i	12	GLU	2.8
32	2a	1219	U	2.8
6	1G	182	LYS	2.8
34	2c	207	VAL	2.8
35	1d	170	VAL	2.8
42	2k	14	VAL	2.8
1	1A	271(J)	C	2.8
1	1A	1075	C	2.8
1	2A	277	C	2.8
26	24	65	ASP	2.8
47	1p	49	LEU	2.8
41	2j	100	THR	2.8
26	14	55	ARG	2.8
44	1m	4	ILE	2.8
47	1p	78	GLY	2.8
50	1s	68	GLY	2.8
21	1Z	136	PHE	2.8
1	1A	275	G	2.8
1	1A	1056	G	2.8
1	1A	2121	G	2.8
32	2a	1023	G	2.8
56	1y	57	G	2.8
56	2y	1	G	2.8
1	2A	2171	A	2.8
33	2b	74	LYS	2.8
35	1d	169	LYS	2.8
56	1y	36	A	2.8

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Mol	Chain	Res	Type	RSRZ
1	2A	2150	U	2.8
32	1a	1000	U	2.8
4	1E	59	VAL	2.8
33	2b	77	ALA	2.8
1	1A	2791	C	2.7
54	1w	2	C	2.7
11	2P	78	PRO	2.7
21	2Z	167	PRO	2.7
8	2I	85	GLU	2.7
33	1b	22	LYS	2.7
1	1A	2125	G	2.7
1	2A	2104	G	2.7
1	2A	2162	G	2.7
1	1A	1105	U	2.7
1	1A	2189	U	2.7
1	2A	2172	U	2.7
9	2N	140	VAL	2.7
20	2Y	55	TYR	2.7
32	2a	1030(C)	G	2.7
32	2a	1252	A	2.7
32	2a	1253	G	2.7
54	1w	6	G	2.7
54	2w	14	A	2.7
56	2y	6	G	2.7
56	2y	52	G	2.7
56	2y	53	G	2.7
32	1a	1040	U	2.7
40	2i	13	ALA	2.7
40	2i	96	LEU	2.7
35	2d	122	ARG	2.7
41	1j	100	THR	2.7
41	1j	78	ASN	2.7
1	2A	2161	C	2.7
32	1a	1039	C	2.7
34	2c	77	ILE	2.7
33	2b	126	GLU	2.7
45	2n	15	LYS	2.7
50	1s	84	GLY	2.7
34	2c	128	PHE	2.7
7	2H	15	VAL	2.7
33	1b	93	VAL	2.7
42	2k	25	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
43	1l	64	TYR	2.7
35	1d	111	ALA	2.7
38	1g	2	ALA	2.7
38	1g	79	ARG	2.7
41	2j	28	ARG	2.7
43	1l	19	ARG	2.7
51	2t	97	ALA	2.7
1	1A	2147	G	2.7
1	1A	2181	G	2.7
32	1a	181	G	2.7
51	2t	9	ASN	2.7
21	1Z	167	PRO	2.7
8	1I	10	GLU	2.7
33	1b	228	GLY	2.7
40	1i	67	GLY	2.7
51	2t	47	GLY	2.7
1	1A	271(O)	C	2.7
32	1a	163	C	2.7
32	2a	1006	C	2.7
41	1j	33	GLN	2.7
7	2H	17	VAL	2.7
22	20	11	ARG	2.7
45	2n	53	LEU	2.7
34	2c	193	TYR	2.7
41	1j	86	MET	2.7
1	2A	271(K)	U	2.7
32	2a	1446	U	2.7
1	2A	652(A)	A	2.7
56	2y	14	A	2.7
14	2S	59	LYS	2.7
1	1A	2207	G	2.7
4	2E	56	PRO	2.7
42	2k	117	ASN	2.7
45	2n	51	GLY	2.7
45	2n	61	TRP	2.7
1	2A	2139	C	2.7
32	2a	1116	C	2.7
54	2w	67	C	2.7
5	2F	6	VAL	2.6
21	2Z	86	VAL	2.6
33	1b	15	VAL	2.6
36	1e	69	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
42	2k	75	TYR	2.6
1	1A	895	U	2.6
1	2A	2189	U	2.6
27	25	29	THR	2.6
32	2a	1000	U	2.6
33	2b	201	ILE	2.6
21	2Z	169	GLU	2.6
48	2q	96	GLU	2.6
56	2y	26	A	2.6
26	14	17	GLY	2.6
1	2A	2181	G	2.6
54	2w	44	G	2.6
55	1x	46	G	2.6
38	2g	76	ARG	2.6
40	1i	10	ARG	2.6
1	2A	271(J)	C	2.6
1	2A	897	C	2.6
8	2I	68	LEU	2.6
32	2a	1007	C	2.6
3	1D	38	LYS	2.6
33	2b	33	TYR	2.6
34	2c	48	TYR	2.6
42	2k	59	TYR	2.6
52	2u	5	ASP	2.6
6	2G	52	ILE	2.6
7	2H	72	ILE	2.6
41	1j	75	ILE	2.6
32	2a	1148	U	2.6
33	1b	126	GLU	2.6
35	1d	179	GLU	2.6
38	1g	84	ASN	2.6
56	1y	20	U	2.6
21	1Z	147	GLY	2.6
41	2j	10	GLY	2.6
51	1t	102	GLY	2.6
1	1A	229	A	2.6
1	1A	890	A	2.6
1	1A	900	A	2.6
1	2A	528	A	2.6
1	2A	2176	A	2.6
56	1y	73	A	2.6
6	1G	21	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
43	2l	41	ARG	2.6
50	2s	29	ARG	2.6
1	1A	271(M)	G	2.6
1	1A	2101	G	2.6
21	1Z	153	SER	2.6
1	1A	34	C	2.6
7	2H	20	ALA	2.6
21	2Z	151	HIS	2.6
32	2a	1260	C	2.6
56	1y	74	C	2.6
7	2H	29	PRO	2.6
40	2i	92	TYR	2.6
42	1k	75	TYR	2.6
21	2Z	170	THR	2.6
35	1d	70	ILE	2.6
38	2g	27	ILE	2.6
41	1j	98	ILE	2.6
1	2A	2897	U	2.6
35	1d	180	GLY	2.6
35	2d	124	GLY	2.6
37	2f	27	GLN	2.6
55	2x	47	U	2.6
40	2i	59	PHE	2.6
45	2n	16	PHE	2.6
7	2H	51	ARG	2.6
33	2b	83	MET	2.6
34	1c	190	ARG	2.6
52	2u	6	ARG	2.6
8	1I	87	LYS	2.6
41	2j	14	LYS	2.6
1	1A	2894	G	2.6
5	2F	21	ALA	2.6
1	2A	2142	C	2.6
32	1a	92	C	2.6
32	2a	1452	C	2.6
54	2w	13	C	2.6
56	1y	67	C	2.6
41	2j	87	THR	2.6
45	2n	21	TYR	2.6
50	2s	26	GLY	2.6
1	1A	2122	U	2.6
1	2A	2895	U	2.6

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Mol	Chain	Res	Type	RSRZ
32	1a	90	U	2.6
33	2b	70	PHE	2.6
40	2i	18	PHE	2.6
12	2Q	6	ARG	2.6
21	2Z	79	ARG	2.6
45	1n	3	ARG	2.6
41	2j	40	LEU	2.5
50	1s	15	LEU	2.5
32	2a	1146	A	2.5
6	2G	28	VAL	2.5
7	2H	44	VAL	2.5
21	2Z	141	VAL	2.5
25	23	58	VAL	2.5
34	2c	195	VAL	2.5
48	2q	23	VAL	2.5
34	2c	149	ALA	2.5
42	1k	15	ALA	2.5
44	1m	5	ALA	2.5
6	1G	52	ILE	2.5
7	1H	92	ILE	2.5
25	23	60	GLU	2.5
34	2c	23	TYR	2.5
40	2i	7	THR	2.5
47	2p	45	THR	2.5
56	1y	18	G	2.5
1	1A	2177	C	2.5
11	1P	44	GLY	2.5
32	1a	1006	C	2.5
32	1a	1115	C	2.5
33	2b	38	GLY	2.5
34	2c	41	GLY	2.5
7	2H	41	MET	2.5
46	2o	88	ARG	2.5
54	1w	60	U	2.5
56	1y	59	U	2.5
19	2X	95	LEU	2.5
45	2n	39	LEU	2.5
50	2s	5	LEU	2.5
21	2Z	96	VAL	2.5
1	2A	1847	A	2.5
32	1a	161	A	2.5
32	2a	1280	A	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	60	ALA	2.5
40	2i	94	ALA	2.5
26	14	57	GLU	2.5
46	2o	3	ILE	2.5
41	2j	48	THR	2.5
20	2Y	107	ASP	2.5
7	2H	174	GLY	2.5
34	1c	13	GLY	2.5
40	2i	36	TYR	2.5
28	26	20	ASN	2.5
47	1p	81	ARG	2.5
1	1A	545	G	2.5
1	2A	171	G	2.5
1	2A	2206	G	2.5
1	1A	1076	C	2.5
1	2A	34	C	2.5
1	2A	2163	C	2.5
20	2Y	94	LYS	2.5
56	2y	34	G	2.5
32	1a	1007	C	2.5
32	2a	1249	C	2.5
1	2A	12	U	2.5
32	2a	1125	U	2.5
21	2Z	126	VAL	2.5
33	1b	7	VAL	2.5
41	2j	72	VAL	2.5
21	2Z	166	SER	2.5
34	2c	19	GLU	2.5
32	1a	160	A	2.5
56	2y	38	A	2.5
7	2H	3	ARG	2.5
17	1V	101	GLY	2.5
21	2Z	131	ARG	2.5
24	22	1	MET	2.5
37	1f	46	ARG	2.5
52	2u	9	ARG	2.5
26	14	16	CYS	2.5
6	2G	53	LEU	2.5
33	2b	10	LEU	2.5
40	1i	19	LEU	2.5
50	2s	22	LEU	2.5
1	1A	2123	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2108	C	2.5
1	2A	2151	G	2.5
32	1a	999	C	2.5
41	2j	62	HIS	2.5
54	2w	68	C	2.5
1	2A	895	U	2.5
32	1a	203	U	2.5
32	2a	1159	U	2.5
8	1I	136	VAL	2.5
40	1i	45	ALA	2.5
21	2Z	142	SER	2.5
21	1Z	171	ILE	2.5
33	2b	129	GLU	2.5
42	2k	29	ILE	2.5
33	2b	8	LYS	2.5
41	2j	66	ARG	2.5
34	2c	171	GLY	2.5
54	2w	7	A	2.5
7	2H	83	TYR	2.5
35	2d	154	ASN	2.5
40	2i	5	TYR	2.5
44	2m	23	TYR	2.5
38	2g	26	PHE	2.5
38	1g	153	HIS	2.4
1	2A	2122	U	2.4
1	2A	2175	C	2.4
6	2G	5	VAL	2.4
7	2H	49	VAL	2.4
17	2V	51	VAL	2.4
38	2g	66	VAL	2.4
50	2s	41	VAL	2.4
56	2y	2	C	2.4
1	1A	2206	G	2.4
32	1a	631	G	2.4
32	1a	1042	G	2.4
32	2a	1010	G	2.4
32	2a	1022	G	2.4
32	2a	1127	G	2.4
56	1y	1	G	2.4
56	1y	22	G	2.4
56	2y	69	G	2.4
34	2c	61	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
40	1i	15	ALA	2.4
8	2I	54	GLN	2.4
33	2b	22	LYS	2.4
51	2t	74	LYS	2.4
7	2H	48	GLY	2.4
35	2d	167	GLY	2.4
38	2g	81	GLY	2.4
51	2t	96	GLY	2.4
39	2h	54	ASP	2.4
50	1s	12	ASP	2.4
1	2A	887	A	2.4
1	2A	1509(B)	A	2.4
21	1Z	150	LEU	2.4
21	2Z	70	LEU	2.4
21	2Z	104	PHE	2.4
33	2b	154	LEU	2.4
37	1f	19	LEU	2.4
40	2i	125	TYR	2.4
50	1s	20	LEU	2.4
41	2j	68	HIS	2.4
41	2j	91	PRO	2.4
6	2G	48	GLU	2.4
32	1a	182	U	2.4
1	1A	645	C	2.4
1	1A	2140	C	2.4
32	1a	1132	C	2.4
32	2a	1369	C	2.4
42	2k	48	ILE	2.4
26	24	68	ARG	2.4
48	1q	97	SER	2.4
1	2A	2152	G	2.4
1	2A	2182	G	2.4
1	2A	2321	G	2.4
32	2a	993	G	2.4
32	2a	1042	G	2.4
54	1w	18	G	2.4
54	1w	19	G	2.4
39	2h	130	GLY	2.4
46	2o	20	GLY	2.4
51	1t	47	GLY	2.4
8	2I	20	ASP	2.4
40	2i	91	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
14	2S	58	LEU	2.4
36	2e	12	LEU	2.4
40	2i	4	TYR	2.4
32	1a	344	A	2.4
32	1a	1503	A	2.4
32	2a	1041	A	2.4
34	2c	73	PRO	2.4
40	2i	41	VAL	2.4
7	2H	58	GLU	2.4
8	1I	63	ALA	2.4
9	2N	61	ARG	2.4
41	1j	66	ARG	2.4
41	2j	26	ALA	2.4
44	1m	3	ARG	2.4
44	2m	76	ALA	2.4
33	1b	95	GLN	2.4
33	1b	211	ILE	2.4
40	2i	63	ILE	2.4
45	2n	7	ILE	2.4
47	1p	5	ARG	2.4
1	1A	12	U	2.4
1	1A	1053	C	2.4
32	2a	999	C	2.4
32	2a	1029	C	2.4
54	2w	4	C	2.4
56	1y	62	C	2.4
43	2l	95	GLY	2.4
1	1A	2124	G	2.4
1	2A	1114	G	2.4
21	1Z	155	LEU	2.4
21	2Z	93	ASP	2.4
40	1i	47	LEU	2.4
44	2m	48	LEU	2.4
40	2i	37	PHE	2.4
45	2n	37	PHE	2.4
34	2c	201	TYR	2.4
29	17	48	LYS	2.4
32	2a	1179	A	2.4
32	2a	1357	A	2.4
35	2d	165	MET	2.4
14	2S	3	ARG	2.4
26	24	58	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
44	2m	3	ARG	2.4
19	2X	91	ALA	2.4
33	1b	13	ALA	2.4
33	2b	29	ALA	2.4
50	1s	40	ILE	2.4
21	1Z	52	SER	2.4
32	2a	1122	U	2.4
18	1W	112	GLY	2.4
21	1Z	69	THR	2.4
34	2c	18	TRP	2.4
35	2d	87	GLY	2.4
36	1e	97	GLY	2.4
36	2e	116	THR	2.4
1	1A	2105	C	2.3
1	1A	2185	C	2.3
7	2H	103	LEU	2.3
21	2Z	76	LEU	2.3
34	1c	101	LEU	2.3
34	2c	47	LEU	2.3
51	1t	99	LEU	2.3
47	1p	80	PHE	2.3
38	2g	37	ASN	2.3
44	2m	12	ASN	2.3
1	2A	2207	G	2.3
32	2a	1011	G	2.3
32	2a	1178	G	2.3
32	2a	1373	G	2.3
21	2Z	9	TYR	2.3
41	2j	7	LYS	2.3
45	2n	17	LYS	2.3
7	2H	39	PRO	2.3
8	2I	107	VAL	2.3
21	2Z	161	VAL	2.3
26	24	3	GLU	2.3
33	2b	175	ARG	2.3
39	2h	129	VAL	2.3
41	1j	44	VAL	2.3
41	2j	61	GLU	2.3
51	2t	8	ARG	2.3
1	2A	655	A	2.3
21	2Z	57	ILE	2.3
33	2b	13	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
33	2b	186	ALA	2.3
34	1c	14	ILE	2.3
36	2e	20	GLN	2.3
40	2i	82	ALA	2.3
41	2j	33	GLN	2.3
44	2m	72	ALA	2.3
14	2S	31	SER	2.3
33	1b	124	SER	2.3
39	2h	3	THR	2.3
33	1b	44	LEU	2.3
35	2d	19	LEU	2.3
39	2h	112	LEU	2.3
40	2i	79	LEU	2.3
45	2n	44	LEU	2.3
51	1t	10	LEU	2.3
52	2u	14	TRP	2.3
40	1i	105	ASP	2.3
32	1a	67	C	2.3
32	2a	980	C	2.3
56	2y	75	C	2.3
34	2c	4	LYS	2.3
34	2c	135	LYS	2.3
41	2j	86	MET	2.3
6	2G	17	PRO	2.3
20	2Y	53	PRO	2.3
47	1p	17	TYR	2.3
52	2u	18	TYR	2.3
32	2a	1182	G	2.3
33	2b	12	GLU	2.3
33	2b	134	GLU	2.3
34	1c	76	VAL	2.3
34	1c	106	VAL	2.3
34	2c	198	VAL	2.3
37	2f	24	GLU	2.3
56	1y	27	G	2.3
21	1Z	165	VAL	2.3
24	12	70	GLN	2.3
46	2o	60	VAL	2.3
50	2s	9	VAL	2.3
6	2G	20	ILE	2.3
33	1b	200	ILE	2.3
33	2b	223	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
36	2e	21	ALA	2.3
44	2m	5	ALA	2.3
1	1A	1177	A	2.3
1	2A	2629	A	2.3
32	2a	1251	A	2.3
32	2a	1256	A	2.3
7	2H	33	LEU	2.3
8	2I	86	THR	2.3
21	1Z	170	THR	2.3
44	2m	92	HIS	2.3
26	14	51	ASP	2.3
37	1f	83	ASP	2.3
5	1F	14	PRO	2.3
6	1G	51	ARG	2.3
29	17	47	ARG	2.3
32	1a	470	C	2.3
41	2j	9	ARG	2.3
41	2j	43	ARG	2.3
8	2I	135	GLU	2.3
21	2Z	2	GLU	2.3
26	14	53	GLU	2.3
40	2i	53	VAL	2.3
37	1f	81	ILE	2.3
33	1b	120	ALA	2.3
44	2m	118	ALA	2.3
1	2A	2191	G	2.3
32	1a	69	G	2.3
56	2y	22	G	2.3
14	2S	27	SER	2.3
21	1Z	166	SER	2.3
27	25	58	LEU	2.3
33	1b	40	HIS	2.3
34	2c	32	LEU	2.3
40	2i	56	LEU	2.3
51	1t	69	GLY	2.3
51	2t	10	LEU	2.3
32	2a	1275	A	2.3
53	1v	12	A	2.3
56	2y	58	A	2.3
20	2Y	21	LYS	2.3
33	2b	152	PHE	2.3
43	1l	126	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
34	1c	62	ASP	2.3
8	2I	82	ARG	2.3
22	10	82	ARG	2.3
24	12	69	ARG	2.3
35	1d	118	ARG	2.3
21	2Z	158	PRO	2.3
34	1c	90	GLU	2.3
43	2l	64	TYR	2.3
1	1A	1104	C	2.3
1	1A	1532	C	2.3
32	1a	217	C	2.3
32	2a	1128	C	2.3
33	2b	68	ILE	2.3
34	1c	39	ILE	2.3
40	2i	65	VAL	2.3
54	2w	3	C	2.3
33	2b	173	ALA	2.3
36	2e	48	ALA	2.3
45	2n	20	ALA	2.3
49	2r	20	ALA	2.3
51	1t	95	ALA	2.3
11	2P	104	GLY	2.2
34	2c	12	LEU	2.2
36	1e	85	GLY	2.2
40	2i	6	GLY	2.2
41	1j	36	GLY	2.2
1	1A	1106	G	2.2
1	1A	2807	G	2.2
5	1F	13	SER	2.2
7	2H	106	THR	2.2
32	1a	1010	G	2.2
32	2a	1202	G	2.2
39	2h	29	SER	2.2
42	1k	51	LYS	2.2
56	1y	5	G	2.2
56	1y	53	G	2.2
1	1A	2892	A	2.2
54	1w	21	A	2.2
1	1A	1101	U	2.2
32	1a	1020	U	2.2
50	2s	34	TRP	2.2
7	2H	10	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
27	25	59	GLU	2.2
5	2F	37	VAL	2.2
7	2H	157	TYR	2.2
7	2H	164	TYR	2.2
11	2P	80	TYR	2.2
12	2Q	32	TYR	2.2
26	24	14	ILE	2.2
40	1i	14	VAL	2.2
45	2n	18	VAL	2.2
46	1o	69	TYR	2.2
47	1p	62	VAL	2.2
12	2Q	28	ALA	2.2
1	1A	2163	C	2.2
1	1A	2188	C	2.2
32	1a	1158	C	2.2
54	1w	13	C	2.2
56	2y	11	C	2.2
11	2P	99	LEU	2.2
21	1Z	102	LEU	2.2
21	2Z	102	LEU	2.2
26	14	64	GLY	2.2
35	1d	188	LEU	2.2
41	1j	31	GLY	2.2
41	2j	16	LEU	2.2
40	1i	126	SER	2.2
48	2q	99	SER	2.2
38	2g	89	MET	2.2
41	1j	79	ARG	2.2
1	1A	171	G	2.2
1	1A	274	G	2.2
1	1A	1055	G	2.2
1	1A	1074	G	2.2
1	2A	2319	G	2.2
6	2G	4	ASP	2.2
32	1a	77	G	2.2
32	1a	142	G	2.2
32	2a	1220	G	2.2
56	1y	44	G	2.2
56	2y	10	G	2.2
6	2G	142	PRO	2.2
1	2A	271(L)	U	2.2
1	2A	900	A	2.2

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Mol	Chain	Res	Type	RSRZ
32	1a	162	A	2.2
35	1d	189	PRO	2.2
32	2a	1086	U	2.2
56	2y	23	A	2.2
14	2S	46	VAL	2.2
14	2S	49	VAL	2.2
27	15	60	VAL	2.2
36	2e	80	ILE	2.2
39	2h	134	ILE	2.2
41	2j	82	ILE	2.2
43	2l	43	VAL	2.2
33	1b	123	ALA	2.2
41	2j	27	ALA	2.2
45	1n	5	ALA	2.2
49	1r	24	ALA	2.2
12	2Q	123	HIS	2.2
33	1b	154	LEU	2.2
33	2b	221	LEU	2.2
45	2n	9	LYS	2.2
51	2t	24	LEU	2.2
6	2G	127	GLY	2.2
40	2i	100	GLY	2.2
50	1s	26	GLY	2.2
1	2A	2177	C	2.2
38	2g	77	SER	2.2
52	2u	17	THR	2.2
6	1G	136	ARG	2.2
12	2Q	10	ARG	2.2
22	20	69	PHE	2.2
25	23	29	ARG	2.2
33	2b	144	ARG	2.2
45	1n	57	ARG	2.2
52	1u	9	ARG	2.2
52	2u	15	ARG	2.2
33	2b	91	PRO	2.2
51	1t	98	PRO	2.2
8	2I	64	GLU	2.2
26	24	30	GLU	2.2
28	26	42	TRP	2.2
1	1A	278	A	2.2
1	1A	892	G	2.2
1	2A	1112	G	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1040	U	2.2
32	2a	1126	U	2.2
32	2a	1176	A	2.2
32	2a	1283	G	2.2
56	1y	21	A	2.2
56	1y	65	G	2.2
56	1y	66	U	2.2
1	2A	1460	A	2.2
32	2a	1346	A	2.2
7	2H	4	ILE	2.2
7	2H	133	VAL	2.2
8	1I	71	ILE	2.2
12	2Q	109	VAL	2.2
39	2h	26	VAL	2.2
44	2m	22	ILE	2.2
48	2q	85	VAL	2.2
12	2Q	22	LYS	2.2
33	1b	34	ALA	2.2
33	2b	88	ALA	2.2
38	1g	151	TYR	2.2
44	2m	120	LYS	2.2
35	2d	155	LEU	2.2
36	2e	123	LEU	2.2
9	2N	1	MET	2.2
34	2c	51	GLY	2.2
40	1i	39	GLY	2.2
42	2k	90	GLY	2.2
6	2G	181	ARG	2.2
15	2T	125	ARG	2.2
26	24	18	CYS	2.2
33	1b	23	ARG	2.2
38	1g	4	ARG	2.2
44	2m	11	ARG	2.2
46	1o	88	ARG	2.2
1	2A	876	C	2.2
1	2A	2183	C	2.2
32	2a	1129	C	2.2
55	2x	16	C	2.2
56	2y	74	C	2.2
7	2H	21	PRO	2.2
33	2b	131	PRO	2.2
21	1Z	2	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
7	2H	92	ILE	2.2
7	2H	141	VAL	2.2
9	1N	9	VAL	2.2
21	2Z	156	LYS	2.2
32	1a	202	U	2.2
32	2a	202	U	2.2
52	2u	13	ILE	2.2
40	2i	86	VAL	2.2
51	1t	74	LYS	2.2
56	2y	59	U	2.2
1	1A	2104	G	2.2
1	2A	6	A	2.2
1	2A	1537	G	2.2
1	2A	2121	G	2.2
8	2I	83	ALA	2.2
14	2S	55	ALA	2.2
32	1a	216	G	2.2
32	1a	1131	G	2.2
32	1a	1279	A	2.2
32	2a	1009	G	2.2
32	2a	1092	A	2.2
32	2a	1124	G	2.2
50	2s	24	ALA	2.2
53	2v	14	A	2.2
56	1y	6	G	2.2
56	2y	24	G	2.2
6	2G	139	LEU	2.1
8	1I	68	LEU	2.1
11	1P	147	LEU	2.1
39	1h	62	TYR	2.1
41	2j	90	LEU	2.1
42	1k	25	TYR	2.1
12	2Q	1	MET	2.1
5	1F	208	GLY	2.1
8	2I	34	GLY	2.1
12	2Q	59	ARG	2.1
11	2P	91	PHE	2.1
41	2j	11	PHE	2.1
1	1A	154(A)	C	2.1
32	1a	840	C	2.1
38	1g	13	GLN	2.1
50	2s	27	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
54	1w	68	C	2.1
56	2y	72	C	2.1
21	1Z	120	ILE	2.1
33	2b	58	ILE	2.1
33	2b	211	ILE	2.1
51	2t	100	ILE	2.1
14	2S	85	VAL	2.1
33	1b	165	VAL	2.1
33	2b	164	VAL	2.1
40	1i	108	VAL	2.1
40	2i	26	VAL	2.1
47	2p	48	TRP	2.1
12	2Q	2	LEU	2.1
34	2c	189	ALA	2.1
35	2d	195	ALA	2.1
36	1e	138	ALA	2.1
36	2e	94	ALA	2.1
2	1B	120	A	2.1
32	2a	977	A	2.1
32	2a	1130	A	2.1
33	1b	38	GLY	2.1
33	1b	203	GLY	2.1
54	2w	21	A	2.1
56	1y	9	A	2.1
56	2y	73	A	2.1
21	2Z	122	ARG	2.1
41	2j	70	ARG	2.1
44	2m	104	ARG	2.1
1	1A	1107	G	2.1
1	1A	2154	G	2.1
1	2A	1115	G	2.1
1	2A	1719	G	2.1
32	2a	1017	G	2.1
54	1w	44	G	2.1
22	20	10	THR	2.1
8	2I	134	PRO	2.1
25	13	2	PRO	2.1
52	1u	23	PRO	2.1
20	2Y	57	GLN	2.1
21	2Z	162	GLU	2.1
33	1b	12	GLU	2.1
18	2W	63	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
33	2b	205	ASP	2.1
36	2e	5	ASP	2.1
39	2h	4	ASP	2.1
40	2i	105	ASP	2.1
41	1j	76	ASN	2.1
47	1p	43	LYS	2.1
26	14	15	ILE	2.1
32	1a	381	C	2.1
32	2a	1119	C	2.1
39	1h	100	ILE	2.1
46	1o	3	ILE	2.1
54	1w	62	C	2.1
7	2H	125	VAL	2.1
14	2S	28	VAL	2.1
20	2Y	42	VAL	2.1
34	1c	70	VAL	2.1
35	2d	112	VAL	2.1
4	2E	204	ALA	2.1
6	2G	152	LEU	2.1
8	1I	38	LEU	2.1
11	2P	103	ALA	2.1
20	2Y	106	LEU	2.1
33	1b	62	ALA	2.1
34	2c	137	ALA	2.1
38	1g	12	LEU	2.1
38	1g	59	LEU	2.1
47	1p	48	TRP	2.1
51	1t	24	LEU	2.1
1	2A	9	U	2.1
14	2S	17	ARG	2.1
26	24	61	ARG	2.1
40	2i	10	ARG	2.1
56	2y	60	U	2.1
33	1b	33	TYR	2.1
35	2d	4	TYR	2.1
40	2i	114	TYR	2.1
1	1A	1762	A	2.1
32	1a	141	A	2.1
32	2a	1016	A	2.1
32	2a	1248	A	2.1
44	2m	37	THR	2.1
5	2F	14	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
26	24	29	PRO	2.1
40	1i	21	PRO	2.1
41	2j	39	PRO	2.1
47	1p	66	PRO	2.1
1	2A	2106	G	2.1
56	2y	44	G	2.1
11	1P	149	GLU	2.1
33	2b	35	GLU	2.1
33	2b	86	GLU	2.1
40	1i	35	GLU	2.1
14	2S	83	LYS	2.1
41	2j	55	LYS	2.1
3	2D	71	ASP	2.1
20	1Y	107	ASP	2.1
41	2j	17	ASP	2.1
47	1p	19	ILE	2.1
50	2s	31	ILE	2.1
5	2F	183	VAL	2.1
23	11	82	LEU	2.1
33	2b	69	LEU	2.1
34	2c	188	LEU	2.1
40	2i	50	LEU	2.1
41	2j	71	LEU	2.1
41	2j	85	LEU	2.1
1	1A	894	C	2.1
6	2G	151	ALA	2.1
7	2H	42	ARG	2.1
7	2H	145	ALA	2.1
8	1I	55	ALA	2.1
11	2P	77	ARG	2.1
12	1Q	6	ARG	2.1
12	2Q	136	ALA	2.1
15	2T	112	ARG	2.1
21	2Z	21	ALA	2.1
30	28	34	TRP	2.1
32	1a	848	C	2.1
34	2c	53	ALA	2.1
44	2m	51	ALA	2.1
56	1y	72	C	2.1
1	1A	1090	U	2.1
1	2A	614(A)	U	2.1
7	2H	66	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
54	1w	45	U	2.1
34	1c	23	TYR	2.1
24	12	37	PHE	2.1
33	2b	125	PRO	2.1
44	2m	41	PRO	2.1
52	2u	23	PRO	2.1
1	2A	901	A	2.1
23	21	81	LYS	2.1
24	22	70	GLN	2.1
32	1a	149	A	2.1
32	2a	1151	A	2.1
32	2a	1503	A	2.1
36	2e	47	LYS	2.1
39	2h	98	LYS	2.1
32	2a	1356	G	2.1
33	2b	140	HIS	2.1
54	2w	18	G	2.1
56	2y	65	G	2.1
21	1Z	133	ILE	2.1
21	2Z	132	ASN	2.1
26	24	15	ILE	2.1
34	2c	84	ILE	2.1
51	1t	100	ILE	2.1
7	2H	79	VAL	2.0
7	2H	88	LEU	2.0
33	2b	230	VAL	2.0
36	2e	69	VAL	2.0
44	2m	17	VAL	2.0
46	1o	57	LEU	2.0
6	2G	115	ARG	2.0
50	2s	81	ARG	2.0
34	2c	92	ALA	2.0
36	2e	86	ALA	2.0
40	1i	13	ALA	2.0
1	1A	1052	C	2.0
1	1A	2179	C	2.0
1	2A	2188	C	2.0
32	2a	1114	C	2.0
32	2a	1363	C	2.0
44	2m	68	GLY	2.0
1	1A	2808	U	2.0
1	2A	271(N)	U	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	877	U	2.0
1	2A	1113	U	2.0
32	2a	1012	U	2.0
32	2a	1358	U	2.0
33	2b	168	THR	2.0
35	1d	51	PRO	2.0
47	1p	32	TYR	2.0
35	2d	127	THR	2.0
35	2d	151	LYS	2.0
45	2n	36	PHE	2.0
47	2p	69	THR	2.0
9	2N	10	GLU	2.0
11	2P	149	GLU	2.0
33	2b	192	SER	2.0
35	2d	28	SER	2.0
48	2q	97	SER	2.0
1	2A	890	A	2.0
1	2A	2809	A	2.0
31	29	20	HIS	2.0
32	2a	532	A	2.0
56	2y	64	A	2.0
51	2t	63	ILE	2.0
41	2j	58	ASP	2.0
51	1t	64	ASP	2.0
7	1H	3	ARG	2.0
50	2s	20	LEU	2.0
41	1j	34	VAL	2.0
41	2j	79	ARG	2.0
44	2m	90	LEU	2.0
24	22	63	VAL	2.0
44	1m	53	VAL	2.0
45	2n	56	VAL	2.0
1	1A	2153	G	2.0
32	1a	102	G	2.0
32	1a	1022	G	2.0
32	2a	1133	G	2.0
33	1b	186	ALA	2.0
41	1j	27	ALA	2.0
42	1k	64	ALA	2.0
42	2k	89	ALA	2.0
49	2r	24	ALA	2.0
17	2V	9	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
34	2c	78	GLY	2.0
46	2o	86	GLY	2.0
52	2u	11	GLY	2.0
46	2o	10	LYS	2.0
21	1Z	159	PRO	2.0
1	1A	877	U	2.0
1	2A	1745(A)	C	2.0
32	2a	1217	C	2.0
50	2s	76	PRO	2.0
7	1H	58	GLU	2.0
8	2I	7	GLU	2.0
26	24	52	THR	2.0
32	2a	204	U	2.0
44	1m	87	TYR	2.0
56	1y	51	U	2.0
56	2y	25	C	2.0
33	1b	50	GLU	2.0
33	1b	231	GLU	2.0
40	1i	103	THR	2.0
56	2y	51	U	2.0
6	2G	148	MET	2.0
7	2H	111	HIS	2.0
33	1b	48	MET	2.0
35	1d	181	MET	2.0
41	1j	35	SER	2.0
16	2U	88	ILE	2.0
33	1b	223	ILE	2.0
34	2c	182	ILE	2.0
43	2l	100	ILE	2.0
14	1S	3	ARG	2.0
14	2S	30	ARG	2.0
26	14	58	ARG	2.0
38	2g	115	ARG	2.0
40	1i	66	ARG	2.0
42	2k	96	ARG	2.0
44	1m	102	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
56	4SU	2y	8	20/21	0.42	0.22	89,98,103,117	0
56	G7M	1y	46	24/25	0.52	0.20	86,91,98,109	0
56	G7M	2y	46	24/25	0.52	0.18	80,89,97,113	0
56	PSU	2y	55	20/21	0.56	0.18	86,91,95,96	0
56	PSU	1y	55	20/21	0.61	0.15	85,89,96,106	0
56	MIA	2y	37	22/30	0.61	0.16	80,87,99,111	0
56	4SU	1y	8	20/21	0.64	0.16	87,92,102,110	0
56	5MU	1y	54	21/22	0.65	0.15	80,86,92,104	0
56	5MU	2y	54	21/22	0.66	0.18	83,89,100,110	0
56	PSU	2y	39	20/21	0.66	0.16	82,86,95,101	0
56	MIA	1y	37	22/30	0.69	0.15	81,86,92,99	0
54	G7M	2w	46	24/25	0.73	0.20	79,88,97,115	0
56	PSU	1y	39	20/21	0.74	0.16	78,84,91,95	0
54	G7M	1w	46	24/25	0.75	0.17	67,79,94,112	0
56	PSU	1y	32	20/21	0.78	0.14	74,84,96,96	0
56	PSU	2y	32	20/21	0.79	0.12	78,83,93,103	0
54	4SU	2w	8	20/21	0.80	0.17	82,87,99,99	0
54	PSU	2w	55	20/21	0.84	0.12	65,77,83,87	0
54	4SU	1w	8	20/21	0.85	0.16	75,79,87,88	0
54	MIA	2w	37	25/30	0.88	0.15	59,70,78,93	0
32	2MG	2a	1207	24/25	0.89	0.13	64,78,80,81	0
54	PSU	2w	32	20/21	0.89	0.13	64,77,81,82	0
43	0TD	2l	92	10/11	0.89	0.14	57,60,71,78	0
54	PSU	1w	55	20/21	0.90	0.11	49,68,71,73	0
55	PSU	2x	55	20/21	0.90	0.11	63,71,77,82	0
32	G7M	2a	527	24/25	0.90	0.14	55,60,65,72	0
54	5MU	2w	54	21/22	0.91	0.11	68,73,77,80	0
54	MIA	1w	37	29/30	0.91	0.17	44,53,68,84	0
55	4SU	2x	8	20/21	0.92	0.12	65,70,73,74	0
55	5MC	2x	32	21/22	0.92	0.13	59,64,69,77	0
32	5MC	2a	967	21/22	0.92	0.13	58,64,70,74	0
1	5MU	2A	1915	21/22	0.92	0.11	57,63,68,68	0
54	PSU	2w	39	20/21	0.92	0.12	63,73,79,79	0
55	PSU	1x	55	20/21	0.93	0.10	57,59,70,74	0
43	0TD	1l	92	10/11	0.93	0.11	40,48,50,65	0
32	M2G	2a	966	25/26	0.93	0.14	55,62,73,76	0
55	5MU	2x	54	21/22	0.93	0.12	64,74,77,78	0
54	PSU	1w	32	20/21	0.94	0.12	56,61,67,68	0
55	4SU	1x	8	20/21	0.94	0.10	54,60,69,71	0
55	5MU	1x	54	21/22	0.94	0.10	58,63,68,72	0
1	PSU	2A	1917	20/21	0.94	0.09	51,58,67,68	0
32	5MC	2a	1400	21/22	0.94	0.14	55,62,69,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	PSU	2a	516	20/21	0.94	0.11	56,65,70,71	0
32	MA6	1a	1519	24/25	0.95	0.10	35,44,48,56	0
1	5MU	1A	1915	21/22	0.95	0.10	41,50,55,55	0
1	OMC	2A	1920	21/22	0.95	0.10	49,56,60,64	0
32	4OC	2a	1402	22/23	0.95	0.10	50,55,59,64	0
32	5MC	2a	1404	21/22	0.95	0.09	45,50,54,58	0
55	5MC	1x	32	21/22	0.95	0.11	45,51,57,63	0
32	2MG	1a	1207	24/25	0.95	0.10	60,65,68,69	0
1	PSU	2A	1911	20/21	0.95	0.09	49,59,65,65	0
1	5MC	2A	1962	21/22	0.96	0.09	41,49,52,65	0
54	8AN	2w	76	22/23	0.96	0.09	35,40,43,47	0
32	5MC	2a	1407	21/22	0.96	0.10	44,51,55,58	0
32	UR3	2a	1498	21/22	0.96	0.10	49,55,57,59	0
32	MA6	2a	1518	24/25	0.96	0.10	50,58,62,63	0
32	MA6	2a	1519	24/25	0.96	0.12	52,58,61,63	0
55	8AN	2x	76	22/23	0.96	0.09	33,39,45,58	0
32	5MC	1a	967	21/22	0.96	0.09	43,52,56,61	0
1	5MC	1A	1942	21/22	0.96	0.09	27,39,43,54	0
54	PSU	1w	39	20/21	0.96	0.08	51,59,64,74	0
32	PSU	1a	516	20/21	0.96	0.08	41,53,57,58	0
54	5MU	1w	54	21/22	0.96	0.10	39,55,65,68	0
32	G7M	1a	527	24/25	0.96	0.09	36,42,48,50	0
32	M2G	1a	966	25/26	0.96	0.10	43,50,54,56	0
1	MA6	2A	2058	24/25	0.97	0.09	31,40,49,56	0
1	OMU	2A	2552	21/22	0.97	0.08	38,44,48,54	0
1	PSU	2A	2605	20/21	0.97	0.07	34,40,42,43	0
1	PSU	1A	1911	20/21	0.97	0.08	41,45,50,52	0
55	8AN	1x	76	22/23	0.97	0.07	20,25,30,37	0
1	PSU	1A	1917	20/21	0.97	0.07	40,47,51,53	0
32	5MC	1a	1400	21/22	0.97	0.09	42,48,50,52	0
32	4OC	1a	1402	22/23	0.97	0.10	39,43,46,47	0
32	5MC	1a	1404	21/22	0.97	0.08	29,39,42,44	0
1	5MU	2A	1939	21/22	0.97	0.08	28,39,44,46	0
1	5MC	2A	1942	21/22	0.97	0.08	44,51,56,61	0
32	5MC	1a	1407	21/22	0.97	0.08	33,38,44,46	0
1	PSU	1A	2605	20/21	0.98	0.06	24,28,31,34	0
1	5MU	1A	1939	21/22	0.98	0.06	21,28,32,33	0
1	OMC	1A	1920	21/22	0.98	0.08	37,43,47,50	0
32	UR3	1a	1498	21/22	0.98	0.07	36,41,43,44	0
32	MA6	1a	1518	24/25	0.98	0.08	33,41,44,45	0
1	5MC	1A	1962	21/22	0.98	0.06	26,34,41,42	0
1	MA6	1A	2058	24/25	0.98	0.07	15,26,33,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	OMG	2A	2251	24/25	0.98	0.08	36,42,44,46	0
1	2MA	2A	2503	23/24	0.98	0.08	29,40,43,47	0
1	2MA	1A	2503	23/24	0.98	0.06	18,24,26,29	0
1	OMU	1A	2552	21/22	0.98	0.07	25,28,31,34	0
54	8AN	1w	76	22/23	0.99	0.06	19,25,26,27	0
1	OMG	1A	2251	24/25	0.99	0.04	21,24,27,28	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	2A	3400	1/1	0.43	0.42	88,88,88,88	0
57	MG	10	108	1/1	0.47	0.41	62,62,62,62	0
57	MG	20	102	1/1	0.55	0.31	69,69,69,69	0
57	MG	2y	103	1/1	0.58	0.20	80,80,80,80	0
57	MG	1B	221	1/1	0.61	0.29	64,64,64,64	0
57	MG	2A	3642	1/1	0.61	0.26	66,66,66,66	0
57	MG	1A	3227	1/1	0.61	0.17	66,66,66,66	0
57	MG	1a	1761	1/1	0.61	0.22	73,73,73,73	0
57	MG	1A	4028	1/1	0.62	0.37	76,76,76,76	0
57	MG	2A	3747	1/1	0.64	0.22	78,78,78,78	0
57	MG	1A	3655	1/1	0.64	0.24	53,53,53,53	0
57	MG	1A	3694	1/1	0.64	0.24	69,69,69,69	0
57	MG	1A	3970	1/1	0.65	0.27	61,61,61,61	0
57	MG	2A	3364	1/1	0.65	0.57	79,79,79,79	0
57	MG	2a	1618	1/1	0.65	0.34	80,80,80,80	0
57	MG	2A	3696	1/1	0.65	0.22	69,69,69,69	0
57	MG	2A	3614	1/1	0.66	0.29	67,67,67,67	0
57	MG	2A	3088	1/1	0.66	0.27	76,76,76,76	0
57	MG	2A	3763	1/1	0.66	0.20	64,64,64,64	0
57	MG	2y	105	1/1	0.66	0.33	82,82,82,82	0
57	MG	1A	3961	1/1	0.67	0.17	73,73,73,73	0
57	MG	1A	3481	1/1	0.67	0.22	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1799	1/1	0.67	0.27	71,71,71,71	0
57	MG	2a	1782	1/1	0.68	0.29	73,73,73,73	0
57	MG	1A	4005	1/1	0.68	0.22	52,52,52,52	0
57	MG	1A	3660	1/1	0.68	0.27	72,72,72,72	0
57	MG	2a	1784	1/1	0.69	0.36	77,77,77,77	0
57	MG	2a	1793	1/1	0.69	0.35	73,73,73,73	0
57	MG	2v	103	1/1	0.69	0.31	78,78,78,78	0
57	MG	1A	3556	1/1	0.69	0.16	32,32,32,32	0
57	MG	1B	222	1/1	0.69	0.19	54,54,54,54	0
57	MG	2a	1619	1/1	0.70	0.18	68,68,68,68	0
57	MG	2a	1780	1/1	0.70	0.30	76,76,76,76	0
57	MG	2A	3647	1/1	0.70	0.20	69,69,69,69	0
57	MG	2A	3497	1/1	0.70	0.35	76,76,76,76	0
57	MG	2A	3345	1/1	0.71	0.27	77,77,77,77	0
57	MG	2A	3450	1/1	0.71	0.34	76,76,76,76	0
57	MG	1B	229	1/1	0.71	0.27	74,74,74,74	0
57	MG	2A	3591	1/1	0.71	0.26	66,66,66,66	0
57	MG	2a	1761	1/1	0.72	0.44	71,71,71,71	0
57	MG	1A	3985	1/1	0.72	0.17	59,59,59,59	0
57	MG	1A	3589	1/1	0.72	0.19	76,76,76,76	0
57	MG	1A	3465	1/1	0.72	0.25	74,74,74,74	0
57	MG	1B	230	1/1	0.72	0.17	73,73,73,73	0
57	MG	1U	209	1/1	0.72	0.42	64,64,64,64	0
57	MG	1A	4051	1/1	0.72	0.20	74,74,74,74	0
57	MG	2a	1706	1/1	0.72	0.27	76,76,76,76	0
57	MG	2A	3618	1/1	0.73	0.24	73,73,73,73	0
57	MG	1A	3535	1/1	0.73	0.21	65,65,65,65	0
57	MG	1E	313	1/1	0.73	0.28	66,66,66,66	0
57	MG	1T	202	1/1	0.73	0.23	66,66,66,66	0
57	MG	1A	3980	1/1	0.73	0.23	48,48,48,48	0
57	MG	1A	3965	1/1	0.73	0.15	79,79,79,79	0
57	MG	1a	1649	1/1	0.74	0.23	68,68,68,68	0
57	MG	1A	4011	1/1	0.74	0.13	63,63,63,63	0
57	MG	1A	3367	1/1	0.74	0.25	68,68,68,68	0
57	MG	1A	4034	1/1	0.74	0.26	68,68,68,68	0
57	MG	2A	3588	1/1	0.74	0.26	73,73,73,73	0
57	MG	1A	3929	1/1	0.74	0.14	40,40,40,40	0
57	MG	2a	1766	1/1	0.74	0.20	71,71,71,71	0
57	MG	2A	3276	1/1	0.75	0.34	72,72,72,72	0
57	MG	1A	3941	1/1	0.75	0.22	48,48,48,48	0
57	MG	1A	3973	1/1	0.75	0.14	48,48,48,48	0
57	MG	1A	3918	1/1	0.75	0.22	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	1776	1/1	0.75	0.30	72,72,72,72	0
57	MG	2A	3690	1/1	0.75	0.14	64,64,64,64	0
57	MG	1A	3571	1/1	0.75	0.19	58,58,58,58	0
57	MG	1A	3997	1/1	0.75	0.23	59,59,59,59	0
57	MG	2A	3539	1/1	0.75	0.20	59,59,59,59	0
57	MG	2j	201	1/1	0.75	0.15	76,76,76,76	0
57	MG	2l	203	1/1	0.75	0.21	71,71,71,71	0
57	MG	2A	3818	1/1	0.75	0.23	73,73,73,73	0
57	MG	2w	107	1/1	0.75	0.27	79,79,79,79	0
57	MG	1x	107	1/1	0.75	0.14	70,70,70,70	0
57	MG	1B	207	1/1	0.75	0.21	69,69,69,69	0
57	MG	2A	3183	1/1	0.76	0.28	80,80,80,80	0
57	MG	2A	3718	1/1	0.76	0.18	44,44,44,44	0
57	MG	1A	3972	1/1	0.76	0.22	66,66,66,66	0
57	MG	2A	3277	1/1	0.76	0.41	79,79,79,79	0
57	MG	2A	3605	1/1	0.76	0.19	46,46,46,46	0
57	MG	2A	3841	1/1	0.76	0.19	68,68,68,68	0
57	MG	1A	3926	1/1	0.76	0.17	73,73,73,73	0
57	MG	1A	4077	1/1	0.76	0.19	64,64,64,64	0
57	MG	2l	205	1/1	0.76	0.25	72,72,72,72	0
57	MG	1A	3764	1/1	0.76	0.12	53,53,53,53	0
57	MG	1B	220	1/1	0.76	0.17	68,68,68,68	0
57	MG	2a	1721	1/1	0.76	0.28	75,75,75,75	0
57	MG	1A	3628	1/1	0.76	0.31	70,70,70,70	0
57	MG	2A	3712	1/1	0.77	0.19	39,39,39,39	0
57	MG	2a	1722	1/1	0.77	0.20	75,75,75,75	0
57	MG	2a	1735	1/1	0.77	0.14	85,85,85,85	0
57	MG	2A	3291	1/1	0.77	0.32	61,61,61,61	0
57	MG	2a	1603	1/1	0.77	0.17	76,76,76,76	0
57	MG	2a	1767	1/1	0.77	0.22	70,70,70,70	0
57	MG	2A	3318	1/1	0.77	0.20	78,78,78,78	0
57	MG	2A	3569	1/1	0.77	0.18	71,71,71,71	0
57	MG	1a	1749	1/1	0.77	0.17	70,70,70,70	0
57	MG	2a	1716	1/1	0.78	0.26	79,79,79,79	0
57	MG	2A	3651	1/1	0.78	0.25	60,60,60,60	0
57	MG	2A	3512	1/1	0.78	0.17	53,53,53,53	0
57	MG	1A	3903	1/1	0.78	0.15	57,57,57,57	0
57	MG	2A	3547	1/1	0.78	0.17	61,61,61,61	0
57	MG	2A	3560	1/1	0.78	0.16	64,64,64,64	0
57	MG	2A	3563	1/1	0.78	0.18	60,60,60,60	0
57	MG	1A	3712	1/1	0.78	0.12	33,33,33,33	0
57	MG	2A	3805	1/1	0.78	0.21	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3307	1/1	0.78	0.19	66,66,66,66	0
57	MG	2A	3821	1/1	0.78	0.24	72,72,72,72	0
57	MG	1A	3507	1/1	0.78	0.52	71,71,71,71	0
57	MG	2a	1797	1/1	0.78	0.36	74,74,74,74	0
57	MG	2A	3851	1/1	0.78	0.16	65,65,65,65	0
57	MG	1w	106	1/1	0.78	0.25	83,83,83,83	0
57	MG	1V	208	1/1	0.78	0.16	59,59,59,59	0
57	MG	1A	3892	1/1	0.78	0.11	70,70,70,70	0
57	MG	15	106	1/1	0.78	0.25	54,54,54,54	0
57	MG	1A	3897	1/1	0.78	0.22	59,59,59,59	0
57	MG	2a	1708	1/1	0.78	0.39	75,75,75,75	0
57	MG	2A	3355	1/1	0.79	0.30	71,71,71,71	0
57	MG	2a	1666	1/1	0.79	0.29	68,68,68,68	0
57	MG	1A	3547	1/1	0.79	0.17	64,64,64,64	0
57	MG	2A	3625	1/1	0.79	0.27	79,79,79,79	0
57	MG	2A	3101	1/1	0.79	0.19	73,73,73,73	0
57	MG	2A	3420	1/1	0.79	0.15	70,70,70,70	0
57	MG	2A	3106	1/1	0.79	0.19	76,76,76,76	0
57	MG	2A	3663	1/1	0.79	0.16	84,84,84,84	0
57	MG	2A	3469	1/1	0.79	0.34	78,78,78,78	0
57	MG	2A	3149	1/1	0.79	0.42	79,79,79,79	0
57	MG	2A	3709	1/1	0.79	0.22	76,76,76,76	0
57	MG	2A	3502	1/1	0.79	0.17	57,57,57,57	0
57	MG	1A	3762	1/1	0.79	0.25	64,64,64,64	0
57	MG	1a	1696	1/1	0.79	0.22	60,60,60,60	0
57	MG	1A	3920	1/1	0.79	0.14	73,73,73,73	0
57	MG	2A	3556	1/1	0.79	0.17	78,78,78,78	0
57	MG	1A	3485	1/1	0.79	0.16	65,65,65,65	0
57	MG	2A	3299	1/1	0.79	0.22	71,71,71,71	0
57	MG	2A	3829	1/1	0.79	0.21	69,69,69,69	0
57	MG	1A	3477	1/1	0.79	0.29	74,74,74,74	0
57	MG	1A	3188	1/1	0.79	0.15	74,74,74,74	0
57	MG	1B	228	1/1	0.79	0.17	67,67,67,67	0
57	MG	2A	3598	1/1	0.79	0.21	51,51,51,51	0
57	MG	2A	3354	1/1	0.79	0.25	74,74,74,74	0
57	MG	1A	3438	1/1	0.80	0.17	63,63,63,63	0
57	MG	1a	1737	1/1	0.80	0.22	60,60,60,60	0
57	MG	2B	210	1/1	0.80	0.17	82,82,82,82	0
57	MG	1A	3478	1/1	0.80	0.18	70,70,70,70	0
57	MG	2A	3579	1/1	0.80	0.16	54,54,54,54	0
57	MG	2a	1610	1/1	0.80	0.34	70,70,70,70	0
57	MG	1A	3888	1/1	0.80	0.16	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	3702	1/1	0.80	0.16	68,68,68,68	0
57	MG	2a	1660	1/1	0.80	0.27	70,70,70,70	0
57	MG	1O	206	1/1	0.80	0.29	66,66,66,66	0
57	MG	2a	1684	1/1	0.80	0.31	69,69,69,69	0
57	MG	2a	1689	1/1	0.80	0.29	67,67,67,67	0
57	MG	1A	3976	1/1	0.80	0.22	60,60,60,60	0
57	MG	2A	3611	1/1	0.80	0.17	65,65,65,65	0
57	MG	2A	3346	1/1	0.80	0.16	67,67,67,67	0
57	MG	2A	3073	1/1	0.80	0.18	57,57,57,57	0
57	MG	1A	3375	1/1	0.80	0.25	68,68,68,68	0
57	MG	1B	214	1/1	0.80	0.16	61,61,61,61	0
57	MG	2A	3386	1/1	0.80	0.31	67,67,67,67	0
57	MG	2A	3392	1/1	0.80	0.16	65,65,65,65	0
57	MG	1A	3948	1/1	0.80	0.14	68,68,68,68	0
57	MG	2A	3403	1/1	0.80	0.14	70,70,70,70	0
57	MG	2A	3124	1/1	0.80	0.12	71,71,71,71	0
57	MG	2A	3704	1/1	0.80	0.09	82,82,82,82	0
57	MG	2A	3434	1/1	0.80	0.21	61,61,61,61	0
57	MG	1A	3754	1/1	0.80	0.23	58,58,58,58	0
57	MG	1A	3964	1/1	0.80	0.19	59,59,59,59	0
57	MG	2A	3186	1/1	0.80	0.12	69,69,69,69	0
57	MG	2A	3217	1/1	0.80	0.17	67,67,67,67	0
57	MG	2A	3235	1/1	0.80	0.42	76,76,76,76	0
57	MG	2A	3243	1/1	0.80	0.29	65,65,65,65	0
57	MG	2A	3272	1/1	0.80	0.15	71,71,71,71	0
57	MG	2A	3274	1/1	0.80	0.14	69,69,69,69	0
57	MG	2y	104	1/1	0.80	0.28	82,82,82,82	0
57	MG	2A	3832	1/1	0.80	0.17	64,64,64,64	0
57	MG	1A	3746	1/1	0.81	0.20	64,64,64,64	0
57	MG	2A	3670	1/1	0.81	0.25	62,62,62,62	0
57	MG	2a	1670	1/1	0.81	0.41	74,74,74,74	0
57	MG	1A	4010	1/1	0.81	0.16	69,69,69,69	0
57	MG	1A	3632	1/1	0.81	0.12	66,66,66,66	0
57	MG	2a	1690	1/1	0.81	0.26	64,64,64,64	0
57	MG	2a	1695	1/1	0.81	0.28	68,68,68,68	0
57	MG	1A	3267	1/1	0.81	0.16	66,66,66,66	0
57	MG	2A	3343	1/1	0.81	0.10	81,81,81,81	0
57	MG	1A	3164	1/1	0.81	0.20	73,73,73,73	0
57	MG	1a	1744	1/1	0.81	0.18	68,68,68,68	0
57	MG	1A	4046	1/1	0.81	0.19	72,72,72,72	0
57	MG	2a	1728	1/1	0.81	0.15	68,68,68,68	0
57	MG	2A	3760	1/1	0.81	0.22	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3761	1/1	0.81	0.20	72,72,72,72	0
57	MG	2A	3571	1/1	0.81	0.24	70,70,70,70	0
57	MG	2A	3205	1/1	0.81	0.22	69,69,69,69	0
57	MG	1A	3812	1/1	0.81	0.19	57,57,57,57	0
57	MG	2A	3372	1/1	0.81	0.22	74,74,74,74	0
57	MG	1A	4055	1/1	0.81	0.12	59,59,59,59	0
57	MG	2a	1783	1/1	0.81	0.32	65,65,65,65	0
57	MG	1A	3853	1/1	0.81	0.14	45,45,45,45	0
57	MG	2a	1787	1/1	0.81	0.24	62,62,62,62	0
57	MG	2A	3255	1/1	0.81	0.17	68,68,68,68	0
57	MG	2A	3263	1/1	0.81	0.38	73,73,73,73	0
57	MG	2a	1798	1/1	0.81	0.26	68,68,68,68	0
57	MG	2B	202	1/1	0.81	0.17	67,67,67,67	0
57	MG	1A	3925	1/1	0.81	0.14	74,74,74,74	0
57	MG	2N	201	1/1	0.81	0.13	76,76,76,76	0
57	MG	2A	3623	1/1	0.81	0.21	66,66,66,66	0
57	MG	1x	111	1/1	0.81	0.24	71,71,71,71	0
57	MG	2A	3046	1/1	0.81	0.29	68,68,68,68	0
57	MG	1A	4004	1/1	0.81	0.13	37,37,37,37	0
57	MG	2A	3278	1/1	0.81	0.25	73,73,73,73	0
57	MG	1A	3341	1/1	0.82	0.15	65,65,65,65	0
57	MG	2A	3621	1/1	0.82	0.22	69,69,69,69	0
57	MG	1A	3669	1/1	0.82	0.21	59,59,59,59	0
57	MG	1A	3874	1/1	0.82	0.13	48,48,48,48	0
57	MG	1A	4031	1/1	0.82	0.13	54,54,54,54	0
57	MG	1A	3887	1/1	0.82	0.13	32,32,32,32	0
57	MG	1A	3306	1/1	0.82	0.34	71,71,71,71	0
57	MG	2B	201	1/1	0.82	0.23	67,67,67,67	0
57	MG	1A	3933	1/1	0.82	0.13	36,36,36,36	0
57	MG	2a	1765	1/1	0.82	0.26	76,76,76,76	0
57	MG	1x	104	1/1	0.82	0.18	69,69,69,69	0
57	MG	2F	3302	1/1	0.82	0.17	56,56,56,56	0
57	MG	2A	3678	1/1	0.82	0.21	70,70,70,70	0
57	MG	1A	3788	1/1	0.82	0.23	73,73,73,73	0
57	MG	20	104	1/1	0.82	0.19	67,67,67,67	0
57	MG	1A	4060	1/1	0.82	0.18	47,47,47,47	0
57	MG	2a	1606	1/1	0.82	0.19	70,70,70,70	0
57	MG	2A	3375	1/1	0.82	0.21	78,78,78,78	0
57	MG	2a	1613	1/1	0.82	0.14	70,70,70,70	0
57	MG	1A	3987	1/1	0.82	0.14	36,36,36,36	0
57	MG	1A	3791	1/1	0.82	0.12	52,52,52,52	0
57	MG	2a	1807	1/1	0.82	0.12	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1620	1/1	0.82	0.22	65,65,65,65	0
57	MG	2a	1643	1/1	0.82	0.36	84,84,84,84	0
57	MG	14	101	1/1	0.82	0.16	71,71,71,71	0
57	MG	2v	102	1/1	0.82	0.26	68,68,68,68	0
57	MG	2A	3093	1/1	0.82	0.21	60,60,60,60	0
57	MG	1A	3792	1/1	0.82	0.16	68,68,68,68	0
57	MG	2A	3290	1/1	0.82	0.20	71,71,71,71	0
57	MG	1A	3904	1/1	0.82	0.13	36,36,36,36	0
57	MG	2A	3794	1/1	0.82	0.19	50,50,50,50	0
57	MG	2A	3171	1/1	0.83	0.14	50,50,50,50	0
57	MG	2A	3332	1/1	0.83	0.29	68,68,68,68	0
57	MG	2A	3341	1/1	0.83	0.34	62,62,62,62	0
57	MG	1a	1762	1/1	0.83	0.16	47,47,47,47	0
57	MG	1a	1777	1/1	0.83	0.15	71,71,71,71	0
57	MG	2a	1703	1/1	0.83	0.21	70,70,70,70	0
57	MG	2A	3201	1/1	0.83	0.21	76,76,76,76	0
57	MG	2A	3581	1/1	0.83	0.26	62,62,62,62	0
57	MG	2a	1713	1/1	0.83	0.23	72,72,72,72	0
57	MG	1A	3636	1/1	0.83	0.14	34,34,34,34	0
57	MG	1A	3506	1/1	0.83	0.20	67,67,67,67	0
57	MG	2A	3359	1/1	0.83	0.30	69,69,69,69	0
57	MG	1A	3966	1/1	0.83	0.10	66,66,66,66	0
57	MG	2A	3238	1/1	0.83	0.16	73,73,73,73	0
57	MG	2a	1752	1/1	0.83	0.14	68,68,68,68	0
57	MG	2A	3835	1/1	0.83	0.20	67,67,67,67	0
57	MG	2A	3840	1/1	0.83	0.32	71,71,71,71	0
57	MG	1a	1662	1/1	0.83	0.15	58,58,58,58	0
57	MG	2A	3849	1/1	0.83	0.18	61,61,61,61	0
57	MG	1A	3968	1/1	0.83	0.14	65,65,65,65	0
57	MG	1a	1721	1/1	0.83	0.24	67,67,67,67	0
57	MG	2A	3264	1/1	0.83	0.19	62,62,62,62	0
57	MG	1a	1723	1/1	0.83	0.24	67,67,67,67	0
57	MG	1a	1730	1/1	0.83	0.21	61,61,61,61	0
57	MG	1A	3163	1/1	0.83	0.17	67,67,67,67	0
57	MG	2a	1792	1/1	0.83	0.14	64,64,64,64	0
57	MG	2A	3448	1/1	0.83	0.33	75,75,75,75	0
57	MG	1A	3418	1/1	0.83	0.23	75,75,75,75	0
57	MG	2A	3665	1/1	0.83	0.21	67,67,67,67	0
57	MG	1a	1747	1/1	0.83	0.17	65,65,65,65	0
57	MG	2A	3672	1/1	0.83	0.17	62,62,62,62	0
57	MG	1A	4090	1/1	0.83	0.21	60,60,60,60	0
57	MG	2A	3679	1/1	0.83	0.20	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	3146	1/1	0.83	0.23	69,69,69,69	0
57	MG	2A	3695	1/1	0.83	0.19	69,69,69,69	0
57	MG	11	105	1/1	0.83	0.20	76,76,76,76	0
57	MG	2a	1653	1/1	0.83	0.30	68,68,68,68	0
57	MG	2A	3168	1/1	0.83	0.15	60,60,60,60	0
57	MG	2A	3310	1/1	0.83	0.16	68,68,68,68	0
57	MG	2A	3301	1/1	0.84	0.22	66,66,66,66	0
57	MG	2A	3169	1/1	0.84	0.16	64,64,64,64	0
57	MG	1A	3320	1/1	0.84	0.17	61,61,61,61	0
57	MG	1B	225	1/1	0.84	0.17	57,57,57,57	0
57	MG	2A	3720	1/1	0.84	0.17	60,60,60,60	0
57	MG	2A	3320	1/1	0.84	0.14	62,62,62,62	0
57	MG	2A	3327	1/1	0.84	0.20	68,68,68,68	0
57	MG	1A	3423	1/1	0.84	0.14	59,59,59,59	0
57	MG	2A	3335	1/1	0.84	0.19	70,70,70,70	0
57	MG	2A	3188	1/1	0.84	0.23	61,61,61,61	0
57	MG	2A	3578	1/1	0.84	0.12	37,37,37,37	0
57	MG	1a	1641	1/1	0.84	0.20	64,64,64,64	0
57	MG	1w	108	1/1	0.84	0.20	80,80,80,80	0
57	MG	2A	3826	1/1	0.84	0.18	68,68,68,68	0
57	MG	2A	3206	1/1	0.84	0.17	74,74,74,74	0
57	MG	2A	3348	1/1	0.84	0.31	67,67,67,67	0
57	MG	2A	3834	1/1	0.84	0.24	73,73,73,73	0
57	MG	1A	3797	1/1	0.84	0.18	53,53,53,53	0
57	MG	2A	3231	1/1	0.84	0.18	70,70,70,70	0
57	MG	1a	1659	1/1	0.84	0.25	73,73,73,73	0
57	MG	1A	3758	1/1	0.84	0.13	71,71,71,71	0
57	MG	2A	3022	1/1	0.84	0.18	74,74,74,74	0
57	MG	2A	3038	1/1	0.84	0.38	75,75,75,75	0
57	MG	1A	3424	1/1	0.84	0.16	59,59,59,59	0
57	MG	1F	303	1/1	0.84	0.15	72,72,72,72	0
57	MG	2B	216	1/1	0.84	0.14	61,61,61,61	0
57	MG	1G	203	1/1	0.84	0.13	67,67,67,67	0
57	MG	2A	3402	1/1	0.84	0.34	63,63,63,63	0
57	MG	1A	4024	1/1	0.84	0.21	61,61,61,61	0
57	MG	2a	1795	1/1	0.84	0.18	69,69,69,69	0
57	MG	2A	3413	1/1	0.84	0.32	74,74,74,74	0
57	MG	1A	3366	1/1	0.84	0.30	70,70,70,70	0
57	MG	1A	4029	1/1	0.84	0.18	79,79,79,79	0
57	MG	2a	1810	1/1	0.84	0.36	68,68,68,68	0
57	MG	2A	3671	1/1	0.84	0.36	67,67,67,67	0
57	MG	2A	3442	1/1	0.84	0.20	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3785	1/1	0.84	0.17	58,58,58,58	0
57	MG	1W	205	1/1	0.84	0.20	43,43,43,43	0
57	MG	2A	3462	1/1	0.84	0.21	68,68,68,68	0
57	MG	2w	102	1/1	0.84	0.11	78,78,78,78	0
57	MG	2w	103	1/1	0.84	0.20	75,75,75,75	0
57	MG	2a	1629	1/1	0.84	0.15	86,86,86,86	0
57	MG	2x	106	1/1	0.84	0.12	40,40,40,40	0
57	MG	2a	1637	1/1	0.84	0.29	71,71,71,71	0
57	MG	1a	1758	1/1	0.84	0.17	55,55,55,55	0
57	MG	1A	3395	1/1	0.84	0.13	71,71,71,71	0
57	MG	2A	3635	1/1	0.85	0.18	62,62,62,62	0
57	MG	2A	3639	1/1	0.85	0.15	57,57,57,57	0
57	MG	1A	3868	1/1	0.85	0.10	54,54,54,54	0
57	MG	2a	1607	1/1	0.85	0.35	68,68,68,68	0
57	MG	1a	1804	1/1	0.85	0.16	69,69,69,69	0
57	MG	1a	1807	1/1	0.85	0.12	78,78,78,78	0
57	MG	1a	1809	1/1	0.85	0.15	64,64,64,64	0
57	MG	2A	3664	1/1	0.85	0.12	69,69,69,69	0
57	MG	1A	3870	1/1	0.85	0.10	28,28,28,28	0
57	MG	2A	3669	1/1	0.85	0.24	77,77,77,77	0
57	MG	2a	1634	1/1	0.85	0.29	63,63,63,63	0
57	MG	1A	3938	1/1	0.85	0.17	47,47,47,47	0
57	MG	1a	1640	1/1	0.85	0.18	67,67,67,67	0
57	MG	1x	106	1/1	0.85	0.17	69,69,69,69	0
57	MG	2a	1655	1/1	0.85	0.16	64,64,64,64	0
57	MG	1A	3760	1/1	0.85	0.23	70,70,70,70	0
57	MG	1A	3684	1/1	0.85	0.10	51,51,51,51	0
57	MG	2a	1668	1/1	0.85	0.18	61,61,61,61	0
57	MG	2A	3680	1/1	0.85	0.19	64,64,64,64	0
57	MG	2a	1675	1/1	0.85	0.26	67,67,67,67	0
57	MG	1A	3229	1/1	0.85	0.14	65,65,65,65	0
57	MG	1A	4019	1/1	0.85	0.11	54,54,54,54	0
57	MG	1a	1668	1/1	0.85	0.19	74,74,74,74	0
57	MG	2A	3701	1/1	0.85	0.18	73,73,73,73	0
57	MG	2A	3702	1/1	0.85	0.19	63,63,63,63	0
57	MG	2A	3050	1/1	0.85	0.21	65,65,65,65	0
57	MG	2A	3706	1/1	0.85	0.23	71,71,71,71	0
57	MG	2a	1710	1/1	0.85	0.18	64,64,64,64	0
57	MG	2A	3708	1/1	0.85	0.16	75,75,75,75	0
57	MG	2A	3054	1/1	0.85	0.16	66,66,66,66	0
57	MG	2A	3710	1/1	0.85	0.13	68,68,68,68	0
57	MG	2A	3289	1/1	0.85	0.21	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	3500	1/1	0.85	0.33	74,74,74,74	0
57	MG	2A	3062	1/1	0.85	0.10	55,55,55,55	0
57	MG	2A	3741	1/1	0.85	0.17	67,67,67,67	0
57	MG	2a	1754	1/1	0.85	0.18	69,69,69,69	0
57	MG	1a	1695	1/1	0.85	0.27	64,64,64,64	0
57	MG	2A	3753	1/1	0.85	0.12	65,65,65,65	0
57	MG	1A	3212	1/1	0.85	0.23	71,71,71,71	0
57	MG	1A	3065	1/1	0.85	0.26	62,62,62,62	0
57	MG	1A	3736	1/1	0.85	0.20	76,76,76,76	0
57	MG	2a	1779	1/1	0.85	0.22	70,70,70,70	0
57	MG	2A	3765	1/1	0.85	0.13	83,83,83,83	0
57	MG	2A	3784	1/1	0.85	0.12	72,72,72,72	0
57	MG	1A	3742	1/1	0.85	0.11	26,26,26,26	0
57	MG	2A	3804	1/1	0.85	0.17	45,45,45,45	0
57	MG	1A	3914	1/1	0.85	0.23	65,65,65,65	0
57	MG	2A	3134	1/1	0.85	0.32	69,69,69,69	0
57	MG	2A	3138	1/1	0.85	0.29	65,65,65,65	0
57	MG	2A	3330	1/1	0.85	0.29	79,79,79,79	0
57	MG	1A	3585	1/1	0.85	0.14	56,56,56,56	0
57	MG	1A	3410	1/1	0.85	0.22	59,59,59,59	0
57	MG	2A	3584	1/1	0.85	0.23	67,67,67,67	0
57	MG	2A	3339	1/1	0.85	0.22	73,73,73,73	0
57	MG	2f	202	1/1	0.85	0.21	75,75,75,75	0
57	MG	2A	3162	1/1	0.85	0.15	67,67,67,67	0
57	MG	1A	3923	1/1	0.85	0.13	75,75,75,75	0
57	MG	1A	4058	1/1	0.85	0.20	64,64,64,64	0
57	MG	1a	1759	1/1	0.85	0.12	62,62,62,62	0
57	MG	1A	3850	1/1	0.85	0.12	41,41,41,41	0
57	MG	1A	3595	1/1	0.85	0.16	69,69,69,69	0
57	MG	1A	4088	1/1	0.85	0.22	71,71,71,71	0
57	MG	2A	3193	1/1	0.85	0.22	66,66,66,66	0
57	MG	2E	309	1/1	0.85	0.20	56,56,56,56	0
57	MG	2y	101	1/1	0.85	0.13	80,80,80,80	0
57	MG	1a	1791	1/1	0.85	0.16	56,56,56,56	0
57	MG	2A	3627	1/1	0.85	0.14	67,67,67,67	0
57	MG	2A	3632	1/1	0.85	0.14	74,74,74,74	0
57	MG	1a	1752	1/1	0.86	0.14	75,75,75,75	0
57	MG	2a	1616	1/1	0.86	0.16	60,60,60,60	0
57	MG	2A	3684	1/1	0.86	0.12	67,67,67,67	0
57	MG	1a	1753	1/1	0.86	0.13	54,54,54,54	0
57	MG	1A	3487	1/1	0.86	0.19	64,64,64,64	0
57	MG	2a	1622	1/1	0.86	0.24	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	3293	1/1	0.86	0.21	61,61,61,61	0
57	MG	2A	3697	1/1	0.86	0.17	64,64,64,64	0
57	MG	2a	1636	1/1	0.86	0.23	70,70,70,70	0
57	MG	1A	3861	1/1	0.86	0.12	42,42,42,42	0
57	MG	2a	1641	1/1	0.86	0.24	67,67,67,67	0
57	MG	1A	3637	1/1	0.86	0.11	27,27,27,27	0
57	MG	2A	3703	1/1	0.86	0.23	59,59,59,59	0
57	MG	2A	3304	1/1	0.86	0.12	63,63,63,63	0
57	MG	2a	1657	1/1	0.86	0.17	68,68,68,68	0
57	MG	1a	1612	1/1	0.86	0.32	66,66,66,66	0
57	MG	1a	1633	1/1	0.86	0.25	63,63,63,63	0
57	MG	1A	3492	1/1	0.86	0.26	61,61,61,61	0
57	MG	2A	3166	1/1	0.86	0.21	74,74,74,74	0
57	MG	1A	3579	1/1	0.86	0.17	55,55,55,55	0
57	MG	2A	3572	1/1	0.86	0.16	68,68,68,68	0
57	MG	2A	3577	1/1	0.86	0.10	44,44,44,44	0
57	MG	2A	3723	1/1	0.86	0.14	57,57,57,57	0
57	MG	2a	1691	1/1	0.86	0.16	62,62,62,62	0
57	MG	2a	1694	1/1	0.86	0.37	71,71,71,71	0
57	MG	2A	3724	1/1	0.86	0.16	55,55,55,55	0
57	MG	1a	1645	1/1	0.86	0.33	67,67,67,67	0
57	MG	2a	1704	1/1	0.86	0.22	75,75,75,75	0
57	MG	1E	311	1/1	0.86	0.09	25,25,25,25	0
57	MG	2A	3749	1/1	0.86	0.14	67,67,67,67	0
57	MG	1a	1650	1/1	0.86	0.16	59,59,59,59	0
57	MG	2A	3758	1/1	0.86	0.10	77,77,77,77	0
57	MG	1a	1814	1/1	0.86	0.14	58,58,58,58	0
57	MG	2a	1719	1/1	0.86	0.22	58,58,58,58	0
57	MG	1A	4067	1/1	0.86	0.25	64,64,64,64	0
57	MG	1A	3726	1/1	0.86	0.13	35,35,35,35	0
57	MG	2a	1724	1/1	0.86	0.22	77,77,77,77	0
57	MG	1x	101	1/1	0.86	0.30	70,70,70,70	0
57	MG	2A	3774	1/1	0.86	0.14	53,53,53,53	0
57	MG	2a	1737	1/1	0.86	0.22	80,80,80,80	0
57	MG	2A	3203	1/1	0.86	0.17	64,64,64,64	0
57	MG	2A	3609	1/1	0.86	0.13	68,68,68,68	0
57	MG	2a	1760	1/1	0.86	0.17	54,54,54,54	0
57	MG	2A	3798	1/1	0.86	0.10	57,57,57,57	0
57	MG	1A	3810	1/1	0.86	0.16	70,70,70,70	0
57	MG	1A	4089	1/1	0.86	0.21	64,64,64,64	0
57	MG	1Q	205	1/1	0.86	0.14	58,58,58,58	0
57	MG	2A	3620	1/1	0.86	0.13	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	1a	1702	1/1	0.86	0.29	76,76,76,76	0
57	MG	2A	3360	1/1	0.86	0.18	62,62,62,62	0
57	MG	1A	3734	1/1	0.86	0.08	39,39,39,39	0
57	MG	2A	3833	1/1	0.86	0.22	70,70,70,70	0
57	MG	1A	3814	1/1	0.86	0.21	45,45,45,45	0
57	MG	2a	1786	1/1	0.86	0.29	68,68,68,68	0
57	MG	1A	3840	1/1	0.86	0.11	23,23,23,23	0
57	MG	2A	3839	1/1	0.86	0.17	67,67,67,67	0
57	MG	2A	3247	1/1	0.86	0.35	67,67,67,67	0
57	MG	2A	3249	1/1	0.86	0.23	77,77,77,77	0
57	MG	1A	3981	1/1	0.86	0.14	51,51,51,51	0
57	MG	2A	3643	1/1	0.86	0.20	70,70,70,70	0
57	MG	2a	1804	1/1	0.86	0.26	65,65,65,65	0
57	MG	2a	1806	1/1	0.86	0.26	67,67,67,67	0
57	MG	2A	3856	1/1	0.86	0.20	69,69,69,69	0
57	MG	2A	3644	1/1	0.86	0.21	72,72,72,72	0
57	MG	1a	1739	1/1	0.86	0.18	55,55,55,55	0
57	MG	2B	206	1/1	0.86	0.23	66,66,66,66	0
57	MG	2A	3057	1/1	0.86	0.28	71,71,71,71	0
57	MG	2A	3660	1/1	0.86	0.19	64,64,64,64	0
57	MG	2q	202	1/1	0.86	0.20	74,74,74,74	0
57	MG	2A	3268	1/1	0.86	0.22	64,64,64,64	0
57	MG	1a	1742	1/1	0.86	0.18	66,66,66,66	0
57	MG	2A	3425	1/1	0.86	0.19	68,68,68,68	0
57	MG	2A	3067	1/1	0.86	0.33	71,71,71,71	0
57	MG	1X	107	1/1	0.86	0.15	56,56,56,56	0
57	MG	2a	1602	1/1	0.86	0.11	79,79,79,79	0
57	MG	1Y	201	1/1	0.86	0.13	56,56,56,56	0
57	MG	1A	3404	1/1	0.86	0.19	67,67,67,67	0
57	MG	2A	3286	1/1	0.86	0.16	69,69,69,69	0
57	MG	2A	3467	1/1	0.86	0.21	60,60,60,60	0
57	MG	1A	3352	1/1	0.87	0.15	59,59,59,59	0
57	MG	1A	3393	1/1	0.87	0.20	57,57,57,57	0
57	MG	1A	3427	1/1	0.87	0.18	66,66,66,66	0
57	MG	2a	1624	1/1	0.87	0.13	71,71,71,71	0
57	MG	2A	3251	1/1	0.87	0.27	64,64,64,64	0
57	MG	1A	3359	1/1	0.87	0.11	51,51,51,51	0
57	MG	1A	3494	1/1	0.87	0.17	65,65,65,65	0
57	MG	2A	3470	1/1	0.87	0.19	66,66,66,66	0
57	MG	2A	3473	1/1	0.87	0.11	62,62,62,62	0
57	MG	2A	3479	1/1	0.87	0.12	53,53,53,53	0
57	MG	1A	3696	1/1	0.87	0.11	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1x	109	1/1	0.87	0.26	66,66,66,66	0
57	MG	1a	1654	1/1	0.87	0.13	57,57,57,57	0
57	MG	2A	3507	1/1	0.87	0.10	40,40,40,40	0
57	MG	2A	3007	1/1	0.87	0.26	63,63,63,63	0
57	MG	2A	3525	1/1	0.87	0.18	52,52,52,52	0
57	MG	1A	3699	1/1	0.87	0.12	54,54,54,54	0
57	MG	2a	1673	1/1	0.87	0.24	61,61,61,61	0
57	MG	1A	3449	1/1	0.87	0.14	67,67,67,67	0
57	MG	2A	3043	1/1	0.87	0.17	58,58,58,58	0
57	MG	2A	3743	1/1	0.87	0.12	63,63,63,63	0
57	MG	1A	3994	1/1	0.87	0.13	60,60,60,60	0
57	MG	1a	1670	1/1	0.87	0.13	62,62,62,62	0
57	MG	1a	1682	1/1	0.87	0.21	67,67,67,67	0
57	MG	2A	3755	1/1	0.87	0.13	47,47,47,47	0
57	MG	2a	1702	1/1	0.87	0.29	67,67,67,67	0
57	MG	2A	3757	1/1	0.87	0.14	46,46,46,46	0
57	MG	1a	1692	1/1	0.87	0.22	65,65,65,65	0
57	MG	1A	3704	1/1	0.87	0.15	53,53,53,53	0
57	MG	2A	3064	1/1	0.87	0.17	73,73,73,73	0
57	MG	1A	3806	1/1	0.87	0.10	42,42,42,42	0
57	MG	1A	3607	1/1	0.87	0.09	26,26,26,26	0
57	MG	2A	3079	1/1	0.87	0.18	60,60,60,60	0
57	MG	1a	1717	1/1	0.87	0.16	74,74,74,74	0
57	MG	2A	3787	1/1	0.87	0.08	58,58,58,58	0
57	MG	2A	3090	1/1	0.87	0.15	72,72,72,72	0
57	MG	1A	3717	1/1	0.87	0.08	20,20,20,20	0
57	MG	2A	3800	1/1	0.87	0.13	68,68,68,68	0
57	MG	2a	1732	1/1	0.87	0.15	67,67,67,67	0
57	MG	1D	310	1/1	0.87	0.17	51,51,51,51	0
57	MG	1a	1727	1/1	0.87	0.30	67,67,67,67	0
57	MG	2a	1738	1/1	0.87	0.10	66,66,66,66	0
57	MG	1A	3613	1/1	0.87	0.07	37,37,37,37	0
57	MG	2A	3819	1/1	0.87	0.13	68,68,68,68	0
57	MG	2A	3610	1/1	0.87	0.24	54,54,54,54	0
57	MG	1a	1731	1/1	0.87	0.11	55,55,55,55	0
57	MG	2a	1764	1/1	0.87	0.28	80,80,80,80	0
57	MG	1A	3829	1/1	0.87	0.08	21,21,21,21	0
57	MG	1E	315	1/1	0.87	0.12	58,58,58,58	0
57	MG	1A	4020	1/1	0.87	0.09	28,28,28,28	0
57	MG	2a	1772	1/1	0.87	0.15	60,60,60,60	0
57	MG	2A	3154	1/1	0.87	0.22	67,67,67,67	0
57	MG	1A	4021	1/1	0.87	0.09	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3363	1/1	0.87	0.19	61,61,61,61	0
57	MG	1A	3934	1/1	0.87	0.17	55,55,55,55	0
57	MG	1A	3848	1/1	0.87	0.17	58,58,58,58	0
57	MG	1A	3524	1/1	0.87	0.22	59,59,59,59	0
57	MG	1A	3131	1/1	0.87	0.22	51,51,51,51	0
57	MG	2A	3184	1/1	0.87	0.18	64,64,64,64	0
57	MG	1A	4045	1/1	0.87	0.20	60,60,60,60	0
57	MG	1A	3743	1/1	0.87	0.09	25,25,25,25	0
57	MG	2B	205	1/1	0.87	0.21	63,63,63,63	0
57	MG	2A	3381	1/1	0.87	0.23	50,50,50,50	0
57	MG	2A	3648	1/1	0.87	0.25	58,58,58,58	0
57	MG	2a	1801	1/1	0.87	0.19	72,72,72,72	0
57	MG	2B	212	1/1	0.87	0.25	71,71,71,71	0
57	MG	2B	215	1/1	0.87	0.19	72,72,72,72	0
57	MG	2A	3649	1/1	0.87	0.16	58,58,58,58	0
57	MG	2a	1809	1/1	0.87	0.21	57,57,57,57	0
57	MG	2B	218	1/1	0.87	0.24	68,68,68,68	0
57	MG	2A	3383	1/1	0.87	0.22	39,39,39,39	0
57	MG	2F	3301	1/1	0.87	0.11	59,59,59,59	0
57	MG	1A	3962	1/1	0.87	0.14	73,73,73,73	0
57	MG	2A	3390	1/1	0.87	0.23	67,67,67,67	0
57	MG	2V	202	1/1	0.87	0.14	62,62,62,62	0
57	MG	1A	3863	1/1	0.87	0.22	62,62,62,62	0
57	MG	1a	1789	1/1	0.87	0.10	69,69,69,69	0
57	MG	11	103	1/1	0.87	0.15	62,62,62,62	0
57	MG	1A	3244	1/1	0.87	0.26	63,63,63,63	0
57	MG	2w	104	1/1	0.87	0.15	72,72,72,72	0
57	MG	2A	3410	1/1	0.87	0.29	69,69,69,69	0
57	MG	1A	3869	1/1	0.87	0.14	67,67,67,67	0
57	MG	1A	4061	1/1	0.87	0.14	53,53,53,53	0
57	MG	2y	102	1/1	0.87	0.14	82,82,82,82	0
57	MG	1a	1602	1/1	0.87	0.19	60,60,60,60	0
57	MG	2A	3428	1/1	0.87	0.13	71,71,71,71	0
57	MG	1A	3646	1/1	0.87	0.24	64,64,64,64	0
57	MG	1A	3365	1/1	0.88	0.28	70,70,70,70	0
57	MG	26	101	1/1	0.88	0.22	64,64,64,64	0
57	MG	1A	3787	1/1	0.88	0.24	63,63,63,63	0
57	MG	2A	3141	1/1	0.88	0.17	58,58,58,58	0
57	MG	1A	3416	1/1	0.88	0.20	64,64,64,64	0
57	MG	1a	1757	1/1	0.88	0.16	72,72,72,72	0
57	MG	2A	3352	1/1	0.88	0.18	65,65,65,65	0
57	MG	1A	4068	1/1	0.88	0.13	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3659	1/1	0.88	0.16	56,56,56,56	0
57	MG	1A	3896	1/1	0.88	0.13	52,52,52,52	0
57	MG	1A	3206	1/1	0.88	0.12	51,51,51,51	0
57	MG	1A	3902	1/1	0.88	0.09	38,38,38,38	0
57	MG	1a	1763	1/1	0.88	0.15	49,49,49,49	0
57	MG	2A	3369	1/1	0.88	0.23	62,62,62,62	0
57	MG	2a	1625	1/1	0.88	0.15	71,71,71,71	0
57	MG	1A	3332	1/1	0.88	0.17	57,57,57,57	0
57	MG	2A	3178	1/1	0.88	0.23	64,64,64,64	0
57	MG	2A	3180	1/1	0.88	0.22	65,65,65,65	0
57	MG	2A	3182	1/1	0.88	0.14	63,63,63,63	0
57	MG	2a	1640	1/1	0.88	0.15	65,65,65,65	0
57	MG	1a	1788	1/1	0.88	0.30	75,75,75,75	0
57	MG	1A	3372	1/1	0.88	0.12	55,55,55,55	0
57	MG	2a	1644	1/1	0.88	0.32	81,81,81,81	0
57	MG	2A	3185	1/1	0.88	0.39	75,75,75,75	0
57	MG	2A	3397	1/1	0.88	0.33	62,62,62,62	0
57	MG	2A	3692	1/1	0.88	0.15	55,55,55,55	0
57	MG	1B	208	1/1	0.88	0.24	71,71,71,71	0
57	MG	1a	1793	1/1	0.88	0.14	70,70,70,70	0
57	MG	2A	3189	1/1	0.88	0.21	60,60,60,60	0
57	MG	2A	3404	1/1	0.88	0.26	62,62,62,62	0
57	MG	1a	1798	1/1	0.88	0.19	59,59,59,59	0
57	MG	1A	3908	1/1	0.88	0.08	43,43,43,43	0
57	MG	1a	1802	1/1	0.88	0.11	66,66,66,66	0
57	MG	1B	215	1/1	0.88	0.11	59,59,59,59	0
57	MG	1A	3910	1/1	0.88	0.14	48,48,48,48	0
57	MG	2A	3212	1/1	0.88	0.16	63,63,63,63	0
57	MG	2A	3214	1/1	0.88	0.16	62,62,62,62	0
57	MG	1A	3069	1/1	0.88	0.14	59,59,59,59	0
57	MG	2a	1696	1/1	0.88	0.16	67,67,67,67	0
57	MG	2a	1698	1/1	0.88	0.23	72,72,72,72	0
57	MG	2a	1701	1/1	0.88	0.18	63,63,63,63	0
57	MG	1a	1653	1/1	0.88	0.24	61,61,61,61	0
57	MG	1f	3101	1/1	0.88	0.16	48,48,48,48	0
57	MG	1A	3714	1/1	0.88	0.13	38,38,38,38	0
57	MG	1A	3387	1/1	0.88	0.15	53,53,53,53	0
57	MG	1A	3276	1/1	0.88	0.23	66,66,66,66	0
57	MG	1a	1664	1/1	0.88	0.29	60,60,60,60	0
57	MG	1A	3924	1/1	0.88	0.15	58,58,58,58	0
57	MG	2A	3254	1/1	0.88	0.10	66,66,66,66	0
57	MG	1A	3298	1/1	0.88	0.18	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	3501	1/1	0.88	0.20	55,55,55,55	0
57	MG	2A	3257	1/1	0.88	0.15	59,59,59,59	0
57	MG	2A	3503	1/1	0.88	0.24	61,61,61,61	0
57	MG	2A	3261	1/1	0.88	0.13	66,66,66,66	0
57	MG	1x	108	1/1	0.88	0.14	67,67,67,67	0
57	MG	1D	302	1/1	0.88	0.24	60,60,60,60	0
57	MG	2A	3532	1/1	0.88	0.10	40,40,40,40	0
57	MG	2A	3266	1/1	0.88	0.13	68,68,68,68	0
57	MG	2a	1750	1/1	0.88	0.14	78,78,78,78	0
57	MG	2A	3778	1/1	0.88	0.14	39,39,39,39	0
57	MG	2A	3781	1/1	0.88	0.12	46,46,46,46	0
57	MG	2A	3544	1/1	0.88	0.16	57,57,57,57	0
57	MG	1a	1688	1/1	0.88	0.15	71,71,71,71	0
57	MG	1A	3835	1/1	0.88	0.10	44,44,44,44	0
57	MG	1A	3476	1/1	0.88	0.12	68,68,68,68	0
57	MG	2A	3030	1/1	0.88	0.11	54,54,54,54	0
57	MG	2A	3565	1/1	0.88	0.11	39,39,39,39	0
57	MG	2a	1769	1/1	0.88	0.17	68,68,68,68	0
57	MG	2A	3568	1/1	0.88	0.21	56,56,56,56	0
57	MG	1A	3847	1/1	0.88	0.19	68,68,68,68	0
57	MG	2a	1777	1/1	0.88	0.16	67,67,67,67	0
57	MG	1a	1697	1/1	0.88	0.22	63,63,63,63	0
57	MG	1A	3551	1/1	0.88	0.16	52,52,52,52	0
57	MG	2a	1781	1/1	0.88	0.22	62,62,62,62	0
57	MG	2A	3574	1/1	0.88	0.14	59,59,59,59	0
57	MG	2A	3287	1/1	0.88	0.18	76,76,76,76	0
57	MG	2A	3830	1/1	0.88	0.11	58,58,58,58	0
57	MG	1a	1709	1/1	0.88	0.10	52,52,52,52	0
57	MG	1a	1716	1/1	0.88	0.13	60,60,60,60	0
57	MG	2a	1789	1/1	0.88	0.11	61,61,61,61	0
57	MG	1A	3240	1/1	0.88	0.14	56,56,56,56	0
57	MG	2A	3583	1/1	0.88	0.16	47,47,47,47	0
57	MG	1A	4030	1/1	0.88	0.14	63,63,63,63	0
57	MG	1N	201	1/1	0.88	0.12	47,47,47,47	0
57	MG	2A	3066	1/1	0.88	0.23	58,58,58,58	0
57	MG	1O	205	1/1	0.88	0.11	67,67,67,67	0
57	MG	2A	3850	1/1	0.88	0.13	56,56,56,56	0
57	MG	2a	1805	1/1	0.88	0.28	68,68,68,68	0
57	MG	1A	3557	1/1	0.88	0.15	57,57,57,57	0
57	MG	1A	3406	1/1	0.88	0.18	71,71,71,71	0
57	MG	2A	3317	1/1	0.88	0.27	73,73,73,73	0
57	MG	1A	3680	1/1	0.88	0.14	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	2e	201	1/1	0.88	0.10	63,63,63,63	0
57	MG	2A	3319	1/1	0.88	0.13	78,78,78,78	0
57	MG	2g	201	1/1	0.88	0.14	77,77,77,77	0
57	MG	1A	3574	1/1	0.88	0.08	35,35,35,35	0
57	MG	2B	207	1/1	0.88	0.12	69,69,69,69	0
57	MG	1a	1741	1/1	0.88	0.17	66,66,66,66	0
57	MG	1A	3685	1/1	0.88	0.11	57,57,57,57	0
57	MG	2B	214	1/1	0.88	0.26	70,70,70,70	0
57	MG	1A	3686	1/1	0.88	0.18	59,59,59,59	0
57	MG	2A	3333	1/1	0.88	0.17	64,64,64,64	0
57	MG	2B	217	1/1	0.88	0.30	73,73,73,73	0
57	MG	2A	3116	1/1	0.88	0.16	58,58,58,58	0
57	MG	2A	3629	1/1	0.88	0.14	60,60,60,60	0
57	MG	2A	3338	1/1	0.88	0.13	58,58,58,58	0
57	MG	1A	3780	1/1	0.88	0.22	44,44,44,44	0
57	MG	2A	3636	1/1	0.88	0.15	60,60,60,60	0
57	MG	2T	203	1/1	0.88	0.22	69,69,69,69	0
57	MG	2A	3340	1/1	0.88	0.45	53,53,53,53	0
57	MG	2A	3640	1/1	0.88	0.15	67,67,67,67	0
57	MG	1w	104	1/1	0.89	0.14	72,72,72,72	0
57	MG	1A	3915	1/1	0.89	0.15	58,58,58,58	0
57	MG	1A	4033	1/1	0.89	0.13	55,55,55,55	0
57	MG	2A	3270	1/1	0.89	0.22	65,65,65,65	0
57	MG	2B	213	1/1	0.89	0.25	61,61,61,61	0
57	MG	1a	1603	1/1	0.89	0.22	65,65,65,65	0
57	MG	1A	3153	1/1	0.89	0.18	64,64,64,64	0
57	MG	1a	1630	1/1	0.89	0.22	66,66,66,66	0
57	MG	1A	3024	1/1	0.89	0.20	76,76,76,76	0
57	MG	1A	3282	1/1	0.89	0.09	36,36,36,36	0
57	MG	2D	307	1/1	0.89	0.12	60,60,60,60	0
57	MG	2E	307	1/1	0.89	0.10	36,36,36,36	0
57	MG	2A	3282	1/1	0.89	0.22	68,68,68,68	0
57	MG	2A	3284	1/1	0.89	0.13	49,49,49,49	0
57	MG	1A	3291	1/1	0.89	0.25	60,60,60,60	0
57	MG	1x	110	1/1	0.89	0.11	27,27,27,27	0
57	MG	2Q	202	1/1	0.89	0.23	65,65,65,65	0
57	MG	2A	3288	1/1	0.89	0.18	62,62,62,62	0
57	MG	1A	3803	1/1	0.89	0.12	59,59,59,59	0
57	MG	1x	113	1/1	0.89	0.14	55,55,55,55	0
57	MG	2A	3001	1/1	0.89	0.36	64,64,64,64	0
57	MG	2A	3003	1/1	0.89	0.17	55,55,55,55	0
57	MG	28	101	1/1	0.89	0.21	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	28	102	1/1	0.89	0.18	63,63,63,63	0
57	MG	1A	4056	1/1	0.89	0.13	49,49,49,49	0
57	MG	1A	3582	1/1	0.89	0.14	55,55,55,55	0
57	MG	2a	1604	1/1	0.89	0.22	60,60,60,60	0
57	MG	1A	3409	1/1	0.89	0.15	66,66,66,66	0
57	MG	1A	3232	1/1	0.89	0.18	64,64,64,64	0
57	MG	2a	1609	1/1	0.89	0.18	66,66,66,66	0
57	MG	2A	3308	1/1	0.89	0.17	61,61,61,61	0
57	MG	2a	1611	1/1	0.89	0.24	71,71,71,71	0
57	MG	2A	3626	1/1	0.89	0.14	58,58,58,58	0
57	MG	1a	1656	1/1	0.89	0.31	63,63,63,63	0
57	MG	2A	3314	1/1	0.89	0.13	57,57,57,57	0
57	MG	1a	1657	1/1	0.89	0.35	74,74,74,74	0
57	MG	1A	4062	1/1	0.89	0.17	41,41,41,41	0
57	MG	1a	1660	1/1	0.89	0.34	63,63,63,63	0
57	MG	2A	3637	1/1	0.89	0.12	58,58,58,58	0
57	MG	1A	3813	1/1	0.89	0.10	43,43,43,43	0
57	MG	2A	3325	1/1	0.89	0.16	64,64,64,64	0
57	MG	2a	1630	1/1	0.89	0.25	72,72,72,72	0
57	MG	2A	3641	1/1	0.89	0.16	65,65,65,65	0
57	MG	1A	3937	1/1	0.89	0.09	53,53,53,53	0
57	MG	2A	3329	1/1	0.89	0.15	74,74,74,74	0
57	MG	1a	1665	1/1	0.89	0.16	50,50,50,50	0
57	MG	1A	4073	1/1	0.89	0.09	73,73,73,73	0
57	MG	2a	1642	1/1	0.89	0.14	54,54,54,54	0
57	MG	1A	3705	1/1	0.89	0.09	25,25,25,25	0
57	MG	2A	3068	1/1	0.89	0.21	56,56,56,56	0
57	MG	2a	1651	1/1	0.89	0.35	74,74,74,74	0
57	MG	2A	3336	1/1	0.89	0.21	73,73,73,73	0
57	MG	2A	3652	1/1	0.89	0.13	58,58,58,58	0
57	MG	1a	1672	1/1	0.89	0.33	65,65,65,65	0
57	MG	1a	1674	1/1	0.89	0.13	65,65,65,65	0
57	MG	1a	1678	1/1	0.89	0.19	55,55,55,55	0
57	MG	1A	3413	1/1	0.89	0.18	53,53,53,53	0
57	MG	2A	3091	1/1	0.89	0.13	74,74,74,74	0
57	MG	1A	3600	1/1	0.89	0.11	43,43,43,43	0
57	MG	1A	3953	1/1	0.89	0.13	40,40,40,40	0
57	MG	2a	1680	1/1	0.89	0.21	63,63,63,63	0
57	MG	1A	3956	1/1	0.89	0.08	41,41,41,41	0
57	MG	2a	1688	1/1	0.89	0.23	72,72,72,72	0
57	MG	1A	3300	1/1	0.89	0.17	55,55,55,55	0
57	MG	2A	3676	1/1	0.89	0.10	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1B	212	1/1	0.89	0.22	63,63,63,63	0
57	MG	2A	3129	1/1	0.89	0.14	66,66,66,66	0
57	MG	1A	3610	1/1	0.89	0.10	43,43,43,43	0
57	MG	1a	1706	1/1	0.89	0.20	65,65,65,65	0
57	MG	2A	3140	1/1	0.89	0.23	64,64,64,64	0
57	MG	1A	3730	1/1	0.89	0.07	71,71,71,71	0
57	MG	2A	3693	1/1	0.89	0.21	71,71,71,71	0
57	MG	1a	1715	1/1	0.89	0.15	60,60,60,60	0
57	MG	1A	3210	1/1	0.89	0.23	49,49,49,49	0
57	MG	2A	3153	1/1	0.89	0.15	61,61,61,61	0
57	MG	2A	3382	1/1	0.89	0.34	55,55,55,55	0
57	MG	1A	3852	1/1	0.89	0.13	62,62,62,62	0
57	MG	2A	3385	1/1	0.89	0.29	58,58,58,58	0
57	MG	1A	3496	1/1	0.89	0.16	66,66,66,66	0
57	MG	1A	3969	1/1	0.89	0.09	49,49,49,49	0
57	MG	2a	1720	1/1	0.89	0.24	67,67,67,67	0
57	MG	1A	3023	1/1	0.89	0.18	54,54,54,54	0
57	MG	2A	3394	1/1	0.89	0.31	63,63,63,63	0
57	MG	1A	3329	1/1	0.89	0.24	54,54,54,54	0
57	MG	1A	3744	1/1	0.89	0.11	42,42,42,42	0
57	MG	1B	234	1/1	0.89	0.17	70,70,70,70	0
57	MG	2A	3719	1/1	0.89	0.18	61,61,61,61	0
57	MG	1a	1738	1/1	0.89	0.11	72,72,72,72	0
57	MG	1A	3745	1/1	0.89	0.09	40,40,40,40	0
57	MG	1A	3978	1/1	0.89	0.08	40,40,40,40	0
57	MG	2A	3729	1/1	0.89	0.18	42,42,42,42	0
57	MG	2A	3740	1/1	0.89	0.11	56,56,56,56	0
57	MG	1A	3522	1/1	0.89	0.18	63,63,63,63	0
57	MG	1A	3748	1/1	0.89	0.12	52,52,52,52	0
57	MG	1A	3984	1/1	0.89	0.11	55,55,55,55	0
57	MG	1A	3880	1/1	0.89	0.10	43,43,43,43	0
57	MG	2A	3430	1/1	0.89	0.17	64,64,64,64	0
57	MG	1A	3886	1/1	0.89	0.09	30,30,30,30	0
57	MG	1A	3642	1/1	0.89	0.08	43,43,43,43	0
57	MG	2A	3445	1/1	0.89	0.28	65,65,65,65	0
57	MG	2a	1773	1/1	0.89	0.18	70,70,70,70	0
57	MG	2A	3759	1/1	0.89	0.13	65,65,65,65	0
57	MG	2A	3200	1/1	0.89	0.19	59,59,59,59	0
57	MG	1A	3755	1/1	0.89	0.12	43,43,43,43	0
57	MG	1A	3999	1/1	0.89	0.11	56,56,56,56	0
57	MG	1A	3643	1/1	0.89	0.12	40,40,40,40	0
57	MG	2A	3770	1/1	0.89	0.17	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1Q	207	1/1	0.89	0.18	60,60,60,60	0
57	MG	2A	3777	1/1	0.89	0.12	61,61,61,61	0
57	MG	1A	3425	1/1	0.89	0.24	72,72,72,72	0
57	MG	1A	3379	1/1	0.89	0.14	67,67,67,67	0
57	MG	1A	3898	1/1	0.89	0.14	53,53,53,53	0
57	MG	2A	3481	1/1	0.89	0.30	55,55,55,55	0
57	MG	2A	3790	1/1	0.89	0.13	44,44,44,44	0
57	MG	2A	3791	1/1	0.89	0.12	60,60,60,60	0
57	MG	2A	3496	1/1	0.89	0.14	57,57,57,57	0
57	MG	2A	3224	1/1	0.89	0.16	59,59,59,59	0
57	MG	1A	3430	1/1	0.89	0.11	48,48,48,48	0
57	MG	2A	3802	1/1	0.89	0.14	74,74,74,74	0
57	MG	1A	3773	1/1	0.89	0.13	52,52,52,52	0
57	MG	2A	3236	1/1	0.89	0.27	56,56,56,56	0
57	MG	2A	3807	1/1	0.89	0.11	40,40,40,40	0
57	MG	2A	3808	1/1	0.89	0.09	49,49,49,49	0
57	MG	1A	3777	1/1	0.89	0.19	60,60,60,60	0
57	MG	2A	3242	1/1	0.89	0.15	61,61,61,61	0
57	MG	2A	3509	1/1	0.89	0.10	48,48,48,48	0
57	MG	2A	3511	1/1	0.89	0.16	54,54,54,54	0
57	MG	1Z	302	1/1	0.89	0.10	59,59,59,59	0
57	MG	2l	201	1/1	0.89	0.14	65,65,65,65	0
57	MG	2A	3522	1/1	0.89	0.16	44,44,44,44	0
57	MG	2l	204	1/1	0.89	0.12	62,62,62,62	0
57	MG	2A	3245	1/1	0.89	0.14	62,62,62,62	0
57	MG	2A	3526	1/1	0.89	0.19	71,71,71,71	0
57	MG	2v	101	1/1	0.89	0.28	61,61,61,61	0
57	MG	2A	3527	1/1	0.89	0.15	60,60,60,60	0
57	MG	10	105	1/1	0.89	0.26	61,61,61,61	0
57	MG	2A	3538	1/1	0.89	0.17	74,74,74,74	0
57	MG	1A	3907	1/1	0.89	0.12	50,50,50,50	0
57	MG	11	102	1/1	0.89	0.14	62,62,62,62	0
57	MG	1A	3245	1/1	0.89	0.10	49,49,49,49	0
57	MG	2A	3555	1/1	0.89	0.14	68,68,68,68	0
57	MG	1A	3555	1/1	0.89	0.12	58,58,58,58	0
57	MG	13	103	1/1	0.89	0.14	59,59,59,59	0
57	MG	2A	3259	1/1	0.89	0.41	68,68,68,68	0
57	MG	1A	3392	1/1	0.89	0.14	57,57,57,57	0
57	MG	15	105	1/1	0.89	0.12	47,47,47,47	0
57	MG	2A	3406	1/1	0.90	0.21	55,55,55,55	0
57	MG	2A	3005	1/1	0.90	0.26	60,60,60,60	0
57	MG	1A	4040	1/1	0.90	0.15	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	3383	1/1	0.90	0.13	48,48,48,48	0
57	MG	1A	3630	1/1	0.90	0.11	40,40,40,40	0
57	MG	2A	3426	1/1	0.90	0.15	59,59,59,59	0
57	MG	1A	3343	1/1	0.90	0.24	65,65,65,65	0
57	MG	1A	3955	1/1	0.90	0.10	50,50,50,50	0
57	MG	2A	3432	1/1	0.90	0.12	73,73,73,73	0
57	MG	2a	1614	1/1	0.90	0.12	67,67,67,67	0
57	MG	1A	3388	1/1	0.90	0.17	54,54,54,54	0
57	MG	2a	1617	1/1	0.90	0.23	69,69,69,69	0
57	MG	2A	3681	1/1	0.90	0.17	66,66,66,66	0
57	MG	2A	3437	1/1	0.90	0.31	71,71,71,71	0
57	MG	2A	3689	1/1	0.90	0.12	57,57,57,57	0
57	MG	2A	3256	1/1	0.90	0.12	71,71,71,71	0
57	MG	10	102	1/1	0.90	0.14	58,58,58,58	0
57	MG	1a	1725	1/1	0.90	0.14	61,61,61,61	0
57	MG	2a	1628	1/1	0.90	0.29	67,67,67,67	0
57	MG	1A	3518	1/1	0.90	0.12	51,51,51,51	0
57	MG	2A	3451	1/1	0.90	0.12	57,57,57,57	0
57	MG	2a	1633	1/1	0.90	0.35	62,62,62,62	0
57	MG	2A	3457	1/1	0.90	0.20	59,59,59,59	0
57	MG	2a	1635	1/1	0.90	0.23	70,70,70,70	0
57	MG	1A	3391	1/1	0.90	0.13	50,50,50,50	0
57	MG	1A	3429	1/1	0.90	0.15	68,68,68,68	0
57	MG	1a	1733	1/1	0.90	0.12	74,74,74,74	0
57	MG	1A	3876	1/1	0.90	0.10	61,61,61,61	0
57	MG	1A	3162	1/1	0.90	0.15	55,55,55,55	0
57	MG	1A	3652	1/1	0.90	0.12	29,29,29,29	0
57	MG	1A	3431	1/1	0.90	0.20	65,65,65,65	0
57	MG	2a	1645	1/1	0.90	0.15	80,80,80,80	0
57	MG	1A	3657	1/1	0.90	0.10	59,59,59,59	0
57	MG	1A	3890	1/1	0.90	0.09	53,53,53,53	0
57	MG	1A	3432	1/1	0.90	0.23	55,55,55,55	0
57	MG	2A	3279	1/1	0.90	0.13	62,62,62,62	0
57	MG	1A	3263	1/1	0.90	0.07	40,40,40,40	0
57	MG	2A	3100	1/1	0.90	0.28	69,69,69,69	0
57	MG	2A	3506	1/1	0.90	0.16	56,56,56,56	0
57	MG	2A	3726	1/1	0.90	0.15	61,61,61,61	0
57	MG	1a	1750	1/1	0.90	0.12	64,64,64,64	0
57	MG	2a	1674	1/1	0.90	0.30	70,70,70,70	0
57	MG	2A	3731	1/1	0.90	0.15	71,71,71,71	0
57	MG	2a	1677	1/1	0.90	0.17	64,64,64,64	0
57	MG	2A	3104	1/1	0.90	0.23	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1682	1/1	0.90	0.37	64,64,64,64	0
57	MG	1a	1605	1/1	0.90	0.10	61,61,61,61	0
57	MG	2a	1687	1/1	0.90	0.16	73,73,73,73	0
57	MG	2A	3113	1/1	0.90	0.20	72,72,72,72	0
57	MG	2A	3519	1/1	0.90	0.12	64,64,64,64	0
57	MG	2A	3114	1/1	0.90	0.22	60,60,60,60	0
57	MG	2A	3751	1/1	0.90	0.16	50,50,50,50	0
57	MG	2A	3115	1/1	0.90	0.30	65,65,65,65	0
57	MG	1A	3784	1/1	0.90	0.14	61,61,61,61	0
57	MG	2A	3121	1/1	0.90	0.35	70,70,70,70	0
57	MG	2A	3122	1/1	0.90	0.15	57,57,57,57	0
57	MG	2A	3537	1/1	0.90	0.08	49,49,49,49	0
57	MG	1a	1621	1/1	0.90	0.28	63,63,63,63	0
57	MG	1A	3362	1/1	0.90	0.14	52,52,52,52	0
57	MG	2A	3540	1/1	0.90	0.12	45,45,45,45	0
57	MG	2a	1705	1/1	0.90	0.12	60,60,60,60	0
57	MG	2A	3543	1/1	0.90	0.09	47,47,47,47	0
57	MG	2a	1707	1/1	0.90	0.22	60,60,60,60	0
57	MG	1A	3900	1/1	0.90	0.15	57,57,57,57	0
57	MG	2A	3773	1/1	0.90	0.08	38,38,38,38	0
57	MG	2A	3545	1/1	0.90	0.14	71,71,71,71	0
57	MG	1A	3983	1/1	0.90	0.17	55,55,55,55	0
57	MG	2a	1717	1/1	0.90	0.12	68,68,68,68	0
57	MG	2a	1718	1/1	0.90	0.19	78,78,78,78	0
57	MG	2A	3550	1/1	0.90	0.14	57,57,57,57	0
57	MG	2A	3311	1/1	0.90	0.15	55,55,55,55	0
57	MG	2A	3312	1/1	0.90	0.13	60,60,60,60	0
57	MG	1A	3464	1/1	0.90	0.15	53,53,53,53	0
57	MG	1A	3569	1/1	0.90	0.14	45,45,45,45	0
57	MG	1A	3151	1/1	0.90	0.18	61,61,61,61	0
57	MG	1A	3470	1/1	0.90	0.14	61,61,61,61	0
57	MG	1A	3303	1/1	0.90	0.12	61,61,61,61	0
57	MG	2A	3570	1/1	0.90	0.24	62,62,62,62	0
57	MG	1A	3269	1/1	0.90	0.12	64,64,64,64	0
57	MG	1A	3241	1/1	0.90	0.17	68,68,68,68	0
57	MG	2A	3164	1/1	0.90	0.10	69,69,69,69	0
57	MG	2A	3806	1/1	0.90	0.10	56,56,56,56	0
57	MG	2a	1759	1/1	0.90	0.15	52,52,52,52	0
57	MG	1A	3588	1/1	0.90	0.12	50,50,50,50	0
57	MG	1A	3480	1/1	0.90	0.15	53,53,53,53	0
57	MG	1a	1801	1/1	0.90	0.11	49,49,49,49	0
57	MG	1A	3593	1/1	0.90	0.11	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	1803	1/1	0.90	0.14	62,62,62,62	0
57	MG	1A	3411	1/1	0.90	0.23	50,50,50,50	0
57	MG	2A	3828	1/1	0.90	0.10	54,54,54,54	0
57	MG	1a	1805	1/1	0.90	0.15	70,70,70,70	0
57	MG	1E	310	1/1	0.90	0.16	60,60,60,60	0
57	MG	1A	3825	1/1	0.90	0.13	66,66,66,66	0
57	MG	1A	3279	1/1	0.90	0.26	62,62,62,62	0
57	MG	2A	3607	1/1	0.90	0.12	46,46,46,46	0
57	MG	2A	3608	1/1	0.90	0.16	42,42,42,42	0
57	MG	1b	301	1/1	0.90	0.13	63,63,63,63	0
57	MG	1A	4023	1/1	0.90	0.13	47,47,47,47	0
57	MG	1a	1671	1/1	0.90	0.12	69,69,69,69	0
57	MG	2A	3844	1/1	0.90	0.12	61,61,61,61	0
57	MG	2A	3351	1/1	0.90	0.36	65,65,65,65	0
57	MG	2A	3615	1/1	0.90	0.24	70,70,70,70	0
57	MG	2a	1788	1/1	0.90	0.25	58,58,58,58	0
57	MG	2A	3617	1/1	0.90	0.15	63,63,63,63	0
57	MG	2A	3853	1/1	0.90	0.14	67,67,67,67	0
57	MG	2A	3192	1/1	0.90	0.17	62,62,62,62	0
57	MG	1A	3601	1/1	0.90	0.14	49,49,49,49	0
57	MG	2A	3195	1/1	0.90	0.35	68,68,68,68	0
57	MG	1w	107	1/1	0.90	0.09	79,79,79,79	0
57	MG	1G	202	1/1	0.90	0.21	62,62,62,62	0
57	MG	2a	1802	1/1	0.90	0.24	68,68,68,68	0
57	MG	1A	3928	1/1	0.90	0.12	26,26,26,26	0
57	MG	2B	208	1/1	0.90	0.14	57,57,57,57	0
57	MG	2B	209	1/1	0.90	0.19	59,59,59,59	0
57	MG	2A	3368	1/1	0.90	0.11	67,67,67,67	0
57	MG	2A	3204	1/1	0.90	0.16	55,55,55,55	0
57	MG	1a	1679	1/1	0.90	0.32	68,68,68,68	0
57	MG	2A	3373	1/1	0.90	0.16	64,64,64,64	0
57	MG	1A	3140	1/1	0.90	0.09	49,49,49,49	0
57	MG	1a	1684	1/1	0.90	0.24	67,67,67,67	0
57	MG	1a	1686	1/1	0.90	0.10	55,55,55,55	0
57	MG	2A	3216	1/1	0.90	0.22	66,66,66,66	0
57	MG	2A	3384	1/1	0.90	0.25	54,54,54,54	0
57	MG	2E	303	1/1	0.90	0.14	65,65,65,65	0
57	MG	1N	207	1/1	0.90	0.16	47,47,47,47	0
57	MG	1A	3417	1/1	0.90	0.15	70,70,70,70	0
57	MG	2A	3226	1/1	0.90	0.17	63,63,63,63	0
57	MG	2A	3645	1/1	0.90	0.13	48,48,48,48	0
57	MG	2A	3228	1/1	0.90	0.12	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	2O	3900	1/1	0.90	0.12	60,60,60,60	0
57	MG	1A	3612	1/1	0.90	0.10	35,35,35,35	0
57	MG	2A	3234	1/1	0.90	0.17	81,81,81,81	0
57	MG	1x	112	1/1	0.90	0.11	69,69,69,69	0
57	MG	2x	105	1/1	0.90	0.24	67,67,67,67	0
57	MG	2A	3401	1/1	0.90	0.23	56,56,56,56	0
57	MG	2A	3654	1/1	0.90	0.19	48,48,48,48	0
57	MG	25	105	1/1	0.90	0.13	63,63,63,63	0
57	MG	1A	3288	1/1	0.90	0.16	44,44,44,44	0
57	MG	1A	3616	1/1	0.90	0.07	34,34,34,34	0
57	MG	1A	4039	1/1	0.90	0.14	41,41,41,41	0
59	A1AE1	2A	3855	76/76	0.90	0.15	46,60,66,71	0
57	MG	1A	3894	1/1	0.91	0.08	66,66,66,66	0
57	MG	1O	204	1/1	0.91	0.09	45,45,45,45	0
57	MG	20	103	1/1	0.91	0.28	70,70,70,70	0
57	MG	2A	3353	1/1	0.91	0.24	49,49,49,49	0
57	MG	25	101	1/1	0.91	0.08	68,68,68,68	0
57	MG	1A	3664	1/1	0.91	0.11	53,53,53,53	0
57	MG	1A	3774	1/1	0.91	0.16	48,48,48,48	0
57	MG	1A	3666	1/1	0.91	0.10	49,49,49,49	0
57	MG	1A	3305	1/1	0.91	0.12	61,61,61,61	0
57	MG	2A	3361	1/1	0.91	0.13	64,64,64,64	0
57	MG	2A	3159	1/1	0.91	0.22	59,59,59,59	0
57	MG	2A	3366	1/1	0.91	0.22	58,58,58,58	0
57	MG	2a	1605	1/1	0.91	0.34	72,72,72,72	0
57	MG	1A	3782	1/1	0.91	0.09	44,44,44,44	0
57	MG	1A	4014	1/1	0.91	0.08	47,47,47,47	0
57	MG	2a	1608	1/1	0.91	0.20	64,64,64,64	0
57	MG	1A	3783	1/1	0.91	0.15	57,57,57,57	0
57	MG	1A	3673	1/1	0.91	0.13	60,60,60,60	0
57	MG	2A	3650	1/1	0.91	0.17	69,69,69,69	0
57	MG	1A	3679	1/1	0.91	0.16	74,74,74,74	0
57	MG	2A	3378	1/1	0.91	0.19	56,56,56,56	0
57	MG	2A	3380	1/1	0.91	0.21	44,44,44,44	0
57	MG	2A	3655	1/1	0.91	0.10	69,69,69,69	0
57	MG	1A	3185	1/1	0.91	0.10	51,51,51,51	0
57	MG	1A	3683	1/1	0.91	0.09	50,50,50,50	0
57	MG	1A	3912	1/1	0.91	0.13	57,57,57,57	0
57	MG	2a	1621	1/1	0.91	0.13	74,74,74,74	0
57	MG	1A	3790	1/1	0.91	0.09	53,53,53,53	0
57	MG	2a	1623	1/1	0.91	0.15	54,54,54,54	0
57	MG	1A	3584	1/1	0.91	0.14	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3666	1/1	0.91	0.10	61,61,61,61	0
57	MG	10	110	1/1	0.91	0.13	54,54,54,54	0
57	MG	2A	3388	1/1	0.91	0.13	37,37,37,37	0
57	MG	10	111	1/1	0.91	0.25	70,70,70,70	0
57	MG	1A	3916	1/1	0.91	0.10	66,66,66,66	0
57	MG	1a	1770	1/1	0.91	0.10	68,68,68,68	0
57	MG	1A	3313	1/1	0.91	0.14	63,63,63,63	0
57	MG	2A	3399	1/1	0.91	0.18	52,52,52,52	0
57	MG	1a	1786	1/1	0.91	0.24	52,52,52,52	0
57	MG	1a	1787	1/1	0.91	0.29	56,56,56,56	0
57	MG	1A	3369	1/1	0.91	0.26	65,65,65,65	0
57	MG	2A	3687	1/1	0.91	0.16	75,75,75,75	0
57	MG	1A	4038	1/1	0.91	0.14	32,32,32,32	0
57	MG	1a	1790	1/1	0.91	0.26	59,59,59,59	0
57	MG	13	104	1/1	0.91	0.09	50,50,50,50	0
57	MG	2a	1647	1/1	0.91	0.10	64,64,64,64	0
57	MG	2a	1648	1/1	0.91	0.22	52,52,52,52	0
57	MG	1A	3921	1/1	0.91	0.15	67,67,67,67	0
57	MG	1A	3799	1/1	0.91	0.08	65,65,65,65	0
57	MG	2A	3416	1/1	0.91	0.14	48,48,48,48	0
57	MG	2A	3417	1/1	0.91	0.15	65,65,65,65	0
57	MG	1A	3688	1/1	0.91	0.09	23,23,23,23	0
57	MG	2A	3207	1/1	0.91	0.21	47,47,47,47	0
57	MG	2a	1667	1/1	0.91	0.32	77,77,77,77	0
57	MG	15	107	1/1	0.91	0.12	63,63,63,63	0
57	MG	2a	1669	1/1	0.91	0.22	63,63,63,63	0
57	MG	18	105	1/1	0.91	0.14	53,53,53,53	0
57	MG	2A	3705	1/1	0.91	0.20	67,67,67,67	0
57	MG	1A	3805	1/1	0.91	0.12	54,54,54,54	0
57	MG	1A	3314	1/1	0.91	0.09	54,54,54,54	0
57	MG	2A	3223	1/1	0.91	0.19	54,54,54,54	0
57	MG	2a	1679	1/1	0.91	0.23	55,55,55,55	0
57	MG	1a	1604	1/1	0.91	0.12	60,60,60,60	0
57	MG	2A	3439	1/1	0.91	0.19	63,63,63,63	0
57	MG	2a	1683	1/1	0.91	0.12	68,68,68,68	0
57	MG	2A	3716	1/1	0.91	0.15	60,60,60,60	0
57	MG	1A	3808	1/1	0.91	0.12	57,57,57,57	0
57	MG	1a	1609	1/1	0.91	0.40	61,61,61,61	0
57	MG	1a	1811	1/1	0.91	0.14	74,74,74,74	0
57	MG	1A	3373	1/1	0.91	0.23	58,58,58,58	0
57	MG	1a	1613	1/1	0.91	0.11	57,57,57,57	0
57	MG	2a	1693	1/1	0.91	0.12	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	1e	201	1/1	0.91	0.12	68,68,68,68	0
57	MG	1A	4057	1/1	0.91	0.18	58,58,58,58	0
57	MG	2A	3241	1/1	0.91	0.14	48,48,48,48	0
57	MG	1n	101	1/1	0.91	0.37	65,65,65,65	0
57	MG	1v	101	1/1	0.91	0.20	68,68,68,68	0
57	MG	1a	1622	1/1	0.91	0.21	60,60,60,60	0
57	MG	2A	3745	1/1	0.91	0.16	72,72,72,72	0
57	MG	2A	3475	1/1	0.91	0.16	41,41,41,41	0
57	MG	2A	3748	1/1	0.91	0.09	48,48,48,48	0
57	MG	2A	3478	1/1	0.91	0.10	35,35,35,35	0
57	MG	1a	1623	1/1	0.91	0.25	63,63,63,63	0
57	MG	1A	3930	1/1	0.91	0.13	38,38,38,38	0
57	MG	2A	3486	1/1	0.91	0.17	68,68,68,68	0
57	MG	2a	1711	1/1	0.91	0.16	57,57,57,57	0
57	MG	2A	3489	1/1	0.91	0.09	46,46,46,46	0
57	MG	2A	3492	1/1	0.91	0.10	52,52,52,52	0
57	MG	1A	3123	1/1	0.91	0.14	51,51,51,51	0
57	MG	1A	3599	1/1	0.91	0.14	52,52,52,52	0
57	MG	1A	3936	1/1	0.91	0.10	49,49,49,49	0
57	MG	1A	3322	1/1	0.91	0.13	52,52,52,52	0
57	MG	1A	3203	1/1	0.91	0.23	53,53,53,53	0
57	MG	2A	3769	1/1	0.91	0.10	62,62,62,62	0
57	MG	1A	3071	1/1	0.91	0.14	38,38,38,38	0
57	MG	1A	3713	1/1	0.91	0.13	34,34,34,34	0
57	MG	1A	4079	1/1	0.91	0.19	39,39,39,39	0
57	MG	2a	1734	1/1	0.91	0.16	65,65,65,65	0
57	MG	1A	3075	1/1	0.91	0.15	31,31,31,31	0
57	MG	1A	3843	1/1	0.91	0.14	42,42,42,42	0
57	MG	1A	3080	1/1	0.91	0.16	58,58,58,58	0
57	MG	1B	206	1/1	0.91	0.19	52,52,52,52	0
57	MG	1A	3960	1/1	0.91	0.08	54,54,54,54	0
57	MG	2a	1753	1/1	0.91	0.09	67,67,67,67	0
57	MG	1A	3348	1/1	0.91	0.10	50,50,50,50	0
57	MG	2a	1757	1/1	0.91	0.14	65,65,65,65	0
57	MG	2A	3275	1/1	0.91	0.29	63,63,63,63	0
57	MG	1A	3534	1/1	0.91	0.14	40,40,40,40	0
57	MG	2A	3797	1/1	0.91	0.08	56,56,56,56	0
57	MG	2a	1762	1/1	0.91	0.20	58,58,58,58	0
57	MG	2A	3529	1/1	0.91	0.09	55,55,55,55	0
57	MG	2A	3009	1/1	0.91	0.23	63,63,63,63	0
57	MG	1a	1666	1/1	0.91	0.26	63,63,63,63	0
57	MG	1B	213	1/1	0.91	0.14	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3031	1/1	0.91	0.11	44,44,44,44	0
57	MG	2a	1771	1/1	0.91	0.33	67,67,67,67	0
57	MG	2A	3283	1/1	0.91	0.11	56,56,56,56	0
57	MG	1a	1669	1/1	0.91	0.22	68,68,68,68	0
57	MG	1A	3294	1/1	0.91	0.10	47,47,47,47	0
57	MG	1A	3538	1/1	0.91	0.18	43,43,43,43	0
57	MG	1A	3856	1/1	0.91	0.11	37,37,37,37	0
57	MG	1a	1673	1/1	0.91	0.25	62,62,62,62	0
57	MG	2A	3822	1/1	0.91	0.14	58,58,58,58	0
57	MG	2A	3823	1/1	0.91	0.19	68,68,68,68	0
57	MG	1A	3967	1/1	0.91	0.09	54,54,54,54	0
57	MG	2A	3059	1/1	0.91	0.23	61,61,61,61	0
57	MG	1a	1676	1/1	0.91	0.26	52,52,52,52	0
57	MG	2A	3297	1/1	0.91	0.21	60,60,60,60	0
57	MG	1A	3860	1/1	0.91	0.09	25,25,25,25	0
57	MG	2A	3566	1/1	0.91	0.17	60,60,60,60	0
57	MG	2a	1791	1/1	0.91	0.15	62,62,62,62	0
57	MG	1B	224	1/1	0.91	0.08	49,49,49,49	0
57	MG	1A	3546	1/1	0.91	0.25	54,54,54,54	0
57	MG	1B	227	1/1	0.91	0.09	40,40,40,40	0
57	MG	1A	3446	1/1	0.91	0.11	43,43,43,43	0
57	MG	1A	3448	1/1	0.91	0.15	69,69,69,69	0
57	MG	2A	3573	1/1	0.91	0.17	45,45,45,45	0
57	MG	2A	3848	1/1	0.91	0.23	62,62,62,62	0
57	MG	2A	3085	1/1	0.91	0.17	60,60,60,60	0
57	MG	1A	3640	1/1	0.91	0.12	29,29,29,29	0
57	MG	1a	1693	1/1	0.91	0.30	64,64,64,64	0
57	MG	1A	3353	1/1	0.91	0.29	38,38,38,38	0
57	MG	1B	236	1/1	0.91	0.10	42,42,42,42	0
57	MG	2A	3094	1/1	0.91	0.14	45,45,45,45	0
57	MG	2A	3096	1/1	0.91	0.19	58,58,58,58	0
57	MG	2A	3323	1/1	0.91	0.17	61,61,61,61	0
57	MG	1A	3401	1/1	0.91	0.18	43,43,43,43	0
57	MG	2A	3326	1/1	0.91	0.30	69,69,69,69	0
57	MG	1A	3248	1/1	0.91	0.25	53,53,53,53	0
57	MG	1E	308	1/1	0.91	0.16	52,52,52,52	0
57	MG	2A	3105	1/1	0.91	0.17	66,66,66,66	0
57	MG	1A	3558	1/1	0.91	0.12	40,40,40,40	0
57	MG	2A	3112	1/1	0.91	0.20	58,58,58,58	0
57	MG	1a	1711	1/1	0.91	0.17	46,46,46,46	0
57	MG	1A	3224	1/1	0.91	0.16	68,68,68,68	0
57	MG	2A	3337	1/1	0.91	0.24	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	2A	3616	1/1	0.91	0.23	61,61,61,61	0
57	MG	1A	3759	1/1	0.91	0.10	59,59,59,59	0
57	MG	1A	3166	1/1	0.91	0.10	57,57,57,57	0
57	MG	2w	105	1/1	0.91	0.22	51,51,51,51	0
57	MG	1a	1718	1/1	0.91	0.19	55,55,55,55	0
57	MG	2x	101	1/1	0.91	0.19	41,41,41,41	0
57	MG	2x	103	1/1	0.91	0.27	69,69,69,69	0
57	MG	1A	3364	1/1	0.91	0.30	47,47,47,47	0
57	MG	1F	313	1/1	0.91	0.11	52,52,52,52	0
57	MG	2A	3624	1/1	0.91	0.14	62,62,62,62	0
57	MG	2A	3344	1/1	0.91	0.18	60,60,60,60	0
57	MG	1A	3988	1/1	0.91	0.11	33,33,33,33	0
57	MG	1A	3662	1/1	0.91	0.17	59,59,59,59	0
57	MG	1A	3996	1/1	0.91	0.06	14,14,14,14	0
57	MG	2A	3631	1/1	0.91	0.13	58,58,58,58	0
57	MG	1a	1810	1/1	0.92	0.15	54,54,54,54	0
57	MG	2A	3376	1/1	0.92	0.26	65,65,65,65	0
57	MG	1A	3456	1/1	0.92	0.16	59,59,59,59	0
57	MG	2A	3379	1/1	0.92	0.33	53,53,53,53	0
57	MG	1a	1812	1/1	0.92	0.12	55,55,55,55	0
57	MG	1A	3457	1/1	0.92	0.11	66,66,66,66	0
57	MG	1a	1658	1/1	0.92	0.26	64,64,64,64	0
57	MG	2A	3646	1/1	0.92	0.12	49,49,49,49	0
57	MG	1d	301	1/1	0.92	0.14	59,59,59,59	0
57	MG	1A	3239	1/1	0.92	0.18	62,62,62,62	0
57	MG	1A	3905	1/1	0.92	0.13	64,64,64,64	0
57	MG	1h	201	1/1	0.92	0.10	72,72,72,72	0
57	MG	1B	235	1/1	0.92	0.12	48,48,48,48	0
57	MG	2A	3389	1/1	0.92	0.10	49,49,49,49	0
57	MG	1A	3346	1/1	0.92	0.29	44,44,44,44	0
57	MG	2A	3210	1/1	0.92	0.12	53,53,53,53	0
57	MG	2A	3657	1/1	0.92	0.10	61,61,61,61	0
57	MG	1A	3399	1/1	0.92	0.21	44,44,44,44	0
57	MG	1A	4006	1/1	0.92	0.08	44,44,44,44	0
57	MG	2a	1615	1/1	0.92	0.20	56,56,56,56	0
57	MG	2A	3661	1/1	0.92	0.11	69,69,69,69	0
57	MG	1A	3473	1/1	0.92	0.13	60,60,60,60	0
57	MG	1A	3119	1/1	0.92	0.16	54,54,54,54	0
57	MG	1A	3271	1/1	0.92	0.10	28,28,28,28	0
57	MG	1x	102	1/1	0.92	0.17	55,55,55,55	0
57	MG	1A	3272	1/1	0.92	0.24	48,48,48,48	0
57	MG	1x	105	1/1	0.92	0.12	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3592	1/1	0.92	0.08	31,31,31,31	0
57	MG	2A	3409	1/1	0.92	0.13	51,51,51,51	0
57	MG	1A	3061	1/1	0.92	0.23	48,48,48,48	0
57	MG	2a	1627	1/1	0.92	0.14	58,58,58,58	0
57	MG	1F	304	1/1	0.92	0.09	65,65,65,65	0
57	MG	2A	3415	1/1	0.92	0.23	64,64,64,64	0
57	MG	1A	3312	1/1	0.92	0.12	54,54,54,54	0
57	MG	1A	3002	1/1	0.92	0.10	48,48,48,48	0
57	MG	2A	3240	1/1	0.92	0.23	67,67,67,67	0
57	MG	2A	3685	1/1	0.92	0.09	42,42,42,42	0
57	MG	1A	4026	1/1	0.92	0.27	67,67,67,67	0
57	MG	1a	1680	1/1	0.92	0.18	57,57,57,57	0
57	MG	2a	1638	1/1	0.92	0.29	65,65,65,65	0
57	MG	2a	1639	1/1	0.92	0.24	66,66,66,66	0
57	MG	1a	1681	1/1	0.92	0.35	57,57,57,57	0
57	MG	1A	3706	1/1	0.92	0.11	44,44,44,44	0
57	MG	2A	3246	1/1	0.92	0.12	60,60,60,60	0
57	MG	1N	205	1/1	0.92	0.17	48,48,48,48	0
57	MG	2A	3435	1/1	0.92	0.20	64,64,64,64	0
57	MG	2A	3004	1/1	0.92	0.30	63,63,63,63	0
57	MG	2A	3699	1/1	0.92	0.10	58,58,58,58	0
57	MG	2A	3250	1/1	0.92	0.17	57,57,57,57	0
57	MG	2A	3441	1/1	0.92	0.14	53,53,53,53	0
57	MG	2a	1652	1/1	0.92	0.10	75,75,75,75	0
57	MG	1a	1685	1/1	0.92	0.17	58,58,58,58	0
57	MG	2a	1654	1/1	0.92	0.15	64,64,64,64	0
57	MG	1A	3280	1/1	0.92	0.21	55,55,55,55	0
57	MG	2A	3446	1/1	0.92	0.19	51,51,51,51	0
57	MG	1O	201	1/1	0.92	0.10	68,68,68,68	0
57	MG	2a	1661	1/1	0.92	0.19	52,52,52,52	0
57	MG	2a	1662	1/1	0.92	0.12	58,58,58,58	0
57	MG	1a	1690	1/1	0.92	0.22	56,56,56,56	0
57	MG	2A	3023	1/1	0.92	0.13	56,56,56,56	0
57	MG	2A	3456	1/1	0.92	0.10	47,47,47,47	0
57	MG	2A	3258	1/1	0.92	0.15	63,63,63,63	0
57	MG	2A	3713	1/1	0.92	0.11	56,56,56,56	0
57	MG	2A	3028	1/1	0.92	0.24	67,67,67,67	0
57	MG	2A	3717	1/1	0.92	0.40	48,48,48,48	0
57	MG	2A	3260	1/1	0.92	0.16	58,58,58,58	0
57	MG	2a	1676	1/1	0.92	0.18	62,62,62,62	0
57	MG	1A	3822	1/1	0.92	0.17	40,40,40,40	0
57	MG	1A	3415	1/1	0.92	0.17	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3034	1/1	0.92	0.09	39,39,39,39	0
57	MG	1A	3828	1/1	0.92	0.10	46,46,46,46	0
57	MG	1A	3606	1/1	0.92	0.07	28,28,28,28	0
57	MG	1A	3832	1/1	0.92	0.13	22,22,22,22	0
57	MG	2A	3730	1/1	0.92	0.09	57,57,57,57	0
57	MG	2A	3047	1/1	0.92	0.09	52,52,52,52	0
57	MG	2A	3485	1/1	0.92	0.12	53,53,53,53	0
57	MG	2A	3273	1/1	0.92	0.16	59,59,59,59	0
57	MG	2A	3742	1/1	0.92	0.15	65,65,65,65	0
57	MG	1S	3603	1/1	0.92	0.09	59,59,59,59	0
57	MG	1T	201	1/1	0.92	0.10	57,57,57,57	0
57	MG	1A	3316	1/1	0.92	0.11	62,62,62,62	0
57	MG	2A	3058	1/1	0.92	0.23	60,60,60,60	0
57	MG	1A	3317	1/1	0.92	0.16	61,61,61,61	0
57	MG	2A	3750	1/1	0.92	0.12	64,64,64,64	0
57	MG	1A	4041	1/1	0.92	0.11	48,48,48,48	0
57	MG	2A	3280	1/1	0.92	0.16	63,63,63,63	0
57	MG	1A	4042	1/1	0.92	0.19	66,66,66,66	0
57	MG	2A	3504	1/1	0.92	0.14	53,53,53,53	0
57	MG	2A	3065	1/1	0.92	0.23	65,65,65,65	0
57	MG	1A	3319	1/1	0.92	0.19	69,69,69,69	0
57	MG	1A	3419	1/1	0.92	0.15	49,49,49,49	0
57	MG	1A	3509	1/1	0.92	0.11	50,50,50,50	0
57	MG	2A	3762	1/1	0.92	0.11	74,74,74,74	0
57	MG	2A	3070	1/1	0.92	0.12	58,58,58,58	0
57	MG	1a	1722	1/1	0.92	0.12	55,55,55,55	0
57	MG	2A	3074	1/1	0.92	0.15	53,53,53,53	0
57	MG	1A	3627	1/1	0.92	0.07	29,29,29,29	0
57	MG	2A	3082	1/1	0.92	0.14	65,65,65,65	0
57	MG	1A	3514	1/1	0.92	0.20	46,46,46,46	0
57	MG	1A	3949	1/1	0.92	0.13	52,52,52,52	0
57	MG	1A	3004	1/1	0.92	0.13	43,43,43,43	0
57	MG	2a	1723	1/1	0.92	0.17	63,63,63,63	0
57	MG	2A	3533	1/1	0.92	0.13	45,45,45,45	0
57	MG	2A	3535	1/1	0.92	0.25	59,59,59,59	0
57	MG	2a	1730	1/1	0.92	0.10	64,64,64,64	0
57	MG	2a	1731	1/1	0.92	0.14	62,62,62,62	0
57	MG	1A	3371	1/1	0.92	0.16	66,66,66,66	0
57	MG	2A	3789	1/1	0.92	0.15	61,61,61,61	0
57	MG	2A	3305	1/1	0.92	0.26	54,54,54,54	0
57	MG	1A	3523	1/1	0.92	0.20	59,59,59,59	0
57	MG	1A	3101	1/1	0.92	0.11	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	1749	1/1	0.92	0.20	68,68,68,68	0
57	MG	2A	3796	1/1	0.92	0.10	75,75,75,75	0
57	MG	2A	3541	1/1	0.92	0.10	44,44,44,44	0
57	MG	2A	3095	1/1	0.92	0.13	49,49,49,49	0
57	MG	11	104	1/1	0.92	0.08	45,45,45,45	0
57	MG	1A	3529	1/1	0.92	0.09	40,40,40,40	0
57	MG	12	102	1/1	0.92	0.13	49,49,49,49	0
57	MG	2A	3548	1/1	0.92	0.19	63,63,63,63	0
57	MG	2A	3549	1/1	0.92	0.12	55,55,55,55	0
57	MG	1A	3866	1/1	0.92	0.10	39,39,39,39	0
57	MG	2a	1763	1/1	0.92	0.10	59,59,59,59	0
57	MG	2A	3553	1/1	0.92	0.15	63,63,63,63	0
57	MG	2A	3810	1/1	0.92	0.10	41,41,41,41	0
57	MG	2A	3815	1/1	0.92	0.16	52,52,52,52	0
57	MG	1A	4072	1/1	0.92	0.19	58,58,58,58	0
57	MG	1A	3324	1/1	0.92	0.19	57,57,57,57	0
57	MG	2a	1770	1/1	0.92	0.19	65,65,65,65	0
57	MG	2A	3820	1/1	0.92	0.15	60,60,60,60	0
57	MG	2A	3557	1/1	0.92	0.26	65,65,65,65	0
57	MG	2A	3111	1/1	0.92	0.18	42,42,42,42	0
57	MG	1a	1748	1/1	0.92	0.09	69,69,69,69	0
57	MG	1A	3756	1/1	0.92	0.08	42,42,42,42	0
57	MG	1A	3238	1/1	0.92	0.13	56,56,56,56	0
57	MG	1A	3330	1/1	0.92	0.18	43,43,43,43	0
57	MG	2A	3328	1/1	0.92	0.21	67,67,67,67	0
57	MG	2A	3831	1/1	0.92	0.12	53,53,53,53	0
57	MG	1A	3545	1/1	0.92	0.11	56,56,56,56	0
57	MG	1A	3331	1/1	0.92	0.21	59,59,59,59	0
57	MG	1A	4093	1/1	0.92	0.25	53,53,53,53	0
57	MG	1B	202	1/1	0.92	0.31	64,64,64,64	0
57	MG	2A	3837	1/1	0.92	0.09	59,59,59,59	0
57	MG	1A	3884	1/1	0.92	0.12	60,60,60,60	0
57	MG	1A	3885	1/1	0.92	0.07	48,48,48,48	0
57	MG	1A	3656	1/1	0.92	0.17	57,57,57,57	0
57	MG	1B	210	1/1	0.92	0.15	60,60,60,60	0
57	MG	1a	1776	1/1	0.92	0.09	67,67,67,67	0
57	MG	1B	211	1/1	0.92	0.17	50,50,50,50	0
57	MG	1A	3385	1/1	0.92	0.14	57,57,57,57	0
57	MG	2a	1799	1/1	0.92	0.24	67,67,67,67	0
57	MG	2A	3342	1/1	0.92	0.10	70,70,70,70	0
57	MG	1A	3548	1/1	0.92	0.21	51,51,51,51	0
57	MG	2A	3592	1/1	0.92	0.17	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	1624	1/1	0.92	0.26	60,60,60,60	0
57	MG	2A	3604	1/1	0.92	0.13	61,61,61,61	0
57	MG	1a	1625	1/1	0.92	0.22	53,53,53,53	0
57	MG	1A	3776	1/1	0.92	0.15	60,60,60,60	0
57	MG	2A	3347	1/1	0.92	0.22	72,72,72,72	0
57	MG	1a	1632	1/1	0.92	0.25	67,67,67,67	0
57	MG	1a	1792	1/1	0.92	0.20	60,60,60,60	0
57	MG	1A	3264	1/1	0.92	0.15	58,58,58,58	0
57	MG	1a	1637	1/1	0.92	0.15	54,54,54,54	0
57	MG	1a	1638	1/1	0.92	0.23	58,58,58,58	0
57	MG	2A	3173	1/1	0.92	0.24	66,66,66,66	0
57	MG	2A	3356	1/1	0.92	0.15	65,65,65,65	0
57	MG	2A	3357	1/1	0.92	0.13	69,69,69,69	0
57	MG	2A	3619	1/1	0.92	0.14	52,52,52,52	0
57	MG	2r	101	1/1	0.92	0.14	72,72,72,72	0
57	MG	2t	201	1/1	0.92	0.15	57,57,57,57	0
57	MG	2A	3358	1/1	0.92	0.18	70,70,70,70	0
57	MG	2A	3176	1/1	0.92	0.12	43,43,43,43	0
57	MG	2D	308	1/1	0.92	0.07	27,27,27,27	0
57	MG	2w	101	1/1	0.92	0.29	67,67,67,67	0
57	MG	2E	302	1/1	0.92	0.20	60,60,60,60	0
57	MG	1A	3982	1/1	0.92	0.08	33,33,33,33	0
57	MG	2E	306	1/1	0.92	0.12	56,56,56,56	0
57	MG	1A	3439	1/1	0.92	0.13	58,58,58,58	0
57	MG	2A	3362	1/1	0.92	0.16	66,66,66,66	0
57	MG	1A	3665	1/1	0.92	0.20	50,50,50,50	0
57	MG	1B	223	1/1	0.92	0.15	64,64,64,64	0
57	MG	1A	3333	1/1	0.92	0.17	46,46,46,46	0
57	MG	1a	1806	1/1	0.92	0.14	54,54,54,54	0
57	MG	2P	201	1/1	0.92	0.11	54,54,54,54	0
57	MG	2P	202	1/1	0.92	0.09	62,62,62,62	0
57	MG	2A	3370	1/1	0.92	0.13	68,68,68,68	0
57	MG	2A	3371	1/1	0.92	0.13	69,69,69,69	0
57	MG	1A	3336	1/1	0.92	0.20	45,45,45,45	0
59	A1AE1	1A	4094	76/76	0.92	0.12	29,49,58,64	0
57	MG	1A	3297	1/1	0.92	0.28	60,60,60,60	0
57	MG	1A	3796	1/1	0.93	0.09	20,20,20,20	0
57	MG	1a	1800	1/1	0.93	0.18	67,67,67,67	0
57	MG	20	101	1/1	0.93	0.11	58,58,58,58	0
57	MG	1A	3445	1/1	0.93	0.09	45,45,45,45	0
57	MG	1A	3798	1/1	0.93	0.12	65,65,65,65	0
57	MG	2A	3374	1/1	0.93	0.18	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	3337	1/1	0.93	0.17	59,59,59,59	0
57	MG	25	103	1/1	0.93	0.13	58,58,58,58	0
57	MG	1A	3800	1/1	0.93	0.10	20,20,20,20	0
57	MG	2A	3377	1/1	0.93	0.18	45,45,45,45	0
57	MG	1a	1626	1/1	0.93	0.15	52,52,52,52	0
57	MG	1a	1627	1/1	0.93	0.24	61,61,61,61	0
57	MG	2A	3191	1/1	0.93	0.15	59,59,59,59	0
57	MG	1a	1629	1/1	0.93	0.20	48,48,48,48	0
57	MG	1A	3801	1/1	0.93	0.09	25,25,25,25	0
57	MG	1A	3304	1/1	0.93	0.18	65,65,65,65	0
57	MG	2A	3197	1/1	0.93	0.08	47,47,47,47	0
57	MG	1A	3678	1/1	0.93	0.07	27,27,27,27	0
57	MG	1A	4092	1/1	0.93	0.26	61,61,61,61	0
57	MG	1A	3150	1/1	0.93	0.18	38,38,38,38	0
57	MG	1a	1639	1/1	0.93	0.14	61,61,61,61	0
57	MG	2A	3656	1/1	0.93	0.09	36,36,36,36	0
57	MG	2a	1612	1/1	0.93	0.20	63,63,63,63	0
57	MG	1A	3453	1/1	0.93	0.10	48,48,48,48	0
57	MG	1B	204	1/1	0.93	0.18	56,56,56,56	0
57	MG	2A	3393	1/1	0.93	0.26	64,64,64,64	0
57	MG	1A	3560	1/1	0.93	0.08	44,44,44,44	0
57	MG	2A	3662	1/1	0.93	0.12	60,60,60,60	0
57	MG	2A	3208	1/1	0.93	0.22	58,58,58,58	0
57	MG	1a	1646	1/1	0.93	0.18	49,49,49,49	0
57	MG	2A	3211	1/1	0.93	0.17	64,64,64,64	0
57	MG	1A	3566	1/1	0.93	0.09	53,53,53,53	0
57	MG	2A	3667	1/1	0.93	0.13	69,69,69,69	0
57	MG	1A	3275	1/1	0.93	0.14	59,59,59,59	0
57	MG	1a	1651	1/1	0.93	0.27	68,68,68,68	0
57	MG	1w	105	1/1	0.93	0.13	71,71,71,71	0
57	MG	1A	3942	1/1	0.93	0.07	12,12,12,12	0
57	MG	2A	3675	1/1	0.93	0.14	38,38,38,38	0
57	MG	1A	3946	1/1	0.93	0.09	61,61,61,61	0
57	MG	1a	1655	1/1	0.93	0.22	64,64,64,64	0
57	MG	2a	1632	1/1	0.93	0.26	48,48,48,48	0
57	MG	1A	3394	1/1	0.93	0.10	58,58,58,58	0
57	MG	2A	3414	1/1	0.93	0.29	53,53,53,53	0
57	MG	2A	3230	1/1	0.93	0.12	51,51,51,51	0
57	MG	2A	3683	1/1	0.93	0.14	52,52,52,52	0
57	MG	1A	3818	1/1	0.93	0.17	38,38,38,38	0
57	MG	2A	3232	1/1	0.93	0.12	64,64,64,64	0
57	MG	2A	3686	1/1	0.93	0.12	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3419	1/1	0.93	0.12	63,63,63,63	0
57	MG	2A	3233	1/1	0.93	0.15	59,59,59,59	0
57	MG	1A	3460	1/1	0.93	0.10	55,55,55,55	0
57	MG	1A	3575	1/1	0.93	0.10	44,44,44,44	0
57	MG	2A	3427	1/1	0.93	0.23	62,62,62,62	0
57	MG	1A	3826	1/1	0.93	0.07	34,34,34,34	0
57	MG	1A	3827	1/1	0.93	0.08	37,37,37,37	0
57	MG	2A	3239	1/1	0.93	0.19	61,61,61,61	0
57	MG	2a	1649	1/1	0.93	0.14	70,70,70,70	0
57	MG	2a	1650	1/1	0.93	0.08	60,60,60,60	0
57	MG	2A	3433	1/1	0.93	0.08	55,55,55,55	0
57	MG	1A	3307	1/1	0.93	0.17	44,44,44,44	0
57	MG	1A	3398	1/1	0.93	0.18	61,61,61,61	0
57	MG	1A	3830	1/1	0.93	0.06	28,28,28,28	0
57	MG	1A	3350	1/1	0.93	0.11	56,56,56,56	0
57	MG	1A	3472	1/1	0.93	0.21	56,56,56,56	0
57	MG	1A	3311	1/1	0.93	0.13	47,47,47,47	0
57	MG	2A	3443	1/1	0.93	0.09	35,35,35,35	0
57	MG	1A	3841	1/1	0.93	0.15	76,76,76,76	0
57	MG	1A	3083	1/1	0.93	0.20	42,42,42,42	0
57	MG	2A	3711	1/1	0.93	0.15	60,60,60,60	0
57	MG	2A	3447	1/1	0.93	0.13	59,59,59,59	0
57	MG	1A	3356	1/1	0.93	0.08	37,37,37,37	0
57	MG	2A	3715	1/1	0.93	0.09	47,47,47,47	0
57	MG	2a	1671	1/1	0.93	0.11	62,62,62,62	0
57	MG	2A	3449	1/1	0.93	0.31	68,68,68,68	0
57	MG	1A	3407	1/1	0.93	0.17	58,58,58,58	0
57	MG	1A	3168	1/1	0.93	0.09	46,46,46,46	0
57	MG	1A	3851	1/1	0.93	0.21	24,24,24,24	0
57	MG	2A	3010	1/1	0.93	0.21	52,52,52,52	0
57	MG	2A	3722	1/1	0.93	0.09	56,56,56,56	0
57	MG	2A	3459	1/1	0.93	0.25	45,45,45,45	0
57	MG	2A	3015	1/1	0.93	0.15	67,67,67,67	0
57	MG	2A	3017	1/1	0.93	0.12	59,59,59,59	0
57	MG	2A	3728	1/1	0.93	0.15	42,42,42,42	0
57	MG	1A	3977	1/1	0.93	0.11	58,58,58,58	0
57	MG	1A	3597	1/1	0.93	0.09	34,34,34,34	0
57	MG	1A	3718	1/1	0.93	0.10	54,54,54,54	0
57	MG	1A	3719	1/1	0.93	0.09	21,21,21,21	0
57	MG	2A	3476	1/1	0.93	0.17	53,53,53,53	0
57	MG	2A	3477	1/1	0.93	0.19	69,69,69,69	0
57	MG	1A	3857	1/1	0.93	0.13	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	3361	1/1	0.93	0.12	56,56,56,56	0
57	MG	2A	3267	1/1	0.93	0.14	58,58,58,58	0
57	MG	2a	1697	1/1	0.93	0.10	63,63,63,63	0
57	MG	1A	3182	1/1	0.93	0.09	44,44,44,44	0
57	MG	2a	1699	1/1	0.93	0.20	62,62,62,62	0
57	MG	1A	3486	1/1	0.93	0.21	50,50,50,50	0
57	MG	1a	1689	1/1	0.93	0.14	64,64,64,64	0
57	MG	2A	3490	1/1	0.93	0.11	62,62,62,62	0
57	MG	1A	3864	1/1	0.93	0.07	32,32,32,32	0
57	MG	2A	3493	1/1	0.93	0.10	36,36,36,36	0
57	MG	2A	3756	1/1	0.93	0.13	40,40,40,40	0
57	MG	2A	3495	1/1	0.93	0.08	35,35,35,35	0
57	MG	1A	3735	1/1	0.93	0.09	26,26,26,26	0
57	MG	2a	1709	1/1	0.93	0.16	48,48,48,48	0
57	MG	2A	3051	1/1	0.93	0.09	48,48,48,48	0
57	MG	1A	3867	1/1	0.93	0.10	48,48,48,48	0
57	MG	1G	204	1/1	0.93	0.19	60,60,60,60	0
57	MG	2a	1715	1/1	0.93	0.19	61,61,61,61	0
57	MG	1A	3281	1/1	0.93	0.17	53,53,53,53	0
57	MG	1A	3491	1/1	0.93	0.07	47,47,47,47	0
57	MG	2A	3060	1/1	0.93	0.16	55,55,55,55	0
57	MG	1A	3609	1/1	0.93	0.09	55,55,55,55	0
57	MG	1A	3247	1/1	0.93	0.13	47,47,47,47	0
57	MG	2A	3508	1/1	0.93	0.08	48,48,48,48	0
57	MG	1A	3286	1/1	0.93	0.15	35,35,35,35	0
57	MG	2A	3285	1/1	0.93	0.13	56,56,56,56	0
57	MG	1A	3877	1/1	0.93	0.10	72,72,72,72	0
57	MG	2A	3779	1/1	0.93	0.09	41,41,41,41	0
57	MG	2a	1729	1/1	0.93	0.09	60,60,60,60	0
57	MG	2A	3780	1/1	0.93	0.25	60,60,60,60	0
57	MG	1a	1714	1/1	0.93	0.13	68,68,68,68	0
57	MG	1A	3495	1/1	0.93	0.09	61,61,61,61	0
57	MG	1A	3881	1/1	0.93	0.11	58,58,58,58	0
57	MG	1A	4013	1/1	0.93	0.09	56,56,56,56	0
57	MG	1A	3070	1/1	0.93	0.16	40,40,40,40	0
57	MG	2A	3292	1/1	0.93	0.19	67,67,67,67	0
57	MG	2a	1744	1/1	0.93	0.14	68,68,68,68	0
57	MG	2a	1745	1/1	0.93	0.12	61,61,61,61	0
57	MG	2a	1746	1/1	0.93	0.13	76,76,76,76	0
57	MG	1A	3753	1/1	0.93	0.27	29,29,29,29	0
57	MG	2A	3295	1/1	0.93	0.15	65,65,65,65	0
57	MG	1A	3262	1/1	0.93	0.09	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	3187	1/1	0.93	0.14	60,60,60,60	0
57	MG	1V	203	1/1	0.93	0.35	45,45,45,45	0
57	MG	2A	3302	1/1	0.93	0.09	38,38,38,38	0
57	MG	2a	1758	1/1	0.93	0.19	50,50,50,50	0
57	MG	2A	3803	1/1	0.93	0.08	57,57,57,57	0
57	MG	1a	1726	1/1	0.93	0.12	54,54,54,54	0
57	MG	1A	3422	1/1	0.93	0.10	54,54,54,54	0
57	MG	2A	3306	1/1	0.93	0.17	53,53,53,53	0
57	MG	1W	201	1/1	0.93	0.11	57,57,57,57	0
57	MG	1A	3325	1/1	0.93	0.11	56,56,56,56	0
57	MG	2A	3309	1/1	0.93	0.09	49,49,49,49	0
57	MG	2A	3812	1/1	0.93	0.11	54,54,54,54	0
57	MG	1A	4025	1/1	0.93	0.25	56,56,56,56	0
57	MG	2a	1768	1/1	0.93	0.18	70,70,70,70	0
57	MG	1A	3635	1/1	0.93	0.12	34,34,34,34	0
57	MG	2A	3098	1/1	0.93	0.16	48,48,48,48	0
57	MG	1Z	301	1/1	0.93	0.14	63,63,63,63	0
57	MG	2A	3554	1/1	0.93	0.14	65,65,65,65	0
57	MG	2A	3315	1/1	0.93	0.14	69,69,69,69	0
57	MG	2a	1775	1/1	0.93	0.19	64,64,64,64	0
57	MG	1A	3295	1/1	0.93	0.17	53,53,53,53	0
57	MG	2A	3102	1/1	0.93	0.17	55,55,55,55	0
57	MG	2a	1778	1/1	0.93	0.13	55,55,55,55	0
57	MG	1a	1740	1/1	0.93	0.09	57,57,57,57	0
57	MG	1A	3519	1/1	0.93	0.11	39,39,39,39	0
57	MG	2A	3322	1/1	0.93	0.11	55,55,55,55	0
57	MG	1A	3638	1/1	0.93	0.07	30,30,30,30	0
57	MG	2A	3324	1/1	0.93	0.31	51,51,51,51	0
57	MG	2A	3110	1/1	0.93	0.10	73,73,73,73	0
57	MG	2a	1785	1/1	0.93	0.27	64,64,64,64	0
57	MG	1A	3046	1/1	0.93	0.09	24,24,24,24	0
57	MG	1a	1746	1/1	0.93	0.14	57,57,57,57	0
57	MG	1A	3426	1/1	0.93	0.13	67,67,67,67	0
57	MG	1A	3901	1/1	0.93	0.07	42,42,42,42	0
57	MG	1A	3233	1/1	0.93	0.14	72,72,72,72	0
57	MG	1A	3644	1/1	0.93	0.10	34,34,34,34	0
57	MG	2A	3120	1/1	0.93	0.19	71,71,71,71	0
57	MG	1A	3779	1/1	0.93	0.09	55,55,55,55	0
57	MG	2A	3580	1/1	0.93	0.10	49,49,49,49	0
57	MG	1A	3376	1/1	0.93	0.16	53,53,53,53	0
57	MG	1A	3146	1/1	0.93	0.14	57,57,57,57	0
57	MG	2a	1800	1/1	0.93	0.19	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3852	1/1	0.93	0.13	69,69,69,69	0
57	MG	2A	3126	1/1	0.93	0.12	59,59,59,59	0
57	MG	2a	1803	1/1	0.93	0.20	56,56,56,56	0
57	MG	2A	3854	1/1	0.93	0.11	68,68,68,68	0
57	MG	2A	3586	1/1	0.93	0.09	41,41,41,41	0
57	MG	2A	3127	1/1	0.93	0.13	49,49,49,49	0
57	MG	2A	3128	1/1	0.93	0.14	51,51,51,51	0
57	MG	2B	203	1/1	0.93	0.23	68,68,68,68	0
57	MG	2B	204	1/1	0.93	0.15	73,73,73,73	0
57	MG	2d	302	1/1	0.93	0.11	62,62,62,62	0
57	MG	1A	3382	1/1	0.93	0.13	57,57,57,57	0
57	MG	2A	3593	1/1	0.93	0.17	71,71,71,71	0
57	MG	1A	3302	1/1	0.93	0.10	52,52,52,52	0
57	MG	1A	4048	1/1	0.93	0.15	32,32,32,32	0
57	MG	1A	3911	1/1	0.93	0.17	48,48,48,48	0
57	MG	1A	3544	1/1	0.93	0.20	56,56,56,56	0
57	MG	2A	3144	1/1	0.93	0.15	51,51,51,51	0
57	MG	1A	3659	1/1	0.93	0.08	63,63,63,63	0
57	MG	1A	3437	1/1	0.93	0.16	39,39,39,39	0
57	MG	2A	3349	1/1	0.93	0.22	57,57,57,57	0
57	MG	1a	1601	1/1	0.93	0.17	59,59,59,59	0
57	MG	1a	1778	1/1	0.93	0.10	63,63,63,63	0
57	MG	2A	3156	1/1	0.93	0.21	58,58,58,58	0
57	MG	2D	306	1/1	0.93	0.17	62,62,62,62	0
57	MG	1a	1779	1/1	0.93	0.07	67,67,67,67	0
57	MG	1A	3334	1/1	0.93	0.28	47,47,47,47	0
57	MG	1A	4059	1/1	0.93	0.20	34,34,34,34	0
57	MG	1A	3204	1/1	0.93	0.14	50,50,50,50	0
57	MG	2E	304	1/1	0.93	0.15	63,63,63,63	0
57	MG	2w	106	1/1	0.93	0.17	64,64,64,64	0
57	MG	2A	3167	1/1	0.93	0.13	49,49,49,49	0
57	MG	2A	3622	1/1	0.93	0.09	56,56,56,56	0
57	MG	1A	3919	1/1	0.93	0.11	49,49,49,49	0
57	MG	2E	310	1/1	0.93	0.14	45,45,45,45	0
57	MG	1a	1606	1/1	0.93	0.16	58,58,58,58	0
57	MG	1A	3443	1/1	0.93	0.18	52,52,52,52	0
57	MG	2F	3303	1/1	0.93	0.09	44,44,44,44	0
57	MG	2A	3172	1/1	0.93	0.25	69,69,69,69	0
57	MG	1a	1611	1/1	0.93	0.12	64,64,64,64	0
57	MG	1A	4063	1/1	0.93	0.20	60,60,60,60	0
57	MG	2A	3177	1/1	0.93	0.17	45,45,45,45	0
57	MG	1A	3793	1/1	0.93	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	1O	203	1/1	0.94	0.18	59,59,59,59	0
57	MG	2A	3248	1/1	0.94	0.21	68,68,68,68	0
57	MG	2A	3024	1/1	0.94	0.13	54,54,54,54	0
57	MG	2A	3668	1/1	0.94	0.07	32,32,32,32	0
57	MG	2A	3027	1/1	0.94	0.16	55,55,55,55	0
57	MG	1a	1687	1/1	0.94	0.17	53,53,53,53	0
57	MG	2A	3253	1/1	0.94	0.11	62,62,62,62	0
57	MG	1A	3692	1/1	0.94	0.22	58,58,58,58	0
57	MG	1A	3177	1/1	0.94	0.15	33,33,33,33	0
57	MG	1A	3695	1/1	0.94	0.14	41,41,41,41	0
57	MG	1a	1691	1/1	0.94	0.14	55,55,55,55	0
57	MG	2A	3440	1/1	0.94	0.09	46,46,46,46	0
57	MG	2A	3042	1/1	0.94	0.15	65,65,65,65	0
57	MG	1A	3475	1/1	0.94	0.10	69,69,69,69	0
57	MG	2A	3044	1/1	0.94	0.14	67,67,67,67	0
57	MG	1A	3697	1/1	0.94	0.09	62,62,62,62	0
57	MG	1S	3601	1/1	0.94	0.20	46,46,46,46	0
57	MG	1A	3178	1/1	0.94	0.11	41,41,41,41	0
57	MG	1A	3701	1/1	0.94	0.08	29,29,29,29	0
57	MG	2A	3052	1/1	0.94	0.21	69,69,69,69	0
57	MG	1A	3615	1/1	0.94	0.09	31,31,31,31	0
57	MG	1a	1705	1/1	0.94	0.19	66,66,66,66	0
57	MG	2A	3452	1/1	0.94	0.11	45,45,45,45	0
57	MG	2A	3694	1/1	0.94	0.09	51,51,51,51	0
57	MG	2A	3271	1/1	0.94	0.10	70,70,70,70	0
57	MG	1T	204	1/1	0.94	0.14	55,55,55,55	0
57	MG	1U	204	1/1	0.94	0.16	37,37,37,37	0
57	MG	1A	4032	1/1	0.94	0.12	55,55,55,55	0
57	MG	2A	3463	1/1	0.94	0.11	49,49,49,49	0
57	MG	2A	3465	1/1	0.94	0.13	48,48,48,48	0
57	MG	1A	3054	1/1	0.94	0.11	44,44,44,44	0
57	MG	1A	3428	1/1	0.94	0.14	66,66,66,66	0
57	MG	1A	4035	1/1	0.94	0.10	51,51,51,51	0
57	MG	1A	3549	1/1	0.94	0.07	23,23,23,23	0
57	MG	1X	105	1/1	0.94	0.11	51,51,51,51	0
57	MG	1a	1720	1/1	0.94	0.11	44,44,44,44	0
57	MG	1A	3708	1/1	0.94	0.09	25,25,25,25	0
57	MG	1A	3811	1/1	0.94	0.07	25,25,25,25	0
57	MG	1A	3086	1/1	0.94	0.11	42,42,42,42	0
57	MG	2A	3480	1/1	0.94	0.09	22,22,22,22	0
57	MG	2A	3714	1/1	0.94	0.08	52,52,52,52	0
57	MG	1A	3554	1/1	0.94	0.10	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3081	1/1	0.94	0.23	53,53,53,53	0
57	MG	1A	4043	1/1	0.94	0.09	41,41,41,41	0
57	MG	2A	3488	1/1	0.94	0.08	55,55,55,55	0
57	MG	10	103	1/1	0.94	0.10	45,45,45,45	0
57	MG	1A	3042	1/1	0.94	0.07	29,29,29,29	0
57	MG	1A	3815	1/1	0.94	0.12	34,34,34,34	0
57	MG	1a	1732	1/1	0.94	0.20	72,72,72,72	0
57	MG	2a	1656	1/1	0.94	0.08	56,56,56,56	0
57	MG	1A	3816	1/1	0.94	0.13	36,36,36,36	0
57	MG	1A	3817	1/1	0.94	0.07	39,39,39,39	0
57	MG	2A	3727	1/1	0.94	0.10	39,39,39,39	0
57	MG	2A	3294	1/1	0.94	0.10	59,59,59,59	0
57	MG	2A	3498	1/1	0.94	0.07	29,29,29,29	0
57	MG	1A	4052	1/1	0.94	0.09	55,55,55,55	0
57	MG	2A	3296	1/1	0.94	0.15	69,69,69,69	0
57	MG	2A	3733	1/1	0.94	0.12	71,71,71,71	0
57	MG	2A	3735	1/1	0.94	0.12	52,52,52,52	0
57	MG	2A	3736	1/1	0.94	0.12	67,67,67,67	0
57	MG	1A	3716	1/1	0.94	0.08	34,34,34,34	0
57	MG	1A	3005	1/1	0.94	0.16	64,64,64,64	0
57	MG	2A	3300	1/1	0.94	0.14	62,62,62,62	0
57	MG	1A	3277	1/1	0.94	0.13	59,59,59,59	0
57	MG	1A	3403	1/1	0.94	0.14	36,36,36,36	0
57	MG	2a	1678	1/1	0.94	0.18	53,53,53,53	0
57	MG	2A	3746	1/1	0.94	0.15	66,66,66,66	0
57	MG	1A	3639	1/1	0.94	0.09	52,52,52,52	0
57	MG	2a	1681	1/1	0.94	0.16	53,53,53,53	0
57	MG	1a	1745	1/1	0.94	0.10	56,56,56,56	0
57	MG	2A	3510	1/1	0.94	0.10	48,48,48,48	0
57	MG	1A	3729	1/1	0.94	0.10	30,30,30,30	0
57	MG	2a	1685	1/1	0.94	0.33	57,57,57,57	0
57	MG	2a	1686	1/1	0.94	0.22	63,63,63,63	0
57	MG	1A	3488	1/1	0.94	0.25	56,56,56,56	0
57	MG	2A	3515	1/1	0.94	0.13	46,46,46,46	0
57	MG	1A	3732	1/1	0.94	0.07	37,37,37,37	0
57	MG	2A	3520	1/1	0.94	0.11	41,41,41,41	0
57	MG	2A	3521	1/1	0.94	0.11	40,40,40,40	0
57	MG	1A	3190	1/1	0.94	0.12	44,44,44,44	0
57	MG	1A	3940	1/1	0.94	0.11	49,49,49,49	0
57	MG	17	103	1/1	0.94	0.24	52,52,52,52	0
57	MG	17	106	1/1	0.94	0.09	59,59,59,59	0
57	MG	2A	3528	1/1	0.94	0.06	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1756	1/1	0.94	0.09	61,61,61,61	0
57	MG	18	101	1/1	0.94	0.18	52,52,52,52	0
57	MG	2A	3766	1/1	0.94	0.08	54,54,54,54	0
57	MG	1A	3192	1/1	0.94	0.08	48,48,48,48	0
57	MG	18	106	1/1	0.94	0.16	62,62,62,62	0
57	MG	2A	3772	1/1	0.94	0.13	38,38,38,38	0
57	MG	2A	3536	1/1	0.94	0.11	68,68,68,68	0
57	MG	19	101	1/1	0.94	0.24	54,54,54,54	0
57	MG	2A	3123	1/1	0.94	0.11	54,54,54,54	0
57	MG	1A	4069	1/1	0.94	0.07	55,55,55,55	0
57	MG	1A	3836	1/1	0.94	0.11	29,29,29,29	0
57	MG	1a	1768	1/1	0.94	0.21	60,60,60,60	0
57	MG	1A	3944	1/1	0.94	0.06	27,27,27,27	0
57	MG	1a	1771	1/1	0.94	0.09	68,68,68,68	0
57	MG	1A	3197	1/1	0.94	0.09	49,49,49,49	0
57	MG	1A	3738	1/1	0.94	0.13	51,51,51,51	0
57	MG	1A	4082	1/1	0.94	0.20	38,38,38,38	0
57	MG	1A	4083	1/1	0.94	0.20	42,42,42,42	0
57	MG	1a	1783	1/1	0.94	0.11	56,56,56,56	0
57	MG	1A	4087	1/1	0.94	0.12	51,51,51,51	0
57	MG	1A	3645	1/1	0.94	0.06	21,21,21,21	0
57	MG	1A	3844	1/1	0.94	0.13	55,55,55,55	0
57	MG	1a	1619	1/1	0.94	0.08	50,50,50,50	0
57	MG	1a	1620	1/1	0.94	0.24	64,64,64,64	0
57	MG	1A	3845	1/1	0.94	0.08	31,31,31,31	0
57	MG	2A	3562	1/1	0.94	0.16	62,62,62,62	0
57	MG	1A	3846	1/1	0.94	0.08	49,49,49,49	0
57	MG	2A	3564	1/1	0.94	0.19	65,65,65,65	0
57	MG	1A	3957	1/1	0.94	0.08	47,47,47,47	0
57	MG	2A	3165	1/1	0.94	0.10	62,62,62,62	0
57	MG	2A	3567	1/1	0.94	0.17	61,61,61,61	0
57	MG	2a	1736	1/1	0.94	0.11	60,60,60,60	0
57	MG	1a	1796	1/1	0.94	0.10	48,48,48,48	0
57	MG	1A	3959	1/1	0.94	0.11	49,49,49,49	0
57	MG	2a	1739	1/1	0.94	0.14	60,60,60,60	0
57	MG	2a	1740	1/1	0.94	0.09	50,50,50,50	0
57	MG	1A	3161	1/1	0.94	0.12	45,45,45,45	0
57	MG	1A	3648	1/1	0.94	0.08	33,33,33,33	0
57	MG	1A	3650	1/1	0.94	0.13	46,46,46,46	0
57	MG	1A	3048	1/1	0.94	0.12	49,49,49,49	0
57	MG	1A	3747	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3175	1/1	0.94	0.11	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3126	1/1	0.94	0.09	42,42,42,42	0
57	MG	2A	3827	1/1	0.94	0.19	57,57,57,57	0
57	MG	2a	1755	1/1	0.94	0.22	59,59,59,59	0
57	MG	1A	3377	1/1	0.94	0.08	49,49,49,49	0
57	MG	1A	3583	1/1	0.94	0.16	54,54,54,54	0
57	MG	1A	3658	1/1	0.94	0.09	41,41,41,41	0
57	MG	1a	1808	1/1	0.94	0.14	59,59,59,59	0
57	MG	1A	3081	1/1	0.94	0.09	61,61,61,61	0
57	MG	1B	217	1/1	0.94	0.10	45,45,45,45	0
57	MG	2A	3587	1/1	0.94	0.07	36,36,36,36	0
57	MG	1A	3862	1/1	0.94	0.15	37,37,37,37	0
57	MG	1A	3513	1/1	0.94	0.24	53,53,53,53	0
57	MG	1A	3586	1/1	0.94	0.08	26,26,26,26	0
57	MG	1a	1647	1/1	0.94	0.09	54,54,54,54	0
57	MG	2A	3190	1/1	0.94	0.10	54,54,54,54	0
57	MG	2A	3601	1/1	0.94	0.08	43,43,43,43	0
57	MG	2A	3846	1/1	0.94	0.08	69,69,69,69	0
57	MG	2A	3847	1/1	0.94	0.12	66,66,66,66	0
57	MG	2A	3602	1/1	0.94	0.10	47,47,47,47	0
57	MG	2A	3603	1/1	0.94	0.10	56,56,56,56	0
57	MG	2A	3365	1/1	0.94	0.15	75,75,75,75	0
57	MG	1A	3455	1/1	0.94	0.08	55,55,55,55	0
57	MG	2A	3606	1/1	0.94	0.10	48,48,48,48	0
57	MG	2A	3367	1/1	0.94	0.24	71,71,71,71	0
57	MG	1A	3761	1/1	0.94	0.11	31,31,31,31	0
57	MG	1A	3318	1/1	0.94	0.25	50,50,50,50	0
57	MG	1a	1652	1/1	0.94	0.13	56,56,56,56	0
57	MG	2A	3196	1/1	0.94	0.20	63,63,63,63	0
57	MG	2A	3612	1/1	0.94	0.15	60,60,60,60	0
57	MG	1k	201	1/1	0.94	0.14	45,45,45,45	0
57	MG	2A	3198	1/1	0.94	0.16	70,70,70,70	0
57	MG	1l	3200	1/1	0.94	0.06	73,73,73,73	0
57	MG	1A	3138	1/1	0.94	0.07	36,36,36,36	0
57	MG	1A	3765	1/1	0.94	0.09	39,39,39,39	0
57	MG	1w	101	1/1	0.94	0.14	51,51,51,51	0
57	MG	1w	103	1/1	0.94	0.23	63,63,63,63	0
57	MG	1A	3766	1/1	0.94	0.06	26,26,26,26	0
57	MG	1A	3768	1/1	0.94	0.07	29,29,29,29	0
57	MG	2a	1794	1/1	0.94	0.14	59,59,59,59	0
57	MG	1A	3770	1/1	0.94	0.08	38,38,38,38	0
57	MG	2A	3209	1/1	0.94	0.23	61,61,61,61	0
57	MG	1A	3667	1/1	0.94	0.12	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	3458	1/1	0.94	0.18	44,44,44,44	0
57	MG	1A	3671	1/1	0.94	0.10	54,54,54,54	0
57	MG	1A	3672	1/1	0.94	0.13	67,67,67,67	0
57	MG	2A	3630	1/1	0.94	0.15	58,58,58,58	0
57	MG	1E	301	1/1	0.94	0.11	40,40,40,40	0
57	MG	1A	3082	1/1	0.94	0.08	67,67,67,67	0
57	MG	2A	3221	1/1	0.94	0.28	51,51,51,51	0
57	MG	2A	3391	1/1	0.94	0.37	67,67,67,67	0
57	MG	1A	3998	1/1	0.94	0.13	52,52,52,52	0
57	MG	2a	1808	1/1	0.94	0.21	54,54,54,54	0
57	MG	1a	1667	1/1	0.94	0.14	68,68,68,68	0
57	MG	1A	3386	1/1	0.94	0.13	62,62,62,62	0
57	MG	2d	301	1/1	0.94	0.32	57,57,57,57	0
57	MG	2A	3395	1/1	0.94	0.31	62,62,62,62	0
57	MG	2A	3227	1/1	0.94	0.25	52,52,52,52	0
57	MG	1A	4001	1/1	0.94	0.09	37,37,37,37	0
57	MG	1A	3321	1/1	0.94	0.12	57,57,57,57	0
57	MG	1A	3889	1/1	0.94	0.11	62,62,62,62	0
57	MG	1A	3467	1/1	0.94	0.24	34,34,34,34	0
57	MG	1F	310	1/1	0.94	0.12	54,54,54,54	0
57	MG	1A	4007	1/1	0.94	0.09	41,41,41,41	0
57	MG	1A	3681	1/1	0.94	0.14	52,52,52,52	0
57	MG	2q	201	1/1	0.94	0.09	65,65,65,65	0
57	MG	2R	201	1/1	0.94	0.14	61,61,61,61	0
57	MG	2T	201	1/1	0.94	0.09	61,61,61,61	0
57	MG	2T	202	1/1	0.94	0.10	65,65,65,65	0
57	MG	2A	3408	1/1	0.94	0.17	42,42,42,42	0
57	MG	1A	3358	1/1	0.94	0.11	46,46,46,46	0
57	MG	2W	201	1/1	0.94	0.10	46,46,46,46	0
57	MG	1A	3537	1/1	0.94	0.10	36,36,36,36	0
57	MG	2A	3653	1/1	0.94	0.10	45,45,45,45	0
57	MG	2A	3412	1/1	0.94	0.15	50,50,50,50	0
57	MG	1I	201	1/1	0.94	0.07	52,52,52,52	0
57	MG	21	101	1/1	0.94	0.19	47,47,47,47	0
57	MG	1A	3265	1/1	0.94	0.09	58,58,58,58	0
57	MG	25	102	1/1	0.94	0.20	48,48,48,48	0
57	MG	1A	3608	1/1	0.94	0.06	23,23,23,23	0
57	MG	25	104	1/1	0.94	0.07	50,50,50,50	0
57	MG	1a	1683	1/1	0.94	0.24	55,55,55,55	0
57	MG	2A	3016	1/1	0.94	0.14	49,49,49,49	0
57	MG	2x	107	1/1	0.94	0.17	53,53,53,53	0
57	MG	27	102	1/1	0.94	0.10	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3244	1/1	0.94	0.13	58,58,58,58	0
57	MG	1A	3539	1/1	0.94	0.25	41,41,41,41	0
57	MG	28	103	1/1	0.94	0.29	59,59,59,59	0
57	MG	29	101	1/1	0.94	0.21	65,65,65,65	0
58	K	2A	3423	1/1	0.94	0.07	52,52,52,52	0
57	MG	2A	3422	1/1	0.94	0.27	60,60,60,60	0
57	MG	1A	3690	1/1	0.94	0.09	27,27,27,27	0
60	ZN	24	501	1/1	0.94	0.13	118,118,118,118	0
57	MG	1l	3201	1/1	0.95	0.14	54,54,54,54	0
57	MG	1m	3001	1/1	0.95	0.13	56,56,56,56	0
57	MG	2A	3213	1/1	0.95	0.31	61,61,61,61	0
57	MG	2a	1601	1/1	0.95	0.08	55,55,55,55	0
57	MG	1a	1635	1/1	0.95	0.28	62,62,62,62	0
57	MG	1n	102	1/1	0.95	0.08	45,45,45,45	0
57	MG	1r	101	1/1	0.95	0.21	58,58,58,58	0
57	MG	2A	3219	1/1	0.95	0.21	57,57,57,57	0
57	MG	2A	3220	1/1	0.95	0.25	43,43,43,43	0
57	MG	1A	3839	1/1	0.95	0.07	31,31,31,31	0
57	MG	1A	3620	1/1	0.95	0.06	20,20,20,20	0
57	MG	1w	102	1/1	0.95	0.10	50,50,50,50	0
57	MG	1A	3963	1/1	0.95	0.07	53,53,53,53	0
57	MG	1A	3621	1/1	0.95	0.07	19,19,19,19	0
57	MG	2A	3677	1/1	0.95	0.09	47,47,47,47	0
57	MG	1B	216	1/1	0.95	0.10	50,50,50,50	0
57	MG	2A	3431	1/1	0.95	0.09	47,47,47,47	0
57	MG	1a	1642	1/1	0.95	0.10	50,50,50,50	0
57	MG	1A	3842	1/1	0.95	0.07	41,41,41,41	0
57	MG	1A	3360	1/1	0.95	0.09	47,47,47,47	0
57	MG	1A	3235	1/1	0.95	0.06	37,37,37,37	0
57	MG	1a	1648	1/1	0.95	0.10	51,51,51,51	0
57	MG	1x	103	1/1	0.95	0.14	44,44,44,44	0
57	MG	1A	3122	1/1	0.95	0.09	41,41,41,41	0
57	MG	2A	3237	1/1	0.95	0.26	65,65,65,65	0
57	MG	1A	3301	1/1	0.95	0.07	55,55,55,55	0
57	MG	1A	3737	1/1	0.95	0.14	58,58,58,58	0
57	MG	1A	3050	1/1	0.95	0.10	47,47,47,47	0
57	MG	1A	3740	1/1	0.95	0.04	23,23,23,23	0
57	MG	1A	3077	1/1	0.95	0.15	38,38,38,38	0
57	MG	1A	3027	1/1	0.95	0.20	34,34,34,34	0
57	MG	1A	3136	1/1	0.95	0.12	41,41,41,41	0
57	MG	2a	1631	1/1	0.95	0.21	43,43,43,43	0
57	MG	2A	3698	1/1	0.95	0.20	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1B	232	1/1	0.95	0.06	44,44,44,44	0
57	MG	2A	3700	1/1	0.95	0.06	38,38,38,38	0
57	MG	1A	3979	1/1	0.95	0.09	59,59,59,59	0
57	MG	1x	114	1/1	0.95	0.07	62,62,62,62	0
57	MG	2A	3455	1/1	0.95	0.28	57,57,57,57	0
57	MG	1A	3530	1/1	0.95	0.06	40,40,40,40	0
57	MG	2A	3002	1/1	0.95	0.21	49,49,49,49	0
57	MG	2A	3458	1/1	0.95	0.21	54,54,54,54	0
57	MG	1A	3057	1/1	0.95	0.05	45,45,45,45	0
57	MG	2A	3460	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3641	1/1	0.95	0.14	45,45,45,45	0
57	MG	2A	3252	1/1	0.95	0.08	52,52,52,52	0
57	MG	2A	3464	1/1	0.95	0.42	72,72,72,72	0
57	MG	2a	1646	1/1	0.95	0.12	58,58,58,58	0
57	MG	1A	3186	1/1	0.95	0.11	35,35,35,35	0
57	MG	2A	3006	1/1	0.95	0.12	45,45,45,45	0
57	MG	1D	312	1/1	0.95	0.09	50,50,50,50	0
57	MG	1A	3433	1/1	0.95	0.11	51,51,51,51	0
57	MG	2A	3471	1/1	0.95	0.10	45,45,45,45	0
57	MG	1A	3040	1/1	0.95	0.11	40,40,40,40	0
57	MG	2A	3474	1/1	0.95	0.08	46,46,46,46	0
57	MG	1A	3249	1/1	0.95	0.07	47,47,47,47	0
57	MG	2A	3721	1/1	0.95	0.12	62,62,62,62	0
57	MG	1A	3865	1/1	0.95	0.07	69,69,69,69	0
57	MG	1A	3992	1/1	0.95	0.10	53,53,53,53	0
57	MG	2a	1659	1/1	0.95	0.48	68,68,68,68	0
57	MG	1A	3541	1/1	0.95	0.20	44,44,44,44	0
57	MG	2A	3262	1/1	0.95	0.16	50,50,50,50	0
57	MG	1E	316	1/1	0.95	0.05	37,37,37,37	0
57	MG	2a	1664	1/1	0.95	0.28	65,65,65,65	0
57	MG	1A	3995	1/1	0.95	0.08	53,53,53,53	0
57	MG	2A	3484	1/1	0.95	0.10	62,62,62,62	0
57	MG	2A	3265	1/1	0.95	0.14	56,56,56,56	0
57	MG	1A	3757	1/1	0.95	0.08	42,42,42,42	0
57	MG	2A	3732	1/1	0.95	0.08	57,57,57,57	0
57	MG	1A	3260	1/1	0.95	0.11	50,50,50,50	0
57	MG	2a	1672	1/1	0.95	0.10	53,53,53,53	0
57	MG	1a	1677	1/1	0.95	0.24	59,59,59,59	0
57	MG	1F	312	1/1	0.95	0.12	30,30,30,30	0
57	MG	1A	3440	1/1	0.95	0.17	46,46,46,46	0
57	MG	2A	3036	1/1	0.95	0.12	43,43,43,43	0
57	MG	1F	314	1/1	0.95	0.16	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3039	1/1	0.95	0.07	51,51,51,51	0
57	MG	2A	3744	1/1	0.95	0.07	40,40,40,40	0
57	MG	2A	3041	1/1	0.95	0.19	54,54,54,54	0
57	MG	1A	3651	1/1	0.95	0.06	28,28,28,28	0
57	MG	2A	3499	1/1	0.95	0.10	64,64,64,64	0
57	MG	1A	3442	1/1	0.95	0.14	55,55,55,55	0
57	MG	1A	3654	1/1	0.95	0.15	40,40,40,40	0
57	MG	1H	201	1/1	0.95	0.24	48,48,48,48	0
57	MG	1A	3144	1/1	0.95	0.34	34,34,34,34	0
57	MG	2A	3281	1/1	0.95	0.23	62,62,62,62	0
57	MG	2A	3754	1/1	0.95	0.16	59,59,59,59	0
57	MG	1A	3021	1/1	0.95	0.14	51,51,51,51	0
57	MG	1N	202	1/1	0.95	0.08	47,47,47,47	0
57	MG	1A	3378	1/1	0.95	0.10	49,49,49,49	0
57	MG	2a	1692	1/1	0.95	0.09	56,56,56,56	0
57	MG	1N	206	1/1	0.95	0.10	46,46,46,46	0
57	MG	2A	3055	1/1	0.95	0.12	51,51,51,51	0
57	MG	2A	3056	1/1	0.95	0.15	64,64,64,64	0
57	MG	1A	3148	1/1	0.95	0.14	38,38,38,38	0
57	MG	1A	3552	1/1	0.95	0.07	24,24,24,24	0
57	MG	2A	3518	1/1	0.95	0.14	50,50,50,50	0
57	MG	2A	3764	1/1	0.95	0.06	63,63,63,63	0
57	MG	1O	202	1/1	0.95	0.20	54,54,54,54	0
57	MG	1A	3771	1/1	0.95	0.07	33,33,33,33	0
57	MG	2A	3768	1/1	0.95	0.07	49,49,49,49	0
57	MG	1A	3381	1/1	0.95	0.15	39,39,39,39	0
57	MG	1A	4016	1/1	0.95	0.10	55,55,55,55	0
57	MG	1A	4018	1/1	0.95	0.09	48,48,48,48	0
57	MG	1a	1701	1/1	0.95	0.19	56,56,56,56	0
57	MG	1A	3450	1/1	0.95	0.30	56,56,56,56	0
57	MG	1a	1703	1/1	0.95	0.15	59,59,59,59	0
57	MG	1A	3775	1/1	0.95	0.20	47,47,47,47	0
57	MG	1Q	208	1/1	0.95	0.08	37,37,37,37	0
57	MG	1A	3193	1/1	0.95	0.25	56,56,56,56	0
57	MG	2A	3534	1/1	0.95	0.06	41,41,41,41	0
57	MG	1A	3149	1/1	0.95	0.06	34,34,34,34	0
57	MG	2A	3080	1/1	0.95	0.08	44,44,44,44	0
57	MG	1A	3778	1/1	0.95	0.10	53,53,53,53	0
57	MG	1A	3199	1/1	0.95	0.13	47,47,47,47	0
57	MG	1A	3559	1/1	0.95	0.14	50,50,50,50	0
57	MG	1U	203	1/1	0.95	0.09	36,36,36,36	0
57	MG	1A	3200	1/1	0.95	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	1U	205	1/1	0.95	0.10	30,30,30,30	0
57	MG	1U	207	1/1	0.95	0.19	46,46,46,46	0
57	MG	2a	1725	1/1	0.95	0.12	61,61,61,61	0
57	MG	2a	1727	1/1	0.95	0.08	60,60,60,60	0
57	MG	1A	3010	1/1	0.95	0.14	52,52,52,52	0
57	MG	2A	3801	1/1	0.95	0.07	23,23,23,23	0
57	MG	1A	3323	1/1	0.95	0.25	36,36,36,36	0
57	MG	1V	206	1/1	0.95	0.13	57,57,57,57	0
57	MG	1V	207	1/1	0.95	0.07	34,34,34,34	0
57	MG	2a	1733	1/1	0.95	0.12	69,69,69,69	0
57	MG	1A	3461	1/1	0.95	0.11	25,25,25,25	0
57	MG	2A	3551	1/1	0.95	0.10	54,54,54,54	0
57	MG	1A	3676	1/1	0.95	0.08	52,52,52,52	0
57	MG	1A	3389	1/1	0.95	0.10	42,42,42,42	0
57	MG	2A	3321	1/1	0.95	0.09	62,62,62,62	0
57	MG	1X	103	1/1	0.95	0.10	50,50,50,50	0
57	MG	2A	3813	1/1	0.95	0.08	55,55,55,55	0
57	MG	1A	3273	1/1	0.95	0.18	54,54,54,54	0
57	MG	1a	1736	1/1	0.95	0.11	46,46,46,46	0
57	MG	2A	3109	1/1	0.95	0.07	41,41,41,41	0
57	MG	2a	1747	1/1	0.95	0.13	50,50,50,50	0
57	MG	1X	106	1/1	0.95	0.06	45,45,45,45	0
57	MG	1A	3906	1/1	0.95	0.10	67,67,67,67	0
57	MG	2a	1751	1/1	0.95	0.12	65,65,65,65	0
57	MG	1A	3578	1/1	0.95	0.06	28,28,28,28	0
57	MG	1A	3087	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3909	1/1	0.95	0.12	26,26,26,26	0
57	MG	1Z	303	1/1	0.95	0.16	53,53,53,53	0
57	MG	2a	1756	1/1	0.95	0.08	53,53,53,53	0
57	MG	1A	3682	1/1	0.95	0.08	53,53,53,53	0
57	MG	2A	3117	1/1	0.95	0.11	60,60,60,60	0
57	MG	1A	3794	1/1	0.95	0.09	53,53,53,53	0
57	MG	10	104	1/1	0.95	0.18	49,49,49,49	0
57	MG	1A	3094	1/1	0.95	0.21	36,36,36,36	0
57	MG	10	107	1/1	0.95	0.06	41,41,41,41	0
57	MG	2A	3576	1/1	0.95	0.14	60,60,60,60	0
57	MG	1A	3913	1/1	0.95	0.09	59,59,59,59	0
57	MG	2A	3836	1/1	0.95	0.09	42,42,42,42	0
57	MG	2A	3125	1/1	0.95	0.29	62,62,62,62	0
57	MG	1A	3154	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3278	1/1	0.95	0.14	43,43,43,43	0
57	MG	1A	3474	1/1	0.95	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3917	1/1	0.95	0.08	68,68,68,68	0
57	MG	1A	4053	1/1	0.95	0.08	30,30,30,30	0
57	MG	1A	3397	1/1	0.95	0.20	40,40,40,40	0
57	MG	12	101	1/1	0.95	0.10	49,49,49,49	0
57	MG	1A	3689	1/1	0.95	0.10	32,32,32,32	0
57	MG	2A	3589	1/1	0.95	0.12	49,49,49,49	0
57	MG	2A	3350	1/1	0.95	0.12	38,38,38,38	0
57	MG	1A	3802	1/1	0.95	0.06	34,34,34,34	0
57	MG	2A	3145	1/1	0.95	0.28	55,55,55,55	0
57	MG	1A	3155	1/1	0.95	0.07	28,28,28,28	0
57	MG	1A	3213	1/1	0.95	0.09	51,51,51,51	0
57	MG	2A	3150	1/1	0.95	0.16	35,35,35,35	0
57	MG	2A	3152	1/1	0.95	0.11	66,66,66,66	0
57	MG	15	102	1/1	0.95	0.17	35,35,35,35	0
57	MG	1A	3215	1/1	0.95	0.12	56,56,56,56	0
57	MG	1a	1773	1/1	0.95	0.07	64,64,64,64	0
57	MG	1a	1775	1/1	0.95	0.07	77,77,77,77	0
57	MG	2A	3160	1/1	0.95	0.10	37,37,37,37	0
57	MG	2A	3161	1/1	0.95	0.07	51,51,51,51	0
57	MG	2A	3363	1/1	0.95	0.18	53,53,53,53	0
57	MG	1A	3222	1/1	0.95	0.10	40,40,40,40	0
57	MG	2B	211	1/1	0.95	0.24	68,68,68,68	0
57	MG	1A	3594	1/1	0.95	0.06	30,30,30,30	0
57	MG	16	101	1/1	0.95	0.07	59,59,59,59	0
57	MG	2a	1796	1/1	0.95	0.16	68,68,68,68	0
57	MG	1A	3927	1/1	0.95	0.17	48,48,48,48	0
57	MG	1a	1781	1/1	0.95	0.08	58,58,58,58	0
57	MG	1a	1782	1/1	0.95	0.07	53,53,53,53	0
57	MG	1A	4064	1/1	0.95	0.12	39,39,39,39	0
57	MG	1a	1784	1/1	0.95	0.06	51,51,51,51	0
57	MG	2D	303	1/1	0.95	0.17	52,52,52,52	0
57	MG	1A	3283	1/1	0.95	0.23	60,60,60,60	0
57	MG	18	104	1/1	0.95	0.11	48,48,48,48	0
57	MG	2A	3174	1/1	0.95	0.12	52,52,52,52	0
57	MG	2E	301	1/1	0.95	0.15	59,59,59,59	0
57	MG	1A	3338	1/1	0.95	0.11	51,51,51,51	0
57	MG	1A	3284	1/1	0.95	0.11	49,49,49,49	0
57	MG	1A	3342	1/1	0.95	0.09	42,42,42,42	0
57	MG	1A	3223	1/1	0.95	0.09	54,54,54,54	0
57	MG	1A	3604	1/1	0.95	0.05	31,31,31,31	0
57	MG	2E	308	1/1	0.95	0.12	74,74,74,74	0
57	MG	1A	4078	1/1	0.95	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3017	1/1	0.95	0.11	49,49,49,49	0
57	MG	2E	311	1/1	0.95	0.12	55,55,55,55	0
57	MG	1A	4081	1/1	0.95	0.08	43,43,43,43	0
57	MG	1A	3104	1/1	0.95	0.12	47,47,47,47	0
57	MG	1A	3711	1/1	0.95	0.06	36,36,36,36	0
57	MG	2G	201	1/1	0.95	0.09	57,57,57,57	0
57	MG	2A	3187	1/1	0.95	0.09	70,70,70,70	0
57	MG	1A	4084	1/1	0.95	0.11	57,57,57,57	0
57	MG	2A	3387	1/1	0.95	0.21	58,58,58,58	0
57	MG	1A	3292	1/1	0.95	0.26	54,54,54,54	0
57	MG	1A	3293	1/1	0.95	0.11	50,50,50,50	0
57	MG	1a	1614	1/1	0.95	0.20	61,61,61,61	0
57	MG	2R	202	1/1	0.95	0.06	41,41,41,41	0
57	MG	1a	1615	1/1	0.95	0.12	41,41,41,41	0
57	MG	1a	1618	1/1	0.95	0.08	48,48,48,48	0
57	MG	1A	3112	1/1	0.95	0.17	49,49,49,49	0
57	MG	2U	201	1/1	0.95	0.13	48,48,48,48	0
57	MG	1A	3945	1/1	0.95	0.08	40,40,40,40	0
57	MG	1A	4091	1/1	0.95	0.08	47,47,47,47	0
57	MG	2X	101	1/1	0.95	0.12	57,57,57,57	0
57	MG	1A	3049	1/1	0.95	0.09	50,50,50,50	0
57	MG	1A	3296	1/1	0.95	0.14	55,55,55,55	0
57	MG	2x	102	1/1	0.95	0.20	63,63,63,63	0
57	MG	1A	4095	1/1	0.95	0.06	42,42,42,42	0
57	MG	1A	3165	1/1	0.95	0.09	44,44,44,44	0
57	MG	1A	3831	1/1	0.95	0.11	32,32,32,32	0
57	MG	23	101	1/1	0.95	0.15	64,64,64,64	0
57	MG	1A	3512	1/1	0.95	0.09	47,47,47,47	0
57	MG	1A	3833	1/1	0.95	0.08	31,31,31,31	0
57	MG	2A	3405	1/1	0.95	0.08	46,46,46,46	0
57	MG	1A	3617	1/1	0.95	0.07	42,42,42,42	0
57	MG	1A	3727	1/1	0.95	0.10	57,57,57,57	0
57	MG	1A	3837	1/1	0.95	0.08	27,27,27,27	0
57	MG	1a	1634	1/1	0.95	0.08	60,60,60,60	0
57	MG	27	103	1/1	0.95	0.10	55,55,55,55	0
60	ZN	14	102	1/1	0.95	0.11	107,107,107,107	0
57	MG	2A	3411	1/1	0.95	0.34	60,60,60,60	0
57	MG	1A	3781	1/1	0.96	0.07	36,36,36,36	0
57	MG	2A	3491	1/1	0.96	0.08	40,40,40,40	0
57	MG	2A	3075	1/1	0.96	0.15	50,50,50,50	0
57	MG	2A	3076	1/1	0.96	0.21	41,41,41,41	0
57	MG	2a	1626	1/1	0.96	0.23	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3078	1/1	0.96	0.14	30,30,30,30	0
57	MG	1W	206	1/1	0.96	0.07	47,47,47,47	0
57	MG	1A	3444	1/1	0.96	0.23	41,41,41,41	0
57	MG	1a	1729	1/1	0.96	0.10	49,49,49,49	0
57	MG	2A	3725	1/1	0.96	0.09	52,52,52,52	0
57	MG	1A	3038	1/1	0.96	0.17	30,30,30,30	0
57	MG	2A	3083	1/1	0.96	0.09	48,48,48,48	0
57	MG	1A	3266	1/1	0.96	0.09	53,53,53,53	0
57	MG	1A	3447	1/1	0.96	0.11	47,47,47,47	0
57	MG	2A	3089	1/1	0.96	0.11	55,55,55,55	0
57	MG	1A	3060	1/1	0.96	0.04	24,24,24,24	0
57	MG	1a	1735	1/1	0.96	0.07	47,47,47,47	0
57	MG	2A	3298	1/1	0.96	0.08	56,56,56,56	0
57	MG	1A	3268	1/1	0.96	0.06	54,54,54,54	0
57	MG	1A	3789	1/1	0.96	0.08	61,61,61,61	0
57	MG	2A	3738	1/1	0.96	0.09	71,71,71,71	0
57	MG	1A	3001	1/1	0.96	0.06	42,42,42,42	0
57	MG	10	101	1/1	0.96	0.17	42,42,42,42	0
57	MG	1A	3270	1/1	0.96	0.12	40,40,40,40	0
57	MG	2A	3513	1/1	0.96	0.10	46,46,46,46	0
57	MG	2A	3099	1/1	0.96	0.09	48,48,48,48	0
57	MG	1A	3670	1/1	0.96	0.07	48,48,48,48	0
57	MG	1A	3454	1/1	0.96	0.06	53,53,53,53	0
57	MG	1A	3205	1/1	0.96	0.09	49,49,49,49	0
57	MG	1A	3098	1/1	0.96	0.14	31,31,31,31	0
57	MG	1A	3007	1/1	0.96	0.09	22,22,22,22	0
57	MG	10	109	1/1	0.96	0.20	64,64,64,64	0
57	MG	2A	3108	1/1	0.96	0.27	58,58,58,58	0
57	MG	2A	3313	1/1	0.96	0.15	55,55,55,55	0
57	MG	1A	3562	1/1	0.96	0.05	32,32,32,32	0
57	MG	1A	3563	1/1	0.96	0.09	12,12,12,12	0
57	MG	1A	3327	1/1	0.96	0.13	46,46,46,46	0
57	MG	1a	1751	1/1	0.96	0.06	76,76,76,76	0
57	MG	1A	3568	1/1	0.96	0.07	31,31,31,31	0
57	MG	1A	4066	1/1	0.96	0.10	50,50,50,50	0
57	MG	1A	3043	1/1	0.96	0.06	31,31,31,31	0
57	MG	11	106	1/1	0.96	0.09	53,53,53,53	0
57	MG	1A	3105	1/1	0.96	0.10	36,36,36,36	0
57	MG	1A	3573	1/1	0.96	0.07	52,52,52,52	0
57	MG	1a	1760	1/1	0.96	0.06	65,65,65,65	0
57	MG	13	102	1/1	0.96	0.10	46,46,46,46	0
57	MG	2A	3542	1/1	0.96	0.12	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	3214	1/1	0.96	0.26	47,47,47,47	0
57	MG	1A	3106	1/1	0.96	0.17	45,45,45,45	0
57	MG	1A	4076	1/1	0.96	0.08	58,58,58,58	0
57	MG	2A	3771	1/1	0.96	0.11	74,74,74,74	0
57	MG	1A	3396	1/1	0.96	0.12	39,39,39,39	0
57	MG	2A	3331	1/1	0.96	0.10	63,63,63,63	0
57	MG	15	104	1/1	0.96	0.13	32,32,32,32	0
57	MG	2A	3776	1/1	0.96	0.06	36,36,36,36	0
57	MG	1A	3216	1/1	0.96	0.27	37,37,37,37	0
57	MG	2A	3334	1/1	0.96	0.08	61,61,61,61	0
57	MG	1A	3581	1/1	0.96	0.07	24,24,24,24	0
57	MG	2A	3130	1/1	0.96	0.08	67,67,67,67	0
57	MG	2A	3133	1/1	0.96	0.08	43,43,43,43	0
57	MG	1A	3691	1/1	0.96	0.04	14,14,14,14	0
57	MG	2A	3137	1/1	0.96	0.12	38,38,38,38	0
57	MG	2A	3788	1/1	0.96	0.10	62,62,62,62	0
57	MG	1A	3219	1/1	0.96	0.05	28,28,28,28	0
57	MG	1A	3335	1/1	0.96	0.09	45,45,45,45	0
57	MG	1A	3939	1/1	0.96	0.06	52,52,52,52	0
57	MG	2A	3793	1/1	0.96	0.05	56,56,56,56	0
57	MG	2A	3142	1/1	0.96	0.18	40,40,40,40	0
57	MG	1A	4086	1/1	0.96	0.11	53,53,53,53	0
57	MG	1A	3221	1/1	0.96	0.08	47,47,47,47	0
57	MG	1A	3402	1/1	0.96	0.27	35,35,35,35	0
57	MG	1A	3110	1/1	0.96	0.10	38,38,38,38	0
57	MG	1A	3943	1/1	0.96	0.14	25,25,25,25	0
57	MG	2A	3151	1/1	0.96	0.09	53,53,53,53	0
57	MG	1A	3820	1/1	0.96	0.14	41,41,41,41	0
57	MG	2a	1700	1/1	0.96	0.20	64,64,64,64	0
57	MG	1A	3026	1/1	0.96	0.07	34,34,34,34	0
57	MG	1A	3823	1/1	0.96	0.09	28,28,28,28	0
57	MG	1A	3947	1/1	0.96	0.09	69,69,69,69	0
57	MG	2A	3158	1/1	0.96	0.08	42,42,42,42	0
57	MG	1B	201	1/1	0.96	0.21	52,52,52,52	0
57	MG	2A	3809	1/1	0.96	0.13	37,37,37,37	0
57	MG	1A	3824	1/1	0.96	0.11	31,31,31,31	0
57	MG	2A	3811	1/1	0.96	0.14	57,57,57,57	0
57	MG	1a	1607	1/1	0.96	0.29	66,66,66,66	0
57	MG	1a	1795	1/1	0.96	0.12	71,71,71,71	0
57	MG	2A	3163	1/1	0.96	0.06	60,60,60,60	0
57	MG	2a	1712	1/1	0.96	0.11	53,53,53,53	0
57	MG	2A	3816	1/1	0.96	0.07	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	1714	1/1	0.96	0.18	46,46,46,46	0
57	MG	1B	203	1/1	0.96	0.09	46,46,46,46	0
57	MG	1a	1610	1/1	0.96	0.09	52,52,52,52	0
57	MG	2A	3585	1/1	0.96	0.11	62,62,62,62	0
57	MG	1A	3113	1/1	0.96	0.09	43,43,43,43	0
57	MG	1B	205	1/1	0.96	0.06	51,51,51,51	0
57	MG	1A	3951	1/1	0.96	0.06	28,28,28,28	0
57	MG	2A	3825	1/1	0.96	0.15	49,49,49,49	0
57	MG	1A	3952	1/1	0.96	0.06	31,31,31,31	0
57	MG	1A	3591	1/1	0.96	0.05	31,31,31,31	0
57	MG	1a	1616	1/1	0.96	0.05	41,41,41,41	0
57	MG	1A	3703	1/1	0.96	0.05	42,42,42,42	0
57	MG	2A	3594	1/1	0.96	0.06	34,34,34,34	0
57	MG	2A	3595	1/1	0.96	0.06	54,54,54,54	0
57	MG	2A	3596	1/1	0.96	0.16	58,58,58,58	0
57	MG	2A	3597	1/1	0.96	0.09	44,44,44,44	0
57	MG	1A	3116	1/1	0.96	0.14	41,41,41,41	0
57	MG	1A	3287	1/1	0.96	0.09	53,53,53,53	0
57	MG	1A	3958	1/1	0.96	0.07	39,39,39,39	0
57	MG	1A	3483	1/1	0.96	0.13	35,35,35,35	0
57	MG	1A	3117	1/1	0.96	0.05	38,38,38,38	0
57	MG	2A	3179	1/1	0.96	0.07	47,47,47,47	0
57	MG	1A	3290	1/1	0.96	0.14	37,37,37,37	0
57	MG	1A	3412	1/1	0.96	0.08	54,54,54,54	0
57	MG	1a	1813	1/1	0.96	0.12	57,57,57,57	0
57	MG	1B	218	1/1	0.96	0.19	47,47,47,47	0
57	MG	2a	1741	1/1	0.96	0.21	57,57,57,57	0
57	MG	1A	3008	1/1	0.96	0.05	28,28,28,28	0
57	MG	1A	3489	1/1	0.96	0.07	22,22,22,22	0
57	MG	1A	3602	1/1	0.96	0.08	44,44,44,44	0
57	MG	1e	202	1/1	0.96	0.13	53,53,53,53	0
57	MG	2a	1748	1/1	0.96	0.09	70,70,70,70	0
57	MG	1A	3838	1/1	0.96	0.09	24,24,24,24	0
57	MG	1A	3603	1/1	0.96	0.12	53,53,53,53	0
57	MG	1A	3490	1/1	0.96	0.12	50,50,50,50	0
57	MG	1B	226	1/1	0.96	0.09	46,46,46,46	0
57	MG	1A	3605	1/1	0.96	0.05	30,30,30,30	0
57	MG	1A	3723	1/1	0.96	0.05	40,40,40,40	0
57	MG	1A	3169	1/1	0.96	0.16	41,41,41,41	0
57	MG	1A	3073	1/1	0.96	0.10	38,38,38,38	0
57	MG	1A	3493	1/1	0.96	0.09	48,48,48,48	0
57	MG	1t	201	1/1	0.96	0.10	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	3237	1/1	0.96	0.17	43,43,43,43	0
57	MG	1A	3031	1/1	0.96	0.32	31,31,31,31	0
57	MG	1A	3733	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3611	1/1	0.96	0.09	43,43,43,43	0
57	MG	1A	3033	1/1	0.96	0.08	39,39,39,39	0
57	MG	1D	311	1/1	0.96	0.17	28,28,28,28	0
57	MG	1A	3500	1/1	0.96	0.08	49,49,49,49	0
57	MG	1D	313	1/1	0.96	0.11	38,38,38,38	0
57	MG	1D	314	1/1	0.96	0.19	37,37,37,37	0
57	MG	1A	3503	1/1	0.96	0.11	38,38,38,38	0
57	MG	1E	307	1/1	0.96	0.17	29,29,29,29	0
57	MG	1A	3504	1/1	0.96	0.21	38,38,38,38	0
57	MG	2D	302	1/1	0.96	0.08	51,51,51,51	0
57	MG	2A	3407	1/1	0.96	0.20	50,50,50,50	0
57	MG	2D	305	1/1	0.96	0.26	45,45,45,45	0
57	MG	1A	3421	1/1	0.96	0.12	38,38,38,38	0
57	MG	1A	3619	1/1	0.96	0.06	27,27,27,27	0
57	MG	1A	3184	1/1	0.96	0.07	33,33,33,33	0
57	MG	1E	314	1/1	0.96	0.11	40,40,40,40	0
57	MG	1A	3990	1/1	0.96	0.07	44,44,44,44	0
57	MG	1a	1661	1/1	0.96	0.38	69,69,69,69	0
57	MG	1A	3127	1/1	0.96	0.08	52,52,52,52	0
57	MG	1a	1663	1/1	0.96	0.11	55,55,55,55	0
57	MG	1A	3625	1/1	0.96	0.10	50,50,50,50	0
57	MG	1A	3626	1/1	0.96	0.09	61,61,61,61	0
57	MG	1F	306	1/1	0.96	0.07	34,34,34,34	0
57	MG	2A	3229	1/1	0.96	0.08	53,53,53,53	0
57	MG	1A	3299	1/1	0.96	0.09	44,44,44,44	0
57	MG	1A	3242	1/1	0.96	0.10	39,39,39,39	0
57	MG	1A	3751	1/1	0.96	0.07	50,50,50,50	0
57	MG	1A	3128	1/1	0.96	0.06	39,39,39,39	0
57	MG	2F	3304	1/1	0.96	0.13	42,42,42,42	0
57	MG	1G	201	1/1	0.96	0.15	38,38,38,38	0
57	MG	1A	3515	1/1	0.96	0.08	40,40,40,40	0
57	MG	1A	4002	1/1	0.96	0.05	39,39,39,39	0
57	MG	1A	4003	1/1	0.96	0.05	20,20,20,20	0
57	MG	1a	1675	1/1	0.96	0.16	37,37,37,37	0
57	MG	2Q	201	1/1	0.96	0.13	58,58,58,58	0
57	MG	1A	3633	1/1	0.96	0.06	30,30,30,30	0
57	MG	1A	3871	1/1	0.96	0.08	44,44,44,44	0
57	MG	1A	3872	1/1	0.96	0.09	40,40,40,40	0
57	MG	1A	3079	1/1	0.96	0.10	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1N	204	1/1	0.96	0.22	55,55,55,55	0
57	MG	1A	3246	1/1	0.96	0.12	38,38,38,38	0
57	MG	2A	3025	1/1	0.96	0.15	44,44,44,44	0
57	MG	1A	3052	1/1	0.96	0.06	37,37,37,37	0
57	MG	2A	3444	1/1	0.96	0.07	46,46,46,46	0
57	MG	2A	3673	1/1	0.96	0.10	56,56,56,56	0
57	MG	2Y	201	1/1	0.96	0.20	60,60,60,60	0
57	MG	2Z	301	1/1	0.96	0.13	67,67,67,67	0
57	MG	1A	3368	1/1	0.96	0.11	56,56,56,56	0
57	MG	1A	3189	1/1	0.96	0.09	41,41,41,41	0
57	MG	1A	3526	1/1	0.96	0.10	37,37,37,37	0
57	MG	2f	201	1/1	0.96	0.09	39,39,39,39	0
57	MG	1A	3527	1/1	0.96	0.18	50,50,50,50	0
57	MG	2A	3035	1/1	0.96	0.11	56,56,56,56	0
57	MG	1A	3528	1/1	0.96	0.19	47,47,47,47	0
57	MG	23	103	1/1	0.96	0.10	49,49,49,49	0
57	MG	2l	202	1/1	0.96	0.10	65,65,65,65	0
57	MG	1A	3037	1/1	0.96	0.06	31,31,31,31	0
57	MG	1A	3251	1/1	0.96	0.07	43,43,43,43	0
57	MG	1Q	202	1/1	0.96	0.21	44,44,44,44	0
57	MG	1A	4022	1/1	0.96	0.06	36,36,36,36	0
57	MG	1A	3532	1/1	0.96	0.14	39,39,39,39	0
57	MG	1A	3435	1/1	0.96	0.09	52,52,52,52	0
57	MG	2A	3045	1/1	0.96	0.13	56,56,56,56	0
57	MG	1A	3436	1/1	0.96	0.18	43,43,43,43	0
57	MG	2A	3691	1/1	0.96	0.08	42,42,42,42	0
57	MG	2A	3461	1/1	0.96	0.09	51,51,51,51	0
57	MG	1S	3602	1/1	0.96	0.08	51,51,51,51	0
57	MG	1A	3893	1/1	0.96	0.07	62,62,62,62	0
57	MG	1A	3772	1/1	0.96	0.07	43,43,43,43	0
57	MG	1A	3895	1/1	0.96	0.12	43,43,43,43	0
57	MG	2A	3053	1/1	0.96	0.16	60,60,60,60	0
57	MG	1T	203	1/1	0.96	0.16	63,63,63,63	0
57	MG	1a	1704	1/1	0.96	0.24	58,58,58,58	0
57	MG	1A	3252	1/1	0.96	0.10	42,42,42,42	0
57	MG	2A	3472	1/1	0.96	0.11	60,60,60,60	0
57	MG	1A	3374	1/1	0.96	0.19	51,51,51,51	0
57	MG	1A	3055	1/1	0.96	0.15	48,48,48,48	0
57	MG	1A	3899	1/1	0.96	0.05	46,46,46,46	0
57	MG	1U	206	1/1	0.96	0.35	39,39,39,39	0
57	MG	1A	3540	1/1	0.96	0.29	44,44,44,44	0
57	MG	2A	3063	1/1	0.96	0.07	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	3056	1/1	0.96	0.09	35,35,35,35	0
57	MG	1V	202	1/1	0.96	0.21	41,41,41,41	0
57	MG	1A	4036	1/1	0.96	0.33	41,41,41,41	0
58	K	1A	3508	1/1	0.96	0.06	36,36,36,36	0
57	MG	1A	4037	1/1	0.96	0.06	42,42,42,42	0
57	MG	1A	3441	1/1	0.96	0.06	52,52,52,52	0
57	MG	1A	3145	1/1	0.96	0.20	56,56,56,56	0
57	MG	2A	3071	1/1	0.96	0.08	49,49,49,49	0
57	MG	1A	3084	1/1	0.96	0.05	28,28,28,28	0
62	PHE	2w	108	11/12	0.96	0.12	35,38,45,45	0
63	FME	2x	108	10/11	0.96	0.11	34,43,46,53	0
57	MG	1A	3883	1/1	0.97	0.04	53,53,53,53	0
57	MG	1A	4012	1/1	0.97	0.06	15,15,15,15	0
57	MG	1A	3208	1/1	0.97	0.19	27,27,27,27	0
57	MG	2A	3225	1/1	0.97	0.08	44,44,44,44	0
57	MG	1A	3459	1/1	0.97	0.09	41,41,41,41	0
57	MG	1A	4015	1/1	0.97	0.11	44,44,44,44	0
57	MG	1A	3550	1/1	0.97	0.06	30,30,30,30	0
57	MG	1A	4017	1/1	0.97	0.07	39,39,39,39	0
57	MG	1A	3108	1/1	0.97	0.17	35,35,35,35	0
57	MG	1A	3109	1/1	0.97	0.16	36,36,36,36	0
57	MG	1A	3767	1/1	0.97	0.08	30,30,30,30	0
57	MG	2A	3012	1/1	0.97	0.06	35,35,35,35	0
57	MG	2A	3014	1/1	0.97	0.14	39,39,39,39	0
57	MG	1A	3462	1/1	0.97	0.08	47,47,47,47	0
57	MG	2A	3454	1/1	0.97	0.11	36,36,36,36	0
57	MG	1A	3891	1/1	0.97	0.05	45,45,45,45	0
57	MG	1A	3769	1/1	0.97	0.04	30,30,30,30	0
57	MG	2A	3019	1/1	0.97	0.18	59,59,59,59	0
57	MG	1A	3014	1/1	0.97	0.10	38,38,38,38	0
57	MG	1A	3111	1/1	0.97	0.18	33,33,33,33	0
57	MG	1A	3466	1/1	0.97	0.14	33,33,33,33	0
57	MG	2A	3707	1/1	0.97	0.17	43,43,43,43	0
57	MG	1A	4027	1/1	0.97	0.07	36,36,36,36	0
57	MG	2A	3026	1/1	0.97	0.05	39,39,39,39	0
57	MG	1A	3022	1/1	0.97	0.15	34,34,34,34	0
57	MG	1A	3468	1/1	0.97	0.24	36,36,36,36	0
57	MG	2A	3029	1/1	0.97	0.08	42,42,42,42	0
57	MG	1A	3159	1/1	0.97	0.08	22,22,22,22	0
57	MG	1A	3661	1/1	0.97	0.04	13,13,13,13	0
57	MG	2A	3032	1/1	0.97	0.11	43,43,43,43	0
57	MG	2A	3033	1/1	0.97	0.07	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	1P	206	1/1	0.97	0.10	41,41,41,41	0
57	MG	1Q	201	1/1	0.97	0.19	35,35,35,35	0
57	MG	1A	3561	1/1	0.97	0.08	24,24,24,24	0
57	MG	2A	3037	1/1	0.97	0.07	24,24,24,24	0
57	MG	1A	3663	1/1	0.97	0.08	34,34,34,34	0
57	MG	1Q	206	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3218	1/1	0.97	0.08	27,27,27,27	0
57	MG	1A	3039	1/1	0.97	0.17	32,32,32,32	0
57	MG	1R	201	1/1	0.97	0.14	37,37,37,37	0
57	MG	1R	203	1/1	0.97	0.06	33,33,33,33	0
57	MG	2A	3482	1/1	0.97	0.12	38,38,38,38	0
57	MG	1A	3565	1/1	0.97	0.07	35,35,35,35	0
57	MG	1A	3114	1/1	0.97	0.14	60,60,60,60	0
57	MG	1a	1694	1/1	0.97	0.12	47,47,47,47	0
57	MG	2A	3487	1/1	0.97	0.07	41,41,41,41	0
57	MG	1A	3567	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3028	1/1	0.97	0.15	35,35,35,35	0
57	MG	2A	3734	1/1	0.97	0.06	49,49,49,49	0
57	MG	1A	3006	1/1	0.97	0.07	34,34,34,34	0
57	MG	1a	1700	1/1	0.97	0.14	59,59,59,59	0
57	MG	2A	3737	1/1	0.97	0.10	49,49,49,49	0
57	MG	1A	3786	1/1	0.97	0.05	40,40,40,40	0
57	MG	2A	3739	1/1	0.97	0.04	51,51,51,51	0
57	MG	2A	3269	1/1	0.97	0.16	55,55,55,55	0
57	MG	2A	3494	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3570	1/1	0.97	0.10	56,56,56,56	0
57	MG	2a	1663	1/1	0.97	0.13	45,45,45,45	0
57	MG	1U	202	1/1	0.97	0.11	41,41,41,41	0
57	MG	2a	1665	1/1	0.97	0.09	49,49,49,49	0
57	MG	1A	3072	1/1	0.97	0.12	42,42,42,42	0
57	MG	1A	3675	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3225	1/1	0.97	0.17	47,47,47,47	0
57	MG	1a	1707	1/1	0.97	0.11	51,51,51,51	0
57	MG	2A	3061	1/1	0.97	0.11	43,43,43,43	0
57	MG	1a	1708	1/1	0.97	0.07	58,58,58,58	0
57	MG	1A	3479	1/1	0.97	0.05	49,49,49,49	0
57	MG	1a	1710	1/1	0.97	0.05	36,36,36,36	0
57	MG	2A	3752	1/1	0.97	0.11	72,72,72,72	0
57	MG	1A	4049	1/1	0.97	0.05	35,35,35,35	0
57	MG	1a	1713	1/1	0.97	0.10	51,51,51,51	0
57	MG	1A	3121	1/1	0.97	0.29	31,31,31,31	0
57	MG	1A	3577	1/1	0.97	0.06	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3167	1/1	0.97	0.15	41,41,41,41	0
57	MG	1V	205	1/1	0.97	0.11	31,31,31,31	0
57	MG	2A	3072	1/1	0.97	0.06	50,50,50,50	0
57	MG	1A	4054	1/1	0.97	0.06	61,61,61,61	0
57	MG	2A	3514	1/1	0.97	0.08	34,34,34,34	0
57	MG	1a	1719	1/1	0.97	0.07	46,46,46,46	0
57	MG	1A	3795	1/1	0.97	0.12	44,44,44,44	0
57	MG	1A	3482	1/1	0.97	0.10	39,39,39,39	0
57	MG	2A	3077	1/1	0.97	0.08	43,43,43,43	0
57	MG	1A	3351	1/1	0.97	0.06	47,47,47,47	0
57	MG	1A	3484	1/1	0.97	0.18	44,44,44,44	0
57	MG	2A	3524	1/1	0.97	0.07	33,33,33,33	0
57	MG	1A	3414	1/1	0.97	0.28	56,56,56,56	0
57	MG	1A	3289	1/1	0.97	0.09	41,41,41,41	0
57	MG	1X	104	1/1	0.97	0.10	41,41,41,41	0
57	MG	1A	3032	1/1	0.97	0.06	48,48,48,48	0
57	MG	2A	3084	1/1	0.97	0.06	46,46,46,46	0
57	MG	2A	3530	1/1	0.97	0.07	38,38,38,38	0
57	MG	2A	3531	1/1	0.97	0.07	41,41,41,41	0
57	MG	1A	3088	1/1	0.97	0.06	31,31,31,31	0
57	MG	2A	3086	1/1	0.97	0.06	56,56,56,56	0
57	MG	2A	3087	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3587	1/1	0.97	0.05	14,14,14,14	0
57	MG	2A	3303	1/1	0.97	0.25	66,66,66,66	0
57	MG	2A	3786	1/1	0.97	0.06	60,60,60,60	0
57	MG	1A	3804	1/1	0.97	0.25	41,41,41,41	0
57	MG	1Y	202	1/1	0.97	0.13	47,47,47,47	0
57	MG	1A	3357	1/1	0.97	0.09	46,46,46,46	0
57	MG	1A	3234	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3931	1/1	0.97	0.09	26,26,26,26	0
57	MG	2A	3792	1/1	0.97	0.06	37,37,37,37	0
57	MG	1A	3693	1/1	0.97	0.10	62,62,62,62	0
57	MG	1A	4070	1/1	0.97	0.07	61,61,61,61	0
57	MG	2A	3097	1/1	0.97	0.12	61,61,61,61	0
57	MG	1A	3809	1/1	0.97	0.09	46,46,46,46	0
57	MG	2A	3546	1/1	0.97	0.08	26,26,26,26	0
57	MG	1A	3935	1/1	0.97	0.10	47,47,47,47	0
57	MG	1A	4074	1/1	0.97	0.06	49,49,49,49	0
57	MG	1A	4075	1/1	0.97	0.06	39,39,39,39	0
57	MG	2A	3316	1/1	0.97	0.11	56,56,56,56	0
57	MG	1A	3420	1/1	0.97	0.20	42,42,42,42	0
57	MG	1A	3170	1/1	0.97	0.12	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	3236	1/1	0.97	0.06	35,35,35,35	0
57	MG	1A	3174	1/1	0.97	0.14	29,29,29,29	0
57	MG	2A	3107	1/1	0.97	0.13	50,50,50,50	0
57	MG	11	101	1/1	0.97	0.34	42,42,42,42	0
57	MG	1A	4080	1/1	0.97	0.19	48,48,48,48	0
57	MG	2a	1726	1/1	0.97	0.09	76,76,76,76	0
57	MG	2A	3561	1/1	0.97	0.07	53,53,53,53	0
57	MG	1A	3698	1/1	0.97	0.06	41,41,41,41	0
57	MG	1A	3175	1/1	0.97	0.15	34,34,34,34	0
57	MG	1A	3596	1/1	0.97	0.06	46,46,46,46	0
57	MG	1a	1754	1/1	0.97	0.07	58,58,58,58	0
57	MG	2A	3817	1/1	0.97	0.13	56,56,56,56	0
57	MG	1A	3124	1/1	0.97	0.11	32,32,32,32	0
57	MG	1A	4085	1/1	0.97	0.06	50,50,50,50	0
57	MG	1A	3598	1/1	0.97	0.08	41,41,41,41	0
57	MG	13	101	1/1	0.97	0.08	34,34,34,34	0
57	MG	2A	3118	1/1	0.97	0.11	34,34,34,34	0
57	MG	1A	3497	1/1	0.97	0.10	57,57,57,57	0
57	MG	2A	3824	1/1	0.97	0.07	53,53,53,53	0
57	MG	1A	3091	1/1	0.97	0.07	35,35,35,35	0
57	MG	1A	3181	1/1	0.97	0.11	29,29,29,29	0
57	MG	2a	1743	1/1	0.97	0.10	60,60,60,60	0
57	MG	1A	3093	1/1	0.97	0.14	37,37,37,37	0
57	MG	2A	3575	1/1	0.97	0.09	55,55,55,55	0
57	MG	1a	1767	1/1	0.97	0.05	63,63,63,63	0
57	MG	1A	3709	1/1	0.97	0.06	46,46,46,46	0
57	MG	1a	1769	1/1	0.97	0.07	53,53,53,53	0
57	MG	15	103	1/1	0.97	0.18	31,31,31,31	0
57	MG	1A	3950	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3710	1/1	0.97	0.04	30,30,30,30	0
57	MG	2A	3582	1/1	0.97	0.09	40,40,40,40	0
57	MG	1A	3505	1/1	0.97	0.14	34,34,34,34	0
57	MG	2A	3131	1/1	0.97	0.13	48,48,48,48	0
57	MG	2A	3838	1/1	0.97	0.10	51,51,51,51	0
57	MG	1A	3074	1/1	0.97	0.14	33,33,33,33	0
57	MG	1A	3045	1/1	0.97	0.04	21,21,21,21	0
57	MG	2A	3135	1/1	0.97	0.18	38,38,38,38	0
57	MG	2A	3842	1/1	0.97	0.06	45,45,45,45	0
57	MG	2A	3843	1/1	0.97	0.06	56,56,56,56	0
57	MG	17	101	1/1	0.97	0.05	30,30,30,30	0
57	MG	2A	3845	1/1	0.97	0.06	61,61,61,61	0
57	MG	1A	3133	1/1	0.97	0.21	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	2A	3139	1/1	0.97	0.11	47,47,47,47	0
57	MG	1a	1780	1/1	0.97	0.06	66,66,66,66	0
57	MG	17	104	1/1	0.97	0.07	34,34,34,34	0
57	MG	17	105	1/1	0.97	0.17	54,54,54,54	0
57	MG	1A	3715	1/1	0.97	0.07	30,30,30,30	0
57	MG	17	107	1/1	0.97	0.14	29,29,29,29	0
57	MG	1a	1785	1/1	0.97	0.04	52,52,52,52	0
57	MG	2A	3147	1/1	0.97	0.07	54,54,54,54	0
57	MG	2A	3148	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3370	1/1	0.97	0.10	40,40,40,40	0
57	MG	18	102	1/1	0.97	0.20	44,44,44,44	0
57	MG	1A	3135	1/1	0.97	0.12	45,45,45,45	0
57	MG	1A	3834	1/1	0.97	0.10	45,45,45,45	0
57	MG	1A	3434	1/1	0.97	0.07	35,35,35,35	0
57	MG	1B	209	1/1	0.97	0.14	49,49,49,49	0
57	MG	2A	3155	1/1	0.97	0.18	46,46,46,46	0
57	MG	1A	3100	1/1	0.97	0.29	38,38,38,38	0
57	MG	2A	3157	1/1	0.97	0.10	47,47,47,47	0
57	MG	1A	3720	1/1	0.97	0.04	33,33,33,33	0
57	MG	1A	3722	1/1	0.97	0.06	67,67,67,67	0
57	MG	2A	3613	1/1	0.97	0.14	47,47,47,47	0
57	MG	1A	3516	1/1	0.97	0.12	33,33,33,33	0
57	MG	1A	3724	1/1	0.97	0.05	28,28,28,28	0
57	MG	1A	3076	1/1	0.97	0.14	34,34,34,34	0
57	MG	1A	3250	1/1	0.97	0.11	38,38,38,38	0
57	MG	2a	1790	1/1	0.97	0.27	56,56,56,56	0
57	MG	1a	1608	1/1	0.97	0.07	45,45,45,45	0
57	MG	1A	3728	1/1	0.97	0.09	57,57,57,57	0
57	MG	1A	3614	1/1	0.97	0.05	27,27,27,27	0
57	MG	1A	3520	1/1	0.97	0.17	32,32,32,32	0
57	MG	1A	3521	1/1	0.97	0.13	40,40,40,40	0
57	MG	1A	3139	1/1	0.97	0.20	37,37,37,37	0
57	MG	2A	3170	1/1	0.97	0.08	33,33,33,33	0
57	MG	1A	3102	1/1	0.97	0.16	32,32,32,32	0
57	MG	1A	3258	1/1	0.97	0.20	33,33,33,33	0
57	MG	1A	3259	1/1	0.97	0.09	42,42,42,42	0
57	MG	2A	3628	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3623	1/1	0.97	0.04	20,20,20,20	0
57	MG	1A	3315	1/1	0.97	0.12	38,38,38,38	0
57	MG	1A	3855	1/1	0.97	0.07	42,42,42,42	0
57	MG	1A	3739	1/1	0.97	0.08	51,51,51,51	0
57	MG	2A	3634	1/1	0.97	0.21	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3380	1/1	0.97	0.11	38,38,38,38	0
57	MG	1B	231	1/1	0.97	0.09	57,57,57,57	0
57	MG	1A	3141	1/1	0.97	0.09	27,27,27,27	0
57	MG	2A	3638	1/1	0.97	0.24	35,35,35,35	0
57	MG	2A	3181	1/1	0.97	0.06	54,54,54,54	0
57	MG	1A	3261	1/1	0.97	0.10	30,30,30,30	0
57	MG	1A	3194	1/1	0.97	0.09	51,51,51,51	0
57	MG	1A	3989	1/1	0.97	0.05	39,39,39,39	0
57	MG	1a	1628	1/1	0.97	0.16	59,59,59,59	0
57	MG	1A	3533	1/1	0.97	0.13	54,54,54,54	0
57	MG	2A	3398	1/1	0.97	0.10	55,55,55,55	0
57	MG	1D	303	1/1	0.97	0.15	42,42,42,42	0
57	MG	1D	304	1/1	0.97	0.12	39,39,39,39	0
57	MG	1D	306	1/1	0.97	0.11	38,38,38,38	0
57	MG	1D	309	1/1	0.97	0.08	45,45,45,45	0
57	MG	1A	3384	1/1	0.97	0.09	46,46,46,46	0
57	MG	1A	3993	1/1	0.97	0.07	26,26,26,26	0
57	MG	1A	3142	1/1	0.97	0.09	27,27,27,27	0
57	MG	1A	3103	1/1	0.97	0.07	37,37,37,37	0
57	MG	2V	201	1/1	0.97	0.18	44,44,44,44	0
57	MG	1A	3749	1/1	0.97	0.05	21,21,21,21	0
57	MG	1A	3750	1/1	0.97	0.06	19,19,19,19	0
57	MG	1E	303	1/1	0.97	0.16	47,47,47,47	0
57	MG	2A	3199	1/1	0.97	0.06	56,56,56,56	0
57	MG	1a	1644	1/1	0.97	0.15	47,47,47,47	0
57	MG	1E	304	1/1	0.97	0.12	45,45,45,45	0
57	MG	2A	3202	1/1	0.97	0.13	51,51,51,51	0
57	MG	1A	3018	1/1	0.97	0.09	22,22,22,22	0
57	MG	1A	3451	1/1	0.97	0.10	34,34,34,34	0
57	MG	1A	4000	1/1	0.97	0.09	48,48,48,48	0
57	MG	1A	3452	1/1	0.97	0.15	33,33,33,33	0
57	MG	2A	3418	1/1	0.97	0.13	37,37,37,37	0
57	MG	1E	312	1/1	0.97	0.10	28,28,28,28	0
57	MG	2x	104	1/1	0.97	0.08	53,53,53,53	0
57	MG	1A	3201	1/1	0.97	0.05	44,44,44,44	0
57	MG	1A	3543	1/1	0.97	0.07	28,28,28,28	0
57	MG	1A	3078	1/1	0.97	0.09	41,41,41,41	0
57	MG	1A	3147	1/1	0.97	0.08	41,41,41,41	0
57	MG	1F	301	1/1	0.97	0.14	39,39,39,39	0
57	MG	27	101	1/1	0.97	0.18	60,60,60,60	0
57	MG	1A	3047	1/1	0.97	0.11	29,29,29,29	0
57	MG	2A	3429	1/1	0.97	0.17	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	3107	1/1	0.97	0.18	37,37,37,37	0
57	MG	2A	3215	1/1	0.97	0.43	40,40,40,40	0
57	MG	1A	4009	1/1	0.97	0.07	32,32,32,32	0
57	MG	1F	307	1/1	0.97	0.06	36,36,36,36	0
57	MG	2A	3218	1/1	0.97	0.15	45,45,45,45	0
60	ZN	2Y	202	1/1	0.97	0.05	90,90,90,90	0
57	MG	1F	308	1/1	0.97	0.12	27,27,27,27	0
60	ZN	2n	501	1/1	0.97	0.05	81,81,81,81	0
62	PHE	1w	109	11/12	0.97	0.08	19,25,28,30	0
57	MG	1A	3882	1/1	0.97	0.08	37,37,37,37	0
63	FME	1x	115	10/11	0.97	0.12	21,25,29,39	10
57	MG	2A	3438	1/1	0.97	0.09	47,47,47,47	0
57	MG	1A	3536	1/1	0.98	0.12	29,29,29,29	0
57	MG	1A	3339	1/1	0.98	0.08	42,42,42,42	0
57	MG	1A	3463	1/1	0.98	0.13	46,46,46,46	0
57	MG	2A	3468	1/1	0.98	0.05	62,62,62,62	0
57	MG	1A	3285	1/1	0.98	0.15	34,34,34,34	0
57	MG	1A	3020	1/1	0.98	0.06	17,17,17,17	0
57	MG	1A	3115	1/1	0.98	0.06	50,50,50,50	0
57	MG	1A	3618	1/1	0.98	0.09	25,25,25,25	0
57	MG	1A	3542	1/1	0.98	0.12	32,32,32,32	0
57	MG	1B	219	1/1	0.98	0.05	36,36,36,36	0
57	MG	1A	3405	1/1	0.98	0.13	37,37,37,37	0
57	MG	1A	3344	1/1	0.98	0.13	35,35,35,35	0
57	MG	1A	3622	1/1	0.98	0.04	28,28,28,28	0
57	MG	1A	4008	1/1	0.98	0.06	12,12,12,12	0
57	MG	1a	1699	1/1	0.98	0.05	29,29,29,29	0
57	MG	1A	3095	1/1	0.98	0.27	29,29,29,29	0
57	MG	10	106	1/1	0.98	0.08	44,44,44,44	0
57	MG	1A	3471	1/1	0.98	0.08	36,36,36,36	0
57	MG	2A	3483	1/1	0.98	0.08	43,43,43,43	0
57	MG	2A	3658	1/1	0.98	0.05	61,61,61,61	0
57	MG	1A	3408	1/1	0.98	0.08	40,40,40,40	0
57	MG	1A	3347	1/1	0.98	0.10	34,34,34,34	0
57	MG	1A	3807	1/1	0.98	0.05	44,44,44,44	0
57	MG	1A	3096	1/1	0.98	0.05	36,36,36,36	0
57	MG	1A	3629	1/1	0.98	0.08	22,22,22,22	0
57	MG	1A	3349	1/1	0.98	0.21	36,36,36,36	0
57	MG	2A	3008	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3118	1/1	0.98	0.05	32,32,32,32	0
57	MG	1B	233	1/1	0.98	0.07	61,61,61,61	0
57	MG	2A	3011	1/1	0.98	0.04	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3721	1/1	0.98	0.09	40,40,40,40	0
57	MG	1a	1712	1/1	0.98	0.09	44,44,44,44	0
57	MG	1A	3097	1/1	0.98	0.12	33,33,33,33	0
57	MG	1A	3634	1/1	0.98	0.09	30,30,30,30	0
57	MG	1D	301	1/1	0.98	0.10	32,32,32,32	0
57	MG	2A	3018	1/1	0.98	0.10	39,39,39,39	0
57	MG	1A	3553	1/1	0.98	0.04	39,39,39,39	0
57	MG	2A	3020	1/1	0.98	0.05	23,23,23,23	0
57	MG	2A	3021	1/1	0.98	0.16	45,45,45,45	0
57	MG	1A	3725	1/1	0.98	0.05	22,22,22,22	0
57	MG	1A	3120	1/1	0.98	0.14	28,28,28,28	0
57	MG	2A	3505	1/1	0.98	0.04	43,43,43,43	0
57	MG	2A	3682	1/1	0.98	0.05	49,49,49,49	0
57	MG	1D	305	1/1	0.98	0.09	21,21,21,21	0
57	MG	1A	3063	1/1	0.98	0.18	30,30,30,30	0
57	MG	15	101	1/1	0.98	0.08	42,42,42,42	0
57	MG	1D	307	1/1	0.98	0.07	31,31,31,31	0
57	MG	1A	3819	1/1	0.98	0.09	34,34,34,34	0
57	MG	2A	3688	1/1	0.98	0.04	34,34,34,34	0
57	MG	1A	3354	1/1	0.98	0.06	31,31,31,31	0
57	MG	2D	301	1/1	0.98	0.09	37,37,37,37	0
57	MG	1A	3821	1/1	0.98	0.20	34,34,34,34	0
57	MG	1A	3099	1/1	0.98	0.04	32,32,32,32	0
57	MG	2D	304	1/1	0.98	0.27	45,45,45,45	0
57	MG	1A	3064	1/1	0.98	0.04	15,15,15,15	0
57	MG	1A	3731	1/1	0.98	0.04	40,40,40,40	0
57	MG	2A	3516	1/1	0.98	0.11	32,32,32,32	0
57	MG	2A	3517	1/1	0.98	0.07	35,35,35,35	0
57	MG	1A	3243	1/1	0.98	0.07	39,39,39,39	0
57	MG	1A	3195	1/1	0.98	0.11	37,37,37,37	0
57	MG	2A	3194	1/1	0.98	0.12	45,45,45,45	0
57	MG	1A	3196	1/1	0.98	0.04	34,34,34,34	0
57	MG	2E	305	1/1	0.98	0.05	44,44,44,44	0
57	MG	1a	1734	1/1	0.98	0.12	51,51,51,51	0
57	MG	2A	3523	1/1	0.98	0.06	50,50,50,50	0
57	MG	1E	305	1/1	0.98	0.07	34,34,34,34	0
57	MG	1E	306	1/1	0.98	0.10	27,27,27,27	0
57	MG	2A	3040	1/1	0.98	0.13	57,57,57,57	0
57	MG	1A	3016	1/1	0.98	0.10	28,28,28,28	0
57	MG	1A	3198	1/1	0.98	0.14	37,37,37,37	0
57	MG	1E	309	1/1	0.98	0.09	28,28,28,28	0
57	MG	1A	3564	1/1	0.98	0.07	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3932	1/1	0.98	0.06	29,29,29,29	0
57	MG	2F	3305	1/1	0.98	0.19	43,43,43,43	0
57	MG	1A	3647	1/1	0.98	0.09	32,32,32,32	0
57	MG	1A	3156	1/1	0.98	0.15	35,35,35,35	0
57	MG	2A	3048	1/1	0.98	0.09	23,23,23,23	0
57	MG	2A	3049	1/1	0.98	0.11	41,41,41,41	0
57	MG	1A	3158	1/1	0.98	0.11	32,32,32,32	0
57	MG	1A	3741	1/1	0.98	0.06	27,27,27,27	0
57	MG	1A	3066	1/1	0.98	0.24	45,45,45,45	0
57	MG	1A	3202	1/1	0.98	0.18	39,39,39,39	0
57	MG	1A	4044	1/1	0.98	0.20	39,39,39,39	0
57	MG	1A	3653	1/1	0.98	0.04	33,33,33,33	0
57	MG	1F	305	1/1	0.98	0.13	34,34,34,34	0
57	MG	1A	3067	1/1	0.98	0.12	37,37,37,37	0
57	MG	1A	4047	1/1	0.98	0.16	26,26,26,26	0
57	MG	1A	3253	1/1	0.98	0.13	23,23,23,23	0
57	MG	1a	1755	1/1	0.98	0.07	47,47,47,47	0
57	MG	1F	309	1/1	0.98	0.12	31,31,31,31	0
57	MG	1A	3068	1/1	0.98	0.05	30,30,30,30	0
57	MG	2A	3222	1/1	0.98	0.20	37,37,37,37	0
57	MG	1F	311	1/1	0.98	0.05	54,54,54,54	0
57	MG	1A	3572	1/1	0.98	0.07	23,23,23,23	0
57	MG	2A	3552	1/1	0.98	0.07	40,40,40,40	0
57	MG	1A	3308	1/1	0.98	0.20	33,33,33,33	0
57	MG	1A	3309	1/1	0.98	0.16	32,32,32,32	0
57	MG	1a	1617	1/1	0.98	0.08	53,53,53,53	0
57	MG	1A	3310	1/1	0.98	0.15	36,36,36,36	0
57	MG	23	102	1/1	0.98	0.07	47,47,47,47	0
57	MG	2a	1774	1/1	0.98	0.06	52,52,52,52	0
57	MG	1A	3498	1/1	0.98	0.14	36,36,36,36	0
57	MG	2A	3558	1/1	0.98	0.08	33,33,33,33	0
57	MG	1A	3129	1/1	0.98	0.12	25,25,25,25	0
57	MG	1A	3130	1/1	0.98	0.21	35,35,35,35	0
57	MG	1A	3580	1/1	0.98	0.07	27,27,27,27	0
57	MG	1A	3849	1/1	0.98	0.04	35,35,35,35	0
57	MG	1A	3011	1/1	0.98	0.04	25,25,25,25	0
57	MG	1a	1774	1/1	0.98	0.05	58,58,58,58	0
57	MG	1A	3209	1/1	0.98	0.12	29,29,29,29	0
57	MG	1N	203	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3954	1/1	0.98	0.06	26,26,26,26	0
57	MG	2A	3396	1/1	0.98	0.27	54,54,54,54	0
57	MG	1A	3132	1/1	0.98	0.15	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	3668	1/1	0.98	0.10	28,28,28,28	0
57	MG	1A	4065	1/1	0.98	0.07	46,46,46,46	0
57	MG	1A	3854	1/1	0.98	0.08	45,45,45,45	0
57	MG	1A	3211	1/1	0.98	0.13	44,44,44,44	0
57	MG	1A	3044	1/1	0.98	0.09	32,32,32,32	0
57	MG	1A	3763	1/1	0.98	0.17	25,25,25,25	0
57	MG	1a	1636	1/1	0.98	0.14	55,55,55,55	0
57	MG	1A	3858	1/1	0.98	0.06	31,31,31,31	0
57	MG	1A	4071	1/1	0.98	0.04	49,49,49,49	0
57	MG	1P	202	1/1	0.98	0.18	30,30,30,30	0
57	MG	1P	203	1/1	0.98	0.12	33,33,33,33	0
57	MG	2A	3092	1/1	0.98	0.13	37,37,37,37	0
57	MG	1P	205	1/1	0.98	0.09	58,58,58,58	0
57	MG	1A	3511	1/1	0.98	0.06	24,24,24,24	0
57	MG	1a	1643	1/1	0.98	0.12	42,42,42,42	0
57	MG	1A	3134	1/1	0.98	0.14	33,33,33,33	0
57	MG	1a	1794	1/1	0.98	0.06	25,25,25,25	0
57	MG	1A	3036	1/1	0.98	0.20	29,29,29,29	0
57	MG	1Q	203	1/1	0.98	0.07	28,28,28,28	0
57	MG	2A	3590	1/1	0.98	0.04	40,40,40,40	0
57	MG	1a	1797	1/1	0.98	0.12	57,57,57,57	0
57	MG	1Q	204	1/1	0.98	0.05	42,42,42,42	0
57	MG	1A	3674	1/1	0.98	0.14	53,53,53,53	0
57	MG	1A	3015	1/1	0.98	0.08	47,47,47,47	0
57	MG	2A	3421	1/1	0.98	0.08	48,48,48,48	0
57	MG	1A	3590	1/1	0.98	0.08	22,22,22,22	0
57	MG	1A	3171	1/1	0.98	0.21	39,39,39,39	0
57	MG	1A	3173	1/1	0.98	0.26	38,38,38,38	0
57	MG	2A	3599	1/1	0.98	0.10	43,43,43,43	0
57	MG	2A	3600	1/1	0.98	0.06	38,38,38,38	0
57	MG	1R	202	1/1	0.98	0.24	40,40,40,40	0
57	MG	1A	3517	1/1	0.98	0.44	45,45,45,45	0
57	MG	2A	3782	1/1	0.98	0.07	40,40,40,40	0
57	MG	1A	3971	1/1	0.98	0.06	39,39,39,39	0
57	MG	2A	3785	1/1	0.98	0.04	53,53,53,53	0
57	MG	1A	3137	1/1	0.98	0.10	44,44,44,44	0
57	MG	1A	3029	1/1	0.98	0.13	22,22,22,22	0
57	MG	1A	3975	1/1	0.98	0.07	50,50,50,50	0
57	MG	1A	3176	1/1	0.98	0.05	38,38,38,38	0
57	MG	1A	3274	1/1	0.98	0.04	31,31,31,31	0
57	MG	1A	3089	1/1	0.98	0.29	39,39,39,39	0
57	MG	2A	3436	1/1	0.98	0.04	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	3390	1/1	0.98	0.15	34,34,34,34	0
57	MG	1A	3687	1/1	0.98	0.07	47,47,47,47	0
57	MG	2A	3119	1/1	0.98	0.05	45,45,45,45	0
57	MG	1A	3878	1/1	0.98	0.09	36,36,36,36	0
57	MG	1A	3879	1/1	0.98	0.06	29,29,29,29	0
57	MG	2A	3799	1/1	0.98	0.06	64,64,64,64	0
57	MG	1A	3090	1/1	0.98	0.09	48,48,48,48	0
57	MG	1A	3525	1/1	0.98	0.07	49,49,49,49	0
57	MG	1A	3180	1/1	0.98	0.05	42,42,42,42	0
57	MG	1V	201	1/1	0.98	0.12	26,26,26,26	0
57	MG	1A	3986	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3226	1/1	0.98	0.06	34,34,34,34	0
57	MG	1V	204	1/1	0.98	0.25	32,32,32,32	0
57	MG	1A	3059	1/1	0.98	0.07	32,32,32,32	0
57	MG	1A	3228	1/1	0.98	0.09	49,49,49,49	0
57	MG	1A	3030	1/1	0.98	0.26	34,34,34,34	0
57	MG	2a	1658	1/1	0.98	0.05	59,59,59,59	0
57	MG	2A	3132	1/1	0.98	0.10	40,40,40,40	0
57	MG	2A	3453	1/1	0.98	0.05	44,44,44,44	0
57	MG	1A	3531	1/1	0.98	0.16	33,33,33,33	0
57	MG	1A	3230	1/1	0.98	0.16	47,47,47,47	0
57	MG	2A	3814	1/1	0.98	0.06	62,62,62,62	0
57	MG	1W	202	1/1	0.98	0.12	36,36,36,36	0
57	MG	1W	203	1/1	0.98	0.14	45,45,45,45	0
60	ZN	1n	103	1/1	0.98	0.04	57,57,57,57	0
57	MG	1W	204	1/1	0.98	0.08	32,32,32,32	0
57	MG	2A	3633	1/1	0.98	0.05	42,42,42,42	0
60	ZN	25	106	1/1	0.98	0.04	57,57,57,57	0
57	MG	1A	3231	1/1	0.98	0.08	24,24,24,24	0
57	MG	1A	3183	1/1	0.98	0.09	22,22,22,22	0
57	MG	1X	102	1/1	0.98	0.07	43,43,43,43	0
57	MG	1A	3400	1/1	0.98	0.08	40,40,40,40	0
57	MG	2A	3143	1/1	0.98	0.08	35,35,35,35	0
57	MG	18	103	1/1	0.99	0.11	44,44,44,44	0
57	MG	1A	3859	1/1	0.99	0.06	34,34,34,34	0
57	MG	1a	1728	1/1	0.99	0.19	40,40,40,40	0
57	MG	1A	3257	1/1	0.99	0.19	31,31,31,31	0
57	MG	1A	3677	1/1	0.99	0.03	28,28,28,28	0
57	MG	1A	3345	1/1	0.99	0.15	29,29,29,29	0
57	MG	1A	3051	1/1	0.99	0.08	35,35,35,35	0
57	MG	1A	3207	1/1	0.99	0.17	32,32,32,32	0
57	MG	1A	3035	1/1	0.99	0.12	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	3053	1/1	0.99	0.04	21,21,21,21	0
57	MG	2A	3795	1/1	0.99	0.08	38,38,38,38	0
57	MG	1A	3012	1/1	0.99	0.07	15,15,15,15	0
57	MG	2A	3103	1/1	0.99	0.06	28,28,28,28	0
57	MG	2A	3559	1/1	0.99	0.04	38,38,38,38	0
57	MG	1X	101	1/1	0.99	0.22	33,33,33,33	0
57	MG	1A	3092	1/1	0.99	0.04	21,21,21,21	0
57	MG	1A	3152	1/1	0.99	0.08	12,12,12,12	0
57	MG	1A	3191	1/1	0.99	0.15	30,30,30,30	0
57	MG	1A	3025	1/1	0.99	0.14	31,31,31,31	0
57	MG	1A	3355	1/1	0.99	0.13	36,36,36,36	0
57	MG	1a	1743	1/1	0.99	0.04	47,47,47,47	0
57	MG	1A	3922	1/1	0.99	0.06	42,42,42,42	0
57	MG	1A	3873	1/1	0.99	0.05	32,32,32,32	0
57	MG	1A	3974	1/1	0.99	0.05	28,28,28,28	0
57	MG	1A	3172	1/1	0.99	0.21	31,31,31,31	0
57	MG	1A	3875	1/1	0.99	0.04	15,15,15,15	0
57	MG	1A	3003	1/1	0.99	0.05	27,27,27,27	0
57	MG	1A	3217	1/1	0.99	0.13	30,30,30,30	0
57	MG	1A	3649	1/1	0.99	0.02	14,14,14,14	0
57	MG	1P	201	1/1	0.99	0.17	36,36,36,36	0
57	MG	1D	308	1/1	0.99	0.10	36,36,36,36	0
57	MG	1A	3326	1/1	0.99	0.12	36,36,36,36	0
57	MG	1P	204	1/1	0.99	0.21	30,30,30,30	0
57	MG	2A	3424	1/1	0.99	0.07	21,21,21,21	0
57	MG	1A	3009	1/1	0.99	0.08	25,25,25,25	0
57	MG	1A	3328	1/1	0.99	0.11	39,39,39,39	0
57	MG	1A	3058	1/1	0.99	0.11	35,35,35,35	0
57	MG	1A	3220	1/1	0.99	0.17	31,31,31,31	0
57	MG	1A	3157	1/1	0.99	0.06	28,28,28,28	0
57	MG	1A	3125	1/1	0.99	0.05	14,14,14,14	0
57	MG	1E	302	1/1	0.99	0.13	29,29,29,29	0
57	MG	1a	1631	1/1	0.99	0.10	24,24,24,24	0
57	MG	1a	1764	1/1	0.99	0.05	61,61,61,61	0
57	MG	1a	1765	1/1	0.99	0.06	51,51,51,51	0
57	MG	1a	1766	1/1	0.99	0.05	51,51,51,51	0
57	MG	1A	3700	1/1	0.99	0.10	28,28,28,28	0
57	MG	1A	3576	1/1	0.99	0.08	24,24,24,24	0
57	MG	2a	1742	1/1	0.99	0.05	59,59,59,59	0
57	MG	2A	3136	1/1	0.99	0.05	40,40,40,40	0
57	MG	2X	102	1/1	0.99	0.12	51,51,51,51	0
57	MG	1a	1698	1/1	0.99	0.14	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	3499	1/1	0.99	0.07	28,28,28,28	0
57	MG	1A	3019	1/1	0.99	0.04	42,42,42,42	0
57	MG	1A	3991	1/1	0.99	0.06	54,54,54,54	0
57	MG	1A	3501	1/1	0.99	0.16	30,30,30,30	0
57	MG	1A	3502	1/1	0.99	0.14	33,33,33,33	0
57	MG	1A	3179	1/1	0.99	0.11	23,23,23,23	0
57	MG	2A	3069	1/1	0.99	0.04	30,30,30,30	0
57	MG	1A	3752	1/1	0.99	0.05	23,23,23,23	0
57	MG	1A	3707	1/1	0.99	0.11	35,35,35,35	0
57	MG	1A	3160	1/1	0.99	0.03	32,32,32,32	0
57	MG	1A	4050	1/1	0.99	0.05	50,50,50,50	0
57	MG	1A	3041	1/1	0.99	0.04	32,32,32,32	0
57	MG	1U	201	1/1	0.99	0.07	33,33,33,33	0
57	MG	1A	3469	1/1	0.99	0.14	33,33,33,33	0
57	MG	1A	3624	1/1	0.99	0.03	30,30,30,30	0
57	MG	2A	3767	1/1	0.99	0.04	48,48,48,48	0
57	MG	1F	302	1/1	0.99	0.10	33,33,33,33	0
57	MG	1A	3085	1/1	0.99	0.10	19,19,19,19	0
57	MG	1A	3034	1/1	0.99	0.08	22,22,22,22	0
57	MG	1A	3510	1/1	0.99	0.06	35,35,35,35	0
57	MG	17	102	1/1	0.99	0.09	29,29,29,29	0
57	MG	1U	208	1/1	0.99	0.18	31,31,31,31	0
57	MG	1A	3062	1/1	0.99	0.06	15,15,15,15	0
60	ZN	1Y	203	1/1	0.99	0.03	66,66,66,66	0
57	MG	2A	3775	1/1	0.99	0.11	43,43,43,43	0
60	ZN	15	108	1/1	0.99	0.02	41,41,41,41	0
57	MG	1A	3340	1/1	0.99	0.10	23,23,23,23	0
57	MG	2A	3013	1/1	0.99	0.06	44,44,44,44	0
57	MG	1A	3254	1/1	0.99	0.14	30,30,30,30	0
57	MG	1A	3631	1/1	0.99	0.02	27,27,27,27	0
60	ZN	29	102	1/1	0.99	0.03	61,61,61,61	0
57	MG	2A	3466	1/1	0.99	0.04	69,69,69,69	0
61	SF4	1d	302	8/8	0.99	0.04	54,57,62,67	0
61	SF4	2d	303	8/8	0.99	0.05	62,68,72,74	0
57	MG	1A	3255	1/1	0.99	0.12	35,35,35,35	0
57	MG	1a	1724	1/1	0.99	0.05	50,50,50,50	0
57	MG	2A	3783	1/1	0.99	0.06	39,39,39,39	0
57	MG	1A	3256	1/1	0.99	0.10	31,31,31,31	0
60	ZN	19	102	1/1	1.00	0.03	40,40,40,40	0
57	MG	2A	3674	1/1	1.00	0.06	35,35,35,35	0
57	MG	1A	3013	1/1	1.00	0.04	28,28,28,28	0
57	MG	1a	1772	1/1	1.00	0.02	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3143	1/1	1.00	0.12	25,25,25,25	0
60	ZN	26	102	1/1	1.00	0.02	51,51,51,51	0
60	ZN	16	102	1/1	1.00	0.02	42,42,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.