Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:41 AM UTC

PDB ID	:	4Y4P / pdb_00004y4p
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome with rRNA modifications and bound to mRNA and A-, P- and E-site tRNAs at 2.5A resolution
Authors	:	Polikanov, Y.S.; Melnikov, S.V.; Soll, D.; Steitz, T.A.
Deposited on	:	2015-02-10
Resolution	:	2.50 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:

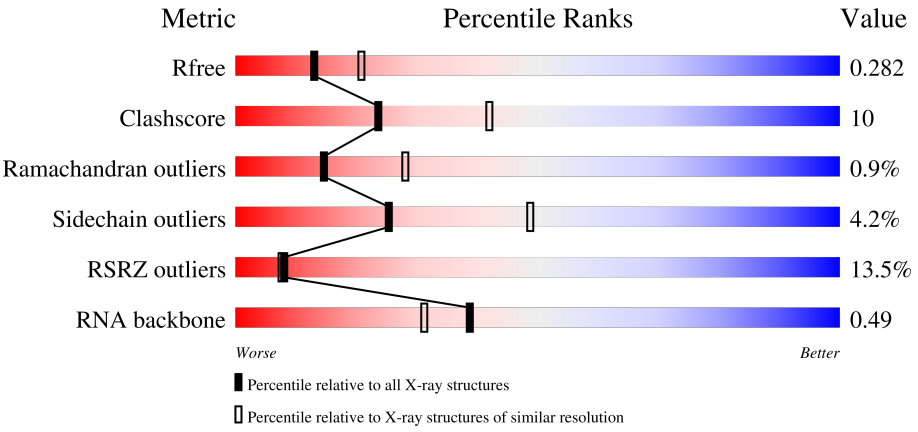
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.48.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 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	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)
RNA backbone	3690	1181 (2.80-2.20)

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	6% 65% 27% 6%
1	2A	2915	4% 53% 34% 9%
2	1B	121	% 71% 25%
2	2B	121	12% 36% 45% 17%

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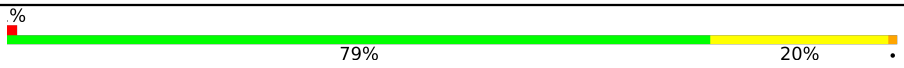
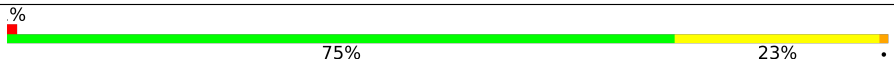
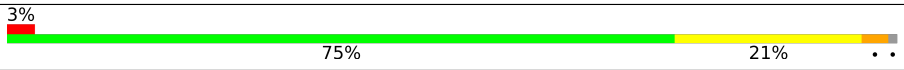
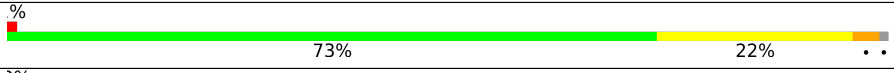
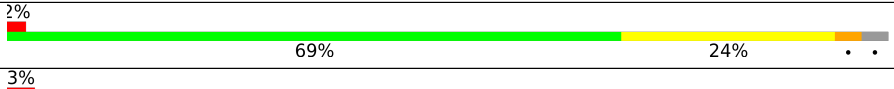
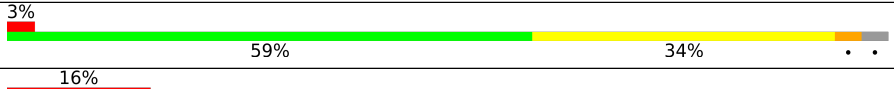
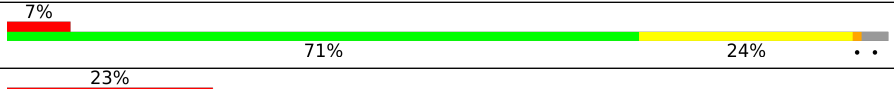
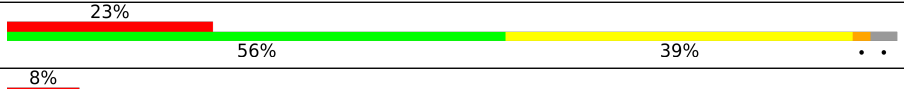
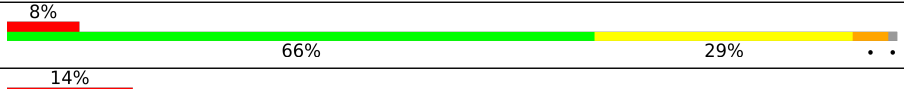
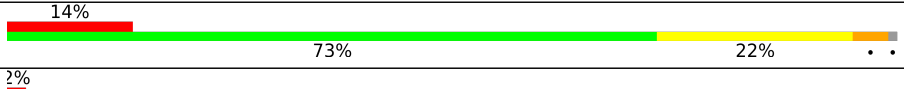
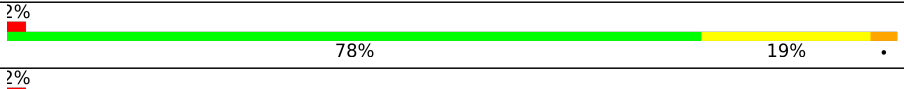
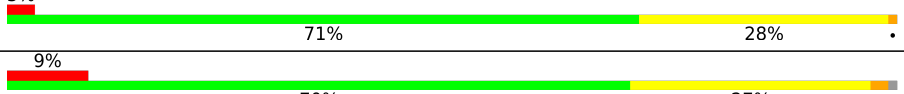
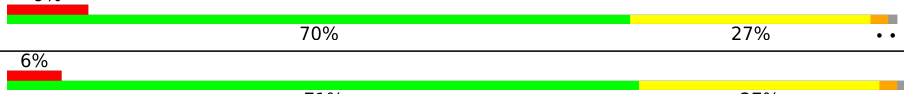
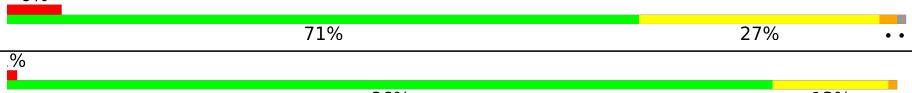
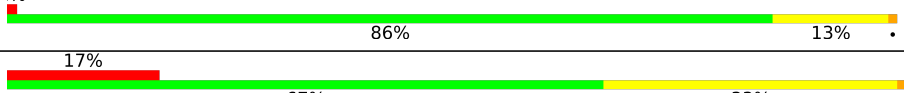
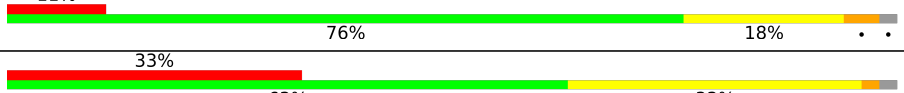
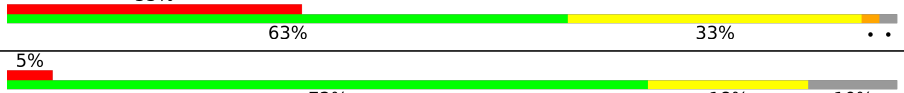
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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Mol	Chain	Length	Quality of chain
15	2T	146	2% 58% 32% 10%
16	1U	118	2% 81% 17%
16	2U	118	% 75% 23%
17	1V	101	3% 82% 15%
17	2V	101	5% 72% 23%
18	1W	113	2% 87% 10%
18	2W	113	2% 78% 20%
19	1X	96	3% 85% 10%
19	2X	96	% 65% 32%
20	1Y	110	8% 69% 24% 5%
20	2Y	110	12% 64% 32%
21	1Z	206	10% 53% 19% 25%
21	2Z	206	47% 44% 30% 22%
22	10	85	78% 18%
22	20	85	20% 69% 28%
23	11	98	% 81% 18%
23	21	98	13% 70% 29%
24	12	72	7% 74% 24%
24	22	72	4% 71% 26%
25	13	60	2% 80% 17%
25	23	60	3% 68% 30%
26	14	71	31% 55% 31% 11%
26	24	71	51% 39% 44% 14%
27	15	60	2% 80% 15%
27	25	60	2% 75% 18% 5%

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Mol	Chain	Length	Quality of chain
28	16	54	2% 69% 24% 6%
28	26	54	6% 76% 22%
29	17	49	10% 78% 20%
29	27	49	4% 71% 24%
30	18	65	6% 66% 31%
30	28	65	2% 66% 29%
31	19	37	84% 16%
31	29	37	14% 76% 24%
32	1a	1521	7% 57% 35% 7%
32	2a	1521	18% 48% 41% 9%
33	1b	256	27% 57% 30% 10%
33	2b	256	57% 40% 47% 10%
34	1c	239	23% 64% 22% 14%
34	2c	239	56% 55% 30% 14%
35	1d	209	17% 70% 26%
35	2d	209	17% 72% 26%
36	1e	162	14% 64% 27% 9%
36	2e	162	41% 57% 31% 9%
37	1f	101	5% 67% 32%
37	2f	101	6% 74% 25%
38	1g	156	23% 72% 25%
38	2g	156	28% 76% 20%
39	1h	138	11% 74% 25%
39	2h	138	32% 75% 24%
40	1i	128	26% 68% 28%

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Mol	Chain	Length	Quality of chain
40	2i	128	70% 48% 48%
41	1j	105	31% 50% 40% 8%
41	2j	105	70% 47% 41% 9%
42	1k	129	10% 72% 15% 12%
42	2k	129	13% 66% 21% 12%
43	1l	132	11% 70% 20% 8%
43	2l	132	12% 60% 30% 8%
44	1m	126	10% 71% 26%
44	2m	126	55% 56% 38%
45	1n	61	13% 67% 23% 8%
45	2n	61	89% 48% 49%
46	1o	89	16% 78% 19%
46	2o	89	15% 70% 27%
47	1p	88	31% 65% 24% 5% 7%
47	2p	88	18% 59% 32% 7%
48	1q	105	7% 71% 23% 6%
48	2q	105	20% 69% 26% 6%
49	1r	88	7% 59% 18% 23%
49	2r	88	10% 53% 23% 23%
50	1s	93	20% 59% 28% 11%
50	2s	93	69% 56% 29% 11%
51	1t	106	22% 67% 20% 9%
51	2t	106	10% 68% 21% 9%
52	1u	27	33% 52% 33% 15%
52	2u	27	63% 44% 41% 15%

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Mol	Chain	Length	Quality of chain
53	1v	24	29% 29% 17% 8% 46%
53	2v	24	29% 38% 8% 8% 46%
54	1w	76	28% 34% 50% 12%
54	1y	76	20% 32% 42% 22%
54	2w	76	26% 16% 53% 24% 5%
54	2y	76	20% 29% 45% 20%
55	1x	77	6% 66% 26% 6%
55	2x	77	4% 42% 44% 13%

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
54	PSU	2y	55	-	-	X	-

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 300910 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 53 is a RNA chain called mRNA.

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1592	713	285	518	74	2			
54	1y	74	Total	C	N	O	P	S	0	0	0
			1585	707	285	518	74	1			
54	2w	72	Total	C	N	O	P	S	0	0	0
			1544	690	278	502	72	2			
54	2y	73	Total	C	N	O	P	S	0	0	0
			1565	698	283	510	73	1			

- Molecule 55 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
55	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	1141	Total	Mg	0	0
			1141	1141		
56	1B	37	Total	Mg	0	0
			37	37		
56	1D	12	Total	Mg	0	0
			12	12		
56	1E	11	Total	Mg	0	0
			11	11		
56	1F	8	Total	Mg	0	0
			8	8		
56	1G	5	Total	Mg	0	0
			5	5		
56	1I	1	Total	Mg	0	0
			1	1		
56	1N	6	Total	Mg	0	0
			6	6		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1O	7	Total Mg 7 7	0	0
56	1P	4	Total Mg 4 4	0	0
56	1Q	6	Total Mg 6 6	0	0
56	1R	3	Total Mg 3 3	0	0
56	1S	3	Total Mg 3 3	0	0
56	1T	2	Total Mg 2 2	0	0
56	1U	8	Total Mg 8 8	0	0
56	1V	3	Total Mg 3 3	0	0
56	1W	5	Total Mg 5 5	0	0
56	1X	6	Total Mg 6 6	0	0
56	1Y	3	Total Mg 3 3	0	0
56	1Z	3	Total Mg 3 3	0	0
56	10	6	Total Mg 6 6	0	0
56	11	3	Total Mg 3 3	0	0
56	12	1	Total Mg 1 1	0	0
56	13	3	Total Mg 3 3	0	0
56	15	2	Total Mg 2 2	0	0
56	16	3	Total Mg 3 3	0	0
56	17	1	Total Mg 1 1	0	0
56	18	3	Total Mg 3 3	0	0
56	19	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1a	229	Total Mg 229 229	0	0
56	1b	2	Total Mg 2 2	0	0
56	1d	1	Total Mg 1 1	0	0
56	1e	1	Total Mg 1 1	0	0
56	1f	2	Total Mg 2 2	0	0
56	1l	3	Total Mg 3 3	0	0
56	1n	2	Total Mg 2 2	0	0
56	1s	1	Total Mg 1 1	0	0
56	1t	1	Total Mg 1 1	0	0
56	1v	1	Total Mg 1 1	0	0
56	1w	11	Total Mg 11 11	0	0
56	1x	16	Total Mg 16 16	0	0
56	1y	4	Total Mg 4 4	0	0
56	2A	909	Total Mg 909 909	0	0
56	2B	21	Total Mg 21 21	0	0
56	2D	5	Total Mg 5 5	0	0
56	2E	9	Total Mg 9 9	0	0
56	2F	4	Total Mg 4 4	0	0
56	2G	1	Total Mg 1 1	0	0
56	2N	1	Total Mg 1 1	0	0
56	2O	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	2P	1	Total Mg 1 1	0	0
56	2Q	3	Total Mg 3 3	0	0
56	2R	1	Total Mg 1 1	0	0
56	2T	3	Total Mg 3 3	0	0
56	2U	4	Total Mg 4 4	0	0
56	2V	1	Total Mg 1 1	0	0
56	2W	3	Total Mg 3 3	0	0
56	2X	3	Total Mg 3 3	0	0
56	2Y	1	Total Mg 1 1	0	0
56	2Z	1	Total Mg 1 1	0	0
56	20	3	Total Mg 3 3	0	0
56	23	2	Total Mg 2 2	0	0
56	25	4	Total Mg 4 4	0	0
56	27	1	Total Mg 1 1	0	0
56	28	2	Total Mg 2 2	0	0
56	2a	244	Total Mg 244 244	0	0
56	2d	1	Total Mg 1 1	0	0
56	2e	1	Total Mg 1 1	0	0
56	2f	1	Total Mg 1 1	0	0
56	2g	1	Total Mg 1 1	0	0
56	2i	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	2j	2	Total Mg 2 2	0	0
56	2l	2	Total Mg 2 2	0	0
56	2n	1	Total Mg 1 1	0	0
56	2q	2	Total Mg 2 2	0	0
56	2r	2	Total Mg 2 2	0	0
56	2t	1	Total Mg 1 1	0	0
56	2v	2	Total Mg 2 2	0	0
56	2w	8	Total Mg 8 8	0	0
56	2x	5	Total Mg 5 5	0	0
56	2y	7	Total Mg 7 7	0	0

- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1A	1	Total K 1 1	0	0
57	2A	1	Total K 1 1	0	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1Y	1	Total Zn 1 1	0	0
58	14	1	Total Zn 1 1	0	0
58	15	1	Total Zn 1 1	0	0
58	16	1	Total Zn 1 1	0	0
58	19	1	Total Zn 1 1	0	0

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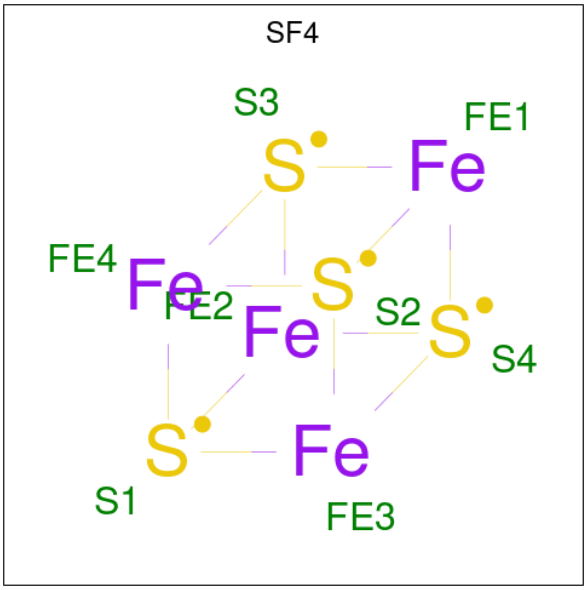
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1n	1	Total Zn 1 1	0	0
58	2Y	1	Total Zn 1 1	0	0
58	24	1	Total Zn 1 1	0	0
58	25	1	Total Zn 1 1	0	0
58	26	1	Total Zn 1 1	0	0
58	29	1	Total Zn 1 1	0	0
58	2n	1	Total Zn 1 1	0	0

- Molecule 59 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1d	1	Total Fe S 8 4 4	0	0
59	2d	1	Total Fe S 8 4 4	0	0

- Molecule 60 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	2238	Total O 2238 2238	0	0
60	1B	68	Total O 68 68	0	0
60	1D	28	Total O 28 28	0	0
60	1E	28	Total O 28 28	0	0
60	1F	13	Total O 13 13	0	0
60	1G	7	Total O 7 7	0	0
60	1H	2	Total O 2 2	0	0
60	1I	3	Total O 3 3	0	0
60	1N	7	Total O 7 7	0	0
60	1O	8	Total O 8 8	0	0
60	1P	23	Total O 23 23	0	0
60	1Q	14	Total O 14 14	0	0
60	1R	14	Total O 14 14	0	0
60	1S	5	Total O 5 5	0	0
60	1T	8	Total O 8 8	0	0
60	1U	11	Total O 11 11	0	0
60	1V	9	Total O 9 9	0	0
60	1W	6	Total O 6 6	0	0
60	1X	8	Total O 8 8	0	0
60	1Y	4	Total O 4 4	0	0
60	1Z	1	Total O 1 1	0	0
60	10	12	Total O 12 12	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	11	10	Total O 10 10	0	0
60	12	4	Total O 4 4	0	0
60	13	6	Total O 6 6	0	0
60	14	1	Total O 1 1	0	0
60	15	6	Total O 6 6	0	0
60	16	3	Total O 3 3	0	0
60	17	9	Total O 9 9	0	0
60	18	13	Total O 13 13	0	0
60	1a	438	Total O 438 438	0	0
60	1b	1	Total O 1 1	0	0
60	1d	1	Total O 1 1	0	0
60	1e	1	Total O 1 1	0	0
60	1f	1	Total O 1 1	0	0
60	1g	1	Total O 1 1	0	0
60	1i	1	Total O 1 1	0	0
60	1l	8	Total O 8 8	0	0
60	1m	2	Total O 2 2	0	0
60	1o	1	Total O 1 1	0	0
60	1p	1	Total O 1 1	0	0
60	1q	4	Total O 4 4	0	0
60	1u	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1v	5	Total O 5 5	0	0
60	1w	21	Total O 21 21	0	0
60	1x	15	Total O 15 15	0	0
60	1y	1	Total O 1 1	0	0
60	2A	1389	Total O 1389 1389	0	0
60	2B	26	Total O 26 26	0	0
60	2D	28	Total O 28 28	0	0
60	2E	16	Total O 16 16	0	0
60	2F	16	Total O 16 16	0	0
60	2H	1	Total O 1 1	0	0
60	2I	4	Total O 4 4	0	0
60	2N	1	Total O 1 1	0	0
60	2P	14	Total O 14 14	0	0
60	2Q	2	Total O 2 2	0	0
60	2R	2	Total O 2 2	0	0
60	2T	6	Total O 6 6	0	0
60	2U	2	Total O 2 2	0	0
60	2V	2	Total O 2 2	0	0
60	2W	2	Total O 2 2	0	0
60	2X	5	Total O 5 5	0	0
60	2Y	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	2Z	2	Total O 2 2	0	0
60	20	7	Total O 7 7	0	0
60	21	12	Total O 12 12	0	0
60	22	1	Total O 1 1	0	0
60	23	1	Total O 1 1	0	0
60	25	4	Total O 4 4	0	0
60	26	1	Total O 1 1	0	0
60	27	4	Total O 4 4	0	0
60	28	6	Total O 6 6	0	0
60	29	1	Total O 1 1	0	0
60	2a	377	Total O 377 377	0	0
60	2d	1	Total O 1 1	0	0
60	2e	2	Total O 2 2	0	0
60	2g	1	Total O 1 1	0	0
60	2i	1	Total O 1 1	0	0
60	2j	4	Total O 4 4	0	0
60	2l	5	Total O 5 5	0	0
60	2o	1	Total O 1 1	0	0
60	2p	2	Total O 2 2	0	0
60	2q	1	Total O 1 1	0	0
60	2r	1	Total O 1 1	0	0

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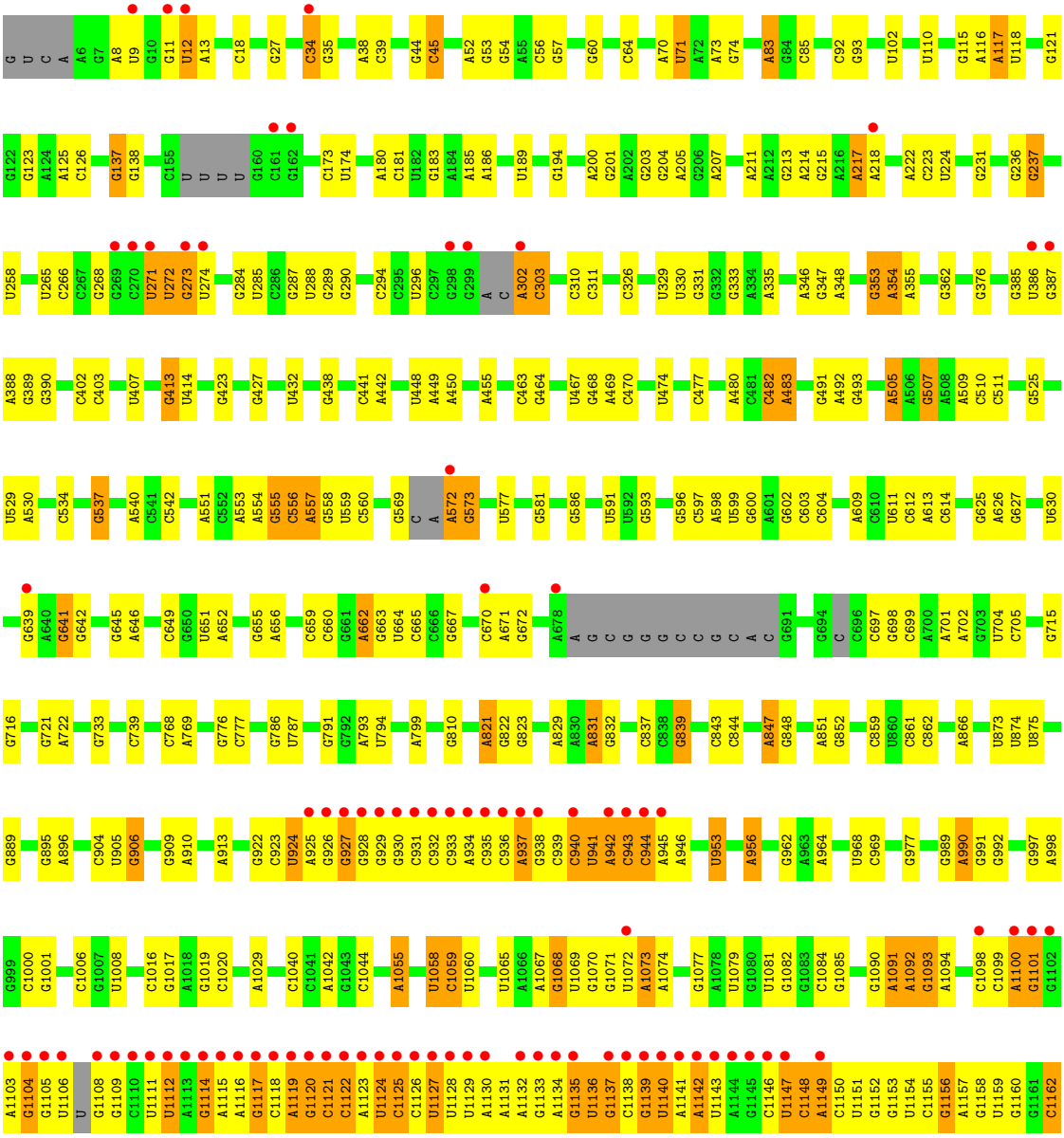
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	2t	4	Total O 4 4	0	0
60	2u	1	Total O 1 1	0	0
60	2v	1	Total O 1 1	0	0
60	2w	2	Total O 2 2	0	0
60	2x	7	Total O 7 7	0	0
60	2y	19	Total O 19 19	0	0

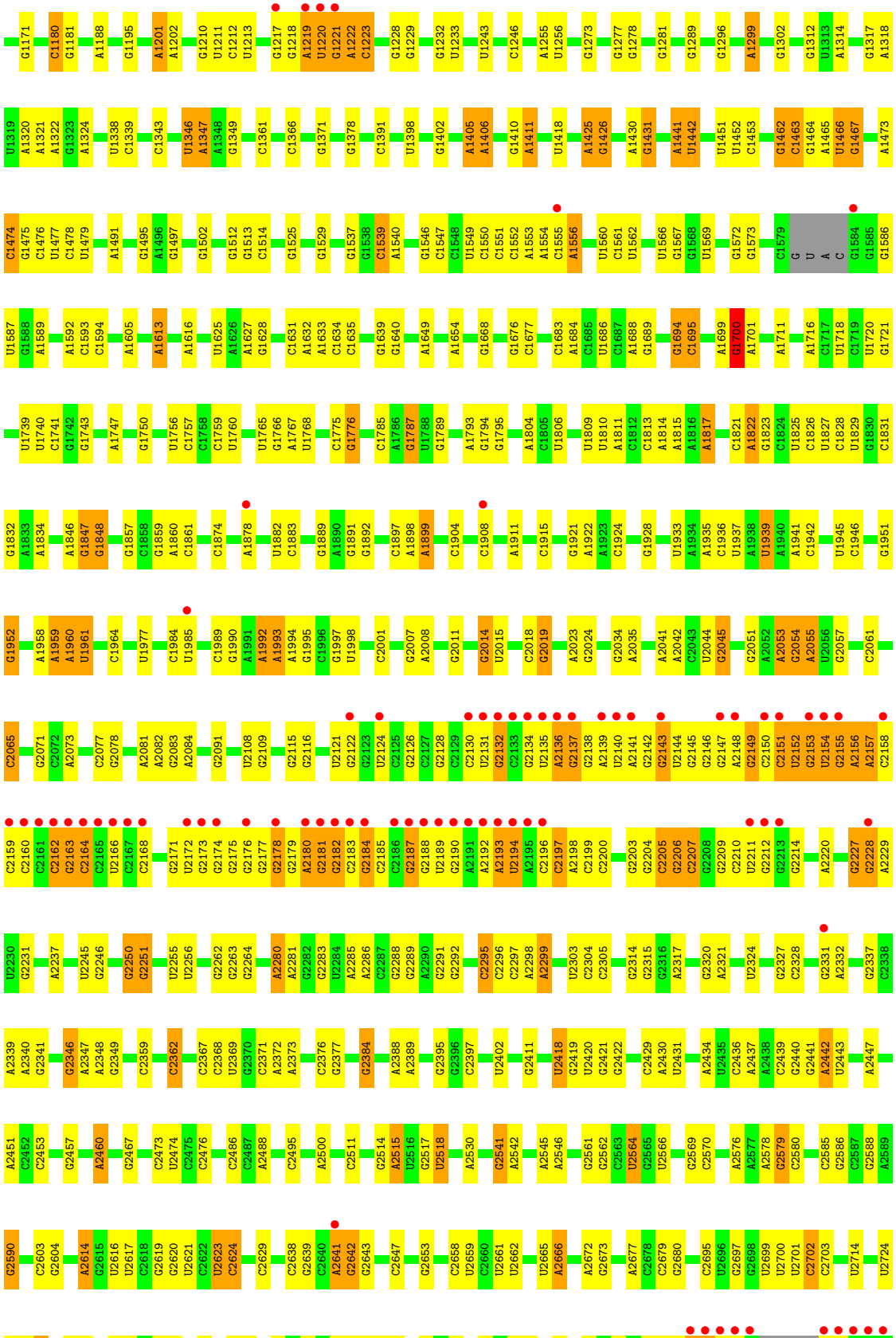
3 Residue-property plots (i)

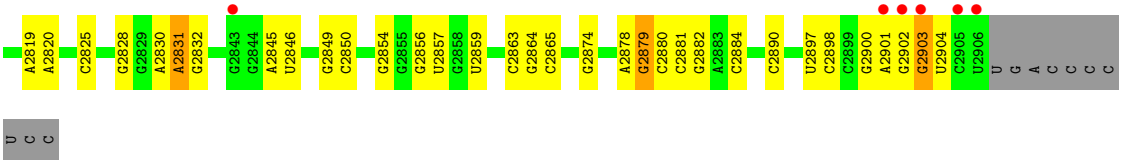
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 23S Ribosomal RNA

Chain 1A:

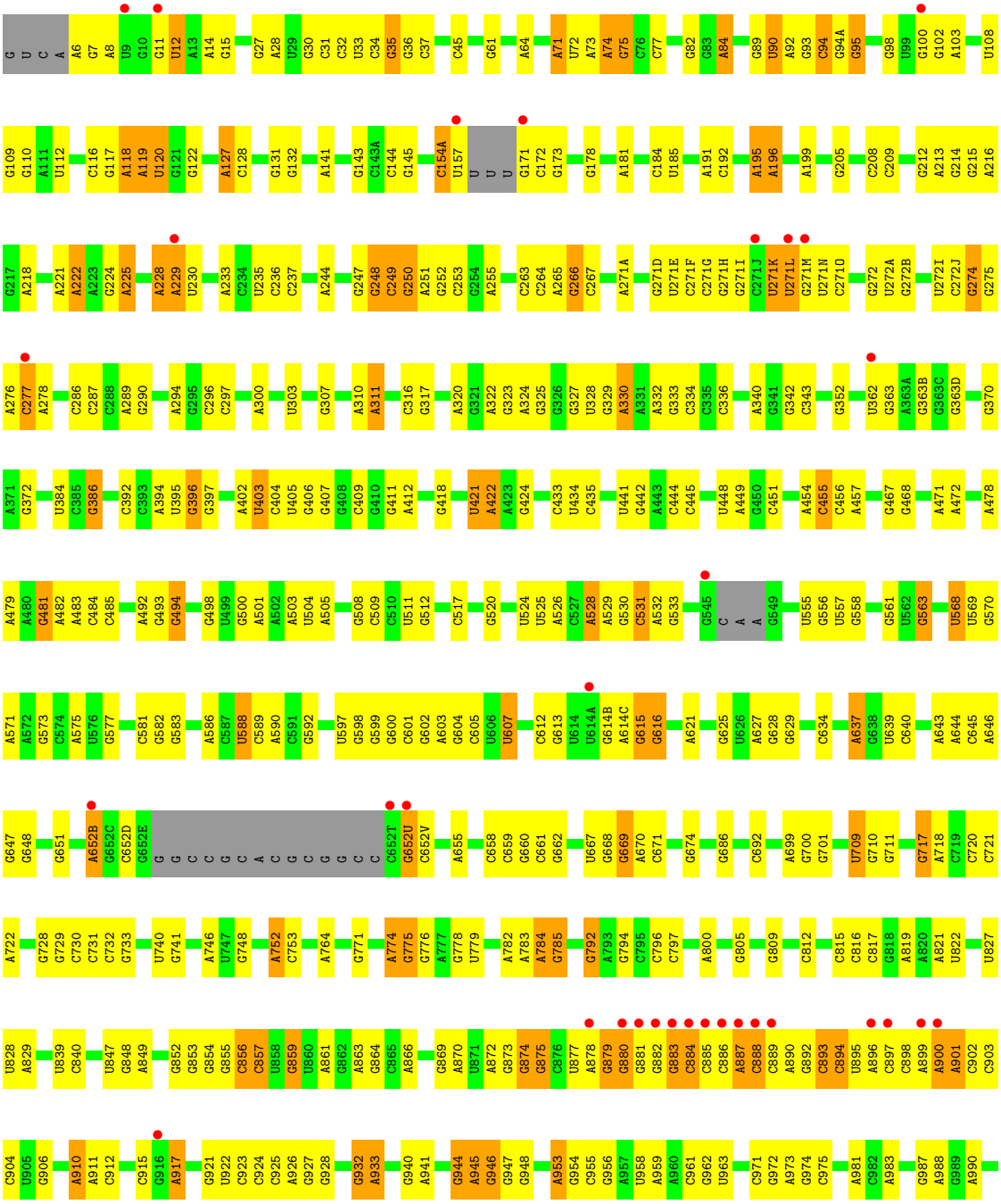


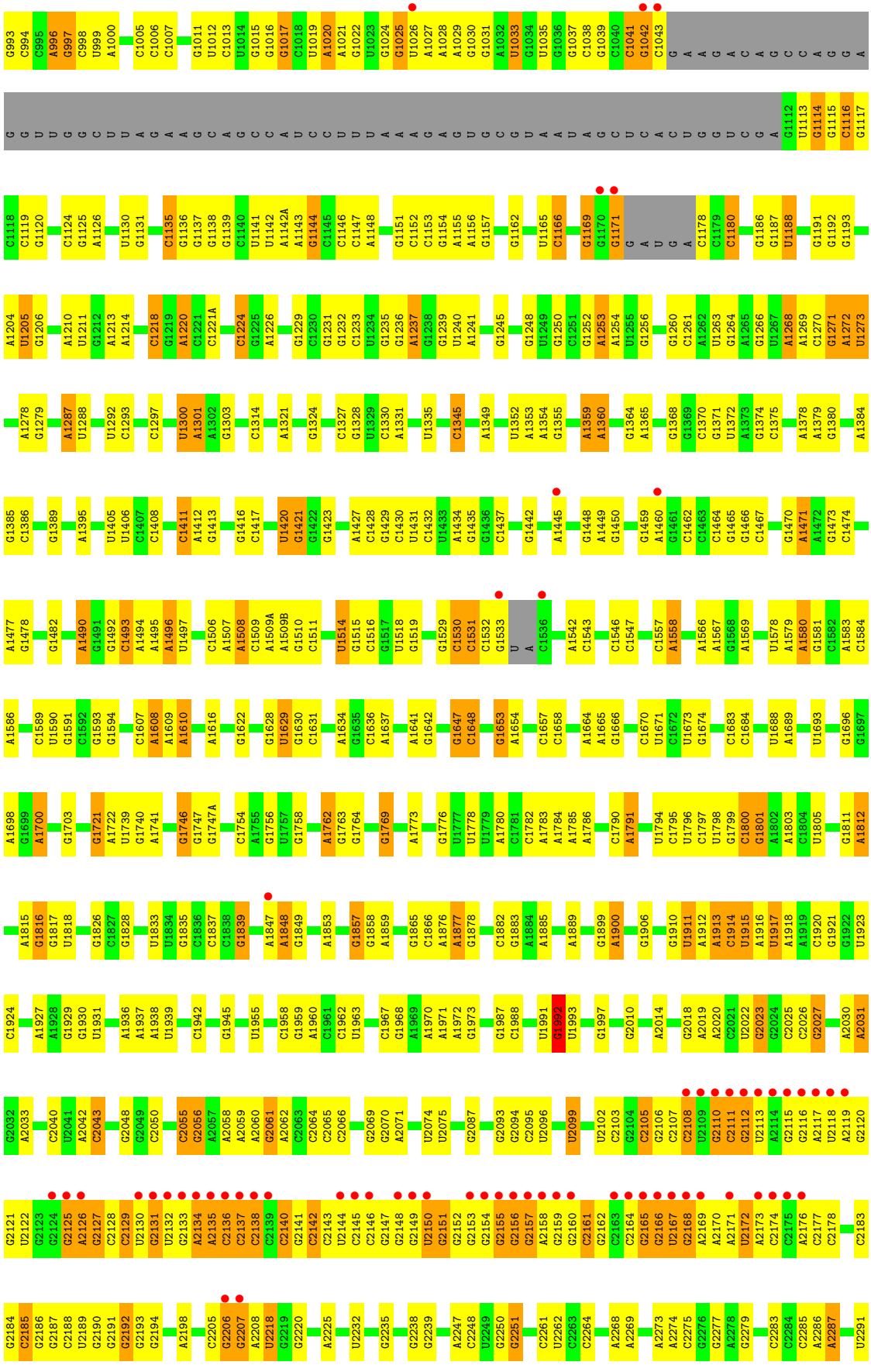




• Molecule 1: 23S Ribosomal RNA

Chain 2A:

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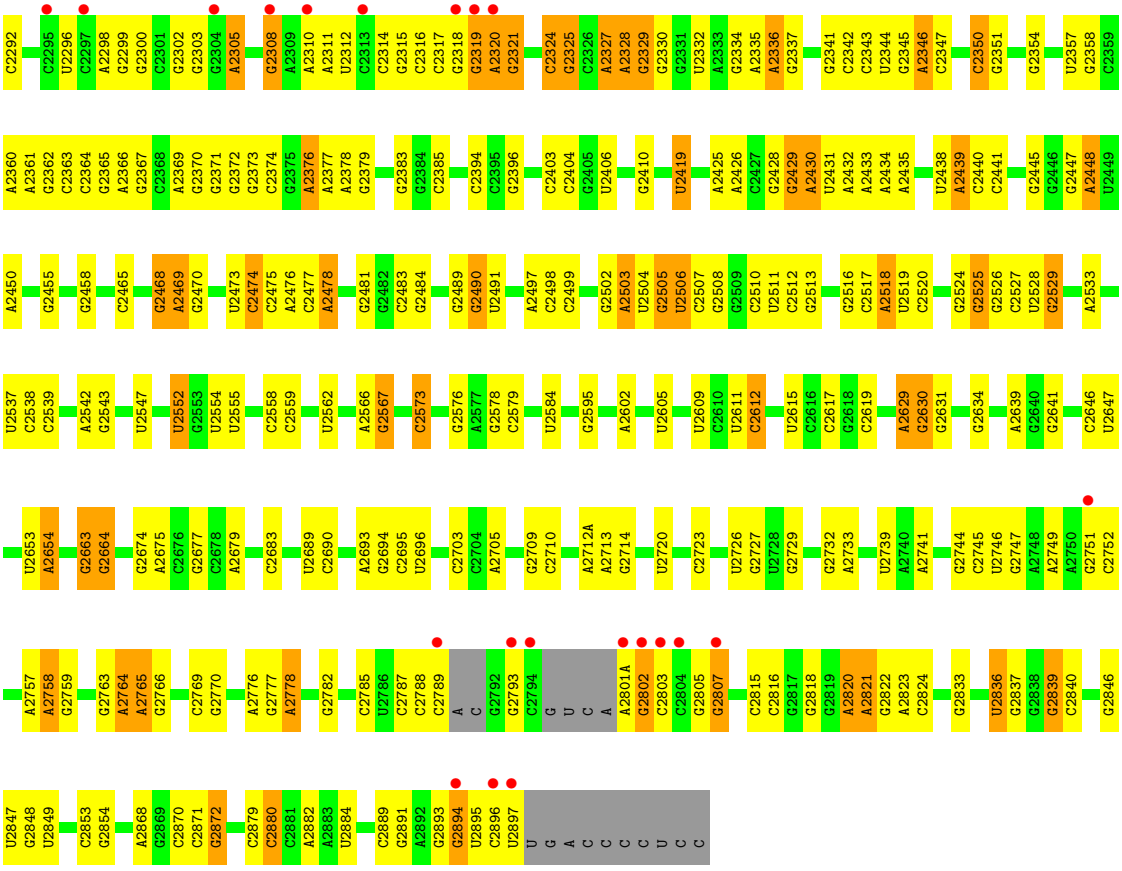
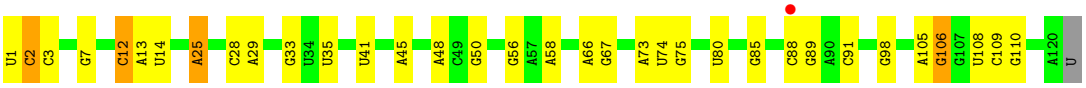
C1005 C1006 C1007
G1011 U1012 C1013 U1014 G1015 G1016 G1017 C1018 U1019 A1020 A1021 G1022 U1023 G1024 G1025 U1026 A1027 A1028 A1029 G1030 G1031 A1032 U1033 G1034 U1035 G1036 G1037 C1038 G1039 C1040 C1041 G1042 C1043
G A A G A C A G
G G U U G G C U U A G A A G C A A G C C G U A A C C C A U C U U A A G C C G U A A C C C A U C U U A A G C C G U A A C C C A U C U U



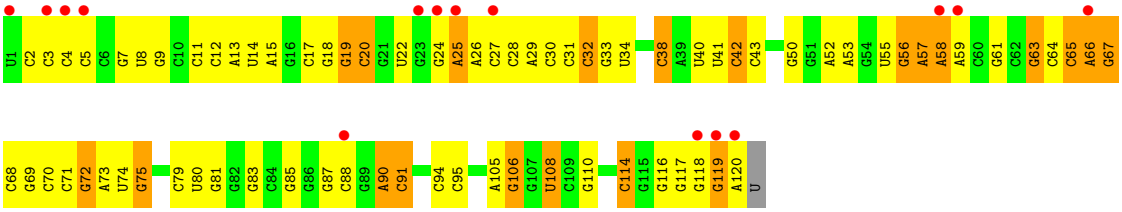
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



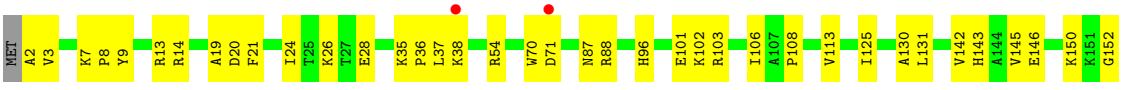
• Molecule 2: 5S Ribosomal RNA

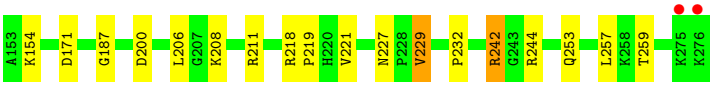
Chain 2B:



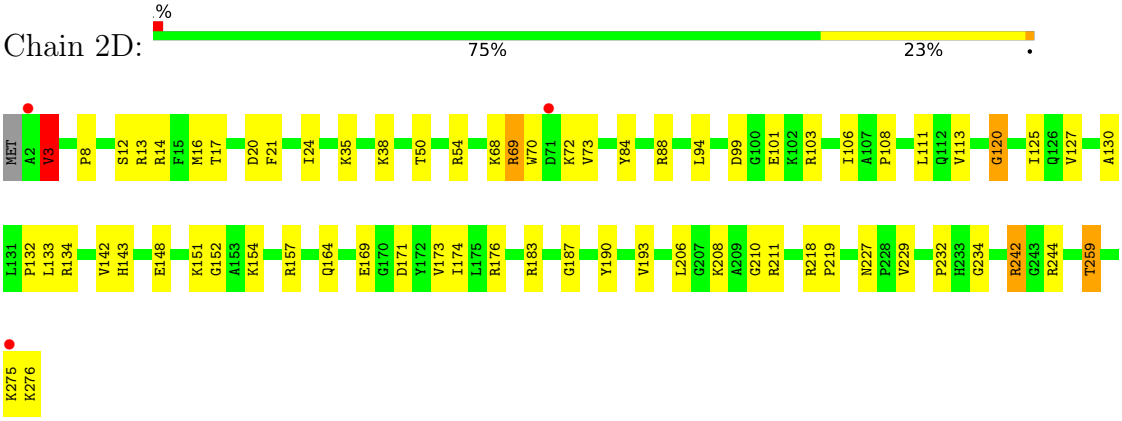
• Molecule 3: 50S ribosomal protein L2

Chain 1D:

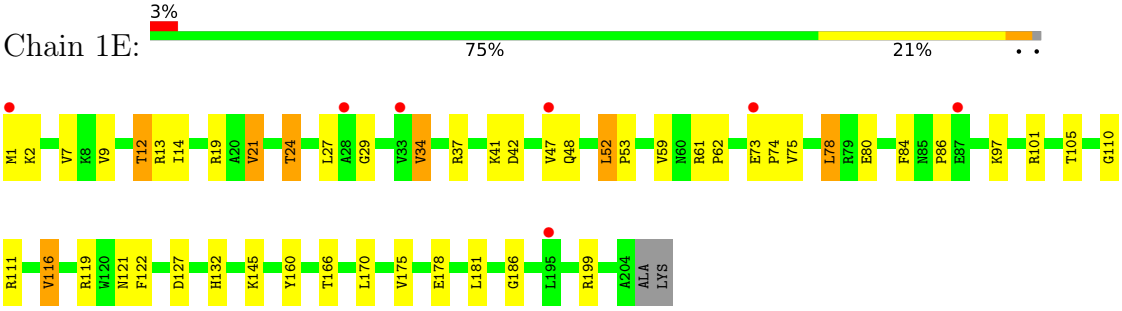




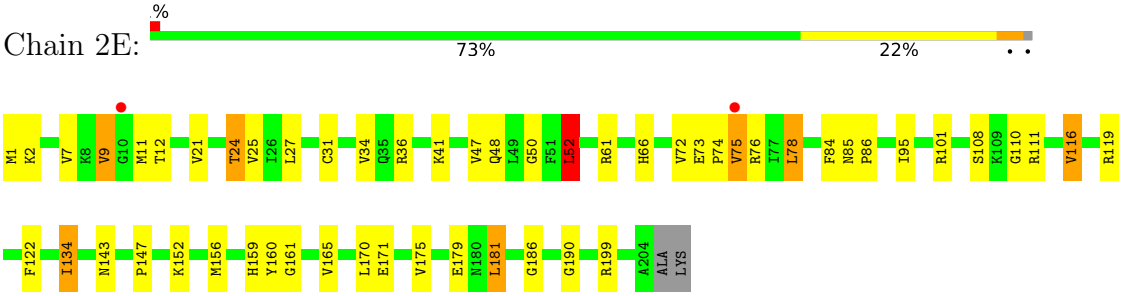
• Molecule 3: 50S ribosomal protein L2



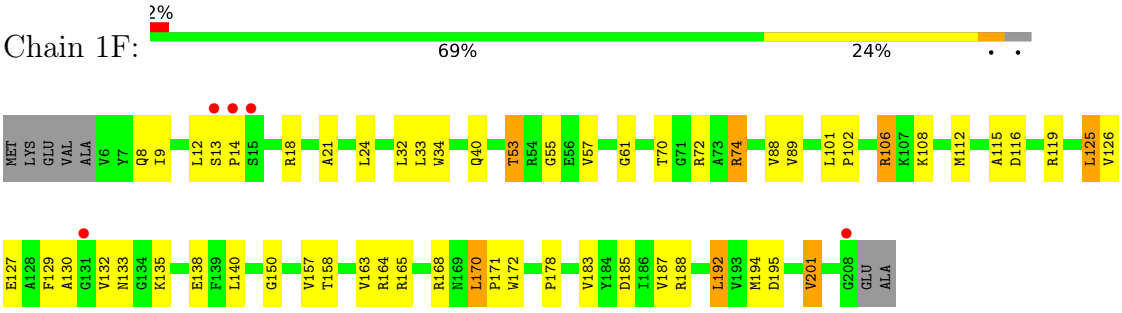
• Molecule 4: 50S ribosomal protein L3



• Molecule 4: 50S ribosomal protein L3

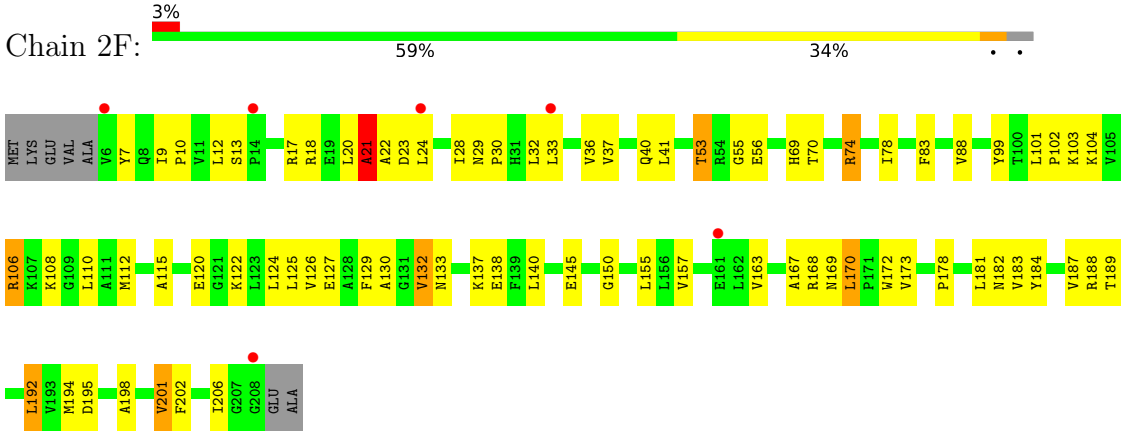


• Molecule 5: 50S ribosomal protein L4



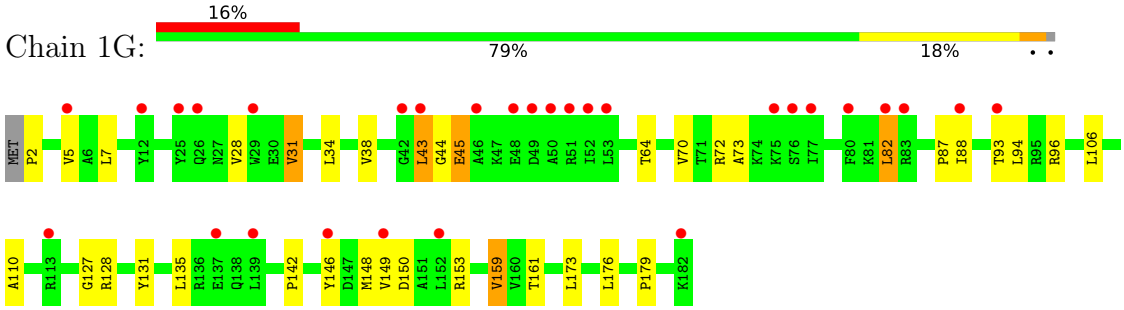
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



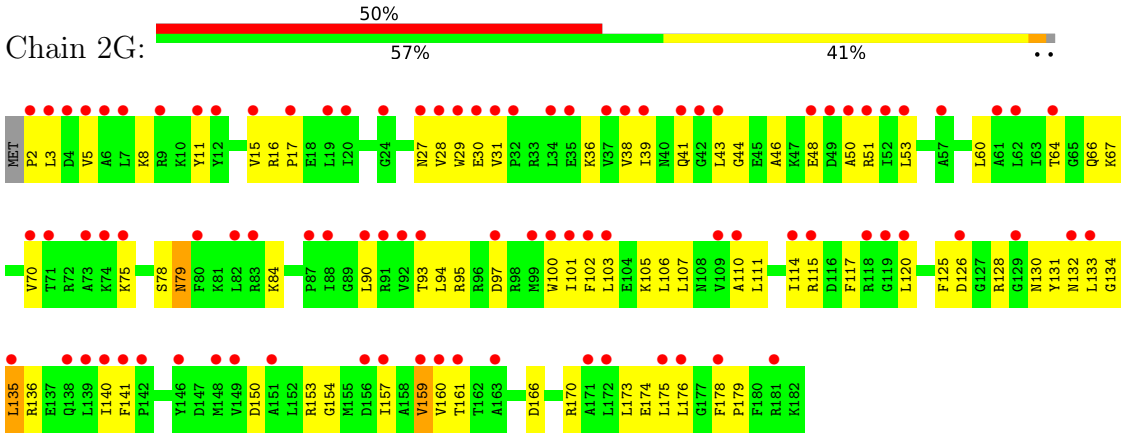
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



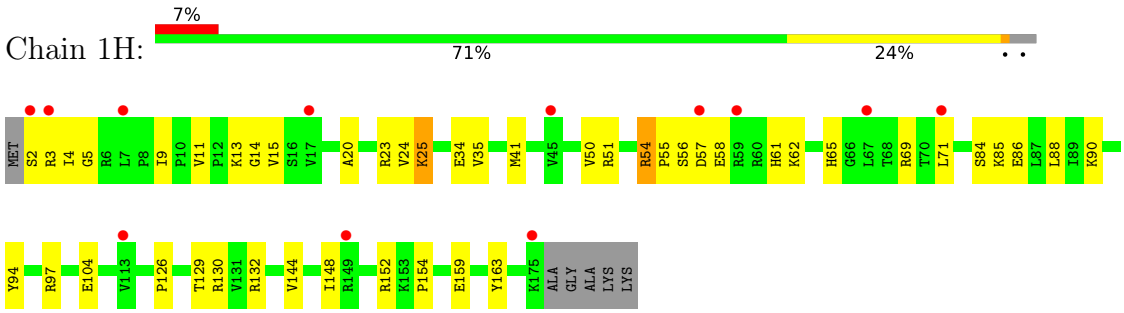
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



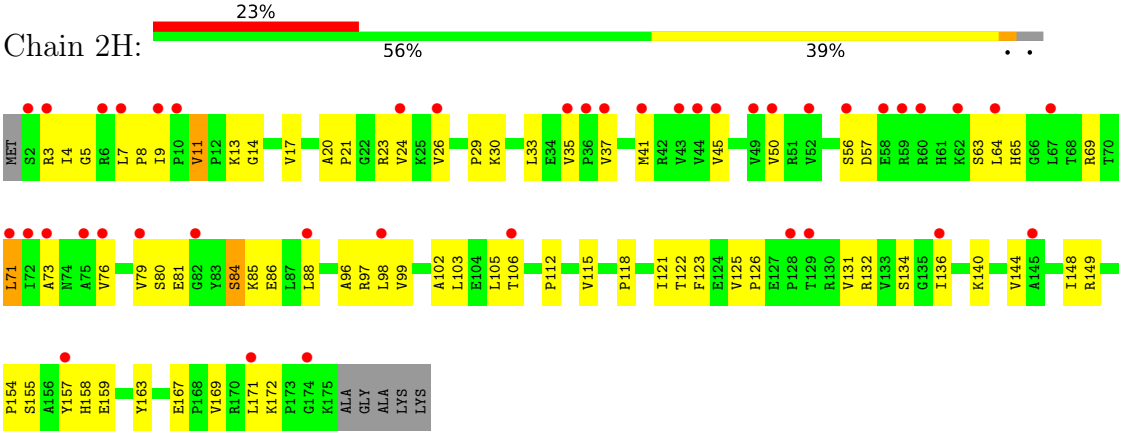
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



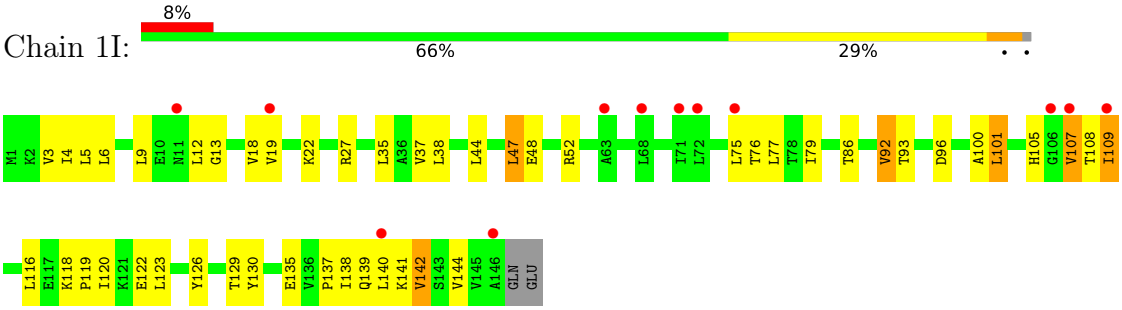
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



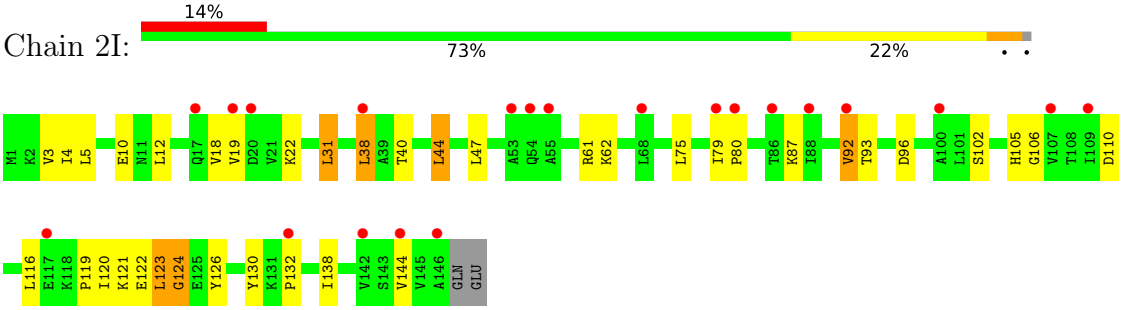
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



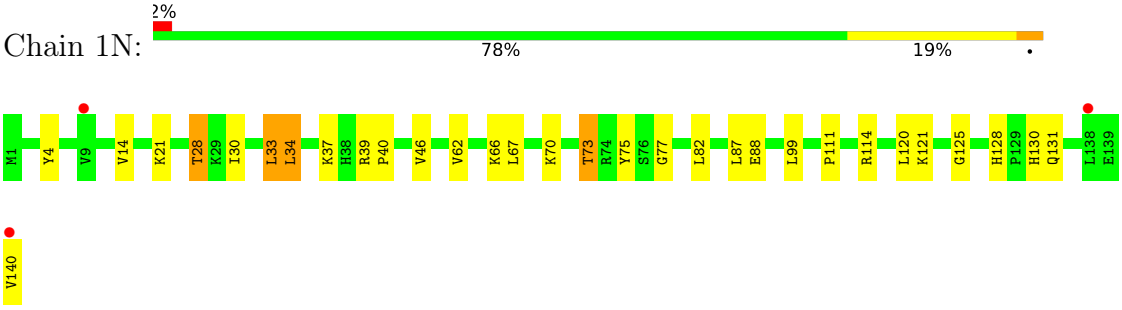
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



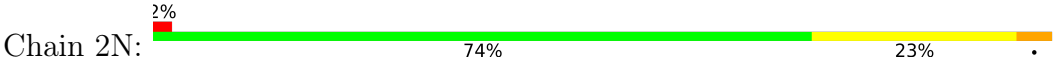
• Molecule 9: 50S ribosomal protein L13

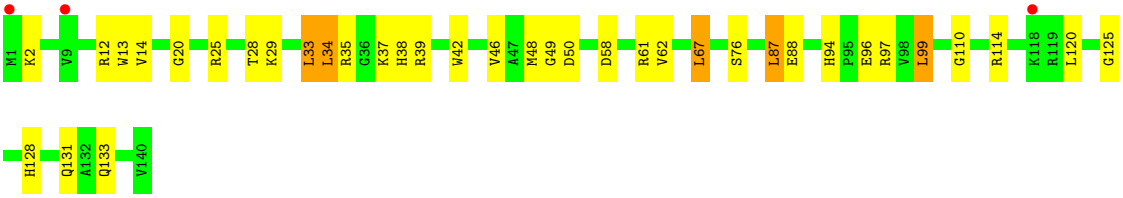
Chain 1N:



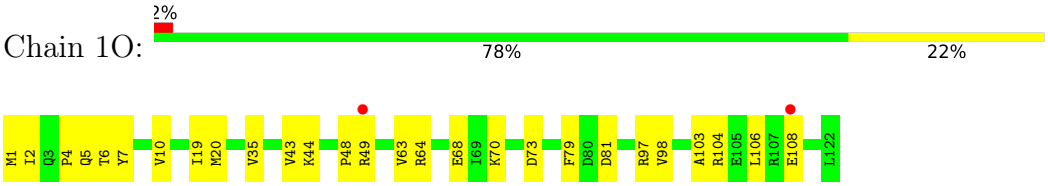
• Molecule 9: 50S ribosomal protein L13

Chain 2N:

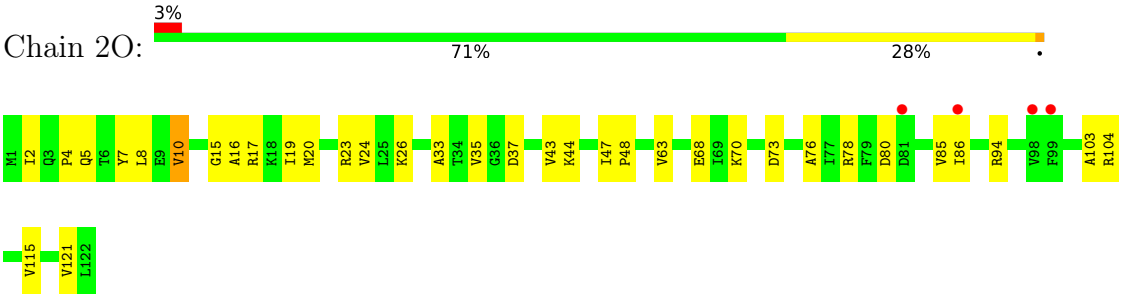




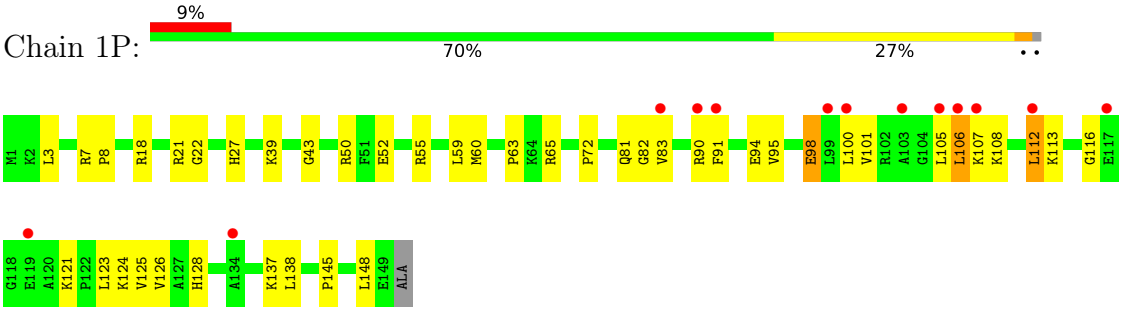
• Molecule 10: 50S ribosomal protein L14



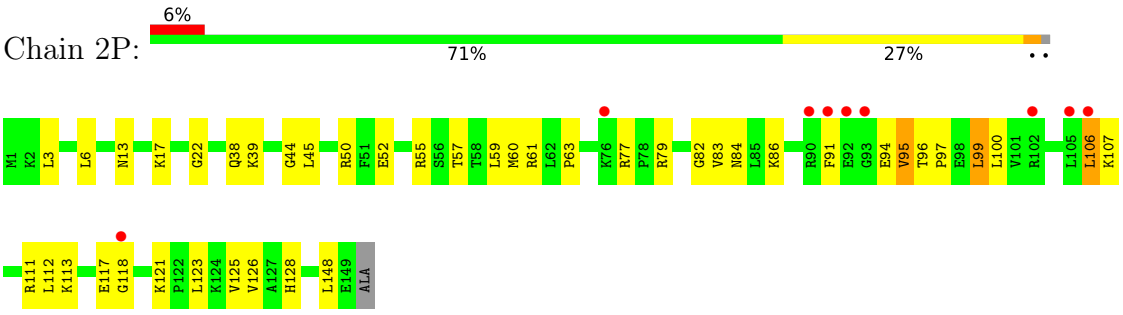
• Molecule 10: 50S ribosomal protein L14



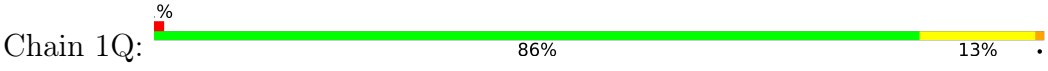
• Molecule 11: 50S ribosomal protein L15

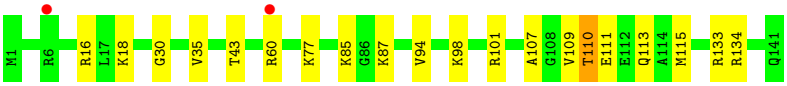


• Molecule 11: 50S ribosomal protein L15



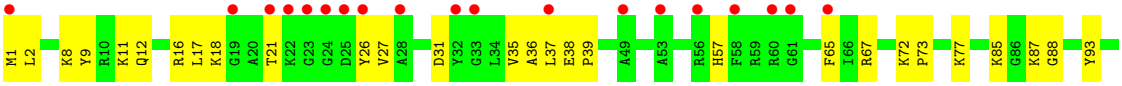
• Molecule 12: 50S ribosomal protein L16

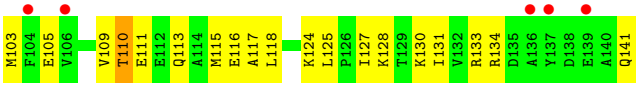




• Molecule 12: 50S ribosomal protein L16

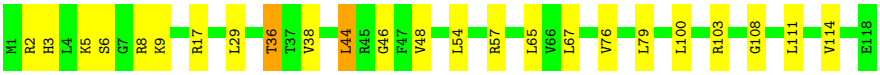
Chain 2Q:





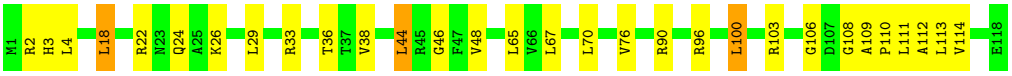
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



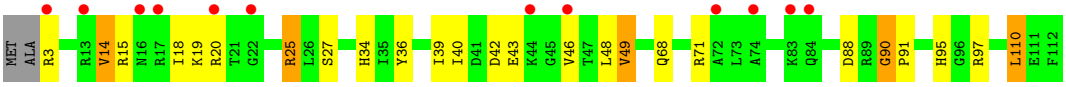
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



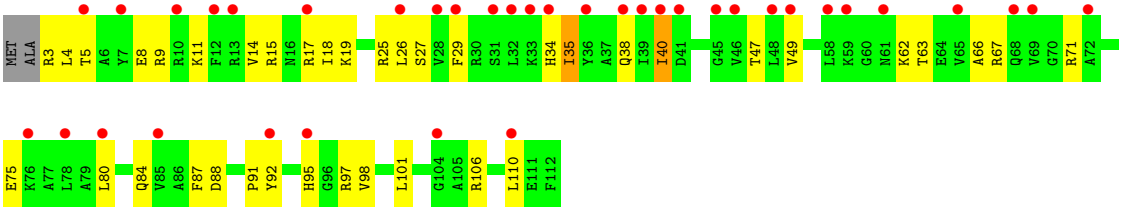
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



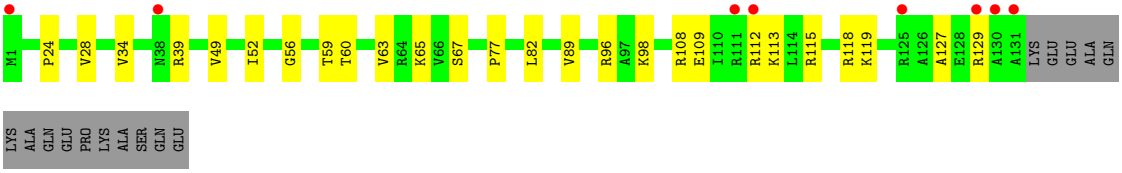
• Molecule 14: 50S ribosomal protein L18

Chain 2S:

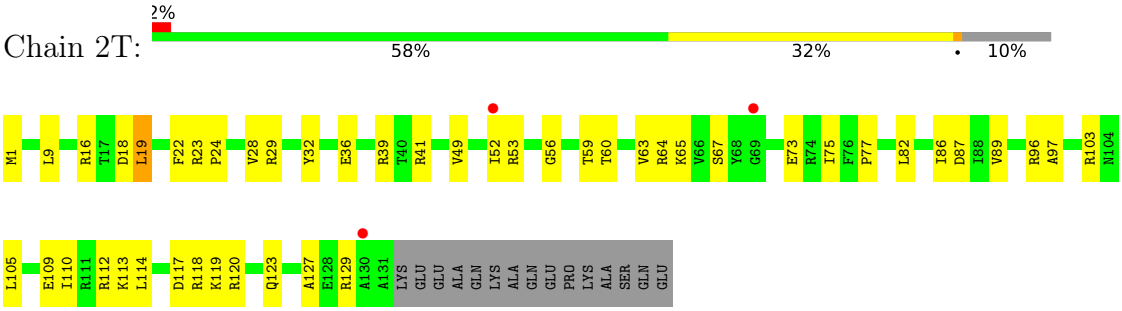


• Molecule 15: 50S ribosomal protein L19

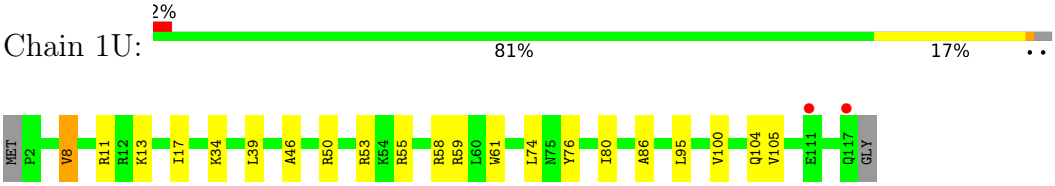
Chain 1T:



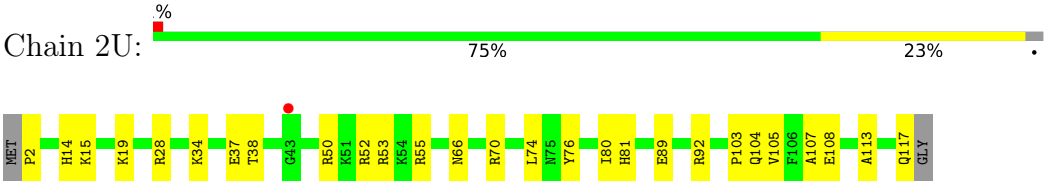
• Molecule 15: 50S ribosomal protein L19



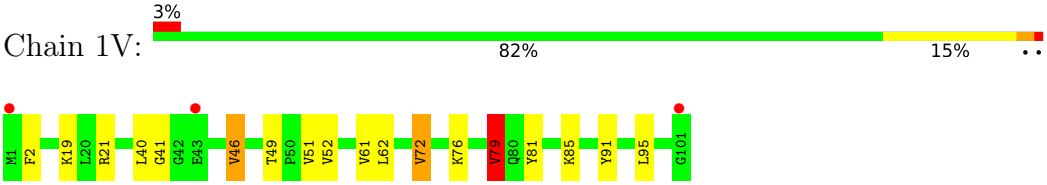
• Molecule 16: 50S ribosomal protein L20



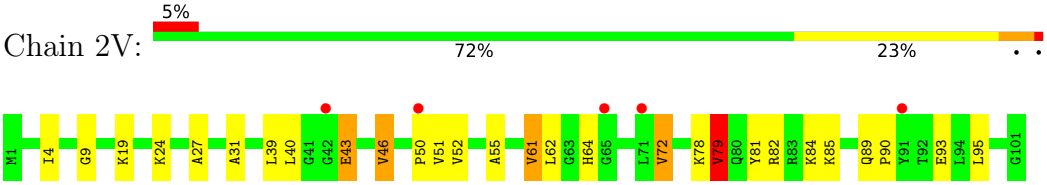
• Molecule 16: 50S ribosomal protein L20



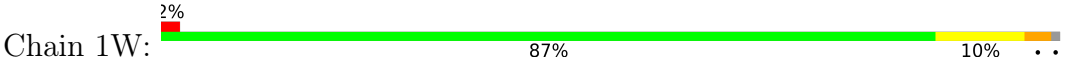
• Molecule 17: 50S ribosomal protein L21



• Molecule 17: 50S ribosomal protein L21



• Molecule 18: 50S ribosomal protein L22



• Molecule 18: 50S ribosomal protein L22

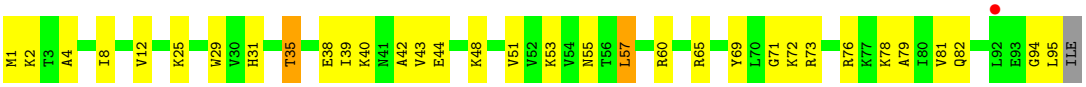
Chain 2W:

• Molecule 19: 50S ribosomal protein L23

Chain 1X:

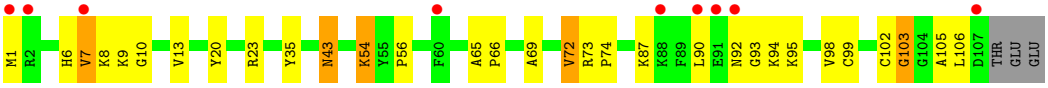
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



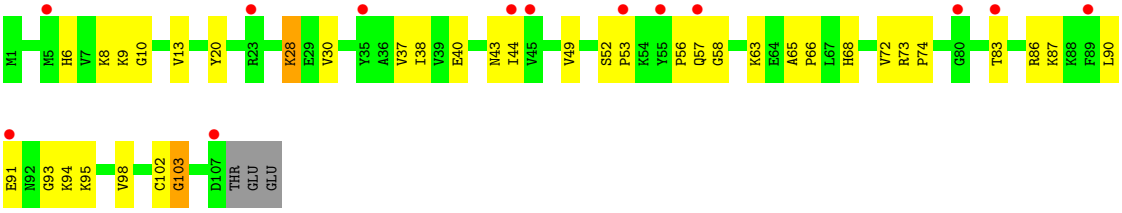
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



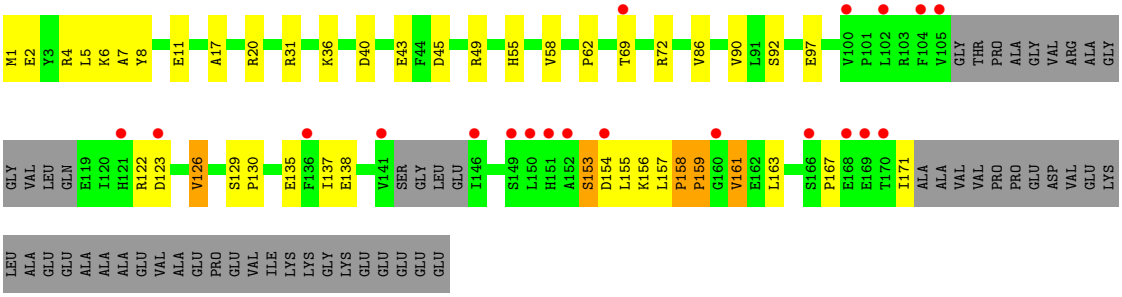
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



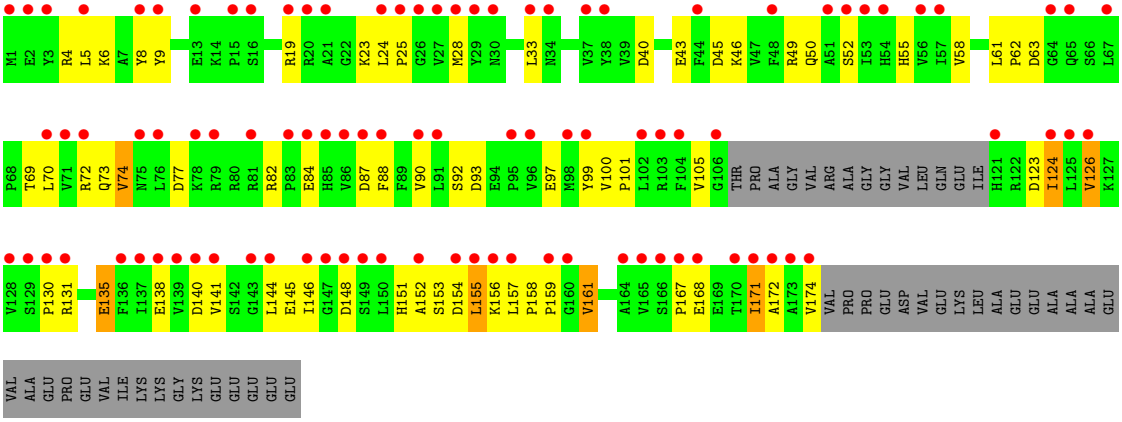
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



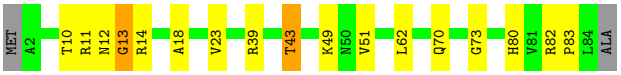
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



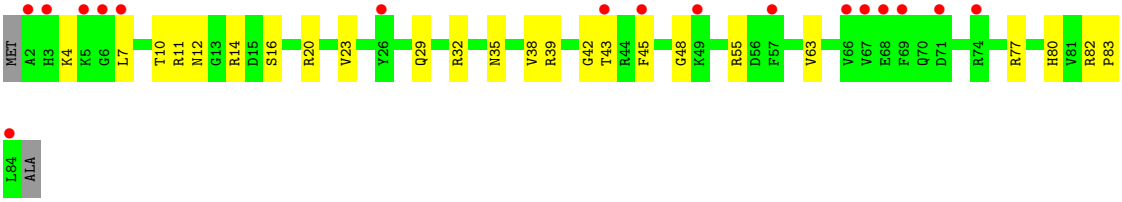
• Molecule 22: 50S ribosomal protein L27

Chain 10:



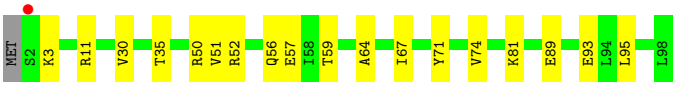
• Molecule 22: 50S ribosomal protein L27

Chain 20:

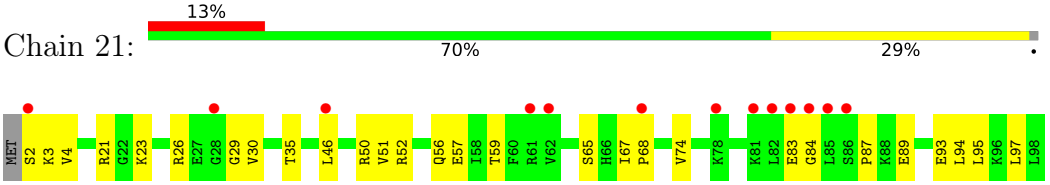


• Molecule 23: 50S ribosomal protein L28

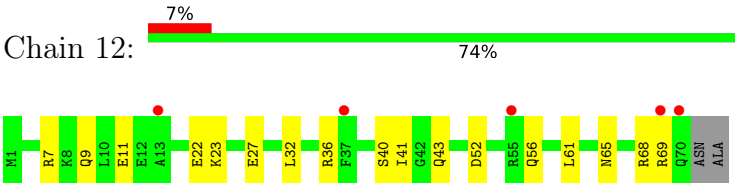
Chain 11:



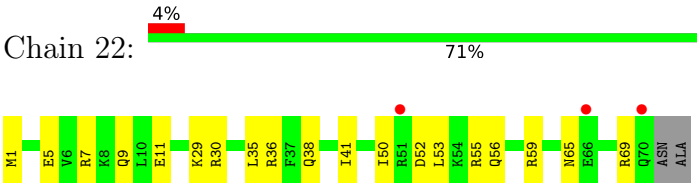
• Molecule 23: 50S ribosomal protein L28



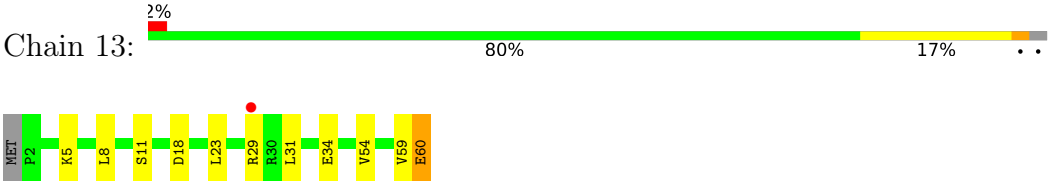
• Molecule 24: 50S ribosomal protein L29



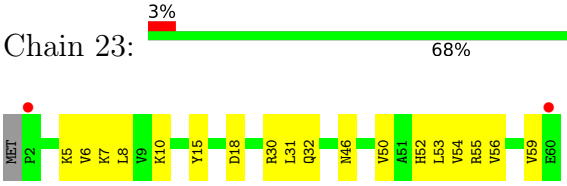
• Molecule 24: 50S ribosomal protein L29



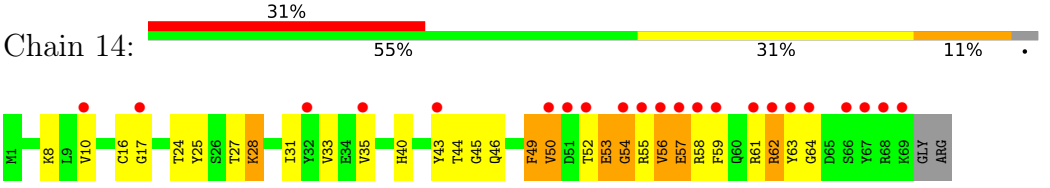
• Molecule 25: 50S ribosomal protein L30



• Molecule 25: 50S ribosomal protein L30

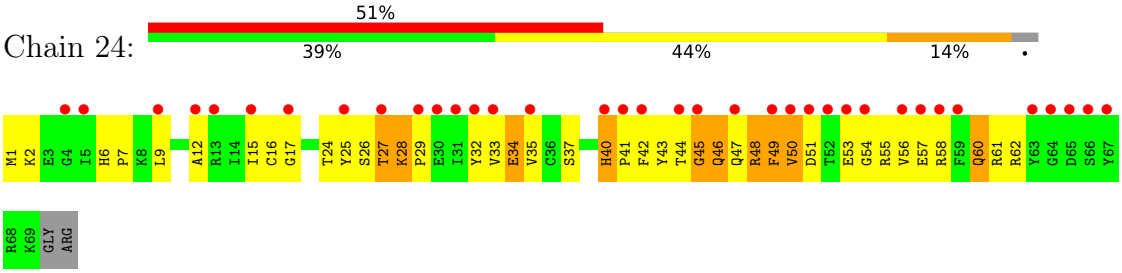


• Molecule 26: 50S ribosomal protein L31



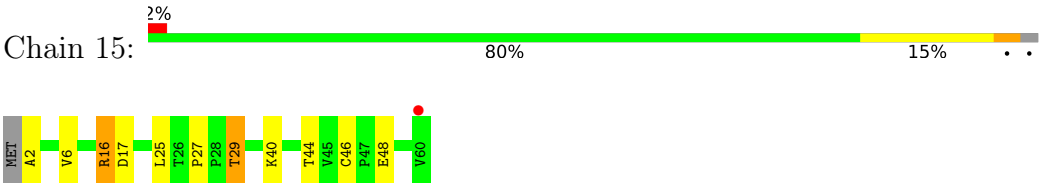
• Molecule 26: 50S ribosomal protein L31

Chain 24:



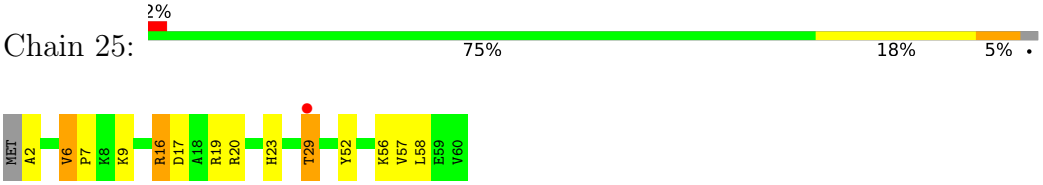
• Molecule 27: 50S ribosomal protein L32

Chain 15:



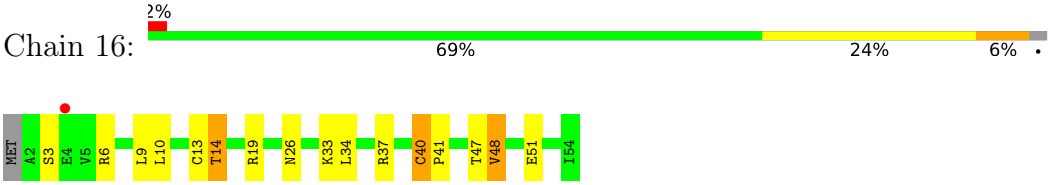
• Molecule 27: 50S ribosomal protein L32

Chain 25:



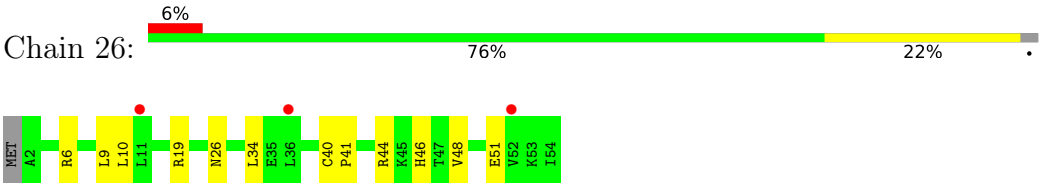
• Molecule 28: 50S ribosomal protein L33

Chain 16:



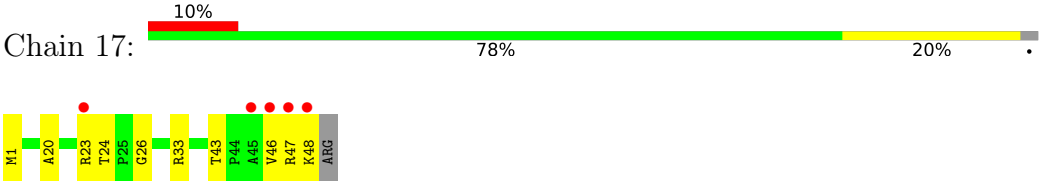
• Molecule 28: 50S ribosomal protein L33

Chain 26:



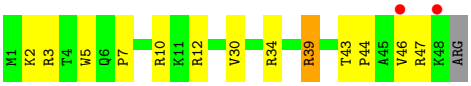
• Molecule 29: 50S ribosomal protein L34

Chain 17:



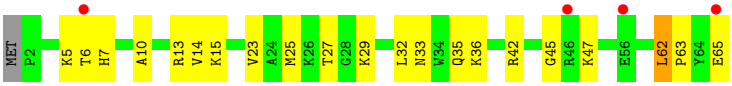
• Molecule 29: 50S ribosomal protein L34

Chain 27:



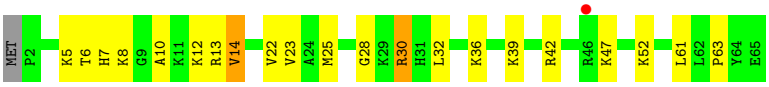
• Molecule 30: 50S ribosomal protein L35

Chain 18:



• Molecule 30: 50S ribosomal protein L35

Chain 28:

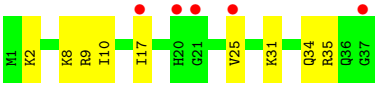


• Molecule 31: 50S ribosomal protein L36

Chain 19:

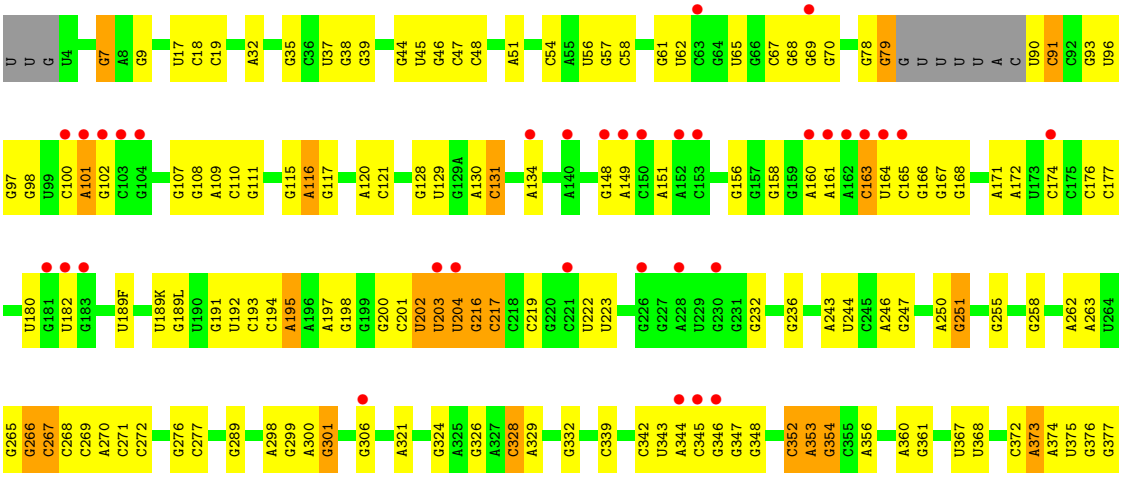
• Molecule 31: 50S ribosomal protein L36

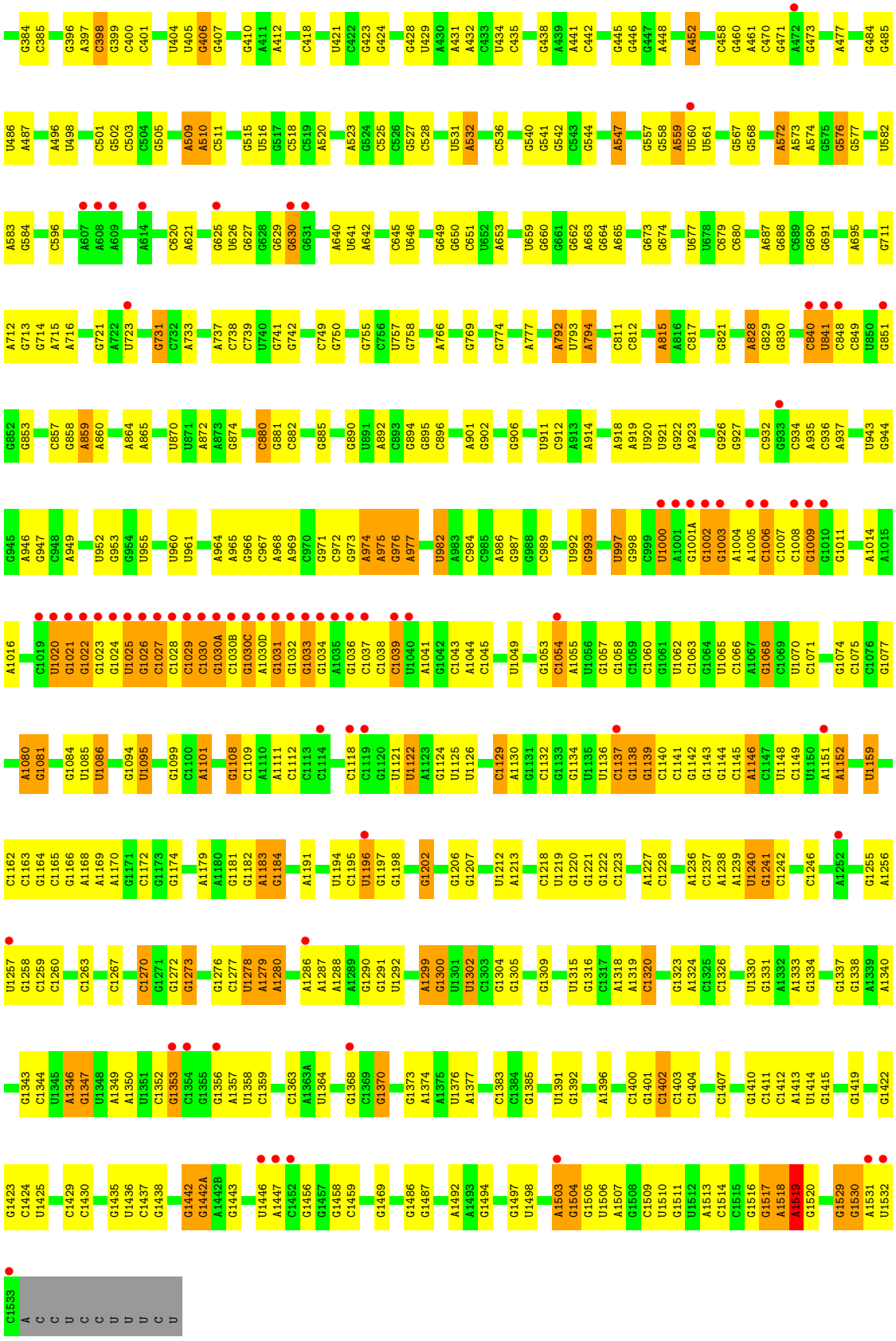
Chain 29:



• Molecule 32: 16S Ribosomal RNA

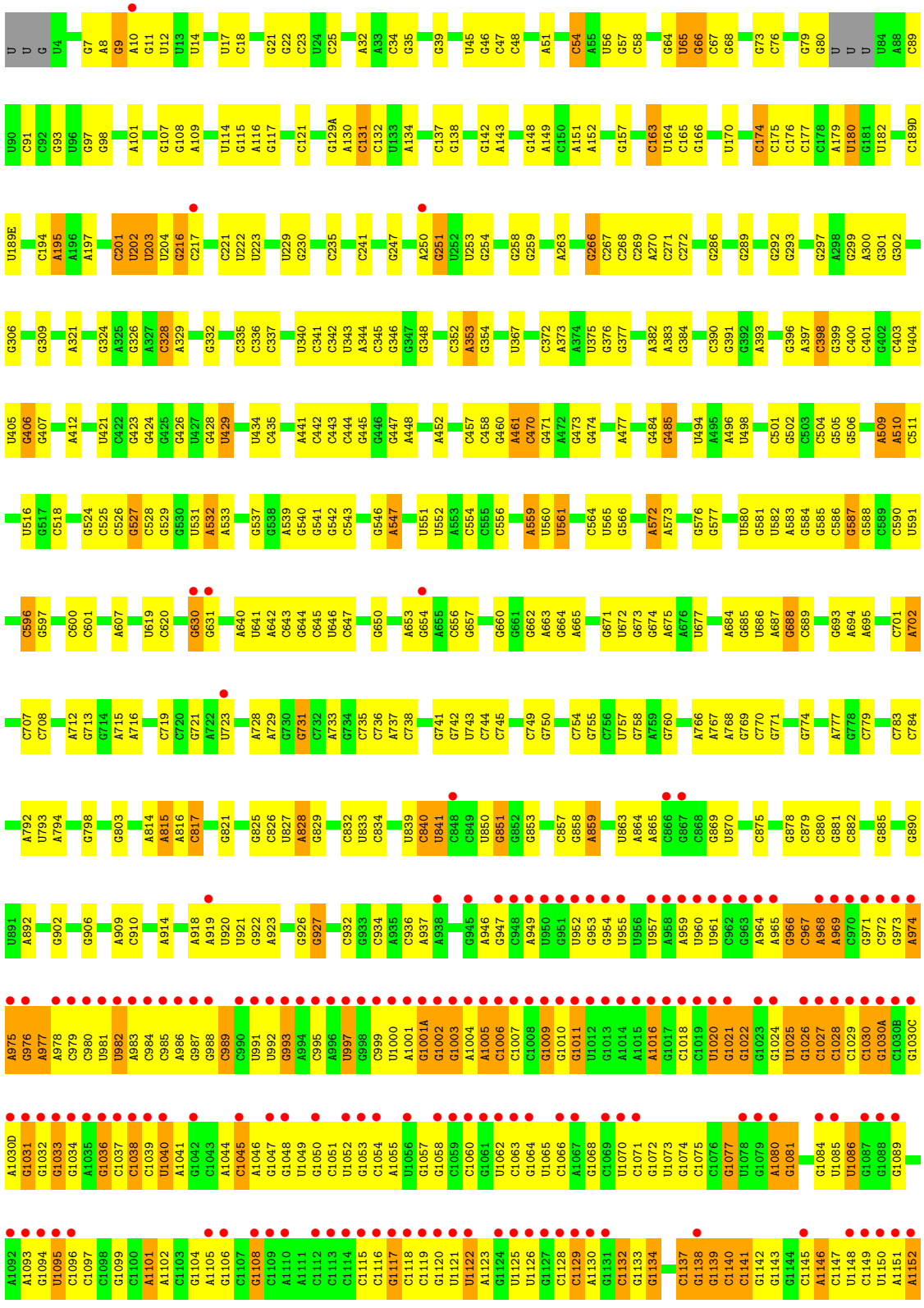
Chain 1a:

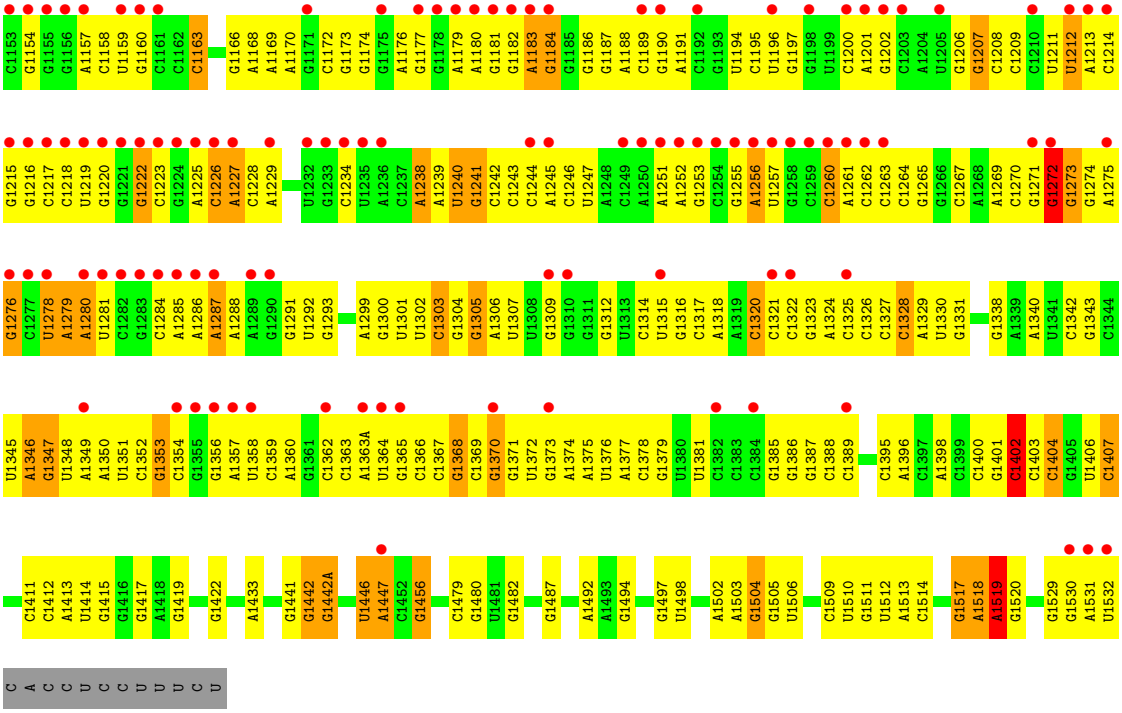




• Molecule 32: 16S Ribosomal RNA

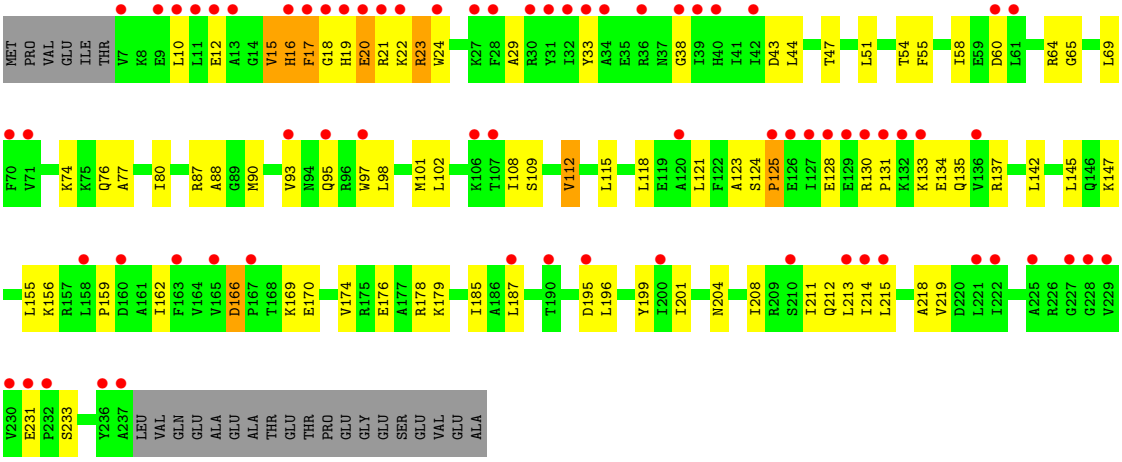
Chain 2a:





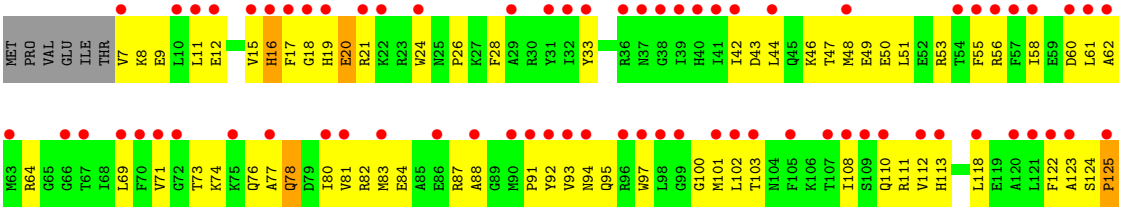
• Molecule 33: 30S ribosomal protein S2

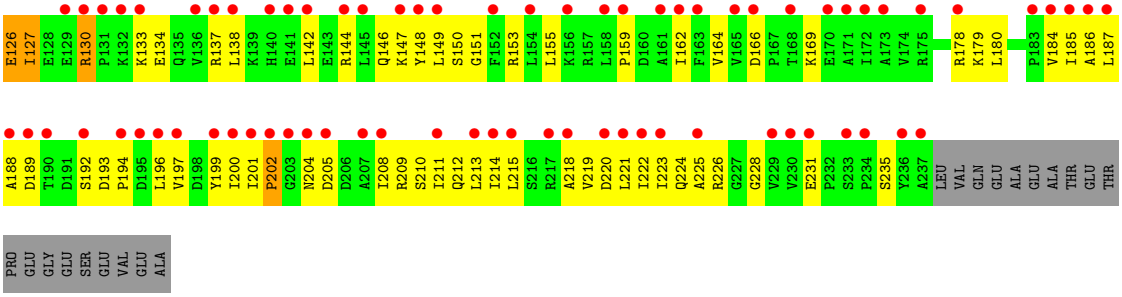
Chain 1b:



• Molecule 33: 30S ribosomal protein S2

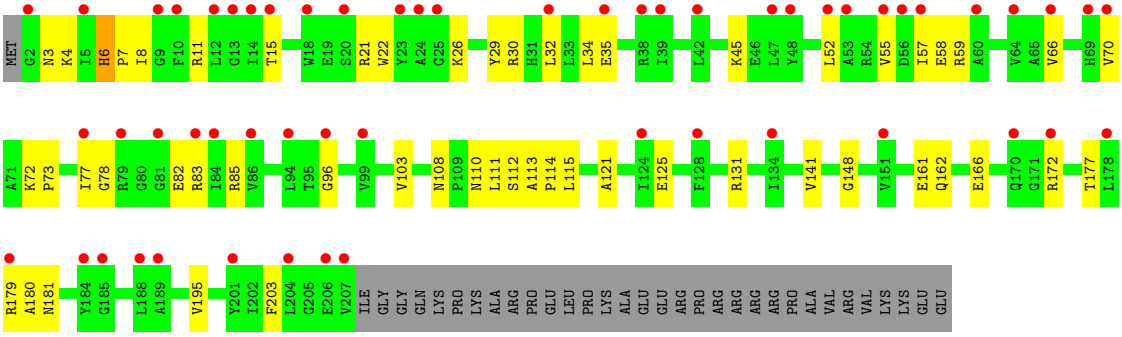
Chain 2b:





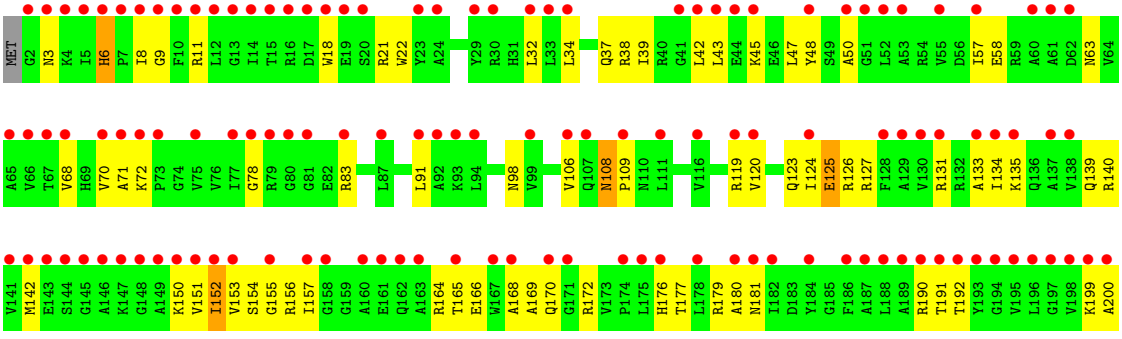
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



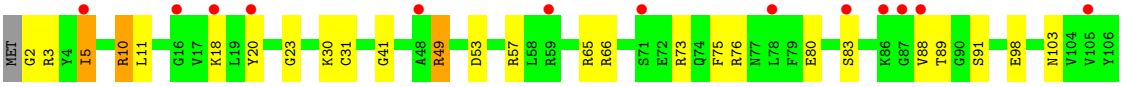
• Molecule 34: 30S ribosomal protein S3

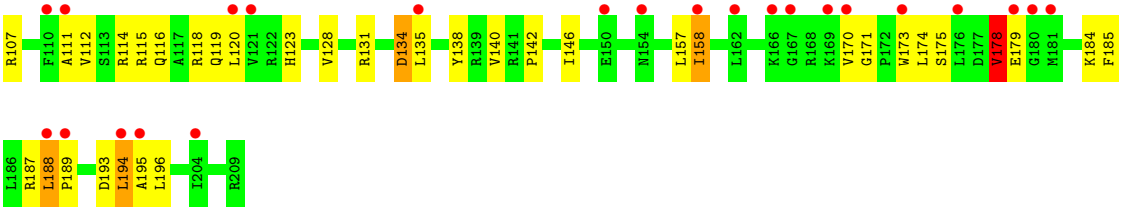
Chain 2c:



• Molecule 35: 30S ribosomal protein S4

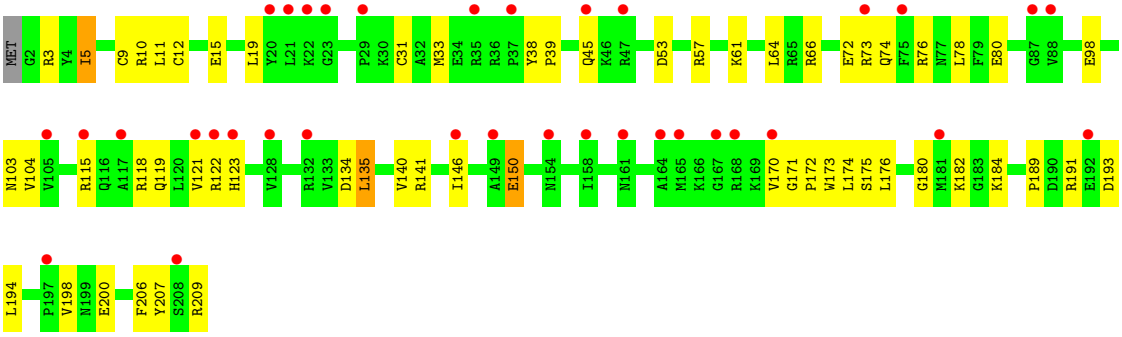
Chain 1d:





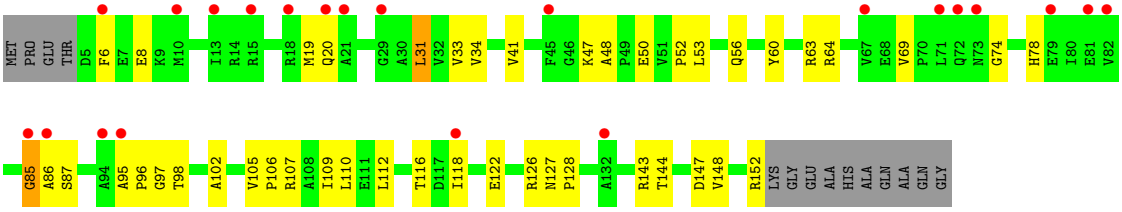
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



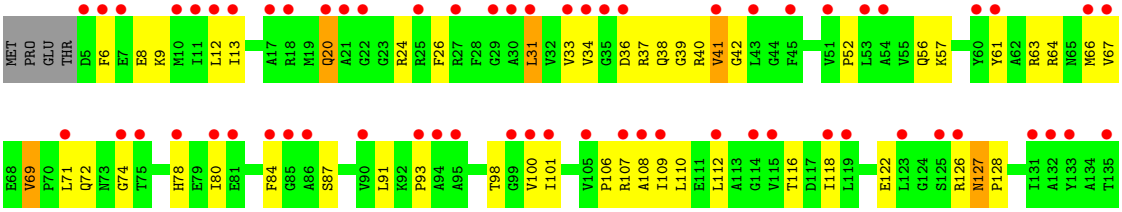
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



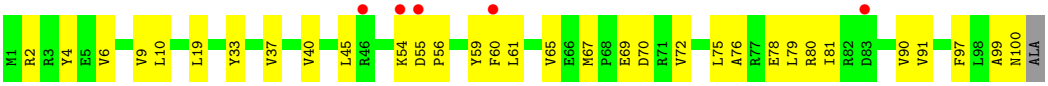
• Molecule 36: 30S ribosomal protein S5

Chain 2e:

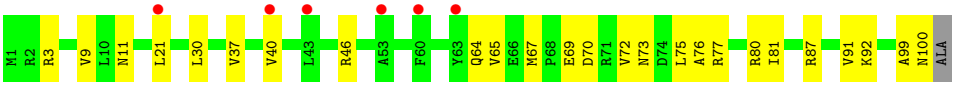


• Molecule 37: 30S ribosomal protein S6

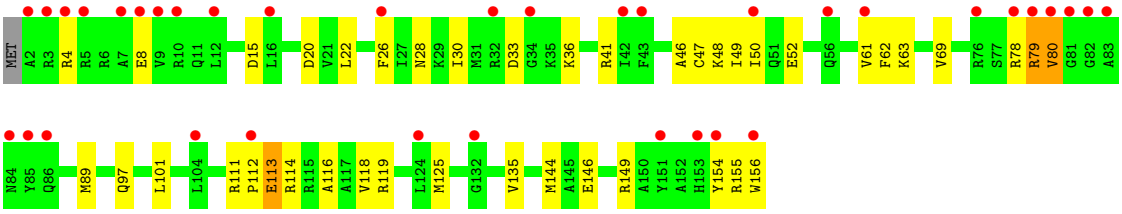
Chain 1f:



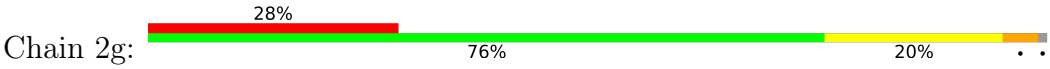
• Molecule 37: 30S ribosomal protein S6

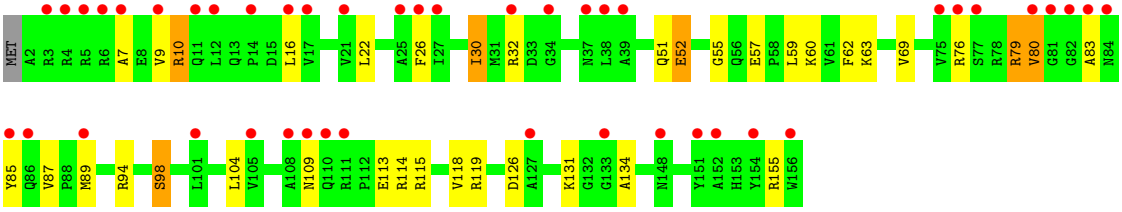


• Molecule 38: 30S ribosomal protein S7

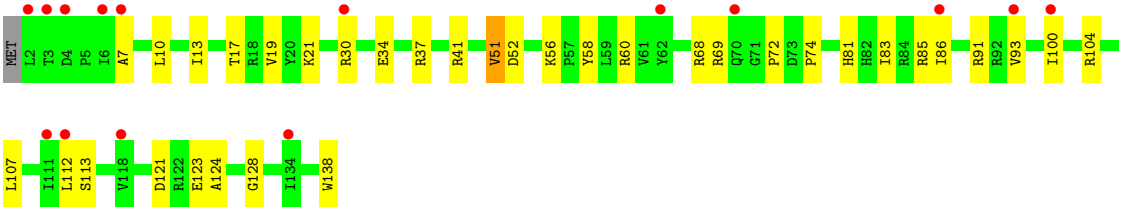


• Molecule 38: 30S ribosomal protein S7

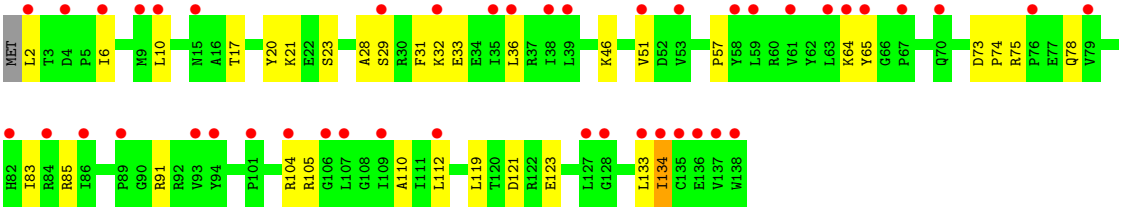




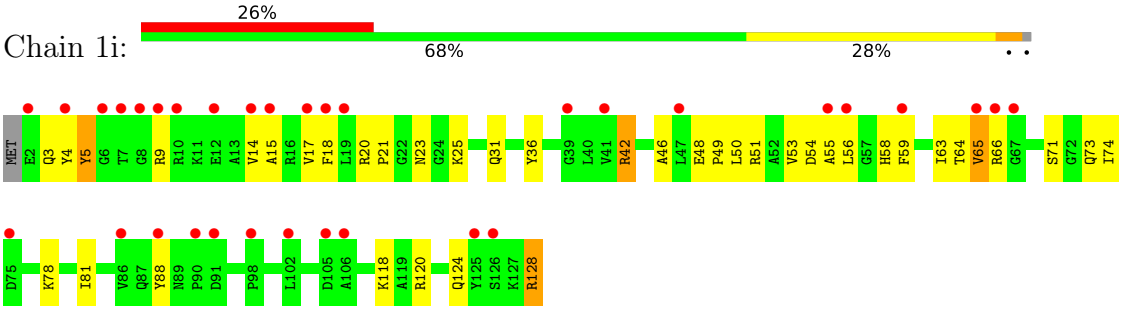
• Molecule 39: 30S ribosomal protein S8



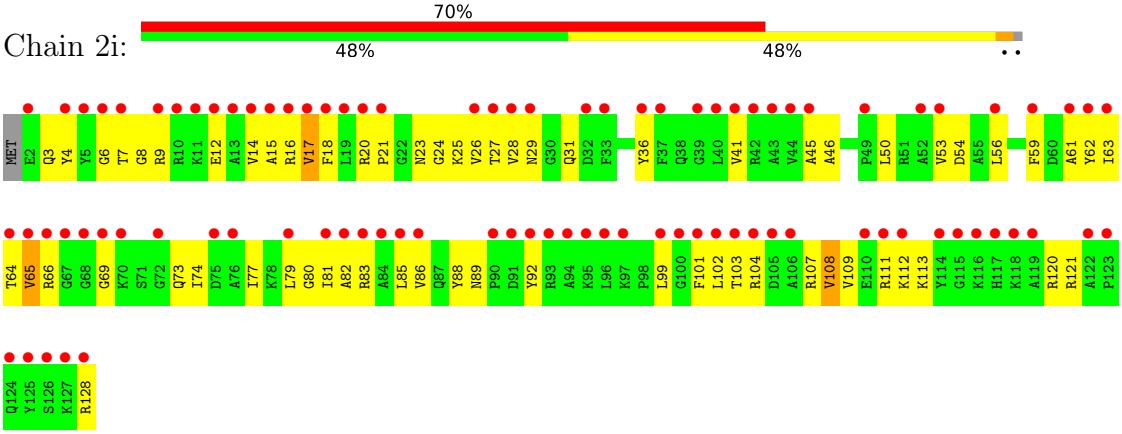
• Molecule 39: 30S ribosomal protein S8



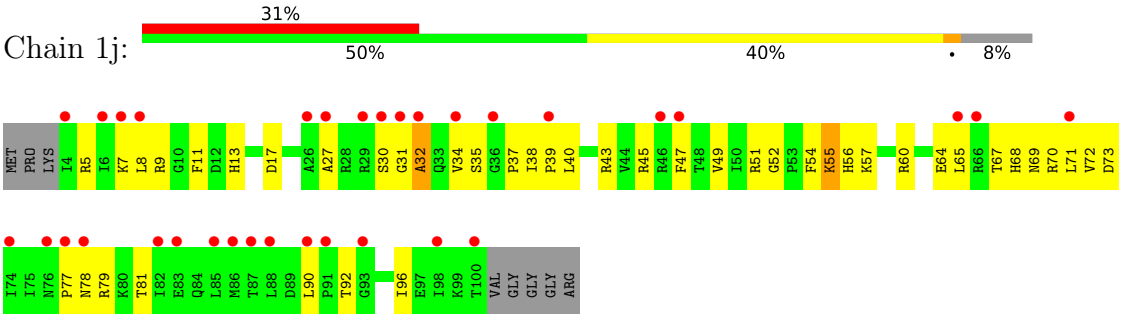
• Molecule 40: 30S ribosomal protein S9



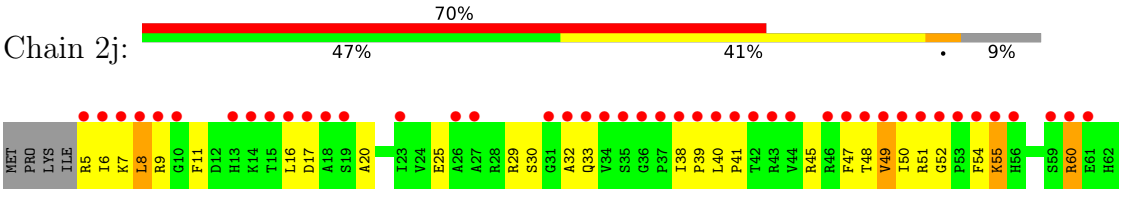
• Molecule 40: 30S ribosomal protein S9

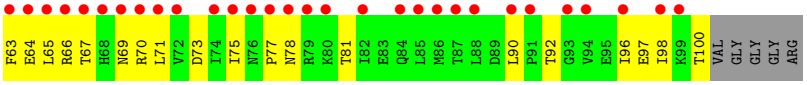


• Molecule 41: 30S ribosomal protein S10



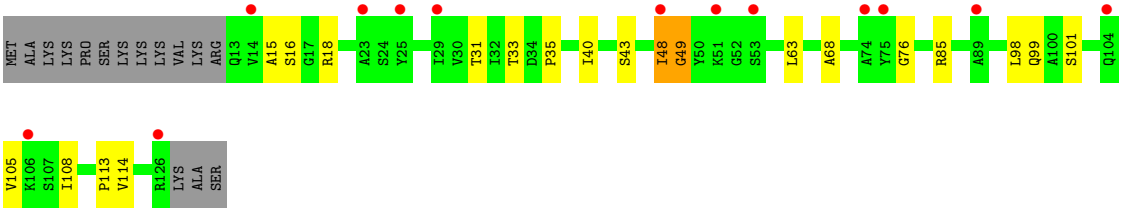
• Molecule 41: 30S ribosomal protein S10





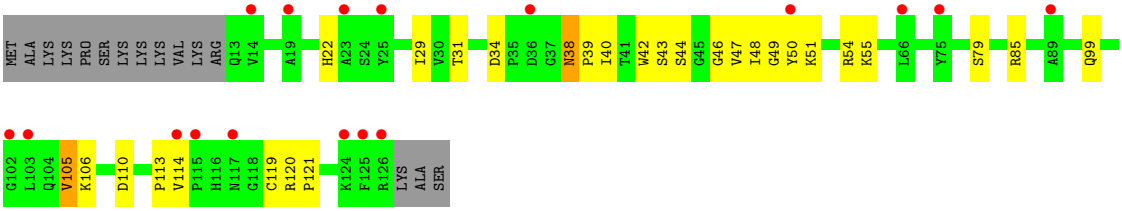
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



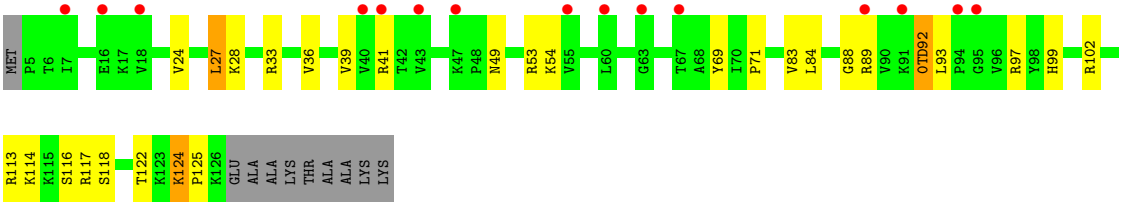
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



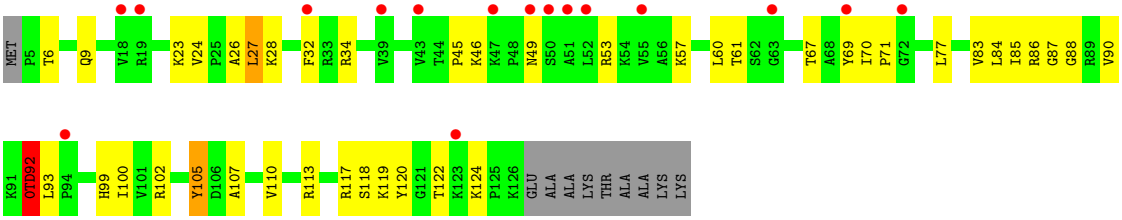
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



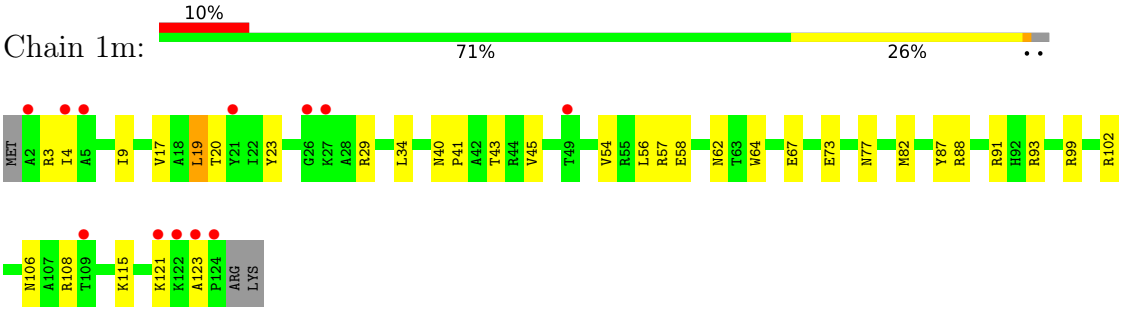
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



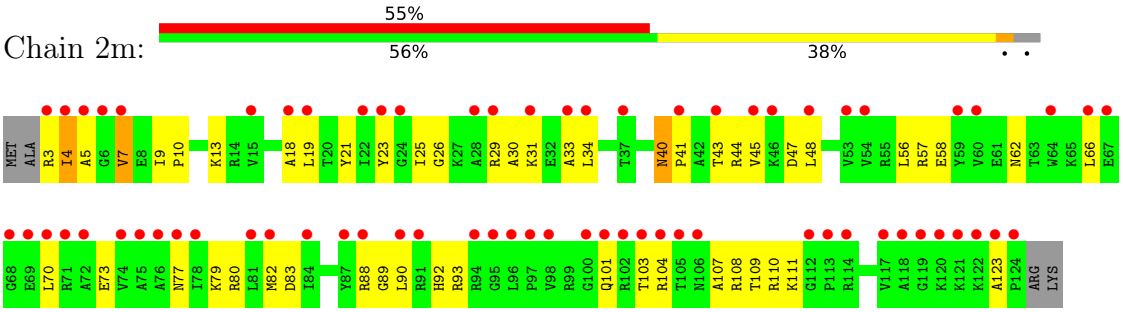
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



• Molecule 44: 30S ribosomal protein S13

Chain 2m:

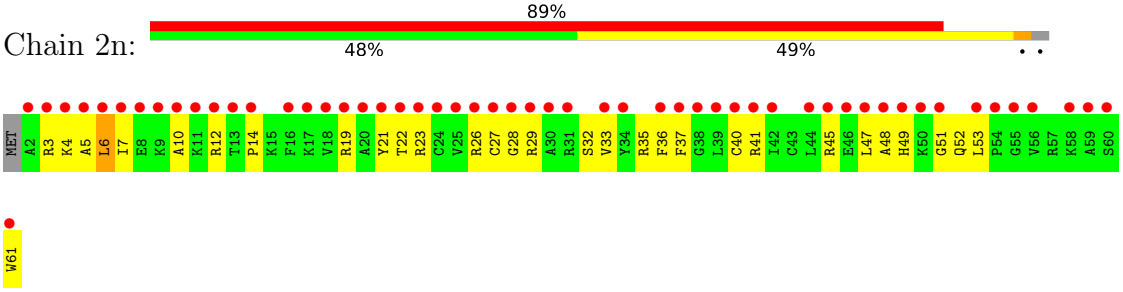


• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:

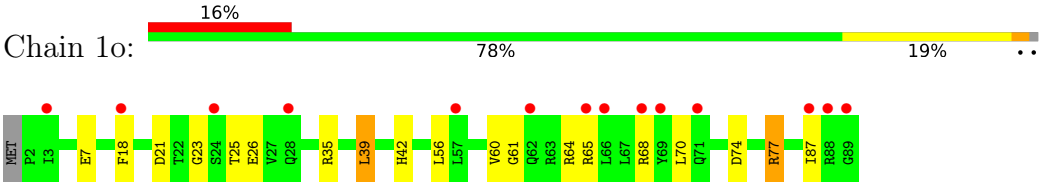
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:



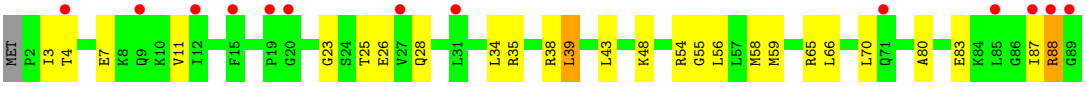
• Molecule 46: 30S ribosomal protein S15

Chain 1o:



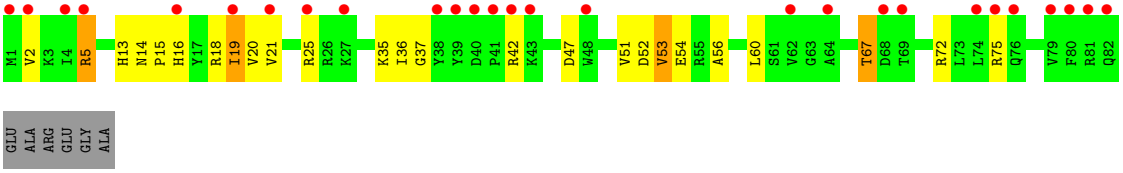
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



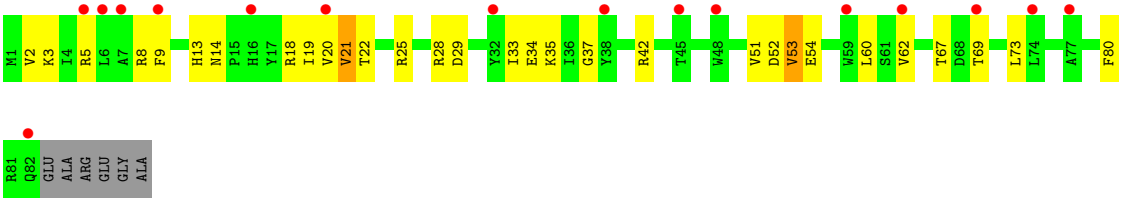
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



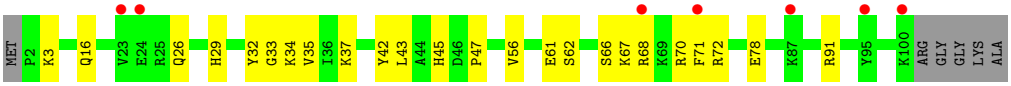
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



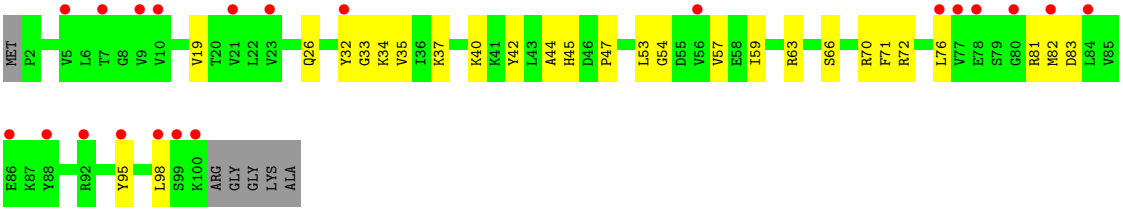
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



• Molecule 48: 30S ribosomal protein S17

Chain 2q:

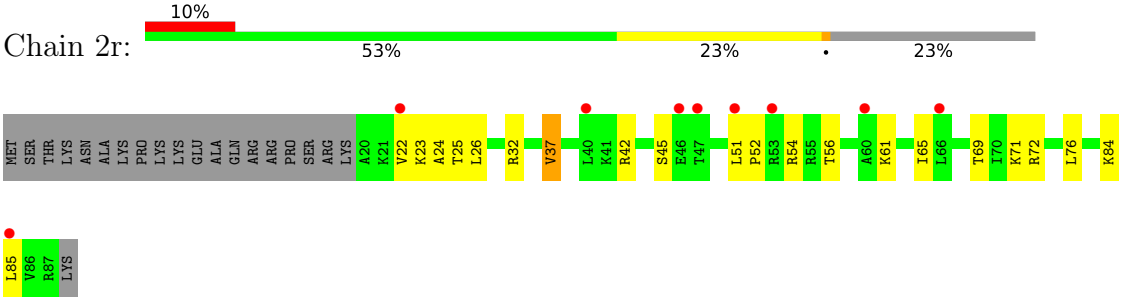


• Molecule 49: 30S ribosomal protein S18

Chain 1r:

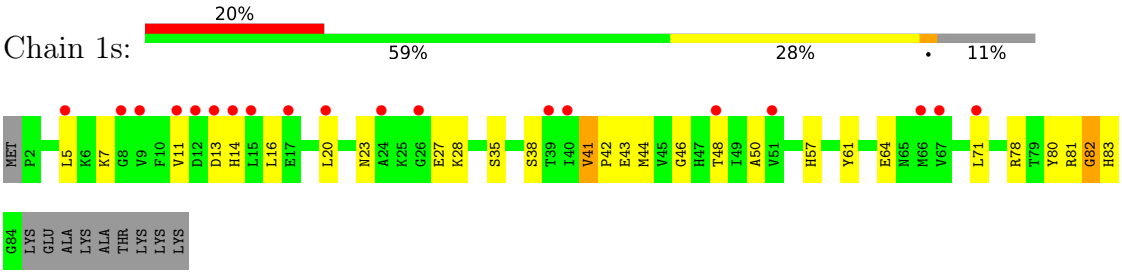
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



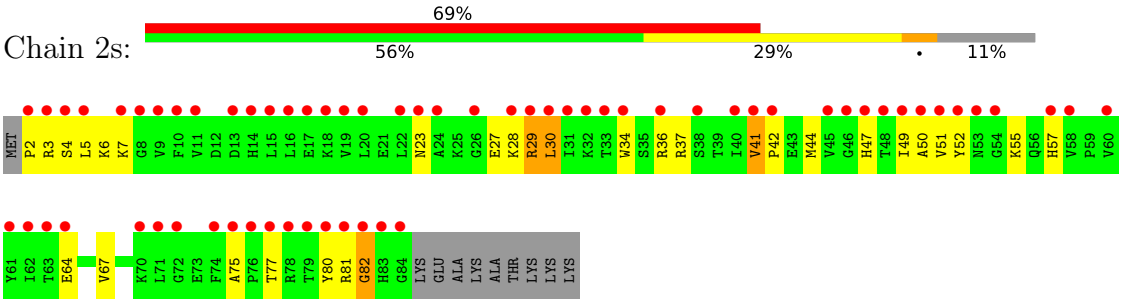
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



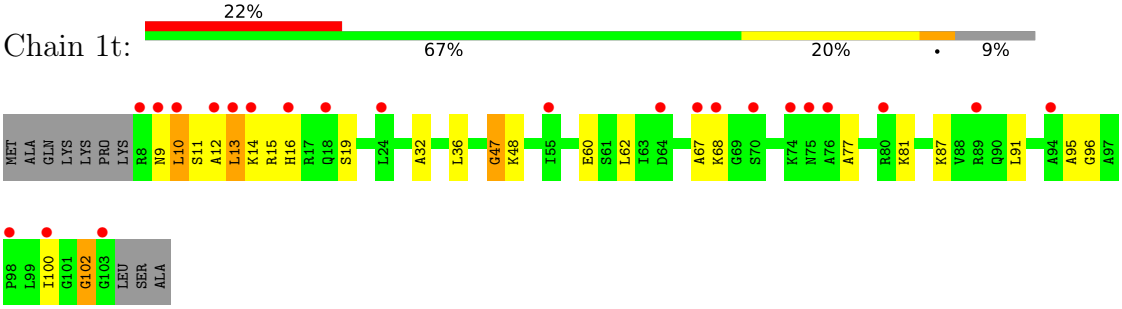
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



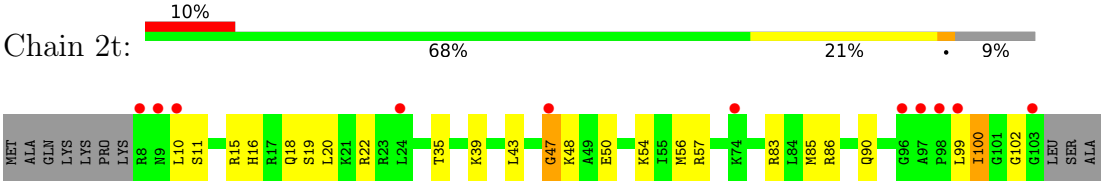
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



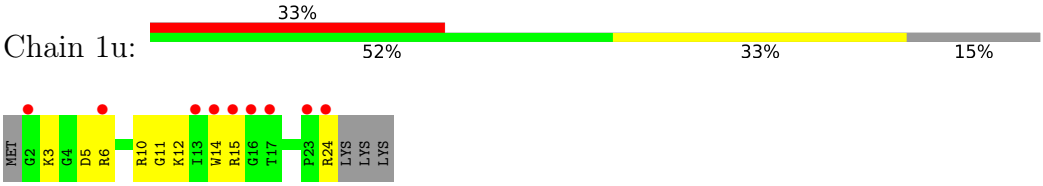
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



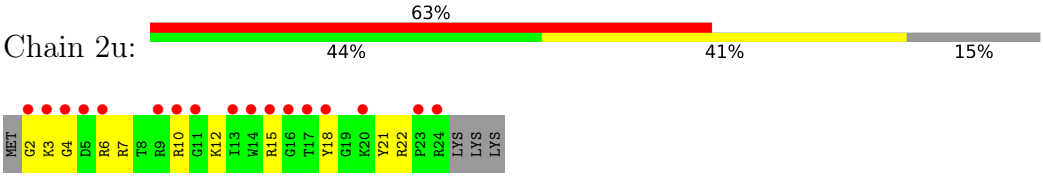
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



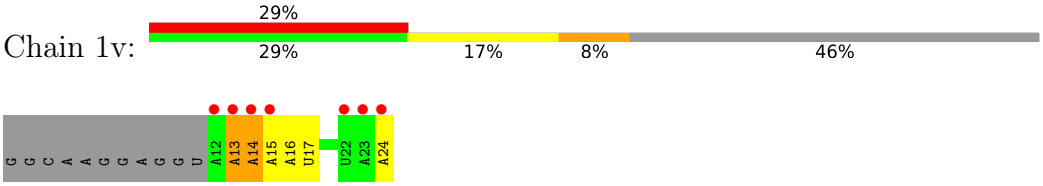
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



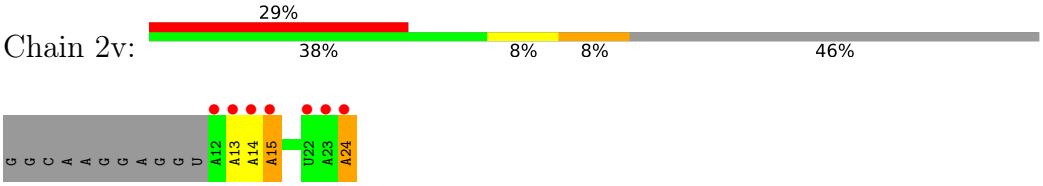
• Molecule 53: mRNA

Chain 1v:



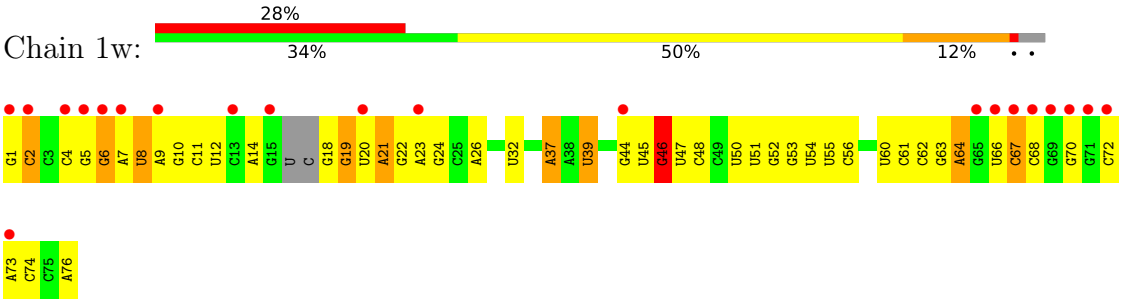
• Molecule 53: mRNA

Chain 2v:



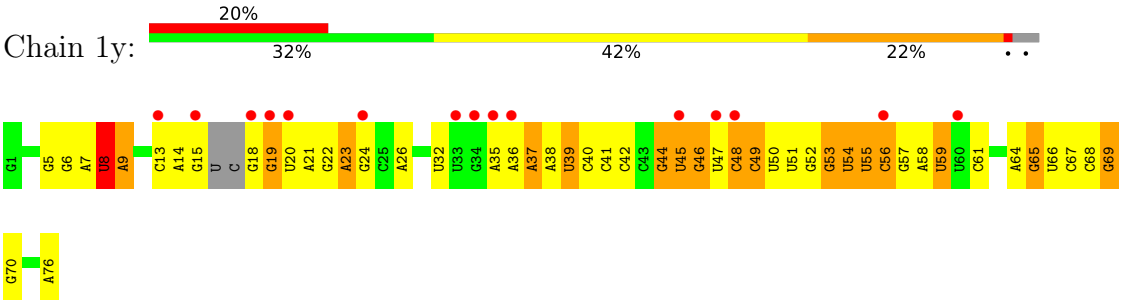
• Molecule 54: A-site and E-site tRNAs

Chain 1w:



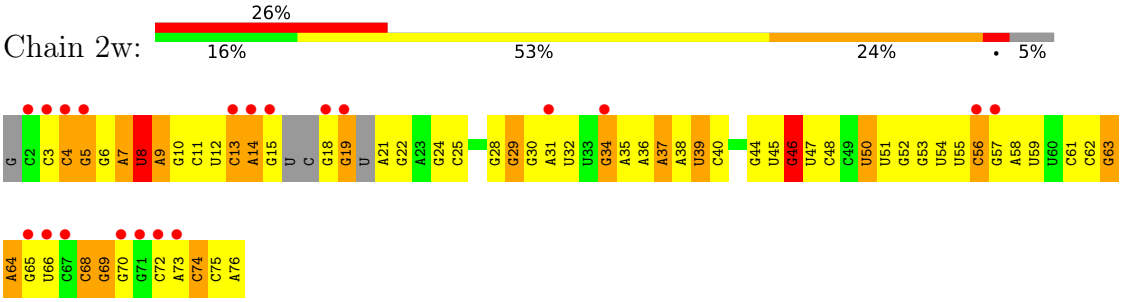
• Molecule 54: A-site and E-site tRNAs

Chain 1y:



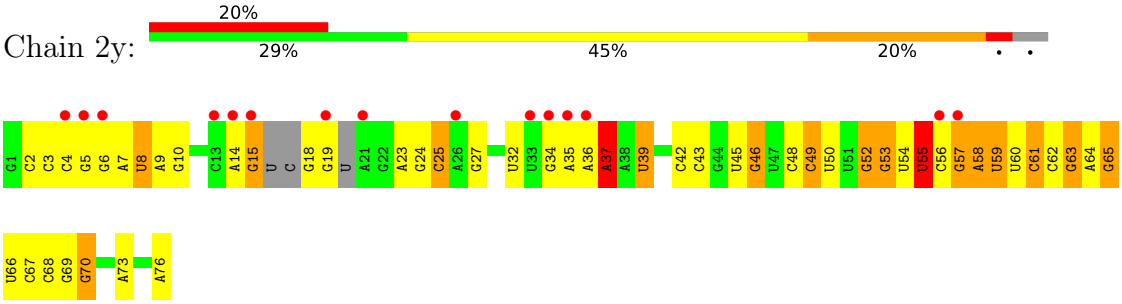
• Molecule 54: A-site and E-site tRNAs

Chain 2w:



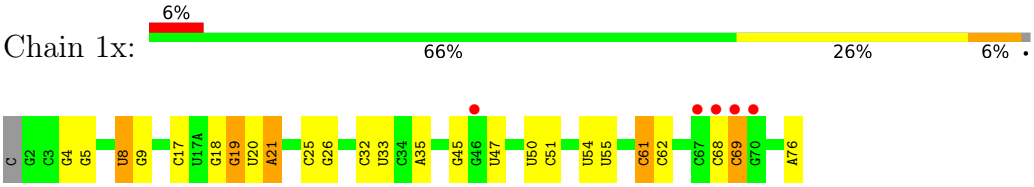
• Molecule 54: A-site and E-site tRNAs

Chain 2y:



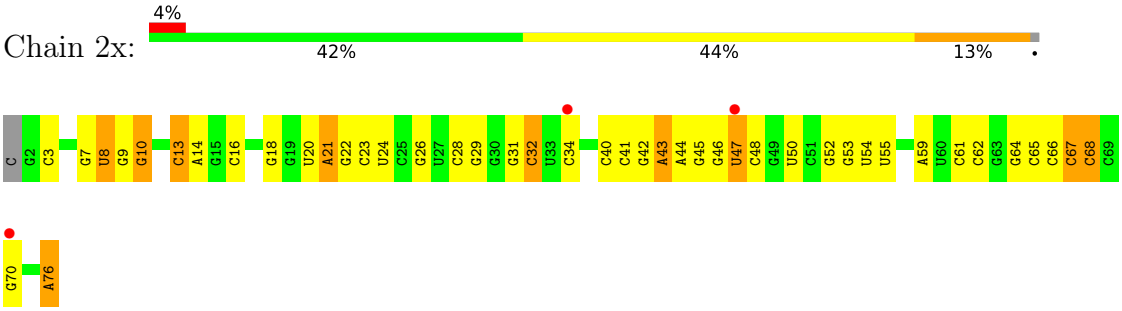
• Molecule 55: P-site tRNA

Chain 1x:



• Molecule 55: P-site tRNA

Chain 2x:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.70Å 450.05Å 624.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	122.01 – 2.50 122.01 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (122.01-2.50) 97.8 (122.01-2.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.22 (at 2.52Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.231 , 0.281 0.232 , 0.282	Depositor DCC
R_{free} test set	98495 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	47.4	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 57.4	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	0.91	EDS
Total number of atoms	300910	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% 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: 0TD, 4OC, MA6, 5MC, OMG, UR3, MG, M2G, PSU, 7MG, 2MG, 2MA, MIA, ZN, K, 4SU, SF4, 5MU, 2MU

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	0.34	0/69009	0.51	3/107712 (0.0%)
1	2A	0.28	0/67293	0.49	1/105034 (0.0%)
2	1B	0.26	0/2882	0.41	0/4494
2	2B	0.30	0/2879	0.48	0/4487
3	1D	0.56	0/2186	0.90	2/2944 (0.1%)
3	2D	0.49	0/2186	0.93	4/2944 (0.1%)
4	1E	0.57	0/1592	0.93	0/2149
4	2E	0.49	0/1592	0.94	4/2149 (0.2%)
5	1F	0.55	0/1619	0.89	3/2193 (0.1%)
5	2F	0.46	0/1615	0.93	3/2188 (0.1%)
6	1G	0.44	0/1448	0.87	3/1957 (0.2%)
6	2G	0.44	0/1453	1.00	6/1963 (0.3%)
7	1H	0.49	0/1356	0.92	3/1834 (0.2%)
7	2H	0.44	0/1356	0.92	2/1834 (0.1%)
8	1I	0.42	0/1112	0.88	1/1514 (0.1%)
8	2I	0.41	0/1079	0.92	4/1475 (0.3%)
9	1N	0.54	0/1144	0.90	2/1543 (0.1%)
9	2N	0.46	0/1144	0.99	6/1543 (0.4%)
10	1O	0.54	0/943	0.88	0/1269
10	2O	0.44	0/943	0.84	0/1269
11	1P	0.54	0/1152	0.86	2/1533 (0.1%)
11	2P	0.43	0/1152	0.97	4/1533 (0.3%)
12	1Q	0.54	0/1143	0.79	0/1527
12	2Q	0.46	0/1143	0.91	0/1527
13	1R	0.59	0/982	0.88	1/1312 (0.1%)
13	2R	0.52	0/982	0.85	0/1312
14	1S	0.45	0/883	0.85	3/1176 (0.3%)
14	2S	0.45	0/880	0.92	1/1172 (0.1%)
15	1T	0.50	0/1105	0.85	0/1477
15	2T	0.45	0/1097	0.85	2/1468 (0.1%)
16	1U	0.61	0/977	0.86	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.48	0/977	0.88	0/1301
17	1V	0.58	0/782	0.88	0/1049
17	2V	0.45	0/782	0.91	0/1049
18	1W	0.63	0/897	0.92	0/1205
18	2W	0.50	0/897	0.86	0/1205
19	1X	0.53	0/764	0.88	2/1025 (0.2%)
19	2X	0.49	0/764	0.88	0/1025
20	1Y	0.49	0/819	0.85	0/1095
20	2Y	0.41	0/819	0.91	2/1095 (0.2%)
21	1Z	0.45	0/1267	0.98	5/1717 (0.3%)
21	2Z	0.41	0/1299	0.93	1/1763 (0.1%)
22	10	0.53	0/662	0.97	1/881 (0.1%)
22	20	0.41	0/662	0.93	2/881 (0.2%)
23	11	0.50	0/762	0.85	0/1014
23	21	0.46	0/762	0.87	0/1014
24	12	0.51	0/590	0.79	0/781
24	22	0.41	0/590	0.80	0/781
25	13	0.56	0/474	0.93	2/635 (0.3%)
25	23	0.42	0/469	0.88	0/630
26	14	0.44	0/565	1.08	6/761 (0.8%)
26	24	0.50	0/545	1.06	5/737 (0.7%)
27	15	0.60	0/469	0.86	1/635 (0.2%)
27	25	0.49	0/469	0.91	0/635
28	16	0.55	0/460	0.79	2/613 (0.3%)
28	26	0.41	0/456	0.77	0/608
29	17	0.54	0/426	0.93	1/561 (0.2%)
29	27	0.57	0/426	0.92	0/561
30	18	0.53	0/525	0.90	2/691 (0.3%)
30	28	0.47	0/525	0.90	2/691 (0.3%)
31	19	0.51	0/310	0.89	0/407
31	29	0.46	0/310	0.92	0/407
32	1a	0.24	0/35795	0.44	0/55864
32	2a	0.24	1/35886 (0.0%)	0.45	2/56005 (0.0%)
33	1b	0.42	0/1881	0.96	10/2542 (0.4%)
33	2b	0.44	0/1860	0.98	5/2518 (0.2%)
34	1c	0.39	0/1572	0.88	5/2126 (0.2%)
34	2c	0.47	0/1566	0.97	9/2119 (0.4%)
35	1d	0.40	0/1685	0.87	2/2262 (0.1%)
35	2d	0.42	0/1704	0.86	4/2284 (0.2%)
36	1e	0.43	0/1145	0.92	4/1543 (0.3%)
36	2e	0.45	0/1149	1.01	4/1548 (0.3%)
37	1f	0.43	0/823	0.80	0/1115
37	2f	0.42	0/829	0.81	2/1123 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.42	0/1250	0.87	1/1679 (0.1%)
38	2g	0.38	0/1254	0.90	2/1683 (0.1%)
39	1h	0.40	0/1108	0.90	1/1494 (0.1%)
39	2h	0.39	0/1108	0.90	3/1494 (0.2%)
40	1i	0.41	0/1002	0.91	1/1346 (0.1%)
40	2i	0.42	0/997	0.91	0/1343
41	1j	0.39	0/722	0.95	4/982 (0.4%)
41	2j	0.47	0/727	1.03	5/988 (0.5%)
42	1k	0.44	0/844	0.86	2/1145 (0.2%)
42	2k	0.41	0/848	0.85	2/1149 (0.2%)
43	1l	0.43	0/937	0.86	2/1260 (0.2%)
43	2l	0.41	0/937	0.94	4/1260 (0.3%)
44	1m	0.41	0/969	0.89	1/1302 (0.1%)
44	2m	0.43	0/961	0.91	4/1291 (0.3%)
45	1n	0.39	0/501	0.81	0/664
45	2n	0.39	0/501	0.84	0/664
46	1o	0.41	0/739	0.83	1/985 (0.1%)
46	2o	0.38	0/739	0.82	0/985
47	1p	0.40	0/697	0.83	1/939 (0.1%)
47	2p	0.41	0/693	0.77	0/935
48	1q	0.40	0/836	0.84	0/1117
48	2q	0.37	0/836	0.80	0/1117
49	1r	0.43	0/560	0.80	0/746
49	2r	0.36	0/560	0.79	0/746
50	1s	0.38	0/667	0.94	1/900 (0.1%)
50	2s	0.54	0/661	1.10	3/893 (0.3%)
51	1t	0.37	0/730	0.85	0/965
51	2t	0.43	0/729	0.84	1/965 (0.1%)
52	1u	0.32	0/203	0.79	0/266
52	2u	0.38	0/203	0.80	0/266
53	1v	0.24	0/310	0.38	0/480
53	2v	0.32	0/310	0.43	0/480
54	1w	0.30	1/1606 (0.1%)	0.44	0/2497
54	1y	0.29	1/1606 (0.1%)	0.44	0/2497
54	2w	0.31	0/1556	0.43	0/2418
54	2y	0.30	0/1583	0.48	0/2459
55	1x	0.30	0/1725	0.45	0/2689
55	2x	0.27	1/1725 (0.1%)	0.42	0/2689
All	All	0.35	4/316686 (0.0%)	0.62	180/474113 (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
43	2l	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1y	8	4SU	O3'-P	5.24	1.61	1.56
54	1w	8	4SU	O3'-P	5.23	1.61	1.56
32	2a	1498	UR3	O3'-P	5.16	1.61	1.56
55	2x	8	4SU	O3'-P	5.15	1.61	1.56

All (180) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
21	1Z	158	PRO	CA-C-N	10.29	132.70	119.84
21	1Z	158	PRO	C-N-CA	10.29	132.70	119.84
9	2N	125	GLY	CA-C-N	8.71	128.44	119.56
9	2N	125	GLY	C-N-CA	8.71	128.44	119.56
33	1b	123	ALA	N-CA-C	-8.18	103.29	113.18
11	2P	22	GLY	CA-C-N	8.01	127.58	118.85
11	2P	22	GLY	C-N-CA	8.01	127.58	118.85
26	14	54	GLY	N-CA-C	7.92	126.70	115.30
34	2c	48	TYR	N-CA-C	-7.92	102.64	111.82
46	1o	87	ILE	N-CA-C	7.62	118.90	111.67
22	20	82	ARG	CA-C-N	7.56	127.57	119.78
22	20	82	ARG	C-N-CA	7.56	127.57	119.78
1	1A	2014	G	C2'-C3'-O3'	7.05	120.08	109.50
50	2s	82	GLY	N-CA-C	7.04	120.30	111.85
41	2j	90	LEU	CA-C-N	7.01	128.60	119.84
41	2j	90	LEU	C-N-CA	7.01	128.60	119.84
34	1c	72	LYS	CA-C-N	6.96	128.55	119.84
34	1c	72	LYS	C-N-CA	6.96	128.55	119.84
33	2b	130	ARG	CA-C-N	6.94	126.97	119.89
33	2b	130	ARG	C-N-CA	6.94	126.97	119.89
6	2G	48	GLU	N-CA-C	-6.85	104.06	113.18
9	1N	125	GLY	CA-C-N	6.84	126.54	119.56
9	1N	125	GLY	C-N-CA	6.84	126.54	119.56
41	2j	52	GLY	CA-C-N	6.82	126.42	119.19
41	2j	52	GLY	C-N-CA	6.82	126.42	119.19
39	2h	73	ASP	CA-C-N	6.80	127.76	120.83
39	2h	73	ASP	C-N-CA	6.80	127.76	120.83
8	2I	124	GLY	N-CA-C	6.77	119.56	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	2P	44	GLY	CA-C-N	6.67	133.71	121.70
11	2P	44	GLY	C-N-CA	6.67	133.71	121.70
47	1p	5	ARG	N-CA-C	6.53	117.75	108.74
42	1k	40	ILE	N-CA-C	-6.52	106.62	111.90
11	1P	22	GLY	CA-C-N	6.49	125.92	118.85
11	1P	22	GLY	C-N-CA	6.49	125.92	118.85
43	2l	105	TYR	CB-CA-C	-6.48	108.41	117.23
34	2c	6	HIS	CA-C-N	6.37	126.06	119.56
34	2c	6	HIS	C-N-CA	6.37	126.06	119.56
35	2d	171	GLY	CA-C-N	6.36	126.11	119.05
35	2d	171	GLY	C-N-CA	6.36	126.11	119.05
37	2f	11	ASN	CA-C-N	6.22	125.85	119.56
37	2f	11	ASN	C-N-CA	6.22	125.85	119.56
6	2G	44	GLY	N-CA-C	-6.18	106.80	115.32
34	2c	108	ASN	CA-C-N	6.14	126.04	119.28
34	2c	108	ASN	C-N-CA	6.14	126.04	119.28
43	2l	119	LYS	N-CA-C	-6.03	101.99	110.50
5	1F	89	VAL	N-CA-C	6.01	116.07	110.42
26	14	40	HIS	CA-C-N	6.00	126.16	119.32
26	14	40	HIS	C-N-CA	6.00	126.16	119.32
5	1F	9	ILE	CA-C-N	5.94	125.88	119.76
5	1F	9	ILE	C-N-CA	5.94	125.88	119.76
50	2s	30	LEU	N-CA-C	5.93	118.83	110.23
43	2l	28	LYS	N-CA-C	5.90	119.39	111.24
9	2N	94	HIS	CA-C-N	5.86	125.72	119.28
9	2N	94	HIS	C-N-CA	5.86	125.72	119.28
41	2j	60	ARG	N-CA-C	5.85	117.48	109.18
1	2A	1992	G	C2'-C3'-O3'	5.83	118.25	109.50
21	1Z	157	LEU	CA-C-N	5.81	126.36	120.38
21	1Z	157	LEU	C-N-CA	5.81	126.36	120.38
7	1H	54	ARG	CA-C-N	5.81	125.43	119.56
7	1H	54	ARG	C-N-CA	5.81	125.43	119.56
38	2g	10	ARG	N-CA-C	5.79	118.62	110.23
43	1l	124	LYS	CA-C-N	5.75	125.71	119.78
43	1l	124	LYS	C-N-CA	5.75	125.71	119.78
8	2I	132	PRO	N-CA-C	-5.75	108.07	114.92
20	2Y	91	GLU	N-CA-C	-5.72	106.26	113.18
4	2E	190	GLY	CA-C-N	5.70	125.89	120.31
4	2E	190	GLY	C-N-CA	5.70	125.89	120.31
32	2a	1272	G	N1-C2-N2	-5.68	99.14	116.20
44	2m	107	ALA	N-CA-C	-5.67	104.58	112.30
30	18	62	LEU	CA-C-N	5.67	125.29	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
30	18	62	LEU	C-N-CA	5.67	125.29	119.56
4	2E	31	CYS	CA-C-N	5.66	125.42	119.76
4	2E	31	CYS	C-N-CA	5.66	125.42	119.76
20	2Y	93	GLY	N-CA-C	-5.66	107.17	113.79
44	1m	106	ASN	CB-CA-C	-5.66	110.07	116.63
50	1s	82	GLY	N-CA-C	5.65	118.93	111.52
50	2s	34	TRP	N-CA-C	-5.64	105.74	113.30
8	2I	31	LEU	CA-C-N	-5.63	113.87	119.56
8	2I	31	LEU	C-N-CA	-5.63	113.87	119.56
33	1b	18	GLY	N-CA-C	5.62	118.59	112.29
29	17	47	ARG	N-CA-C	5.62	117.48	111.36
7	1H	9	ILE	N-CA-C	5.60	113.42	107.76
5	2F	21	ALA	CA-C-N	5.59	131.77	121.70
5	2F	21	ALA	C-N-CA	5.59	131.77	121.70
35	2d	39	PRO	CA-C-N	5.59	125.56	120.03
35	2d	39	PRO	C-N-CA	5.59	125.56	120.03
28	16	40	CYS	CA-C-N	5.58	125.10	119.19
28	16	40	CYS	C-N-CA	5.58	125.10	119.19
3	2D	244	ARG	CA-C-N	-5.57	114.64	120.38
3	2D	244	ARG	C-N-CA	-5.57	114.64	120.38
14	1S	90	GLY	CA-C-N	5.57	125.66	119.87
14	1S	90	GLY	C-N-CA	5.57	125.66	119.87
34	2c	125	GLU	N-CA-C	-5.53	106.37	113.23
36	1e	48	ALA	N-CA-C	5.53	113.20	108.22
38	1g	114	ARG	N-CA-C	5.52	116.98	110.97
26	24	60	GLN	N-CA-C	-5.52	105.81	112.54
8	1I	13	GLY	N-CA-C	5.51	118.79	110.75
6	1G	45	GLU	N-CA-C	-5.50	105.83	112.54
14	2S	40	ILE	N-CA-C	5.50	115.81	108.11
43	2l	23	LYS	N-CA-C	-5.49	105.80	112.88
44	2m	40	ASN	CA-C-N	5.47	125.14	119.56
44	2m	40	ASN	C-N-CA	5.47	125.14	119.56
25	13	11	SER	CA-C-N	5.47	125.95	120.04
25	13	11	SER	C-N-CA	5.47	125.95	120.04
39	2h	134	ILE	N-CA-C	5.45	115.54	110.42
33	1b	65	GLY	N-CA-C	-5.44	105.45	114.48
36	2e	127	ASN	CA-C-N	5.44	124.89	119.24
36	2e	127	ASN	C-N-CA	5.44	124.89	119.24
35	1d	188	LEU	CA-C-N	5.43	125.35	119.76
35	1d	188	LEU	C-N-CA	5.43	125.35	119.76
26	24	28	LYS	CA-C-N	5.43	125.08	119.05
26	24	28	LYS	C-N-CA	5.43	125.08	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2D	120	GLY	CA-C-N	5.43	125.25	119.28
3	2D	120	GLY	C-N-CA	5.43	125.25	119.28
5	2F	9	ILE	N-CA-C	5.42	113.80	107.89
22	10	13	GLY	N-CA-C	5.40	125.98	113.18
6	1G	96	ARG	CB-CA-C	-5.38	110.35	116.54
33	2b	130	ARG	N-CA-C	5.37	117.37	110.39
41	1j	90	LEU	CA-C-N	5.37	126.55	119.84
41	1j	90	LEU	C-N-CA	5.37	126.55	119.84
36	2e	98	THR	N-CA-C	5.36	117.12	111.28
33	1b	128	GLU	N-CA-C	-5.36	106.59	113.02
3	1D	7	LYS	CA-C-N	5.35	126.52	119.84
3	1D	7	LYS	C-N-CA	5.35	126.52	119.84
34	1c	6	HIS	CA-C-N	5.33	125.00	119.56
34	1c	6	HIS	C-N-CA	5.33	125.00	119.56
30	28	52	LYS	CA-C-N	-5.32	113.14	119.05
30	28	52	LYS	C-N-CA	-5.32	113.14	119.05
7	2H	11	VAL	CA-C-N	5.30	125.59	119.92
7	2H	11	VAL	C-N-CA	5.30	125.59	119.92
33	1b	38	GLY	N-CA-C	-5.29	107.95	115.30
19	1X	94	GLY	CA-C-N	5.28	131.20	121.70
19	1X	94	GLY	C-N-CA	5.28	131.20	121.70
33	2b	193	ASP	CA-C-N	5.28	124.46	118.97
33	2b	193	ASP	C-N-CA	5.28	124.46	118.97
40	1i	5	TYR	N-CA-C	5.26	118.03	109.24
21	1Z	153	SER	N-CA-C	5.25	117.43	111.02
27	15	27	PRO	O-C-N	5.25	123.72	121.31
9	2N	110	GLY	CA-C-N	5.25	124.70	119.24
9	2N	110	GLY	C-N-CA	5.25	124.70	119.24
33	1b	156	LYS	N-CA-C	-5.25	106.67	114.64
34	2c	126	ARG	N-CA-C	-5.25	106.73	113.02
36	2e	26	PHE	N-CA-C	5.23	117.48	109.95
41	1j	52	GLY	CA-C-N	5.22	124.83	119.56
41	1j	52	GLY	C-N-CA	5.22	124.83	119.56
6	2G	78	SER	N-CA-C	5.22	116.65	111.07
36	1e	98	THR	N-CA-C	5.21	116.65	111.07
33	1b	23	ARG	N-CA-C	-5.21	106.69	112.57
26	14	52	THR	N-CA-C	-5.20	104.69	112.54
14	1S	40	ILE	N-CA-C	5.18	115.37	108.11
6	2G	141	PHE	CA-C-N	5.17	124.83	119.56
6	2G	141	PHE	C-N-CA	5.17	124.83	119.56
15	2T	19	LEU	CA-C-N	5.16	125.07	119.85
15	2T	19	LEU	C-N-CA	5.16	125.07	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
36	1e	127	ASN	CA-C-N	5.16	124.61	119.24
36	1e	127	ASN	C-N-CA	5.16	124.61	119.24
38	2g	114	ARG	N-CA-C	5.15	116.58	110.97
21	2Z	52	SER	CB-CA-C	-5.13	110.67	116.63
26	24	40	HIS	CA-C-N	5.11	125.15	119.32
26	24	40	HIS	C-N-CA	5.11	125.15	119.32
6	2G	160	VAL	N-CA-C	5.11	115.27	108.11
33	1b	166	ASP	CA-C-N	5.11	124.90	119.28
33	1b	166	ASP	C-N-CA	5.11	124.90	119.28
39	1h	100	ILE	N-CA-C	5.11	113.96	108.95
42	2k	38	ASN	CA-C-N	5.10	125.03	119.78
42	2k	38	ASN	C-N-CA	5.10	125.03	119.78
32	2a	1272	G	N3-C2-N2	5.09	135.16	119.90
1	1A	2014	G	P-O3'-C3'	5.06	127.79	120.20
44	2m	7	VAL	N-CA-C	5.06	116.96	109.17
34	1c	96	GLY	N-CA-C	-5.06	108.34	115.32
34	2c	72	LYS	CA-C-N	5.05	126.15	119.84
34	2c	72	LYS	C-N-CA	5.05	126.15	119.84
1	1A	1700	G	C2'-C3'-O3'	5.04	117.05	109.50
6	1G	127	GLY	N-CA-C	-5.04	107.70	114.25
33	1b	15	VAL	N-CA-C	5.03	119.80	109.34
51	2t	11	SER	N-CA-C	-5.03	106.74	112.92
42	1k	49	GLY	N-CA-C	5.02	125.09	113.18
26	14	28	LYS	CA-C-N	5.01	124.61	119.05
26	14	28	LYS	C-N-CA	5.01	124.61	119.05
13	1R	38	VAL	CB-CA-C	-5.00	108.94	113.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	2l	92	0TD	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31193	632	0
1	2A	60322	0	30425	882	0
2	1B	2577	0	1305	22	0
2	2B	2575	0	1303	65	0
3	1D	2136	0	2218	47	0
3	2D	2136	0	2218	62	0
4	1E	1559	0	1618	34	0
4	2E	1559	0	1618	38	0
5	1F	1584	0	1625	36	0
5	2F	1580	0	1619	55	0
6	1G	1423	0	1436	22	0
6	2G	1428	0	1438	73	0
7	1H	1330	0	1407	28	0
7	2H	1330	0	1407	46	0
8	1I	1097	0	1140	33	0
8	2I	1064	0	1082	25	0
9	1N	1117	0	1184	21	0
9	2N	1117	0	1184	22	0
10	1O	933	0	996	20	0
10	2O	933	0	996	25	0
11	1P	1135	0	1212	36	0
11	2P	1135	0	1212	34	0
12	1Q	1122	0	1179	15	0
12	2Q	1122	0	1179	35	0
13	1R	968	0	1033	12	0
13	2R	968	0	1033	21	0
14	1S	873	0	927	19	0
14	2S	870	0	923	31	0
15	1T	1091	0	1151	19	0
15	2T	1083	0	1136	36	0
16	1U	959	0	1019	18	0
16	2U	959	0	1019	26	0
17	1V	771	0	830	10	0
17	2V	771	0	830	23	0
18	1W	886	0	940	8	0
18	2W	886	0	940	14	0
19	1X	750	0	814	10	0
19	2X	750	0	814	28	0
20	1Y	806	0	881	21	0
20	2Y	806	0	881	25	0
21	1Z	1240	0	1240	25	0
21	2Z	1271	0	1273	48	0
22	10	653	0	674	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	20	653	0	674	20	0
23	11	755	0	826	11	0
23	21	755	0	826	21	0
24	12	588	0	643	11	0
24	22	588	0	643	17	0
25	13	469	0	518	6	0
25	23	464	0	514	12	0
26	14	552	0	533	21	0
26	24	532	0	503	39	0
27	15	455	0	465	7	0
27	25	455	0	465	12	0
28	16	453	0	473	13	0
28	26	449	0	469	10	0
29	17	418	0	467	9	0
29	27	418	0	467	17	0
30	18	517	0	582	18	0
30	28	517	0	582	19	0
31	19	307	0	335	4	0
31	29	307	0	335	8	0
32	1a	32246	0	16295	441	0
32	2a	32327	0	16339	638	0
33	1b	1846	0	1867	60	0
33	2b	1825	0	1828	107	0
34	1c	1548	0	1535	35	0
34	2c	1542	0	1517	56	0
35	1d	1655	0	1672	51	0
35	2d	1674	0	1714	43	0
36	1e	1129	0	1185	30	0
36	2e	1133	0	1191	39	0
37	1f	810	0	804	25	0
37	2f	816	0	808	17	0
38	1g	1231	0	1238	29	0
38	2g	1235	0	1249	27	0
39	1h	1088	0	1126	27	0
39	2h	1088	0	1126	27	0
40	1i	983	0	986	28	0
40	2i	978	0	966	54	0
41	1j	709	0	650	32	0
41	2j	714	0	672	37	0
42	1k	829	0	825	9	0
42	2k	833	0	836	19	0
43	1l	932	0	981	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	2l	932	0	981	28	0
44	1m	958	0	1002	25	0
44	2m	950	0	988	49	0
45	1n	492	0	529	19	0
45	2n	492	0	529	37	0
46	1o	728	0	760	16	0
46	2o	728	0	760	18	0
47	1p	681	0	697	20	0
47	2p	677	0	686	19	0
48	1q	823	0	891	26	0
48	2q	823	0	891	17	0
49	1r	555	0	618	12	0
49	2r	555	0	618	15	0
50	1s	652	0	662	24	0
50	2s	646	0	644	27	0
51	1t	728	0	798	15	0
51	2t	727	0	796	18	0
52	1u	199	0	208	8	0
52	2u	199	0	208	12	0
53	1v	277	0	140	3	0
53	2v	277	0	140	3	0
54	1w	1592	0	819	35	0
54	1y	1585	0	804	40	0
54	2w	1544	0	788	47	0
54	2y	1565	0	795	53	0
55	1x	1625	0	828	15	0
55	2x	1625	0	828	24	0
56	10	6	0	0	0	0
56	11	3	0	0	0	0
56	12	1	0	0	0	0
56	13	3	0	0	0	0
56	15	2	0	0	0	0
56	16	3	0	0	0	0
56	17	1	0	0	0	0
56	18	3	0	0	0	0
56	19	2	0	0	0	0
56	1A	1141	0	0	0	0
56	1B	37	0	0	0	0
56	1D	12	0	0	0	0
56	1E	11	0	0	0	0
56	1F	8	0	0	0	0
56	1G	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1I	1	0	0	0	0
56	1N	6	0	0	0	0
56	1O	7	0	0	0	0
56	1P	4	0	0	0	0
56	1Q	6	0	0	0	0
56	1R	3	0	0	0	0
56	1S	3	0	0	0	0
56	1T	2	0	0	0	0
56	1U	8	0	0	0	0
56	1V	3	0	0	0	0
56	1W	5	0	0	0	0
56	1X	6	0	0	0	0
56	1Y	3	0	0	0	0
56	1Z	3	0	0	0	0
56	1a	229	0	0	0	0
56	1b	2	0	0	0	0
56	1d	1	0	0	0	0
56	1e	1	0	0	0	0
56	1f	2	0	0	0	0
56	1l	3	0	0	0	0
56	1n	2	0	0	0	0
56	1s	1	0	0	0	0
56	1t	1	0	0	0	0
56	1v	1	0	0	0	0
56	1w	11	0	0	0	0
56	1x	16	0	0	0	0
56	1y	4	0	0	0	0
56	20	3	0	0	0	0
56	23	2	0	0	0	0
56	25	4	0	0	0	0
56	27	1	0	0	0	0
56	28	2	0	0	0	0
56	2A	909	0	0	0	0
56	2B	21	0	0	0	0
56	2D	5	0	0	0	0
56	2E	9	0	0	0	0
56	2F	4	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	1	0	0	0	0
56	2P	1	0	0	0	0
56	2Q	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2R	1	0	0	0	0
56	2T	3	0	0	0	0
56	2U	4	0	0	0	0
56	2V	1	0	0	0	0
56	2W	3	0	0	0	0
56	2X	3	0	0	0	0
56	2Y	1	0	0	0	0
56	2Z	1	0	0	0	0
56	2a	244	0	0	0	0
56	2d	1	0	0	0	0
56	2e	1	0	0	0	0
56	2f	1	0	0	0	0
56	2g	1	0	0	0	0
56	2i	1	0	0	0	0
56	2j	2	0	0	0	0
56	2l	2	0	0	0	0
56	2n	1	0	0	0	0
56	2q	2	0	0	0	0
56	2r	2	0	0	0	0
56	2t	1	0	0	0	0
56	2v	2	0	0	0	0
56	2w	8	0	0	0	0
56	2x	5	0	0	0	0
56	2y	7	0	0	0	0
57	1A	1	0	0	0	0
57	2A	1	0	0	0	0
58	14	1	0	0	0	0
58	15	1	0	0	0	0
58	16	1	0	0	0	0
58	19	1	0	0	0	0
58	1Y	1	0	0	0	0
58	1n	1	0	0	0	0
58	24	1	0	0	0	0
58	25	1	0	0	0	0
58	26	1	0	0	0	0
58	29	1	0	0	0	0
58	2Y	1	0	0	0	0
58	2n	1	0	0	0	0
59	1d	8	0	0	0	0
59	2d	8	0	0	1	0
60	10	12	0	0	0	0
60	11	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	12	4	0	0	0	0
60	13	6	0	0	0	0
60	14	1	0	0	0	0
60	15	6	0	0	0	0
60	16	3	0	0	0	0
60	17	9	0	0	0	0
60	18	13	0	0	1	0
60	1A	2238	0	0	95	0
60	1B	68	0	0	3	0
60	1D	28	0	0	1	0
60	1E	28	0	0	3	0
60	1F	13	0	0	1	0
60	1G	7	0	0	1	0
60	1H	2	0	0	0	0
60	1I	3	0	0	0	0
60	1N	7	0	0	1	0
60	1O	8	0	0	0	0
60	1P	23	0	0	3	0
60	1Q	14	0	0	0	0
60	1R	14	0	0	0	0
60	1S	5	0	0	0	0
60	1T	8	0	0	1	0
60	1U	11	0	0	1	0
60	1V	9	0	0	0	0
60	1W	6	0	0	0	0
60	1X	8	0	0	2	0
60	1Y	4	0	0	0	0
60	1Z	1	0	0	0	0
60	1a	438	0	0	28	0
60	1b	1	0	0	0	0
60	1d	1	0	0	0	0
60	1e	1	0	0	0	0
60	1f	1	0	0	0	0
60	1g	1	0	0	0	0
60	1i	1	0	0	0	0
60	1l	8	0	0	0	0
60	1m	2	0	0	0	0
60	1o	1	0	0	0	0
60	1p	1	0	0	0	0
60	1q	4	0	0	0	0
60	1u	1	0	0	1	0
60	1v	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	1w	21	0	0	1	0
60	1x	15	0	0	0	0
60	1y	1	0	0	0	0
60	20	7	0	0	0	0
60	21	12	0	0	0	0
60	22	1	0	0	0	0
60	23	1	0	0	0	0
60	25	4	0	0	1	0
60	26	1	0	0	0	0
60	27	4	0	0	1	0
60	28	6	0	0	2	0
60	29	1	0	0	0	0
60	2A	1389	0	0	90	0
60	2B	26	0	0	1	0
60	2D	28	0	0	2	0
60	2E	16	0	0	0	0
60	2F	16	0	0	0	0
60	2H	1	0	0	0	0
60	2I	4	0	0	0	0
60	2N	1	0	0	0	0
60	2P	14	0	0	1	0
60	2Q	2	0	0	0	0
60	2R	2	0	0	0	0
60	2T	6	0	0	0	0
60	2U	2	0	0	0	0
60	2V	2	0	0	0	0
60	2W	2	0	0	0	0
60	2X	5	0	0	0	0
60	2Y	1	0	0	1	0
60	2Z	2	0	0	0	0
60	2a	377	0	0	34	0
60	2d	1	0	0	0	0
60	2e	2	0	0	0	0
60	2g	1	0	0	0	0
60	2i	1	0	0	0	0
60	2j	4	0	0	0	0
60	2l	5	0	0	1	0
60	2o	1	0	0	0	0
60	2p	2	0	0	0	0
60	2q	1	0	0	0	0
60	2r	1	0	0	1	0
60	2t	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	2u	1	0	0	1	0
60	2v	1	0	0	0	0
60	2w	2	0	0	0	0
60	2x	7	0	0	0	0
60	2y	19	0	0	5	0
All	All	300910	0	196690	4749	0

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

All (4749) 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:1128:U:H3	1:1A:1132:A:N6	1.34	1.25
1:2A:2136:C:N4	1:2A:2155:G:H1	1.44	1.15
55:1x:4:G:H1	55:1x:69:C:N4	1.48	1.10
32:2a:997:U:H3	32:2a:1044:A:N6	1.49	1.10
1:1A:1128:U:O4	1:1A:1132:A:N1	1.85	1.09
1:2A:2138:C:N4	1:2A:2153:G:H1	1.48	1.09
54:2w:50:U:H3	54:2w:64:A:N6	1.50	1.07
54:1w:6:G:H1	54:1w:67:C:N4	1.55	1.05
54:1w:7:A:N6	54:1w:66:U:H3	1.55	1.03
1:1A:1740:U:H1'	3:1D:14:ARG:HH22	1.22	1.01
32:2a:1089:G:H1	32:2a:1096:C:N4	1.62	0.98
32:1a:998:G:H1	32:1a:1043:C:H42	1.08	0.98
1:1A:2122:G:H1	1:1A:2211:U:H3	1.14	0.96
1:2A:1693:U:H1'	3:2D:14:ARG:HH22	1.31	0.95
32:2a:1000:U:H3	32:2a:1041:A:N6	1.62	0.95
54:2y:5:G:H1	54:2y:68:C:H42	1.01	0.95
32:1a:1004:A:N6	32:1a:1037:C:N3	2.14	0.94
44:2m:3:ARG:HG2	44:2m:9:ILE:H	1.31	0.94
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.50	0.94
1:2A:2129:C:H42	1:2A:2159:G:H1	1.06	0.93
1:1A:1105:G:H1	1:1A:1125:C:H42	0.99	0.93
1:1A:2511:C:OP1	60:1A:5012:HOH:O	1.83	0.93
1:1A:2439:C:OP1	60:1A:5528:HOH:O	1.87	0.93
1:1A:2702:C:OP1	13:1R:17:ARG:NH2	2.01	0.93
32:2a:1002:G:H1	32:2a:1038:C:H42	1.11	0.93
20:1Y:92:ASN:HB3	20:1Y:94:LYS:H	1.33	0.92
54:2y:55:PSU:HN1	54:2y:57:G:H5"	1.30	0.92
1:1A:2143:G:H1	1:1A:2199:C:H42	1.07	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1011:G:H1	32:2a:1018:C:H42	1.17	0.92
54:1w:7:A:H61	54:1w:66:U:H3	0.98	0.92
1:2A:1171:G:N2	1:2A:1178:C:N3	2.18	0.92
32:2a:1133:G:H1	32:2a:1141:C:H42	1.13	0.91
54:1w:6:G:H1	54:1w:67:C:H42	0.91	0.91
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.53	0.90
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.35	0.90
54:2y:15:G:H22	54:2y:48:C:H42	1.15	0.90
1:2A:2127:G:N2	1:2A:2161:C:C2	2.40	0.90
32:1a:1009:G:O6	32:1a:1020:U:O2	1.90	0.90
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.21	0.89
54:2y:50:U:H3	54:2y:64:A:H61	1.18	0.89
1:2A:2136:C:N4	1:2A:2155:G:N1	2.19	0.89
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.06	0.89
54:2w:4:C:H42	54:2w:69:G:H1	1.18	0.89
1:1A:1099:C:H42	1:1A:1152:G:H1	1.17	0.88
32:2a:1089:G:H1	32:2a:1096:C:H42	0.92	0.88
1:1A:1105:G:H1	1:1A:1125:C:N4	1.71	0.88
22:10:10:THR:HG22	22:10:12:ASN:H	1.37	0.88
32:2a:1000:U:H3	32:2a:1041:A:H61	0.88	0.88
1:2A:2136:C:N3	1:2A:2155:G:N2	2.22	0.87
32:2a:975:A:H4'	32:2a:976:G:H5"	1.57	0.86
36:1e:78:HIS:HE1	36:1e:143:ARG:H	1.20	0.86
1:1A:2121:U:H3	1:1A:2212:G:H1	0.91	0.85
1:2A:854:G:H2'	1:2A:855:G:H8	1.38	0.85
1:2A:2014:A:H4'	18:2W:92:ARG:HH22	1.37	0.85
1:2A:2127:G:N1	1:2A:2161:C:C4	2.44	0.85
1:2A:1689:A:H62	1:2A:1698:A:H2	1.20	0.85
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.21	0.85
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.57	0.85
1:2A:2345:G:H4'	1:2A:2346:A:H5"	1.58	0.85
11:2P:52:GLU:OE1	11:2P:55:ARG:NH1	2.08	0.85
1:1A:303:C:H42	1:1A:385:G:H1	1.21	0.85
1:1A:1378:G:OP1	60:1A:4704:HOH:O	1.94	0.85
54:2y:5:G:H1	54:2y:68:C:N4	1.74	0.85
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.24	0.85
1:2A:2807:G:N1	1:2A:2893:G:O6	2.09	0.85
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.11	0.85
1:1A:1694:G:OP1	60:1A:5101:HOH:O	1.94	0.85
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.10	0.85
54:1w:6:G:N2	54:1w:67:C:N3	2.24	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:559:A:H4'	32:2a:560:U:H3'	1.59	0.84
1:1A:1740:U:O2	3:1D:14:ARG:NH2	2.11	0.84
1:1A:1111:U:O2	1:1A:1119:A:N6	2.11	0.84
32:2a:1029:C:C4	32:2a:1032:G:N1	2.46	0.84
32:2a:597:G:OP2	60:2a:3377:HOH:O	1.96	0.84
1:1A:929:G:H1	1:1A:940:C:H42	1.25	0.83
32:1a:559:A:H4'	32:1a:560:U:H3'	1.59	0.83
1:2A:2127:G:C2	1:2A:2161:C:N3	2.46	0.83
55:1x:4:G:N2	55:1x:69:C:N3	2.24	0.83
1:1A:2831:A:OP2	60:1A:5352:HOH:O	1.97	0.83
23:21:2:SER:HB3	23:21:46:LEU:HD12	1.60	0.83
1:2A:2099:U:H3	1:2A:2190:G:H1	1.22	0.83
1:1A:2158:C:N3	1:1A:2177:G:N2	2.26	0.83
17:2V:72:VAL:HG13	17:2V:85:LYS:HB2	1.61	0.83
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.12	0.83
32:1a:998:G:H1	32:1a:1043:C:N4	1.77	0.82
54:2w:50:U:H3	54:2w:64:A:H61	0.83	0.82
32:1a:189(F):U:H3	48:1q:72:ARG:HH22	1.28	0.82
1:2A:1204:A:H2	1:2A:1241:A:H62	1.28	0.82
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.60	0.82
1:2A:2138:C:N3	1:2A:2153:G:N2	2.24	0.82
32:1a:1162:C:H42	32:1a:1174:G:H1	1.23	0.82
1:1A:2143:G:H1	1:1A:2199:C:N4	1.78	0.82
1:2A:2129:C:N4	1:2A:2159:G:H1	1.77	0.82
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.61	0.81
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.62	0.81
1:1A:889:G:N7	60:1A:5371:HOH:O	2.14	0.81
1:2A:2524:G:N7	60:2A:5109:HOH:O	2.13	0.81
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.62	0.81
3:2D:13:ARG:NH1	3:2D:16:MET:SD	2.54	0.81
32:2a:406:G:H21	35:2d:119:GLN:HE22	1.27	0.81
1:1A:2152:U:H2'	1:1A:2180:A:H61	1.45	0.81
41:1j:38:ILE:HD11	41:1j:71:LEU:HD23	1.63	0.81
1:1A:1140:U:H1'	1:1A:1143:U:H5	1.46	0.81
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.63	0.81
32:2a:1329:A:OP2	52:2u:7:ARG:NH1	2.13	0.80
1:2A:1021:A:H62	1:2A:1141:U:H3	1.28	0.80
1:1A:2832:G:OP2	60:1A:5352:HOH:O	1.98	0.80
32:1a:664:G:H22	32:1a:741:G:H1	1.26	0.80
7:2H:84:SER:HB3	7:2H:132:ARG:HH11	1.47	0.80
1:1A:2158:C:N4	1:1A:2177:G:N1	2.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1389:G:N7	60:2A:4894:HOH:O	2.14	0.80
54:2w:4:C:N4	54:2w:69:G:H1	1.78	0.80
1:1A:1108:G:H1	1:1A:1123:A:H61	1.30	0.80
32:1a:1027:C:C2	32:1a:1034:G:N2	2.50	0.80
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.64	0.80
1:1A:2156:A:C4	1:1A:2180:A:H2	1.99	0.80
33:1b:118:LEU:HB3	33:1b:142:LEU:HD12	1.63	0.80
1:2A:2822:G:OP2	60:2A:5369:HOH:O	1.99	0.80
1:2A:962:G:OP1	60:2A:4399:HOH:O	2.00	0.79
1:2A:1647:G:OP1	60:2A:4350:HOH:O	2.00	0.79
32:1a:1196:U:H3	34:1c:162:GLN:HE22	1.30	0.79
1:2A:1670:C:OP1	60:2A:4902:HOH:O	2.00	0.79
38:1g:50:ILE:HD13	38:1g:125:MET:HG2	1.64	0.79
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.15	0.79
3:1D:242:ARG:NH1	60:1D:412:HOH:O	2.16	0.79
1:2A:2127:G:C2	1:2A:2161:C:C4	2.71	0.79
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.63	0.79
32:2a:1055:A:N7	32:2a:1200:C:N4	2.31	0.79
5:1F:70:THR:HG23	5:1F:72:ARG:H	1.48	0.79
1:2A:711:G:N2	1:2A:720:C:O2	2.16	0.79
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.64	0.79
32:1a:299:G:O6	60:1a:1950:HOH:O	2.01	0.79
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.64	0.79
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.65	0.78
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.15	0.78
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	1.64	0.78
1:2A:882:G:H2'	1:2A:883:G:H8	1.48	0.78
32:2a:1002:G:H1	32:2a:1038:C:N4	1.80	0.78
1:2A:1818:U:OP2	3:2D:157:ARG:NH1	2.16	0.78
32:2a:1011:G:H1	32:2a:1018:C:N4	1.80	0.78
32:1a:78:G:C6	32:1a:91:C:N4	2.51	0.78
32:1a:101:A:N7	60:1a:2034:HOH:O	2.17	0.78
33:1b:93:VAL:HG21	33:1b:97:TRP:HD1	1.49	0.78
32:2a:130:A:H5'	48:2q:63:ARG:HH11	1.46	0.78
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.16	0.78
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.15	0.78
54:2y:18:G:N2	54:2y:55:PSU:N3	2.26	0.78
32:2a:1004:A:N6	32:2a:1037:C:O2	2.15	0.78
32:2a:1133:G:H1	32:2a:1141:C:N4	1.80	0.78
1:1A:294:C:H42	1:1A:390:G:H1	1.29	0.78
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:27:GLU:HB2	50:1s:28:LYS:HA	1.63	0.78
1:1A:1151:U:H2'	1:1A:1152:G:C8	2.18	0.78
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.19	0.78
1:1A:2146:G:H1	1:1A:2196:C:H42	1.31	0.78
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.47	0.78
54:2y:15:G:H22	54:2y:48:C:N4	1.82	0.78
1:1A:1085:G:H1	1:1A:1162:C:H42	1.31	0.78
1:2A:1634:A:OP1	60:2A:4877:HOH:O	2.01	0.78
1:1A:1044:C:OP1	60:1A:4714:HOH:O	2.02	0.77
1:1A:2460:A:OP1	60:1A:5012:HOH:O	2.01	0.77
1:2A:948:G:OP1	60:2A:4399:HOH:O	2.00	0.77
32:1a:997:U:H3	32:1a:1044:A:H61	1.31	0.77
1:2A:2287:A:H62	1:2A:2344:U:H3	1.33	0.77
41:1j:30:SER:HG	41:1j:81:THR:HG1	1.23	0.77
49:1r:52:PRO:HB2	49:1r:54:ARG:HG2	1.66	0.77
32:2a:987:G:H1	32:2a:1218:C:H42	1.32	0.77
33:1b:33:TYR:HB2	33:1b:43:ASP:HB2	1.64	0.77
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.01	0.77
2:2B:7:G:H1	2:2B:114:C:H42	1.33	0.77
2:2B:27:C:N4	2:2B:56:G:O6	2.18	0.77
1:2A:2127:G:C6	1:2A:2161:C:N4	2.53	0.77
32:1a:532:A:N6	32:1a:1206:G:O2'	2.17	0.77
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.17	0.77
1:2A:1826:G:H4'	3:2D:242:ARG:HE	1.47	0.77
40:1i:31:GLN:HE21	40:1i:36:TYR:HD1	1.30	0.77
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	1.67	0.77
1:1A:1711:A:OP1	60:1A:5025:HOH:O	2.02	0.77
60:1A:5352:HOH:O	4:1E:110:GLY:O	2.02	0.77
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.67	0.77
32:1a:766:A:OP2	60:1a:1932:HOH:O	2.01	0.77
15:1T:98:LYS:NZ	60:1T:8106:HOH:O	2.17	0.76
1:1A:925:A:N6	1:1A:945:A:O2'	2.17	0.76
32:1a:156:G:N2	32:1a:165:C:O2	2.18	0.76
1:2A:424:G:N7	60:2A:5062:HOH:O	2.18	0.76
54:1y:50:U:O4	54:1y:64:A:N1	2.19	0.76
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.68	0.76
32:2a:117:G:OP2	60:2a:3619:HOH:O	2.04	0.76
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.67	0.76
1:1A:2007:G:OP2	60:1A:5698:HOH:O	2.02	0.76
1:2A:2126:A:N6	1:2A:2162:G:O2'	2.18	0.76
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1030:C:N4	32:2a:1031:G:H1	1.82	0.76
2:2B:17:C:O2	2:2B:67:G:N2	2.17	0.76
32:2a:1028:C:N3	32:2a:1033:G:O6	2.19	0.76
1:1A:1055:A:OP2	9:1N:37:LYS:NZ	2.19	0.76
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.04	0.76
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.68	0.76
32:2a:107:G:N7	51:2t:15:ARG:NH2	2.34	0.76
32:2a:151:A:N6	32:2a:170:U:O2	2.19	0.76
32:2a:532:A:N6	32:2a:1206:G:O2'	2.19	0.76
32:1a:1518:MA6:N6	32:1a:1519:MA6:H103	2.02	0.75
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.19	0.75
1:2A:1155:A:H5"	16:2U:55:ARG:HH11	1.50	0.75
32:2a:596:C:O2	32:2a:644:G:N2	2.18	0.75
32:2a:770:C:OP1	60:2a:3457:HOH:O	2.03	0.75
54:2y:10:G:H1	54:2y:25:C:H42	1.31	0.75
1:2A:1783:A:OP2	60:2A:4560:HOH:O	2.03	0.75
1:1A:2227:G:H3'	1:1A:2228:G:C8	2.22	0.75
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.68	0.75
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.68	0.75
32:2a:554:C:O2'	60:2a:3651:HOH:O	2.03	0.75
1:1A:1151:U:H2'	1:1A:1152:G:H8	1.51	0.75
32:1a:1030:C:H42	32:1a:1031:G:H1	1.34	0.75
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.52	0.75
32:2a:1328:C:OP1	52:2u:21:TYR:OH	2.05	0.75
10:1O:20:MET:HE3	10:1O:44:LYS:HE3	1.69	0.75
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.20	0.75
1:2A:2332:U:O4	60:2A:4436:HOH:O	2.04	0.75
32:2a:988:G:H1	32:2a:1217:C:H42	1.32	0.75
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.67	0.75
41:2j:8:LEU:HB2	41:2j:96:ILE:HG12	1.68	0.75
1:2A:1693:U:O2	3:2D:14:ARG:NH2	2.18	0.75
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.18	0.75
32:1a:1469:G:N7	60:1a:2194:HOH:O	2.20	0.75
32:2a:547:A:OP1	60:2a:3518:HOH:O	2.04	0.75
1:1A:1099:C:N4	1:1A:1152:G:H1	1.85	0.75
1:2A:2308:G:O6	1:2A:2311:A:N6	2.19	0.75
32:2a:1128:C:O2'	32:2a:1147:C:N3	2.20	0.75
54:2y:15:G:N2	54:2y:48:C:H42	1.85	0.74
32:2a:1025:U:H3	32:2a:1036:G:H1	0.78	0.74
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.69	0.74
40:1i:9:ARG:HG2	40:1i:14:VAL:HG12	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:880:G:N2	1:2A:898:C:O2	2.19	0.74
40:2i:50:LEU:HD13	40:2i:56:LEU:HA	1.69	0.74
2:2B:22:U:H3	2:2B:61:G:H1	1.36	0.74
22:20:10:THR:HG22	22:20:12:ASN:H	1.52	0.74
34:2c:9:GLY:HA3	45:2n:49:HIS:HA	1.69	0.74
1:1A:1059:C:OP2	60:1A:5073:HOH:O	2.04	0.74
32:1a:1108:G:O6	60:1a:2308:HOH:O	2.05	0.74
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.50	0.74
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.69	0.74
1:1A:786:G:OP1	60:1A:5040:HOH:O	2.06	0.74
1:2A:2884:U:OP2	60:2A:4309:HOH:O	2.06	0.74
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.70	0.74
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.50	0.74
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.68	0.74
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.70	0.74
54:2w:8:4SU:S4	54:2w:13:C:O2'	2.46	0.74
1:1A:493:G:OP1	29:17:33:ARG:NH1	2.22	0.73
30:18:6:THR:HG22	30:18:63:PRO:HD2	1.70	0.73
33:1b:121:LEU:HD11	33:1b:130:ARG:HH22	1.53	0.73
44:1m:3:ARG:NH2	44:1m:9:ILE:O	2.20	0.73
1:2A:2310:A:N1	6:2G:79:ASN:ND2	2.36	0.73
9:2N:128:HIS:O	9:2N:131:GLN:NE2	2.21	0.73
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.88	0.73
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.69	0.73
54:2w:4:C:N3	54:2w:69:G:N2	2.36	0.73
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.22	0.73
32:2a:1089:G:N2	32:2a:1096:C:N3	2.34	0.73
1:1A:2145:G:H1	1:1A:2197:C:H42	1.34	0.73
1:2A:1156:A:OP2	60:2A:4427:HOH:O	2.07	0.73
2:2B:117:G:N7	60:2B:3126:HOH:O	2.22	0.73
54:2w:14:A:H61	54:2w:21:A:H2	1.35	0.73
1:1A:1123:A:H2'	1:1A:1124:U:H4'	1.70	0.73
1:2A:792:G:O6	60:2A:4331:HOH:O	2.06	0.73
3:2D:152:GLY:O	60:2D:427:HOH:O	2.05	0.73
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	1.69	0.73
12:2Q:26:TYR:O	12:2Q:67:ARG:NH1	2.21	0.73
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.70	0.73
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.24	0.73
32:2a:1026:G:O6	32:2a:1036:G:N2	2.22	0.73
32:1a:574:A:OP2	60:1a:2133:HOH:O	2.07	0.73
22:10:11:ARG:O	22:10:14:ARG:NH2	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:23:ASN:HB2	40:1i:25:LYS:HD3	1.70	0.72
41:2j:6:ILE:HG12	41:2j:98:ILE:HG13	1.71	0.72
54:2w:19:G:H1	54:2w:56:C:H42	1.36	0.72
32:1a:1025:U:O2	32:1a:1036:G:O6	2.06	0.72
35:1d:134:ASP:N	35:1d:134:ASP:OD1	2.20	0.72
55:2x:7:G:H5"	55:2x:8:4SU:H5	1.71	0.72
54:2y:50:U:H3	54:2y:64:A:N6	1.87	0.72
32:1a:78:G:N1	32:1a:91:C:C4	2.57	0.72
1:2A:794:G:OP1	60:2A:4747:HOH:O	2.07	0.72
32:2a:396:G:O2'	32:2a:398:C:OP1	2.04	0.72
43:2l:86:ARG:NH1	60:2l:303:HOH:O	2.22	0.72
1:1A:1848:G:OP1	3:1D:88:ARG:NH2	2.22	0.72
35:1d:107:ARG:HH21	35:1d:194:LEU:HD21	1.55	0.72
1:2A:822:U:OP2	60:2A:4800:HOH:O	2.07	0.72
1:2A:1671:U:OP2	60:2A:4902:HOH:O	2.08	0.72
32:2a:927:G:O2'	60:2a:3660:HOH:O	2.06	0.72
32:2a:1317:C:O2	50:2s:37:ARG:NH1	2.23	0.72
1:1A:2421:G:O2'	60:1A:5384:HOH:O	2.06	0.72
1:2A:854:G:H2'	1:2A:855:G:C8	2.23	0.72
1:1A:1101:G:H1	1:1A:1150:C:H42	1.37	0.72
1:1A:2820:A:N6	1:1A:2900:G:O2'	2.22	0.72
32:1a:812:C:N3	60:1a:1935:HOH:O	2.23	0.72
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.71	0.72
1:1A:2695:C:O2	10:1O:70:LYS:NZ	2.18	0.72
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.23	0.72
32:1a:473:G:OP2	47:1p:75:ARG:NH1	2.23	0.72
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.72	0.72
46:1o:26:GLU:OE2	46:1o:77:ARG:NE	2.23	0.72
1:2A:728:G:H5"	3:2D:13:ARG:HH21	1.55	0.72
1:2A:2822:G:N7	60:2A:5368:HOH:O	2.23	0.72
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.72	0.72
23:21:21:ARG:HD3	23:21:35:THR:HG21	1.72	0.72
1:1A:2180:A:O2'	1:1A:2181:G:OP2	2.07	0.72
32:1a:1008:C:N3	32:1a:1021:G:O6	2.23	0.72
32:2a:1271:G:N2	32:2a:1272:G:N7	2.38	0.72
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	1.72	0.72
54:2w:11:C:H42	54:2w:24:G:H1	1.38	0.72
1:1A:701:A:OP2	60:1A:4755:HOH:O	2.08	0.71
1:1A:1829:U:H5'	3:1D:259:THR:HG22	1.72	0.71
1:2A:531:C:OP1	1:2A:561:G:N1	2.22	0.71
1:2A:1566:A:OP1	3:2D:211:ARG:NH1	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2288:G:N7	60:1A:5504:HOH:O	2.23	0.71
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.21	0.71
33:2b:7:VAL:HG12	33:2b:8:LYS:H	1.56	0.71
33:2b:71:VAL:HB	33:2b:164:VAL:HA	1.72	0.71
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.72	0.71
32:1a:266:G:H5"	32:1a:268:C:H41	1.56	0.71
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.71	0.71
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.70	0.71
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.70	0.71
7:2H:7:LEU:HD12	7:2H:8:PRO:HD2	1.72	0.71
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.72	0.71
1:1A:1810:U:OP2	60:1A:5038:HOH:O	2.06	0.71
1:1A:873:U:OP1	60:1A:5528:HOH:O	2.08	0.71
1:2A:987:G:O2'	1:2A:1000:A:N3	2.23	0.71
1:1A:1939:PSU:O2	60:1A:5275:HOH:O	2.08	0.71
32:1a:894:G:N7	60:1a:2251:HOH:O	2.23	0.71
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.24	0.71
1:2A:467:G:OP2	29:27:34:ARG:HD3	1.90	0.71
1:2A:1271:G:OP2	60:2A:4350:HOH:O	2.08	0.71
32:2a:115:G:OP2	60:2a:3350:HOH:O	2.07	0.71
32:2a:444:C:H2'	32:2a:445:G:H8	1.56	0.71
1:2A:1031:G:H5"	31:29:8:LYS:HE3	1.73	0.71
1:2A:1693:U:H1'	3:2D:14:ARG:NH2	2.04	0.71
5:2F:140:LEU:HD11	5:2F:170:LEU:HD11	1.71	0.71
1:1A:927:G:H2'	1:1A:928:G:H8	1.54	0.71
1:1A:943:C:N3	1:1A:944:C:N4	2.38	0.71
1:1A:1069:U:OP2	60:1A:4871:HOH:O	2.08	0.71
1:1A:1716:A:OP2	60:1A:4989:HOH:O	2.07	0.71
1:1A:2798:C:OP1	4:1E:41:LYS:NZ	2.18	0.71
14:1S:68:GLN:HG3	14:1S:71:ARG:HH21	1.55	0.71
34:1c:32:LEU:HD23	34:1c:59:ARG:HD3	1.72	0.71
1:2A:692:C:O2'	3:2D:38:LYS:NZ	2.21	0.71
32:2a:1260:C:O2	32:2a:1274:G:N2	2.23	0.71
55:2x:3:C:H42	55:2x:70:G:H1	1.39	0.71
1:1A:2772:G:N7	60:1A:4321:HOH:O	2.24	0.71
39:2h:21:LYS:O	39:2h:65:TYR:OH	2.09	0.71
1:1A:331:G:N7	60:1A:4450:HOH:O	2.24	0.70
1:1A:1924:C:OP1	3:1D:242:ARG:NH1	2.22	0.70
1:2A:568:U:O4	60:2A:4947:HOH:O	2.08	0.70
32:1a:515:G:N7	60:1a:2127:HOH:O	2.25	0.70
6:2G:79:ASN:N	6:2G:79:ASN:OD1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2776:G:OP2	60:1A:4740:HOH:O	2.09	0.70
1:2A:2677:G:N3	60:2A:5258:HOH:O	2.24	0.70
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.72	0.70
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.72	0.70
32:2a:201:C:H42	32:2a:216:G:H1	1.36	0.70
1:1A:1299:A:OP1	60:1A:5877:HOH:O	2.08	0.70
26:14:53:GLU:HG3	26:14:54:GLY:H	1.55	0.70
1:2A:131:G:OP1	60:2A:4066:HOH:O	2.08	0.70
1:2A:2490:G:O6	60:2A:4471:HOH:O	2.09	0.70
32:2a:1274:G:N2	32:2a:1275:A:N7	2.38	0.70
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.72	0.70
1:1A:2802:C:O2	1:1A:2903:G:N2	2.22	0.70
32:1a:972:C:O2'	41:1j:55:LYS:O	2.10	0.70
1:2A:2478:A:OP2	31:29:2:LYS:NZ	2.24	0.70
1:1A:928:G:N2	1:1A:943:C:O2	2.25	0.70
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.63	0.70
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.72	0.70
1:1A:1296:G:OP2	11:1P:21:ARG:NH1	2.25	0.70
1:1A:1740:U:H1'	3:1D:14:ARG:NH2	2.04	0.70
1:1A:2440:G:OP1	60:1A:5528:HOH:O	2.08	0.70
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.24	0.70
32:1a:1370:G:N7	60:1a:1970:HOH:O	2.24	0.70
1:2A:89:G:H3'	1:2A:90:U:H5"	1.72	0.70
1:2A:882:G:H2'	1:2A:883:G:C8	2.26	0.70
1:2A:1466:G:HO2'	1:2A:1546:C:HO2'	1.31	0.70
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.73	0.70
32:2a:953:G:H5'	32:2a:965:A:H61	1.55	0.70
34:2c:18:TRP:O	34:2c:21:ARG:NH1	2.23	0.70
1:1A:1361:C:OP2	60:1A:4704:HOH:O	2.09	0.70
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.38	0.70
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.25	0.70
26:24:34:GLU:OE1	44:2m:3:ARG:N	2.25	0.70
33:2b:58:ILE:HG21	33:2b:222:ILE:HG22	1.74	0.70
1:1A:1060:U:OP2	60:1A:5073:HOH:O	2.10	0.70
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.72	0.70
32:1a:1136:U:H5"	32:1a:1137:C:C4	2.27	0.70
1:2A:109:G:N7	60:2A:5070:HOH:O	2.25	0.70
2:2B:41:U:H5	6:2G:70:VAL:H	1.40	0.70
32:2a:986:A:N3	50:2s:52:TYR:OH	2.24	0.70
1:1A:1857:G:H4'	3:1D:242:ARG:HE	1.56	0.69
1:1A:2045:G:H5'	1:1A:2629:C:H4'	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2149:G:H1	1:1A:2183:C:H42	1.37	0.69
1:1A:2641:A:O2'	1:1A:2642:G:OP2	2.10	0.69
1:2A:1973:G:OP1	60:2A:5051:HOH:O	2.10	0.69
1:2A:2710:C:N4	60:2A:4933:HOH:O	2.24	0.69
24:22:1:MET:N	24:22:52:ASP:OD1	2.23	0.69
32:2a:864:A:OP2	60:2a:3438:HOH:O	2.10	0.69
32:1a:200:G:H1	32:1a:217:C:H42	1.39	0.69
32:1a:525:C:OP1	43:1l:89:ARG:NH1	2.25	0.69
54:1w:5:G:H2'	54:1w:6:G:H8	1.57	0.69
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.75	0.69
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.74	0.69
32:2a:654:G:O6	32:2a:754:C:N4	2.20	0.69
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.65	0.69
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.25	0.69
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.26	0.69
5:2F:20:LEU:HD13	5:2F:125:LEU:HD13	1.74	0.69
32:1a:1027:C:C4	32:1a:1034:G:C2	2.80	0.69
36:2e:78:HIS:CD2	39:2h:104:ARG:HD2	2.27	0.69
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.73	0.69
1:2A:963:U:OP2	60:2A:4399:HOH:O	2.09	0.69
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.10	0.69
6:2G:15:VAL:HG13	6:2G:175:LEU:HD23	1.74	0.69
32:2a:664:G:H22	32:2a:741:G:H1	1.38	0.69
32:2a:972:C:O2'	41:2j:55:LYS:O	2.08	0.69
1:1A:1312:G:O5'	18:1W:15:ARG:NH2	2.25	0.69
32:2a:403:C:O2'	35:2d:122:ARG:NH2	2.26	0.69
49:2r:26:LEU:HD11	49:2r:42:ARG:HD3	1.74	0.69
1:1A:1785:C:H5	15:1T:96:ARG:NH2	1.91	0.69
1:1A:2362:C:OP2	60:1A:5166:HOH:O	2.09	0.69
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.58	0.69
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.58	0.69
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.73	0.69
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.74	0.69
42:2k:54:ARG:NH1	54:2y:39:PSU:O2'	2.26	0.69
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.73	0.69
50:1s:28:LYS:NZ	50:1s:46:GLY:O	2.25	0.69
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.26	0.69
32:2a:583:A:OP2	60:2a:3403:HOH:O	2.11	0.69
37:2f:46:ARG:HH22	49:2r:37:VAL:HG11	1.55	0.69
1:2A:1016:G:O6	1:2A:1147:C:N4	2.26	0.69
11:2P:95:VAL:HA	11:2P:99:LEU:HD21	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:815:A:N7	32:2a:1509:C:O2'	2.26	0.69
32:1a:1198:G:OP1	60:1a:2016:HOH:O	2.10	0.68
1:2A:775:G:O3'	60:2A:4370:HOH:O	2.10	0.68
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.75	0.68
32:2a:1191:A:OP2	34:2c:3:ASN:ND2	2.26	0.68
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	1.74	0.68
1:1A:2384:G:O6	60:1A:4543:HOH:O	2.06	0.68
32:1a:148:G:H2'	32:1a:149:A:H8	1.58	0.68
1:2A:1278:A:OP1	13:2R:36:THR:HG22	1.93	0.68
1:2A:2250:G:OP1	12:2Q:85:LYS:NZ	2.26	0.68
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.29	0.68
32:2a:673:G:H2'	32:2a:674:G:C8	2.27	0.68
1:2A:307:G:N1	1:2A:310:A:OP2	2.27	0.68
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.29	0.68
32:2a:148:G:H2'	32:2a:149:A:H8	1.56	0.68
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.27	0.68
32:1a:324:G:N7	60:1a:2314:HOH:O	2.25	0.68
37:1f:37:VAL:HA	37:1f:65:VAL:HG12	1.74	0.68
1:2A:249:C:O2	30:28:12:LYS:NZ	2.25	0.68
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.25	0.68
32:2a:1302:U:OP2	44:2m:21:TYR:OH	2.06	0.68
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.74	0.68
32:1a:376:G:H5"	47:1p:5:ARG:HG2	1.75	0.68
32:1a:829:G:O6	60:1a:2228:HOH:O	2.09	0.68
1:1A:1990:G:OP1	60:1A:4816:HOH:O	2.11	0.68
32:1a:1292:U:P	38:1g:41:ARG:HH22	2.16	0.68
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.26	0.68
32:2a:953:G:H5'	32:2a:965:A:N6	2.09	0.68
54:2w:18:G:O2'	54:2w:57:G:N2	2.26	0.68
54:2y:10:G:H1	54:2y:25:C:N4	1.92	0.68
1:1A:1552:C:H2'	1:1A:1553:A:H8	1.59	0.68
32:1a:1075:C:OP1	33:1b:179:LYS:NZ	2.21	0.68
36:1e:85:GLY:O	36:1e:87:SER:N	2.23	0.68
1:2A:2305:A:H5"	6:2G:134:GLY:HA3	1.76	0.68
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.75	0.68
41:2j:8:LEU:HG	41:2j:70:ARG:HB2	1.76	0.68
4:1E:127:ASP:OD2	60:1E:411:HOH:O	2.10	0.68
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.74	0.68
32:2a:407:G:H5"	35:2d:115:ARG:HG2	1.74	0.68
50:2s:27:GLU:HB2	50:2s:28:LYS:HA	1.76	0.68
1:1A:1100:A:H61	1:1A:1151:U:H3	1.42	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:156:G:N1	32:1a:165:C:N3	2.38	0.68
54:1y:7:A:O2'	54:1y:49:C:OP2	2.09	0.68
4:2E:52:LEU:HB3	4:2E:76:ARG:HD3	1.76	0.68
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.77	0.67
35:1d:178:VAL:HG12	35:1d:179:GLU:H	1.59	0.67
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.76	0.67
32:2a:1226:C:H41	44:2m:104:ARG:HG2	1.59	0.67
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.26	0.67
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.76	0.67
1:1A:1431:G:O2'	1:1A:1442:U:O2	2.09	0.67
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.29	0.67
32:1a:62:U:OP1	32:1a:385:C:O2'	2.13	0.67
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.12	0.67
4:2E:27:LEU:HD22	15:2T:1:MET:HE1	1.74	0.67
32:2a:1518:MA6:N6	32:2a:1519:MA6:H103	2.09	0.67
1:1A:2850:C:OP2	60:1A:5118:HOH:O	2.12	0.67
1:1A:2884:C:OP1	60:1A:5250:HOH:O	2.11	0.67
1:2A:481:G:N7	60:2A:5310:HOH:O	2.27	0.67
1:2A:922:U:O2'	22:20:29:GLN:NE2	2.27	0.67
1:2A:2268:A:OP1	60:2A:4307:HOH:O	2.11	0.67
7:1H:94:TYR:OH	7:1H:152:ARG:NH1	2.26	0.67
32:2a:266:G:H5"	32:2a:268:C:H41	1.58	0.67
1:1A:1202:A:OP1	16:1U:55:ARG:NH1	2.28	0.67
32:1a:1086:U:H3	32:1a:1099:G:H22	1.42	0.67
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.30	0.67
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.74	0.67
1:1A:1228:G:O2'	25:13:29:ARG:NH1	2.26	0.67
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.28	0.67
2:2B:55:U:H1'	6:2G:29:TRP:HD1	1.59	0.67
32:2a:1028:C:O2	32:2a:1033:G:N1	2.26	0.67
1:2A:821:A:N1	60:2A:4282:HOH:O	2.27	0.67
1:2A:1024:G:OP2	60:2A:4644:HOH:O	2.13	0.67
1:2A:1803:A:O2'	3:2D:259:THR:HG21	1.95	0.67
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.28	0.67
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.75	0.67
38:2g:59:LEU:HG	38:2g:63:LYS:HE2	1.75	0.67
1:1A:2286:A:OP2	60:1A:5505:HOH:O	2.13	0.67
60:1A:5352:HOH:O	13:1R:3:HIS:NE2	2.27	0.67
6:1G:45:GLU:OE2	60:1G:3104:HOH:O	2.12	0.67
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.77	0.67
18:2W:34:ASN:OD1	18:2W:37:ARG:NH2	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:51:VAL:HG12	47:2p:53:VAL:H	1.59	0.67
14:1S:15:ARG:O	14:1S:19:LYS:HG2	1.94	0.67
32:1a:975:A:H4'	32:1a:976:G:H5"	1.76	0.67
1:2A:1218:C:H42	1:2A:1231:G:H1	1.43	0.67
2:2B:55:U:O2'	6:2G:27:ASN:ND2	2.25	0.67
32:2a:1271:G:H2'	32:2a:1272:G:H5"	1.76	0.67
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.10	0.67
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.60	0.67
1:1A:290:G:N7	60:1A:5216:HOH:O	2.28	0.66
1:1A:787:U:OP2	60:1A:4742:HOH:O	2.12	0.66
1:2A:861:A:N3	2:2B:79:C:O2'	2.27	0.66
1:2A:2143:C:H2'	1:2A:2144:U:O4'	1.95	0.66
32:2a:1030:C:H42	32:2a:1031:G:H1	1.42	0.66
32:2a:1075:C:H5"	33:2b:179:LYS:HZ3	1.58	0.66
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.74	0.66
42:2k:51:LYS:HA	42:2k:55:LYS:HE3	1.77	0.66
1:1A:593:G:O6	60:1A:5012:HOH:O	2.11	0.66
1:1A:1997:G:OP2	60:1A:4758:HOH:O	2.12	0.66
32:1a:407:G:H5"	35:1d:115:ARG:HG2	1.78	0.66
1:2A:2782:G:OP2	60:2A:4806:HOH:O	2.12	0.66
17:2V:40:LEU:HB2	17:2V:46:VAL:HG13	1.76	0.66
1:1A:715:G:N7	60:1A:5891:HOH:O	2.28	0.66
1:1A:2564:2MU:OP2	60:1A:5027:HOH:O	2.12	0.66
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.75	0.66
32:2a:1160:G:OP1	33:2b:133:LYS:NZ	2.28	0.66
32:2a:1239:A:H62	32:2a:1299:A:H62	1.41	0.66
48:2q:95:TYR:HA	48:2q:98:LEU:HD12	1.76	0.66
1:1A:2158:C:N4	1:1A:2177:G:C6	2.63	0.66
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.28	0.66
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.77	0.66
5:2F:40:GLN:HE22	5:2F:184:TYR:H	1.42	0.66
1:1A:1070:G:OP2	60:1A:4871:HOH:O	2.13	0.66
32:1a:1162:C:N4	32:1a:1174:G:H1	1.92	0.66
32:1a:134:A:H61	47:1p:25:ARG:HH12	1.43	0.66
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.28	0.66
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.77	0.66
32:2a:1060:C:H5"	41:2j:51:ARG:HG2	1.76	0.66
54:2y:55:PSU:N1	54:2y:57:G:H5"	2.08	0.66
32:1a:401:C:P	35:1d:73:ARG:HH21	2.18	0.66
1:2A:1648:C:OP1	60:2A:4350:HOH:O	2.12	0.66
1:2A:2518:A:OP2	60:2A:4219:HOH:O	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.28	0.66
32:2a:952:U:H2'	32:2a:953:G:C8	2.30	0.66
32:2a:1226:C:O2'	44:2m:111:LYS:NZ	2.25	0.66
24:12:52:ASP:O	24:12:56:GLN:HG3	1.96	0.66
32:2a:952:U:H2'	32:2a:953:G:H8	1.60	0.66
1:1A:2055:A:OP1	60:1A:4436:HOH:O	2.12	0.66
32:1a:116:A:OP1	60:1a:2042:HOH:O	2.12	0.66
1:2A:731:C:OP1	60:2A:4876:HOH:O	2.13	0.66
1:2A:2362:G:N3	60:2A:5180:HOH:O	2.29	0.66
26:24:24:THR:OG1	26:24:25:TYR:N	2.29	0.66
32:2a:1316:G:N7	50:2s:7:LYS:NZ	2.42	0.66
1:1A:1649:A:OP1	60:1A:5524:HOH:O	2.13	0.66
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.78	0.66
36:1e:78:HIS:CE1	36:1e:143:ARG:H	2.10	0.66
1:2A:1959:G:N7	60:2A:4532:HOH:O	2.29	0.66
7:2H:35:VAL:HG13	7:2H:71:LEU:HD22	1.78	0.66
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.61	0.66
1:1A:265:U:O4	60:1A:5675:HOH:O	2.10	0.65
1:1A:930:G:H22	1:1A:939:C:H42	1.42	0.65
1:1A:1077:G:H5"	31:19:8:LYS:HE3	1.77	0.65
4:1E:119:ARG:HD2	4:1E:160:TYR:HB2	1.77	0.65
32:1a:558:G:OP1	60:1a:1950:HOH:O	2.14	0.65
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.61	0.65
54:1w:7:A:N1	54:1w:66:U:O2	2.29	0.65
1:2A:322:A:OP2	5:2F:169:ASN:HB2	1.96	0.65
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.78	0.65
1:1A:1159:U:H2'	1:1A:1160:G:H8	1.61	0.65
1:1A:2164:C:N3	1:1A:2171:G:O6	2.30	0.65
8:1I:4:ILE:HG12	8:1I:18:VAL:HG22	1.77	0.65
54:1w:5:G:H2'	54:1w:6:G:C8	2.31	0.65
6:2G:120:LEU:N	6:2G:179:PRO:O	2.25	0.65
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.77	0.65
54:2w:53:G:H1	54:2w:61:C:H42	1.44	0.65
1:1A:2158:C:N3	1:1A:2177:G:C2	2.65	0.65
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.30	0.65
1:2A:1395:A:OP1	60:2A:4567:HOH:O	2.13	0.65
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.78	0.65
13:2R:24:GLN:HE22	13:2R:36:THR:HG21	1.61	0.65
32:2a:1264:C:N4	32:2a:1265:G:O6	2.29	0.65
46:2o:4:THR:OG1	46:2o:7:GLU:OE1	2.12	0.65
1:1A:1441:A:OP1	60:1A:5524:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:16:HIS:HD2	33:1b:204:ASN:H	1.44	0.65
32:2a:504:C:OP1	60:2a:3526:HOH:O	2.15	0.65
32:2a:712:A:N6	60:2a:3344:HOH:O	2.29	0.65
1:1A:625:G:O2'	1:1A:702:A:N6	2.29	0.65
5:1F:13:SER:OG	5:1F:127:GLU:OE1	2.12	0.65
32:1a:1191:A:OP1	34:1c:4:LYS:NZ	2.30	0.65
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.24	0.65
54:2w:51:U:H3	54:2w:63:G:H1	1.44	0.65
1:1A:992:G:OP2	60:1A:5140:HOH:O	2.15	0.65
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.32	0.65
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.79	0.65
54:2w:50:U:O2	54:2w:64:A:N1	2.30	0.65
32:1a:161:A:N1	32:1a:347:G:O2'	2.30	0.65
32:1a:649:G:H2'	32:1a:650:G:H8	1.62	0.65
1:2A:2136:C:H42	1:2A:2155:G:H1	1.32	0.65
32:2a:157:G:H1	32:2a:164:U:H3	1.44	0.65
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.78	0.65
54:2y:57:G:N2	60:2y:3116:HOH:O	2.29	0.65
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.62	0.65
32:2a:406:G:N2	35:2d:119:GLN:HE22	1.94	0.65
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.27	0.64
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.79	0.64
1:2A:2058:A:OP1	60:2A:4924:HOH:O	2.13	0.64
1:2A:2141:G:O6	1:2A:2150:U:O2	2.15	0.64
2:2B:66:A:H61	2:2B:108:U:H2'	1.62	0.64
41:2j:32:ALA:HB1	41:2j:33:GLN:HA	1.79	0.64
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.25	0.64
54:2y:6:G:H1	54:2y:67:C:H42	1.43	0.64
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.32	0.64
1:2A:897:C:H1'	54:2w:56:C:H5	1.63	0.64
32:2a:1004:A:N6	32:2a:1037:C:H1'	2.11	0.64
1:1A:83:A:H5'	20:1Y:8:LYS:HG2	1.78	0.64
1:1A:1243:U:O4	60:1A:5606:HOH:O	2.08	0.64
1:1A:1105:G:N2	1:1A:1125:C:N3	2.42	0.64
1:2A:1434:A:H61	1:2A:1558:A:H62	1.43	0.64
1:2A:2042:A:OP1	60:2A:4114:HOH:O	2.15	0.64
1:2A:2499:C:OP2	60:2A:4650:HOH:O	2.15	0.64
6:2G:135:LEU:HD21	6:2G:157:ILE:HD12	1.78	0.64
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.61	0.64
32:2a:949:A:H1'	32:2a:1364:U:H3	1.62	0.64
34:2c:39:ILE:HG23	34:2c:91:LEU:HD11	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:117:ARG:HG2	43:2l:122:THR:HB	1.79	0.64
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.33	0.64
5:1F:133:ASN:N	5:1F:138:GLU:OE1	2.31	0.64
32:1a:677:U:H3	32:1a:713:G:H22	1.46	0.64
7:2H:96:ALA:HB1	7:2H:103:LEU:HD11	1.80	0.64
23:21:50:ARG:NH1	23:21:57:GLU:OE2	2.23	0.64
32:2a:1009:G:H22	32:2a:1021:G:H1'	1.62	0.64
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	1.79	0.64
7:1H:3:ARG:NH1	7:1H:5:GLY:H	1.96	0.64
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.78	0.64
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.30	0.64
2:2B:14:U:OP2	2:2B:70:C:O2'	2.13	0.64
5:2F:12:LEU:HB2	5:2F:124:LEU:HD11	1.79	0.64
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.13	0.64
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.79	0.64
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.63	0.64
32:1a:107:G:N7	51:1t:15:ARG:NH2	2.46	0.64
35:1d:175:SER:HB3	35:1d:184:LYS:HB3	1.79	0.64
1:2A:1411:C:H42	1:2A:1591:G:H1	1.46	0.64
1:2A:2759:G:OP2	60:2A:4824:HOH:O	2.15	0.64
29:27:34:ARG:HE	29:27:39:ARG:HG2	1.63	0.64
5:1F:108:LYS:HG2	5:1F:112:MET:HE2	1.80	0.64
54:1y:8:4SU:H4'	54:1y:48:C:H4'	1.80	0.64
1:2A:494:G:OP1	18:2W:8:ARG:NH1	2.31	0.64
1:2A:1033:U:OP1	31:29:9:ARG:NH2	2.22	0.64
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.12	0.64
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.62	0.64
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.12	0.64
47:2p:52:ASP:O	47:2p:54:GLU:N	2.30	0.64
55:2x:40:C:H2'	55:2x:41:C:H6	1.63	0.64
1:1A:1452:U:H2'	1:1A:1453:C:C6	2.32	0.64
1:1A:2562:G:OP1	60:1A:4989:HOH:O	2.15	0.64
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.78	0.64
1:2A:132:G:O6	60:2A:4610:HOH:O	2.11	0.64
1:2A:449:A:OP2	60:2A:4655:HOH:O	2.15	0.64
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.28	0.64
10:1O:104:ARG:CZ	15:1T:34:VAL:HG11	2.28	0.64
26:14:56:VAL:HG23	26:14:57:GLU:H	1.61	0.64
32:1a:45:U:H2'	32:1a:46:G:C8	2.33	0.64
32:1a:102:G:O6	60:1a:2035:HOH:O	2.09	0.64
1:2A:322:A:OP1	5:2F:168:ARG:HD2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1355:G:O6	60:2A:5022:HOH:O	2.13	0.64
32:2a:1145:C:H4'	32:2a:1146:A:H5'	1.79	0.64
54:2y:67:C:H2'	54:2y:68:C:H6	1.63	0.64
1:1A:2149:G:H1	1:1A:2183:C:N4	1.96	0.63
32:1a:944:G:OP1	60:1a:2092:HOH:O	2.15	0.63
32:1a:953:G:H5'	32:1a:965:A:H61	1.61	0.63
5:2F:145:GLU:OE1	5:2F:145:GLU:N	2.31	0.63
7:2H:125:VAL:HG12	7:2H:131:VAL:HG22	1.80	0.63
33:2b:87:ARG:NH1	33:2b:220:ASP:OD1	2.31	0.63
34:2c:151:VAL:HG22	34:2c:200:ALA:HA	1.80	0.63
1:1A:2128:G:H1	1:1A:2205:C:H42	1.44	0.63
32:1a:1027:C:N4	32:1a:1034:G:C6	2.67	0.63
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.80	0.63
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.80	0.63
1:2A:1011:G:OP2	16:2U:70:ARG:NH2	2.31	0.63
12:2Q:11:LYS:HE3	12:2Q:88:GLY:O	1.97	0.63
32:2a:1029:C:C2	32:2a:1032:G:N2	2.66	0.63
32:2a:1163:C:H42	32:2a:1173:G:H1	1.47	0.63
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.80	0.63
33:2b:218:ALA:O	33:2b:222:ILE:HG23	1.98	0.63
34:2c:43:LEU:HD21	34:2c:91:LEU:HD13	1.80	0.63
1:1A:121:G:OP2	60:1A:4220:HOH:O	2.15	0.63
3:1D:8:PRO:HB3	3:1D:14:ARG:HD2	1.79	0.63
1:2A:370:G:N7	60:2A:4061:HOH:O	2.30	0.63
1:2A:1673:U:O2'	60:2A:4420:HOH:O	2.13	0.63
1:2A:1833:U:OP1	60:2A:5389:HOH:O	2.15	0.63
36:2e:8:GLU:HG2	36:2e:34:VAL:HG23	1.81	0.63
32:1a:1095:U:OP2	60:1a:2308:HOH:O	2.16	0.63
1:2A:1920:4OC:HM22	1:2A:1921:G:H5'	1.80	0.63
1:2A:2498:C:OP2	60:2A:4650:HOH:O	2.15	0.63
5:2F:110:LEU:HD21	5:2F:181:LEU:HD23	1.81	0.63
54:2y:18:G:H22	54:2y:55:PSU:HN3	1.41	0.63
32:1a:120:A:OP1	60:1a:2280:HOH:O	2.15	0.63
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.22	0.63
47:1p:51:VAL:HG12	47:1p:53:VAL:H	1.64	0.63
32:2a:1190:G:H5'	34:2c:176:HIS:HE1	1.62	0.63
33:2b:55:PHE:HE1	33:2b:218:ALA:HA	1.64	0.63
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.80	0.63
26:14:24:THR:OG1	26:14:25:TYR:N	2.30	0.63
1:1A:1718:U:O4	60:1A:4989:HOH:O	2.13	0.63
19:1X:88:LYS:HE2	19:1X:93:GLU:HG3	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:60:MET:HA	30:18:13:ARG:NH1	2.13	0.63
33:1b:174:VAL:O	33:1b:178:ARG:HG2	1.99	0.63
47:1p:13:HIS:O	47:1p:42:ARG:NH1	2.32	0.63
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.30	0.63
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.28	0.63
32:2a:17:U:H2'	32:2a:18:C:C6	2.34	0.63
1:1A:1513:G:O2'	1:1A:1593:C:O2'	2.17	0.62
8:1I:77:LEU:HD12	8:1I:101:LEU:HD13	1.81	0.62
32:1a:1237:C:O2'	32:1a:1300:G:N2	2.26	0.62
33:1b:51:LEU:HD22	33:1b:55:PHE:HE2	1.63	0.62
1:2A:2746:U:OP1	7:2H:85:LYS:NZ	2.28	0.62
3:2D:69:ARG:HE	3:2D:130:ALA:HB2	1.64	0.62
32:2a:1239:A:H4'	32:2a:1240:U:H5"	1.79	0.62
1:1A:1103:A:N6	1:1A:1133:G:OP2	2.31	0.62
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.64	0.62
32:1a:38:G:O6	60:1a:2178:HOH:O	2.13	0.62
1:2A:875:G:O6	1:2A:902:C:N4	2.32	0.62
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.39	0.62
29:27:34:ARG:HG3	29:27:34:ARG:HH11	1.63	0.62
32:2a:997:U:H3	32:2a:1044:A:H61	0.73	0.62
32:2a:1132:C:H42	32:2a:1142:G:H1	1.46	0.62
41:2j:30:SER:O	41:2j:81:THR:OG1	2.17	0.62
54:2y:7:A:O2'	54:2y:49:C:O4'	2.16	0.62
1:1A:1834:A:O2'	3:1D:259:THR:HG21	1.99	0.62
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.81	0.62
1:1A:303:C:N3	1:1A:385:G:N2	2.43	0.62
1:1A:414:U:O4	60:1A:5867:HOH:O	2.10	0.62
1:1A:1103:A:H61	1:1A:1127:U:H3	1.46	0.62
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.33	0.62
1:2A:829:A:N7	1:2A:2248:C:H5'	2.13	0.62
1:2A:900:A:O2'	1:2A:901:A:OP1	2.15	0.62
32:2a:1414:U:O4	60:2a:3578:HOH:O	2.14	0.62
1:1A:2328:C:O2'	6:1G:128:ARG:NH2	2.32	0.62
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.33	0.62
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.32	0.62
55:1x:4:G:H1	55:1x:69:C:H42	0.72	0.62
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.81	0.62
2:2B:31:C:H4'	6:2G:29:TRP:CZ2	2.35	0.62
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.81	0.62
32:2a:640:A:N6	60:2a:3376:HOH:O	2.32	0.62
1:1A:1104:G:H1	1:1A:1126:C:H42	1.46	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.18	0.62
26:24:33:VAL:HG12	26:24:35:VAL:H	1.64	0.62
32:1a:1270:C:OP2	52:1u:24:ARG:NH2	2.33	0.62
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.32	0.62
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	1.81	0.62
32:2a:1029:C:N3	32:2a:1032:G:N2	2.47	0.62
32:2a:1029:C:N4	32:2a:1032:G:N1	2.48	0.62
38:2g:16:LEU:HD21	40:2i:45:ALA:HB2	1.80	0.62
17:1V:72:VAL:HG13	17:1V:85:LYS:HB3	1.81	0.62
1:2A:271(G):C:H2'	1:2A:271(H):G:H8	1.65	0.62
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.31	0.62
1:2A:2318:G:H21	14:2S:3:ARG:HD3	1.64	0.62
32:2a:64:G:H4'	32:2a:65:U:H3'	1.81	0.62
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.33	0.62
43:1l:117:ARG:HG2	43:1l:122:THR:HB	1.82	0.62
32:2a:1075:C:H5"	33:2b:179:LYS:NZ	2.14	0.62
34:2c:47:LEU:HD12	34:2c:68:VAL:HG11	1.82	0.62
1:1A:2130:C:H2'	1:1A:2131:U:H6	1.65	0.62
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	1.81	0.62
32:2a:646:U:H2'	32:2a:647:C:C6	2.34	0.62
32:2a:1020:U:H2'	32:2a:1021:G:H8	1.63	0.62
33:2b:118:LEU:O	33:2b:122:PHE:HB3	2.00	0.62
44:2m:31:LYS:HA	44:2m:34:LEU:HD12	1.82	0.62
1:1A:1219:A:H4'	1:1A:1220:U:OP1	1.99	0.61
1:1A:2150:C:H42	1:1A:2182:G:H1	1.47	0.61
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.30	0.61
32:1a:1166:G:N2	32:1a:1170:A:OP2	2.33	0.61
1:2A:848:G:C2	1:2A:933:A:H1'	2.35	0.61
1:2A:2138:C:H42	1:2A:2153:G:H1	0.71	0.61
1:2A:2663:G:H3'	1:2A:2664:G:H8	1.64	0.61
37:2f:99:ALA:HB1	49:2r:23:LYS:HE3	1.81	0.61
1:1A:1159:U:H2'	1:1A:1160:G:C8	2.35	0.61
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.23	0.61
21:2Z:4:ARG:HG2	21:2Z:58:VAL:HB	1.82	0.61
5:1F:140:LEU:HD11	5:1F:170:LEU:HD11	1.81	0.61
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.83	0.61
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.82	0.61
32:2a:1219:U:OP1	45:2n:19:ARG:NH1	2.32	0.61
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.81	0.61
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.00	0.61
15:1T:65:LYS:HE3	15:1T:67:SER:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.32	0.61
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.82	0.61
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.28	0.61
24:22:1:MET:SD	24:22:56:GLN:NE2	2.73	0.61
8:1I:140:LEU:HD22	8:1I:142:VAL:HG13	1.82	0.61
12:1Q:18:LYS:O	12:1Q:98:LYS:NZ	2.27	0.61
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.81	0.61
32:1a:1000:U:O4	32:1a:1041:A:N1	2.33	0.61
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	1.81	0.61
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	1.83	0.61
44:2m:89:GLY:O	44:2m:93:ARG:HG3	2.01	0.61
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.35	0.61
1:2A:2396:G:O2'	60:2A:5236:HOH:O	2.16	0.61
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.34	0.61
32:2a:947:G:H1	32:2a:1234:C:H42	1.48	0.61
32:2a:1312:G:H5'	50:2s:5:LEU:HD11	1.82	0.61
33:2b:71:VAL:HG21	33:2b:164:VAL:HG22	1.81	0.61
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.66	0.61
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	1.82	0.61
54:1w:66:U:H2'	54:1w:67:C:C6	2.35	0.61
2:2B:43:C:O4'	6:2G:66:GLN:NE2	2.33	0.61
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.32	0.61
1:2A:2484:G:H1'	12:2Q:124:LYS:HD2	1.83	0.61
10:2O:80:ASP:OD2	15:2T:64:ARG:NH2	2.34	0.61
32:2a:45:U:H2'	32:2a:46:G:C8	2.36	0.61
32:2a:980:C:H1'	45:2n:19:ARG:HA	1.83	0.61
32:2a:1347:G:H22	32:2a:1373:G:H2'	1.66	0.61
54:2w:68:C:H2'	54:2w:69:G:H8	1.65	0.61
54:2y:18:G:N2	54:2y:55:PSU:C4	2.68	0.61
33:1b:60:ASP:O	33:1b:64:ARG:HG2	2.01	0.61
41:1j:65:LEU:HD13	45:1n:56:VAL:HG22	1.82	0.61
32:2a:771:G:N7	60:2a:3539:HOH:O	2.31	0.61
32:2a:983:A:N1	32:2a:1222:G:N2	2.47	0.61
32:2a:1011:G:N2	32:2a:1018:C:N3	2.48	0.61
32:2a:1134:G:H1	32:2a:1140:C:H42	1.49	0.61
1:1A:799:A:H3'	29:17:1:MET:HE1	1.83	0.60
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.81	0.60
32:1a:946:A:H2'	32:1a:947:G:C8	2.35	0.60
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.66	0.60
8:2I:93:THR:H	8:2I:96:ASP:HB2	1.66	0.60
54:2w:39:PSU:H2'	54:2w:40:C:H6	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:276:G:O3'	48:1q:68:ARG:NH1	2.34	0.60
32:1a:1228:C:OP1	44:1m:115:LYS:NZ	2.34	0.60
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.82	0.60
48:2q:26:GLN:HG2	48:2q:37:LYS:HG2	1.83	0.60
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.37	0.60
1:2A:1300:U:H4'	1:2A:1301:A:H5"	1.81	0.60
8:2I:124:GLY:H	8:2I:144:VAL:HG23	1.65	0.60
7:1H:56:SER:HB3	7:1H:61:HIS:ND1	2.17	0.60
41:1j:5:ARG:NH1	41:1j:71:LEU:HD21	2.16	0.60
1:2A:422:A:OP2	60:2A:4062:HOH:O	2.16	0.60
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.35	0.60
1:2A:2324:C:H5"	1:2A:2325:G:H5'	1.84	0.60
2:2B:24:G:H4'	2:2B:25:A:N7	2.17	0.60
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.01	0.60
54:2w:9:A:H5'	54:2w:46:7MG:HN22	1.66	0.60
1:1A:555:G:N1	1:1A:2045:G:OP1	2.30	0.60
1:1A:1451:U:H2'	1:1A:1452:U:C6	2.37	0.60
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.25	0.60
33:1b:16:HIS:CG	33:1b:17:PHE:H	2.20	0.60
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.34	0.60
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.17	0.60
32:2a:328:C:H4'	32:2a:329:A:H5'	1.83	0.60
33:2b:78:GLN:O	33:2b:94:ASN:ND2	2.34	0.60
44:2m:25:ILE:HD11	44:2m:66:LEU:HD13	1.83	0.60
45:2n:4:LYS:HA	45:2n:7:ILE:HG12	1.82	0.60
32:1a:625:G:H4'	47:1p:16:HIS:CD2	2.36	0.60
34:1c:26:LYS:HE2	41:1j:45:ARG:HH22	1.67	0.60
42:2k:31:THR:HG23	42:2k:42:TRP:HB3	1.82	0.60
1:1A:1405:A:H2'	1:1A:1406:A:H5'	1.83	0.60
1:1A:2175:G:H2'	1:1A:2176:G:C8	2.36	0.60
1:1A:2624:C:OP2	27:15:2:ALA:N	2.34	0.60
1:2A:1812:A:OP2	60:2A:5276:HOH:O	2.16	0.60
2:2B:40:U:H2'	26:24:2:LYS:HE3	1.83	0.60
2:2B:83:G:H1	2:2B:94:C:H42	1.48	0.60
1:1A:181:C:OP1	60:1A:4235:HOH:O	2.17	0.60
32:1a:584:G:H5'	48:1q:91:ARG:HH22	1.66	0.60
16:2U:66:ASN:HD21	16:2U:70:ARG:HH21	1.50	0.60
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.65	0.60
1:1A:2348:A:H61	22:10:43:THR:HG22	1.67	0.60
32:1a:78:G:C2	32:1a:91:C:N3	2.69	0.60
37:1f:97:PHE:HD2	49:1r:31:LEU:HD11	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.35	0.60
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.36	0.60
1:2A:2144:U:H1'	1:2A:2148:G:N2	2.17	0.60
32:2a:1029:C:N4	32:2a:1032:G:C6	2.70	0.60
1:1A:2349:G:OP1	60:1A:4319:HOH:O	2.17	0.60
26:14:54:GLY:N	26:14:55:ARG:HA	2.17	0.60
32:1a:1503:A:O2'	53:1v:13:A:N1	2.34	0.60
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.84	0.60
1:2A:615:G:OP1	5:2F:40:GLN:HG2	2.02	0.60
46:2o:28:GLN:HE21	46:2o:66:LEU:HD21	1.67	0.60
1:1A:2776:G:N7	60:1A:4738:HOH:O	2.31	0.59
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.84	0.59
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.84	0.59
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.17	0.59
54:1y:19:G:N2	54:1y:56:C:N3	2.50	0.59
4:1E:29:GLY:HA3	60:1E:419:HOH:O	2.00	0.59
32:1a:262:A:H2'	32:1a:263:A:C8	2.37	0.59
2:2B:42:C:O2'	6:2G:67:LYS:O	2.13	0.59
3:2D:164:GLN:HB3	3:2D:176:ARG:HG2	1.84	0.59
6:2G:173:LEU:HD23	6:2G:176:LEU:HD12	1.85	0.59
37:2f:3:ARG:HD3	37:2f:64:GLN:HE21	1.67	0.59
48:2q:32:TYR:O	48:2q:34:LYS:N	2.33	0.59
54:2y:55:PSU:HN1	54:2y:57:G:C5'	2.12	0.59
54:2y:67:C:H2'	54:2y:68:C:C6	2.37	0.59
1:2A:2156:G:H2'	1:2A:2157:G:C2	2.37	0.59
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.84	0.59
4:2E:179:GLU:HG3	15:2T:9:LEU:HD21	1.84	0.59
19:2X:29:TRP:CZ3	19:2X:76:ARG:HG3	2.36	0.59
32:2a:35:G:O2'	43:2l:118:SER:O	2.16	0.59
32:2a:1126:U:H3	41:2j:40:LEU:HD11	1.66	0.59
7:1H:97:ARG:NE	7:1H:104:GLU:OE1	2.35	0.59
41:1j:54:PHE:O	41:1j:56:HIS:N	2.34	0.59
40:2i:77:ILE:O	40:2i:81:ILE:HG12	2.03	0.59
1:1A:2766:A:O2'	31:19:15:LYS:NZ	2.35	0.59
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.84	0.59
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.84	0.59
32:1a:890:G:O2'	32:1a:906:G:O6	2.18	0.59
33:1b:74:LYS:HD2	33:1b:166:ASP:HB2	1.84	0.59
1:2A:1253:A:OP1	60:2A:4014:HOH:O	2.16	0.59
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.37	0.59
19:2X:48:LYS:NZ	24:22:30:ARG:HH22	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.17	0.59
1:1A:1140:U:H1'	1:1A:1143:U:C5	2.34	0.59
1:1A:2430:A:OP2	30:18:29:LYS:NZ	2.36	0.59
1:1A:2825:C:H5'	27:15:29:THR:HG21	1.84	0.59
8:1I:126:TYR:HB2	8:1I:142:VAL:HG23	1.84	0.59
1:2A:2096:U:H3	1:2A:2193:G:H1	1.49	0.59
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.17	0.59
21:2Z:45:ASP:O	21:2Z:49:ARG:HG2	2.01	0.59
54:2y:7:A:H61	54:2y:66:U:H3	1.50	0.59
1:1A:1100:A:N6	1:1A:1151:U:H3	2.01	0.59
32:1a:164:U:H2'	32:1a:165:C:C6	2.37	0.59
32:1a:997:U:H3	32:1a:1044:A:N6	1.99	0.59
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.17	0.59
1:2A:2376:A:H3'	1:2A:2377:A:H8	1.66	0.59
1:2A:2448:A:OP1	60:2A:4843:HOH:O	2.16	0.59
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.83	0.59
54:2w:9:A:O2'	54:2w:10:G:N7	2.34	0.59
1:1A:2150:C:H2'	1:1A:2151:C:O4'	2.01	0.59
2:1B:66:A:H61	2:1B:109:C:H5'	1.67	0.59
32:2a:448:A:P	32:2a:485:G:H22	2.26	0.59
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.85	0.59
32:1a:376:G:O3'	47:1p:5:ARG:HD2	2.02	0.59
32:1a:1007:C:N3	32:1a:1022:G:O6	2.36	0.59
32:1a:1037:C:H2'	32:1a:1038:C:H6	1.67	0.59
32:1a:1385:G:N7	60:1a:2216:HOH:O	2.32	0.59
1:2A:848:G:N3	1:2A:933:A:H1'	2.17	0.59
1:2A:878:A:H61	1:2A:899:A:H1'	1.66	0.59
1:2A:1220:A:OP2	16:2U:19:LYS:NZ	2.34	0.59
1:1A:1410:G:P	23:11:3:LYS:HG3	2.43	0.59
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.85	0.59
22:10:70:GLN:OE1	22:10:80:HIS:NE2	2.31	0.59
54:1w:66:U:H2'	54:1w:67:C:H6	1.66	0.59
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.20	0.59
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.03	0.59
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.85	0.59
9:2N:67:LEU:HD12	9:2N:87:LEU:HD13	1.85	0.59
19:2X:48:LYS:HZ3	24:22:30:ARG:HH22	1.48	0.59
44:2m:3:ARG:HG2	44:2m:9:ILE:N	2.12	0.59
1:1A:2297:C:OP2	28:16:6:ARG:NH1	2.35	0.58
32:1a:1302:U:H5	44:1m:17:VAL:HG21	1.68	0.58
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:51:U:H2'	54:1w:52:G:C8	2.38	0.58
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.33	0.58
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.02	0.58
30:28:30:ARG:O	60:28:201:HOH:O	2.16	0.58
32:2a:1005:A:OP1	32:2a:1006:C:N4	2.36	0.58
35:2d:61:LYS:NZ	35:2d:72:GLU:OE1	2.34	0.58
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	1.85	0.58
1:1A:83:A:H5"	20:1Y:8:LYS:HE3	1.85	0.58
1:1A:997:G:OP1	12:1Q:16:ARG:NH2	2.35	0.58
1:1A:2146:G:H1	1:1A:2196:C:N4	2.00	0.58
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.18	0.58
1:2A:855:G:H2'	1:2A:856:C:C6	2.38	0.58
34:2c:131:ARG:HH11	34:2c:166:GLU:HG3	1.68	0.58
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.02	0.58
1:1A:2879:G:H2'	1:1A:2880:C:O4'	2.03	0.58
31:19:2:LYS:HE2	31:19:31:LYS:O	2.03	0.58
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.37	0.58
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.16	0.58
51:1t:10:LEU:HG	51:1t:12:ALA:H	1.68	0.58
1:2A:271(G):C:H2'	1:2A:271(H):G:C8	2.38	0.58
1:2A:307:G:H21	1:2A:330:A:H62	1.52	0.58
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.35	0.58
1:2A:2394:C:OP2	30:28:30:ARG:NH1	2.35	0.58
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.86	0.58
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.84	0.58
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.86	0.58
54:2y:9:A:H4'	54:2y:46:7MG:H5'	1.85	0.58
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.85	0.58
32:1a:158:G:N2	32:1a:163:C:O2	2.33	0.58
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.72	0.58
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.85	0.58
34:1c:52:LEU:HD21	34:1c:55:VAL:HG23	1.85	0.58
43:1l:39:VAL:HG11	43:1l:41:ARG:HH11	1.68	0.58
32:2a:375:U:OP1	47:2p:69:THR:HG21	2.01	0.58
32:2a:662:G:H2'	32:2a:663:A:C8	2.39	0.58
33:2b:208:ILE:HD13	33:2b:211:ILE:HD12	1.84	0.58
1:1A:2130:C:H2'	1:1A:2131:U:C6	2.39	0.58
1:1A:2145:G:H1	1:1A:2197:C:N4	2.01	0.58
2:1B:89:G:OP1	60:1B:3145:HOH:O	2.17	0.58
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.21	0.58
1:2A:2439:A:N6	55:2x:76:A:OP1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:187:VAL:HG12	11:2P:3:LEU:HD12	1.85	0.58
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.03	0.58
26:24:16:CYS:SG	26:24:17:GLY:N	2.77	0.58
32:2a:645:C:OP2	60:2a:3322:HOH:O	2.17	0.58
32:2a:890:G:O2'	32:2a:906:G:O6	2.18	0.58
32:2a:1027:C:N4	32:2a:1036:G:O6	2.36	0.58
44:2m:79:LYS:NZ	44:2m:83:ASP:OD2	2.33	0.58
49:2r:61:LYS:O	49:2r:65:ILE:HG12	2.03	0.58
1:1A:173:C:H2'	1:1A:174:U:C6	2.39	0.58
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.39	0.58
1:2A:903:C:H2'	1:2A:904:C:C6	2.39	0.58
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.86	0.58
11:2P:39:LYS:HB2	11:2P:45:LEU:HG	1.85	0.58
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.39	0.58
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.03	0.58
41:2j:17:ASP:OD1	41:2j:70:ARG:NE	2.33	0.58
54:2y:58:A:N3	54:2y:60:U:N3	2.51	0.58
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.38	0.58
26:14:57:GLU:HB3	26:14:58:ARG:HA	1.85	0.58
1:2A:2317:C:N4	1:2A:2318:G:O6	2.36	0.58
3:2D:3:VAL:HG13	3:2D:17:THR:HB	1.86	0.58
3:2D:101:GLU:OE2	3:2D:103:ARG:NH1	2.35	0.58
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.19	0.58
1:1A:810:G:OP1	60:1A:5161:HOH:O	2.17	0.58
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.67	0.58
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.50	0.58
37:1f:97:PHE:CD2	49:1r:31:LEU:HD11	2.39	0.58
41:1j:27:ALA:HB2	41:1j:81:THR:HG21	1.86	0.58
54:1w:4:C:H2'	54:1w:5:G:H8	1.68	0.58
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.39	0.58
32:2a:1007:C:N3	32:2a:1022:G:O6	2.36	0.58
43:2l:92:0TD:O	43:2l:93:LEU:HD23	2.03	0.58
1:1A:1834:A:H4'	3:1D:259:THR:HG23	1.85	0.58
32:1a:1159:U:OP1	33:1b:133:LYS:NZ	2.35	0.58
37:1f:10:LEU:HB2	37:1f:59:TYR:HB3	1.86	0.58
1:2A:2469:A:H3'	1:2A:2470:G:H8	1.69	0.58
11:2P:60:MET:HA	30:28:13:ARG:NH1	2.19	0.58
14:2S:92:TYR:HB3	14:2S:98:VAL:HG21	1.85	0.58
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.69	0.58
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.86	0.58
39:2h:20:TYR:OH	39:2h:78:GLN:NE2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:61:GLY:O	60:1F:407:HOH:O	2.17	0.58
37:1f:60:PHE:CE2	49:1r:78:LEU:HD21	2.39	0.58
37:1f:100:ASN:HB2	49:1r:28:GLU:HA	1.85	0.58
1:2A:108:U:H2'	1:2A:109:G:H8	1.68	0.58
1:2A:247:G:H4'	1:2A:386:G:C5	2.39	0.58
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.68	0.58
33:2b:146:GLN:O	33:2b:150:SER:HB3	2.04	0.58
35:2d:119:GLN:HG3	35:2d:123:HIS:CD2	2.39	0.58
39:2h:110:ALA:HB3	39:2h:121:ASP:HB3	1.86	0.58
1:1A:1232:G:H5"	17:1V:81:TYR:CE1	2.38	0.57
11:1P:94:GLU:OE2	11:1P:124:LYS:NZ	2.37	0.57
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.69	0.57
7:2H:17:VAL:HG13	7:2H:26:VAL:HG22	1.85	0.57
32:2a:76:C:H42	32:2a:93:G:H1	1.50	0.57
32:2a:974:A:OP2	45:2n:41:ARG:NH1	2.37	0.57
38:2g:113:GLU:HG3	38:2g:118:VAL:HG12	1.86	0.57
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.86	0.57
32:1a:582:U:OP1	46:1o:64:ARG:NH1	2.37	0.57
1:2A:1448:G:N7	60:2A:4812:HOH:O	2.33	0.57
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.39	0.57
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.04	0.57
1:2A:2141:G:H2'	1:2A:2142:C:O4'	2.04	0.57
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.69	0.57
31:29:10:ILE:HD11	31:29:34:GLN:HE21	1.68	0.57
32:2a:953:G:O6	44:2m:104:ARG:NH2	2.38	0.57
1:1A:701:A:N7	60:1A:4756:HOH:O	2.33	0.57
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.86	0.57
32:1a:1030:C:N3	32:1a:1031:G:N2	2.53	0.57
50:1s:11:VAL:HG12	50:1s:13:ASP:H	1.69	0.57
1:2A:2031:A:N3	1:2A:2455:G:O2'	2.32	0.57
2:2B:50:G:OP1	14:2S:63:THR:N	2.36	0.57
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.38	0.57
20:2Y:28:LYS:HG3	20:2Y:40:GLU:HG2	1.85	0.57
30:28:28:GLY:O	30:28:36:LYS:NZ	2.27	0.57
32:2a:67:C:H2'	32:2a:68:G:C8	2.38	0.57
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.34	0.57
1:1A:2457:G:OP1	5:1F:74:ARG:NH2	2.36	0.57
32:1a:1037:C:H2'	32:1a:1038:C:C6	2.39	0.57
34:1c:30:ARG:NH1	45:1n:35:ARG:O	2.37	0.57
40:1i:53:VAL:O	40:1i:55:ALA:N	2.37	0.57
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:397:G:N7	60:2A:4631:HOH:O	2.32	0.57
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.86	0.57
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.40	0.57
1:2A:2318:G:H21	14:2S:3:ARG:CD	2.17	0.57
22:20:11:ARG:O	22:20:14:ARG:NH2	2.36	0.57
32:2a:1226:C:N4	44:2m:104:ARG:HG2	2.19	0.57
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.39	0.57
54:2w:39:PSU:H2'	54:2w:40:C:C6	2.37	0.57
27:15:16:ARG:HG3	27:15:17:ASP:N	2.19	0.57
1:2A:2129:C:N3	1:2A:2159:G:N2	2.46	0.57
7:2H:159:GLU:HG2	7:2H:169:VAL:HG11	1.87	0.57
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.39	0.57
33:2b:97:TRP:HH2	33:2b:102:LEU:HD13	1.69	0.57
44:2m:92:HIS:HA	44:2m:110:ARG:HH21	1.68	0.57
60:1A:6276:HOH:O	3:1D:14:ARG:HG3	2.04	0.57
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.86	0.57
33:1b:134:GLU:HA	33:1b:137:ARG:HE	1.70	0.57
1:2A:1021:A:N6	1:2A:1141:U:H3	2.00	0.57
32:2a:565:U:OP2	32:2a:566:G:O2'	2.17	0.57
32:2a:966:M2G:HM22	55:2x:34:C:H5'	1.86	0.57
33:2b:126:GLU:CD	33:2b:126:GLU:H	2.12	0.57
32:1a:404:U:H2'	32:1a:405:U:C6	2.40	0.57
32:1a:405:U:OP2	35:1d:3:ARG:NH1	2.38	0.57
37:1f:75:LEU:O	37:1f:79:LEU:HG	2.05	0.57
38:1g:46:ALA:HA	38:1g:49:ILE:HD12	1.87	0.57
1:2A:1857:G:O2'	1:2A:1885:A:N6	2.35	0.57
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.04	0.57
11:2P:79:ARG:O	11:2P:111:ARG:N	2.33	0.57
14:2S:67:ARG:HG2	14:2S:71:ARG:HD2	1.87	0.57
32:2a:1244:C:H42	32:2a:1293:G:H1	1.52	0.57
32:2a:1328:C:O2'	44:2m:29:ARG:NE	2.38	0.57
38:2g:80:VAL:HB	38:2g:85:TYR:HE2	1.69	0.57
40:2i:7:THR:H	40:2i:83:ARG:HD2	1.70	0.57
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.39	0.57
1:1A:2699:U:OP2	60:1A:4849:HOH:O	2.17	0.57
60:1A:6427:HOH:O	28:16:19:ARG:HD2	2.04	0.57
32:1a:662:G:H2'	32:1a:663:A:C8	2.38	0.57
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.85	0.57
1:2A:212:G:H2'	1:2A:213:A:O4'	2.05	0.57
1:2A:296:C:O3'	20:2Y:95:LYS:NZ	2.38	0.57
1:2A:2269:A:OP1	60:2A:4307:HOH:O	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:33:ALA:HB1	44:2m:56:LEU:HD11	1.87	0.57
3:1D:125:ILE:HB	37:1f:81:ILE:HD11	1.86	0.57
21:1Z:126:VAL:HG13	21:1Z:161:VAL:HG23	1.85	0.57
32:1a:108:G:N1	51:1t:15:ARG:HG2	2.19	0.57
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.34	0.57
54:1w:4:C:H2'	54:1w:5:G:C8	2.40	0.57
1:2A:276:A:H5"	1:2A:277:C:H5'	1.85	0.57
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.20	0.57
54:2w:12:U:H3'	54:2w:13:C:H5"	1.85	0.57
54:2y:2:C:H2'	54:2y:3:C:H6	1.68	0.57
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.20	0.56
9:1N:67:LEU:HD12	9:1N:87:LEU:HD22	1.86	0.56
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.87	0.56
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.31	0.56
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.51	0.56
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.39	0.56
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.40	0.56
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.39	0.56
33:2b:73:THR:HA	33:2b:94:ASN:O	2.05	0.56
33:2b:74:LYS:HD2	33:2b:166:ASP:HB2	1.86	0.56
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.06	0.56
32:1a:56:U:H2'	32:1a:57:G:C8	2.39	0.56
32:1a:1030(A):G:H1'	32:1a:1031:G:H1	1.69	0.56
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.19	0.56
37:1f:60:PHE:HE2	49:1r:78:LEU:HD21	1.69	0.56
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.87	0.56
32:2a:148:G:H2'	32:2a:149:A:C8	2.38	0.56
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.39	0.56
32:2a:1314:C:N4	50:2s:2:PRO:O	2.38	0.56
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.87	0.56
44:2m:13:LYS:NZ	44:2m:21:TYR:OH	2.38	0.56
45:2n:12:ARG:NH1	45:2n:14:PRO:HA	2.20	0.56
1:1A:346:A:OP1	5:1F:168:ARG:HD2	2.05	0.56
1:1A:641:G:OP1	5:1F:40:GLN:HG2	2.05	0.56
1:1A:1346:U:H4'	1:1A:1347:A:H5"	1.87	0.56
1:1A:2155:G:O2'	1:1A:2178:G:N2	2.38	0.56
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.40	0.56
11:1P:106:LEU:HD13	11:1P:112:LEU:HG	1.86	0.56
32:1a:673:G:H2'	32:1a:674:G:C8	2.39	0.56
32:1a:1095:U:OP1	32:1a:1108:G:N1	2.38	0.56
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:128:ARG:NH2	55:1x:33:U:OP2	2.39	0.56
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.38	0.56
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.23	0.56
1:2A:740:U:H2'	1:2A:741:G:C8	2.40	0.56
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.38	0.56
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.40	0.56
2:2B:57:A:N3	6:2G:29:TRP:HB3	2.20	0.56
16:2U:50:ARG:HH12	17:2V:72:VAL:HA	1.71	0.56
32:2a:297:G:N2	32:2a:300:A:OP2	2.38	0.56
32:2a:1030(A):G:N1	32:2a:1030(D):A:OP2	2.38	0.56
32:2a:1343:G:H1'	40:2i:121:ARG:HH12	1.71	0.56
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.87	0.56
40:2i:4:TYR:O	40:2i:18:PHE:HA	2.05	0.56
45:2n:32:SER:O	45:2n:32:SER:OG	2.21	0.56
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.87	0.56
32:1a:1002:G:H3'	32:1a:1003:G:C4'	2.35	0.56
39:1h:86:ILE:HG22	39:1h:93:VAL:HG21	1.88	0.56
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.88	0.56
1:2A:1530:C:HO2'	1:2A:1531:C:P	2.29	0.56
52:2u:2:GLY:N	60:2u:101:HOH:O	2.37	0.56
1:1A:1108:G:P	1:1A:1116:A:H1'	2.46	0.56
1:1A:2008:A:OP2	60:1A:5695:HOH:O	2.17	0.56
38:1g:20:ASP:OD2	38:1g:63:LYS:NZ	2.37	0.56
40:1i:50:LEU:HD23	40:1i:81:ILE:HD11	1.87	0.56
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.31	0.56
7:2H:99:VAL:N	7:2H:102:ALA:O	2.38	0.56
32:2a:506:G:H1	32:2a:525:C:H42	1.53	0.56
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.87	0.56
40:2i:24:GLY:HA2	40:2i:59:PHE:O	2.05	0.56
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.86	0.56
44:2m:10:PRO:HD2	44:2m:18:ALA:HA	1.88	0.56
1:1A:1133:G:H2'	1:1A:1135:G:C8	2.41	0.56
1:1A:2647:C:O2'	4:1E:80:GLU:OE2	2.21	0.56
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.86	0.56
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.87	0.56
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.41	0.56
1:2A:994:C:O2'	1:2A:996:A:OP1	2.23	0.56
6:2G:102:PHE:HZ	6:2G:157:ILE:HD13	1.71	0.56
33:2b:15:VAL:O	33:2b:17:PHE:N	2.39	0.56
38:2g:89:MET:SD	38:2g:155:ARG:HB2	2.45	0.56
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1221:G:H1'	1:1A:1222:A:H5"	1.88	0.56
1:1A:2434:A:O4'	54:1y:76:A:N6	2.39	0.56
21:1Z:154:ASP:OD1	21:1Z:154:ASP:N	2.36	0.56
33:1b:115:LEU:HD13	33:1b:145:LEU:HB3	1.86	0.56
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.88	0.56
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.40	0.56
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.20	0.56
6:2G:75:LYS:HA	6:2G:84:LYS:HD2	1.88	0.56
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.38	0.56
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.86	0.56
32:2a:585:G:OP1	48:2q:37:LYS:NZ	2.31	0.56
1:1A:1000:C:OP1	12:1Q:87:LYS:HE3	2.06	0.56
1:1A:1699:A:OP1	13:1R:8:ARG:NH1	2.37	0.56
24:12:23:LYS:O	24:12:27:GLU:HG3	2.06	0.56
32:1a:67:C:H2'	32:1a:68:G:C8	2.40	0.56
32:1a:1027:C:C4	32:1a:1034:G:N1	2.74	0.56
41:1j:5:ARG:NH2	41:1j:73:ASP:OD2	2.39	0.56
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.40	0.56
1:2A:884:C:N3	1:2A:893:C:O2'	2.35	0.56
1:2A:887:A:H4'	1:2A:888:C:C5	2.40	0.56
1:2A:2127:G:N1	1:2A:2161:C:N4	2.53	0.56
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	1.87	0.56
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.37	0.56
20:2Y:94:LYS:NZ	60:2Y:601:HOH:O	2.38	0.56
26:24:9:LEU:HD23	26:24:27:THR:HG23	1.88	0.56
32:2a:560:U:H5'	32:2a:566:G:N2	2.21	0.56
32:2a:987:G:H1	32:2a:1218:C:N4	2.00	0.56
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.39	0.56
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.41	0.56
1:2A:500:G:N1	1:2A:503:A:OP2	2.38	0.56
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.40	0.56
6:2G:41:GLN:HE21	6:2G:153:ARG:HB3	1.70	0.56
6:2G:170:ARG:HH12	6:2G:174:GLU:CD	2.13	0.56
29:27:34:ARG:NE	29:27:39:ARG:HG2	2.20	0.56
32:2a:644:G:OP1	60:2a:3318:HOH:O	2.18	0.56
32:2a:1133:G:N2	32:2a:1141:C:N3	2.52	0.56
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.39	0.56
32:2a:1225:A:OP1	44:2m:103:THR:OG1	2.21	0.56
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.41	0.56
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.88	0.55
21:1Z:138:GLU:H	21:1Z:156:LYS:NZ	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:93:VAL:HG21	33:1b:97:TRP:CD1	2.35	0.55
54:1w:26:A:H61	54:1w:44:G:H1	1.55	0.55
6:2G:36:LYS:HD3	6:2G:95:ARG:NH1	2.21	0.55
14:2S:67:ARG:O	14:2S:71:ARG:HG3	2.05	0.55
28:26:10:LEU:HD13	28:26:19:ARG:HD3	1.88	0.55
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.41	0.55
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	1.87	0.55
32:2a:1395:C:O2'	32:2a:1401:G:O2'	2.21	0.55
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.88	0.55
39:1h:124:ALA:O	39:1h:128:GLY:N	2.39	0.55
47:1p:52:ASP:O	47:1p:54:GLU:N	2.39	0.55
1:2A:236:C:H2'	1:2A:237:C:H6	1.70	0.55
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.38	0.55
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.04	0.55
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	1.88	0.55
1:1A:611:U:H2'	1:1A:612:C:C6	2.41	0.55
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.39	0.55
26:14:63:TYR:N	26:14:64:GLY:HA2	2.21	0.55
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.40	0.55
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.88	0.55
54:1y:15:G:H22	54:1y:48:C:H42	1.54	0.55
54:1y:55:PSU:N1	54:1y:57:G:OP2	2.40	0.55
1:2A:2882:A:OP1	13:2R:96:ARG:NE	2.39	0.55
3:2D:127:VAL:HA	3:2D:193:VAL:HG23	1.88	0.55
3:2D:232:PRO:O	60:2D:404:HOH:O	2.18	0.55
13:2R:100:LEU:HD11	13:2R:113:LEU:HD23	1.89	0.55
15:2T:16:ARG:NH2	15:2T:18:ASP:OD2	2.39	0.55
32:2a:671:G:H5'	37:2f:77:ARG:HH22	1.72	0.55
32:2a:1003:G:N2	32:2a:1025:U:O4	2.40	0.55
32:2a:1009:G:N2	32:2a:1021:G:H1'	2.21	0.55
32:2a:1096:C:O2	32:2a:1170:A:O2'	2.24	0.55
1:1A:1109:G:N2	1:1A:1122:C:O2'	2.39	0.55
1:1A:1233:U:H4'	17:1V:79:VAL:HG22	1.88	0.55
32:1a:396:G:O2'	32:1a:398:C:OP1	2.17	0.55
32:1a:955:U:O2'	50:1s:83:HIS:HD2	1.90	0.55
6:2G:131:TYR:HE2	6:2G:133:LEU:HD23	1.72	0.55
27:25:56:LYS:NZ	27:25:58:LEU:O	2.39	0.55
1:1A:2157:A:H5'	1:1A:2182:G:H4'	1.87	0.55
5:1F:125:LEU:HD12	5:1F:194:MET:HB2	1.87	0.55
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.21	0.55
23:11:50:ARG:HD2	23:11:57:GLU:OE2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:17:ARG:HH21	10:2O:47:ILE:HG21	1.71	0.55
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.38	0.55
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.88	0.55
43:2l:57:LYS:HG2	43:2l:67:THR:HG22	1.88	0.55
1:1A:1111:U:H5"	1:1A:1112:U:OP2	2.06	0.55
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.54	0.55
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.22	0.55
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.20	0.55
32:1a:1316:G:OP1	45:1n:17:LYS:NZ	2.39	0.55
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.40	0.55
51:1t:13:LEU:HD12	51:1t:14:LYS:N	2.21	0.55
1:2A:403:U:H4'	1:2A:404:C:H5'	1.88	0.55
1:2A:482:A:H1'	1:2A:498:G:N2	2.22	0.55
1:2A:1865:G:N2	1:2A:1877:A:OP2	2.39	0.55
9:2N:12:ARG:NH2	9:2N:50:ASP:OD2	2.39	0.55
32:2a:8:A:N6	35:2d:209:ARG:HB2	2.21	0.55
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.06	0.55
1:1A:1108:G:OP1	1:1A:1116:A:O2'	2.23	0.55
1:1A:2227:G:H8	1:1A:2228:G:N7	2.04	0.55
32:1a:102:G:O2'	32:1a:151:A:N3	2.35	0.55
32:1a:1352:C:H2'	32:1a:1353:G:C8	2.41	0.55
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.42	0.55
3:2D:171:ASP:O	3:2D:187:GLY:N	2.37	0.55
32:2a:542:G:OP1	35:2d:10:ARG:NH2	2.23	0.55
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.07	0.55
54:2y:8:4SU:H1'	54:2y:48:C:H1'	1.89	0.55
1:1A:1108:G:H1	1:1A:1123:A:N6	2.03	0.55
18:1W:68:ARG:HH11	18:1W:111:HIS:HA	1.71	0.55
54:1y:36:A:H2'	54:1y:37:MIA:O4'	2.07	0.55
1:2A:863:A:H2'	1:2A:864:G:C8	2.41	0.55
32:2a:986:A:H2'	32:2a:987:G:O4'	2.06	0.55
33:2b:144:ARG:NH2	33:2b:148:TYR:OH	2.39	0.55
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.89	0.55
1:1A:1827:U:H2'	1:1A:1828:C:C6	2.41	0.55
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.89	0.55
1:2A:93:G:H2'	1:2A:94:C:C6	2.42	0.55
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.36	0.55
7:2H:41:MET:HE2	7:2H:64:LEU:HB2	1.88	0.55
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.89	0.55
32:2a:130:A:O2'	32:2a:131:C:O5'	2.25	0.55
32:2a:946:A:H2'	32:2a:947:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:16:HIS:O	51:2t:19:SER:OG	2.19	0.55
1:1A:843:C:H2'	1:1A:844:C:C6	2.42	0.55
1:1A:1633:A:H2'	1:1A:1634:C:C6	2.41	0.55
11:1P:91:PHE:O	11:1P:121:LYS:NZ	2.36	0.55
1:2A:668:G:H5'	1:2A:669:G:OP2	2.07	0.55
1:2A:1041:C:H1'	1:2A:1115:G:N2	2.22	0.55
1:2A:1580:A:H3'	1:2A:1581:G:H8	1.72	0.55
32:2a:501:C:H2'	32:2a:502:G:H8	1.71	0.55
32:2a:728:A:H2'	32:2a:729:A:C8	2.42	0.55
32:2a:1239:A:H62	32:2a:1299:A:N6	2.04	0.55
34:2c:6:HIS:CG	45:2n:49:HIS:HB3	2.42	0.55
34:2c:134:ILE:HD11	34:2c:153:VAL:HG23	1.88	0.55
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.89	0.54
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.88	0.54
1:2A:586:A:N1	1:2A:809:G:O2'	2.31	0.54
3:2D:103:ARG:HG3	3:2D:103:ARG:HH11	1.71	0.54
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.89	0.54
32:2a:34:C:H2'	32:2a:35:G:H8	1.72	0.54
33:2b:134:GLU:HA	33:2b:137:ARG:HE	1.73	0.54
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.89	0.54
1:1A:85:C:H4'	1:1A:102:U:H1'	1.89	0.54
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	1.87	0.54
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.40	0.54
40:1i:65:VAL:HG11	40:1i:73:GLN:HB3	1.89	0.54
50:1s:20:LEU:HD23	50:1s:23:ASN:HD22	1.72	0.54
1:2A:643:A:N1	1:2A:2369:A:O2'	2.39	0.54
9:2N:35:ARG:HD3	9:2N:37:LYS:HD2	1.88	0.54
32:2a:551:U:H2'	32:2a:552:U:C6	2.42	0.54
55:2x:44:A:H2'	55:2x:45:G:C8	2.42	0.54
54:2y:35:A:H2'	54:2y:36:A:O4'	2.08	0.54
1:1A:294:C:N3	1:1A:390:G:N2	2.44	0.54
1:1A:2784:C:H2'	1:1A:2785:C:H6	1.72	0.54
32:1a:328:C:H4'	32:1a:329:A:H5'	1.88	0.54
32:1a:1236:A:H4'	32:1a:1304:G:H4'	1.88	0.54
32:1a:1350:A:O2'	38:1g:33:ASP:OD1	2.21	0.54
54:1w:51:U:H2'	54:1w:52:G:H8	1.71	0.54
1:2A:1423:G:OP1	1:2A:1492:G:O2'	2.26	0.54
1:2A:1762:A:N1	60:2A:4405:HOH:O	2.34	0.54
5:2F:184:TYR:CZ	5:2F:188:ARG:HD2	2.41	0.54
19:2X:60:ARG:NH2	29:27:47:ARG:HH12	2.05	0.54
32:2a:719:C:N4	49:2r:71:LYS:HE2	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.07	0.54
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.07	0.54
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.88	0.54
34:2c:119:ARG:HE	34:2c:140:ARG:NH2	2.05	0.54
1:1A:602:G:H2'	1:1A:603:C:C6	2.43	0.54
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.73	0.54
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.89	0.54
32:1a:1144:G:H21	32:1a:1146:A:H62	1.55	0.54
1:2A:955:C:OP1	12:2Q:87:LYS:HE3	2.07	0.54
1:2A:2815:C:H2'	1:2A:2816:C:H6	1.72	0.54
6:2G:11:TYR:O	6:2G:16:ARG:HG2	2.06	0.54
25:23:8:LEU:HG	25:23:31:LEU:HD23	1.90	0.54
32:2a:1318:A:O2'	50:2s:37:ARG:HB2	2.08	0.54
33:2b:15:VAL:HG12	33:2b:209:ARG:HD2	1.88	0.54
36:2e:78:HIS:HD2	39:2h:104:ARG:HD2	1.73	0.54
1:1A:2148:A:N3	1:1A:2149:G:H1'	2.23	0.54
32:1a:998:G:N2	32:1a:1043:C:N3	2.46	0.54
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.08	0.54
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.90	0.54
54:1y:48:C:C2	54:1y:59:U:H1'	2.42	0.54
1:2A:652(D):C:H42	1:2A:652(U):G:H1	1.54	0.54
2:2B:28:C:H2'	2:2B:29:A:O4'	2.07	0.54
7:2H:20:ALA:HB3	7:2H:23:ARG:HG3	1.90	0.54
10:2O:73:ASP:OD2	15:2T:32:TYR:OH	2.20	0.54
32:2a:1010:G:N2	32:2a:1020:U:HO2'	2.06	0.54
50:2s:52:TYR:HB2	50:2s:57:HIS:CE1	2.42	0.54
1:1A:525:G:N7	60:1A:5331:HOH:O	2.33	0.54
1:1A:2603:C:H2'	1:1A:2604:G:C8	2.41	0.54
1:1A:2880:C:H2'	1:1A:2881:C:O4'	2.07	0.54
26:14:59:PHE:CE2	50:1s:64:GLU:HB3	2.43	0.54
42:1k:99:GLN:HE21	42:1k:108:ILE:HD11	1.72	0.54
48:1q:45:HIS:NE2	48:1q:47:PRO:HG3	2.23	0.54
22:20:32:ARG:H	22:20:35:ASN:ND2	2.06	0.54
32:2a:646:U:H2'	32:2a:647:C:H6	1.73	0.54
34:2c:131:ARG:HD3	34:2c:166:GLU:OE2	2.07	0.54
38:2g:94:ARG:O	38:2g:98:SER:OG	2.25	0.54
39:2h:17:THR:HA	39:2h:65:TYR:HE1	1.72	0.54
1:1A:1091:A:H4'	1:1A:1091:A:OP1	2.07	0.54
1:1A:1466:U:O2'	1:1A:1467:G:OP1	2.21	0.54
1:1A:2759:U:OP1	7:1H:85:LYS:NZ	2.32	0.54
1:1A:2801:C:OP1	4:1E:61:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.88	0.54
1:2A:637:A:H2'	11:2P:117:GLU:OE2	2.08	0.54
3:2D:8:PRO:HB3	3:2D:14:ARG:HD2	1.89	0.54
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.90	0.54
9:2N:20:GLY:HA2	9:2N:61:ARG:HG3	1.88	0.54
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.41	0.54
21:2Z:50:GLN:OE1	21:2Z:50:GLN:N	2.41	0.54
32:2a:179:A:H2'	32:2a:180:U:C6	2.43	0.54
33:2b:78:GLN:NE2	33:2b:95:GLN:OE1	2.40	0.54
33:2b:185:ILE:HG22	33:2b:199:TYR:HD2	1.72	0.54
34:2c:134:ILE:HG22	34:2c:168:ALA:HB3	1.90	0.54
1:1A:123:G:H21	29:17:48:LYS:HG2	1.72	0.54
1:1A:1131:A:HO2'	1:1A:1150:C:HO2'	1.53	0.54
1:1A:1289:G:O3'	11:1P:7:ARG:NH2	2.41	0.54
1:1A:2159:C:H2'	1:1A:2160:C:C6	2.43	0.54
1:1A:2348:A:H61	22:10:43:THR:CG2	2.19	0.54
54:1w:6:G:N1	54:1w:67:C:N4	2.27	0.54
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.90	0.54
15:2T:49:VAL:HG12	15:2T:63:VAL:HG22	1.90	0.54
17:2V:62:LEU:CD1	17:2V:95:LEU:HB2	2.38	0.54
26:24:60:GLN:O	26:24:62:ARG:N	2.40	0.54
32:2a:1345:U:OP2	60:2a:3494:HOH:O	2.18	0.54
38:2g:59:LEU:O	38:2g:63:LYS:HG3	2.08	0.54
54:2w:19:G:H1	54:2w:56:C:N4	2.05	0.54
54:2w:36:A:H2'	54:2w:37:MIA:H8	1.90	0.54
1:1A:1695:C:OP1	60:1A:5101:HOH:O	2.17	0.54
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	1.89	0.54
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.43	0.54
15:1T:127:ALA:C	15:1T:129:ARG:H	2.16	0.54
32:1a:731:G:H5'	32:1a:766:A:H4'	1.90	0.54
32:1a:1030:C:N3	32:1a:1031:G:C2	2.75	0.54
54:1w:63:G:H2'	54:1w:64:A:C8	2.42	0.54
1:2A:2142:C:H2'	1:2A:2143:C:O4'	2.08	0.54
1:2A:2474:C:H5"	1:2A:2475:C:OP2	2.08	0.54
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.07	0.54
7:2H:3:ARG:HH22	7:2H:65:HIS:HB3	1.72	0.54
32:2a:509:A:N3	32:2a:543:C:O2'	2.38	0.54
32:2a:1359:C:OP2	45:2n:35:ARG:NH1	2.41	0.54
54:2w:74:C:N4	54:2w:75:C:O2	2.40	0.54
1:1A:231:G:C8	30:18:5:LYS:HG2	2.43	0.54
1:1A:1700:G:H3'	13:1R:2:ARG:HD3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:128:G:O2'	48:1q:3:LYS:NZ	2.41	0.54
34:1c:78:GLY:HA3	34:1c:83:ARG:H	1.73	0.54
48:1q:45:HIS:CD2	48:1q:47:PRO:HG3	2.43	0.54
1:2A:72:U:OP1	60:2A:4855:HOH:O	2.19	0.54
1:2A:728:G:H4'	3:2D:13:ARG:HE	1.73	0.54
54:2y:42:C:H2'	54:2y:43:C:H6	1.73	0.54
1:1A:1137:G:C6	1:1A:1147:U:C2	2.96	0.53
1:1A:2367:C:H1'	22:10:39:ARG:HH21	1.73	0.53
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.90	0.53
15:1T:24:PRO:HA	15:1T:49:VAL:HG23	1.89	0.53
40:1i:55:ALA:HA	40:1i:58:HIS:HD2	1.73	0.53
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.08	0.53
1:2A:2430:A:OP2	60:2A:4409:HOH:O	2.17	0.53
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.88	0.53
32:2a:1129:C:OP2	40:2i:66:ARG:NH1	2.41	0.53
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.76	0.53
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	1.90	0.53
46:2o:26:GLU:OE1	46:2o:26:GLU:N	2.39	0.53
50:2s:80:TYR:O	50:2s:82:GLY:N	2.42	0.53
54:2y:18:G:N1	54:2y:55:PSU:C4	2.71	0.53
1:1A:18:C:O2'	1:1A:577:U:OP1	2.21	0.53
1:1A:1462:G:O2'	1:1A:1463:C:OP2	2.24	0.53
1:1A:2071:G:N7	60:1A:5009:HOH:O	2.33	0.53
40:1i:128:ARG:NH1	55:1x:35:A:OP2	2.41	0.53
1:2A:2134:A:H2'	1:2A:2134:A:N3	2.23	0.53
2:2B:14:U:O2	2:2B:108:U:H4'	2.07	0.53
32:2a:643:C:H2'	32:2a:644:G:H8	1.73	0.53
54:2y:6:G:N2	54:2y:67:C:N3	2.56	0.53
1:1A:1105:G:H2'	1:1A:1106:U:C5	2.43	0.53
1:1A:1552:C:H2'	1:1A:1553:A:C8	2.41	0.53
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.21	0.53
32:1a:1151:A:O2'	32:1a:1152:A:H8	1.92	0.53
35:1d:98:GLU:HG3	35:1d:189:PRO:HG2	1.88	0.53
1:2A:1152:C:H2'	1:2A:1153:C:H6	1.72	0.53
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.89	0.53
33:2b:186:ALA:O	33:2b:201:ILE:N	2.37	0.53
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.55	0.53
1:1A:1775:C:H5'	1:1A:1776:G:OP2	2.08	0.53
1:1A:2642:G:H2'	1:1A:2643:G:C8	2.43	0.53
32:1a:715:A:H2'	32:1a:716:A:C8	2.44	0.53
35:1d:23:GLY:HA3	35:1d:112:VAL:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.41	0.53
32:2a:1108:G:O6	60:2a:3564:HOH:O	2.18	0.53
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.23	0.53
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.44	0.53
51:2t:86:ARG:O	51:2t:90:GLN:HB2	2.08	0.53
1:1A:302:A:H2'	1:1A:303:C:C6	2.43	0.53
1:1A:551:A:O2'	1:1A:2065:C:O2	2.26	0.53
1:1A:927:G:H2'	1:1A:928:G:C8	2.40	0.53
6:1G:150:ASP:OD1	6:1G:150:ASP:N	2.41	0.53
15:1T:49:VAL:HG12	15:1T:63:VAL:HG22	1.90	0.53
32:1a:78:G:N1	32:1a:91:C:N4	2.55	0.53
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.09	0.53
1:2A:320:A:OP2	5:2F:137:LYS:NZ	2.29	0.53
1:2A:568:U:H5'	1:2A:945:A:N1	2.23	0.53
4:2E:11:MET:HG2	4:2E:24:THR:HB	1.90	0.53
15:2T:118:ARG:HG2	32:2a:1442(A):G:C8	2.44	0.53
32:2a:1122:U:H2'	32:2a:1123:A:H8	1.73	0.53
34:2c:47:LEU:HD22	34:2c:50:ALA:HB3	1.89	0.53
40:2i:8:GLY:O	40:2i:15:ALA:N	2.37	0.53
1:1A:2193:A:O2'	1:1A:2194:U:H5"	2.09	0.53
33:1b:166:ASP:O	33:1b:170:GLU:N	2.42	0.53
36:1e:60:TYR:OH	36:1e:64:ARG:NH2	2.35	0.53
39:1h:51:VAL:HG11	39:1h:60:ARG:HH12	1.72	0.53
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.07	0.53
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.42	0.53
20:2Y:30:VAL:HG22	20:2Y:37:VAL:HG12	1.90	0.53
32:2a:132:C:O2	32:2a:230:G:N2	2.30	0.53
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.42	0.53
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.90	0.53
1:1A:1961:5MU:OP1	1:1A:2616:U:O2'	2.27	0.53
1:1A:2011:G:O6	60:1A:5950:HOH:O	2.19	0.53
9:1N:4:TYR:CE2	16:1U:100:VAL:HG11	2.43	0.53
21:1Z:1:MET:HE2	21:1Z:135:GLU:HB2	1.91	0.53
21:1Z:163:LEU:HD23	21:1Z:167:PRO:HG3	1.91	0.53
54:1y:40:C:H2'	54:1y:41:C:H6	1.73	0.53
1:2A:2148:G:H2'	1:2A:2149:G:C8	2.44	0.53
1:2A:2497:A:H5"	60:2A:4025:HOH:O	2.09	0.53
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.91	0.53
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.91	0.53
23:21:56:GLN:HE21	23:21:87:PRO:HG3	1.74	0.53
32:2a:393:A:OP1	60:2a:3393:HOH:O	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:825:G:H1	32:2a:875:C:H42	1.57	0.53
32:2a:988:G:H1	32:2a:1217:C:N4	2.01	0.53
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.24	0.53
1:1A:1101:G:H1	1:1A:1150:C:N4	2.04	0.53
1:1A:1898:A:H2'	1:1A:1899:A:C8	2.43	0.53
1:1A:2812:A:H1'	1:1A:2904:U:H1'	1.90	0.53
32:1a:625:G:H2'	32:1a:626:U:C6	2.44	0.53
54:1w:9:A:O2'	54:1w:10:G:N7	2.42	0.53
54:1y:23:A:H2'	54:1y:24:G:C8	2.44	0.53
1:2A:796:C:H2'	1:2A:797:C:C6	2.44	0.53
1:2A:884:C:H3'	1:2A:885:C:C6	2.44	0.53
5:2F:13:SER:HB3	5:2F:127:GLU:HG3	1.90	0.53
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HG22	1.90	0.53
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.33	0.53
32:2a:501:C:H2'	32:2a:502:G:C8	2.43	0.53
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.09	0.53
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.89	0.53
32:1a:620:C:H2'	32:1a:621:A:O4'	2.09	0.53
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.24	0.53
32:1a:757:U:H2'	32:1a:758:G:O4'	2.09	0.53
32:1a:1029:C:N3	32:1a:1032:G:O6	2.42	0.53
32:1a:1239:A:H4'	32:1a:1240:U:H5"	1.90	0.53
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.91	0.53
1:2A:2019:A:N7	27:25:9:LYS:HE2	2.24	0.53
1:2A:2184:G:H2'	1:2A:2185:C:C6	2.43	0.53
1:2A:2468:G:C2	1:2A:2481:G:N3	2.77	0.53
7:2H:98:LEU:HB2	7:2H:125:VAL:HG22	1.90	0.53
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.91	0.53
1:1A:904:C:H4'	22:10:23:VAL:HG21	1.89	0.53
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	1.90	0.53
26:14:33:VAL:HG12	26:14:35:VAL:H	1.74	0.53
32:1a:458:C:H2'	32:1a:460:G:O4'	2.09	0.53
44:1m:4:ILE:HD12	44:1m:57:ARG:HA	1.91	0.53
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.09	0.53
2:2B:31:C:H4'	6:2G:29:TRP:HZ2	1.74	0.53
6:2G:41:GLN:HG3	6:2G:154:GLY:O	2.09	0.53
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	1.90	0.53
32:2a:537:G:H5"	43:2l:113:ARG:NH1	2.24	0.53
1:1A:1040:C:OP1	16:1U:53:ARG:NH2	2.42	0.52
1:1A:1201:A:OP1	16:1U:55:ARG:HD2	2.10	0.52
1:1A:1338:U:H2'	1:1A:1339:C:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1915:C:OP1	60:1A:5837:HOH:O	2.19	0.52
1:1A:2250:G:N3	1:1A:2250:G:H2'	2.23	0.52
32:1a:167:G:H2'	32:1a:168:G:C8	2.45	0.52
39:1h:91:ARG:HD3	48:1q:32:TYR:O	2.08	0.52
1:2A:11:G:C2'	1:2A:12:U:H5'	2.39	0.52
1:2A:144:C:H2'	1:2A:145:G:H8	1.74	0.52
3:2D:169:GLU:HG2	3:2D:174:ILE:HD11	1.90	0.52
6:2G:5:VAL:H	6:2G:8:LYS:HE2	1.74	0.52
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.91	0.52
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.24	0.52
32:2a:1169:A:H2'	32:2a:1170:A:C8	2.44	0.52
32:2a:1227:A:OP2	44:2m:111:LYS:HE2	2.09	0.52
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.22	0.52
32:2a:1314:C:OP1	50:2s:6:LYS:NZ	2.31	0.52
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.27	0.52
46:2o:87:ILE:O	46:2o:88:ARG:HB3	2.09	0.52
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.10	0.52
1:1A:2175:G:H2'	1:1A:2176:G:H8	1.73	0.52
9:1N:70:LYS:HD3	9:1N:87:LEU:HD12	1.91	0.52
19:1X:35:THR:HG22	19:1X:38:GLU:HB2	1.91	0.52
32:1a:865:A:H2	32:1a:918:A:H4'	1.75	0.52
42:1k:48:ILE:HD12	42:1k:63:LEU:HB2	1.91	0.52
1:2A:236:C:H2'	1:2A:237:C:C6	2.44	0.52
1:2A:455:C:N3	1:2A:472:A:H2'	2.24	0.52
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.09	0.52
2:2B:4:C:H42	2:2B:117:G:H1	1.56	0.52
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.45	0.52
32:2a:1106:G:H5"	34:2c:172:ARG:HB3	1.91	0.52
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.89	0.52
40:2i:31:GLN:HE21	40:2i:36:TYR:HD1	1.56	0.52
54:2w:11:C:N4	54:2w:24:G:H1	2.05	0.52
55:2x:47:U:N3	55:2x:50:U:OP1	2.42	0.52
1:1A:831:A:N6	3:1D:229:VAL:HG11	2.24	0.52
1:1A:964:A:N3	2:1B:80:U:O2'	2.35	0.52
1:1A:2147:G:N1	1:1A:2194:U:OP1	2.20	0.52
32:1a:262:A:C6	32:1a:263:A:C6	2.97	0.52
1:2A:981:A:N1	1:2A:2027:G:O2'	2.40	0.52
1:2A:2151:G:H2'	1:2A:2152:G:C8	2.44	0.52
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	1.91	0.52
32:2a:25:C:H5'	32:2a:524:G:H1'	1.90	0.52
32:2a:986:A:H1'	50:2s:55:LYS:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.09	0.52
50:2s:28:LYS:HB3	50:2s:29:ARG:CB	2.39	0.52
1:1A:2661:U:H2'	1:1A:2662:U:C6	2.44	0.52
60:1A:4906:HOH:O	11:1P:39:LYS:HE3	2.09	0.52
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.44	0.52
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.90	0.52
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.09	0.52
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.91	0.52
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.10	0.52
1:2A:1192:G:OP2	11:2P:17:LYS:NZ	2.43	0.52
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.25	0.52
1:2A:2303:G:O2'	6:2G:132:ASN:HB2	2.09	0.52
2:2B:7:G:N2	14:2S:38:GLN:HE22	1.99	0.52
7:2H:33:LEU:HD11	7:2H:136:ILE:HG22	1.90	0.52
9:2N:42:TRP:HA	9:2N:48:MET:HE1	1.91	0.52
1:1A:941:U:O2'	1:1A:942:A:OP1	2.23	0.52
1:1A:1320:A:N3	1:1A:1343:C:H1'	2.24	0.52
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.09	0.52
1:1A:1823:G:O2'	1:1A:1861:C:OP1	2.25	0.52
32:1a:78:G:N2	32:1a:91:C:N3	2.57	0.52
32:1a:148:G:H2'	32:1a:149:A:C8	2.40	0.52
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.45	0.52
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.27	0.52
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.09	0.52
1:2A:928:G:H8	1:2A:928:G:O5'	1.92	0.52
1:2A:1345:C:OP2	60:2A:4866:HOH:O	2.19	0.52
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.24	0.52
1:2A:2128:C:N3	1:2A:2160:G:O6	2.43	0.52
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.08	0.52
21:2Z:73:GLN:O	21:2Z:87:ASP:N	2.34	0.52
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.45	0.52
45:2n:47:LEU:HB3	45:2n:52:GLN:HB2	1.92	0.52
1:1A:1613:A:OP1	3:1D:211:ARG:NH1	2.43	0.52
1:1A:2429:C:OP1	11:1P:65:ARG:NH2	2.43	0.52
26:14:61:ARG:HG3	26:14:62:ARG:N	2.24	0.52
32:1a:1060:C:OP1	45:1n:45:ARG:NH2	2.40	0.52
54:1w:22:G:N7	54:1w:46:7MG:N2	2.53	0.52
54:1y:51:U:H2'	54:1y:52:G:C8	2.45	0.52
19:2X:94:GLY:H	19:2X:95:LEU:HA	1.74	0.52
32:2a:21:G:H2'	32:2a:22:G:C8	2.45	0.52
32:2a:353:A:H5'	32:2a:353:A:H8	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:375:U:O4	60:2a:3562:HOH:O	2.13	0.52
32:2a:1163:C:N4	32:2a:1173:G:H1	2.06	0.52
54:2y:14:A:O2'	54:2y:15:G:OP1	2.24	0.52
1:1A:123:G:N2	29:17:48:LYS:HG2	2.24	0.52
1:1A:1882:U:H2'	1:1A:1883:C:O4'	2.08	0.52
4:1E:111:ARG:HD2	4:1E:160:TYR:CD2	2.45	0.52
8:1I:5:LEU:HD11	8:1I:19:VAL:HG22	1.92	0.52
20:1Y:6:HIS:HE1	20:1Y:72:VAL:O	1.93	0.52
26:14:28:LYS:HE2	26:14:31:ILE:HD11	1.91	0.52
32:1a:1030:C:N4	32:1a:1031:G:H1	2.04	0.52
1:2A:1431:U:H2'	1:2A:1432:C:C6	2.44	0.52
1:2A:2144:U:O2'	1:2A:2147:G:O6	2.23	0.52
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.37	0.52
21:2Z:141:VAL:HG13	21:2Z:144:LEU:HB3	1.92	0.52
32:2a:134:A:H61	47:2p:25:ARG:NH1	2.07	0.52
32:2a:674:G:H2'	32:2a:675:A:H8	1.75	0.52
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.45	0.52
32:2a:1137:C:H5"	32:2a:1138:G:OP1	2.10	0.52
32:2a:1315:U:O2'	32:2a:1360:A:N3	2.32	0.52
1:1A:2227:G:H3'	1:1A:2228:G:N7	2.24	0.52
32:1a:544:G:OP2	35:1d:66:ARG:NH2	2.43	0.52
41:1j:57:LYS:HE2	41:1j:60:ARG:NH2	2.25	0.52
1:2A:1231:G:H2'	1:2A:1232:G:C8	2.45	0.52
1:2A:1805:U:O2	3:2D:50:THR:HB	2.10	0.52
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.35	0.52
14:2S:35:ILE:HG12	14:2S:101:LEU:HD12	1.90	0.52
33:2b:103:THR:HA	33:2b:180:LEU:HD11	1.92	0.52
1:1A:54:G:O2'	1:1A:125:A:N1	2.38	0.52
1:1A:1115:A:H1'	1:1A:1142:A:H4'	1.90	0.52
33:1b:95:GLN:OE1	33:1b:147:LYS:HG2	2.10	0.52
1:2A:728:G:C5'	3:2D:13:ARG:HH21	2.22	0.52
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.25	0.52
43:2l:86:ARG:HG3	43:2l:87:GLY:O	2.10	0.52
45:2n:47:LEU:O	45:2n:51:GLY:N	2.37	0.52
1:1A:2264:G:OP2	60:1A:5857:HOH:O	2.19	0.52
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.09	0.52
35:1d:65:ARG:HG2	35:1d:75:PHE:CD1	2.45	0.52
40:1i:3:GLN:HE21	40:1i:20:ARG:NH2	2.07	0.52
1:2A:184:C:H2'	1:2A:185:U:C6	2.45	0.52
1:2A:859:G:N2	1:2A:917:A:OP2	2.44	0.52
2:2B:30:C:H2'	2:2B:31:C:H5'	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:173:LEU:O	6:2G:178:PHE:N	2.37	0.52
32:2a:11:G:H1	32:2a:23:C:H42	1.58	0.52
32:2a:494:U:OP2	60:2a:3449:HOH:O	2.19	0.52
32:2a:863:U:O2'	32:2a:865:A:N7	2.42	0.52
32:2a:865:A:N3	32:2a:918:A:O2'	2.36	0.52
32:2a:1057:G:H2'	32:2a:1058:G:O4'	2.10	0.52
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.45	0.52
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.42	0.52
35:2d:172:PRO:HD2	35:2d:173:TRP:CZ3	2.44	0.52
1:1A:704:U:H2'	1:1A:705:C:C6	2.45	0.51
1:1A:1001:G:H5"	12:1Q:77:LYS:HD2	1.92	0.51
5:1F:135:LYS:HB2	5:1F:138:GLU:CD	2.35	0.51
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.25	0.51
32:1a:78:G:N2	32:1a:91:C:C2	2.78	0.51
32:1a:376:G:H5"	47:1p:5:ARG:CG	2.40	0.51
32:1a:1053:G:H4'	32:1a:1054:C:H5'	1.91	0.51
32:1a:1239:A:H62	32:1a:1299:A:N6	2.07	0.51
32:1a:1246:C:H42	32:1a:1291:G:H1	1.58	0.51
41:1j:17:ASP:OD1	41:1j:70:ARG:NE	2.44	0.51
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.45	0.51
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.45	0.51
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.44	0.51
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.55	0.51
2:2B:20:C:H42	2:2B:63:G:H1	1.59	0.51
2:2B:87:G:N2	2:2B:90:A:OP2	2.36	0.51
3:2D:20:ASP:OD1	3:2D:20:ASP:N	2.35	0.51
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.43	0.51
32:2a:1004:A:N3	32:2a:1038:C:C2	2.77	0.51
32:2a:1085:U:H3'	32:2a:1086:U:C6	2.45	0.51
32:2a:1329:A:H5"	44:2m:26:GLY:H	1.75	0.51
33:2b:118:LEU:HD13	33:2b:142:LEU:HB2	1.92	0.51
43:2l:24:VAL:HB	43:2l:27:LEU:HD22	1.91	0.51
1:1A:553:A:O2'	1:1A:554:A:H5'	2.10	0.51
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.92	0.51
26:14:44:THR:O	26:14:46:GLN:N	2.43	0.51
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.92	0.51
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.92	0.51
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.75	0.51
40:1i:4:TYR:CE1	40:1i:88:TYR:HA	2.45	0.51
40:1i:21:PRO:HA	40:1i:59:PHE:HD1	1.75	0.51
44:1m:82:MET:O	44:1m:93:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:996:A:H1'	17:2V:9:GLY:O	2.10	0.51
55:2x:3:C:N4	55:2x:70:G:H1	2.06	0.51
1:1A:1141:A:C8	1:1A:1142:A:C8	2.98	0.51
1:1A:2518:U:O2'	54:1w:76:A:H4'	2.10	0.51
2:1B:25:A:OP2	60:1B:3134:HOH:O	2.19	0.51
12:1Q:16:ARG:HG3	12:1Q:18:LYS:HG3	1.93	0.51
19:1X:57:LEU:HA	60:1X:3101:HOH:O	2.11	0.51
24:12:7:ARG:O	24:12:11:GLU:HG3	2.11	0.51
32:1a:165:C:H2'	32:1a:166:G:C8	2.46	0.51
32:1a:406:G:N2	35:1d:119:GLN:HE22	2.08	0.51
54:1y:5:G:H1'	54:1y:69:G:N2	2.25	0.51
1:2A:77:C:OP1	24:22:59:ARG:HD3	2.10	0.51
1:2A:852:G:H2'	1:2A:853:G:H8	1.75	0.51
1:2A:2127:G:N2	1:2A:2161:C:N3	2.58	0.51
4:2E:1:MET:HE3	4:2E:199:ARG:HD2	1.93	0.51
15:2T:36:GLU:O	15:2T:39:ARG:HG2	2.11	0.51
19:2X:1:MET:H3	24:22:29:LYS:HE3	1.74	0.51
22:20:63:VAL:HG21	22:20:83:PRO:HG3	1.91	0.51
32:2a:572:A:OP1	60:2a:3361:HOH:O	2.19	0.51
32:2a:798:G:N7	60:2a:3535:HOH:O	2.34	0.51
32:2a:828:A:H2'	32:2a:829:G:O4'	2.10	0.51
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	1.92	0.51
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.75	0.51
1:1A:776:G:C6	3:1D:208:LYS:HB2	2.46	0.51
1:1A:831:A:C6	3:1D:229:VAL:HG11	2.45	0.51
1:1A:1832:G:OP2	3:1D:154:LYS:NZ	2.39	0.51
1:1A:2128:G:H1	1:1A:2205:C:N4	2.09	0.51
33:1b:97:TRP:HZ2	33:1b:102:LEU:HD13	1.75	0.51
41:1j:5:ARG:HH11	41:1j:71:LEU:HD21	1.76	0.51
54:1y:67:C:H2'	54:1y:68:C:C6	2.45	0.51
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.46	0.51
6:2G:106:LEU:O	6:2G:111:LEU:HD12	2.10	0.51
11:2P:84:ASN:OD1	11:2P:117:GLU:HB2	2.10	0.51
32:2a:701:C:OP1	32:2a:702:A:O2'	2.19	0.51
32:2a:975:A:N1	41:2j:48:THR:HB	2.25	0.51
32:2a:1010:G:N2	32:2a:1020:U:O2'	2.43	0.51
32:2a:1417:G:O6	60:2a:3547:HOH:O	2.18	0.51
40:2i:85:LEU:HB3	40:2i:92:TYR:HD2	1.75	0.51
54:2w:30:G:O6	54:2w:31:A:N6	2.44	0.51
4:1E:105:THR:OG1	4:1E:166:THR:OG1	2.22	0.51
32:1a:265:G:H2'	32:1a:267:C:H5	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:690:G:C6	32:1a:691:G:C6	2.98	0.51
1:2A:271(K):U:H4'	1:2A:271(L):U:OP2	2.09	0.51
1:2A:1019:U:H3	1:2A:1142(A):A:N6	2.07	0.51
1:2A:1349:A:OP1	60:2A:4475:HOH:O	2.19	0.51
1:2A:1364:G:P	23:21:3:LYS:HG3	2.51	0.51
1:2A:1853:A:N1	1:2A:2087:G:H1'	2.25	0.51
2:2B:24:G:O4'	2:2B:26:A:N6	2.35	0.51
6:2G:3:LEU:HD12	6:2G:8:LYS:NZ	2.25	0.51
32:2a:560:U:H4'	32:2a:561:U:O5'	2.10	0.51
40:2i:108:VAL:HG12	40:2i:109:VAL:H	1.76	0.51
50:2s:80:TYR:C	50:2s:82:GLY:H	2.18	0.51
5:1F:187:VAL:HG12	11:1P:3:LEU:HD12	1.92	0.51
28:16:10:LEU:HD13	28:16:19:ARG:HD3	1.91	0.51
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.32	0.51
33:1b:109:SER:HA	33:1b:112:VAL:HG13	1.92	0.51
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	1.91	0.51
54:1w:66:U:H1'	60:1w:211:HOH:O	2.11	0.51
1:2A:265:A:C8	1:2A:266:G:H1'	2.45	0.51
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.46	0.51
2:2B:24:G:N7	2:2B:56:G:H2'	2.25	0.51
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.91	0.51
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.92	0.51
33:2b:76:GLN:HB2	33:2b:208:ILE:HD11	1.93	0.51
1:1A:1121:C:H2'	1:1A:1122:C:H5'	1.92	0.51
1:1A:1898:A:H2'	1:1A:1899:A:H8	1.76	0.51
1:1A:2801:C:O2'	1:1A:2819:A:N3	2.37	0.51
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.24	0.51
33:1b:101:MET:HA	33:1b:108:ILE:HG13	1.91	0.51
38:1g:22:LEU:HG	38:1g:62:PHE:HE2	1.76	0.51
1:2A:646:A:H2'	1:2A:647:G:O4'	2.11	0.51
1:2A:892:G:H3'	1:2A:893:C:H5"	1.93	0.51
1:2A:2394:C:N3	54:2y:76:A:O2'	2.35	0.51
32:2a:222:U:H2'	32:2a:223:U:C6	2.46	0.51
32:2a:977:A:O2'	32:2a:981:U:N3	2.44	0.51
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.92	0.51
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.44	0.51
1:1A:183:G:OP2	60:1A:4833:HOH:O	2.19	0.51
8:1I:27:ARG:HD3	23:11:71:TYR:CE2	2.45	0.51
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.10	0.51
33:1b:24:TRP:HZ3	33:1b:29:ALA:HB2	1.76	0.51
48:1q:26:GLN:HE21	48:1q:37:LYS:HE3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2815:C:H2'	1:2A:2816:C:C6	2.46	0.51
6:2G:103:LEU:HA	6:2G:106:LEU:HB3	1.93	0.51
32:2a:731:G:OP2	60:2a:3607:HOH:O	2.19	0.51
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.44	0.51
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.24	0.51
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.92	0.51
32:1a:952:U:H2'	32:1a:953:G:C8	2.45	0.51
37:1f:91:VAL:HG11	49:1r:72:ARG:NH1	2.25	0.51
50:1s:41:VAL:HG13	50:1s:43:GLU:H	1.75	0.51
1:2A:208:C:H2'	1:2A:209:C:C6	2.46	0.51
38:2g:79:ARG:HA	38:2g:83:ALA:O	2.11	0.51
54:2y:5:G:N2	54:2y:68:C:N3	2.49	0.51
1:1A:906:G:O2'	1:1A:962:G:O6	2.22	0.51
8:1I:76:THR:HG22	8:1I:141:LYS:HE2	1.93	0.51
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	1.92	0.51
32:1a:163:C:H2'	32:1a:164:U:C6	2.46	0.51
32:1a:943:U:H1'	40:1i:124:GLN:HE22	1.75	0.51
32:1a:1060:C:H5"	41:1j:51:ARG:HG2	1.92	0.51
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.42	0.51
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	1.92	0.51
1:2A:1264:G:H2'	1:2A:2014:A:N6	2.26	0.51
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.11	0.51
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.92	0.51
6:2G:173:LEU:HB3	6:2G:178:PHE:CG	2.46	0.51
32:2a:501:C:OP2	43:2l:124:LYS:NZ	2.38	0.51
32:2a:533:A:OP1	60:2a:3602:HOH:O	2.19	0.51
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.45	0.51
51:2t:35:THR:O	51:2t:39:LYS:N	2.39	0.51
52:2u:3:LYS:HA	52:2u:10:ARG:HG3	1.93	0.51
1:1A:1085:G:H1	1:1A:1162:C:N4	2.07	0.50
1:1A:2053:A:N3	1:1A:2467:G:O2'	2.40	0.50
1:1A:2153:G:H5'	1:1A:2155:G:C8	2.46	0.50
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.45	0.50
7:1H:20:ALA:HB3	7:1H:23:ARG:HB2	1.92	0.50
32:1a:1004:A:H5"	32:1a:1024:G:H1	1.76	0.50
48:1q:56:VAL:HB	48:1q:78:GLU:HB3	1.92	0.50
1:2A:893:C:H2'	1:2A:894:C:C5	2.46	0.50
1:2A:2431:U:OP1	60:2A:4148:HOH:O	2.19	0.50
1:2A:2820:A:OP2	13:2R:2:ARG:NH2	2.44	0.50
21:2Z:77:ASP:N	21:2Z:82:ARG:O	2.34	0.50
32:2a:134:A:H61	47:2p:25:ARG:HH12	1.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:47:PHE:HE2	41:2j:65:LEU:HB2	1.76	0.50
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	1.93	0.50
43:2l:88:GLY:HA3	43:2l:99:HIS:HD2	1.75	0.50
48:2q:40:LYS:HD3	48:2q:42:TYR:OH	2.11	0.50
1:1A:1410:G:OP2	23:11:3:LYS:HG3	2.12	0.50
1:1A:2041:A:O4'	16:1U:34:LYS:HE3	2.11	0.50
1:1A:2163:G:C6	1:1A:2164:C:C2	3.00	0.50
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.91	0.50
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.26	0.50
32:1a:557:G:OP1	60:1a:1945:HOH:O	2.19	0.50
39:1h:81:HIS:N	39:1h:138:TRP:O	2.44	0.50
54:1y:23:A:H2'	54:1y:24:G:H8	1.76	0.50
1:2A:637:A:H5"	11:2P:117:GLU:HG2	1.94	0.50
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.11	0.50
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.11	0.50
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.09	0.50
7:2H:24:VAL:HG13	7:2H:37:VAL:HG21	1.94	0.50
29:27:34:ARG:HG3	29:27:34:ARG:NH1	2.27	0.50
32:2a:271:C:H2'	32:2a:272:C:C6	2.46	0.50
32:2a:1157:A:H5'	32:2a:1158:C:C6	2.45	0.50
1:1A:964:A:H5"	2:1B:98:G:O2'	2.11	0.50
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.47	0.50
32:1a:236:G:H5"	48:1q:42:TYR:OH	2.10	0.50
32:1a:438:G:H4'	35:1d:123:HIS:CE1	2.47	0.50
32:1a:1111:A:N1	34:1c:177:THR:OG1	2.37	0.50
33:1b:213:LEU:HD22	33:1b:214:ILE:HD13	1.94	0.50
44:1m:3:ARG:HH22	44:1m:45:VAL:HG11	1.76	0.50
1:2A:731:C:H5"	60:2A:4876:HOH:O	2.11	0.50
1:2A:1270:C:H5"	1:2A:1271:G:O5'	2.11	0.50
1:2A:1335:U:OP1	19:2X:65:ARG:NH1	2.44	0.50
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.46	0.50
1:2A:2357:U:OP1	22:20:20:ARG:NE	2.35	0.50
1:2A:2506:U:O2'	54:2w:76:A:H4'	2.10	0.50
1:2A:2705:A:OP2	60:2A:4355:HOH:O	2.19	0.50
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.46	0.50
10:2O:10:VAL:HG21	10:2O:16:ALA:HB3	1.93	0.50
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.37	0.50
32:2a:1099:G:OP2	33:2b:144:ARG:NH2	2.44	0.50
32:2a:1207:2MG:H2'	32:2a:1208:C:C6	2.46	0.50
32:2a:1251:A:N1	32:2a:1354:C:O2'	2.42	0.50
32:2a:1342:C:H2'	32:2a:1343:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:236:G:H4'	1:1A:413:G:C5	2.47	0.50
32:1a:1008:C:O2	32:1a:1021:G:N1	2.35	0.50
38:1g:89:MET:SD	38:1g:155:ARG:HB2	2.52	0.50
3:2D:206:LEU:O	3:2D:211:ARG:HD3	2.12	0.50
4:2E:50:GLY:HA3	4:2E:75:VAL:HG11	1.94	0.50
6:2G:110:ALA:HB1	6:2G:140:ILE:HG22	1.93	0.50
10:2O:24:VAL:HG12	10:2O:33:ALA:HB2	1.93	0.50
32:2a:1003:G:H2'	32:2a:1004:A:O4'	2.12	0.50
32:2a:1116:C:H2'	32:2a:1117:G:H5"	1.94	0.50
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.26	0.50
33:2b:60:ASP:O	33:2b:64:ARG:HG2	2.11	0.50
1:1A:928:G:H3'	1:1A:929:G:H8	1.76	0.50
5:1F:150:GLY:HA2	5:1F:172:TRP:CE3	2.47	0.50
14:1S:19:LYS:HE2	14:1S:25:ARG:CZ	2.41	0.50
32:1a:1036:G:H5'	32:1a:1037:C:OP2	2.12	0.50
32:1a:1095:U:P	32:1a:1108:G:H1	2.34	0.50
33:1b:178:ARG:NH1	33:1b:196:LEU:O	2.44	0.50
39:1h:13:ILE:O	39:1h:17:THR:HG23	2.11	0.50
54:1y:18:G:O2'	54:1y:57:G:O6	2.29	0.50
1:2A:557:U:H2'	1:2A:558:G:H8	1.75	0.50
1:2A:746:A:H2'	1:2A:2612:C:H5"	1.93	0.50
1:2A:981:A:OP1	60:2A:4304:HOH:O	2.19	0.50
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.46	0.50
1:2A:1920:4OC:O5'	1:2A:1920:4OC:H6	2.11	0.50
1:2A:2145:C:O2'	1:2A:2147:G:N7	2.44	0.50
1:2A:2167:U:H3'	1:2A:2168:G:H21	1.77	0.50
1:2A:2749:A:H1'	7:2H:63:SER:HB3	1.93	0.50
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	1.93	0.50
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.93	0.50
8:2I:102:SER:O	8:2I:106:GLY:N	2.40	0.50
32:2a:131:C:H2'	32:2a:132:C:C6	2.47	0.50
32:2a:202:U:H3'	32:2a:203:U:C5	2.46	0.50
52:2u:6:ARG:HE	52:2u:15:ARG:NH2	2.10	0.50
1:1A:599:U:H2'	1:1A:600:G:C8	2.46	0.50
1:1A:2143:G:H2'	1:1A:2144:U:C6	2.47	0.50
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	1.92	0.50
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.11	0.50
32:1a:376:G:P	47:1p:67:THR:HG21	2.52	0.50
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.47	0.50
39:1h:19:VAL:HG23	39:1h:21:LYS:HG2	1.94	0.50
1:2A:120:U:H5"	1:2A:122:G:OP2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.28	0.50
1:2A:947:G:H2'	1:2A:948:G:C8	2.47	0.50
1:2A:2319:G:H22	14:2S:3:ARG:HD2	1.76	0.50
1:2A:2342:C:O2'	1:2A:2374:C:OP1	2.29	0.50
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.26	0.50
2:2B:7:G:H5'	14:2S:29:PHE:CE2	2.46	0.50
11:2P:106:LEU:HD13	11:2P:112:LEU:HG	1.93	0.50
34:2c:152:ILE:HG12	34:2c:199:LYS:HB2	1.94	0.50
42:2k:85:ARG:HD3	42:2k:113:PRO:HD3	1.93	0.50
54:2w:5:G:H2'	54:2w:6:G:H8	1.77	0.50
1:1A:1814:A:H5'	1:1A:2620:G:H4'	1.94	0.50
1:1A:1874:C:H5'	3:1D:253:GLN:OE1	2.11	0.50
2:1B:41:U:H5	6:1G:70:VAL:H	1.59	0.50
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.77	0.50
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.11	0.50
8:1I:101:LEU:HG	8:1I:107:VAL:HG13	1.93	0.50
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.93	0.50
19:1X:31:HIS:NE2	60:1X:3103:HOH:O	2.35	0.50
27:15:40:LYS:NZ	27:15:44:THR:O	2.38	0.50
32:1a:277:C:OP1	48:1q:68:ARG:NH2	2.26	0.50
32:1a:1024:G:H2'	32:1a:1025:U:H5"	1.93	0.50
32:1a:1055:A:O2'	34:1c:161:GLU:O	2.29	0.50
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.94	0.50
1:2A:817:C:O2'	1:2A:839:U:H5"	2.11	0.50
1:2A:821:A:H2'	1:2A:946:G:H5"	1.93	0.50
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.12	0.50
1:2A:1218:C:N4	1:2A:1231:G:H1	2.08	0.50
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.92	0.50
1:2A:2315:G:H1'	6:2G:126:ASP:OD2	2.11	0.50
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.45	0.50
4:2E:73:GLU:HG2	4:2E:74:PRO:HD2	1.94	0.50
21:2Z:23:LYS:HD3	21:2Z:40:ASP:HA	1.93	0.50
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.46	0.50
32:2a:735:C:H2'	32:2a:736:C:H6	1.75	0.50
32:2a:1330:U:H4'	44:2m:23:TYR:CZ	2.47	0.50
32:2a:1406:U:H3'	32:2a:1407:5MC:HM53	1.92	0.50
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.42	0.50
43:2l:84:LEU:HB2	43:2l:105:TYR:CE2	2.46	0.50
1:1A:922:G:H2'	1:1A:923:C:O4'	2.11	0.50
1:1A:1452:U:H2'	1:1A:1453:C:H6	1.76	0.50
1:1A:2376:C:H2'	1:1A:2377:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2420:U:H2'	1:1A:2421:G:C8	2.47	0.50
32:1a:445:G:H2'	32:1a:446:G:C8	2.47	0.50
32:1a:739:C:HO2'	46:1o:42:HIS:HD1	1.60	0.50
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.94	0.50
1:2A:71:A:H5"	1:2A:73:A:C8	2.47	0.50
1:2A:863:A:H2'	1:2A:864:G:H8	1.77	0.50
1:2A:1459:G:OP2	60:2A:5251:HOH:O	2.19	0.50
3:2D:176:ARG:HG3	3:2D:176:ARG:O	2.11	0.50
6:2G:120:LEU:HD12	6:2G:178:PHE:HB3	1.93	0.50
27:25:52:TYR:HB3	27:25:57:VAL:HG21	1.94	0.50
32:2a:309:G:O2'	32:2a:607:A:N1	2.44	0.50
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.38	0.50
32:2a:978:A:O2'	32:2a:1322:C:N3	2.43	0.50
33:2b:186:ALA:HB3	33:2b:197:VAL:HG11	1.93	0.50
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.47	0.50
55:2x:23:C:H2'	55:2x:24:U:C6	2.47	0.50
1:1A:268:G:H4'	23:11:81:LYS:HG2	1.93	0.50
1:1A:2141:A:O2'	1:1A:2142:G:H5"	2.12	0.50
1:1A:2251:G:OP2	60:1A:5809:HOH:O	2.20	0.50
40:1i:46:ALA:HA	40:1i:78:LYS:HB2	1.94	0.50
2:2B:33:G:H5'	6:2G:2:PRO:HD3	1.94	0.50
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.93	0.50
32:2a:324:G:N7	60:2a:3432:HOH:O	2.35	0.50
32:2a:448:A:OP2	32:2a:485:G:N2	2.41	0.50
32:2a:660:G:H1	32:2a:745:C:H42	1.60	0.50
32:2a:833:U:H2'	32:2a:834:C:C6	2.47	0.50
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.30	0.50
32:2a:1049:U:C5	32:2a:1201:A:H5'	2.47	0.50
1:1A:1465:A:O2'	1:1A:1467:G:N7	2.41	0.49
1:1A:2661:U:H2'	1:1A:2662:U:H6	1.77	0.49
3:1D:206:LEU:O	3:1D:211:ARG:HD3	2.12	0.49
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.93	0.49
1:2A:1530:C:H1'	1:2A:1531:C:OP1	2.12	0.49
4:2E:101:ARG:HD3	4:2E:170:LEU:C	2.37	0.49
32:2a:993:G:O6	32:2a:1045:C:N4	2.35	0.49
32:2a:1309:G:OP1	44:2m:88:ARG:NH2	2.43	0.49
41:2j:6:ILE:HA	41:2j:97:GLU:O	2.12	0.49
43:2l:46:LYS:HG3	43:2l:92:0TD:CSB	2.42	0.49
1:1A:1546:G:H2'	1:1A:1547:C:C6	2.47	0.49
7:1H:41:MET:HE1	7:1H:54:ARG:HB3	1.95	0.49
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.24	0.49
38:1g:50:ILE:HD13	38:1g:125:MET:CG	2.38	0.49
40:1i:3:GLN:HE21	40:1i:20:ARG:HH21	1.59	0.49
1:2A:2025:C:H2'	1:2A:2026:C:C6	2.47	0.49
6:2G:106:LEU:O	6:2G:110:ALA:HB3	2.13	0.49
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.12	0.49
26:24:40:HIS:CE1	26:24:42:PHE:HB3	2.48	0.49
26:24:48:ARG:HG3	26:24:51:ASP:O	2.12	0.49
32:2a:1104:G:H4'	33:2b:111:ARG:HH21	1.77	0.49
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.11	0.49
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.94	0.49
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.45	0.49
1:1A:929:G:H1	1:1A:940:C:N4	2.01	0.49
1:1A:2185:C:OP1	1:1A:2187:G:N2	2.45	0.49
20:1Y:98:VAL:HG12	20:1Y:105:ALA:HA	1.94	0.49
35:1d:116:GLN:NE2	35:1d:157:LEU:HD21	2.27	0.49
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.47	0.49
1:2A:1882:C:H5"	23:21:26:ARG:HH21	1.77	0.49
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.27	0.49
26:24:46:GLN:C	26:24:48:ARG:H	2.20	0.49
32:2a:989:C:H1'	32:2a:1016:A:H2	1.77	0.49
32:2a:1063:C:H3'	32:2a:1064:G:H2'	1.94	0.49
32:2a:1104:G:H4'	33:2b:111:ARG:NH2	2.27	0.49
32:2a:1242:C:H2'	32:2a:1243:C:O4'	2.12	0.49
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.27	0.49
34:2c:131:ARG:HE	34:2c:135:LYS:HE3	1.76	0.49
38:2g:22:LEU:HG	38:2g:62:PHE:CE2	2.48	0.49
1:1A:1821:C:H5"	1:1A:1822:A:OP1	2.12	0.49
1:1A:1847:G:O2'	1:1A:1848:G:OP2	2.29	0.49
1:1A:2296:C:OP1	28:16:3:SER:OG	2.30	0.49
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.93	0.49
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.45	0.49
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	1.93	0.49
32:1a:811:C:O2'	32:1a:901:A:N1	2.43	0.49
37:1f:97:PHE:N	49:1r:30:ASP:OD1	2.44	0.49
1:2A:32:C:N4	1:2A:33:U:O4	2.46	0.49
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.42	0.49
5:2F:133:ASN:N	5:2F:138:GLU:OE1	2.46	0.49
6:2G:3:LEU:HD22	26:24:25:TYR:CZ	2.46	0.49
6:2G:103:LEU:HD23	6:2G:106:LEU:HD23	1.93	0.49
7:2H:11:VAL:HG21	7:2H:50:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	1.93	0.49
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE2	1.94	0.49
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.94	0.49
32:2a:34:C:H2'	32:2a:35:G:C8	2.47	0.49
32:2a:1502:A:C8	32:2a:1505:G:N2	2.76	0.49
54:2y:65:G:H2'	54:2y:66:U:C6	2.47	0.49
32:1a:164:U:H2'	32:1a:165:C:H6	1.77	0.49
32:1a:737:A:H2'	32:1a:738:C:C6	2.47	0.49
32:1a:741:G:H2'	32:1a:742:G:O4'	2.13	0.49
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.46	0.49
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.94	0.49
1:2A:2490:G:H8	1:2A:2490:G:OP2	1.96	0.49
1:2A:2641:G:H5"	9:2N:76:SER:HB3	1.94	0.49
10:2O:86:ILE:HG22	10:2O:94:ARG:HD2	1.95	0.49
12:2Q:12:GLN:HE21	12:2Q:72:LYS:HG3	1.76	0.49
32:2a:1005:A:H5"	32:2a:1006:C:C5	2.48	0.49
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.11	0.49
43:2l:77:LEU:HD21	43:2l:107:ALA:HB2	1.95	0.49
45:2n:6:LEU:O	45:2n:10:ALA:N	2.45	0.49
1:1A:64:C:H5'	19:1X:71:GLY:HA3	1.94	0.49
1:1A:1466:U:HO2'	1:1A:1467:G:P	2.34	0.49
1:1A:1495:G:H4'	1:1A:1589:A:OP1	2.12	0.49
1:1A:2262:G:OP1	12:1Q:85:LYS:NZ	2.45	0.49
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.47	0.49
1:1A:2476:C:H1'	60:1A:5819:HOH:O	2.11	0.49
1:1A:2576:A:C2	1:1A:2659:U:H4'	2.47	0.49
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.47	0.49
18:1W:67:ASP:OD1	18:1W:67:ASP:N	2.45	0.49
32:1a:841:U:OP1	32:1a:841:U:H6	1.96	0.49
32:1a:1302:U:C5	44:1m:17:VAL:HG21	2.46	0.49
35:1d:11:LEU:HD23	35:1d:66:ARG:HB3	1.95	0.49
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.47	0.49
38:1g:47:CYS:HA	38:1g:50:ILE:HG22	1.93	0.49
54:1y:68:C:H2'	54:1y:69:G:H5"	1.95	0.49
1:2A:456:C:H4'	60:2A:5139:HOH:O	2.11	0.49
2:2B:32:C:H42	2:2B:50:G:H1	1.59	0.49
6:2G:136:ARG:HA	6:2G:154:GLY:HA3	1.93	0.49
15:2T:127:ALA:C	15:2T:129:ARG:H	2.20	0.49
27:25:6:VAL:HG12	60:25:5001:HOH:O	2.13	0.49
32:2a:757:U:H2'	32:2a:758:G:O4'	2.13	0.49
32:2a:936:C:H2'	32:2a:937:A:O4'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1353:G:OP1	52:2u:10:ARG:NH1	2.46	0.49
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.48	0.49
54:2w:72:C:H2'	54:2w:73:A:H8	1.77	0.49
1:1A:510:C:H2'	1:1A:511:C:C6	2.48	0.49
1:1A:1639:G:H2'	1:1A:1640:G:C8	2.48	0.49
1:1A:1809:U:H2'	1:1A:1815:A:N6	2.27	0.49
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.48	0.49
1:1A:2588:G:H1'	60:1A:4548:HOH:O	2.11	0.49
1:1A:2897:U:H2'	1:1A:2898:C:H6	1.78	0.49
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.45	0.49
7:1H:88:LEU:HD23	7:1H:130:ARG:HG2	1.94	0.49
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.45	0.49
1:2A:82:G:N1	1:2A:103:A:OP2	2.37	0.49
1:2A:1021:A:H8	1:2A:1021:A:H3'	1.77	0.49
1:2A:1155:A:H5"	16:2U:55:ARG:NH1	2.25	0.49
1:2A:2121:G:H1	1:2A:2177:C:H42	1.59	0.49
1:2A:2893:G:H5"	1:2A:2894:G:O4'	2.12	0.49
4:2E:2:LYS:HB2	4:2E:95:ILE:HD12	1.95	0.49
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.78	0.49
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.48	0.49
41:2j:7:LYS:HG2	41:2j:71:LEU:HD13	1.95	0.49
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	1.95	0.49
1:1A:1106:U:N3	1:1A:1108:G:O2'	2.43	0.49
1:1A:1952:G:O2'	1:1A:1990:G:O6	2.31	0.49
34:1c:110:ASN:O	34:1c:141:VAL:HG22	2.13	0.49
37:1f:99:ALA:HB1	49:1r:23:LYS:NZ	2.28	0.49
48:1q:26:GLN:HG2	48:1q:37:LYS:HG2	1.94	0.49
54:1y:38:A:H2'	54:1y:39:PSU:O4'	2.12	0.49
1:2A:127:A:H5"	1:2A:128:C:C6	2.47	0.49
1:2A:141:A:C8	1:2A:1408:C:O2'	2.65	0.49
1:2A:1224:C:O2	17:2V:85:LYS:NZ	2.45	0.49
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.43	0.49
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.78	0.49
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.48	0.49
26:24:7:PRO:HB2	26:24:27:THR:HG21	1.95	0.49
26:24:34:GLU:HA	44:2m:57:ARG:NH1	2.28	0.49
26:24:53:GLU:HG2	26:24:54:GLY:H	1.77	0.49
32:2a:1030(A):G:N2	32:2a:1030(D):A:OP2	2.45	0.49
32:2a:1360:A:H8	32:2a:1360:A:OP1	1.96	0.49
34:2c:119:ARG:HE	34:2c:140:ARG:HH21	1.61	0.49
41:2j:47:PHE:N	41:2j:63:PHE:O	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1109:G:O2'	1:1A:1122:C:N4	2.46	0.49
1:1A:1128:U:C4	1:1A:1132:A:N1	2.74	0.49
1:1A:1676:G:H2'	1:1A:1677:C:C6	2.48	0.49
1:1A:2642:G:H2'	1:1A:2643:G:H8	1.78	0.49
6:1G:146:TYR:O	6:1G:149:VAL:HG12	2.13	0.49
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.95	0.49
32:1a:536:C:OP2	60:1a:2236:HOH:O	2.20	0.49
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.48	0.49
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.78	0.49
50:1s:41:VAL:HG12	50:1s:44:MET:HG3	1.93	0.49
1:2A:588:U:H2'	1:2A:589:C:C6	2.48	0.49
1:2A:1263:U:H2'	1:2A:1264:G:C8	2.47	0.49
1:2A:2171:A:N3	1:2A:2172:U:N3	2.61	0.49
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.48	0.49
1:2A:2882:A:H5'	13:2R:96:ARG:HG3	1.95	0.49
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.94	0.49
4:2E:7:VAL:HG12	4:2E:27:LEU:HB3	1.95	0.49
4:2E:52:LEU:O	4:2E:76:ARG:N	2.28	0.49
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.95	0.49
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.38	0.49
26:24:58:ARG:HG3	50:2s:67:VAL:HB	1.95	0.49
32:2a:443:C:H2'	32:2a:444:C:C6	2.48	0.49
32:2a:585:G:O2'	32:2a:879:C:OP1	2.28	0.49
32:2a:664:G:N2	32:2a:741:G:H1	2.05	0.49
32:2a:1048:G:N2	32:2a:1214:C:O2	2.42	0.49
32:2a:1120:G:C6	32:2a:1121:U:C4	3.00	0.49
32:2a:1275:A:H3'	32:2a:1276:G:H8	1.78	0.49
33:2b:74:LYS:HG2	33:2b:169:LYS:HG2	1.94	0.49
48:2q:45:HIS:CD2	48:2q:47:PRO:HD3	2.48	0.49
32:1a:1027:C:N4	32:1a:1034:G:N1	2.61	0.49
32:1a:1288:A:N3	32:1a:1352:C:O2'	2.43	0.49
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.30	0.49
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.37	0.49
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.77	0.49
8:2I:122:GLU:O	8:2I:126:TYR:OH	2.28	0.49
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.13	0.49
12:2Q:118:LEU:HD12	12:2Q:131:ILE:HG23	1.95	0.49
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.20	0.49
21:2Z:92:SER:O	21:2Z:130:PRO:HG3	2.12	0.49
32:2a:596:C:N3	32:2a:644:G:N1	2.37	0.49
32:2a:1001:A:H2'	32:2a:1001(A):G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1208:C:H2'	32:2a:1209:C:H6	1.78	0.49
38:2g:69:VAL:HG11	38:2g:134:ALA:HB1	1.95	0.49
32:1a:567:G:N3	60:1a:1988:HOH:O	2.35	0.48
32:1a:1049:U:OP1	45:1n:3:ARG:HB3	2.13	0.48
38:1g:111:ARG:HG2	38:1g:112:PRO:HD2	1.94	0.48
41:1j:40:LEU:HB2	41:1j:69:ASN:CB	2.43	0.48
44:1m:3:ARG:HG3	44:1m:4:ILE:HG22	1.94	0.48
1:2A:7:G:H4'	9:2N:13:TRP:CZ2	2.48	0.48
1:2A:222:A:H5"	1:2A:421:U:OP1	2.13	0.48
1:2A:1235:G:C6	1:2A:1236:G:N1	2.81	0.48
32:2a:107:G:H2'	32:2a:108:G:O4'	2.13	0.48
32:2a:1207:2MG:H2'	32:2a:1208:C:H6	1.77	0.48
33:2b:124:SER:HB3	33:2b:125:PRO:HD3	1.95	0.48
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.13	0.48
44:2m:30:ALA:O	44:2m:34:LEU:HG	2.13	0.48
51:2t:56:MET:HE3	51:2t:85:MET:HG2	1.95	0.48
54:2w:19:G:N2	54:2w:56:C:N3	2.52	0.48
8:1I:77:LEU:HD21	8:1I:100:ALA:HB1	1.96	0.48
9:1N:114:ARG:HD3	60:1N:303:HOH:O	2.12	0.48
10:1O:64:ARG:HD2	10:1O:81:ASP:OD1	2.13	0.48
32:1a:984:C:H42	32:1a:1221:G:H1	1.60	0.48
32:1a:1164:G:H2'	32:1a:1165:C:C6	2.48	0.48
35:1d:3:ARG:HG3	35:1d:5:ILE:HG23	1.95	0.48
45:1n:6:LEU:HB3	45:1n:23:ARG:NH2	2.28	0.48
1:2A:253:C:OP2	30:28:5:LYS:NZ	2.40	0.48
1:2A:601:C:O2	1:2A:605:C:H4'	2.12	0.48
1:2A:816:C:H2'	1:2A:817:C:H6	1.78	0.48
1:2A:855:G:H1	1:2A:922:U:H3	1.59	0.48
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.48	0.48
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.13	0.48
6:2G:39:ILE:HG12	6:2G:157:ILE:HG12	1.95	0.48
9:2N:33:LEU:HA	9:2N:38:HIS:HD2	1.77	0.48
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.94	0.48
32:2a:137:C:H2'	32:2a:138:G:H8	1.79	0.48
32:2a:194:C:H2'	32:2a:195:A:H5"	1.95	0.48
32:2a:235:C:N4	60:2a:3311:HOH:O	2.46	0.48
32:2a:947:G:H1	32:2a:1234:C:N4	2.10	0.48
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.94	0.48
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.95	0.48
54:2y:10:G:O2'	60:2y:3108:HOH:O	2.20	0.48
54:2y:36:A:H2'	54:2y:37:MIA:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1112:U:H2'	1:1A:1114:G:OP2	2.13	0.48
1:1A:2153:G:H5"	1:1A:2154:U:H3'	1.94	0.48
5:1F:24:LEU:HD23	5:1F:115:ALA:HA	1.95	0.48
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.13	0.48
32:1a:191:G:N2	51:1t:102:GLY:O	2.44	0.48
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.60	0.48
35:1d:76:ARG:O	35:1d:80:GLU:HG2	2.12	0.48
1:2A:531:C:OP1	1:2A:561:G:N2	2.47	0.48
1:2A:1912:A:OP1	60:2A:4443:HOH:O	2.19	0.48
5:2F:20:LEU:HD23	5:2F:22:ALA:HB2	1.95	0.48
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.96	0.48
32:2a:1004:A:C8	32:2a:1005:A:H4'	2.48	0.48
34:2c:42:LEU:HA	34:2c:45:LYS:NZ	2.29	0.48
37:2f:3:ARG:HD3	37:2f:64:GLN:NE2	2.28	0.48
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.28	0.48
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.13	0.48
1:1A:2849:G:H5'	13:1R:46:GLY:HA2	1.94	0.48
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.94	0.48
1:2A:250:G:C6	1:2A:251:A:C6	3.02	0.48
1:2A:1021:A:H3'	1:2A:1021:A:C8	2.48	0.48
1:2A:1580:A:H3'	1:2A:1581:G:C8	2.48	0.48
32:2a:684:A:H1'	42:2k:39:PRO:HD2	1.96	0.48
32:2a:1183:A:O2'	32:2a:1184:G:OP1	2.25	0.48
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.96	0.48
38:2g:126:ASP:HB3	38:2g:131:LYS:HB2	1.94	0.48
1:1A:174:U:H4'	1:1A:207:A:H4'	1.96	0.48
1:1A:1688:A:H2'	1:1A:1689:G:O4'	2.12	0.48
1:1A:1921:G:N3	1:1A:1921:G:H2'	2.27	0.48
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.77	0.48
32:1a:176:C:H2'	32:1a:177:C:C6	2.48	0.48
32:1a:222:U:H2'	32:1a:223:U:C6	2.48	0.48
55:1x:19:G:H4'	55:1x:20:U:OP2	2.12	0.48
1:2A:557:U:H2'	1:2A:558:G:C8	2.49	0.48
1:2A:855:G:C6	1:2A:856:C:N4	2.82	0.48
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.48	0.48
4:2E:111:ARG:HD2	4:2E:160:TYR:CD2	2.47	0.48
5:2F:28:ILE:HG23	5:2F:112:MET:HE3	1.95	0.48
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.95	0.48
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.49	0.48
32:2a:8:A:C6	35:2d:209:ARG:HB2	2.47	0.48
32:2a:1150:U:H4'	41:2j:41:PRO:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1255:G:OP1	41:2j:45:ARG:NH2	2.47	0.48
33:2b:16:HIS:CB	33:2b:210:SER:HB2	2.40	0.48
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.95	0.48
1:1A:310:C:H2'	1:1A:311:C:H6	1.79	0.48
1:1A:1793:A:H2'	60:1A:5028:HOH:O	2.14	0.48
1:1A:1857:G:H4'	3:1D:242:ARG:NE	2.27	0.48
16:1U:59:ARG:HD3	60:1U:305:HOH:O	2.13	0.48
32:1a:266:G:O3'	48:1q:67:LYS:HB2	2.13	0.48
32:1a:659:U:H2'	32:1a:660:G:H8	1.79	0.48
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.14	0.48
40:1i:49:PRO:HD3	40:1i:78:LYS:HG3	1.95	0.48
55:1x:68:C:H2'	55:1x:69:C:C6	2.49	0.48
1:2A:2117:A:O2'	1:2A:2118:U:H5"	2.14	0.48
1:2A:2137:C:N3	1:2A:2155:G:C6	2.82	0.48
2:2B:58:A:H2'	2:2B:59:A:O4'	2.14	0.48
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.44	0.48
10:2O:73:ASP:HB2	15:2T:82:LEU:CD1	2.43	0.48
16:2U:113:ALA:O	16:2U:117:GLN:HG2	2.14	0.48
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.47	0.48
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.95	0.48
19:2X:57:LEU:HD22	19:2X:78:LYS:HE2	1.95	0.48
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.96	0.48
21:2Z:138:GLU:H	21:2Z:156:LYS:HE2	1.79	0.48
21:2Z:171:ILE:HD12	21:2Z:172:ALA:H	1.78	0.48
32:2a:404:U:H2'	32:2a:405:U:C6	2.48	0.48
33:2b:149:LEU:O	33:2b:153:ARG:N	2.42	0.48
40:2i:21:PRO:HA	40:2i:59:PHE:HD1	1.79	0.48
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.79	0.48
44:2m:73:GLU:O	44:2m:77:ASN:ND2	2.46	0.48
49:2r:32:ARG:NE	60:2r:5001:HOH:O	2.46	0.48
1:1A:1785:C:OP1	15:1T:96:ARG:NH1	2.46	0.48
1:1A:2255:U:OP1	60:1A:4235:HOH:O	2.20	0.48
1:1A:2304:C:H2'	1:1A:2305:C:H6	1.78	0.48
8:1I:86:THR:HG22	8:1I:122:GLU:OE1	2.13	0.48
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.45	0.48
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.14	0.48
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.35	0.48
41:1j:31:GLY:HA2	41:1j:32:ALA:O	2.13	0.48
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.57	0.48
1:2A:471:A:H2'	1:2A:472:A:O4'	2.13	0.48
1:2A:652(U):G:H2'	1:2A:652(V):C:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:670:A:H4'	1:2A:671:C:O5'	2.14	0.48
1:2A:1151:G:H4'	16:2U:81:HIS:ND1	2.29	0.48
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.77	0.48
1:2A:2218:U:H1'	23:21:52:ARG:HH12	1.78	0.48
2:2B:11:C:H3'	2:2B:12:C:C6	2.49	0.48
2:2B:55:U:H1'	6:2G:29:TRP:CD1	2.44	0.48
12:2Q:125:LEU:C	12:2Q:127:ILE:H	2.22	0.48
14:2S:34:HIS:O	14:2S:97:ARG:NH2	2.44	0.48
26:24:46:GLN:HE21	26:24:48:ARG:HD3	1.78	0.48
32:2a:909:A:N3	32:2a:1413:A:O2'	2.38	0.48
32:2a:1179:A:H4'	40:2i:103:THR:HA	1.96	0.48
34:2c:18:TRP:HE3	34:2c:18:TRP:H	1.62	0.48
36:2e:71:LEU:O	36:2e:72:GLN:NE2	2.44	0.48
39:2h:29:SER:HB3	39:2h:32:LYS:CG	2.43	0.48
43:2l:71:PRO:O	43:2l:102:ARG:HD2	2.14	0.48
45:2n:27:CYS:SG	45:2n:28:GLY:N	2.87	0.48
45:2n:37:PHE:HE2	45:2n:53:LEU:HD13	1.78	0.48
1:1A:2545:A:H2'	1:1A:2546:A:O4'	2.14	0.48
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.49	0.48
46:1o:39:LEU:HB3	46:1o:56:LEU:HD13	1.95	0.48
1:2A:251:A:C5	1:2A:252:G:H1'	2.48	0.48
1:2A:555:U:O2'	1:2A:556:G:N7	2.43	0.48
1:2A:848:G:C4	1:2A:933:A:H8	2.32	0.48
1:2A:1899:G:O2'	1:2A:1900:A:OP2	2.28	0.48
1:2A:2674:G:H2'	1:2A:2675:A:C8	2.49	0.48
2:2B:75:G:H1	21:2Z:73:GLN:NE2	2.12	0.48
2:2B:75:G:H1	21:2Z:73:GLN:HE22	1.60	0.48
16:2U:28:ARG:NH1	16:2U:38:THR:OG1	2.41	0.48
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.28	0.48
32:2a:1122:U:H2'	32:2a:1123:A:C8	2.48	0.48
34:2c:199:LYS:HB3	34:2c:201:TYR:HE2	1.79	0.48
36:2e:39:GLY:HA2	36:2e:71:LEU:HD13	1.96	0.48
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.95	0.48
38:2g:57:GLU:HG3	38:2g:60:LYS:H	1.78	0.48
47:2p:22:THR:HA	47:2p:33:ILE:HG13	1.96	0.48
49:2r:45:SER:HB3	49:2r:51:LEU:HD21	1.95	0.48
54:2y:6:G:H1	54:2y:67:C:N4	2.11	0.48
1:1A:768:C:H2'	1:1A:769:A:C8	2.48	0.48
1:1A:1099:C:C4	1:1A:1100:A:C8	3.02	0.48
21:1Z:45:ASP:O	21:1Z:49:ARG:HG3	2.13	0.48
32:1a:130:A:O2'	32:1a:131:C:O5'	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:19:HIS:CD2	33:1b:20:GLU:HG3	2.49	0.48
36:1e:148:VAL:HG11	36:1e:152:ARG:HH21	1.78	0.48
1:2A:90:U:H1'	1:2A:92:A:C8	2.49	0.48
1:2A:392:C:H5"	1:2A:409:C:H5"	1.96	0.48
1:2A:1567:A:OP2	3:2D:84:TYR:OH	2.20	0.48
1:2A:1721:G:H8	1:2A:1741:A:H62	1.61	0.48
1:2A:2095:C:H2'	1:2A:2096:U:O4'	2.14	0.48
1:2A:2193:G:H2'	1:2A:2194:G:H8	1.79	0.48
1:2A:2238:G:H5"	60:2A:5271:HOH:O	2.14	0.48
7:2H:106:THR:HG22	7:2H:112:PRO:HB3	1.95	0.48
21:2Z:55:HIS:HE1	21:2Z:135:GLU:HB2	1.77	0.48
32:2a:560:U:H5'	32:2a:566:G:H22	1.78	0.48
32:2a:620:C:H5"	60:2a:3373:HOH:O	2.14	0.48
41:2j:49:VAL:CG2	45:2n:41:ARG:HB2	2.38	0.48
1:1A:441:C:H2'	1:1A:442:A:C8	2.49	0.48
1:1A:1210:G:H2'	1:1A:1211:U:C6	2.49	0.48
3:1D:218:ARG:HB3	3:1D:219:PRO:HD2	1.96	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.62	0.48
19:1X:94:GLY:CA	19:1X:95:LEU:HB2	2.44	0.48
32:1a:19:C:O2'	32:1a:572:A:N1	2.47	0.48
32:1a:271:C:H2'	32:1a:272:C:C6	2.49	0.48
32:1a:642:A:N3	39:1h:113:SER:OG	2.35	0.48
32:1a:1429:C:H2'	32:1a:1430:C:H6	1.78	0.48
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.47	0.48
43:1l:88:GLY:HA3	43:1l:99:HIS:HD2	1.78	0.48
1:2A:74:A:H5'	1:2A:75:G:O4'	2.14	0.48
1:2A:332:A:O2'	1:2A:334:C:OP2	2.26	0.48
1:2A:445:C:OP1	16:2U:2:PRO:HA	2.13	0.48
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.79	0.48
1:2A:2152:G:C2	1:2A:2153:G:H1'	2.49	0.48
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.14	0.48
4:2E:111:ARG:HD2	4:2E:160:TYR:CE2	2.49	0.48
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.43	0.48
14:2S:62:LYS:O	14:2S:66:ALA:N	2.44	0.48
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.62	0.48
21:2Z:154:ASP:OD1	21:2Z:154:ASP:N	2.37	0.48
23:21:50:ARG:HD2	23:21:57:GLU:OE2	2.14	0.48
32:2a:662:G:H2'	32:2a:663:A:H8	1.79	0.48
32:2a:1055:A:H62	32:2a:1200:C:N4	2.11	0.48
32:2a:1271:G:C2	32:2a:1272:G:N7	2.81	0.48
32:2a:1318:A:OP1	50:2s:3:ARG:NH2	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:909:G:H2'	1:1A:910:A:O4'	2.14	0.47
1:1A:2180:A:HO2'	1:1A:2181:G:P	2.37	0.47
2:1B:88:C:H2'	2:1B:89:G:O4'	2.14	0.47
3:1D:20:ASP:OD1	3:1D:20:ASP:N	2.40	0.47
6:1G:7:LEU:HD21	6:1G:176:LEU:HD22	1.96	0.47
32:1a:407:G:H5"	35:1d:115:ARG:CG	2.44	0.47
32:1a:973:G:H3'	32:1a:974:A:H5"	1.96	0.47
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.79	0.47
38:1g:15:ASP:OD1	38:1g:20:ASP:N	2.34	0.47
54:1y:14:A:N6	54:1y:15:G:C6	2.82	0.47
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.13	0.47
1:2A:2192:G:H5'	1:2A:2193:G:OP2	2.14	0.47
2:2B:68:C:H2'	2:2B:69:G:H8	1.78	0.47
7:2H:73:ALA:O	7:2H:76:VAL:HG22	2.14	0.47
32:2a:1075:C:OP1	33:2b:179:LYS:NZ	2.26	0.47
1:1A:721:G:O2'	5:1F:74:ARG:HD3	2.14	0.47
1:1A:1154:U:H2'	1:1A:1155:C:O4'	2.14	0.47
5:1F:150:GLY:HA2	5:1F:172:TRP:CD2	2.48	0.47
11:1P:43:GLY:HA3	60:1P:303:HOH:O	2.13	0.47
14:1S:43:GLU:OE2	22:10:49:LYS:NZ	2.47	0.47
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.79	0.47
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.44	0.47
32:1a:192:U:H2'	32:1a:193:C:H6	1.79	0.47
32:1a:353:A:H5'	32:1a:353:A:H8	1.78	0.47
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.49	0.47
55:1x:4:G:H2'	55:1x:5:G:C8	2.49	0.47
1:2A:75:G:H4'	24:22:55:ARG:NH1	2.29	0.47
1:2A:563:G:H21	16:2U:37:GLU:CD	2.22	0.47
1:2A:906:G:HO2'	12:2Q:67:ARG:HH21	1.58	0.47
1:2A:1790:C:H5"	1:2A:1791:A:OP1	2.14	0.47
1:2A:1968:G:OP1	60:2A:5052:HOH:O	2.20	0.47
1:2A:2498:C:H3'	60:2A:4650:HOH:O	2.13	0.47
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.47	0.47
1:2A:2769:C:H2'	1:2A:2770:G:O4'	2.13	0.47
5:2F:202:PHE:O	5:2F:206:ILE:HG12	2.13	0.47
32:2a:473:G:H2'	32:2a:474:G:H8	1.79	0.47
32:2a:587:G:N1	32:2a:754:C:OP2	2.45	0.47
32:2a:1030:C:N3	32:2a:1031:G:N2	2.57	0.47
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.49	0.47
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.49	0.47
33:2b:81:VAL:HB	33:2b:94:ASN:HD21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.49	0.47
4:1E:24:THR:HG22	4:1E:186:GLY:O	2.13	0.47
32:1a:171:A:H2'	32:1a:172:A:C8	2.48	0.47
32:1a:1030:C:N4	32:1a:1031:G:N1	2.49	0.47
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.79	0.47
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.38	0.47
35:1d:88:VAL:HG22	36:1e:97:GLY:HA2	1.95	0.47
36:1e:78:HIS:HD2	39:1h:104:ARG:HD2	1.78	0.47
1:2A:492:A:H2'	1:2A:493:G:O4'	2.14	0.47
1:2A:1005:C:C2	1:2A:1143:A:C6	3.02	0.47
1:2A:2115:G:H4'	1:2A:2167:U:C4	2.49	0.47
32:2a:406:G:H21	35:2d:119:GLN:NE2	2.05	0.47
32:2a:999:C:H2'	32:2a:1000:U:O4'	2.14	0.47
55:2x:14:A:N6	55:2x:21:A:C2	2.80	0.47
1:1A:968:U:H2'	1:1A:969:C:C6	2.49	0.47
1:1A:1081:U:H2'	1:1A:1082:G:C8	2.49	0.47
7:1H:4:ILE:O	7:1H:69:ARG:HD2	2.14	0.47
1:2A:602:G:O2'	1:2A:655:A:N6	2.47	0.47
1:2A:872:A:H2'	1:2A:873:G:H8	1.78	0.47
1:2A:921:G:C6	1:2A:922:U:C4	3.02	0.47
1:2A:2144:U:H1'	1:2A:2148:G:H22	1.79	0.47
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.49	0.47
23:21:83:GLU:OE1	23:21:83:GLU:N	2.43	0.47
28:26:40:CYS:O	28:26:44:ARG:N	2.48	0.47
32:2a:707:C:H2'	32:2a:708:C:C6	2.49	0.47
32:2a:993:G:N3	32:2a:993:G:H2'	2.29	0.47
32:2a:1138:G:C6	32:2a:1140:C:H1'	2.48	0.47
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.98	0.47
1:1A:2159:C:H2'	1:1A:2160:C:H6	1.80	0.47
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.72	0.47
8:1I:75:LEU:O	8:1I:141:LYS:NZ	2.47	0.47
32:1a:232:G:H1'	32:1a:262:A:N1	2.29	0.47
32:1a:1027:C:N3	32:1a:1034:G:N2	2.62	0.47
33:1b:87:ARG:NH2	33:1b:233:SER:HB3	2.29	0.47
41:1j:27:ALA:HB3	41:1j:34:VAL:HG11	1.96	0.47
48:1q:61:GLU:HA	48:1q:71:PHE:CD1	2.49	0.47
1:2A:910:A:N1	1:2A:2277:G:H1'	2.30	0.47
1:2A:1152:C:H2'	1:2A:1153:C:C6	2.49	0.47
2:2B:118:G:C2	2:2B:119:G:H1'	2.50	0.47
5:2F:40:GLN:NE2	5:2F:182:ASN:HB2	2.30	0.47
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:12:GLN:HE21	12:2Q:73:PRO:HD2	1.80	0.47
21:2Z:151:HIS:ND1	21:2Z:168:GLU:O	2.47	0.47
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.15	0.47
54:2y:15:G:N1	54:2y:48:C:N3	2.53	0.47
1:1A:505:A:N3	1:1A:507:G:H5"	2.28	0.47
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.70	0.47
54:1y:67:C:H2'	54:1y:68:C:H6	1.78	0.47
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.78	0.47
9:2N:25:ARG:O	9:2N:29:LYS:HE2	2.15	0.47
17:2V:4:ILE:HD12	17:2V:39:LEU:HB3	1.97	0.47
32:2a:269:C:H2'	32:2a:270:A:C8	2.49	0.47
32:2a:1086:U:H3	32:2a:1099:G:H22	1.61	0.47
34:2c:63:ASN:HB3	34:2c:98:ASN:HD22	1.79	0.47
40:2i:3:GLN:HE21	40:2i:20:ARG:NH2	2.13	0.47
50:2s:51:VAL:HB	50:2s:75:ALA:HB2	1.95	0.47
1:1A:662:A:H4'	1:1A:663:G:O5'	2.15	0.47
1:1A:2023:A:OP1	13:1R:9:LYS:NZ	2.41	0.47
1:1A:2126:G:H1	1:1A:2207:C:H42	1.61	0.47
1:1A:2614:A:OP1	60:1A:5843:HOH:O	2.20	0.47
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.39	0.47
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.97	0.47
11:1P:90:ARG:NH1	11:1P:105:LEU:HD11	2.30	0.47
32:1a:78:G:C2	32:1a:91:C:C4	3.02	0.47
32:1a:202:U:H3'	32:1a:203:U:C5	2.49	0.47
32:1a:523:A:H61	43:1l:92:0TD:CG	2.27	0.47
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.14	0.47
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.50	0.47
32:1a:1516:G:H2'	32:1a:1518:MA6:OP2	2.15	0.47
35:1d:107:ARG:NH2	35:1d:194:LEU:HD11	2.30	0.47
38:1g:26:PHE:O	38:1g:30:ILE:HD12	2.15	0.47
52:1u:5:ASP:OD2	60:1u:201:HOH:O	2.20	0.47
54:1y:40:C:H2'	54:1y:41:C:C6	2.50	0.47
1:2A:117:G:C6	1:2A:119:A:C6	3.03	0.47
1:2A:118:A:C8	1:2A:119:A:C8	3.03	0.47
1:2A:528:A:H8	9:2N:114:ARG:NH2	2.12	0.47
1:2A:569:U:H5"	60:2A:4285:HOH:O	2.14	0.47
1:2A:839:U:H2'	1:2A:840:C:C6	2.50	0.47
1:2A:912:C:P	12:2Q:8:LYS:HZ3	2.37	0.47
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.20	0.47
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.15	0.47
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2019:A:OP2	27:25:9:LYS:NZ	2.47	0.47
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.49	0.47
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.80	0.47
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.49	0.47
1:2A:2191:G:H2'	1:2A:2192:G:O4'	2.15	0.47
1:2A:2504:U:OP2	60:2A:4333:HOH:O	2.20	0.47
2:2B:105:A:H5'	2:2B:106:G:OP2	2.14	0.47
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.14	0.47
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.26	0.47
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	1.97	0.47
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.96	0.47
11:2P:60:MET:HA	30:28:13:ARG:HH12	1.80	0.47
15:2T:29:ARG:HB3	15:2T:87:ASP:HB2	1.96	0.47
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.32	0.47
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD3	1.95	0.47
32:2a:689:C:OP2	42:2k:55:LYS:HE2	2.15	0.47
32:2a:768:A:N3	32:2a:1512:U:O2'	2.46	0.47
32:2a:976:G:P	45:2n:32:SER:H	2.37	0.47
32:2a:982:U:O2	32:2a:1222:G:N1	2.32	0.47
32:2a:1238:A:C2	32:2a:1303:C:H4'	2.50	0.47
32:2a:1261:A:H3'	32:2a:1262:C:H6	1.80	0.47
32:2a:1328:C:O2'	44:2m:29:ARG:NH2	2.47	0.47
33:2b:223:ILE:O	33:2b:226:ARG:HG2	2.15	0.47
34:2c:47:LEU:CD1	34:2c:68:VAL:HG11	2.43	0.47
36:2e:6:PHE:HB3	36:2e:34:VAL:HG22	1.96	0.47
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.49	0.47
40:2i:23:ASN:ND2	40:2i:25:LYS:HG2	2.30	0.47
40:2i:79:LEU:HD22	40:2i:104:ARG:HB2	1.97	0.47
44:2m:43:THR:HB	44:2m:48:LEU:HD21	1.96	0.47
46:2o:39:LEU:HB3	46:2o:56:LEU:HD13	1.97	0.47
1:1A:180:A:H2'	1:1A:181:C:C6	2.50	0.47
1:1A:704:U:H2'	1:1A:705:C:H6	1.80	0.47
1:1A:2569:G:H2'	1:1A:2570:C:C6	2.50	0.47
2:1B:2:C:H2'	2:1B:3:C:C6	2.50	0.47
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.49	0.47
16:1U:8:VAL:HG23	16:1U:11:ARG:HH21	1.79	0.47
26:14:16:CYS:SG	26:14:17:GLY:N	2.88	0.47
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.97	0.47
32:1a:626:U:C2	32:1a:627:G:C8	3.03	0.47
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.97	0.47
1:2A:1033:U:P	31:29:9:ARG:HH22	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1288:U:O4	13:2R:106:GLY:HA3	2.15	0.47
1:2A:1300:U:H4'	1:2A:1301:A:C5'	2.45	0.47
12:2Q:16:ARG:HG2	12:2Q:18:LYS:HG3	1.97	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.14	0.47
32:2a:176:C:H2'	32:2a:177:C:C6	2.50	0.47
32:2a:376:G:H5"	47:2p:5:ARG:HD2	1.96	0.47
32:2a:964:A:N3	32:2a:969:A:O2'	2.45	0.47
32:2a:974:A:P	45:2n:41:ARG:HH12	2.38	0.47
32:2a:1002:G:C6	32:2a:1003:G:H8	2.33	0.47
32:2a:1128:C:O2'	32:2a:1129:C:OP1	2.32	0.47
32:2a:1152:A:OP1	41:2j:70:ARG:NH2	2.41	0.47
32:2a:1280:A:O2'	32:2a:1281:U:H5'	2.15	0.47
33:2b:178:ARG:NH1	33:2b:196:LEU:O	2.47	0.47
41:2j:64:GLU:OE2	41:2j:66:ARG:NH1	2.48	0.47
1:1A:347:G:C8	5:1F:171:PRO:HG3	2.50	0.47
4:1E:34:VAL:HG22	4:1E:48:GLN:HG2	1.97	0.47
32:1a:129:U:H5'	48:1q:3:LYS:HZ1	1.80	0.47
32:1a:373:A:H2'	32:1a:374:A:H8	1.80	0.47
32:1a:1002:G:N2	32:1a:1004:A:O2'	2.48	0.47
32:1a:1318:A:OP1	50:1s:7:LYS:NZ	2.41	0.47
38:1g:50:ILE:HG12	38:1g:61:VAL:HG11	1.97	0.47
47:1p:56:ALA:O	47:1p:60:LEU:HB2	2.15	0.47
54:1y:19:G:N1	54:1y:56:C:N4	2.62	0.47
1:2A:597:U:H2'	1:2A:598:G:C8	2.50	0.47
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.50	0.47
1:2A:1371:G:H2'	1:2A:1372:U:H5	1.80	0.47
1:2A:2358:G:N2	60:28:203:HOH:O	2.40	0.47
19:2X:72:LYS:HG2	19:2X:73:ARG:O	2.15	0.47
32:2a:109:A:C6	32:2a:326:G:C6	3.03	0.47
32:2a:114:U:O2'	32:2a:115:G:H5'	2.15	0.47
32:2a:991:U:C4	32:2a:1212:U:H1'	2.50	0.47
32:2a:1263:C:N3	32:2a:1272:G:O6	2.48	0.47
33:2b:95:GLN:HB2	33:2b:148:TYR:CD1	2.49	0.47
36:2e:78:HIS:CE1	36:2e:143:ARG:H	2.14	0.47
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.49	0.47
44:2m:13:LYS:O	44:2m:45:VAL:HG23	2.15	0.47
54:2w:58:A:H4'	54:2w:59:U:OP1	2.15	0.47
1:1A:943:C:H5'	54:1w:56:C:OP1	2.15	0.47
1:1A:1091:A:OP1	1:1A:1092:A:H3'	2.14	0.47
1:1A:1120:G:C2	1:1A:1121:C:H1'	2.50	0.47
1:1A:2121:U:O4	1:1A:2212:G:O6	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2124:U:H3	1:1A:2209:G:H1	1.61	0.47
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.48	0.47
8:1I:6:LEU:HD11	8:1I:37:VAL:HG23	1.97	0.47
10:1O:19:ILE:HG22	10:1O:43:VAL:HA	1.96	0.47
17:1V:62:LEU:HD11	17:1V:95:LEU:HB2	1.96	0.47
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.50	0.47
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.98	0.47
1:2A:1115:G:H2'	1:2A:1116:C:O4'	2.15	0.47
1:2A:1169:G:H1	1:2A:1180:C:H42	1.63	0.47
1:2A:2014:A:H4'	18:2W:92:ARG:NH2	2.17	0.47
1:2A:2094:G:P	8:2I:22:LYS:HD2	2.54	0.47
1:2A:2343:C:O2'	1:2A:2373:G:O2'	2.26	0.47
1:2A:2619:C:OP1	4:2E:152:LYS:NZ	2.45	0.47
7:2H:84:SER:HB3	7:2H:132:ARG:NH1	2.23	0.47
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.43	0.47
26:24:16:CYS:HA	26:24:33:VAL:HB	1.96	0.47
32:2a:447:G:O6	32:2a:485:G:O2'	2.30	0.47
32:2a:817:C:OP2	60:2a:3551:HOH:O	2.21	0.47
32:2a:1244:C:N4	32:2a:1293:G:H1	2.13	0.47
33:2b:91:PRO:HA	33:2b:151:GLY:O	2.15	0.47
34:2c:37:GLN:HE22	45:2n:52:GLN:HB3	1.80	0.47
43:2l:46:LYS:HG3	43:2l:92:0TD:H8	1.97	0.47
54:2y:52:G:H5'	54:2y:53:G:OP2	2.15	0.47
1:1A:1324:A:OP1	13:1R:36:THR:HG23	2.15	0.46
1:1A:1473:A:H4'	1:1A:1474:C:O4'	2.15	0.46
1:1A:2579:G:H2'	1:1A:2580:C:C6	2.51	0.46
32:1a:1025:U:O2	32:1a:1036:G:C6	2.68	0.46
33:1b:80:ILE:HG12	33:1b:215:LEU:HD23	1.97	0.46
33:1b:155:LEU:HD21	33:1b:159:PRO:HD3	1.97	0.46
44:1m:3:ARG:NH2	44:1m:45:VAL:HG11	2.30	0.46
54:1y:26:A:H61	54:1y:44:G:H1	1.62	0.46
1:2A:229:A:O5'	1:2A:230:U:H5'	2.15	0.46
1:2A:286:C:H2'	1:2A:287:C:C6	2.50	0.46
1:2A:856:C:O5'	1:2A:856:C:H6	1.98	0.46
1:2A:1024:G:HO2'	1:2A:1144:G:HO2'	1.63	0.46
1:2A:2298:A:N6	1:2A:2318:G:C8	2.84	0.46
1:2A:2639:A:C2	1:2A:2778:A:C8	3.03	0.46
1:2A:2764:A:H5"	1:2A:2765:A:OP2	2.14	0.46
2:2B:83:G:H1	2:2B:94:C:N4	2.13	0.46
4:2E:48:GLN:HE21	4:2E:78:LEU:HG	1.79	0.46
6:2G:126:ASP:HB2	6:2G:130:ASN:HB2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.15	0.46
32:2a:1030(A):G:N2	32:2a:1030(C):G:H3'	2.30	0.46
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.15	0.46
32:2a:1381:U:O2'	38:2g:79:ARG:HD3	2.14	0.46
32:2a:1479:C:H2'	32:2a:1480:G:H8	1.80	0.46
33:2b:134:GLU:HA	33:2b:137:ARG:NE	2.30	0.46
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	1.96	0.46
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.46	0.46
34:2c:125:GLU:HB2	34:2c:190:ARG:NH2	2.30	0.46
45:2n:26:ARG:NH2	45:2n:47:LEU:HD21	2.30	0.46
1:1A:572:A:H1'	1:1A:573:G:OP1	2.14	0.46
1:1A:2045:G:H4'	1:1A:2629:C:O3'	2.15	0.46
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.15	0.46
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.80	0.46
32:1a:713:G:H2'	32:1a:714:G:C8	2.50	0.46
32:1a:841:U:H6	32:1a:841:U:P	2.39	0.46
35:1d:3:ARG:HD3	35:1d:118:ARG:HD2	1.97	0.46
40:1i:5:TYR:HB2	40:1i:18:PHE:CE1	2.51	0.46
55:1x:50:U:H2'	55:1x:51:C:C6	2.50	0.46
1:2A:882:G:H1	1:2A:894:C:H42	1.63	0.46
1:2A:993:G:O6	1:2A:994:C:N4	2.49	0.46
1:2A:2432:A:N1	23:21:35:THR:HG22	2.31	0.46
7:2H:169:VAL:HG12	7:2H:171:LEU:HD23	1.96	0.46
13:2R:18:LEU:HD21	13:2R:22:ARG:CZ	2.45	0.46
32:2a:976:G:C8	32:2a:1358:U:C2	3.03	0.46
32:2a:1050:G:H1'	32:2a:1214:C:O2	2.15	0.46
32:2a:1152:A:P	41:2j:70:ARG:HH22	2.38	0.46
32:2a:1367:C:P	40:2i:112:LYS:HZ1	2.38	0.46
33:2b:192:SER:O	33:2b:194:PRO:HD3	2.16	0.46
34:2c:135:LYS:O	34:2c:139:GLN:HB2	2.15	0.46
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.14	0.46
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.23	0.46
1:1A:273:G:O2'	1:1A:274:U:H5"	2.15	0.46
1:1A:2134:G:H1'	54:1y:19:G:O2'	2.15	0.46
3:1D:8:PRO:HB3	3:1D:14:ARG:CD	2.45	0.46
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.51	0.46
8:1I:109:ILE:HD11	8:1I:130:TYR:CE2	2.51	0.46
8:1I:129:THR:HG22	8:1I:139:GLN:NE2	2.26	0.46
32:1a:1414:U:H3	32:1a:1486:G:H1	1.64	0.46
35:1d:53:ASP:O	35:1d:57:ARG:HG3	2.15	0.46
35:1d:194:LEU:HD12	35:1d:195:ALA:H	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:60:GLU:HG3	51:1t:81:LYS:HD2	1.97	0.46
1:2A:1035:U:H3	1:2A:1120:G:H1	1.64	0.46
1:2A:1171:G:OP2	1:2A:1171:G:H8	1.98	0.46
3:2D:101:GLU:CD	3:2D:103:ARG:HH12	2.22	0.46
15:2T:64:ARG:HG3	15:2T:73:GLU:HG2	1.96	0.46
26:24:15:ILE:HB	26:24:32:TYR:HD1	1.80	0.46
32:2a:857:C:H2'	32:2a:858:G:O4'	2.15	0.46
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.50	0.46
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.16	0.46
32:2a:1388:C:H2'	32:2a:1389:C:C6	2.49	0.46
33:2b:81:VAL:HA	33:2b:215:LEU:HD21	1.98	0.46
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.98	0.46
1:1A:646:A:OP2	11:1P:108:LYS:NZ	2.43	0.46
1:1A:939:C:H2'	1:1A:940:C:C6	2.50	0.46
1:1A:956:A:N1	1:1A:2289:G:H1'	2.31	0.46
1:1A:1103:A:N6	1:1A:1127:U:H3	2.12	0.46
1:1A:1105:G:H2'	1:1A:1106:U:C6	2.51	0.46
1:1A:2148:A:N1	1:1A:2184:G:O2'	2.42	0.46
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	1.98	0.46
32:1a:922:G:C6	32:1a:923:A:C6	3.03	0.46
32:1a:1137:C:H5"	32:1a:1138:G:OP1	2.15	0.46
1:2A:94(A):G:H2'	1:2A:95:G:O4'	2.15	0.46
5:2F:10:PRO:HB3	5:2F:17:ARG:CZ	2.45	0.46
21:2Z:93:ASP:CB	21:2Z:131:ARG:HH22	2.29	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.74	0.46
24:22:38:GLN:O	24:22:41:ILE:HG12	2.14	0.46
26:24:53:GLU:H	26:24:53:GLU:CD	2.23	0.46
32:2a:814:A:N7	32:2a:816:A:C4	2.83	0.46
32:2a:1347:G:H5"	40:2i:107:ARG:HB3	1.98	0.46
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.50	0.46
44:2m:40:ASN:HA	44:2m:41:PRO:HD2	1.83	0.46
54:2w:34:G:H2'	54:2w:35:A:C8	2.50	0.46
1:1A:137:G:O2'	1:1A:138:G:H5'	2.16	0.46
1:1A:559:U:H2'	1:1A:560:C:C6	2.50	0.46
1:1A:581:G:OP1	9:1N:111:PRO:HD2	2.16	0.46
1:1A:953:U:O2'	12:1Q:101:ARG:NH2	2.46	0.46
1:1A:1139:G:H3'	1:1A:1140:U:H5"	1.98	0.46
1:1A:1995:G:OP2	60:1A:4765:HOH:O	2.21	0.46
6:1G:82:LEU:HD21	6:1G:88:ILE:HG21	1.98	0.46
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.97	0.46
32:1a:510:A:H5"	35:1d:49:ARG:HH12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1429:C:H2'	32:1a:1430:C:C6	2.51	0.46
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.81	0.46
48:1q:29:HIS:N	48:1q:34:LYS:O	2.47	0.46
1:2A:448:U:O4	1:2A:583:G:H1'	2.15	0.46
1:2A:647:G:H8	1:2A:647:G:O5'	1.97	0.46
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.97	0.46
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.15	0.46
10:2O:26:LYS:NZ	10:2O:37:ASP:OD2	2.40	0.46
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.97	0.46
26:24:53:GLU:HG3	26:24:56:VAL:HG13	1.98	0.46
32:2a:707:C:H2'	32:2a:708:C:H6	1.80	0.46
32:2a:728:A:H2'	32:2a:729:A:H8	1.81	0.46
33:2b:92:TYR:N	33:2b:151:GLY:O	2.37	0.46
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.30	0.46
35:2d:74:GLN:O	35:2d:78:LEU:HD13	2.16	0.46
36:2e:93:PRO:HG2	39:2h:105:ARG:HE	1.81	0.46
1:1A:265:U:H2'	1:1A:266:C:C6	2.50	0.46
1:1A:1132:A:H5"	1:1A:1132:A:N3	2.30	0.46
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.50	0.46
2:1B:29:A:O2'	2:1B:58:A:N1	2.43	0.46
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.98	0.46
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.98	0.46
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.32	0.46
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	1.98	0.46
32:1a:17:U:H2'	32:1a:18:C:C6	2.51	0.46
32:1a:404:U:H2'	32:1a:405:U:H6	1.80	0.46
32:1a:1309:G:OP1	44:1m:88:ARG:NH2	2.45	0.46
34:1c:35:GLU:CD	34:1c:59:ARG:HH22	2.22	0.46
37:1f:67:MET:SD	37:1f:72:VAL:HG12	2.55	0.46
54:1w:18:G:H4'	54:1w:60:U:C6	2.51	0.46
54:1y:64:A:H2'	54:1y:65:G:C8	2.51	0.46
1:2A:395:U:O2'	1:2A:396:G:N7	2.42	0.46
1:2A:2370:G:C6	1:2A:2371:G:C6	3.04	0.46
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.46	0.46
21:2Z:105:VAL:O	21:2Z:140:ASP:HA	2.16	0.46
28:26:34:LEU:H	28:26:51:GLU:HG2	1.80	0.46
32:2a:643:C:H5'	39:2h:31:PHE:CE1	2.51	0.46
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.50	0.46
32:2a:1251:A:N6	32:2a:1285:A:N1	2.63	0.46
33:2b:58:ILE:HA	33:2b:61:LEU:HB3	1.97	0.46
34:2c:134:ILE:HD11	34:2c:153:VAL:CG2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:48:ILE:O	42:2k:50:TYR:N	2.49	0.46
44:2m:108:ARG:HA	44:2m:108:ARG:HD3	1.78	0.46
47:2p:9:PHE:HE2	47:2p:18:ARG:HD2	1.81	0.46
50:2s:23:ASN:OD1	50:2s:47:HIS:HE1	1.98	0.46
54:2w:11:C:N3	54:2w:24:G:N2	2.63	0.46
1:1A:928:G:C2	1:1A:929:G:H1'	2.51	0.46
1:1A:1897:C:H2'	1:1A:1898:A:O4'	2.16	0.46
26:14:55:ARG:N	26:14:56:VAL:HA	2.31	0.46
32:1a:166:G:H2'	32:1a:167:G:C8	2.50	0.46
35:1d:187:ARG:NH2	35:1d:193:ASP:OD2	2.48	0.46
1:2A:286:C:H2'	1:2A:287:C:H6	1.80	0.46
1:2A:526:A:O2'	1:2A:2043:C:O2	2.30	0.46
1:2A:1231:G:H2'	1:2A:1232:G:H8	1.80	0.46
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.51	0.46
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.16	0.46
1:2A:2059:A:H2'	1:2A:2503:2MA:HM23	1.97	0.46
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.16	0.46
8:2I:123:LEU:HD12	8:2I:123:LEU:HA	1.76	0.46
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.16	0.46
15:2T:19:LEU:HD22	15:2T:86:ILE:HD12	1.96	0.46
25:23:18:ASP:OD1	25:23:18:ASP:N	2.44	0.46
32:2a:340:U:H2'	32:2a:341:C:C6	2.51	0.46
32:2a:399:G:H2'	32:2a:400:C:C6	2.50	0.46
32:2a:693:G:H2'	32:2a:694:A:C8	2.50	0.46
32:2a:922:G:C6	32:2a:923:A:C6	3.03	0.46
33:2b:82:ARG:HG3	33:2b:92:TYR:OH	2.15	0.46
34:2c:34:LEU:HD11	34:2c:38:ARG:HH21	1.80	0.46
36:2e:122:GLU:HB2	36:2e:126:ARG:HH11	1.80	0.46
38:2g:32:ARG:HH21	38:2g:109:ASN:ND2	2.12	0.46
40:2i:29:ASN:ND2	40:2i:65:VAL:O	2.37	0.46
45:2n:29:ARG:HD3	45:2n:40:CYS:HB2	1.97	0.46
46:2o:3:ILE:CD1	46:2o:38:ARG:HE	2.29	0.46
1:1A:1464:G:N7	60:1A:4647:HOH:O	2.36	0.46
1:1A:2740:G:O2'	10:1O:70:LYS:NZ	2.45	0.46
12:1Q:30:GLY:HA2	12:1Q:107:ALA:HB2	1.98	0.46
32:1a:1272:G:H2'	32:1a:1273:G:O4'	2.16	0.46
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	1.97	0.46
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.72	0.46
45:1n:4:LYS:HA	45:1n:7:ILE:HG22	1.98	0.46
45:1n:29:ARG:HD3	45:1n:40:CYS:SG	2.55	0.46
1:2A:1027:A:C6	1:2A:1126:A:C4	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:42:C:C4	2:2B:43:C:C4	3.04	0.46
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.81	0.46
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.42	0.46
21:2Z:155:LEU:HB3	21:2Z:157:LEU:HG	1.97	0.46
32:2a:254:G:OP1	48:2q:66:SER:OG	2.16	0.46
32:2a:986:A:O2'	50:2s:55:LYS:O	2.33	0.46
32:2a:1003:G:C5	32:2a:1004:A:C2	3.04	0.46
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.45	0.46
32:2a:1220:G:O3'	50:2s:36:ARG:HD3	2.16	0.46
32:2a:1240:U:OP2	38:2g:115:ARG:HA	2.16	0.46
32:2a:1272:G:N2	32:2a:1273:G:C4	2.84	0.46
47:2p:21:VAL:HG13	47:2p:34:GLU:HB3	1.98	0.46
1:1A:11:G:H2'	1:1A:12:U:H5"	1.96	0.46
1:1A:1405:A:C2	1:1A:1418:U:O4	2.68	0.46
1:1A:1941:A:O2'	32:1a:1517:G:N3	2.43	0.46
1:1A:2495:C:OP1	54:1w:64:A:H4'	2.16	0.46
2:1B:91:C:H5'	12:1Q:18:LYS:HA	1.97	0.46
4:1E:97:LYS:HE2	4:1E:97:LYS:HB3	1.65	0.46
6:1G:43:LEU:HD11	6:1G:153:ARG:HD2	1.97	0.46
11:1P:128:HIS:NE2	11:1P:148:LEU:HD11	2.30	0.46
32:1a:7:G:H5'	32:1a:298:A:O4'	2.16	0.46
32:1a:1026:G:C8	32:1a:1027:C:O2	2.69	0.46
32:1a:1038:C:C2'	32:1a:1039:C:H5'	2.46	0.46
1:2A:311:A:C6	1:2A:328:U:C4	3.04	0.46
1:2A:774:A:H2'	1:2A:774:A:N3	2.31	0.46
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.51	0.46
1:2A:2156:G:H2'	1:2A:2157:G:C4	2.49	0.46
1:2A:2379:G:O2'	14:2S:17:ARG:NH2	2.48	0.46
1:2A:2595:G:N7	60:2A:5057:HOH:O	2.35	0.46
2:2B:19:G:H2'	2:2B:20:C:O4'	2.15	0.46
3:2D:21:PHE:HB3	3:2D:24:ILE:HD12	1.97	0.46
12:2Q:85:LYS:HG2	22:20:7:LEU:HB2	1.98	0.46
19:2X:44:GLU:O	19:2X:48:LYS:N	2.49	0.46
20:2Y:20:TYR:CE2	20:2Y:43:ASN:HA	2.51	0.46
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.51	0.46
32:2a:428:G:OP2	35:2d:10:ARG:NH1	2.49	0.46
32:2a:539:A:H2'	32:2a:540:G:C8	2.51	0.46
32:2a:1273:G:C5	32:2a:1274:G:C4	3.04	0.46
32:2a:1370:G:N7	40:2i:109:VAL:HG11	2.30	0.46
33:2b:19:HIS:CG	33:2b:20:GLU:H	2.34	0.46
35:2d:173:TRP:CZ3	35:2d:193:ASP:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:69:TYR:CD1	43:2l:90:VAL:HG21	2.51	0.46
44:2m:90:LEU:HD23	44:2m:93:ARG:HD2	1.97	0.46
1:1A:649:C:O2'	1:1A:704:U:OP1	2.32	0.46
1:1A:655:G:OP2	30:18:15:LYS:NZ	2.31	0.46
1:1A:664:U:H2'	1:1A:665:C:C6	2.51	0.46
8:1I:48:GLU:HB3	8:1I:52:ARG:HH12	1.80	0.46
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.17	0.46
34:1c:45:LYS:HB2	34:1c:45:LYS:HE3	1.64	0.46
38:1g:111:ARG:CG	38:1g:112:PRO:HD2	2.45	0.46
48:1q:62:SER:HB3	48:1q:72:ARG:NH2	2.30	0.46
54:1y:52:G:H2'	54:1y:53:G:C8	2.51	0.46
1:2A:600:G:O6	60:2A:4478:HOH:O	2.21	0.46
1:2A:628:G:H2'	1:2A:629:G:C8	2.51	0.46
1:2A:764:A:H5'	3:2D:210:GLY:HA2	1.98	0.46
1:2A:940:G:N3	1:2A:1191:G:H4'	2.31	0.46
1:2A:944:G:H5"	1:2A:945:A:O5'	2.15	0.46
1:2A:1784:A:O2'	60:2A:4593:HOH:O	2.21	0.46
5:2F:7:TYR:O	5:2F:22:ALA:N	2.49	0.46
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.55	0.46
30:28:8:LYS:HB3	30:28:12:LYS:HE3	1.98	0.46
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.51	0.46
54:2w:8:4SU:N3	54:2w:15:G:O6	2.49	0.46
1:1A:667:G:OP1	60:1A:5361:HOH:O	2.21	0.45
1:1A:1137:G:C6	1:1A:1138:C:C4	3.04	0.45
1:1A:2205:C:H2'	1:1A:2206:G:C8	2.47	0.45
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.51	0.45
1:1A:2411:G:H1'	60:1A:6427:HOH:O	2.16	0.45
1:1A:2430:A:H2'	1:1A:2431:U:C6	2.50	0.45
1:1A:2473:C:H2'	1:1A:2474:U:C6	2.51	0.45
1:1A:2864:G:H2'	1:1A:2865:C:C6	2.51	0.45
32:1a:1003:G:N3	32:1a:1004:A:H2	2.14	0.45
32:1a:1437:C:H2'	32:1a:1438:G:H8	1.80	0.45
38:1g:78:ARG:HH21	38:1g:79:ARG:NH1	2.14	0.45
39:1h:104:ARG:HA	39:1h:104:ARG:HD3	1.75	0.45
51:1t:10:LEU:HD12	51:1t:11:SER:H	1.80	0.45
54:1y:9:A:O3'	54:1y:45:U:O2'	2.32	0.45
1:2A:27:G:N2	1:2A:512:G:H1'	2.31	0.45
1:2A:1272:A:H3'	1:2A:1273:U:H5"	1.97	0.45
1:2A:1510:G:H2'	1:2A:1511:C:C6	2.52	0.45
1:2A:2315:G:H2'	1:2A:2316:C:H6	1.81	0.45
5:2F:18:ARG:NH1	5:2F:127:GLU:OE2	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:51:ARG:HA	6:2G:51:ARG:HD3	1.84	0.45
13:2R:103:ARG:HD3	13:2R:108:GLY:O	2.15	0.45
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.42	0.45
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.51	0.45
29:27:2:LYS:NZ	60:27:203:HOH:O	2.49	0.45
32:2a:22:G:H4'	32:2a:885:G:C8	2.52	0.45
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.20	0.45
32:2a:1072:G:C5	32:2a:1073:U:C4	3.04	0.45
34:2c:119:ARG:O	34:2c:123:GLN:HG3	2.17	0.45
35:2d:57:ARG:HB3	35:2d:206:PHE:HB2	1.98	0.45
36:2e:40:ARG:HB3	36:2e:66:MET:HE1	1.98	0.45
38:2g:22:LEU:HG	38:2g:62:PHE:HE2	1.81	0.45
51:2t:50:GLU:HB2	51:2t:99:LEU:HD22	1.97	0.45
1:1A:92:C:H2'	1:1A:93:G:O4'	2.16	0.45
1:1A:602:G:OP1	60:1A:5436:HOH:O	2.21	0.45
1:1A:2331:G:N2	14:1S:3:ARG:HA	2.31	0.45
5:1F:165:ARG:HG3	5:1F:168:ARG:NH2	2.31	0.45
32:1a:110:C:H2'	32:1a:111:G:O4'	2.17	0.45
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.46	0.45
39:1h:51:VAL:HG11	39:1h:60:ARG:NH1	2.31	0.45
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.31	0.45
1:2A:263:C:H2'	1:2A:264:C:O4'	2.17	0.45
1:2A:320:A:H4'	1:2A:322:A:C8	2.51	0.45
1:2A:661:C:H2'	1:2A:662:G:C8	2.52	0.45
1:2A:829:A:C5	1:2A:2248:C:H5'	2.51	0.45
1:2A:1017:G:O6	1:2A:1146:C:N4	2.49	0.45
1:2A:2135:A:H5'	1:2A:2159:G:O2'	2.16	0.45
1:2A:2723:C:OP1	13:2R:3:HIS:ND1	2.25	0.45
10:2O:19:ILE:HG22	10:2O:43:VAL:HA	1.98	0.45
14:2S:11:LYS:HG3	14:2S:91:PRO:HD3	1.97	0.45
19:2X:94:GLY:N	19:2X:95:LEU:HA	2.30	0.45
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.97	0.45
30:28:23:VAL:CG1	30:28:47:LYS:HD3	2.46	0.45
32:2a:909:A:H2'	32:2a:910:C:O4'	2.16	0.45
32:2a:1024:G:H2'	32:2a:1025:U:H5"	1.99	0.45
36:2e:36:ASP:C	36:2e:38:GLN:H	2.24	0.45
36:2e:106:PRO:O	36:2e:110:LEU:HG	2.16	0.45
48:2q:32:TYR:C	48:2q:34:LYS:H	2.23	0.45
1:1A:924:U:H3	1:1A:945:A:H2	1.65	0.45
1:1A:1121:C:O2	1:1A:1122:C:H2'	2.16	0.45
1:1A:1935:A:H4'	1:1A:1936:C:H5"	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:121:ASN:ND2	60:1E:408:HOH:O	2.39	0.45
28:16:13:CYS:SG	28:16:47:THR:HG21	2.57	0.45
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.51	0.45
32:1a:1006:C:N3	32:1a:1023:G:N2	2.64	0.45
34:1c:73:PRO:HB3	34:1c:103:VAL:HG11	1.98	0.45
39:1h:30:ARG:O	39:1h:34:GLU:HG2	2.16	0.45
54:1w:21:A:N6	54:1w:46:7MG:C4	2.84	0.45
54:1y:19:G:C4'	54:1y:57:G:H22	2.28	0.45
1:2A:511:U:H4'	1:2A:1235:G:H4'	1.96	0.45
1:2A:658:C:H2'	1:2A:659:C:C6	2.52	0.45
1:2A:1192:G:O6	60:2A:4615:HOH:O	2.20	0.45
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.16	0.45
1:2A:1857:G:C6	1:2A:1858:G:N1	2.85	0.45
1:2A:2357:U:P	22:20:20:ARG:HE	2.38	0.45
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.51	0.45
1:2A:2516:G:C6	1:2A:2517:C:C4	3.05	0.45
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.52	0.45
32:2a:630:G:H2'	32:2a:631:G:C8	2.51	0.45
32:2a:671:G:H2'	32:2a:672:U:O4'	2.17	0.45
32:2a:881:G:H2'	32:2a:882:C:O4'	2.16	0.45
32:2a:918:A:H2'	32:2a:919:A:O4'	2.15	0.45
32:2a:984:C:H2'	32:2a:985:C:H6	1.81	0.45
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.16	0.45
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.17	0.45
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.81	0.45
48:2q:54:GLY:O	48:2q:81:ARG:N	2.48	0.45
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.17	0.45
54:2w:5:G:H2'	54:2w:6:G:C8	2.52	0.45
1:1A:1281:G:H5"	60:1A:5107:HOH:O	2.16	0.45
1:1A:1539:C:N4	1:1A:2227:G:O2'	2.47	0.45
1:1A:1549:U:H2'	1:1A:1550:C:C6	2.51	0.45
1:1A:1683:C:H2'	1:1A:1684:A:C8	2.51	0.45
1:1A:1945:U:H2'	1:1A:1946:C:C6	2.52	0.45
1:1A:2143:G:N2	1:1A:2199:C:N3	2.48	0.45
1:1A:2178:G:OP2	1:1A:2178:G:H8	1.99	0.45
2:1B:33:G:C2	2:1B:50:G:C2	3.04	0.45
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.16	0.45
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.99	0.45
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.99	0.45
32:1a:711:G:OP1	37:1f:54:LYS:NZ	2.35	0.45
32:1a:830:G:O6	60:1a:2228:HOH:O	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:54:VAL:HA	44:1m:57:ARG:HB3	1.99	0.45
1:2A:709:U:H2'	1:2A:710:G:C8	2.52	0.45
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.32	0.45
1:2A:2330:G:H21	22:20:42:GLY:N	2.15	0.45
1:2A:2473:U:O2	1:2A:2473:U:H2'	2.15	0.45
25:23:10:LYS:NZ	25:23:15:TYR:OH	2.47	0.45
32:2a:920:U:H2'	32:2a:921:U:C6	2.51	0.45
32:2a:1346:A:N7	38:2g:10:ARG:NH1	2.63	0.45
33:2b:224:GLN:HG3	33:2b:225:ALA:N	2.30	0.45
34:2c:108:ASN:HA	34:2c:109:PRO:HD2	1.76	0.45
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.81	0.45
41:2j:5:ARG:HA	41:2j:73:ASP:OD1	2.16	0.45
41:2j:6:ILE:O	41:2j:71:LEU:HD12	2.16	0.45
42:2k:43:SER:HA	42:2k:47:VAL:HG21	1.97	0.45
43:2l:34:ARG:O	43:2l:61:THR:HG23	2.17	0.45
54:2w:28:G:H2'	54:2w:29:G:O4'	2.16	0.45
1:1A:2796:G:N7	60:1A:5760:HOH:O	2.36	0.45
15:1T:127:ALA:C	15:1T:129:ARG:N	2.74	0.45
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.17	0.45
32:1a:343:U:O2'	32:1a:346:G:O6	2.30	0.45
32:1a:1121:U:C2'	32:1a:1122:U:H5'	2.46	0.45
40:1i:48:GLU:CD	40:1i:51:ARG:HD2	2.42	0.45
41:1j:64:GLU:HB3	45:1n:59:ALA:HB2	1.98	0.45
42:1k:15:ALA:HA	42:1k:76:GLY:O	2.17	0.45
54:1w:11:C:H2'	54:1w:12:U:C6	2.52	0.45
1:2A:265:A:H1'	1:2A:266:G:O4'	2.17	0.45
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.51	0.45
1:2A:660:G:H5'	5:2F:99:TYR:CE1	2.52	0.45
1:2A:1007:C:OP1	9:2N:37:LYS:NZ	2.49	0.45
1:2A:1218:C:OP2	16:2U:15:LYS:NZ	2.40	0.45
1:2A:1245:G:OP1	11:2P:13:ASN:ND2	2.36	0.45
24:22:52:ASP:O	24:22:56:GLN:HG3	2.17	0.45
32:2a:45:U:H2'	32:2a:46:G:H8	1.81	0.45
32:2a:509:A:O2'	32:2a:510:A:OP1	2.29	0.45
33:2b:50:GLU:HB3	33:2b:200:ILE:O	2.16	0.45
36:2e:93:PRO:HG2	39:2h:105:ARG:NE	2.32	0.45
40:2i:4:TYR:CZ	40:2i:88:TYR:HD1	2.35	0.45
44:2m:123:ALA:HB2	54:2w:39:PSU:H1'	1.98	0.45
1:1A:348:A:N6	1:1A:362:G:O2'	2.50	0.45
1:1A:2108:U:H2'	1:1A:2109:G:H8	1.81	0.45
1:1A:2150:C:N4	1:1A:2182:G:H1	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.98	0.45
20:1Y:92:ASN:CG	20:1Y:94:LYS:HG2	2.41	0.45
32:1a:1144:G:N2	32:1a:1146:A:H62	2.12	0.45
33:1b:17:PHE:HB3	33:1b:44:LEU:HD11	1.97	0.45
33:1b:21:ARG:O	33:1b:23:ARG:HG3	2.16	0.45
33:1b:133:LYS:O	33:1b:137:ARG:HG3	2.17	0.45
46:1o:64:ARG:HH12	46:1o:68:ARG:NH2	2.15	0.45
52:1u:6:ARG:HH21	52:1u:15:ARG:NH2	2.15	0.45
1:2A:1912:A:C8	1:2A:1918:A:C2	3.05	0.45
1:2A:2562:U:H1'	10:2O:23:ARG:HE	1.81	0.45
2:2B:25:A:H2'	2:2B:26:A:H8	1.82	0.45
19:2X:25:LYS:HA	19:2X:81:VAL:O	2.16	0.45
32:2a:865:A:H2	32:2a:918:A:H4'	1.82	0.45
32:2a:954:G:H2'	32:2a:955:U:O4'	2.16	0.45
32:2a:1269:A:N1	32:2a:1312:G:O2'	2.37	0.45
50:2s:80:TYR:CZ	50:2s:82:GLY:HA2	2.52	0.45
1:1A:2157:A:H2	1:1A:2158:C:C2	2.35	0.45
1:1A:2880:C:OP1	13:1R:57:ARG:NH1	2.37	0.45
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.51	0.45
32:1a:501:C:H2'	32:1a:502:G:C8	2.52	0.45
32:1a:502:G:H2'	32:1a:503:C:O4'	2.17	0.45
32:1a:840:C:H4'	32:1a:841:U:OP1	2.16	0.45
32:1a:920:U:H2'	32:1a:921:U:C6	2.52	0.45
33:1b:131:PRO:O	33:1b:135:GLN:N	2.48	0.45
35:1d:83:SER:HA	35:1d:89:THR:OG1	2.15	0.45
39:1h:56:LYS:HB2	39:1h:58:TYR:HE2	1.82	0.45
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.40	0.45
1:2A:699:A:H2'	1:2A:700:G:O4'	2.17	0.45
1:2A:884:C:H3'	1:2A:885:C:H6	1.82	0.45
1:2A:1910:G:H2'	1:2A:1911:PSU:H6	1.82	0.45
1:2A:2065:C:H2'	1:2A:2066:C:H6	1.82	0.45
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.32	0.45
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.97	0.45
4:2E:24:THR:HG22	4:2E:186:GLY:O	2.17	0.45
7:2H:80:SER:OG	7:2H:81:GLU:OE1	2.33	0.45
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.99	0.45
32:2a:715:A:H2'	32:2a:716:A:C8	2.51	0.45
32:2a:1004:A:N1	32:2a:1037:C:C2	2.85	0.45
32:2a:1256:A:N1	32:2a:1278:U:H1'	2.31	0.45
34:2c:58:GLU:HB3	41:2j:92:THR:OG1	2.17	0.45
40:2i:17:VAL:HG11	40:2i:81:ILE:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:54:ARG:HH22	54:2y:39:PSU:H4'	1.80	0.45
44:2m:40:ASN:HB3	44:2m:43:THR:HG23	1.99	0.45
49:2r:22:VAL:HB	49:2r:56:THR:HA	1.99	0.45
1:1A:34:C:H5"	1:1A:35:G:OP2	2.17	0.45
1:1A:1202:A:P	16:1U:55:ARG:HH11	2.38	0.45
1:1A:1405:A:H2	1:1A:1418:U:O4	2.00	0.45
1:1A:1958:A:OP1	1:1A:1959:A:H5'	2.16	0.45
1:1A:2285:A:H2'	1:1A:2286:A:C8	2.51	0.45
1:1A:2803:A:H5'	1:1A:2902:G:H21	1.82	0.45
5:1F:188:ARG:HA	11:1P:3:LEU:HD11	1.99	0.45
20:1Y:92:ASN:HB3	20:1Y:94:LYS:N	2.16	0.45
32:1a:865:A:C2	32:1a:918:A:H4'	2.51	0.45
34:1c:82:GLU:OE2	34:1c:85:ARG:NH1	2.50	0.45
38:1g:146:GLU:O	38:1g:149:ARG:HB2	2.17	0.45
1:2A:839:U:H1'	1:2A:1191:G:H1'	1.98	0.45
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.51	0.45
1:2A:2129:C:H5'	1:2A:2130:U:OP2	2.17	0.45
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.83	0.45
13:2R:67:LEU:CD1	13:2R:76:VAL:HG21	2.47	0.45
19:2X:35:THR:HG22	19:2X:38:GLU:H	1.81	0.45
21:2Z:146:ILE:HG12	21:2Z:174:VAL:HG13	1.98	0.45
24:22:1:MET:HE3	24:22:5:GLU:HB3	1.99	0.45
25:23:46:ASN:O	25:23:50:VAL:HG22	2.17	0.45
32:2a:741:G:H2'	32:2a:742:G:O4'	2.16	0.45
32:2a:1027:C:H2'	32:2a:1034:G:H22	1.82	0.45
32:2a:1352:C:H42	32:2a:1370:G:H1	1.65	0.45
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.52	0.45
32:2a:1396:A:OP2	60:2a:3396:HOH:O	2.21	0.45
35:2d:180:GLY:O	35:2d:182:LYS:HG3	2.17	0.45
40:2i:16:ARG:HH11	40:2i:64:THR:HG21	1.81	0.45
55:2x:44:A:C6	55:2x:45:G:C6	3.05	0.45
1:1A:1093:G:H2'	1:1A:1156:G:N2	2.32	0.45
3:1D:108:PRO:HB3	3:1D:143:HIS:HE1	1.82	0.45
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.47	0.45
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.52	0.45
9:1N:128:HIS:O	9:1N:131:GLN:NE2	2.50	0.45
32:1a:44:G:C2	32:1a:45:U:H1'	2.52	0.45
32:1a:266:G:H2'	32:1a:266:G:N3	2.32	0.45
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.99	0.45
32:1a:1129:C:H2'	32:1a:1139:G:N7	2.31	0.45
42:1k:98:LEU:O	42:1k:101:SER:OG	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:1l:113:ARG:NH2	43:1l:116:SER:HB2	2.32	0.45
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.77	0.45
1:2A:195:A:H5"	1:2A:196:A:O5'	2.16	0.45
1:2A:322:A:C5	1:2A:340:A:C2	3.05	0.45
1:2A:1374:G:H2'	1:2A:1375:C:C6	2.52	0.45
1:2A:2019:A:O4'	16:2U:34:LYS:HE3	2.17	0.45
1:2A:2262:U:OP2	22:20:16:SER:OG	2.29	0.45
2:2B:7:G:H1	2:2B:114:C:N4	2.08	0.45
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.99	0.45
15:2T:16:ARG:HB3	15:2T:18:ASP:OD1	2.17	0.45
16:2U:52:ARG:HA	16:2U:55:ARG:HE	1.82	0.45
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.98	0.45
32:2a:909:A:H2	32:2a:1413:A:N3	2.15	0.45
32:2a:973:G:H3'	32:2a:974:A:H5"	1.99	0.45
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.46	0.45
32:2a:1264:C:C4	32:2a:1272:G:O6	2.70	0.45
36:2e:69:VAL:HG22	36:2e:71:LEU:HD12	1.98	0.45
1:1A:213:G:H2'	1:1A:214:A:O4'	2.16	0.45
1:1A:597:C:N3	4:1E:145:LYS:NZ	2.65	0.45
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.45	0.45
15:1T:56:GLY:O	15:1T:59:THR:HG22	2.17	0.45
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.17	0.45
18:1W:68:ARG:NH1	18:1W:111:HIS:HA	2.32	0.45
32:1a:1030(B):C:H2'	32:1a:1030(C):G:H5'	1.99	0.45
50:1s:80:TYR:O	50:1s:82:GLY:N	2.48	0.45
55:1x:25:C:H2'	55:1x:26:G:O4'	2.16	0.45
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.62	0.45
1:2A:570:G:H2'	1:2A:2030:A:C5	2.51	0.45
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.81	0.45
1:2A:1353:A:H2'	1:2A:1354:A:C8	2.52	0.45
1:2A:2162:G:H4'	1:2A:2172:U:C2'	2.45	0.45
1:2A:2261:C:O2'	1:2A:2262:U:H5'	2.17	0.45
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.97	0.45
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.99	0.45
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.50	0.45
6:2G:131:TYR:CE2	6:2G:133:LEU:HD23	2.51	0.45
32:2a:229:U:H5"	47:2p:33:ILE:HD13	1.99	0.45
32:2a:767:A:H2'	32:2a:768:A:O4'	2.17	0.45
32:2a:1208:C:H2'	32:2a:1209:C:C6	2.52	0.45
38:2g:26:PHE:O	38:2g:30:ILE:HD12	2.17	0.45
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:51:ARG:HG3	45:2n:45:ARG:NH2	2.32	0.45
47:2p:60:LEU:HD21	47:2p:80:PHE:HE1	1.82	0.45
1:1A:329:U:H2'	1:1A:330:U:C6	2.53	0.44
1:1A:1846:A:OP2	3:1D:54:ARG:NH2	2.37	0.44
1:1A:2304:C:H2'	1:1A:2305:C:C6	2.52	0.44
2:1B:28:C:OP1	14:1S:36:TYR:OH	2.30	0.44
33:1b:54:THR:O	33:1b:58:ILE:HG13	2.17	0.44
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.51	0.44
36:1e:31:LEU:HD23	36:1e:31:LEU:HA	1.75	0.44
37:1f:19:LEU:HD11	37:1f:59:TYR:CE1	2.52	0.44
49:1r:38:GLU:HA	49:1r:41:LYS:HE3	1.99	0.44
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.52	0.44
54:1y:56:C:C2	54:1y:57:G:C8	3.05	0.44
1:2A:61:G:H5'	24:22:50:ILE:HG21	1.99	0.44
1:2A:154(A):C:H42	1:2A:171:G:H1	1.65	0.44
1:2A:639:U:H2'	1:2A:640:C:C6	2.52	0.44
1:2A:947:G:N2	1:2A:971:C:C2	2.85	0.44
1:2A:1466:G:O2'	1:2A:1546:C:O2'	2.09	0.44
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.51	0.44
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.53	0.44
1:2A:2332:U:H5'	1:2A:2336:A:N6	2.33	0.44
26:24:44:THR:O	26:24:45:GLY:C	2.60	0.44
26:24:47:GLN:C	26:24:49:PHE:H	2.24	0.44
32:2a:980:C:H3'	32:2a:981:U:H6	1.80	0.44
32:2a:995:C:N3	32:2a:1046:A:O2'	2.43	0.44
33:2b:48:MET:HE2	33:2b:49:GLU:HB2	1.99	0.44
38:2g:76:ARG:N	38:2g:87:VAL:O	2.48	0.44
1:1A:449:A:H2'	1:1A:450:A:C8	2.53	0.44
1:1A:1550:C:H2'	1:1A:1551:C:H6	1.82	0.44
1:1A:1787:G:H4'	1:1A:1789:G:O4'	2.17	0.44
1:1A:2054:G:H1'	4:1E:145:LYS:HD3	1.99	0.44
1:1A:2764:G:C4	7:1H:2:SER:HA	2.52	0.44
6:1G:43:LEU:HB3	6:1G:44:GLY:H	1.55	0.44
16:1U:104:GLN:NE2	16:1U:105:VAL:HG23	2.32	0.44
30:18:42:ARG:HD2	60:18:212:HOH:O	2.17	0.44
32:1a:1198:G:H5"	60:1a:2016:HOH:O	2.17	0.44
1:2A:275:G:C2	1:2A:276:A:C4	3.05	0.44
1:2A:1462:C:H4'	1:2A:2703:C:H5'	2.00	0.44
1:2A:2184:G:O2'	1:2A:2185:C:H5'	2.17	0.44
1:2A:2350:C:H5"	30:28:42:ARG:HD3	1.99	0.44
7:2H:103:LEU:HB3	7:2H:115:VAL:HB	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:149:ARG:HH12	7:2H:167:GLU:CD	2.25	0.44
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	1.99	0.44
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.53	0.44
32:2a:271:C:H2'	32:2a:272:C:H6	1.82	0.44
32:2a:737:A:H2'	32:2a:738:C:C6	2.52	0.44
32:2a:859:A:OP2	32:2a:869:G:N1	2.40	0.44
32:2a:1009:G:C2	32:2a:1021:G:N3	2.85	0.44
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.51	0.44
32:2a:1349:A:H2'	32:2a:1350:A:H8	1.82	0.44
44:2m:23:TYR:HE2	44:2m:70:LEU:HD22	1.81	0.44
2:1B:12:C:H2'	22:10:73:GLY:HA3	1.99	0.44
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.70	0.44
32:1a:116:A:H8	32:1a:116:A:O5'	2.00	0.44
33:1b:155:LEU:HD12	33:1b:155:LEU:HA	1.87	0.44
55:1x:45:G:H8	55:1x:45:G:O5'	2.00	0.44
1:2A:297:C:OP1	20:2Y:87:LYS:HG3	2.18	0.44
1:2A:1359:A:C2	1:2A:1372:U:O4	2.71	0.44
1:2A:1785:A:OP1	60:2A:4173:HOH:O	2.21	0.44
1:2A:2305:A:H1'	6:2G:136:ARG:HB3	1.98	0.44
1:2A:2853:C:H2'	1:2A:2854:G:H8	1.82	0.44
7:2H:122:THR:O	7:2H:134:SER:OG	2.35	0.44
16:2U:81:HIS:CG	16:2U:117:GLN:HE22	2.35	0.44
26:24:58:ARG:HH21	44:2m:80:ARG:HH22	1.63	0.44
32:2a:1350:A:C2	32:2a:1351:U:C2	3.05	0.44
33:2b:51:LEU:HD22	33:2b:55:PHE:CE2	2.52	0.44
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	1.99	0.44
36:2e:74:GLY:HA3	36:2e:116:THR:HG22	1.98	0.44
38:2g:79:ARG:CG	38:2g:80:VAL:H	2.30	0.44
43:2l:45:PRO:CB	43:2l:92:0TD:OD1	2.66	0.44
54:2w:51:U:H2'	54:2w:52:G:C8	2.52	0.44
1:1A:2108:U:H2'	1:1A:2109:G:C8	2.53	0.44
1:1A:2619:G:H2'	1:1A:2620:G:O4'	2.17	0.44
1:1A:2665:U:H2'	1:1A:2666:A:C8	2.53	0.44
32:1a:405:U:O4	35:1d:2:GLY:N	2.50	0.44
32:1a:828:A:H2'	32:1a:829:G:O4'	2.16	0.44
32:1a:935:A:O2'	32:1a:1383:C:N3	2.47	0.44
32:1a:1025:U:C2	32:1a:1036:G:O6	2.70	0.44
34:1c:73:PRO:O	34:1c:77:ILE:HG12	2.18	0.44
34:1c:121:ALA:O	34:1c:125:GLU:HG3	2.16	0.44
39:1h:81:HIS:ND1	39:1h:138:TRP:OXT	2.41	0.44
41:1j:45:ARG:HG2	41:1j:47:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:721:C:H2'	1:2A:722:A:C8	2.52	0.44
1:2A:911:A:O4'	1:2A:2264:C:H4'	2.17	0.44
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.18	0.44
1:2A:1237:A:OP1	60:2A:4545:HOH:O	2.21	0.44
1:2A:2133:G:C2	1:2A:2157:G:C5	3.06	0.44
1:2A:2184:G:H2'	1:2A:2185:C:H6	1.80	0.44
1:2A:2470:G:O6	1:2A:2481:G:C2	2.70	0.44
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.17	0.44
2:2B:29:A:H2'	2:2B:30:C:C6	2.53	0.44
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.81	0.44
17:2V:31:ALA:O	17:2V:61:VAL:HG12	2.18	0.44
22:20:45:PHE:HE1	22:20:77:ARG:NE	2.14	0.44
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.53	0.44
32:2a:1261:A:H3'	32:2a:1262:C:C6	2.51	0.44
32:2a:1356:G:N2	32:2a:1367:C:C2	2.85	0.44
32:2a:1456:G:O2'	51:2t:39:LYS:HE3	2.17	0.44
33:2b:110:GLN:O	33:2b:113:HIS:HB2	2.18	0.44
33:2b:213:LEU:HD22	33:2b:214:ILE:HD13	1.99	0.44
36:2e:24:ARG:HD2	53:2v:24:A:OP2	2.17	0.44
44:2m:3:ARG:HB3	44:2m:7:VAL:O	2.17	0.44
52:2u:6:ARG:HE	52:2u:15:ARG:CZ	2.31	0.44
55:2x:67:C:C2'	55:2x:68:C:H5'	2.48	0.44
1:1A:1099:C:N3	1:1A:1152:G:N2	2.53	0.44
1:1A:2177:G:H2'	1:1A:2177:G:N3	2.33	0.44
15:1T:39:ARG:NH2	32:1a:345:C:H5"	2.33	0.44
24:12:41:ILE:HG13	24:12:43:GLN:HG3	1.99	0.44
32:1a:37:U:O2'	32:1a:547:A:N1	2.45	0.44
32:1a:952:U:H2'	32:1a:953:G:H8	1.82	0.44
32:1a:1095:U:H5"	32:1a:1109:C:O2	2.16	0.44
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.52	0.44
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	1.99	0.44
38:1g:48:LYS:O	38:1g:52:GLU:HG3	2.17	0.44
54:1w:18:G:H4'	54:1w:60:U:H6	1.81	0.44
1:2A:7:G:N2	1:2A:2896:C:O2	2.49	0.44
1:2A:248:G:C2	1:2A:2431:U:H4'	2.53	0.44
1:2A:441:U:H2'	1:2A:442:G:C8	2.53	0.44
1:2A:973:A:H8	1:2A:973:A:OP1	2.01	0.44
1:2A:1037:G:C2	1:2A:1119:C:C2	3.06	0.44
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.81	0.44
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.18	0.44
1:2A:2168:G:C8	1:2A:2170:A:N7	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:8:LYS:HE2	6:2G:8:LYS:HB3	1.81	0.44
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	2.00	0.44
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.17	0.44
15:2T:56:GLY:O	15:2T:59:THR:HG22	2.17	0.44
20:2Y:86:ARG:HB2	20:2Y:98:VAL:HG23	1.99	0.44
23:21:67:ILE:N	23:21:68:PRO:HD2	2.32	0.44
26:24:57:GLU:CB	26:24:58:ARG:HA	2.48	0.44
32:2a:12:U:H4'	32:2a:526:C:O2'	2.17	0.44
32:2a:336:C:H2'	32:2a:337:C:C6	2.52	0.44
32:2a:922:G:N3	32:2a:1398:A:H2	2.15	0.44
32:2a:1206:G:C6	32:2a:1207:2MG:C4	3.06	0.44
32:2a:1272:G:N2	32:2a:1273:G:N9	2.66	0.44
33:2b:112:VAL:HG22	33:2b:149:LEU:HD13	2.00	0.44
35:2d:12:CYS:SG	35:2d:19:LEU:HB2	2.57	0.44
38:2g:69:VAL:HG13	38:2g:134:ALA:O	2.18	0.44
1:1A:1201:A:P	16:1U:55:ARG:HD2	2.57	0.44
1:1A:1314:A:C2	1:1A:2035:A:C4	3.06	0.44
1:1A:1821:C:H2'	1:1A:1822:A:C5	2.52	0.44
1:1A:2073:A:H5'	1:1A:2590:G:O4'	2.18	0.44
1:1A:2177:G:H3'	1:1A:2178:G:C8	2.52	0.44
1:1A:2205:C:HO2'	1:1A:2206:G:P	2.41	0.44
10:1O:64:ARG:HD3	10:1O:79:PHE:CD1	2.52	0.44
21:1Z:137:ILE:HA	21:1Z:156:LYS:HZ1	1.83	0.44
28:16:34:LEU:H	28:16:51:GLU:HG2	1.83	0.44
32:1a:1014:A:H4'	50:1s:14:HIS:CE1	2.52	0.44
32:1a:1029:C:H41	32:1a:1030(A):G:N2	2.14	0.44
34:1c:113:ALA:HB3	34:1c:114:PRO:HD3	2.00	0.44
35:1d:107:ARG:HH22	35:1d:194:LEU:HD11	1.82	0.44
50:1s:80:TYR:C	50:1s:82:GLY:H	2.25	0.44
1:2A:112:U:H5'	24:22:65:ASN:ND2	2.32	0.44
1:2A:1507:A:O2'	1:2A:1508:A:H8	2.01	0.44
1:2A:2050:C:H1'	4:2E:156:MET:HE2	2.00	0.44
6:2G:173:LEU:HB3	6:2G:178:PHE:CD2	2.53	0.44
32:2a:737:A:H1'	37:2f:73:ASN:HD21	1.83	0.44
32:2a:980:C:H3'	32:2a:981:U:C6	2.52	0.44
32:2a:1000:U:H2'	32:2a:1001:A:C8	2.53	0.44
32:2a:1003:G:N2	32:2a:1025:U:C4	2.85	0.44
32:2a:1029:C:N3	32:2a:1032:G:C2	2.86	0.44
33:2b:9:GLU:O	33:2b:12:GLU:HG2	2.18	0.44
33:2b:43:ASP:OD2	33:2b:46:LYS:N	2.46	0.44
33:2b:91:PRO:HG2	33:2b:155:LEU:HD13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.43	0.44
1:1A:326:C:P	20:1Y:73:ARG:HH22	2.41	0.44
1:1A:556:C:H4'	1:1A:557:A:H5"	1.98	0.44
1:1A:895:G:H2'	1:1A:896:A:C8	2.53	0.44
1:1A:937:A:H2'	1:1A:938:G:O4'	2.17	0.44
1:1A:1115:A:H2'	1:1A:1119:A:N7	2.32	0.44
1:1A:2291:G:O6	22:10:14:ARG:HG3	2.18	0.44
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.98	0.44
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.83	0.44
32:1a:629:G:H2'	32:1a:630:G:O4'	2.18	0.44
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.53	0.44
38:1g:28:ASN:HD21	38:1g:36:LYS:NZ	2.15	0.44
1:2A:674:G:H1'	5:2F:74:ARG:HD3	2.00	0.44
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.52	0.44
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.98	0.44
13:2R:24:GLN:NE2	13:2R:36:THR:HG21	2.32	0.44
26:24:49:PHE:HB3	26:24:50:VAL:H	1.49	0.44
32:2a:444:C:H2'	32:2a:445:G:C8	2.44	0.44
32:2a:540:G:C6	32:2a:541:G:C5	3.06	0.44
32:2a:1350:A:N6	60:2a:3648:HOH:O	2.49	0.44
32:2a:1446:U:O2'	32:2a:1447:A:O5'	2.36	0.44
33:2b:18:GLY:HA3	33:2b:42:ILE:H	1.82	0.44
33:2b:95:GLN:HG3	33:2b:147:LYS:HE2	1.99	0.44
33:2b:127:ILE:O	33:2b:127:ILE:HG12	2.17	0.44
47:2p:69:THR:O	47:2p:73:LEU:HG	2.17	0.44
54:2w:68:C:H2'	54:2w:69:G:C8	2.49	0.44
1:1A:8:A:H2'	1:1A:9:U:C6	2.53	0.44
1:1A:1411:A:O2'	23:11:11:ARG:NH1	2.51	0.44
1:1A:1513:G:H2'	1:1A:1594:C:H41	1.83	0.44
1:1A:1997:G:H2'	1:1A:1998:U:O4'	2.17	0.44
1:1A:2371:C:H2'	1:1A:2372:A:O4'	2.18	0.44
5:1F:158:THR:OG1	5:1F:195:ASP:OD2	2.31	0.44
7:1H:55:PRO:HG2	7:1H:61:HIS:ND1	2.32	0.44
13:1R:103:ARG:HD3	13:1R:108:GLY:O	2.18	0.44
32:1a:881:G:H2'	32:1a:882:C:O4'	2.18	0.44
34:1c:108:ASN:HB3	34:1c:111:LEU:HD12	2.00	0.44
35:1d:88:VAL:HG12	35:1d:91:SER:H	1.83	0.44
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.18	0.44
54:1y:58:A:O2'	54:1y:59:U:OP1	2.33	0.44
1:2A:892:G:H3'	1:2A:893:C:C5'	2.47	0.44
1:2A:1137:G:H2'	1:2A:1138:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2542:A:H4'	1:2A:2543:G:C8	2.53	0.44
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.53	0.44
2:2B:33:G:N3	2:2B:50:G:N2	2.66	0.44
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.82	0.44
3:2D:133:LEU:HB3	3:2D:173:VAL:HG11	1.99	0.44
4:2E:108:SER:HB3	4:2E:165:VAL:CG2	2.47	0.44
7:2H:45:VAL:HG12	7:2H:50:VAL:HG22	1.99	0.44
20:2Y:52:SER:HB2	20:2Y:53:PRO:HD2	2.00	0.44
32:2a:688:G:H2'	32:2a:689:C:H6	1.82	0.44
32:2a:967:5MC:H2'	32:2a:968:A:N7	2.33	0.44
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.33	0.44
39:2h:33:GLU:O	39:2h:36:LEU:N	2.51	0.44
1:1A:1117:G:H1'	1:1A:1135:G:H2'	1.99	0.44
1:1A:1634:C:H2'	1:1A:1635:C:H6	1.82	0.44
18:1W:19:LEU:HB3	27:15:25:LEU:HD11	2.00	0.44
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.50	0.44
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.18	0.44
35:1d:196:LEU:HD12	35:1d:196:LEU:H	1.82	0.44
54:1w:60:U:H5"	54:1w:61:C:H5	1.83	0.44
1:2A:11:G:H2'	1:2A:12:U:H5'	1.99	0.44
1:2A:1664:A:OP1	60:2A:5119:HOH:O	2.21	0.44
2:2B:18:G:O2'	2:2B:19:G:H5'	2.18	0.44
5:2F:155:LEU:HB2	5:2F:189:THR:HG21	2.00	0.44
7:2H:56:SER:OG	7:2H:57:ASP:N	2.50	0.44
7:2H:103:LEU:HD21	7:2H:105:LEU:HD21	2.00	0.44
21:2Z:126:VAL:HG13	21:2Z:161:VAL:HG23	2.00	0.44
32:2a:76:C:N4	32:2a:93:G:H1	2.16	0.44
32:2a:583:A:H2'	32:2a:584:G:O4'	2.17	0.44
32:2a:954:G:H2'	32:2a:955:U:C6	2.53	0.44
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.33	0.44
39:2h:91:ARG:HD3	48:2q:32:TYR:O	2.17	0.44
44:2m:44:ARG:O	44:2m:48:LEU:HG	2.17	0.44
47:2p:14:ASN:OD1	47:2p:42:ARG:NH2	2.50	0.44
48:2q:19:VAL:HG23	48:2q:44:ALA:HB3	2.00	0.44
54:2w:10:G:N2	54:2w:11:C:C2	2.85	0.44
55:2x:20:U:O2	55:2x:20:U:H2'	2.18	0.44
55:2x:50:U:H3	55:2x:64:G:H1	1.64	0.44
54:2y:63:G:H2'	54:2y:64:A:O4'	2.18	0.44
1:1A:71:U:H5'	24:12:61:LEU:HD12	1.99	0.43
1:1A:791:G:OP1	4:1E:132:HIS:ND1	2.41	0.43
1:1A:929:G:H4'	54:1w:19:G:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1149:A:H8	1:1A:1149:A:OP2	2.00	0.43
1:1A:2735:G:H2'	1:1A:2736:C:C6	2.53	0.43
2:1B:66:A:N6	2:1B:109:C:H5'	2.30	0.43
14:1S:27:SER:HA	14:1S:88:ASP:HB3	2.00	0.43
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.82	0.43
32:1a:640:A:C5	32:1a:641:U:C4	3.06	0.43
32:1a:964:A:OP1	60:1a:2017:HOH:O	2.21	0.43
32:1a:1509:C:H2'	32:1a:1510:U:O4'	2.18	0.43
36:1e:78:HIS:CD2	39:1h:104:ARG:HH11	2.36	0.43
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.53	0.43
1:2A:218:A:C2	1:2A:235:U:H4'	2.52	0.43
1:2A:601:C:O2'	5:2F:104:LYS:NZ	2.49	0.43
1:2A:910:A:N3	1:2A:2264:C:O2'	2.40	0.43
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.18	0.43
1:2A:2131:G:N7	1:2A:2133:G:C2	2.86	0.43
1:2A:2168:G:H8	1:2A:2170:A:N7	2.16	0.43
2:2B:17:C:H2'	2:2B:18:G:O4'	2.18	0.43
2:2B:24:G:N2	2:2B:27:C:N3	2.59	0.43
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.18	0.43
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.26	0.43
11:2P:128:HIS:NE2	11:2P:148:LEU:HD11	2.33	0.43
12:2Q:103:MET:HE1	12:2Q:125:LEU:HD13	1.99	0.43
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.81	0.43
32:2a:54:C:N4	32:2a:353:A:OP2	2.42	0.43
32:2a:600:C:H2'	32:2a:601:C:C6	2.53	0.43
32:2a:742:G:P	46:2o:35:ARG:HH22	2.40	0.43
32:2a:1047:G:HO2'	32:2a:1215:G:HO2'	1.58	0.43
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.53	0.43
33:2b:87:ARG:HH11	33:2b:219:VAL:HG12	1.83	0.43
35:2d:76:ARG:O	35:2d:80:GLU:HG2	2.18	0.43
51:2t:43:LEU:O	51:2t:47:GLY:N	2.38	0.43
1:1A:2051:G:H2'	1:1A:2053:A:OP1	2.17	0.43
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.17	0.43
8:1I:135:GLU:C	8:1I:137:PRO:HD3	2.43	0.43
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.17	0.43
32:1a:93:G:H2'	32:1a:96:U:O4'	2.18	0.43
32:1a:160:A:H2'	32:1a:161:A:O4'	2.18	0.43
32:1a:166:G:H2'	32:1a:167:G:H8	1.84	0.43
32:1a:974:A:H8	32:1a:974:A:OP1	2.01	0.43
32:1a:1142:G:H2'	32:1a:1143:G:O4'	2.18	0.43
32:1a:1182:G:H4'	32:1a:1183:A:H5"	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1191:A:H5"	34:1c:4:LYS:NZ	2.33	0.43
33:1b:98:LEU:O	33:1b:101:MET:HG3	2.18	0.43
54:1y:18:G:H1	54:1y:55:PSU:H1'	1.82	0.43
54:1y:41:C:H2'	54:1y:42:C:C6	2.52	0.43
1:2A:93:G:H2'	1:2A:94:C:H6	1.81	0.43
1:2A:652(B):A:H61	1:2A:655:A:H1'	1.82	0.43
1:2A:2010:G:H5"	18:2W:42:ARG:HB2	2.00	0.43
1:2A:2018:G:H2'	1:2A:2019:A:O4'	2.18	0.43
1:2A:2311:A:O2'	1:2A:2312:U:O4'	2.32	0.43
1:2A:2343:C:O3'	1:2A:2373:G:H4'	2.18	0.43
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.52	0.43
1:2A:2745:C:C4	1:2A:2746:U:C4	3.06	0.43
1:2A:2787:C:H2'	1:2A:2788:C:H6	1.84	0.43
2:2B:3:C:H2'	2:2B:4:C:C6	2.54	0.43
6:2G:41:GLN:NE2	6:2G:153:ARG:HB3	2.33	0.43
6:2G:70:VAL:HA	6:2G:90:LEU:HD23	1.99	0.43
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.43	0.43
10:2O:7:TYR:CZ	10:2O:44:LYS:HG3	2.54	0.43
15:2T:73:GLU:OE2	15:2T:103:ARG:NE	2.37	0.43
15:2T:105:LEU:HB2	15:2T:110:ILE:HG13	2.00	0.43
22:20:38:VAL:HG11	22:20:45:PHE:HD2	1.83	0.43
26:24:60:GLN:O	26:24:62:ARG:HG2	2.18	0.43
32:2a:163:C:H2'	32:2a:164:U:C6	2.53	0.43
32:2a:165:C:H2'	32:2a:166:G:C8	2.53	0.43
32:2a:174:C:H2'	32:2a:175:C:H6	1.83	0.43
32:2a:1000:U:O2	32:2a:1041:A:N1	2.51	0.43
32:2a:1077:G:N1	32:2a:1080:A:OP2	2.49	0.43
32:2a:1080:A:H5"	32:2a:1081:G:OP2	2.18	0.43
33:2b:17:PHE:HB2	33:2b:44:LEU:HD11	2.00	0.43
34:2c:120:VAL:HG13	34:2c:133:ALA:HB1	2.00	0.43
39:2h:20:TYR:HD1	39:2h:65:TYR:CD1	2.35	0.43
40:2i:18:PHE:O	40:2i:61:ALA:HA	2.18	0.43
43:2l:6:THR:HG23	43:2l:9:GLN:OE1	2.18	0.43
54:2y:18:G:O6	54:2y:55:PSU:H1'	2.18	0.43
1:1A:1212:C:H2'	1:1A:1213:U:C6	2.54	0.43
1:1A:2190:G:O6	1:1A:2193:A:H5"	2.18	0.43
1:1A:2198:A:H2'	1:1A:2199:C:C6	2.53	0.43
5:1F:32:LEU:HD13	5:1F:112:MET:HE1	1.99	0.43
11:1P:121:LYS:O	11:1P:123:LEU:N	2.51	0.43
21:1Z:158:PRO:HA	21:1Z:159:PRO:HD3	1.93	0.43
32:1a:345:C:H5'	32:1a:346:G:C4	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:626:U:H2'	32:1a:627:G:H8	1.83	0.43
53:1v:14:A:H2'	53:1v:14:A:N3	2.33	0.43
1:2A:118:A:N3	1:2A:178:G:H1'	2.33	0.43
1:2A:848:G:C4	1:2A:933:A:C8	3.05	0.43
1:2A:1171:G:N2	1:2A:1178:C:C4	2.86	0.43
1:2A:1529:G:O6	1:2A:1530:C:N4	2.51	0.43
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.51	0.43
1:2A:1945:G:O6	1:2A:1960:A:N6	2.52	0.43
1:2A:2065:C:H4'	1:2A:2251:OMG:HM22	2.00	0.43
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.53	0.43
1:2A:2752:C:H6	1:2A:2752:C:O5'	2.02	0.43
3:2D:227:ASN:C	3:2D:234:GLY:HA3	2.44	0.43
7:2H:3:ARG:HH12	7:2H:5:GLY:CA	2.30	0.43
7:2H:97:ARG:O	7:2H:103:LEU:HD12	2.18	0.43
26:24:12:ALA:CB	26:24:26:SER:HB3	2.49	0.43
26:24:41:PRO:HG3	26:24:49:PHE:CZ	2.53	0.43
32:2a:108:G:N1	51:2t:15:ARG:HG2	2.32	0.43
32:2a:1134:G:H1	32:2a:1140:C:N4	2.12	0.43
32:2a:1261:A:C8	32:2a:1275:A:C6	3.06	0.43
32:2a:1272:G:N2	32:2a:1273:G:C8	2.73	0.43
32:2a:1307:U:O5'	32:2a:1307:U:H6	2.01	0.43
33:2b:77:ALA:HA	33:2b:80:ILE:HG22	1.99	0.43
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	1.99	0.43
46:2o:43:LEU:HD12	46:2o:56:LEU:HD22	1.99	0.43
55:2x:21:A:N6	55:2x:46:G:N3	2.66	0.43
1:1A:44:G:H5"	1:1A:45:C:OP1	2.17	0.43
1:1A:333:G:N3	1:1A:353:G:O2'	2.46	0.43
1:1A:1071:G:O2'	60:1A:4871:HOH:O	2.09	0.43
1:1A:1104:G:H1	1:1A:1126:C:N4	2.13	0.43
1:1A:2874:G:OP1	15:1T:119:LYS:HD2	2.19	0.43
60:1A:5923:HOH:O	9:1N:73:THR:HG21	2.18	0.43
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	2.01	0.43
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.53	0.43
32:1a:509:A:O2'	32:1a:510:A:OP1	2.29	0.43
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.33	0.43
51:1t:16:HIS:O	51:1t:19:SER:OG	2.29	0.43
1:2A:171:G:H2'	1:2A:172:C:C6	2.53	0.43
1:2A:990:A:N6	1:2A:1186:G:H1'	2.34	0.43
1:2A:1155:A:OP1	16:2U:55:ARG:HD2	2.19	0.43
1:2A:1913:A:H4'	1:2A:1914:C:C5'	2.49	0.43
1:2A:2193:G:H2'	1:2A:2194:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:124:GLY:N	8:2I:144:VAL:HG23	2.32	0.43
16:2U:66:ASN:OD1	16:2U:70:ARG:NE	2.48	0.43
19:2X:55:ASN:O	19:2X:79:ALA:HA	2.18	0.43
32:2a:458:C:H2'	32:2a:460:G:O4'	2.18	0.43
32:2a:783:C:H2'	32:2a:784:C:C6	2.52	0.43
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.50	0.43
32:2a:1029:C:C4	32:2a:1032:G:C2	3.06	0.43
32:2a:1070:U:H2'	32:2a:1071:C:H6	1.83	0.43
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.53	0.43
33:2b:53:ARG:HA	33:2b:56:ARG:HH11	1.84	0.43
33:2b:101:MET:HG2	33:2b:108:ILE:HG21	2.00	0.43
33:2b:164:VAL:HB	33:2b:186:ALA:CB	2.49	0.43
36:2e:108:ALA:O	36:2e:112:LEU:HG	2.17	0.43
42:2k:38:ASN:HA	42:2k:39:PRO:HD3	1.80	0.43
1:1A:237:G:OP1	60:1A:6419:HOH:O	2.21	0.43
1:1A:1098:C:H2'	1:1A:1099:C:H6	1.83	0.43
1:1A:1825:U:H2'	1:1A:1826:C:C6	2.54	0.43
1:1A:2137:G:C2	1:1A:2139:A:N7	2.87	0.43
1:1A:2164:C:O2	1:1A:2171:G:N1	2.35	0.43
1:1A:2641:A:HO2'	1:1A:2642:G:P	2.40	0.43
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.99	0.43
32:1a:1278:U:H5'	32:1a:1279:A:C5'	2.49	0.43
33:1b:76:GLN:OE1	33:1b:76:GLN:N	2.48	0.43
39:1h:7:ALA:HB2	39:1h:85:ARG:HG3	2.00	0.43
40:1i:15:ALA:HB2	40:1i:65:VAL:HG13	2.00	0.43
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.52	0.43
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.17	0.43
1:2A:990:A:C6	1:2A:1186:G:H1'	2.54	0.43
1:2A:1324:G:C2	1:2A:1331:A:C2	3.07	0.43
1:2A:1746:G:C2	1:2A:1747:G:C8	3.06	0.43
1:2A:2489:G:O2'	1:2A:2490:G:H5'	2.19	0.43
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.54	0.43
5:2F:126:VAL:HG21	5:2F:129:PHE:CE1	2.53	0.43
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.99	0.43
7:2H:155:SER:HB3	7:2H:158:HIS:O	2.18	0.43
17:2V:24:LYS:HG3	17:2V:64:HIS:HD2	1.82	0.43
21:2Z:145:GLU:HG3	21:2Z:146:ILE:N	2.33	0.43
23:21:52:ARG:HH21	23:21:57:GLU:HB2	1.83	0.43
32:2a:202:U:H3'	32:2a:203:U:C6	2.53	0.43
32:2a:259:G:OP2	51:2t:83:ARG:NH1	2.51	0.43
32:2a:461:A:O2'	32:2a:470:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1002:G:N2	32:2a:1038:C:N3	2.53	0.43
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.52	0.43
32:2a:1240:U:N3	38:2g:30:ILE:O	2.48	0.43
34:2c:22:TRP:CH2	34:2c:32:LEU:HB3	2.53	0.43
36:2e:41:VAL:O	36:2e:67:VAL:HG12	2.18	0.43
40:2i:7:THR:O	40:2i:83:ARG:NH1	2.51	0.43
45:2n:29:ARG:HD3	45:2n:40:CYS:CB	2.49	0.43
54:2w:10:G:H2'	54:2w:11:C:C6	2.54	0.43
1:1A:2402:U:P	30:18:35:GLN:HE22	2.42	0.43
6:1G:34:LEU:HD23	6:1G:161:THR:HG22	2.01	0.43
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.19	0.43
23:11:50:ARG:HG2	23:11:59:THR:HG22	2.01	0.43
32:1a:35:G:O2'	43:1l:118:SER:O	2.33	0.43
32:1a:540:G:H2'	32:1a:541:G:O4'	2.18	0.43
32:1a:1003:G:C4	32:1a:1004:A:H2	2.37	0.43
35:1d:103:ASN:OD1	35:1d:114:ARG:NE	2.36	0.43
47:1p:19:ILE:N	47:1p:37:GLY:O	2.51	0.43
1:2A:108:U:H2'	1:2A:109:G:C8	2.51	0.43
1:2A:208:C:H2'	1:2A:209:C:H6	1.82	0.43
1:2A:589:C:H2'	1:2A:590:A:C8	2.54	0.43
1:2A:643:A:C8	28:26:44:ARG:NH1	2.87	0.43
1:2A:1226:A:OP1	17:2V:84:LYS:NZ	2.32	0.43
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.17	0.43
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	2.02	0.43
1:2A:2061:G:H5"	1:2A:2503:2MA:C2	2.49	0.43
1:2A:2110:G:H3'	1:2A:2111:C:H5'	2.00	0.43
1:2A:2149:G:C6	1:2A:2150:U:C2	3.07	0.43
5:2F:37:VAL:O	5:2F:41:LEU:HG	2.18	0.43
32:2a:743:U:H2'	32:2a:744:C:C6	2.53	0.43
32:2a:1004:A:H5"	32:2a:1024:G:H22	1.84	0.43
32:2a:1060:C:C5'	41:2j:51:ARG:HG2	2.47	0.43
32:2a:1188:A:H2'	32:2a:1189:C:O4'	2.19	0.43
32:2a:1228:C:H2'	32:2a:1229:A:H8	1.84	0.43
33:2b:153:ARG:HE	33:2b:153:ARG:HB2	1.67	0.43
34:2c:127:ARG:HH22	34:2c:192:THR:HG23	1.84	0.43
39:2h:20:TYR:HE2	39:2h:75:ARG:HD2	1.83	0.43
41:2j:9:ARG:NH2	41:2j:69:ASN:HD21	2.17	0.43
43:2l:110:VAL:HG23	43:2l:120:TYR:HB3	2.01	0.43
44:2m:82:MET:HE3	44:2m:92:HIS:HB3	1.99	0.43
50:2s:64:GLU:H	50:2s:64:GLU:CD	2.26	0.43
55:2x:31:G:H2'	55:2x:32:5MC:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1537:G:O2'	3:1D:101:GLU:HB2	2.18	0.43
1:1A:1566:U:H2'	1:1A:1567:G:O4'	2.18	0.43
1:1A:2314:G:C2	1:1A:2327:G:C2	3.07	0.43
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.17	0.43
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	2.01	0.43
7:1H:25:LYS:HG3	7:1H:34:GLU:HG2	2.00	0.43
7:1H:61:HIS:O	7:1H:65:HIS:HB2	2.19	0.43
27:15:46:CYS:SG	27:15:48:GLU:HB2	2.59	0.43
31:19:32:HIS:O	31:19:34:GLN:HG3	2.18	0.43
32:1a:399:G:H2'	32:1a:400:C:C6	2.54	0.43
32:1a:892:A:O2'	32:1a:1415:G:H4'	2.19	0.43
32:1a:1437:C:H2'	32:1a:1438:G:C8	2.53	0.43
33:1b:178:ARG:NH2	39:1h:74:PRO:HB3	2.33	0.43
48:1q:32:TYR:O	48:1q:34:LYS:N	2.46	0.43
50:1s:27:GLU:OE1	50:1s:27:GLU:N	2.34	0.43
1:2A:37:C:H4'	1:2A:451:C:OP1	2.18	0.43
1:2A:613:G:O2'	1:2A:614(C):A:N1	2.50	0.43
1:2A:874:G:H5'	1:2A:875:G:OP2	2.19	0.43
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.54	0.43
1:2A:2321:G:N3	1:2A:2321:G:H2'	2.34	0.43
1:2A:2629:A:H1'	1:2A:2630:G:H5"	2.01	0.43
12:2Q:73:PRO:HA	12:2Q:93:TYR:CD1	2.53	0.43
32:2a:580:U:H2'	32:2a:581:G:O4'	2.18	0.43
32:2a:586:C:O2'	32:2a:878:G:H4'	2.19	0.43
32:2a:952:U:O2'	32:2a:965:A:N6	2.47	0.43
32:2a:1291:G:C6	32:2a:1292:U:C4	3.06	0.43
42:2k:44:SER:OG	42:2k:47:VAL:HG23	2.19	0.43
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.33	0.43
54:2w:63:G:H2'	54:2w:64:A:H5"	2.01	0.43
1:1A:905:U:O2	1:1A:2280:A:H2'	2.18	0.43
1:1A:1512:G:O2'	1:1A:1592:A:N1	2.51	0.43
1:1A:1908:C:O5'	1:1A:1908:C:H6	2.01	0.43
1:1A:2158:C:C2	1:1A:2177:G:N2	2.86	0.43
1:1A:2283:G:OP1	22:10:18:ALA:HB1	2.18	0.43
7:1H:58:GLU:O	7:1H:62:LYS:HG3	2.18	0.43
11:1P:55:ARG:NH1	60:1P:315:HOH:O	2.52	0.43
32:1a:431:A:H2'	32:1a:432:A:O4'	2.19	0.43
32:1a:1009:G:O6	32:1a:1020:U:C2	2.69	0.43
32:1a:1028:C:C2	32:1a:1029:C:H1'	2.54	0.43
35:1d:138:TYR:HE2	35:1d:140:VAL:HA	1.83	0.43
35:1d:142:PRO:HA	35:1d:185:PHE:HD2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:19:LEU:HD21	44:1m:56:LEU:HD21	1.99	0.43
51:1t:13:LEU:HD12	51:1t:14:LYS:H	1.83	0.43
54:1w:1:G:H2'	54:1w:2:C:C6	2.54	0.43
1:2A:116:C:H2'	1:2A:117:G:O4'	2.19	0.43
1:2A:923:C:C4'	22:20:29:GLN:HE21	2.31	0.43
1:2A:932:G:H4'	1:2A:933:A:O5'	2.18	0.43
1:2A:1204:A:N6	1:2A:1240:U:H2'	2.33	0.43
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.18	0.43
1:2A:1799:G:O2'	3:2D:183:ARG:NH1	2.49	0.43
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.19	0.43
1:2A:2094:G:OP1	8:2I:22:LYS:HD2	2.19	0.43
1:2A:2516:G:O6	1:2A:2517:C:N4	2.51	0.43
6:2G:16:ARG:HB2	6:2G:17:PRO:HD3	2.01	0.43
14:2S:5:THR:OG1	14:2S:8:GLU:HG2	2.18	0.43
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.60	0.43
21:2Z:6:LYS:HE3	21:2Z:8:TYR:HE2	1.83	0.43
32:2a:292:G:N7	32:2a:293:G:H1'	2.33	0.43
32:2a:685:G:C2	32:2a:686:U:C4	3.07	0.43
32:2a:1085:U:H3'	32:2a:1086:U:H6	1.84	0.43
32:2a:1278:U:H5'	32:2a:1279:A:H5'	2.00	0.43
35:2d:150:GLU:H	35:2d:150:GLU:HG3	1.53	0.43
36:2e:9:LYS:HB2	36:2e:112:LEU:HD11	1.99	0.43
36:2e:127:ASN:HA	36:2e:128:PRO:HD3	1.87	0.43
51:2t:50:GLU:HB2	51:2t:99:LEU:CD2	2.48	0.43
54:2w:7:A:N1	54:2w:66:U:O4	2.51	0.43
1:1A:1806:U:OP1	1:1A:2001:C:O2'	2.30	0.43
1:1A:2160:C:C2	1:1A:2176:G:C2	3.06	0.43
1:1A:2162:C:O2	1:1A:2174:G:N2	2.52	0.43
1:1A:2315:G:O6	60:1A:5145:HOH:O	2.20	0.43
29:17:20:ALA:HA	29:17:23:ARG:HH21	1.84	0.43
32:1a:520:A:N1	32:1a:536:C:H1'	2.34	0.43
32:1a:583:A:H2'	32:1a:584:G:O4'	2.19	0.43
32:1a:936:C:H2'	32:1a:937:A:O4'	2.18	0.43
32:1a:1057:G:H2'	32:1a:1058:G:O4'	2.19	0.43
32:1a:1080:A:OP1	36:1e:47:LYS:HD3	2.19	0.43
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.54	0.43
46:1o:61:GLY:O	46:1o:65:ARG:HG3	2.19	0.43
51:1t:36:LEU:HD12	51:1t:62:LEU:HD12	2.01	0.43
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.54	0.43
1:2A:783:A:O2'	1:2A:785:G:OP1	2.30	0.43
1:2A:1260:G:C6	1:2A:1261:C:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1411:C:N4	1:2A:1591:G:H1	2.14	0.43
1:2A:1496:A:OP2	1:2A:1496:A:H8	2.02	0.43
1:2A:1589:C:H2'	1:2A:1590:U:C6	2.54	0.43
1:2A:1776:G:O6	60:2A:4213:HOH:O	2.21	0.43
1:2A:2432:A:C6	1:2A:2433:A:C6	3.07	0.43
7:2H:157:TYR:CE1	7:2H:172:LYS:HG3	2.54	0.43
15:2T:119:LYS:O	15:2T:123:GLN:HG3	2.19	0.43
21:2Z:40:ASP:OD2	21:2Z:43:GLU:HG3	2.18	0.43
24:22:7:ARG:O	24:22:11:GLU:HG3	2.19	0.43
25:23:7:LYS:NZ	25:23:32:GLN:O	2.42	0.43
32:2a:839:U:H3'	32:2a:840:C:H6	1.84	0.43
32:2a:1040:U:C2	32:2a:1041:A:C8	3.07	0.43
34:2c:155:GLY:O	34:2c:157:ILE:N	2.50	0.43
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	2.00	0.43
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	2.00	0.43
41:2j:47:PHE:CE2	41:2j:65:LEU:HB2	2.54	0.43
1:1A:989:G:O3'	60:1A:4831:HOH:O	2.21	0.43
1:1A:1132:A:H5'	1:1A:1133:G:OP1	2.19	0.43
1:1A:1312:G:O2'	1:1A:2034:G:O6	2.36	0.43
1:1A:2802:C:O2'	1:1A:2803:A:H4'	2.18	0.43
3:1D:96:HIS:CD2	3:1D:102:LYS:HE2	2.54	0.43
10:1O:1:MET:HE2	10:1O:1:MET:HB3	1.92	0.43
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.37	0.43
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HG3	2.00	0.43
25:13:5:LYS:NZ	25:13:34:GLU:OE2	2.41	0.43
32:1a:134:A:N1	47:1p:25:ARG:NH1	2.67	0.43
32:1a:374:A:C6	32:1a:375:U:C4	3.07	0.43
32:1a:448:A:C4	32:1a:487:A:C2	3.06	0.43
32:1a:486:U:H2'	32:1a:487:A:C8	2.54	0.43
32:1a:895:G:H2'	32:1a:896:C:C6	2.54	0.43
32:1a:1194:U:H2'	32:1a:1195:C:C6	2.54	0.43
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	2.00	0.43
38:1g:28:ASN:HD21	38:1g:36:LYS:HZ1	1.66	0.43
46:1o:60:VAL:O	46:1o:64:ARG:HB2	2.19	0.43
46:1o:74:ASP:OD2	46:1o:77:ARG:NH1	2.50	0.43
49:1r:58:LEU:HD22	49:1r:62:GLU:HB3	2.00	0.43
1:2A:752:A:P	29:27:3:ARG:HH22	2.42	0.43
1:2A:800:A:H8	1:2A:800:A:OP1	2.01	0.43
1:2A:1857:G:C6	1:2A:1858:G:C6	3.07	0.43
1:2A:1923:U:H2'	1:2A:1924:C:C6	2.54	0.43
1:2A:2125:G:H1'	1:2A:2173:A:N6	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.52	0.43
2:2B:25:A:H2'	2:2B:26:A:C8	2.54	0.43
2:2B:64:C:H2'	2:2B:65:C:C6	2.54	0.43
6:2G:125:PHE:CE2	6:2G:170:ARG:HD3	2.53	0.43
7:2H:69:ARG:O	7:2H:73:ALA:N	2.30	0.43
8:2I:79:ILE:HA	8:2I:80:PRO:HD2	1.92	0.43
9:2N:35:ARG:HB2	9:2N:37:LYS:HG3	2.00	0.43
21:2Z:145:GLU:HB3	21:2Z:148:ASP:CG	2.43	0.43
30:28:14:VAL:HG13	30:28:22:VAL:HG13	2.01	0.43
32:2a:657:G:H4'	46:2o:28:GLN:HG3	2.00	0.43
32:2a:979:C:N4	32:2a:1360:A:H62	2.17	0.43
32:2a:1411:C:H2'	32:2a:1412:C:H6	1.83	0.43
34:2c:6:HIS:CD2	34:2c:8:ILE:H	2.36	0.43
54:2y:18:G:H5'	60:2y:3105:HOH:O	2.19	0.43
1:1A:354:A:HO2'	1:1A:355:A:H8	1.65	0.42
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.84	0.42
1:1A:2121:U:O2	1:1A:2212:G:N2	2.34	0.42
1:1A:2800:C:H1'	4:1E:62:PRO:HG3	2.01	0.42
5:1F:178:PRO:HB2	5:1F:201:VAL:HG21	2.00	0.42
8:1I:116:LEU:HD21	8:1I:119:PRO:HA	1.99	0.42
36:1e:102:ALA:O	36:1e:107:ARG:NH2	2.52	0.42
36:1e:122:GLU:O	36:1e:126:ARG:NH1	2.45	0.42
43:1l:113:ARG:O	43:1l:114:LYS:HD3	2.20	0.42
44:1m:29:ARG:HD3	44:1m:64:TRP:CE2	2.54	0.42
54:1y:52:G:H2'	54:1y:53:G:H8	1.84	0.42
1:2A:64:A:H2	19:2X:69:TYR:CD2	2.37	0.42
1:2A:729:G:OP1	3:2D:12:SER:HB2	2.19	0.42
1:2A:999:U:O2'	1:2A:1000:A:H5'	2.19	0.42
1:2A:1278:A:H2'	1:2A:1279:G:C8	2.54	0.42
1:2A:2558:C:H2'	1:2A:2559:C:O4'	2.18	0.42
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	2.01	0.42
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	1.99	0.42
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.18	0.42
14:2S:25:ARG:HG2	14:2S:40:ILE:HB	2.01	0.42
19:2X:60:ARG:HH22	29:27:47:ARG:NH1	2.17	0.42
21:2Z:100:VAL:HA	21:2Z:101:PRO:HD3	1.86	0.42
32:2a:826:C:H2'	32:2a:827:U:C6	2.54	0.42
32:2a:975:A:H5"	32:2a:1363(A):A:N6	2.34	0.42
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.83	0.42
48:2q:59:ILE:HD12	48:2q:71:PHE:HD2	1.83	0.42
54:2y:49:C:H1'	60:2y:3111:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.54	0.42
2:1B:7:G:N7	60:1B:3119:HOH:O	2.36	0.42
9:1N:67:LEU:HA	9:1N:87:LEU:HD22	2.01	0.42
16:1U:17:ILE:HG23	16:1U:39:LEU:HD12	2.00	0.42
32:1a:129:U:H5'	48:1q:3:LYS:NZ	2.34	0.42
32:1a:1030(C):G:H2'	32:1a:1030(D):A:C8	2.54	0.42
32:1a:1080:A:H5"	32:1a:1081:G:OP2	2.19	0.42
32:1a:1136:U:H5"	32:1a:1137:C:C5	2.54	0.42
32:1a:1359:C:OP1	45:1n:22:THR:OG1	2.34	0.42
35:1d:128:VAL:N	35:1d:131:ARG:O	2.52	0.42
37:1f:70:ASP:OD1	37:1f:70:ASP:N	2.38	0.42
38:1g:78:ARG:HD2	38:1g:156:TRP:CE3	2.54	0.42
50:1s:48:THR:HG22	50:1s:61:TYR:HA	2.01	0.42
1:2A:433:C:O2'	1:2A:434:U:H5'	2.19	0.42
1:2A:878:A:N6	1:2A:899:A:O2'	2.52	0.42
1:2A:1131:G:H8	1:2A:2025:C:H4'	1.84	0.42
1:2A:1630:G:H2'	1:2A:1631:C:C6	2.54	0.42
1:2A:1754:C:H5	15:2T:96:ARG:NH2	2.17	0.42
1:2A:2612:C:OP2	27:25:2:ALA:N	2.52	0.42
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.18	0.42
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.85	0.42
25:23:5:LYS:O	25:23:56:VAL:HA	2.18	0.42
32:2a:390:C:H2'	32:2a:391:G:C8	2.54	0.42
32:2a:779:C:H42	32:2a:803:G:H1	1.66	0.42
32:2a:832:C:N4	32:2a:833:U:C4	2.87	0.42
32:2a:1122:U:H3	32:2a:1151:A:H61	1.66	0.42
32:2a:1132:C:N4	32:2a:1142:G:H1	2.14	0.42
32:2a:1509:C:H2'	32:2a:1510:U:O4'	2.19	0.42
33:2b:134:GLU:O	33:2b:138:LEU:HG	2.19	0.42
33:2b:212:GLN:NE2	33:2b:235:SER:HA	2.34	0.42
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.84	0.42
35:2d:11:LEU:HD23	35:2d:66:ARG:HB3	2.02	0.42
41:2j:25:GLU:OE2	41:2j:29:ARG:NE	2.50	0.42
1:1A:651:U:O4	11:1P:107:LYS:HE2	2.19	0.42
1:1A:1477:U:H2'	1:1A:1478:C:C6	2.55	0.42
1:1A:2145:G:H2'	1:1A:2146:G:C8	2.54	0.42
4:1E:37:ARG:HA	4:1E:42:ASP:OD2	2.19	0.42
14:1S:90:GLY:HA3	14:1S:91:PRO:HD2	1.93	0.42
21:1Z:1:MET:HG3	21:1Z:55:HIS:ND1	2.33	0.42
24:12:61:LEU:HA	24:12:61:LEU:HD23	1.76	0.42
26:14:8:LYS:HE3	26:14:10:VAL:CG1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:63:TYR:N	26:14:63:TYR:CD1	2.87	0.42
32:1a:711:G:H2'	32:1a:712:A:C8	2.54	0.42
32:1a:864:A:H2'	32:1a:865:A:C8	2.54	0.42
32:1a:1004:A:N6	32:1a:1036:G:N2	2.67	0.42
37:1f:10:LEU:HD13	37:1f:61:LEU:HD13	2.00	0.42
1:2A:625:G:N7	11:2P:107:LYS:NZ	2.58	0.42
1:2A:1253:A:H4'	60:2A:4847:HOH:O	2.19	0.42
1:2A:1473:G:C6	1:2A:1474:C:C4	3.07	0.42
14:2S:4:LEU:HD23	14:2S:4:LEU:HA	1.81	0.42
14:2S:80:LEU:HA	14:2S:80:LEU:HD12	1.77	0.42
21:2Z:153:SER:O	21:2Z:155:LEU:N	2.52	0.42
32:2a:137:C:H2'	32:2a:138:G:C8	2.54	0.42
32:2a:840:C:H4'	32:2a:841:U:OP1	2.17	0.42
32:2a:981:U:H5'	45:2n:21:TYR:CE2	2.54	0.42
32:2a:1406:U:O2	32:2a:1517:G:N2	2.53	0.42
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.52	0.42
40:2i:23:ASN:HD21	40:2i:25:LYS:HG2	1.83	0.42
55:2x:28:C:H2'	55:2x:29:G:H8	1.84	0.42
1:1A:125:A:H5"	1:1A:126:C:C6	2.55	0.42
1:1A:469:A:H1'	1:1A:1246:C:O4'	2.19	0.42
1:1A:722:A:C8	1:1A:851:A:C6	3.07	0.42
1:1A:776:G:OP2	3:1D:13:ARG:NH2	2.41	0.42
1:1A:1756:U:H2'	1:1A:1757:C:C6	2.54	0.42
1:1A:2227:G:H5"	1:1A:2228:G:C5	2.55	0.42
5:1F:106:ARG:H	5:1F:106:ARG:HG2	1.50	0.42
21:1Z:123:ASP:OD1	21:1Z:123:ASP:N	2.52	0.42
32:1a:195:A:H4'	51:1t:68:LYS:HE3	2.01	0.42
32:1a:356:A:N3	32:1a:368:U:O2'	2.45	0.42
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.20	0.42
33:1b:12:GLU:O	33:1b:15:VAL:HG22	2.19	0.42
37:1f:55:ASP:HA	37:1f:56:PRO:HD2	1.87	0.42
44:1m:121:LYS:HB2	44:1m:121:LYS:HE2	1.72	0.42
1:2A:14:A:C6	1:2A:526:A:C2	3.07	0.42
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.53	0.42
1:2A:1328:G:H2'	1:2A:1330:C:C5	2.54	0.42
6:2G:107:LEU:HD21	6:2G:178:PHE:CE1	2.54	0.42
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	2.01	0.42
21:2Z:9:TYR:OH	21:2Z:63:ASP:OD2	2.23	0.42
21:2Z:99:TYR:HB3	21:2Z:123:ASP:CG	2.44	0.42
25:23:6:VAL:HA	25:23:56:VAL:HG22	2.00	0.42
26:24:12:ALA:HB3	26:24:26:SER:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:382:A:H2'	32:2a:383:A:C8	2.55	0.42
32:2a:509:A:H2'	32:2a:510:A:C8	2.55	0.42
32:2a:689:C:P	42:2k:46:GLY:HA3	2.59	0.42
33:2b:189:ASP:HB3	33:2b:204:ASN:HA	2.00	0.42
34:2c:9:GLY:N	45:2n:49:HIS:O	2.53	0.42
36:2e:84:PHE:N	36:2e:87:SER:O	2.51	0.42
42:2k:120:ARG:HA	42:2k:121:PRO:HD3	1.90	0.42
55:2x:43:A:H2'	55:2x:44:A:C8	2.54	0.42
1:1A:52:A:H2'	1:1A:53:G:O4'	2.19	0.42
1:1A:284:G:C2	1:1A:285:U:O4	2.72	0.42
1:1A:1122:C:O2'	1:1A:1123:A:N7	2.52	0.42
1:1A:1124:U:H5'	1:1A:1125:C:OP1	2.20	0.42
1:1A:1633:A:H2'	1:1A:1634:C:H6	1.84	0.42
1:1A:2177:G:H3'	1:1A:2178:G:H8	1.85	0.42
1:1A:2658:C:H2'	1:1A:2659:U:O4'	2.19	0.42
4:1E:14:ILE:HG13	4:1E:21:VAL:HG13	2.01	0.42
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.19	0.42
23:11:52:ARG:HD3	23:11:56:GLN:O	2.20	0.42
32:1a:194:C:H2'	32:1a:195:A:H5"	2.02	0.42
32:1a:376:G:OP2	47:1p:67:THR:HG21	2.19	0.42
32:1a:650:G:O2'	32:1a:651:C:H5'	2.20	0.42
32:1a:792:A:O2'	32:1a:794:A:N7	2.48	0.42
32:1a:1112:C:H1'	34:1c:179:ARG:HH11	1.83	0.42
32:1a:1124:G:H5"	41:1j:35:SER:OG	2.20	0.42
32:1a:1309:G:N7	44:1m:99:ARG:NH2	2.67	0.42
35:1d:170:VAL:HG12	35:1d:171:GLY:H	1.84	0.42
1:2A:478:A:N1	1:2A:500:G:H4'	2.34	0.42
1:2A:732:C:H2'	1:2A:733:G:O4'	2.20	0.42
1:2A:1354:A:O3'	3:2D:38:LYS:HE2	2.20	0.42
1:2A:1506:C:H2'	1:2A:1507:A:H5'	2.01	0.42
1:2A:2291:U:O2'	1:2A:2374:C:H1'	2.19	0.42
4:2E:110:GLY:HA2	4:2E:161:GLY:HA3	2.01	0.42
6:2G:150:ASP:OD1	6:2G:150:ASP:N	2.47	0.42
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.20	0.42
32:2a:241:C:C2	32:2a:286:G:C2	3.08	0.42
32:2a:406:G:H4'	35:2d:5:ILE:HD11	2.00	0.42
32:2a:1028:C:N3	32:2a:1033:G:C6	2.87	0.42
32:2a:1346:A:N6	32:2a:1375:A:OP2	2.42	0.42
32:2a:1371:G:C6	32:2a:1372:U:C4	3.08	0.42
35:2d:38:TYR:CE1	35:2d:45:GLN:HG3	2.55	0.42
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:76:ARG:HD3	38:2g:76:ARG:HA	1.79	0.42
43:2l:84:LEU:HD12	43:2l:85:ILE:H	1.84	0.42
44:2m:19:LEU:HD11	44:2m:56:LEU:HD21	2.00	0.42
44:2m:45:VAL:HA	44:2m:48:LEU:HD12	2.01	0.42
54:2y:7:A:N3	60:2y:3111:HOH:O	2.37	0.42
1:1A:1223:C:O5'	1:1A:1223:C:H6	2.02	0.42
1:1A:1550:C:H2'	1:1A:1551:C:C6	2.54	0.42
1:1A:2018:C:H4'	1:1A:2019:G:OP1	2.19	0.42
1:1A:2295:C:H2'	1:1A:2296:C:O4'	2.20	0.42
1:1A:2331:G:H22	14:1S:3:ARG:HA	1.85	0.42
5:1F:32:LEU:HD22	5:1F:112:MET:CE	2.50	0.42
5:1F:34:TRP:CH2	11:1P:8:PRO:HB3	2.54	0.42
21:1Z:17:ALA:HA	21:1Z:20:ARG:NH1	2.34	0.42
32:1a:1223:C:OP2	50:1s:78:ARG:NH2	2.49	0.42
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.20	0.42
41:1j:7:LYS:HE3	41:1j:9:ARG:NH1	2.34	0.42
54:1w:7:A:N6	54:1w:66:U:N3	2.36	0.42
1:2A:6:A:N3	9:2N:133:GLN:NE2	2.67	0.42
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.55	0.42
1:2A:612:C:C2	1:2A:616:G:N2	2.88	0.42
1:2A:778:G:C6	1:2A:779:U:N3	2.88	0.42
1:2A:1683:C:H2'	1:2A:1684:C:C6	2.54	0.42
1:2A:1987:G:H2'	1:2A:1988:C:H6	1.84	0.42
1:2A:2107:C:H5"	1:2A:2108:C:OP2	2.20	0.42
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.18	0.42
1:2A:2801(A):A:H5'	1:2A:2802:G:C8	2.54	0.42
5:2F:120:GLU:HG3	5:2F:122:LYS:HG2	2.01	0.42
12:2Q:31:ASP:HA	12:2Q:134:ARG:HH11	1.85	0.42
21:2Z:171:ILE:HD12	21:2Z:172:ALA:N	2.35	0.42
23:21:94:LEU:O	23:21:97:LEU:HB2	2.18	0.42
28:26:40:CYS:HA	28:26:41:PRO:HD3	1.92	0.42
32:2a:165:C:H2'	32:2a:166:G:H8	1.83	0.42
32:2a:221:C:H2'	32:2a:222:U:H6	1.85	0.42
32:2a:528:C:H5'	32:2a:529:G:OP2	2.20	0.42
32:2a:630:G:H2'	32:2a:631:G:H8	1.85	0.42
32:2a:731:G:H5'	32:2a:766:A:H4'	2.00	0.42
34:2c:164:ARG:HG2	34:2c:165:THR:N	2.35	0.42
55:2x:10:G:N2	55:2x:26:G:H1'	2.35	0.42
1:1A:27:G:C2	1:1A:537:G:N3	2.87	0.42
1:1A:1525:G:N2	1:1A:1562:U:C2	2.87	0.42
1:1A:2324:U:OP1	6:1G:73:ALA:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2760:G:O6	1:1A:2768:C:H5"	2.19	0.42
6:1G:5:VAL:HG12	26:14:25:TYR:CE2	2.55	0.42
7:1H:144:VAL:O	7:1H:148:ILE:HG13	2.19	0.42
28:16:14:THR:HG21	28:16:48:VAL:HG13	2.02	0.42
32:1a:68:G:H1	32:1a:101:A:H61	1.66	0.42
32:1a:428:G:OP2	35:1d:10:ARG:HD2	2.19	0.42
32:1a:501:C:H2'	32:1a:502:G:H8	1.84	0.42
32:1a:815:A:N7	32:1a:1509:C:O2'	2.45	0.42
32:1a:911:U:OP2	43:1l:97:ARG:NH2	2.52	0.42
35:1d:18:LYS:HD2	35:1d:20:TYR:CZ	2.54	0.42
37:1f:6:VAL:HG22	37:1f:90:VAL:HG22	2.01	0.42
42:1k:43:SER:HB3	42:1k:68:ALA:HB2	2.02	0.42
46:1o:74:ASP:CG	46:1o:77:ARG:HB2	2.45	0.42
54:1y:8:4SU:H4'	54:1y:48:C:C4'	2.49	0.42
1:2A:569:U:H1'	1:2A:947:G:O4'	2.20	0.42
1:2A:597:U:H2'	1:2A:598:G:H8	1.85	0.42
1:2A:879:G:C6	1:2A:880:G:C2	3.08	0.42
1:2A:988:A:H5"	25:23:31:LEU:HD11	2.02	0.42
1:2A:1006:C:C2	1:2A:1138:G:N2	2.88	0.42
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.53	0.42
1:2A:2526:G:H2'	1:2A:2527:C:H6	1.83	0.42
1:2A:2639:A:O3'	9:2N:97:ARG:NH2	2.47	0.42
2:2B:13:A:H4'	2:2B:15:A:C5	2.54	0.42
15:2T:22:PHE:CE1	15:2T:52:ILE:HD11	2.54	0.42
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.19	0.42
32:2a:57:G:H2'	32:2a:58:C:C6	2.54	0.42
32:2a:250:A:H4'	32:2a:251:G:O5'	2.20	0.42
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.32	0.42
32:2a:590:C:H2'	32:2a:591:U:C6	2.55	0.42
32:2a:997:U:O2	32:2a:1044:A:N1	2.53	0.42
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.54	0.42
32:2a:1010:G:N1	32:2a:1020:U:H1'	2.35	0.42
32:2a:1097:C:H1'	32:2a:1170:A:H1'	2.01	0.42
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.82	0.42
32:2a:1441:G:H8	32:2a:1441:G:O5'	2.03	0.42
33:2b:162:ILE:O	33:2b:185:ILE:HG12	2.19	0.42
39:2h:104:ARG:HD3	39:2h:104:ARG:HA	1.91	0.42
40:2i:85:LEU:O	40:2i:89:ASN:N	2.50	0.42
44:2m:101:GLN:OE1	44:2m:101:GLN:N	2.53	0.42
47:2p:19:ILE:N	47:2p:37:GLY:O	2.52	0.42
53:2v:14:A:H2'	53:2v:14:A:N3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:44:G:H2'	54:2w:45:U:H5'	2.01	0.42
1:1A:482:C:O2'	1:1A:483:A:OP2	2.35	0.42
1:1A:1478:C:H2'	1:1A:1479:U:O4'	2.20	0.42
1:1A:2132:G:H2'	1:1A:2132:G:OP2	2.19	0.42
1:1A:2541:G:H5"	1:1A:2542:A:H5"	2.02	0.42
1:1A:2623:U:H6	1:1A:2623:U:H5'	1.85	0.42
4:1E:1:MET:HE3	4:1E:199:ARG:HD2	2.01	0.42
4:1E:48:GLN:NE2	4:1E:78:LEU:HG	2.35	0.42
14:1S:110:LEU:HA	14:1S:110:LEU:HD12	1.72	0.42
19:1X:31:HIS:HA	19:1X:32:PRO:HD3	1.94	0.42
32:1a:377:G:P	47:1p:5:ARG:HH11	2.43	0.42
32:1a:977:A:H1'	32:1a:982:U:O4	2.19	0.42
37:1f:33:TYR:OH	37:1f:78:GLU:HG3	2.20	0.42
42:1k:18:ARG:HB2	42:1k:33:THR:OG1	2.19	0.42
1:2A:255:A:O2'	1:2A:384:U:OP1	2.21	0.42
1:2A:652(B):A:N6	1:2A:655:A:H1'	2.34	0.42
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.54	0.42
1:2A:854:G:N2	1:2A:924:C:N3	2.68	0.42
1:2A:881:G:H3'	1:2A:882:G:H8	1.84	0.42
1:2A:1124:C:H2'	1:2A:1125:G:O4'	2.20	0.42
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.20	0.42
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.19	0.42
1:2A:2428:G:H5"	1:2A:2429:G:OP1	2.20	0.42
4:2E:1:MET:O	4:2E:84:PHE:HB2	2.20	0.42
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HB3	2.35	0.42
22:20:48:GLY:HA3	22:20:80:HIS:CE1	2.55	0.42
26:24:34:GLU:HA	44:2m:57:ARG:CZ	2.49	0.42
32:2a:677:U:H1'	42:2k:119:CYS:SG	2.60	0.42
32:2a:1194:U:H2'	32:2a:1195:C:C6	2.55	0.42
36:2e:52:PRO:O	36:2e:56:GLN:HG3	2.19	0.42
41:2j:16:LEU:O	41:2j:20:ALA:N	2.50	0.42
49:2r:24:ALA:C	49:2r:26:LEU:H	2.28	0.42
54:2w:50:U:N3	54:2w:64:A:N6	2.26	0.42
54:2y:59:U:H3'	54:2y:60:U:O2	2.20	0.42
1:1A:223:C:H2'	1:1A:224:U:C6	2.55	0.42
1:1A:2209:G:C6	1:1A:2210:C:C4	3.07	0.42
4:1E:7:VAL:CG1	4:1E:27:LEU:HB3	2.50	0.42
7:1H:3:ARG:HH22	7:1H:65:HIS:HB3	1.85	0.42
32:1a:189(F):U:N3	48:1q:72:ARG:NH2	2.58	0.42
32:1a:192:U:H2'	32:1a:193:C:C6	2.54	0.42
32:1a:269:C:H2'	32:1a:270:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:106:PRO:O	36:1e:110:LEU:HG	2.19	0.42
38:1g:113:GLU:HG3	38:1g:118:VAL:HG12	2.02	0.42
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	2.01	0.42
54:1y:66:U:C4	54:1y:67:C:C4	3.07	0.42
1:2A:30:G:H2'	1:2A:31:C:O4'	2.19	0.42
1:2A:861:A:C2	1:2A:917:A:C4	3.07	0.42
1:2A:1470:G:H5"	1:2A:1471:A:OP1	2.19	0.42
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.20	0.42
1:2A:2363:C:O2	22:20:39:ARG:NH2	2.53	0.42
1:2A:2709:G:O2'	1:2A:2710:C:H5'	2.19	0.42
2:2B:13:A:H2'	2:2B:70:C:O2'	2.20	0.42
2:2B:38:C:O4'	14:2S:95:HIS:NE2	2.53	0.42
4:2E:108:SER:HB3	4:2E:165:VAL:HG21	2.01	0.42
32:2a:189(D):C:H2'	32:2a:189(E):U:O4'	2.19	0.42
32:2a:1120:G:C2	32:2a:1154:G:C2	3.08	0.42
32:2a:1122:U:C2	32:2a:1123:A:C8	3.08	0.42
35:2d:33:MET:HB2	59:2d:501:SF4:S2	2.60	0.42
35:2d:53:ASP:O	35:2d:57:ARG:HG3	2.20	0.42
52:2u:6:ARG:O	52:2u:12:LYS:HE3	2.20	0.42
54:2y:7:A:N6	54:2y:66:U:H3	2.16	0.42
1:1A:207:A:C2	1:1A:224:U:H4'	2.55	0.42
1:1A:698:G:H2'	1:1A:699:C:C6	2.55	0.42
1:1A:1016:C:H2'	1:1A:1017:G:O4'	2.19	0.42
1:1A:1402:G:OP2	60:1A:4902:HOH:O	2.21	0.42
1:1A:2142:G:O2'	1:1A:2143:G:H5'	2.20	0.42
1:1A:2672:A:H2'	1:1A:2673:G:O4'	2.20	0.42
2:1B:74:U:H2'	2:1B:75:G:O4'	2.20	0.42
4:1E:101:ARG:HD3	4:1E:170:LEU:C	2.45	0.42
22:10:82:ARG:HA	22:10:83:PRO:HD3	1.88	0.42
29:17:24:THR:HG22	29:17:26:GLY:H	1.85	0.42
30:18:29:LYS:HE2	30:18:45:GLY:HA2	2.00	0.42
32:1a:69:G:H2'	32:1a:70:G:H8	1.84	0.42
32:1a:69:G:H2'	32:1a:70:G:C8	2.54	0.42
32:1a:117:G:OP2	60:1a:2042:HOH:O	2.21	0.42
32:1a:576:G:O6	32:1a:880:C:O2'	2.30	0.42
32:1a:1129:C:OP1	40:1i:66:ARG:NH1	2.53	0.42
32:1a:1151:A:O4'	41:1j:39:PRO:HB2	2.20	0.42
54:1y:26:A:N6	54:1y:44:G:H1	2.18	0.42
1:2A:27:G:O2'	1:2A:28:A:OP2	2.36	0.42
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.20	0.42
1:2A:648:G:O2'	1:2A:2351:G:OP1	2.21	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:652(D):C:N4	1:2A:652(U):G:H1	2.17	0.42
1:2A:717:G:H2'	1:2A:718:A:O4'	2.20	0.42
1:2A:1042:G:H4'	1:2A:1042:G:OP1	2.19	0.42
1:2A:1490:A:O2'	3:2D:99:ASP:OD1	2.38	0.42
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.55	0.42
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	2.01	0.42
3:2D:275:LYS:HD2	3:2D:275:LYS:HA	1.92	0.42
6:2G:36:LYS:HD3	6:2G:95:ARG:HH12	1.84	0.42
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	2.01	0.42
16:2U:103:PRO:O	16:2U:107:ALA:N	2.53	0.42
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	2.02	0.42
21:2Z:70:LEU:HD23	21:2Z:70:LEU:HA	1.76	0.42
21:2Z:146:ILE:HG12	21:2Z:174:VAL:C	2.45	0.42
25:23:7:LYS:N	25:23:55:ARG:O	2.47	0.42
26:24:28:LYS:HA	26:24:29:PRO:HD3	1.79	0.42
32:2a:152:A:N6	32:2a:170:U:C2	2.88	0.42
32:2a:1030(A):G:N3	32:2a:1030(C):G:C8	2.88	0.42
33:2b:83:MET:O	33:2b:87:ARG:N	2.45	0.42
35:2d:3:ARG:HD3	35:2d:118:ARG:NE	2.34	0.42
36:2e:8:GLU:OE2	36:2e:63:ARG:NH2	2.48	0.42
40:2i:50:LEU:H	40:2i:50:LEU:HG	1.68	0.42
40:2i:63:ILE:HD13	40:2i:77:ILE:HG23	2.02	0.42
46:2o:48:LYS:HA	46:2o:48:LYS:HD3	1.76	0.42
51:2t:54:LYS:HE2	51:2t:54:LYS:HB3	1.83	0.42
55:2x:16:C:H5'	55:2x:59:A:N1	2.34	0.42
1:1A:200:A:H2'	1:1A:201:G:O4'	2.20	0.41
1:1A:1074:A:N6	1:1A:1171:G:H2'	2.35	0.41
1:1A:2116:G:P	8:1I:22:LYS:HD2	2.60	0.41
3:1D:19:ALA:HB3	3:1D:21:PHE:CE1	2.55	0.41
7:1H:90:LYS:HD3	7:1H:159:GLU:HG2	2.01	0.41
11:1P:59:LEU:HD23	30:18:13:ARG:HH11	1.85	0.41
20:1Y:43:ASN:HD22	20:1Y:43:ASN:HA	1.60	0.41
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.84	0.41
28:16:34:LEU:N	28:16:51:GLU:HG2	2.36	0.41
32:1a:79:G:C6	32:1a:90:U:C2	3.08	0.41
32:1a:1263:C:O2	32:1a:1273:G:N2	2.53	0.41
36:1e:52:PRO:HG2	36:1e:53:LEU:HD12	2.02	0.41
38:1g:69:VAL:HG22	38:1g:135:VAL:HG22	2.01	0.41
1:2A:853:G:C2	1:2A:854:G:C4	3.07	0.41
1:2A:1287:A:C5	1:2A:1288:U:C4	3.08	0.41
1:2A:1359:A:N1	1:2A:1372:U:C4	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1866:C:H2'	1:2A:1876:A:O4'	2.20	0.41
1:2A:2298:A:N3	1:2A:2321:G:C2	2.88	0.41
1:2A:2319:G:N2	14:2S:3:ARG:HA	2.35	0.41
1:2A:2507:C:H5"	1:2A:2573:C:C4	2.55	0.41
1:2A:2525:G:N2	1:2A:2539:C:C2	2.88	0.41
1:2A:2820:A:C5	13:2R:4:LEU:HD11	2.55	0.41
8:2I:62:LYS:HB2	8:2I:62:LYS:HE3	1.85	0.41
11:2P:121:LYS:O	11:2P:123:LEU:N	2.53	0.41
17:2V:84:LYS:O	17:2V:85:LYS:HD2	2.19	0.41
20:2Y:73:ARG:HH21	20:2Y:83:THR:C	2.27	0.41
23:21:89:GLU:O	23:21:93:GLU:HG2	2.20	0.41
29:27:5:TRP:CD1	29:27:7:PRO:HD3	2.55	0.41
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.19	0.41
32:2a:946:A:OP2	60:2a:3546:HOH:O	2.22	0.41
32:2a:1093:A:C4	32:2a:1095:U:H5'	2.55	0.41
32:2a:1288:A:N3	32:2a:1352:C:O2'	2.46	0.41
32:2a:1312:G:H1	32:2a:1325:C:H42	1.67	0.41
33:2b:130:ARG:HD3	33:2b:130:ARG:HA	1.82	0.41
1:1A:116:A:C8	1:1A:117:A:C8	3.08	0.41
1:1A:1073:A:C2	1:1A:2500:A:H5'	2.55	0.41
1:1A:1091:A:O2'	1:1A:1093:G:C4	2.67	0.41
1:1A:1553:A:O2'	1:1A:1556:A:N6	2.53	0.41
1:1A:1827:U:H2'	1:1A:1828:C:H6	1.85	0.41
1:1A:2346:G:H4'	1:1A:2347:A:OP2	2.20	0.41
1:1A:2564:2MU:O5'	1:1A:2564:2MU:H6	2.20	0.41
1:1A:2641:A:H1'	1:1A:2642:G:O5'	2.20	0.41
1:1A:2666:A:N1	1:1A:2677:A:H5"	2.35	0.41
1:1A:2764:G:H4'	7:1H:4:ILE:HD11	2.02	0.41
15:1T:118:ARG:HG2	32:1a:1442(A):G:C8	2.54	0.41
17:1V:21:ARG:NH1	17:1V:91:TYR:CZ	2.89	0.41
18:1W:73:ALA:HB3	18:1W:106:ILE:HD12	2.02	0.41
25:13:59:VAL:O	25:13:60:GLU:HG2	2.20	0.41
28:16:33:LYS:HA	28:16:51:GLU:OE2	2.20	0.41
29:17:46:VAL:HG13	29:17:48:LYS:NZ	2.35	0.41
30:18:33:ASN:HA	30:18:36:LYS:HD2	2.03	0.41
32:1a:243:A:H4'	32:1a:244:U:H5"	2.02	0.41
32:1a:528:C:H41	43:1l:49:ASN:CG	2.28	0.41
32:1a:1219:U:OP1	45:1n:19:ARG:NH2	2.49	0.41
32:1a:1518:MA6:C6	32:1a:1519:MA6:H103	2.49	0.41
33:1b:97:TRP:HH2	33:1b:176:GLU:CD	2.28	0.41
36:1e:85:GLY:C	36:1e:87:SER:H	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:20:LEU:HD23	50:1s:23:ASN:ND2	2.34	0.41
1:2A:84:A:N1	1:2A:98:G:O2'	2.36	0.41
1:2A:322:A:H4'	1:2A:323:G:OP2	2.19	0.41
1:2A:925:C:H2'	1:2A:926:A:H8	1.84	0.41
1:2A:945:A:C4	1:2A:2448:A:C2	3.08	0.41
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.54	0.41
1:2A:1113:U:H2'	1:2A:1114:G:C8	2.55	0.41
1:2A:1157:G:O2'	25:23:31:LEU:HD12	2.20	0.41
1:2A:1478:G:O2'	1:2A:1558:A:N1	2.48	0.41
1:2A:1628:G:H2'	1:2A:1629:U:C6	2.55	0.41
1:2A:2112:G:C2	1:2A:2113:U:H1'	2.55	0.41
1:2A:2694:G:C6	1:2A:2695:C:C4	3.08	0.41
8:2I:110:ASP:H	8:2I:130:TYR:HH	1.60	0.41
16:2U:104:GLN:O	16:2U:107:ALA:HB3	2.21	0.41
32:2a:270:A:H2'	32:2a:271:C:C6	2.56	0.41
32:2a:677:U:H3	32:2a:713:G:H22	1.68	0.41
32:2a:735:C:H2'	32:2a:736:C:C6	2.55	0.41
32:2a:1054:C:C4	54:2w:34:G:H1'	2.55	0.41
33:2b:188:ALA:HB1	33:2b:192:SER:OG	2.21	0.41
39:2h:112:LEU:HD22	39:2h:133:LEU:HA	2.02	0.41
50:2s:64:GLU:O	50:2s:67:VAL:HG23	2.20	0.41
1:1A:110:U:H5'	24:12:65:ASN:ND2	2.34	0.41
1:1A:467:U:H2'	1:1A:468:G:C8	2.56	0.41
1:1A:613:A:H2'	1:1A:614:C:O4'	2.20	0.41
1:1A:831:A:O4'	3:1D:227:ASN:ND2	2.53	0.41
1:1A:847:A:H8	1:1A:847:A:OP1	2.03	0.41
1:1A:904:C:N4	1:1A:905:U:O4	2.53	0.41
12:1Q:60:ARG:HH21	54:1w:53:G:P	2.43	0.41
23:11:51:VAL:HG11	23:11:74:VAL:HG21	2.02	0.41
28:16:9:LEU:HD13	28:16:51:GLU:HB2	2.01	0.41
32:1a:90:U:H4'	32:1a:91:C:OP1	2.19	0.41
32:1a:109:A:C6	32:1a:326:G:C6	3.09	0.41
32:1a:1027:C:C5	32:1a:1028:C:C4	3.08	0.41
32:1a:1084:G:C5	32:1a:1085:U:C4	3.08	0.41
32:1a:1443:G:N2	32:1a:1459:C:O2	2.44	0.41
43:1l:24:VAL:HB	43:1l:27:LEU:HD22	2.00	0.41
44:1m:123:ALA:HB2	54:1w:39:PSU:H1'	2.02	0.41
54:1y:58:A:HO2'	54:1y:59:U:P	2.43	0.41
1:2A:144:C:H2'	1:2A:145:G:C8	2.54	0.41
1:2A:274:G:H2'	1:2A:275:G:C8	2.56	0.41
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:336:C:H4'	20:2Y:6:HIS:CD2	2.55	0.41
1:2A:484:C:H2'	1:2A:485:C:C6	2.56	0.41
1:2A:524:U:H2'	1:2A:525:U:C6	2.55	0.41
1:2A:971:C:H2'	1:2A:972:G:O4'	2.21	0.41
1:2A:1913:A:H4'	1:2A:1914:C:O5'	2.18	0.41
1:2A:2164:C:C5	1:2A:2165:G:H1'	2.55	0.41
1:2A:2372:G:H1'	28:26:46:HIS:CE1	2.55	0.41
1:2A:2776:A:H4'	1:2A:2777:G:H5"	2.01	0.41
5:2F:29:ASN:HA	5:2F:30:PRO:HD3	1.92	0.41
5:2F:192:LEU:HD22	5:2F:194:MET:HG3	2.02	0.41
11:2P:55:ARG:HA	60:2P:4007:HOH:O	2.20	0.41
17:2V:19:LYS:HE3	17:2V:62:LEU:HD21	2.02	0.41
21:2Z:24:LEU:HA	21:2Z:25:PRO:HD3	1.90	0.41
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.20	0.41
27:25:16:ARG:HG3	27:25:17:ASP:N	2.36	0.41
32:2a:66:G:H8	32:2a:66:G:OP1	2.02	0.41
32:2a:130:A:N3	32:2a:263:A:O2'	2.44	0.41
32:2a:131:C:H2'	32:2a:132:C:H6	1.85	0.41
32:2a:1173:G:H2'	32:2a:1174:G:C8	2.55	0.41
33:2b:33:TYR:HB2	33:2b:43:ASP:HA	2.01	0.41
38:2g:16:LEU:HD22	40:2i:41:VAL:O	2.21	0.41
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	2.02	0.41
45:2n:21:TYR:HE1	45:2n:23:ARG:NE	2.17	0.41
47:2p:13:HIS:O	47:2p:42:ARG:NH1	2.53	0.41
1:1A:287:G:N7	1:1A:448:U:H2'	2.35	0.41
1:1A:491:G:C6	1:1A:492:A:N6	2.89	0.41
1:1A:672:G:O5'	1:1A:672:G:H8	2.04	0.41
1:1A:2854:G:O6	60:1A:5078:HOH:O	2.22	0.41
1:1A:2856:G:H2'	1:1A:2857:U:O4'	2.20	0.41
1:1A:2881:C:N3	60:1A:5080:HOH:O	2.37	0.41
3:1D:130:ALA:C	3:1D:131:LEU:HD12	2.45	0.41
4:1E:52:LEU:HA	4:1E:53:PRO:HD3	1.92	0.41
9:1N:73:THR:OG1	9:1N:82:LEU:HD11	2.21	0.41
10:1O:7:TYR:HE2	10:1O:20:MET:HE2	1.84	0.41
16:1U:34:LYS:HA	16:1U:34:LYS:HD3	1.57	0.41
32:1a:343:U:O2'	32:1a:344:A:H2'	2.20	0.41
32:1a:944:G:O6	32:1a:1337:G:H8	2.03	0.41
32:1a:949:A:H1'	32:1a:1364:U:H3	1.84	0.41
43:1l:33:ARG:HA	43:1l:33:ARG:HD3	1.92	0.41
1:2A:342:G:O2'	1:2A:343:C:H5'	2.20	0.41
1:2A:479:A:O2'	1:2A:481:G:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:588:U:O5'	1:2A:588:U:H6	2.04	0.41
1:2A:881:G:H3'	1:2A:882:G:C8	2.55	0.41
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.56	0.41
1:2A:2653:U:H5"	1:2A:2654:A:OP2	2.21	0.41
3:2D:72:LYS:HD2	3:2D:103:ARG:NH1	2.36	0.41
3:2D:132:PRO:HD3	3:2D:190:TYR:CZ	2.55	0.41
7:2H:30:LYS:N	7:2H:79:VAL:O	2.50	0.41
32:2a:619:U:C2	35:2d:135:LEU:HD22	2.56	0.41
32:2a:1004:A:H1'	32:2a:1038:C:O2	2.20	0.41
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.14	0.41
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.20	0.41
45:2n:3:ARG:HG3	45:2n:4:LYS:N	2.34	0.41
54:2y:58:A:H4'	54:2y:59:U:OP1	2.20	0.41
1:1A:215:G:H21	1:1A:217:A:H62	1.67	0.41
1:1A:402:C:H2'	1:1A:403:C:C6	2.55	0.41
1:1A:1273:G:OP1	16:1U:13:LYS:HG2	2.21	0.41
2:1B:14:U:O2	2:1B:108:U:H4'	2.20	0.41
5:1F:8:GLN:HE22	5:1F:21:ALA:HA	1.85	0.41
5:1F:164:ARG:O	5:1F:168:ARG:HB2	2.20	0.41
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	2.01	0.41
8:1I:47:LEU:HA	8:1I:47:LEU:HD23	1.79	0.41
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.55	0.41
11:1P:27:HIS:HB2	60:1P:321:HOH:O	2.19	0.41
11:1P:126:VAL:HG12	11:1P:148:LEU:HD23	2.03	0.41
12:1Q:134:ARG:CZ	21:1Z:122:ARG:HH21	2.33	0.41
17:1V:2:PHE:CE2	17:1V:41:GLY:HA3	2.55	0.41
32:1a:250:A:H4'	32:1a:251:G:O5'	2.20	0.41
32:1a:277:C:P	48:1q:68:ARG:HH22	2.41	0.41
32:1a:418:C:H1'	32:1a:540:G:O2'	2.20	0.41
32:1a:1152:A:OP1	41:1j:68:HIS:ND1	2.53	0.41
32:1a:1218:C:OP2	45:1n:9:LYS:NZ	2.53	0.41
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.49	0.41
35:1d:178:VAL:O	35:1d:179:GLU:HB2	2.20	0.41
38:1g:97:GLN:O	38:1g:101:LEU:HG	2.20	0.41
38:1g:144:MET:HE2	38:1g:144:MET:HB3	1.73	0.41
1:2A:191:A:H2'	1:2A:192:C:C6	2.54	0.41
1:2A:927:G:H2'	1:2A:928:G:O4'	2.20	0.41
1:2A:1213:A:H2'	1:2A:1214:A:O4'	2.20	0.41
1:2A:1297:C:OP1	1:2A:2710:C:H4'	2.21	0.41
1:2A:2365:G:O6	30:28:39:LYS:HE3	2.20	0.41
3:2D:16:MET:HE3	3:2D:16:MET:HB2	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:195:ASP:HB3	5:2F:198:ALA:H	1.85	0.41
7:2H:4:ILE:O	7:2H:69:ARG:HD2	2.20	0.41
8:2I:61:ARG:HD3	8:2I:61:ARG:HA	1.75	0.41
8:2I:116:LEU:HD11	8:2I:120:ILE:HG13	2.02	0.41
19:2X:35:THR:O	19:2X:39:ILE:HG13	2.21	0.41
26:24:40:HIS:O	26:24:44:THR:HG22	2.20	0.41
32:2a:1004:A:C8	32:2a:1005:A:C4'	3.04	0.41
32:2a:1115:C:H2'	32:2a:1116:C:C6	2.56	0.41
32:2a:1306:A:N6	32:2a:1331:G:O4'	2.53	0.41
33:2b:47:THR:O	33:2b:51:LEU:HG	2.21	0.41
42:2k:79:SER:HB2	42:2k:106:LYS:HD3	2.03	0.41
46:2o:55:GLY:O	46:2o:59:MET:HG3	2.21	0.41
1:1A:386:U:H6	1:1A:386:U:H2'	1.69	0.41
1:1A:493:G:P	29:17:33:ARG:HH12	2.43	0.41
1:1A:821:A:H2'	1:1A:821:A:N3	2.36	0.41
1:1A:1277:G:H2'	1:1A:1278:G:C8	2.56	0.41
1:1A:1668:G:OP2	60:1A:5519:HOH:O	2.22	0.41
1:1A:2157:A:H2'	1:1A:2157:A:N3	2.35	0.41
1:1A:2418:U:C2	11:1P:72:PRO:HG2	2.55	0.41
1:1A:2638:C:H2'	1:1A:2639:G:O4'	2.20	0.41
60:1A:6391:HOH:O	9:1N:28:THR:HG23	2.20	0.41
3:1D:70:TRP:CE2	3:1D:150:LYS:HD3	2.56	0.41
9:1N:39:ARG:HA	9:1N:40:PRO:HD3	1.92	0.41
15:1T:108:ARG:HG3	15:1T:109:GLU:N	2.34	0.41
32:1a:266:G:H4'	32:1a:267:C:C5	2.55	0.41
32:1a:360:A:C6	32:1a:361:G:C6	3.09	0.41
32:1a:438:G:H4'	35:1d:123:HIS:ND1	2.35	0.41
32:1a:645:C:H2'	32:1a:646:U:C6	2.56	0.41
33:1b:47:THR:O	33:1b:51:LEU:HG	2.20	0.41
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.66	0.41
37:1f:9:VAL:HG22	37:1f:60:PHE:CE1	2.55	0.41
41:1j:49:VAL:HG21	45:1n:41:ARG:O	2.20	0.41
46:1o:74:ASP:OD2	46:1o:77:ARG:HB2	2.20	0.41
54:1y:22:G:C2	54:1y:23:A:C5	3.08	0.41
1:2A:996:A:C2	1:2A:997:G:C8	3.09	0.41
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.09	0.41
1:2A:1232:G:H2'	1:2A:1233:C:C6	2.56	0.41
1:2A:1359:A:H2'	1:2A:1360:A:H5'	2.03	0.41
1:2A:1431:U:H2'	1:2A:1432:C:H6	1.84	0.41
1:2A:2539:C:H4'	31:29:35:ARG:NH2	2.36	0.41
2:2B:41:U:O4	6:2G:70:VAL:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:91:C:H5'	12:2Q:18:LYS:HA	2.02	0.41
9:2N:34:LEU:O	9:2N:49:GLY:HA3	2.20	0.41
32:2a:56:U:H2'	32:2a:57:G:C8	2.55	0.41
32:2a:56:U:H2'	32:2a:57:G:H8	1.85	0.41
32:2a:299:G:H8	32:2a:299:G:O5'	2.03	0.41
32:2a:457:C:H2'	32:2a:458:C:H6	1.85	0.41
32:2a:1085:U:H3'	32:2a:1086:U:C5	2.56	0.41
33:2b:58:ILE:O	33:2b:62:ALA:N	2.45	0.41
33:2b:224:GLN:HA	33:2b:228:GLY:O	2.20	0.41
40:2i:69:GLY:O	40:2i:73:GLN:HG3	2.21	0.41
45:2n:36:PHE:HD2	45:2n:37:PHE:CD1	2.39	0.41
52:2u:7:ARG:HG2	52:2u:21:TYR:CZ	2.56	0.41
1:1A:861:C:H2'	1:1A:862:C:C6	2.56	0.41
1:1A:1560:U:O2'	1:1A:1561:C:H5'	2.20	0.41
1:1A:2190:G:N1	1:1A:2193:A:C8	2.88	0.41
1:1A:2245:U:H2'	1:1A:2246:G:C8	2.55	0.41
1:1A:2327:G:H2'	1:1A:2328:C:C6	2.56	0.41
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.21	0.41
9:1N:33:LEU:HD12	9:1N:33:LEU:HA	1.80	0.41
11:1P:81:GLN:NE2	11:1P:105:LEU:O	2.54	0.41
11:1P:116:GLY:O	11:1P:137:LYS:NZ	2.42	0.41
23:11:89:GLU:O	23:11:93:GLU:HG2	2.21	0.41
32:1a:1349:A:OP2	40:1i:118:LYS:HE2	2.20	0.41
33:1b:33:TYR:HB2	33:1b:43:ASP:CB	2.43	0.41
39:1h:72:PRO:O	39:1h:74:PRO:HD3	2.21	0.41
40:1i:55:ALA:HA	40:1i:58:HIS:CD2	2.55	0.41
42:1k:98:LEU:HD23	42:1k:98:LEU:HA	1.87	0.41
50:1s:27:GLU:CB	50:1s:28:LYS:HA	2.40	0.41
51:1t:67:ALA:HB2	51:1t:77:ALA:HB2	2.03	0.41
54:1w:26:A:N6	54:1w:44:G:H1	2.19	0.41
1:2A:829:A:N7	1:2A:2247:A:O2'	2.45	0.41
1:2A:953:A:C2	1:2A:954:G:C8	3.09	0.41
1:2A:1288:U:C2	1:2A:1327:C:O2	2.74	0.41
1:2A:1826:G:H4'	3:2D:242:ARG:HH21	1.84	0.41
1:2A:1848:A:C4	1:2A:1849:G:C8	3.09	0.41
1:2A:2135:A:H2'	1:2A:2136:C:C6	2.56	0.41
1:2A:2335:A:C8	1:2A:2337:G:C5	3.09	0.41
1:2A:2366:A:H2'	1:2A:2367:G:O4'	2.20	0.41
1:2A:2584:U:H6	1:2A:2584:U:O5'	2.04	0.41
1:2A:2747:G:H21	1:2A:2757:A:H62	1.67	0.41
3:2D:68:LYS:C	3:2D:70:TRP:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:121:ILE:HD11	7:2H:140:LYS:HG2	2.02	0.41
29:27:30:VAL:O	29:27:34:ARG:HG2	2.21	0.41
32:2a:9:G:H2'	32:2a:10:A:H8	1.86	0.41
32:2a:1074:G:O2'	32:2a:1101:A:N1	2.51	0.41
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.20	0.41
32:2a:1364:U:O2'	32:2a:1365:G:H5'	2.20	0.41
32:2a:1411:C:H2'	32:2a:1412:C:C6	2.56	0.41
33:2b:100:GLY:HA2	33:2b:103:THR:OG1	2.19	0.41
1:1A:739:C:O2'	3:1D:38:LYS:NZ	2.47	0.41
1:1A:2023:A:H2'	1:1A:2024:G:C8	2.55	0.41
25:13:18:ASP:OD1	25:13:18:ASP:N	2.49	0.41
29:17:46:VAL:HG13	29:17:48:LYS:HZ3	1.86	0.41
32:1a:204:U:H4'	32:1a:216:G:O5'	2.20	0.41
32:1a:769:G:H4'	32:1a:1513:A:H4'	2.02	0.41
32:1a:872:A:C8	32:1a:874:G:C8	3.09	0.41
32:1a:1030(A):G:O2'	32:1a:1031:G:N2	2.54	0.41
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.21	0.41
32:1a:1396:A:H2	36:1e:19:MET:HG3	1.85	0.41
32:1a:1458:G:H5'	51:1t:32:ALA:HB2	2.03	0.41
33:1b:178:ARG:HB3	39:1h:72:PRO:HA	2.02	0.41
37:1f:2:ARG:HB2	37:1f:4:TYR:CE2	2.56	0.41
46:1o:18:PHE:CE2	46:1o:21:ASP:HB2	2.56	0.41
55:1x:17:C:OP1	55:1x:61:C:H5"	2.21	0.41
54:1y:41:C:H2'	54:1y:42:C:H6	1.86	0.41
1:2A:7:G:H4'	9:2N:13:TRP:CH2	2.55	0.41
1:2A:394:A:C6	1:2A:395:U:C4	3.09	0.41
1:2A:468:G:N7	29:27:39:ARG:NH2	2.69	0.41
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.20	0.41
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.56	0.41
2:2B:11:C:H3'	2:2B:12:C:H6	1.86	0.41
5:2F:23:ASP:O	5:2F:24:LEU:HD12	2.21	0.41
8:2I:87:LYS:NZ	8:2I:122:GLU:OE2	2.53	0.41
12:2Q:85:LYS:HG2	22:20:7:LEU:CB	2.50	0.41
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	2.02	0.41
16:2U:89:GLU:HB2	17:2V:50:PRO:HB3	2.01	0.41
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	2.03	0.41
26:24:62:ARG:HA	26:24:62:ARG:HD3	1.75	0.41
29:27:34:ARG:NH2	29:27:39:ARG:HG2	2.35	0.41
32:2a:429:U:H3'	35:2d:9:CYS:SG	2.60	0.41
32:2a:1168:A:H2'	32:2a:1169:A:C8	2.56	0.41
32:2a:1274:G:N2	32:2a:1275:A:H62	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1326:C:H5”	52:2u:18:TYR:O	2.19	0.41
32:2a:1327:C:H2’	32:2a:1328:C:C6	2.55	0.41
32:2a:1371:G:OP1	40:2i:12:GLU:HB2	2.20	0.41
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2’	2.31	0.41
33:2b:185:ILE:HG22	33:2b:199:TYR:CD2	2.52	0.41
34:2c:179:ARG:NH1	34:2c:206:GLU:HB2	2.36	0.41
34:2c:190:ARG:HG2	34:2c:191:THR:N	2.34	0.41
35:2d:176:LEU:HD12	35:2d:182:LYS:O	2.20	0.41
41:2j:38:ILE:HG13	41:2j:71:LEU:HB3	2.03	0.41
45:2n:3:ARG:HG3	45:2n:4:LYS:H	1.85	0.41
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	2.02	0.41
49:2r:25:THR:HG23	49:2r:26:LEU:HD12	2.02	0.41
55:2x:61:C:H2’	55:2x:62:C:H6	1.86	0.41
54:2y:3:C:N3	54:2y:70:G:O6	2.54	0.41
1:1A:271:U:H4’	1:1A:272:U:OP2	2.18	0.41
1:1A:310:C:H2’	1:1A:311:C:C6	2.55	0.41
1:1A:463:C:H2’	1:1A:464:G:C8	2.56	0.41
1:1A:1118:C:H2’	1:1A:1139:G:O6	2.20	0.41
1:1A:1140:U:O2’	1:1A:1141:A:N7	2.51	0.41
1:1A:1720:U:OP1	60:1A:5027:HOH:O	2.21	0.41
1:1A:1739:U:O2’	1:1A:1740:U:H2’	2.20	0.41
1:1A:1765:U:H2’	1:1A:1766:G:O4’	2.21	0.41
1:1A:2136:A:H2	1:1A:2190:G:H1’	1.85	0.41
1:1A:2158:C:C4	1:1A:2177:G:N1	2.88	0.41
1:1A:2331:G:N1	14:1S:3:ARG:HA	2.36	0.41
3:1D:35:LYS:HB2	3:1D:36:PRO:HD2	2.02	0.41
3:1D:37:LEU:HD22	3:1D:87:ASN:ND2	2.36	0.41
4:1E:2:LYS:HA	4:1E:84:PHE:CE1	2.56	0.41
7:1H:56:SER:OG	7:1H:57:ASP:N	2.54	0.41
8:1I:118:LYS:HA	8:1I:119:PRO:HD3	1.95	0.41
11:1P:98:GLU:O	11:1P:101:VAL:HG12	2.21	0.41
20:1Y:65:ALA:HA	20:1Y:66:PRO:HD3	1.93	0.41
21:1Z:6:LYS:HD3	21:1Z:8:TYR:OH	2.20	0.41
21:1Z:126:VAL:CG1	21:1Z:161:VAL:HG23	2.51	0.41
32:1a:243:A:C2	32:1a:246:A:C8	3.09	0.41
32:1a:277:C:H5”	48:1q:68:ARG:NH2	2.36	0.41
32:1a:486:U:H2’	32:1a:487:A:H8	1.85	0.41
32:1a:584:G:H5’	48:1q:91:ARG:NH2	2.34	0.41
32:1a:857:C:H2’	32:1a:858:G:O4’	2.21	0.41
32:1a:918:A:H2’	32:1a:919:A:O4’	2.20	0.41
32:1a:1330:U:H2’	32:1a:1331:G:H5’	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:79:ARG:CG	38:1g:80:VAL:H	2.33	0.41
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	2.03	0.41
44:1m:3:ARG:HG3	44:1m:4:ILE:N	2.36	0.41
54:1y:7:A:OP1	54:1y:8:4SU:H5	2.20	0.41
1:2A:109:G:H2'	1:2A:110:G:O4'	2.21	0.41
1:2A:195:A:N7	60:2A:4402:HOH:O	2.37	0.41
1:2A:224:G:H2'	1:2A:225:A:O4'	2.21	0.41
1:2A:228:A:O2'	1:2A:229:A:H4'	2.21	0.41
1:2A:289:A:H2'	1:2A:290:G:O4'	2.21	0.41
1:2A:372:G:H8	23:21:65:SER:O	2.04	0.41
1:2A:484:C:H2'	1:2A:485:C:H6	1.86	0.41
1:2A:571:A:O2'	17:2V:78:LYS:HE2	2.21	0.41
1:2A:956:G:H5"	12:2Q:77:LYS:HD2	2.02	0.41
1:2A:1567:A:H2'	3:2D:84:TYR:HE2	1.85	0.41
1:2A:1785:A:N6	60:2A:5150:HOH:O	2.54	0.41
1:2A:2848:G:C8	15:2T:97:ALA:HB2	2.56	0.41
60:2A:4018:HOH:O	16:2U:14:HIS:HE1	2.04	0.41
2:2B:94:C:H2'	2:2B:95:C:C6	2.56	0.41
4:2E:50:GLY:CA	4:2E:75:VAL:HG11	2.50	0.41
7:2H:9:ILE:HG12	7:2H:69:ARG:HG3	2.03	0.41
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.49	0.41
8:2I:75:LEU:HD22	8:2I:105:HIS:CD2	2.55	0.41
11:2P:57:THR:O	11:2P:61:ARG:HG3	2.21	0.41
14:2S:8:GLU:HG2	14:2S:8:GLU:H	1.54	0.41
15:2T:23:ARG:NH1	15:2T:120:ARG:HD3	2.35	0.41
16:2U:104:GLN:O	16:2U:108:GLU:HG3	2.21	0.41
17:2V:62:LEU:HD22	17:2V:93:GLU:HG2	2.01	0.41
18:2W:45:TYR:OH	18:2W:49:LYS:NZ	2.45	0.41
21:2Z:61:LEU:HA	21:2Z:62:PRO:HD3	1.94	0.41
21:2Z:138:GLU:H	21:2Z:156:LYS:CE	2.34	0.41
21:2Z:158:PRO:HA	21:2Z:159:PRO:HD3	1.92	0.41
23:21:30:VAL:HG21	54:2y:76:A:H5"	2.02	0.41
26:24:44:THR:O	26:24:46:GLN:N	2.54	0.41
28:26:9:LEU:HD13	28:26:51:GLU:HB2	2.03	0.41
32:2a:142:G:H2'	32:2a:143:A:C8	2.56	0.41
32:2a:302:G:N3	32:2a:556:C:H4'	2.36	0.41
32:2a:641:U:O3'	32:2a:642:A:H8	2.03	0.41
32:2a:957:U:H2'	32:2a:959:A:OP2	2.21	0.41
32:2a:1028:C:O5'	32:2a:1028:C:H6	2.04	0.41
32:2a:1031:G:H5"	32:2a:1032:G:OP2	2.21	0.41
32:2a:1101:A:H4'	32:2a:1102:A:O5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1186:G:H21	45:2n:61:TRP:C	2.28	0.41
32:2a:1385:G:H2'	32:2a:1386:G:H8	1.84	0.41
32:2a:1417:G:C6	32:2a:1482:G:C6	3.09	0.41
33:2b:28:PHE:CD1	33:2b:194:PRO:HG3	2.56	0.41
33:2b:110:GLN:HG2	33:2b:111:ARG:HH12	1.85	0.41
35:2d:191:ARG:NH2	35:2d:200:GLU:OE1	2.51	0.41
36:2e:145:LYS:O	36:2e:149:GLU:HB2	2.20	0.41
40:2i:18:PHE:HD2	40:2i:62:TYR:HD2	1.69	0.41
40:2i:86:VAL:HA	40:2i:89:ASN:O	2.21	0.41
41:2j:54:PHE:O	41:2j:55:LYS:HG2	2.21	0.41
43:2l:26:ALA:HB1	43:2l:60:LEU:HD22	2.02	0.41
51:2t:43:LEU:HD23	51:2t:43:LEU:HA	1.94	0.41
53:2v:14:A:H2	53:2v:15:A:C4	2.39	0.41
1:1A:38:A:H2'	1:1A:39:C:C6	2.56	0.41
1:1A:572:A:H61	17:1V:19:LYS:H	1.69	0.41
1:1A:1116:A:N6	1:1A:1142:A:N3	2.68	0.41
1:1A:2196:C:OP2	1:1A:2196:C:H6	2.04	0.41
1:1A:2679:C:H2'	1:1A:2680:G:O4'	2.20	0.41
1:1A:2801:C:P	4:1E:61:ARG:HH21	2.44	0.41
1:1A:2804:C:H2'	1:1A:2805:G:C8	2.55	0.41
3:1D:171:ASP:O	3:1D:187:GLY:N	2.45	0.41
6:1G:173:LEU:HD23	6:1G:176:LEU:HD12	2.03	0.41
10:1O:49:ARG:HH12	32:1a:1423:G:P	2.44	0.41
26:14:49:PHE:HB3	26:14:50:VAL:H	1.39	0.41
32:1a:560:U:H6	32:1a:560:U:H2'	1.69	0.41
32:1a:1024:G:N2	32:1a:1025:U:C6	2.89	0.41
34:1c:6:HIS:HA	34:1c:7:PRO:HD3	1.78	0.41
34:1c:30:ARG:O	34:1c:34:LEU:N	2.43	0.41
48:1q:43:LEU:HD11	48:1q:68:ARG:NH1	2.36	0.41
54:1w:37:MIA:H162	54:1w:37:MIA:H121	1.75	0.41
1:2A:35:G:H2'	1:2A:36:G:O4'	2.20	0.41
1:2A:581:C:H2'	1:2A:582:G:C8	2.56	0.41
1:2A:815:C:C2	1:2A:1193:G:C2	3.08	0.41
1:2A:1464:C:H2'	1:2A:1465:G:C8	2.56	0.41
1:2A:1529:G:C6	1:2A:1530:C:C4	3.09	0.41
1:2A:1859:A:N6	1:2A:1883:G:O2'	2.53	0.41
1:2A:2055:C:H5'	1:2A:2056:G:O5'	2.21	0.41
1:2A:2140:C:O2	1:2A:2140:C:H2'	2.21	0.41
1:2A:2148:G:H2'	1:2A:2149:G:N7	2.35	0.41
1:2A:2336:A:H61	22:20:43:THR:HG22	1.85	0.41
1:2A:2510:C:C4	1:2A:2511:U:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2512:C:H5”	1:2A:2513:G:OP2	2.21	0.41
1:2A:2519:U:H5’	1:2A:2567:G:H21	1.86	0.41
1:2A:2679:A:C2	1:2A:2729:G:C2	3.09	0.41
1:2A:2741:A:N6	1:2A:2763:G:O2’	2.54	0.41
1:2A:2839:G:C6	1:2A:2840:C:N3	2.89	0.41
2:2B:71:C:H2’	2:2B:72:G:C8	2.56	0.41
5:2F:29:ASN:O	5:2F:112:MET:HE1	2.21	0.41
11:2P:52:GLU:HB3	11:2P:55:ARG:CZ	2.50	0.41
11:2P:94:GLU:HG2	11:2P:96:THR:HG23	2.03	0.41
12:2Q:31:ASP:HA	12:2Q:134:ARG:NH1	2.36	0.41
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.21	0.41
13:2R:109:ALA:HA	13:2R:110:PRO:HD2	1.91	0.41
17:2V:27:ALA:O	17:2V:64:HIS:HE1	2.04	0.41
28:26:34:LEU:N	28:26:51:GLU:HG2	2.36	0.41
32:2a:1030(A):G:C2	32:2a:1030(D):A:OP2	2.75	0.41
32:2a:1053:G:H4’	32:2a:1054:C:H3’	2.03	0.41
32:2a:1301:U:O2’	32:2a:1302:U:H5’	2.21	0.41
32:2a:1369:C:H2’	32:2a:1370:G:O4’	2.21	0.41
32:2a:1378:C:N4	32:2a:1379:G:N3	2.69	0.41
32:2a:1511:G:H2’	32:2a:1512:U:O4’	2.21	0.41
36:2e:34:VAL:O	36:2e:42:GLY:N	2.51	0.41
40:2i:20:ARG:HA	40:2i:21:PRO:HD3	1.97	0.41
51:2t:20:LEU:HD23	51:2t:20:LEU:HA	1.80	0.41
54:2w:28:G:C2	54:2w:29:G:H1’	2.56	0.41
55:2x:21:A:H62	55:2x:46:G:H2’	1.86	0.41
1:1A:943:C:H2’	1:1A:944:C:C6	2.56	0.40
1:1A:1759:C:H2’	1:1A:1760:U:O4’	2.22	0.40
1:1A:2156:A:C5	1:1A:2180:A:H2	2.35	0.40
1:1A:2742:G:H2’	1:1A:2743:C:O4’	2.21	0.40
3:1D:21:PHE:HB3	3:1D:24:ILE:HD12	2.02	0.40
5:1F:12:LEU:HB3	5:1F:126:VAL:HG12	2.03	0.40
21:1Z:4:ARG:HG2	21:1Z:58:VAL:HB	2.01	0.40
23:11:64:ALA:HA	23:11:67:ILE:HG13	2.02	0.40
28:16:10:LEU:O	28:16:51:GLU:HA	2.20	0.40
32:1a:345:C:H5’	32:1a:346:G:C5	2.56	0.40
35:1d:175:SER:CB	35:1d:184:LYS:HB3	2.48	0.40
35:1d:188:LEU:HA	35:1d:189:PRO:HD3	1.85	0.40
36:1e:78:HIS:HE1	36:1e:143:ARG:N	2.02	0.40
43:1l:39:VAL:HG11	43:1l:41:ARG:NH1	2.35	0.40
43:1l:54:LYS:N	43:1l:54:LYS:HD2	2.35	0.40
50:1s:35:SER:HB3	50:1s:38:SER:OG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:71:LEU:HD23	50:1s:71:LEU:HA	1.69	0.40
52:1u:11:GLY:O	52:1u:15:ARG:HG2	2.22	0.40
1:2A:1188:U:C4'	17:2V:79:VAL:HG22	2.49	0.40
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.87	0.40
1:2A:2528:U:O2'	1:2A:2529:G:H3'	2.21	0.40
6:2G:46:ALA:HB2	6:2G:53:LEU:HG	2.02	0.40
9:2N:99:LEU:HD23	9:2N:99:LEU:HA	1.89	0.40
15:2T:113:LYS:O	15:2T:114:LEU:HD23	2.21	0.40
18:2W:60:ASN:HD22	18:2W:60:ASN:N	2.19	0.40
21:2Z:28:MET:HA	21:2Z:88:PHE:O	2.21	0.40
32:2a:142:G:H2'	32:2a:143:A:H8	1.86	0.40
32:2a:377:G:OP1	47:2p:3:LYS:HE2	2.21	0.40
32:2a:560:U:H6	32:2a:560:U:H2'	1.51	0.40
32:2a:1222:G:C6	32:2a:1223:C:C4	3.09	0.40
32:2a:1247:U:H1'	32:2a:1291:G:N2	2.36	0.40
32:2a:1278:U:H5'	32:2a:1279:A:C5'	2.51	0.40
34:2c:131:ARG:NE	34:2c:135:LYS:HE3	2.35	0.40
40:2i:82:ALA:HA	40:2i:85:LEU:HD12	2.03	0.40
45:2n:32:SER:O	45:2n:40:CYS:HA	2.21	0.40
52:2u:18:TYR:HD1	52:2u:22:ARG:O	2.03	0.40
54:2y:4:C:H2'	54:2y:5:G:H5'	2.03	0.40
54:2y:60:U:O2'	54:2y:61:C:H5'	2.21	0.40
1:1A:1058:U:O4	9:1N:28:THR:HG21	2.21	0.40
1:1A:1229:G:H5'	25:13:29:ARG:NH1	2.36	0.40
1:1A:1572:G:C6	1:1A:1573:G:C2	3.08	0.40
1:1A:2368:C:H2'	1:1A:2369:U:O4'	2.21	0.40
12:1Q:43:THR:HA	12:1Q:94:VAL:HG12	2.03	0.40
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.57	0.40
32:1a:57:G:H2'	32:1a:58:C:C6	2.57	0.40
32:1a:69:G:C2	32:1a:70:G:C5	3.10	0.40
32:1a:679:C:H2'	32:1a:680:C:C6	2.55	0.40
32:1a:911:U:H2'	32:1a:912:C:C6	2.56	0.40
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.21	0.40
33:1b:90:MET:HE2	33:1b:90:MET:HA	2.03	0.40
33:1b:118:LEU:HD13	33:1b:142:LEU:HB2	2.03	0.40
36:1e:105:VAL:HG21	36:1e:128:PRO:HB3	2.04	0.40
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.54	0.40
55:1x:61:C:H2'	55:1x:62:C:H6	1.85	0.40
1:2A:64:A:O3'	19:2X:71:GLY:HA3	2.20	0.40
1:2A:84:A:H5"	20:2Y:8:LYS:HE3	2.02	0.40
1:2A:244:A:C2	1:2A:255:A:C4	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:272:G:H4'	1:2A:272(A):U:H5"	2.02	0.40
1:2A:582:G:H2'	1:2A:583:G:C8	2.56	0.40
1:2A:778:G:C5	1:2A:779:U:C4	3.09	0.40
1:2A:1021:A:C8	1:2A:1021:A:C3'	3.04	0.40
1:2A:1263:U:C4	1:2A:1264:G:C6	3.08	0.40
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.57	0.40
1:2A:2070:G:H2'	1:2A:2071:A:H8	1.85	0.40
1:2A:2369:A:C6	1:2A:2370:G:C5	3.09	0.40
1:2A:2419:U:O5'	1:2A:2419:U:H6	2.04	0.40
1:2A:2533:A:O2'	1:2A:2664:G:H5"	2.21	0.40
6:2G:27:ASN:O	6:2G:30:GLU:HB3	2.20	0.40
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	2.02	0.40
6:2G:111:LEU:HD23	6:2G:117:PHE:CE1	2.56	0.40
7:2H:115:VAL:HG12	7:2H:123:PHE:CE2	2.56	0.40
10:2O:2:ILE:HB	10:2O:33:ALA:HB3	2.03	0.40
17:2V:89:GLN:HA	17:2V:90:PRO:HD3	1.88	0.40
18:2W:11:ARG:NH1	18:2W:99:ARG:O	2.54	0.40
21:2Z:46:LYS:O	21:2Z:50:GLN:NE2	2.50	0.40
32:2a:343:U:O2'	32:2a:344:A:H2'	2.21	0.40
32:2a:1084:G:OP1	32:2a:1086:U:C2	2.74	0.40
32:2a:1305:G:C2	32:2a:1331:G:N3	2.89	0.40
32:2a:1316:G:H2'	32:2a:1318:A:OP2	2.21	0.40
34:2c:120:VAL:HG11	34:2c:134:ILE:HD13	2.04	0.40
36:2e:100:VAL:O	36:2e:107:ARG:NH1	2.37	0.40
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.56	0.40
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.86	0.40
1:1A:1068:G:N7	9:1N:66:LYS:HE2	2.36	0.40
1:1A:1136:U:N3	1:1A:1148:C:H1'	2.37	0.40
1:1A:1891:G:N2	1:1A:1904:C:O2	2.51	0.40
1:1A:2081:A:C8	1:1A:2515:2MA:HM22	2.56	0.40
1:1A:2132:G:OP1	1:1A:2140:U:N3	2.54	0.40
2:1B:12:C:H4'	2:1B:13:A:OP1	2.22	0.40
8:1I:9:LEU:HD21	8:1I:35:LEU:HD13	2.02	0.40
8:1I:122:GLU:HB2	8:1I:126:TYR:OH	2.21	0.40
24:12:9:GLN:HE22	24:12:56:GLN:HB3	1.86	0.40
32:1a:100:C:H2'	32:1a:101:A:C8	2.56	0.40
32:1a:270:A:H2'	32:1a:271:C:C6	2.57	0.40
32:1a:352:C:H4'	32:1a:354:G:OP1	2.21	0.40
32:1a:659:U:H2'	32:1a:660:G:C8	2.55	0.40
32:1a:859:A:H2'	32:1a:860:A:O4'	2.21	0.40
32:1a:1241:G:H2'	32:1a:1242:C:H6	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1258:G:H2'	32:1a:1259:C:C6	2.57	0.40
32:1a:1424:C:H2'	32:1a:1425:U:O4'	2.21	0.40
43:1l:28:LYS:HB2	43:1l:33:ARG:HH21	1.85	0.40
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.22	0.40
1:2A:30:G:C6	1:2A:31:C:C4	3.09	0.40
1:2A:569:U:C4	1:2A:570:G:C6	3.10	0.40
1:2A:644:A:C2	1:2A:2369:A:H1'	2.56	0.40
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.56	0.40
1:2A:848:G:H2'	1:2A:849:A:C8	2.55	0.40
1:2A:1015:G:H2'	1:2A:1016:G:C8	2.41	0.40
1:2A:1266:G:O4'	18:2W:15:ARG:NH2	2.54	0.40
1:2A:2048:G:OP1	60:2A:4976:HOH:O	2.22	0.40
1:2A:2064:C:H1'	1:2A:2450:A:C2	2.56	0.40
1:2A:2070:G:H2'	1:2A:2071:A:O4'	2.21	0.40
1:2A:2525:G:C2	1:2A:2539:C:C2	3.09	0.40
2:2B:80:U:O2'	2:2B:81:G:H8	2.05	0.40
5:2F:78:ILE:HA	5:2F:83:PHE:CD2	2.56	0.40
6:2G:16:ARG:HH11	6:2G:16:ARG:HG3	1.85	0.40
6:2G:111:LEU:HA	6:2G:114:ILE:HD12	2.01	0.40
11:2P:95:VAL:HG23	11:2P:100:LEU:HD21	2.03	0.40
11:2P:126:VAL:HG12	11:2P:148:LEU:CD2	2.51	0.40
29:27:34:ARG:HH21	29:27:39:ARG:HG2	1.85	0.40
30:28:61:LEU:C	30:28:63:PRO:HD3	2.47	0.40
32:2a:434:U:H2'	32:2a:435:C:C6	2.57	0.40
32:2a:975:A:C5	32:2a:1357:A:H2	2.39	0.40
32:2a:1304:G:C6	32:2a:1305:G:N1	2.89	0.40
32:2a:1327:C:H2'	32:2a:1328:C:H6	1.86	0.40
33:2b:88:ALA:CB	33:2b:222:ILE:HD11	2.51	0.40
38:2g:52:GLU:H	38:2g:52:GLU:HG2	1.72	0.40
39:2h:46:LYS:HA	39:2h:64:LYS:HE3	2.02	0.40
39:2h:85:ARG:HD2	39:2h:134:ILE:O	2.21	0.40
41:2j:50:ILE:HA	41:2j:60:ARG:HD3	2.03	0.40
1:1A:56:C:H2'	1:1A:57:G:O4'	2.21	0.40
1:1A:540:A:H1'	1:1A:604:C:H1'	2.04	0.40
1:1A:831:A:C8	1:1A:839:G:C5	3.09	0.40
1:1A:1371:G:OP1	60:1A:5441:HOH:O	2.22	0.40
1:1A:2863:C:H2'	1:1A:2864:G:C8	2.57	0.40
9:1N:121:LYS:HD3	9:1N:130:HIS:CE1	2.56	0.40
11:1P:21:ARG:HA	11:1P:21:ARG:HD3	1.95	0.40
14:1S:25:ARG:HB3	14:1S:25:ARG:HH11	1.87	0.40
16:1U:46:ALA:O	16:1U:50:ARG:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1W:13:SER:HA	18:1W:14:PRO:HD3	1.92	0.40
21:1Z:40:ASP:OD2	21:1Z:43:GLU:HG3	2.21	0.40
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.53	0.40
22:10:62:LEU:HA	22:10:62:LEU:HD23	1.89	0.40
26:14:62:ARG:HB3	26:14:63:TYR:H	1.65	0.40
32:1a:198:G:O6	32:1a:219:C:N4	2.55	0.40
32:1a:434:U:H2'	32:1a:435:C:C6	2.57	0.40
32:1a:848:C:H2'	32:1a:849:C:H6	1.86	0.40
32:1a:986:A:H2'	32:1a:987:G:O4'	2.21	0.40
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.56	0.40
34:1c:22:TRP:HB3	34:1c:59:ARG:HB2	2.02	0.40
34:1c:112:SER:HB3	34:1c:115:LEU:HB2	2.03	0.40
37:1f:69:GLU:CD	37:1f:69:GLU:H	2.29	0.40
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.77	0.40
1:2A:185:U:H4'	1:2A:218:A:H4'	2.02	0.40
1:2A:1028:A:H2'	1:2A:1029:A:C8	2.56	0.40
1:2A:1515:G:C2	1:2A:1516:C:C2	3.10	0.40
1:2A:1688:U:H2'	1:2A:1698:A:N6	2.36	0.40
1:2A:2118:U:N3	1:2A:2149:G:H1'	2.36	0.40
1:2A:2128:C:H6	1:2A:2128:C:O5'	2.04	0.40
1:2A:2187:G:C6	1:2A:2188:C:C4	3.10	0.40
5:2F:108:LYS:HE2	5:2F:108:LYS:HB2	1.88	0.40
6:2G:107:LEU:HA	6:2G:111:LEU:HD13	2.04	0.40
32:2a:253:U:H2'	32:2a:254:G:H8	1.87	0.40
32:2a:527:7MG:O6	43:2l:49:ASN:ND2	2.55	0.40
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.86	0.40
37:2f:70:ASP:OD1	37:2f:70:ASP:N	2.39	0.40
37:2f:91:VAL:HG12	37:2f:92:LYS:O	2.22	0.40
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.56	0.40
55:2x:66:C:H2'	55:2x:67:C:O4'	2.22	0.40
1:1A:510:C:H2'	1:1A:511:C:H6	1.87	0.40
1:1A:591:U:H5'	1:1A:990:A:N6	2.37	0.40
1:1A:645:G:N3	1:1A:645:G:H2'	2.35	0.40
1:1A:1111:U:H1'	1:1A:1120:G:C2	2.56	0.40
1:1A:1120:G:N1	1:1A:1121:C:H1'	2.37	0.40
1:1A:1140:U:H2'	1:1A:1141:A:C8	2.56	0.40
1:1A:1476:C:H2'	1:1A:1477:U:C6	2.56	0.40
1:1A:1992:A:H4'	1:1A:1993:A:OP1	2.21	0.40
1:1A:2180:A:H1'	1:1A:2181:G:O5'	2.22	0.40
1:1A:2388:A:H2'	1:1A:2389:A:O4'	2.21	0.40
1:1A:2697:G:H5'	10:1O:68:GLU:OE2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2724:U:OP1	1:1A:2727:G:H4'	2.21	0.40
4:1E:178:GLU:H	4:1E:178:GLU:CD	2.28	0.40
11:1P:18:ARG:NH2	11:1P:21:ARG:NH1	2.69	0.40
14:1S:46:VAL:HG12	14:1S:48:LEU:HD12	2.02	0.40
32:1a:255:G:H1'	48:1q:16:GLN:OE1	2.21	0.40
32:1a:300:A:H2'	32:1a:301:G:O4'	2.22	0.40
32:1a:993:G:H2'	32:1a:993:G:N3	2.36	0.40
32:1a:1152:A:H5'	41:1j:13:HIS:CG	2.57	0.40
32:1a:1168:A:H2'	32:1a:1169:A:C8	2.56	0.40
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.57	0.40
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.56	0.40
38:1g:50:ILE:HD11	38:1g:61:VAL:HG21	2.03	0.40
42:1k:16:SER:O	42:1k:35:PRO:HD3	2.20	0.40
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.86	0.40
44:1m:73:GLU:HG2	44:1m:77:ASN:ND2	2.37	0.40
47:1p:14:ASN:N	47:1p:15:PRO:HD3	2.36	0.40
47:1p:18:ARG:HD3	47:1p:35:LYS:HD2	2.04	0.40
53:1v:16:A:H2'	53:1v:17:U:O4'	2.21	0.40
55:1x:8:4SU:O2	55:1x:21:A:H2	2.04	0.40
1:2A:274:G:H2'	1:2A:275:G:H8	1.86	0.40
1:2A:877:U:O2'	1:2A:900:A:N6	2.55	0.40
1:2A:993:G:C2	1:2A:1162:G:C2	3.09	0.40
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.56	0.40
1:2A:1858:G:O6	60:2A:4492:HOH:O	2.21	0.40
1:2A:2205:C:H1'	1:2A:2220:G:N2	2.37	0.40
1:2A:2299:G:H2'	1:2A:2300:G:H8	1.87	0.40
1:2A:2505:G:O6	1:2A:2576:G:H2'	2.22	0.40
1:2A:2615:U:C2	27:25:7:PRO:HA	2.56	0.40
1:2A:2720:U:C4	1:2A:2872:G:C6	3.10	0.40
1:2A:2836:U:H2'	1:2A:2837:G:H8	1.81	0.40
10:2O:104:ARG:HH21	15:2T:36:GLU:CD	2.29	0.40
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.56	0.40
24:22:35:LEU:CD1	24:22:53:LEU:HD12	2.51	0.40
32:2a:14:U:H5"	60:2a:3397:HOH:O	2.21	0.40
32:2a:335:C:O2'	32:2a:1433:A:N3	2.48	0.40
32:2a:582:U:C2	32:2a:760:G:C6	3.10	0.40
32:2a:850:U:H2'	32:2a:851:G:H5"	2.03	0.40
32:2a:1027:C:H2'	32:2a:1034:G:N2	2.36	0.40
32:2a:1128:C:O2'	32:2a:1129:C:P	2.79	0.40
36:2e:40:ARG:HB3	36:2e:66:MET:CE	2.51	0.40
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:3:GLN:HE21	40:2i:20:ARG:HH21	1.68	0.40
40:2i:18:PHE:HB2	40:2i:62:TYR:O	2.22	0.40
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.37	0.40
46:2o:80:ALA:O	46:2o:83:GLU:HG2	2.22	0.40
54:2w:21:A:N6	54:2w:46:7MG:C4	2.90	0.40
54:2y:66:U:O4	54:2y:67:C:N4	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
3	2D	273/276 (99%)	260 (95%)	11 (4%)	2 (1%)	19	35
4	1E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	25	44
4	2E	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	25	44
5	1F	201/210 (96%)	198 (98%)	2 (1%)	1 (0%)	25	44
5	2F	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	13	25
6	1G	179/182 (98%)	170 (95%)	9 (5%)	0	100	100
6	2G	179/182 (98%)	168 (94%)	10 (6%)	1 (1%)	22	39
7	1H	172/180 (96%)	164 (95%)	7 (4%)	1 (1%)	22	39
7	2H	172/180 (96%)	158 (92%)	12 (7%)	2 (1%)	11	21
8	1I	144/148 (97%)	132 (92%)	12 (8%)	0	100	100
8	2I	144/148 (97%)	128 (89%)	14 (10%)	2 (1%)	9	17
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	2N	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	19	35
10	1O	120/122 (98%)	112 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
10	2O	120/122 (98%)	114 (95%)	6 (5%)	0	100 100
11	1P	147/150 (98%)	139 (95%)	8 (5%)	0	100 100
11	2P	147/150 (98%)	137 (93%)	10 (7%)	0	100 100
12	1Q	139/141 (99%)	133 (96%)	6 (4%)	0	100 100
12	2Q	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	19 35
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100 100
13	2R	116/118 (98%)	112 (97%)	4 (3%)	0	100 100
14	1S	108/112 (96%)	106 (98%)	2 (2%)	0	100 100
14	2S	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	14 28
15	1T	129/146 (88%)	123 (95%)	6 (5%)	0	100 100
15	2T	129/146 (88%)	125 (97%)	4 (3%)	0	100 100
16	1U	114/118 (97%)	114 (100%)	0	0	100 100
16	2U	114/118 (97%)	114 (100%)	0	0	100 100
17	1V	99/101 (98%)	97 (98%)	1 (1%)	1 (1%)	13 25
17	2V	99/101 (98%)	97 (98%)	1 (1%)	1 (1%)	13 25
18	1W	110/113 (97%)	110 (100%)	0	0	100 100
18	2W	110/113 (97%)	110 (100%)	0	0	100 100
19	1X	93/96 (97%)	90 (97%)	3 (3%)	0	100 100
19	2X	93/96 (97%)	88 (95%)	4 (4%)	1 (1%)	12 23
20	1Y	105/110 (96%)	98 (93%)	5 (5%)	2 (2%)	6 12
20	2Y	105/110 (96%)	99 (94%)	4 (4%)	2 (2%)	6 12
21	1Z	148/206 (72%)	136 (92%)	11 (7%)	1 (1%)	19 35
21	2Z	156/206 (76%)	141 (90%)	15 (10%)	0	100 100
22	10	81/85 (95%)	80 (99%)	0	1 (1%)	11 21
22	20	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	11 21
23	11	95/98 (97%)	92 (97%)	3 (3%)	0	100 100
23	21	95/98 (97%)	91 (96%)	4 (4%)	0	100 100
24	12	68/72 (94%)	68 (100%)	0	0	100 100
24	22	68/72 (94%)	67 (98%)	1 (2%)	0	100 100
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
25	23	57/60 (95%)	53 (93%)	3 (5%)	1 (2%)	7 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
26	14	67/71 (94%)	58 (87%)	4 (6%)	5 (8%)	1 1
26	24	67/71 (94%)	53 (79%)	10 (15%)	4 (6%)	1 1
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
27	25	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
28	26	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
29	17	46/49 (94%)	44 (96%)	2 (4%)	0	100 100
29	27	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	5 9
30	18	62/65 (95%)	62 (100%)	0	0	100 100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100 100
31	19	35/37 (95%)	35 (100%)	0	0	100 100
31	29	35/37 (95%)	35 (100%)	0	0	100 100
33	1b	229/256 (90%)	200 (87%)	22 (10%)	7 (3%)	3 5
33	2b	229/256 (90%)	202 (88%)	19 (8%)	8 (4%)	3 4
34	1c	204/239 (85%)	188 (92%)	15 (7%)	1 (0%)	25 44
34	2c	204/239 (85%)	187 (92%)	15 (7%)	2 (1%)	13 25
35	1d	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	25 44
35	2d	206/209 (99%)	197 (96%)	8 (4%)	1 (0%)	25 44
36	1e	146/162 (90%)	137 (94%)	6 (4%)	3 (2%)	5 10
36	2e	146/162 (90%)	139 (95%)	5 (3%)	2 (1%)	9 17
37	1f	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
37	2f	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
38	1g	153/156 (98%)	144 (94%)	6 (4%)	3 (2%)	6 11
38	2g	153/156 (98%)	143 (94%)	7 (5%)	3 (2%)	6 11
39	1h	135/138 (98%)	133 (98%)	2 (2%)	0	100 100
39	2h	135/138 (98%)	131 (97%)	4 (3%)	0	100 100
40	1i	125/128 (98%)	115 (92%)	9 (7%)	1 (1%)	16 31
40	2i	125/128 (98%)	114 (91%)	10 (8%)	1 (1%)	16 31
41	1j	95/105 (90%)	86 (90%)	4 (4%)	5 (5%)	1 1
41	2j	94/105 (90%)	85 (90%)	5 (5%)	4 (4%)	2 3
42	1k	112/129 (87%)	106 (95%)	4 (4%)	2 (2%)	7 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
42	2k	112/129 (87%)	107 (96%)	3 (3%)	2 (2%)	7 12
43	1l	119/132 (90%)	115 (97%)	4 (3%)	0	100 100
43	2l	119/132 (90%)	112 (94%)	7 (6%)	0	100 100
44	1m	121/126 (96%)	114 (94%)	7 (6%)	0	100 100
44	2m	120/126 (95%)	110 (92%)	9 (8%)	1 (1%)	16 31
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100 100
45	2n	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
46	1o	86/89 (97%)	82 (95%)	4 (5%)	0	100 100
46	2o	86/89 (97%)	81 (94%)	4 (5%)	1 (1%)	11 21
47	1p	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	10 19
47	2p	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	10 19
48	1q	97/105 (92%)	93 (96%)	3 (3%)	1 (1%)	13 25
48	2q	97/105 (92%)	94 (97%)	2 (2%)	1 (1%)	13 25
49	1r	66/88 (75%)	65 (98%)	1 (2%)	0	100 100
49	2r	66/88 (75%)	65 (98%)	1 (2%)	0	100 100
50	1s	81/93 (87%)	75 (93%)	5 (6%)	1 (1%)	11 21
50	2s	81/93 (87%)	74 (91%)	5 (6%)	2 (2%)	4 7
51	1t	94/106 (89%)	87 (93%)	0	7 (7%)	1 1
51	2t	94/106 (89%)	86 (92%)	4 (4%)	4 (4%)	2 3
52	1u	21/27 (78%)	21 (100%)	0	0	100 100
52	2u	21/27 (78%)	21 (100%)	0	0	100 100
All	All	11370/12128 (94%)	10779 (95%)	488 (4%)	103 (1%)	14 28

All (103) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
7	1H	126	PRO
21	1Z	159	PRO
26	14	62	ARG
33	1b	10	LEU
38	1g	79	ARG
40	1i	54	ASP
41	1j	55	LYS
50	1s	81	ARG

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Mol	Chain	Res	Type
51	1t	10	LEU
51	1t	100	ILE
5	2F	21	ALA
5	2F	130	ALA
7	2H	126	PRO
8	2I	10	GLU
17	2V	79	VAL
26	24	55	ARG
26	24	61	ARG
29	27	46	VAL
33	2b	16	HIS
33	2b	123	ALA
34	2c	181	ASN
38	2g	79	ARG
44	2m	4	ILE
50	2s	81	ARG
51	2t	10	LEU
17	1V	79	VAL
26	14	45	GLY
26	14	56	VAL
42	1k	49	GLY
3	2D	69	ARG
6	2G	50	ALA
8	2I	40	THR
14	2S	84	GLN
26	24	45	GLY
40	2i	54	ASP
51	2t	47	GLY
4	1E	52	LEU
22	10	13	GLY
33	1b	17	PHE
38	1g	80	VAL
41	1j	32	ALA
41	1j	77	PRO
41	1j	78	ASN
51	1t	47	GLY
51	1t	96	GLY
51	1t	102	GLY
4	2E	52	LEU
9	2N	2	LYS
19	2X	2	LYS
26	24	46	GLN

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Mol	Chain	Res	Type
33	2b	125	PRO
36	2e	37	ARG
41	2j	77	PRO
48	2q	33	GLY
50	2s	29	ARG
26	14	57	GLU
33	1b	16	HIS
33	1b	20	GLU
33	1b	22	LYS
34	1c	66	VAL
35	1d	178	VAL
36	1e	86	ALA
51	1t	95	ALA
3	2D	3	VAL
20	2Y	103	GLY
33	2b	20	GLU
33	2b	78	GLN
34	2c	156	ARG
38	2g	7	ALA
38	2g	80	VAL
41	2j	78	ASN
51	2t	100	ILE
20	1Y	54	LYS
26	14	53	GLU
33	1b	231	GLU
41	1j	79	ARG
42	1k	105	VAL
20	2Y	57	GLN
22	20	4	LYS
33	2b	21	ARG
33	2b	231	GLU
41	2j	55	LYS
42	2k	49	GLY
46	2o	88	ARG
38	1g	4	ARG
51	1t	9	ASN
7	2H	29	PRO
36	2e	69	VAL
42	2k	105	VAL
47	2p	53	VAL
48	1q	33	GLY
25	23	59	VAL

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Mol	Chain	Res	Type
51	2t	102	GLY
20	1Y	103	GLY
36	1e	69	VAL
36	1e	85	GLY
47	1p	53	VAL
33	2b	202	PRO
41	2j	75	ILE
12	2Q	27	VAL
35	2d	5	ILE
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%)	207 (96%)	8 (4%)	29 55
3	2D	215/218 (99%)	206 (96%)	9 (4%)	25 49
4	1E	164/166 (99%)	152 (93%)	12 (7%)	11 24
4	2E	164/166 (99%)	152 (93%)	12 (7%)	11 24
5	1F	160/166 (96%)	147 (92%)	13 (8%)	9 20
5	2F	159/166 (96%)	149 (94%)	10 (6%)	15 30
6	1G	143/156 (92%)	137 (96%)	6 (4%)	25 49
6	2G	143/156 (92%)	134 (94%)	9 (6%)	15 30
7	1H	144/148 (97%)	139 (96%)	5 (4%)	31 57
7	2H	144/148 (97%)	141 (98%)	3 (2%)	48 74
8	1I	113/124 (91%)	104 (92%)	9 (8%)	10 20
8	2I	105/124 (85%)	99 (94%)	6 (6%)	17 35
9	1N	118/119 (99%)	109 (92%)	9 (8%)	11 22
9	2N	118/119 (99%)	107 (91%)	11 (9%)	7 15
10	1O	100/100 (100%)	97 (97%)	3 (3%)	36 63
10	2O	100/100 (100%)	98 (98%)	2 (2%)	50 75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
11	1P	115/116 (99%)	109 (95%)	6 (5%)	19 39
11	2P	115/116 (99%)	110 (96%)	5 (4%)	25 48
12	1Q	111/111 (100%)	108 (97%)	3 (3%)	40 67
12	2Q	111/111 (100%)	105 (95%)	6 (5%)	18 37
13	1R	101/101 (100%)	91 (90%)	10 (10%)	6 13
13	2R	101/101 (100%)	94 (93%)	7 (7%)	13 26
14	1S	86/88 (98%)	82 (95%)	4 (5%)	22 44
14	2S	85/88 (97%)	81 (95%)	4 (5%)	22 44
15	1T	115/127 (91%)	113 (98%)	2 (2%)	56 79
15	2T	113/127 (89%)	112 (99%)	1 (1%)	75 90
16	1U	93/94 (99%)	90 (97%)	3 (3%)	34 60
16	2U	93/94 (99%)	92 (99%)	1 (1%)	70 87
17	1V	80/82 (98%)	74 (92%)	6 (8%)	11 23
17	2V	80/82 (98%)	73 (91%)	7 (9%)	8 17
18	1W	90/92 (98%)	84 (93%)	6 (7%)	13 28
18	2W	90/92 (98%)	83 (92%)	7 (8%)	10 21
19	1X	77/78 (99%)	75 (97%)	2 (3%)	41 68
19	2X	77/78 (99%)	75 (97%)	2 (3%)	41 68
20	1Y	85/91 (93%)	80 (94%)	5 (6%)	16 33
20	2Y	85/91 (93%)	82 (96%)	3 (4%)	31 57
21	1Z	135/179 (75%)	128 (95%)	7 (5%)	19 39
21	2Z	137/179 (76%)	129 (94%)	8 (6%)	17 34
22	10	65/67 (97%)	64 (98%)	1 (2%)	60 82
22	20	65/67 (97%)	65 (100%)	0	100 100
23	11	80/83 (96%)	77 (96%)	3 (4%)	28 53
23	21	80/83 (96%)	78 (98%)	2 (2%)	42 69
24	12	65/67 (97%)	64 (98%)	1 (2%)	60 82
24	22	65/67 (97%)	65 (100%)	0	100 100
25	13	51/52 (98%)	48 (94%)	3 (6%)	16 33
25	23	50/52 (96%)	48 (96%)	2 (4%)	27 51
26	14	59/63 (94%)	56 (95%)	3 (5%)	20 40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
26	24	53/63 (84%)	47 (89%)	6 (11%)	4 9
27	15	50/52 (96%)	47 (94%)	3 (6%)	16 33
27	25	50/52 (96%)	47 (94%)	3 (6%)	16 33
28	16	51/52 (98%)	48 (94%)	3 (6%)	16 33
28	26	50/52 (96%)	49 (98%)	1 (2%)	50 75
29	17	41/42 (98%)	40 (98%)	1 (2%)	44 70
29	27	41/42 (98%)	39 (95%)	2 (5%)	21 42
30	18	54/55 (98%)	52 (96%)	2 (4%)	29 55
30	28	54/55 (98%)	51 (94%)	3 (6%)	17 36
31	19	34/34 (100%)	34 (100%)	0	100 100
31	29	34/34 (100%)	33 (97%)	1 (3%)	37 64
33	1b	192/220 (87%)	190 (99%)	2 (1%)	73 88
33	2b	187/220 (85%)	182 (97%)	5 (3%)	40 67
34	1c	142/188 (76%)	138 (97%)	4 (3%)	38 65
34	2c	140/188 (74%)	135 (96%)	5 (4%)	30 56
35	1d	169/181 (93%)	160 (95%)	9 (5%)	19 38
35	2d	173/181 (96%)	167 (96%)	6 (4%)	31 57
36	1e	113/123 (92%)	109 (96%)	4 (4%)	31 57
36	2e	114/123 (93%)	109 (96%)	5 (4%)	24 47
37	1f	84/90 (93%)	83 (99%)	1 (1%)	67 86
37	2f	85/90 (94%)	82 (96%)	3 (4%)	31 57
38	1g	119/127 (94%)	117 (98%)	2 (2%)	56 79
38	2g	120/127 (94%)	115 (96%)	5 (4%)	25 49
39	1h	114/119 (96%)	111 (97%)	3 (3%)	41 68
39	2h	114/119 (96%)	111 (97%)	3 (3%)	41 68
40	1i	90/99 (91%)	86 (96%)	4 (4%)	24 47
40	2i	89/99 (90%)	82 (92%)	7 (8%)	10 21
41	1j	66/92 (72%)	66 (100%)	0	100 100
41	2j	69/92 (75%)	66 (96%)	3 (4%)	25 48
42	1k	82/99 (83%)	79 (96%)	3 (4%)	29 55
42	2k	83/99 (84%)	82 (99%)	1 (1%)	67 86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
43	1l	96/108 (89%)	92 (96%)	4 (4%)	25 49
43	2l	96/108 (89%)	94 (98%)	2 (2%)	48 74
44	1m	93/101 (92%)	91 (98%)	2 (2%)	47 73
44	2m	92/101 (91%)	91 (99%)	1 (1%)	70 87
45	1n	49/50 (98%)	43 (88%)	6 (12%)	4 8
45	2n	49/50 (98%)	46 (94%)	3 (6%)	15 32
46	1o	78/80 (98%)	75 (96%)	3 (4%)	28 53
46	2o	78/80 (98%)	76 (97%)	2 (3%)	41 68
47	1p	69/74 (93%)	64 (93%)	5 (7%)	12 24
47	2p	68/74 (92%)	63 (93%)	5 (7%)	11 23
48	1q	94/97 (97%)	93 (99%)	1 (1%)	70 87
48	2q	94/97 (97%)	92 (98%)	2 (2%)	48 74
49	1r	59/77 (77%)	57 (97%)	2 (3%)	32 58
49	2r	59/77 (77%)	56 (95%)	3 (5%)	20 40
50	1s	69/80 (86%)	67 (97%)	2 (3%)	37 64
50	2s	67/80 (84%)	64 (96%)	3 (4%)	23 46
51	1t	70/82 (85%)	69 (99%)	1 (1%)	62 83
51	2t	70/82 (85%)	70 (100%)	0	100 100
52	1u	18/22 (82%)	18 (100%)	0	100 100
52	2u	18/22 (82%)	18 (100%)	0	100 100
All	All	9303/10064 (92%)	8909 (96%)	394 (4%)	25 49

All (394) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	106	ILE
3	1D	113	VAL
3	1D	142	VAL
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	257	LEU
4	1E	9	VAL
4	1E	12	THR

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Mol	Chain	Res	Type
4	1E	19	ARG
4	1E	21	VAL
4	1E	24	THR
4	1E	34	VAL
4	1E	73	GLU
4	1E	75	VAL
4	1E	78	LEU
4	1E	116	VAL
4	1E	175	VAL
4	1E	181	LEU
5	1F	18	ARG
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	125	LEU
5	1F	132	VAL
5	1F	170	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	31	VAL
6	1G	43	LEU
6	1G	82	LEU
6	1G	135	LEU
6	1G	148	MET
6	1G	159	VAL
7	1H	15	VAL
7	1H	25	LYS
7	1H	51	ARG
7	1H	71	LEU
7	1H	129	THR
8	1I	44	LEU
8	1I	47	LEU
8	1I	92	VAL
8	1I	101	LEU
8	1I	107	VAL
8	1I	108	THR
8	1I	109	ILE
8	1I	123	LEU

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Mol	Chain	Res	Type
8	1I	142	VAL
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	46	VAL
9	1N	62	VAL
9	1N	73	THR
9	1N	99	LEU
9	1N	120	LEU
10	1O	10	VAL
10	1O	98	VAL
10	1O	108	GLU
11	1P	83	VAL
11	1P	95	VAL
11	1P	98	GLU
11	1P	106	LEU
11	1P	112	LEU
11	1P	125	VAL
12	1Q	35	VAL
12	1Q	109	VAL
12	1Q	110	THR
13	1R	6	SER
13	1R	29	LEU
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	65	LEU
13	1R	79	LEU
13	1R	100	LEU
13	1R	111	LEU
13	1R	114	VAL
14	1S	14	VAL
14	1S	25	ARG
14	1S	49	VAL
14	1S	110	LEU
15	1T	28	VAL
15	1T	89	VAL
16	1U	8	VAL
16	1U	74	LEU
16	1U	95	LEU
17	1V	46	VAL

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Mol	Chain	Res	Type
17	1V	51	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	72	VAL
17	1V	79	VAL
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	67	ASP
18	1W	78	GLU
18	1W	107	LEU
19	1X	35	THR
19	1X	57	LEU
20	1Y	1	MET
20	1Y	7	VAL
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	90	LEU
21	1Z	5	LEU
21	1Z	86	VAL
21	1Z	126	VAL
21	1Z	129	SER
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	171	ILE
22	10	43	THR
23	11	30	VAL
23	11	35	THR
23	11	95	LEU
24	12	40	SER
25	13	23	LEU
25	13	54	VAL
25	13	60	GLU
26	14	27	THR
26	14	49	PHE
26	14	50	VAL
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
28	16	14	THR
28	16	37	ARG
28	16	48	VAL

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Mol	Chain	Res	Type
29	17	43	THR
30	18	14	VAL
30	18	32	LEU
33	1b	112	VAL
33	1b	208	ILE
34	1c	21	ARG
34	1c	57	ILE
34	1c	70	VAL
34	1c	195	VAL
35	1d	5	ILE
35	1d	10	ARG
35	1d	31	CYS
35	1d	49	ARG
35	1d	134	ASP
35	1d	135	LEU
35	1d	158	ILE
35	1d	178	VAL
35	1d	194	LEU
36	1e	20	GLN
36	1e	31	LEU
36	1e	41	VAL
36	1e	56	GLN
37	1f	40	VAL
38	1g	8	GLU
38	1g	113	GLU
39	1h	51	VAL
39	1h	69	ARG
39	1h	112	LEU
40	1i	42	ARG
40	1i	64	THR
40	1i	65	VAL
40	1i	128	ARG
42	1k	31	THR
42	1k	48	ILE
42	1k	114	VAL
43	1l	27	LEU
43	1l	36	VAL
43	1l	83	VAL
43	1l	84	LEU
44	1m	19	LEU
44	1m	102	ARG
45	1n	3	ARG

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Mol	Chain	Res	Type
45	1n	6	LEU
45	1n	7	ILE
45	1n	22	THR
45	1n	23	ARG
45	1n	33	VAL
46	1o	7	GLU
46	1o	39	LEU
46	1o	77	ARG
47	1p	2	VAL
47	1p	19	ILE
47	1p	20	VAL
47	1p	21	VAL
47	1p	67	THR
48	1q	35	VAL
49	1r	37	VAL
49	1r	76	LEU
50	1s	5	LEU
50	1s	41	VAL
51	1t	13	LEU
3	2D	3	VAL
3	2D	94	LEU
3	2D	106	ILE
3	2D	113	VAL
3	2D	134	ARG
3	2D	142	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	276	LYS
4	2E	9	VAL
4	2E	12	THR
4	2E	21	VAL
4	2E	24	THR
4	2E	34	VAL
4	2E	52	LEU
4	2E	75	VAL
4	2E	78	LEU
4	2E	116	VAL
4	2E	134	ILE
4	2E	175	VAL
4	2E	181	LEU
5	2F	53	THR
5	2F	70	THR

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Mol	Chain	Res	Type
5	2F	74	ARG
5	2F	88	VAL
5	2F	106	ARG
5	2F	132	VAL
5	2F	170	LEU
5	2F	183	VAL
5	2F	192	LEU
5	2F	201	VAL
6	2G	28	VAL
6	2G	31	VAL
6	2G	43	LEU
6	2G	60	LEU
6	2G	79	ASN
6	2G	115	ARG
6	2G	135	LEU
6	2G	159	VAL
6	2G	161	THR
7	2H	71	LEU
7	2H	84	SER
7	2H	88	LEU
8	2I	38	LEU
8	2I	44	LEU
8	2I	47	LEU
8	2I	92	VAL
8	2I	121	LYS
8	2I	123	LEU
9	2N	14	VAL
9	2N	28	THR
9	2N	33	LEU
9	2N	34	LEU
9	2N	46	VAL
9	2N	58	ASP
9	2N	62	VAL
9	2N	67	LEU
9	2N	87	LEU
9	2N	99	LEU
9	2N	120	LEU
10	2O	8	LEU
10	2O	10	VAL
11	2P	83	VAL
11	2P	95	VAL
11	2P	99	LEU

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Mol	Chain	Res	Type
11	2P	106	LEU
11	2P	125	VAL
12	2Q	1	MET
12	2Q	2	LEU
12	2Q	21	THR
12	2Q	35	VAL
12	2Q	109	VAL
12	2Q	110	THR
13	2R	18	LEU
13	2R	29	LEU
13	2R	44	LEU
13	2R	65	LEU
13	2R	100	LEU
13	2R	111	LEU
13	2R	114	VAL
14	2S	35	ILE
14	2S	49	VAL
14	2S	75	GLU
14	2S	110	LEU
15	2T	89	VAL
16	2U	74	LEU
17	2V	43	GLU
17	2V	46	VAL
17	2V	51	VAL
17	2V	61	VAL
17	2V	72	VAL
17	2V	79	VAL
17	2V	82	ARG
18	2W	6	ILE
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	67	ASP
18	2W	100	THR
18	2W	107	LEU
19	2X	35	THR
19	2X	57	LEU
20	2Y	28	LYS
20	2Y	72	VAL
20	2Y	90	LEU
21	2Z	5	LEU
21	2Z	74	VAL

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Mol	Chain	Res	Type
21	2Z	124	ILE
21	2Z	126	VAL
21	2Z	135	GLU
21	2Z	155	LEU
21	2Z	161	VAL
21	2Z	171	ILE
23	21	4	VAL
23	21	95	LEU
25	23	30	ARG
25	23	54	VAL
26	24	27	THR
26	24	34	GLU
26	24	37	SER
26	24	48	ARG
26	24	49	PHE
26	24	50	VAL
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
28	26	48	VAL
29	27	39	ARG
29	27	43	THR
30	28	14	VAL
30	28	30	ARG
30	28	32	LEU
31	29	17	ILE
33	2b	11	LEU
33	2b	93	VAL
33	2b	126	GLU
33	2b	127	ILE
33	2b	221	LEU
34	2c	57	ILE
34	2c	70	VAL
34	2c	124	ILE
34	2c	152	ILE
34	2c	154	SER
35	2d	31	CYS
35	2d	135	LEU
35	2d	141	ARG
35	2d	150	GLU
35	2d	170	VAL
35	2d	194	LEU

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Mol	Chain	Res	Type
36	2e	13	ILE
36	2e	20	GLN
36	2e	31	LEU
36	2e	41	VAL
36	2e	64	ARG
37	2f	21	LEU
37	2f	40	VAL
37	2f	72	VAL
38	2g	9	VAL
38	2g	30	ILE
38	2g	52	GLU
38	2g	98	SER
38	2g	104	LEU
39	2h	2	LEU
39	2h	23	SER
39	2h	51	VAL
40	2i	17	VAL
40	2i	27	THR
40	2i	53	VAL
40	2i	65	VAL
40	2i	102	LEU
40	2i	108	VAL
40	2i	128	ARG
41	2j	8	LEU
41	2j	49	VAL
41	2j	100	THR
42	2k	114	VAL
43	2l	27	LEU
43	2l	83	VAL
44	2m	47	ASP
45	2n	6	LEU
45	2n	22	THR
45	2n	33	VAL
46	2o	39	LEU
46	2o	65	ARG
47	2p	2	VAL
47	2p	20	VAL
47	2p	21	VAL
47	2p	62	VAL
47	2p	67	THR
48	2q	35	VAL
48	2q	83	ASP

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Mol	Chain	Res	Type
49	2r	37	VAL
49	2r	76	LEU
49	2r	84	LYS
50	2s	41	VAL
50	2s	49	ILE
50	2s	77	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (120) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
4	1E	48	GLN
4	1E	121	ASN
5	1F	8	GLN
5	1F	40	GLN
8	1I	104	GLN
8	1I	105	HIS
8	1I	139	GLN
9	1N	56	ASN
10	1O	3	GLN
13	1R	71	GLN
13	1R	91	GLN
14	1S	95	HIS
15	1T	43	GLN
15	1T	90	GLN
16	1U	81	HIS
16	1U	117	GLN
17	1V	80	GLN
18	1W	60	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	43	ASN
21	1Z	73	GLN
23	11	19	GLN
23	11	56	GLN
24	12	9	GLN
25	13	32	GLN
26	14	47	GLN
33	1b	78	GLN
33	1b	113	HIS
33	1b	140	HIS

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Mol	Chain	Res	Type
34	1c	6	HIS
34	1c	98	ASN
34	1c	162	GLN
34	1c	181	ASN
35	1d	74	GLN
35	1d	77	ASN
35	1d	116	GLN
35	1d	123	HIS
35	1d	125	HIS
36	1e	38	GLN
36	1e	78	HIS
36	1e	141	GLN
38	1g	28	ASN
38	1g	86	GLN
38	1g	148	ASN
40	1i	3	GLN
40	1i	31	GLN
40	1i	58	HIS
40	1i	117	HIS
40	1i	124	GLN
41	1j	56	HIS
42	1k	93	GLN
42	1k	99	GLN
43	1l	99	HIS
44	1m	77	ASN
50	1s	23	ASN
50	1s	69	HIS
50	1s	83	HIS
51	1t	75	ASN
3	2D	87	ASN
5	2F	40	GLN
5	2F	69	HIS
6	2G	40	ASN
6	2G	41	GLN
8	2I	104	GLN
8	2I	105	HIS
8	2I	139	GLN
9	2N	38	HIS
12	2Q	12	GLN
12	2Q	57	HIS
13	2R	13	HIS
13	2R	24	GLN

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Mol	Chain	Res	Type
13	2R	31	HIS
14	2S	38	GLN
15	2T	79	HIS
15	2T	90	GLN
16	2U	117	GLN
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	6	HIS
21	2Z	55	HIS
22	20	3	HIS
22	20	35	ASN
23	21	56	GLN
24	22	9	GLN
24	22	70	GLN
26	24	46	GLN
31	29	20	HIS
33	2b	40	HIS
33	2b	94	ASN
33	2b	140	HIS
33	2b	212	GLN
34	2c	37	GLN
34	2c	98	ASN
35	2d	77	ASN
35	2d	119	GLN
35	2d	125	HIS
35	2d	161	ASN
36	2e	78	HIS
37	2f	64	GLN
37	2f	73	ASN
38	2g	28	ASN
38	2g	86	GLN
38	2g	122	HIS
39	2h	78	GLN
40	2i	3	GLN
40	2i	58	HIS
40	2i	124	GLN
42	2k	22	HIS
42	2k	78	GLN
43	2l	99	HIS
44	2m	77	ASN
46	2o	28	GLN

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Mol	Chain	Res	Type
50	2s	47	HIS
50	2s	56	GLN
50	2s	69	HIS
51	2t	75	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	419 (14%)	43 (1%)
1	2A	2791/2915 (95%)	510 (18%)	28 (1%)
2	1B	120/121 (99%)	11 (9%)	1 (0%)
2	2B	118/121 (97%)	35 (29%)	0
32	1a	1497/1521 (98%)	244 (16%)	0
32	2a	1501/1521 (98%)	255 (16%)	0
53	1v	12/24 (50%)	4 (33%)	0
53	2v	12/24 (50%)	3 (25%)	0
54	1w	72/76 (94%)	22 (30%)	0
54	1y	72/76 (94%)	23 (31%)	0
54	2w	69/76 (90%)	27 (39%)	0
54	2y	70/76 (92%)	24 (34%)	0
55	1x	75/77 (97%)	8 (10%)	0
55	2x	75/77 (97%)	16 (21%)	0
All	All	9348/9620 (97%)	1601 (17%)	72 (0%)

All (1601) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	13	A
1	1A	34	C
1	1A	45	C
1	1A	60	G
1	1A	70	A
1	1A	71	U
1	1A	73	A
1	1A	74	G
1	1A	83	A
1	1A	117	A
1	1A	118	U
1	1A	137	G
1	1A	185	A

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Mol	Chain	Res	Type
1	1A	186	A
1	1A	189	U
1	1A	194	G
1	1A	203	G
1	1A	204	G
1	1A	205	A
1	1A	211	A
1	1A	217	A
1	1A	218	A
1	1A	222	A
1	1A	237	G
1	1A	258	U
1	1A	271	U
1	1A	272	U
1	1A	273	G
1	1A	288	U
1	1A	289	G
1	1A	296	U
1	1A	303	C
1	1A	335	A
1	1A	353	G
1	1A	354	A
1	1A	376	G
1	1A	387	G
1	1A	388	A
1	1A	389	G
1	1A	407	U
1	1A	413	G
1	1A	423	G
1	1A	427	G
1	1A	432	U
1	1A	438	G
1	1A	455	A
1	1A	470	C
1	1A	474	U
1	1A	477	C
1	1A	480	A
1	1A	482	C
1	1A	483	A
1	1A	505	A
1	1A	507	G
1	1A	529	U

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Mol	Chain	Res	Type
1	1A	530	A
1	1A	534	C
1	1A	537	G
1	1A	555	G
1	1A	556	C
1	1A	557	A
1	1A	558	G
1	1A	569	G
1	1A	573	G
1	1A	586	G
1	1A	596	G
1	1A	598	A
1	1A	609	A
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	639	G
1	1A	641	G
1	1A	642	G
1	1A	652	A
1	1A	659	C
1	1A	660	C
1	1A	662	A
1	1A	670	C
1	1A	671	A
1	1A	697	C
1	1A	716	G
1	1A	733	G
1	1A	777	C
1	1A	793	A
1	1A	794	U
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	831	A
1	1A	832	G
1	1A	837	C
1	1A	839	G
1	1A	848	G
1	1A	852	G
1	1A	859	C
1	1A	866	A

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Mol	Chain	Res	Type
1	1A	874	U
1	1A	875	U
1	1A	906	G
1	1A	913	A
1	1A	924	U
1	1A	926	G
1	1A	927	G
1	1A	931	C
1	1A	932	C
1	1A	933	C
1	1A	934	A
1	1A	935	C
1	1A	936	C
1	1A	937	A
1	1A	940	C
1	1A	941	U
1	1A	942	A
1	1A	943	C
1	1A	944	C
1	1A	946	A
1	1A	953	U
1	1A	956	A
1	1A	977	G
1	1A	990	A
1	1A	991	G
1	1A	998	A
1	1A	1006	C
1	1A	1008	U
1	1A	1019	G
1	1A	1020	C
1	1A	1029	A
1	1A	1042	A
1	1A	1055	A
1	1A	1058	U
1	1A	1059	C
1	1A	1068	G
1	1A	1072	U
1	1A	1073	A
1	1A	1079	U
1	1A	1084	C
1	1A	1090	G
1	1A	1091	A

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Mol	Chain	Res	Type
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A
1	1A	1100	A
1	1A	1101	G
1	1A	1104	G
1	1A	1112	U
1	1A	1114	G
1	1A	1117	G
1	1A	1119	A
1	1A	1120	G
1	1A	1121	C
1	1A	1122	C
1	1A	1124	U
1	1A	1125	C
1	1A	1127	U
1	1A	1129	U
1	1A	1130	A
1	1A	1134	A
1	1A	1135	G
1	1A	1136	U
1	1A	1137	G
1	1A	1139	G
1	1A	1140	U
1	1A	1142	A
1	1A	1146	C
1	1A	1147	U
1	1A	1148	C
1	1A	1149	A
1	1A	1153	G
1	1A	1156	G
1	1A	1157	A
1	1A	1158	G
1	1A	1162	C
1	1A	1180	C
1	1A	1181	G
1	1A	1195	G
1	1A	1201	A
1	1A	1217	G
1	1A	1218	G
1	1A	1219	A
1	1A	1220	U

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Mol	Chain	Res	Type
1	1A	1221	G
1	1A	1222	A
1	1A	1223	C
1	1A	1256	U
1	1A	1299	A
1	1A	1302	G
1	1A	1317	G
1	1A	1318	A
1	1A	1322	A
1	1A	1346	U
1	1A	1347	A
1	1A	1349	G
1	1A	1366	C
1	1A	1391	C
1	1A	1398	U
1	1A	1405	A
1	1A	1406	A
1	1A	1411	A
1	1A	1426	G
1	1A	1430	A
1	1A	1431	G
1	1A	1441	A
1	1A	1442	U
1	1A	1462	G
1	1A	1463	C
1	1A	1466	U
1	1A	1467	G
1	1A	1474	C
1	1A	1491	A
1	1A	1497	G
1	1A	1502	G
1	1A	1514	C
1	1A	1529	G
1	1A	1539	C
1	1A	1540	A
1	1A	1554	A
1	1A	1555	C
1	1A	1556	A
1	1A	1569	U
1	1A	1586	G
1	1A	1587	U
1	1A	1605	A

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Mol	Chain	Res	Type
1	1A	1613	A
1	1A	1616	A
1	1A	1625	U
1	1A	1627	A
1	1A	1628	G
1	1A	1631	C
1	1A	1632	A
1	1A	1654	A
1	1A	1686	U
1	1A	1694	G
1	1A	1695	C
1	1A	1700	G
1	1A	1701	A
1	1A	1721	G
1	1A	1741	C
1	1A	1743	G
1	1A	1747	A
1	1A	1750	G
1	1A	1767	A
1	1A	1768	U
1	1A	1776	G
1	1A	1787	G
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1811	A
1	1A	1813	C
1	1A	1817	A
1	1A	1822	A
1	1A	1831	C
1	1A	1847	G
1	1A	1848	G
1	1A	1859	G
1	1A	1860	A
1	1A	1878	A
1	1A	1889	G
1	1A	1892	G
1	1A	1899	A
1	1A	1911	A
1	1A	1922	A
1	1A	1928	G
1	1A	1951	G

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Mol	Chain	Res	Type
1	1A	1952	G
1	1A	1959	A
1	1A	1960	A
1	1A	1977	U
1	1A	1985	U
1	1A	1989	C
1	1A	1992	A
1	1A	1993	A
1	1A	1994	A
1	1A	2014	G
1	1A	2015	U
1	1A	2019	G
1	1A	2042	A
1	1A	2045	G
1	1A	2053	A
1	1A	2054	G
1	1A	2055	A
1	1A	2057	G
1	1A	2061	C
1	1A	2065	C
1	1A	2077	C
1	1A	2078	G
1	1A	2082	A
1	1A	2083	G
1	1A	2084	A
1	1A	2091	G
1	1A	2115	G
1	1A	2132	G
1	1A	2135	U
1	1A	2136	A
1	1A	2137	G
1	1A	2138	G
1	1A	2143	G
1	1A	2149	G
1	1A	2151	C
1	1A	2152	U
1	1A	2153	G
1	1A	2154	U
1	1A	2155	G
1	1A	2156	A
1	1A	2157	A
1	1A	2162	C

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Mol	Chain	Res	Type
1	1A	2163	G
1	1A	2164	C
1	1A	2166	U
1	1A	2168	C
1	1A	2172	U
1	1A	2173	G
1	1A	2178	G
1	1A	2179	G
1	1A	2180	A
1	1A	2181	G
1	1A	2182	G
1	1A	2184	G
1	1A	2187	G
1	1A	2188	G
1	1A	2189	U
1	1A	2193	A
1	1A	2194	U
1	1A	2197	C
1	1A	2200	C
1	1A	2203	G
1	1A	2204	G
1	1A	2206	G
1	1A	2207	C
1	1A	2214	G
1	1A	2220	A
1	1A	2227	G
1	1A	2228	G
1	1A	2229	A
1	1A	2231	G
1	1A	2237	A
1	1A	2250	G
1	1A	2251	G
1	1A	2280	A
1	1A	2281	A
1	1A	2292	G
1	1A	2295	C
1	1A	2299	A
1	1A	2317	A
1	1A	2320	G
1	1A	2321	A
1	1A	2332	A
1	1A	2337	G

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Mol	Chain	Res	Type
1	1A	2346	G
1	1A	2359	C
1	1A	2362	C
1	1A	2373	A
1	1A	2384	G
1	1A	2395	G
1	1A	2397	C
1	1A	2418	U
1	1A	2419	G
1	1A	2422	G
1	1A	2436	C
1	1A	2437	A
1	1A	2441	G
1	1A	2442	A
1	1A	2443	U
1	1A	2447	A
1	1A	2451	A
1	1A	2453	C
1	1A	2460	A
1	1A	2486	C
1	1A	2488	A
1	1A	2514	G
1	1A	2517	G
1	1A	2518	U
1	1A	2530	A
1	1A	2541	G
1	1A	2561	G
1	1A	2566	U
1	1A	2578	A
1	1A	2579	G
1	1A	2585	C
1	1A	2586	G
1	1A	2590	G
1	1A	2614	A
1	1A	2621	U
1	1A	2623	U
1	1A	2624	C
1	1A	2641	A
1	1A	2642	G
1	1A	2653	G
1	1A	2666	A
1	1A	2701	U

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Mol	Chain	Res	Type
1	1A	2702	C
1	1A	2703	C
1	1A	2714	U
1	1A	2725	A
1	1A	2726	A
1	1A	2727	G
1	1A	2739	U
1	1A	2746	A
1	1A	2770	A
1	1A	2771	A
1	1A	2778	A
1	1A	2782	C
1	1A	2791	A
1	1A	2803	A
1	1A	2804	C
1	1A	2806	G
1	1A	2813	G
1	1A	2828	G
1	1A	2830	A
1	1A	2831	A
1	1A	2845	A
1	1A	2846	U
1	1A	2879	G
1	1A	2882	G
1	1A	2890	C
1	1A	2901	A
1	1A	2903	G
2	1B	2	C
2	1B	12	C
2	1B	25	A
2	1B	35	U
2	1B	45	A
2	1B	56	G
2	1B	67	G
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G

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Mol	Chain	Res	Type
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	54	C
32	1a	61	G
32	1a	65	U
32	1a	79	G
32	1a	91	C
32	1a	97	G
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	163	C
32	1a	174	C
32	1a	180	U
32	1a	182	U
32	1a	195	A
32	1a	197	A
32	1a	201	C
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	217	C
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	306	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	342	C
32	1a	348	G
32	1a	352	C
32	1a	353	A

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Mol	Chain	Res	Type
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	421	U
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	441	A
32	1a	442	C
32	1a	452	A
32	1a	461	A
32	1a	470	C
32	1a	471	G
32	1a	477	A
32	1a	484	G
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	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	630	G
32	1a	653	A

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Mol	Chain	Res	Type
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	721	G
32	1a	723	U
32	1a	731	G
32	1a	733	A
32	1a	749	C
32	1a	755	G
32	1a	774	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	815	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	853	G
32	1a	859	A
32	1a	870	U
32	1a	880	C
32	1a	885	G
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	932	C
32	1a	934	C
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A

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Mol	Chain	Res	Type
32	1a	982	U
32	1a	989	C
32	1a	992	U
32	1a	993	G
32	1a	997	U
32	1a	1000	U
32	1a	1001(A)	G
32	1a	1002	G
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1011	G
32	1a	1016	A
32	1a	1020	U
32	1a	1021	G
32	1a	1022	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1039	C
32	1a	1045	C
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1080	A
32	1a	1081	G
32	1a	1086	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1108	G
32	1a	1122	U
32	1a	1125	U
32	1a	1129	C

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Mol	Chain	Res	Type
32	1a	1130	A
32	1a	1132	C
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1140	C
32	1a	1141	C
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1163	C
32	1a	1172	C
32	1a	1181	G
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1212	U
32	1a	1213	A
32	1a	1220	G
32	1a	1222	G
32	1a	1227	A
32	1a	1238	A
32	1a	1240	U
32	1a	1241	G
32	1a	1256	A
32	1a	1257	U
32	1a	1260	C
32	1a	1267	C
32	1a	1270	C
32	1a	1273	G
32	1a	1276	G
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1290	G
32	1a	1299	A
32	1a	1300	G

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Mol	Chain	Res	Type
32	1a	1302	U
32	1a	1320	C
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1368	G
32	1a	1370	G
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1456	G
32	1a	1487	G
32	1a	1492	A
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1505	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
32	1a	1532	U
53	1v	13	A
53	1v	14	A
53	1v	15	A
53	1v	24	A
54	1w	2	C
54	1w	6	G
54	1w	8	4SU
54	1w	14	A
54	1w	19	G
54	1w	20	U
54	1w	21	A
54	1w	23	A

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Mol	Chain	Res	Type
54	1w	24	G
54	1w	45	U
54	1w	46	7MG
54	1w	47	U
54	1w	48	C
54	1w	50	U
54	1w	62	C
54	1w	64	A
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	18	G
55	1x	19	G
55	1x	21	A
55	1x	47	U
55	1x	61	C
55	1x	69	C
55	1x	76	A
54	1y	6	G
54	1y	8	4SU
54	1y	9	A
54	1y	13	C
54	1y	19	G
54	1y	20	U
54	1y	21	A
54	1y	23	A
54	1y	35	A
54	1y	44	G
54	1y	45	U
54	1y	46	7MG
54	1y	47	U
54	1y	48	C
54	1y	49	C
54	1y	53	G
54	1y	54	5MU
54	1y	56	C
54	1y	59	U
54	1y	61	C

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Mol	Chain	Res	Type
54	1y	65	G
54	1y	69	G
54	1y	70	G
1	2A	8	A
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	90	U
1	2A	94	C
1	2A	95	G
1	2A	100	G
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	127	A
1	2A	154(A)	C
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	233	A
1	2A	248	G
1	2A	249	C
1	2A	250	G
1	2A	267	C

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Mol	Chain	Res	Type
1	2A	271(A)	A
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	272(I)	U
1	2A	272(J)	C
1	2A	274	G
1	2A	277	C
1	2A	278	A
1	2A	294	A
1	2A	303	U
1	2A	311	A
1	2A	316	C
1	2A	317	G
1	2A	324	A
1	2A	325	G
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	363(B)	G
1	2A	363(D)	G
1	2A	386	G
1	2A	396	G
1	2A	402	A
1	2A	403	U
1	2A	405	U
1	2A	406	G
1	2A	407	G
1	2A	411	G
1	2A	412	A
1	2A	418	G
1	2A	421	U
1	2A	422	A
1	2A	435	C
1	2A	444	C

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Mol	Chain	Res	Type
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	481	G
1	2A	494	G
1	2A	501	A
1	2A	504	U
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	517	C
1	2A	520	G
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	588	U
1	2A	592	G
1	2A	599	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	615	G
1	2A	616	G
1	2A	621	A
1	2A	627	A
1	2A	634	C
1	2A	637	A
1	2A	645	C
1	2A	651	G
1	2A	652(B)	A
1	2A	652(U)	G
1	2A	667	U
1	2A	669	G
1	2A	686	G
1	2A	701	G

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Mol	Chain	Res	Type
1	2A	709	U
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	847	U
1	2A	857	C
1	2A	859	G
1	2A	866	A
1	2A	869	G
1	2A	870	A
1	2A	874	G
1	2A	875	G
1	2A	879	G
1	2A	880	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	894	C
1	2A	895	U
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	915	C
1	2A	917	A

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Mol	Chain	Res	Type
1	2A	932	G
1	2A	933	A
1	2A	941	A
1	2A	944	G
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	958	U
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	997	G
1	2A	998	C
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1020	A
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1041	C
1	2A	1042	G
1	2A	1043	C
1	2A	1114	G
1	2A	1116	C
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142	U
1	2A	1144	G
1	2A	1166	C
1	2A	1169	G
1	2A	1171	G
1	2A	1180	C
1	2A	1188	U

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Mol	Chain	Res	Type
1	2A	1205	U
1	2A	1206	G
1	2A	1210	A
1	2A	1211	U
1	2A	1218	C
1	2A	1220	A
1	2A	1224	C
1	2A	1237	A
1	2A	1248	G
1	2A	1250	G
1	2A	1252	G
1	2A	1253	A
1	2A	1256	G
1	2A	1268	A
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1287	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1321	A
1	2A	1345	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	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1411	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	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	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1494	A
1	2A	1495	A
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1514	U
1	2A	1531	C
1	2A	1532	C
1	2A	1533	G
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1616	A
1	2A	1629	U
1	2A	1647	G
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

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Mol	Chain	Res	Type
1	2A	1722	A
1	2A	1739	U
1	2A	1740	G
1	2A	1746	G
1	2A	1747(A)	G
1	2A	1756	G
1	2A	1758	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1769	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1786	A
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1811	G
1	2A	1812	A
1	2A	1816	G
1	2A	1828	G
1	2A	1835	G
1	2A	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1857	G
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
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	1931	U
1	2A	1936	A
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U

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Mol	Chain	Res	Type
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2027	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2093	G
1	2A	2099	U
1	2A	2105	C
1	2A	2108	C
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2116	G
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U
1	2A	2125	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2137	C
1	2A	2138	C
1	2A	2140	C

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Mol	Chain	Res	Type
1	2A	2142	C
1	2A	2146	C
1	2A	2150	U
1	2A	2151	G
1	2A	2154	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2161	C
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2172	U
1	2A	2174	C
1	2A	2178	C
1	2A	2185	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	2232	U
1	2A	2235	G
1	2A	2239	G
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2302	G
1	2A	2305	A
1	2A	2308	G
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2324	C
1	2A	2325	G

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Mol	Chain	Res	Type
1	2A	2327	A
1	2A	2328	A
1	2A	2329	G
1	2A	2334	G
1	2A	2336	A
1	2A	2341	G
1	2A	2346	A
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2403	C
1	2A	2406	U
1	2A	2410	G
1	2A	2419	U
1	2A	2425	A
1	2A	2426	A
1	2A	2429	G
1	2A	2430	A
1	2A	2434	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2445	G
1	2A	2448	A
1	2A	2458	G
1	2A	2465	C
1	2A	2468	G
1	2A	2469	A
1	2A	2474	C
1	2A	2476	A
1	2A	2477	C
1	2A	2478	A
1	2A	2490	G
1	2A	2491	U
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C

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Mol	Chain	Res	Type
1	2A	2525	G
1	2A	2529	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2629	A
1	2A	2630	G
1	2A	2634	G
1	2A	2654	A
1	2A	2663	G
1	2A	2664	G
1	2A	2689	U
1	2A	2690	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2739	U
1	2A	2744	G
1	2A	2751	G
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2778	A
1	2A	2789	C
1	2A	2793	G
1	2A	2802	G
1	2A	2803	C
1	2A	2807	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2824	C

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Mol	Chain	Res	Type
1	2A	2833	G
1	2A	2836	U
1	2A	2839	G
1	2A	2872	G
1	2A	2879	C
1	2A	2880	C
1	2A	2894	G
1	2A	2895	U
1	2A	2897	U
2	2B	2	C
2	2B	5	C
2	2B	8	U
2	2B	9	G
2	2B	19	G
2	2B	20	C
2	2B	25	A
2	2B	32	C
2	2B	34	U
2	2B	38	C
2	2B	42	C
2	2B	52	A
2	2B	53	A
2	2B	56	G
2	2B	57	A
2	2B	58	A
2	2B	63	G
2	2B	65	C
2	2B	66	A
2	2B	67	G
2	2B	72	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G
2	2B	88	C
2	2B	90	A
2	2B	91	C
2	2B	106	G
2	2B	108	U
2	2B	110	G
2	2B	114	C
2	2B	116	G

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Mol	Chain	Res	Type
2	2B	119	G
2	2B	120	A
32	2a	7	G
32	2a	9	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	54	C
32	2a	65	U
32	2a	66	G
32	2a	73	G
32	2a	79	G
32	2a	80	G
32	2a	89	C
32	2a	91	C
32	2a	97	G
32	2a	98	G
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	163	C
32	2a	174	C
32	2a	180	U
32	2a	182	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	217	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	301	G

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Mol	Chain	Res	Type
32	2a	306	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	342	C
32	2a	348	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	421	U
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	441	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	477	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	531	U
32	2a	532	A
32	2a	547	A
32	2a	559	A
32	2a	561	U

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Mol	Chain	Res	Type
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	587	G
32	2a	588	G
32	2a	596	C
32	2a	630	G
32	2a	650	G
32	2a	653	A
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	702	A
32	2a	721	G
32	2a	723	U
32	2a	731	G
32	2a	733	A
32	2a	749	C
32	2a	755	G
32	2a	774	G
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	815	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	870	U
32	2a	880	C
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G

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Mol	Chain	Res	Type
32	2a	932	C
32	2a	934	C
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	997	U
32	2a	1001(A)	G
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	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1031	G
32	2a	1033	G
32	2a	1036	G
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1045	C
32	2a	1051	C
32	2a	1065	U

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Mol	Chain	Res	Type
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1080	A
32	2a	1081	G
32	2a	1086	U
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1108	G
32	2a	1117	G
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1134	G
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1141	C
32	2a	1146	A
32	2a	1152	A
32	2a	1159	U
32	2a	1163	C
32	2a	1172	C
32	2a	1181	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1222	G
32	2a	1226	C
32	2a	1227	A
32	2a	1238	A
32	2a	1240	U

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Mol	Chain	Res	Type
32	2a	1241	G
32	2a	1256	A
32	2a	1257	U
32	2a	1260	C
32	2a	1267	C
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1276	G
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1287	A
32	2a	1300	G
32	2a	1303	C
32	2a	1305	G
32	2a	1320	C
32	2a	1328	C
32	2a	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1368	G
32	2a	1370	G
32	2a	1402	4OC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1456	G
32	2a	1487	G
32	2a	1492	A
32	2a	1494	G
32	2a	1497	G
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1519	MA6

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Mol	Chain	Res	Type
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	13	A
53	2v	15	A
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	13	C
54	2w	14	A
54	2w	19	G
54	2w	22	G
54	2w	25	C
54	2w	29	G
54	2w	34	G
54	2w	38	A
54	2w	46	7MG
54	2w	47	U
54	2w	48	C
54	2w	50	U
54	2w	56	C
54	2w	62	C
54	2w	63	G
54	2w	64	A
54	2w	65	G
54	2w	68	C
54	2w	69	G
54	2w	70	G
54	2w	74	C
55	2x	9	G
55	2x	10	G
55	2x	13	C
55	2x	18	G
55	2x	21	A
55	2x	22	G
55	2x	42	G

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Mol	Chain	Res	Type
55	2x	43	A
55	2x	47	U
55	2x	48	C
55	2x	52	G
55	2x	53	G
55	2x	65	C
55	2x	67	C
55	2x	68	C
55	2x	76	A
54	2y	15	G
54	2y	19	G
54	2y	23	A
54	2y	24	G
54	2y	25	C
54	2y	27	G
54	2y	34	G
54	2y	37	MIA
54	2y	45	U
54	2y	49	C
54	2y	52	G
54	2y	53	G
54	2y	55	PSU
54	2y	56	C
54	2y	57	G
54	2y	58	A
54	2y	59	U
54	2y	61	C
54	2y	62	C
54	2y	63	G
54	2y	65	G
54	2y	69	G
54	2y	70	G
54	2y	73	A

All (72) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	115	G
1	1A	185	A
1	1A	271	U
1	1A	302	A

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Mol	Chain	Res	Type
1	1A	509	A
1	1A	572	A
1	1A	596	G
1	1A	793	A
1	1A	821	A
1	1A	847	A
1	1A	913	A
1	1A	941	U
1	1A	1019	G
1	1A	1065	U
1	1A	1067	A
1	1A	1093	G
1	1A	1119	A
1	1A	1188	A
1	1A	1201	A
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1255	A
1	1A	1321	A
1	1A	1347	A
1	1A	1425	A
1	1A	1466	U
1	1A	1554	A
1	1A	1654	A
1	1A	1700	G
1	1A	2014	G
1	1A	2156	A
1	1A	2180	A
1	1A	2192	A
1	1A	2203	G
1	1A	2205	C
1	1A	2418	U
1	1A	2442	A
1	1A	2451	A
1	1A	2641	A
1	1A	2701	U
1	1A	2769	U
2	1B	1	U
1	2A	34	C
1	2A	195	A
1	2A	196	A

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Mol	Chain	Res	Type
1	2A	228	A
1	2A	266	G
1	2A	271(K)	U
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	752	A
1	2A	774	A
1	2A	827	U
1	2A	856	C
1	2A	883	G
1	2A	900	A
1	2A	1210	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1608	A
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2119	A
1	2A	2126	A
1	2A	2406	U
1	2A	2439	A
1	2A	2689	U

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

84 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	$\#\|Z\| > 2$
55	5MC	1x	32	55	19,22,23	1.67	3 (15%)	26,32,35	1.23	3 (11%)
32	MA6	2a	1519	32	19,26,27	1.12	2 (10%)	18,38,41	2.25	5 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
55	5MU	1x	54	56,55	19,22,23	1.45	6 (31%)	27,32,35	1.89	6 (22%)
55	PSU	1x	55	56,55	18,21,22	1.35	2 (11%)	21,30,33	2.01	4 (19%)
54	MIA	1y	37	54	17,24,32	0.98	1 (5%)	16,35,47	1.37	2 (12%)
1	5MU	2A	1915	1	19,22,23	1.46	5 (26%)	27,32,35	2.23	6 (22%)
1	PSU	2A	1917	1	18,21,22	1.36	2 (11%)	21,30,33	1.96	3 (14%)
54	4SU	1y	8	54	18,21,22	1.72	4 (22%)	25,30,33	1.88	6 (24%)
54	MIA	2w	37	54	19,27,32	1.80	3 (15%)	18,39,47	1.38	4 (22%)
1	OMG	1A	2263	56,1,55	19,26,27	0.96	1 (5%)	21,38,41	1.05	2 (9%)
32	2MG	2a	1207	32	18,26,27	0.91	1 (5%)	16,38,41	1.37	2 (12%)
1	PSU	2A	1911	1	18,21,22	1.42	2 (11%)	21,30,33	1.84	4 (19%)
54	PSU	2w	39	54	18,21,22	1.35	2 (11%)	21,30,33	1.81	4 (19%)
55	4SU	1x	8	55	18,21,22	2.11	5 (27%)	25,30,33	1.64	6 (24%)
1	2MU	2A	2552	56,1	19,22,24	1.31	2 (10%)	25,31,36	1.80	5 (20%)
32	7MG	2a	527	32,56	23,26,27	1.34	4 (17%)	27,39,42	2.59	6 (22%)
32	PSU	1a	516	32	18,21,22	1.42	3 (16%)	21,30,33	1.88	5 (23%)
54	5MU	2w	54	54	19,22,23	1.39	4 (21%)	27,32,35	1.89	6 (22%)
32	4OC	2a	1402	32,56	20,23,24	0.81	0	25,32,35	1.07	1 (4%)
55	5MU	2x	54	55	19,22,23	1.39	5 (26%)	27,32,35	2.22	6 (22%)
32	5MC	2a	1407	32	19,22,23	1.52	3 (15%)	26,32,35	1.21	4 (15%)
54	PSU	2y	55	54	18,21,22	1.33	3 (16%)	21,30,33	1.91	5 (23%)
1	5MU	1A	1937	1	19,22,23	1.35	5 (26%)	27,32,35	2.18	7 (25%)
54	4SU	2y	8	54	18,21,22	1.87	4 (22%)	25,30,33	2.25	5 (20%)
55	PSU	2x	55	55	18,21,22	1.39	2 (11%)	21,30,33	1.97	4 (19%)
32	5MC	1a	1404	32	19,22,23	1.62	3 (15%)	26,32,35	1.19	3 (11%)
43	0TD	2l	92	43	8,9,10	5.75	3 (37%)	6,11,13	2.22	1 (16%)
54	PSU	2y	39	54	18,21,22	1.36	2 (11%)	21,30,33	1.93	3 (14%)
32	MA6	1a	1519	32	19,26,27	1.14	2 (10%)	18,38,41	1.97	5 (27%)
1	5MU	1A	1961	56,1	19,22,23	1.32	4 (21%)	27,32,35	2.59	6 (22%)
54	PSU	1w	32	56,54	18,21,22	1.35	2 (11%)	21,30,33	2.01	3 (14%)
1	5MU	2A	1939	56,1	19,22,23	1.46	6 (31%)	27,32,35	2.51	6 (22%)
32	5MC	2a	967	32	19,22,23	1.92	2 (10%)	26,32,35	1.16	4 (15%)
32	UR3	1a	1498	32	19,22,23	1.10	1 (5%)	26,32,35	1.83	5 (19%)
1	2MA	1A	2515	56,1	18,25,26	0.81	0	20,37,40	1.92	3 (15%)
32	M2G	2a	966	32	20,27,28	1.32	3 (15%)	19,40,43	1.07	1 (5%)
32	5MC	2a	1400	32	19,22,23	1.68	3 (15%)	26,32,35	1.20	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MC	1A	1964	56,1	19,22,23	1.51	3 (15%)	26,32,35	1.23	2 (7%)
1	PSU	1A	1939	1	18,21,22	1.42	4 (22%)	21,30,33	2.12	4 (19%)
54	PSU	1y	39	54	18,21,22	1.42	2 (11%)	21,30,33	1.84	4 (19%)
1	PSU	1A	1933	1	18,21,22	1.33	2 (11%)	21,30,33	2.07	4 (19%)
32	2MG	1a	1207	32	18,26,27	0.96	1 (5%)	16,38,41	1.11	1 (6%)
54	PSU	1y	32	54	18,21,22	1.41	3 (16%)	21,30,33	1.89	3 (14%)
54	PSU	1w	55	54	18,21,22	1.37	2 (11%)	21,30,33	1.98	3 (14%)
54	PSU	2w	32	54	18,21,22	1.38	2 (11%)	21,30,33	1.99	4 (19%)
43	0TD	1l	92	43	8,9,10	5.73	6 (75%)	6,11,13	4.21	3 (50%)
1	OMG	2A	2251	56,1,55	19,26,27	0.90	1 (5%)	21,38,41	1.19	3 (14%)
54	5MU	2y	54	54	19,22,23	1.51	4 (21%)	27,32,35	2.12	9 (33%)
54	MIA	2y	37	54	17,24,32	0.96	1 (5%)	16,35,47	1.35	2 (12%)
54	7MG	2w	46	54	23,26,27	1.40	3 (13%)	27,39,42	2.47	6 (22%)
32	PSU	2a	516	32	18,21,22	1.34	2 (11%)	21,30,33	1.90	4 (19%)
1	2MU	1A	2564	56,1	19,22,24	1.20	2 (10%)	25,31,36	2.02	6 (24%)
32	5MC	1a	1400	32	19,22,23	1.60	3 (15%)	26,32,35	1.15	2 (7%)
54	PSU	2w	55	56,54	18,21,22	1.38	2 (11%)	21,30,33	1.94	3 (14%)
32	M2G	1a	966	32	20,27,28	1.44	3 (15%)	19,40,43	1.00	1 (5%)
1	4OC	2A	1920	1	19,22,24	0.76	0	25,31,35	0.85	0
32	5MC	1a	967	32	19,22,23	1.67	3 (15%)	26,32,35	1.15	3 (11%)
55	4SU	2x	8	55	18,21,22	2.04	6 (33%)	25,30,33	1.43	5 (20%)
54	7MG	1y	46	54	23,26,27	1.35	4 (17%)	27,39,42	2.61	6 (22%)
32	UR3	2a	1498	32	19,22,23	1.07	2 (10%)	26,32,35	1.81	4 (15%)
54	5MU	1w	54	54	19,22,23	1.47	5 (26%)	27,32,35	2.07	6 (22%)
1	5MC	2A	1942	1	19,22,23	1.50	2 (10%)	26,32,35	1.12	2 (7%)
54	PSU	2y	32	54	18,21,22	1.36	2 (11%)	21,30,33	1.93	4 (19%)
1	PSU	1A	2617	56,1	18,21,22	1.51	4 (22%)	21,30,33	2.12	4 (19%)
32	MA6	2a	1518	32	19,26,27	1.06	2 (10%)	18,38,41	2.30	7 (38%)
1	PSU	2A	2605	1	18,21,22	1.25	2 (11%)	21,30,33	2.18	6 (28%)
54	PSU	1y	55	54	18,21,22	1.33	2 (11%)	21,30,33	2.13	4 (19%)
1	4OC	1A	1942	1	19,22,24	0.78	0	25,31,35	0.97	1 (4%)
32	4OC	1a	1402	32	20,23,24	0.79	0	25,32,35	1.03	2 (8%)
32	5MC	1a	1407	32	19,22,23	1.66	3 (15%)	26,32,35	1.24	4 (15%)
55	5MC	2x	32	55	19,22,23	1.56	3 (15%)	26,32,35	1.19	3 (11%)
32	7MG	1a	527	32,56	23,26,27	1.46	4 (17%)	27,39,42	2.46	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
54	7MG	2y	46	54	23,26,27	1.45	4 (17%)	27,39,42	2.79	6 (22%)
54	4SU	1w	8	54	18,21,22	1.82	5 (27%)	25,30,33	1.99	5 (20%)
32	MA6	1a	1518	32	19,26,27	1.06	1 (5%)	18,38,41	2.36	7 (38%)
54	PSU	1w	39	54	18,21,22	1.37	2 (11%)	21,30,33	1.96	3 (14%)
32	5MC	2a	1404	32	19,22,23	1.70	3 (15%)	26,32,35	1.19	3 (11%)
1	5MC	1A	1984	56,1	19,22,23	1.57	3 (15%)	26,32,35	1.23	5 (19%)
1	2MA	2A	2503	56,1	18,25,26	0.78	0	20,37,40	1.75	2 (10%)
54	MIA	1w	37	54	24,31,32	2.20	3 (12%)	22,44,47	2.48	6 (27%)
54	7MG	1w	46	54	23,26,27	1.48	4 (17%)	27,39,42	2.54	7 (25%)
54	5MU	1y	54	54	19,22,23	1.55	6 (31%)	27,32,35	1.99	6 (22%)
1	5MC	2A	1962	56,1	19,22,23	1.52	3 (15%)	26,32,35	1.29	3 (11%)
54	4SU	2w	8	54	18,21,22	1.81	4 (22%)	25,30,33	2.48	5 (20%)

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
55	5MC	1x	32	55	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	2/7/29/30	0/3/3/3
55	5MU	1x	54	56,55	-	0/7/25/26	0/2/2/2
55	PSU	1x	55	56,55	-	0/7/25/26	0/2/2/2
54	MIA	1y	37	54	-	0/3/25/34	0/3/3/3
1	5MU	2A	1915	1	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
54	4SU	1y	8	54	-	3/7/25/26	0/2/2/2
54	MIA	2w	37	54	-	2/7/29/34	0/3/3/3
1	OMG	1A	2263	56,1,55	-	0/5/27/28	0/3/3/3
32	2MG	2a	1207	32	-	0/5/27/28	0/3/3/3
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
1	2MU	2A	2552	56,1	-	0/9/27/28	0/2/2/2
32	7MG	2a	527	32,56	-	3/7/37/38	0/3/3/3
32	PSU	1a	516	32	-	0/7/25/26	0/2/2/2
54	5MU	2w	54	54	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32,56	-	2/9/29/30	0/2/2/2
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
54	PSU	2y	55	54	-	2/7/25/26	0/2/2/2
1	5MU	1A	1937	1	-	0/7/25/26	0/2/2/2
54	4SU	2y	8	54	-	0/7/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	1/7/12/14	-
54	PSU	2y	39	54	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/7/29/30	0/3/3/3
1	5MU	1A	1961	56,1	-	0/7/25/26	0/2/2/2
54	PSU	1w	32	56,54	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	56,1	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
1	2MA	1A	2515	56,1	-	1/3/25/26	0/3/3/3
32	M2G	2a	966	32	-	0/7/29/30	0/3/3/3
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1964	56,1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1939	1	-	0/7/25/26	0/2/2/2
54	PSU	1y	39	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/5/27/28	0/3/3/3
54	PSU	1y	32	54	-	0/7/25/26	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	3/7/12/14	-
1	OMG	2A	2251	56,1,55	-	0/5/27/28	0/3/3/3
54	5MU	2y	54	54	-	2/7/25/26	0/2/2/2
54	MIA	2y	37	54	-	3/3/25/34	0/3/3/3
54	7MG	2w	46	54	-	4/7/37/38	0/3/3/3
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
1	2MU	1A	2564	56,1	-	0/9/27/28	0/2/2/2
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
54	PSU	2w	55	56,54	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/7/29/30	0/3/3/3
1	4OC	2A	1920	1	-	0/9/27/30	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	1/7/25/26	0/2/2/2
54	7MG	1y	46	54	-	2/7/37/38	0/3/3/3
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	5MU	1w	54	54	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
54	PSU	2y	32	54	-	1/7/25/26	0/2/2/2
1	PSU	1A	2617	56,1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/7/29/30	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
54	PSU	1y	55	54	-	1/7/25/26	0/2/2/2
1	4OC	1A	1942	1	-	1/9/27/30	0/2/2/2
32	4OC	1a	1402	32	-	3/9/29/30	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
32	7MG	1a	527	32,56	-	2/7/37/38	0/3/3/3
54	7MG	2y	46	54	-	3/7/37/38	0/3/3/3
54	4SU	1w	8	54	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/7/29/30	0/3/3/3
54	PSU	1w	39	54	-	1/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1984	56,1	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	56,1	-	1/3/25/26	0/3/3/3
54	MIA	1w	37	54	-	1/11/33/34	0/3/3/3
54	7MG	1w	46	54	-	3/7/37/38	0/3/3/3
54	5MU	1y	54	54	-	3/7/25/26	0/2/2/2
1	5MC	2A	1962	56,1	-	0/7/25/26	0/2/2/2
54	4SU	2w	8	54	-	1/7/25/26	0/2/2/2

All (233) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-15.10	1.67	1.82
43	1l	92	0TD	CB-SB	-15.01	1.67	1.82
32	2a	967	5MC	C5-C4	7.30	1.49	1.44
54	1w	37	MIA	C2-S10	-6.99	1.70	1.75
54	1w	37	MIA	C13-C14	6.94	1.53	1.32
54	2w	37	MIA	C2-S10	-6.20	1.70	1.75
32	2a	1400	5MC	C5-C4	6.11	1.48	1.44
32	1a	967	5MC	C5-C4	6.09	1.48	1.44
32	2a	1404	5MC	C5-C4	6.09	1.48	1.44
32	1a	1407	5MC	C5-C4	5.94	1.48	1.44
55	1x	32	5MC	C5-C4	5.87	1.48	1.44
32	1a	1400	5MC	C5-C4	5.77	1.48	1.44
32	1a	1404	5MC	C5-C4	5.73	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	1984	5MC	C5-C4	5.50	1.48	1.44
1	1A	1964	5MC	C5-C4	5.42	1.48	1.44
55	2x	32	5MC	C5-C4	5.37	1.48	1.44
32	2a	1407	5MC	C5-C4	5.31	1.48	1.44
1	2A	1962	5MC	C5-C4	5.21	1.48	1.44
1	2A	1942	5MC	C5-C4	5.10	1.48	1.44
54	2y	8	4SU	C4-S4	-5.05	1.59	1.68
54	2w	8	4SU	C4-S4	-4.97	1.59	1.68
55	1x	8	4SU	C4-N3	-4.95	1.32	1.37
54	1w	8	4SU	C4-S4	-4.77	1.60	1.68
43	2l	92	0TD	CB-CA	-4.68	1.53	1.54
55	2x	8	4SU	C4-N3	-4.66	1.32	1.37
55	2x	8	4SU	C4-S4	-4.40	1.60	1.68
54	1y	8	4SU	C4-S4	-4.36	1.61	1.68
32	1a	966	M2G	C2-N3	4.26	1.36	1.30
54	1y	32	PSU	C6-C5	4.13	1.39	1.35
55	1x	8	4SU	C4-S4	-4.10	1.61	1.68
54	2w	55	PSU	C6-C5	4.09	1.39	1.35
54	1y	39	PSU	C6-C5	4.05	1.39	1.35
54	1w	55	PSU	C6-C5	4.04	1.39	1.35
55	2x	55	PSU	C6-C5	3.97	1.39	1.35
32	2a	966	M2G	C2-N3	3.96	1.36	1.30
32	1a	527	7MG	C4-N9	-3.88	1.33	1.37
54	2y	32	PSU	C6-C5	3.86	1.39	1.35
1	2A	1911	PSU	C6-C5	3.84	1.39	1.35
55	1x	8	4SU	C2-N3	-3.80	1.31	1.38
54	2y	46	7MG	C5-C4	3.75	1.49	1.37
54	2w	46	7MG	C4-N9	-3.73	1.33	1.37
32	2a	516	PSU	C6-C5	3.72	1.39	1.35
54	2w	39	PSU	C6-C5	3.72	1.39	1.35
54	1w	39	PSU	C6-C5	3.67	1.39	1.35
32	1a	516	PSU	C6-C5	3.63	1.39	1.35
54	1w	46	7MG	C4-N9	-3.61	1.33	1.37
54	2w	32	PSU	C6-C5	3.60	1.39	1.35
54	2y	39	PSU	C6-C5	3.57	1.39	1.35
1	2A	2605	PSU	C6-C5	3.57	1.39	1.35
1	2A	1917	PSU	C6-C5	3.56	1.39	1.35
54	1w	46	7MG	C5-C4	3.52	1.48	1.37
54	1y	55	PSU	C6-C5	3.52	1.39	1.35
54	1y	46	7MG	C5-C4	3.47	1.48	1.37
55	1x	55	PSU	C6-C5	3.45	1.39	1.35
54	2y	54	5MU	C2-N1	3.44	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	527	7MG	C5-C4	3.40	1.48	1.37
54	2w	46	7MG	C5-C4	3.35	1.47	1.37
54	1w	32	PSU	C6-C5	3.35	1.39	1.35
54	1y	8	4SU	C4-N3	-3.32	1.34	1.37
32	2a	527	7MG	C5-C4	3.28	1.47	1.37
43	1l	92	0TD	CSB-SB	-3.27	1.73	1.79
55	1x	8	4SU	C5-C4	-3.26	1.38	1.42
55	2x	8	4SU	C5-C4	-3.16	1.38	1.42
54	1w	8	4SU	C4-N3	-3.15	1.34	1.37
1	2A	1942	5MC	C6-C5	3.14	1.39	1.34
1	1A	1939	PSU	C6-C5	3.14	1.38	1.35
1	1A	1933	PSU	C6-C5	3.13	1.38	1.35
32	2a	1404	5MC	C6-C5	3.10	1.39	1.34
32	1a	966	M2G	C2-N2	3.10	1.40	1.35
54	1y	54	5MU	C6-C5	3.09	1.39	1.34
55	2x	54	5MU	C6-C5	3.04	1.39	1.34
54	1w	54	5MU	C6-C5	3.01	1.39	1.34
54	2y	8	4SU	C4-N3	-2.96	1.34	1.37
54	2w	8	4SU	C2-N1	2.93	1.43	1.38
32	1a	967	5MC	C6-C5	2.93	1.39	1.34
55	2x	8	4SU	C2-N3	-2.92	1.32	1.38
1	1A	2617	PSU	C4-N3	-2.92	1.33	1.38
55	2x	32	5MC	C6-C5	2.92	1.39	1.34
32	1a	1404	5MC	C6-C5	2.91	1.39	1.34
54	2y	55	PSU	C6-C5	2.89	1.38	1.35
54	2w	8	4SU	C4-N3	-2.89	1.34	1.37
54	2w	54	5MU	C6-C5	2.87	1.39	1.34
32	1a	1407	5MC	C6-C5	2.87	1.39	1.34
55	1x	32	5MC	C6-C5	2.87	1.39	1.34
43	1l	92	0TD	CA-N	-2.86	1.39	1.47
54	1y	54	5MU	C2-N1	2.85	1.42	1.38
1	1A	2617	PSU	C2-N1	-2.85	1.32	1.36
1	1A	1939	PSU	C4-N3	-2.85	1.33	1.38
32	2a	527	7MG	C4-N9	-2.84	1.34	1.37
55	1x	54	5MU	C6-C5	2.84	1.39	1.34
54	1w	8	4SU	C5-C4	-2.82	1.39	1.42
1	2A	1915	5MU	C2-N1	2.82	1.42	1.38
1	2A	1939	5MU	C4-C5	2.82	1.49	1.44
1	1A	2263	OMG	C6-N1	-2.81	1.33	1.37
32	1a	1498	UR3	C2-N1	2.81	1.42	1.38
1	2A	1915	5MU	C6-C5	2.81	1.39	1.34
1	1A	1961	5MU	C6-C5	2.80	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1518	MA6	C6-C5	2.79	1.49	1.44
1	2A	1939	5MU	C6-C5	2.79	1.39	1.34
55	1x	54	5MU	C4-N3	-2.79	1.33	1.38
54	2y	8	4SU	C5-C4	-2.78	1.39	1.42
32	1a	1400	5MC	C6-C5	2.78	1.39	1.34
32	2a	967	5MC	C6-C5	2.77	1.39	1.34
1	1A	1933	PSU	C4-N3	-2.77	1.33	1.38
32	2a	1400	5MC	C6-C5	2.76	1.39	1.34
54	2w	37	MIA	C6-C5	2.75	1.49	1.44
32	2a	966	M2G	C2-N2	2.75	1.40	1.35
1	2A	1915	5MU	C4-C5	2.74	1.49	1.44
54	2y	46	7MG	C8-N9	2.73	1.47	1.45
54	2y	8	4SU	C2-N1	2.73	1.42	1.38
43	2l	92	0TD	OD2-CG	-2.69	1.22	1.30
54	1y	54	5MU	C4-N3	-2.69	1.33	1.38
54	2y	37	MIA	C2-N3	2.69	1.36	1.32
55	2x	54	5MU	C4-C5	2.69	1.49	1.44
54	1w	54	5MU	C2-N1	2.68	1.42	1.38
32	2a	1518	MA6	C6-C5	2.68	1.48	1.44
1	1A	2617	PSU	C2-N3	-2.67	1.33	1.37
32	1a	516	PSU	C4-N3	-2.67	1.33	1.38
54	2y	54	5MU	C6-C5	2.67	1.39	1.34
54	1w	54	5MU	C4-C5	2.65	1.49	1.44
43	1l	92	0TD	OD2-CG	-2.64	1.22	1.30
1	2A	1962	5MC	C6-N1	-2.64	1.33	1.38
54	1y	54	5MU	C4-C5	2.64	1.49	1.44
1	1A	2564	2MU	C4-N3	-2.61	1.34	1.38
1	2A	1939	5MU	C4-N3	-2.61	1.34	1.38
1	1A	1937	5MU	C6-C5	2.60	1.38	1.34
1	1A	1984	5MC	C6-N1	-2.60	1.33	1.38
54	1y	37	MIA	C2-N3	2.60	1.36	1.32
54	1y	39	PSU	C4-N3	-2.59	1.34	1.38
54	1w	54	5MU	C4-N3	-2.58	1.34	1.38
1	1A	1961	5MU	C4-N3	-2.56	1.34	1.38
1	2A	1962	5MC	C6-C5	2.56	1.38	1.34
54	1w	39	PSU	C4-N3	-2.56	1.34	1.38
54	2y	46	7MG	C6-N1	-2.53	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.53	1.33	1.38
54	2y	39	PSU	C4-N3	-2.53	1.34	1.38
54	2w	32	PSU	C4-N3	-2.52	1.34	1.38
1	2A	2552	2MU	C4-N3	-2.51	1.34	1.38
1	2A	1911	PSU	C4-N3	-2.51	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1498	UR3	C2-N1	2.51	1.42	1.38
32	1a	1207	2MG	C6-N1	-2.50	1.34	1.37
43	1l	92	0TD	CB-CG	-2.50	1.47	1.52
55	1x	32	5MC	C6-N1	-2.50	1.33	1.38
54	2w	54	5MU	C4-C5	2.49	1.48	1.44
54	2w	46	7MG	C8-N9	2.49	1.47	1.45
1	1A	1964	5MC	C6-C5	2.49	1.38	1.34
54	2w	8	4SU	C5-C4	-2.48	1.39	1.42
54	1w	46	7MG	C8-N9	2.48	1.47	1.45
54	1w	46	7MG	C6-N1	-2.48	1.34	1.38
54	2y	54	5MU	C4-C5	2.47	1.48	1.44
54	2w	54	5MU	C2-N1	2.47	1.42	1.38
1	1A	1937	5MU	C4-N3	-2.46	1.34	1.38
54	2w	39	PSU	C4-N3	-2.46	1.34	1.38
55	2x	55	PSU	C4-N3	-2.46	1.34	1.38
55	1x	54	5MU	C4-C5	2.45	1.48	1.44
54	2y	55	PSU	C4-N3	-2.45	1.34	1.38
54	1w	32	PSU	C4-N3	-2.45	1.34	1.38
54	2y	54	5MU	C4-N3	-2.43	1.34	1.38
54	1y	8	4SU	C5-C4	-2.42	1.39	1.42
55	1x	8	4SU	O2-C2	2.42	1.27	1.23
54	1w	37	MIA	C6-C5	2.41	1.48	1.44
54	2w	55	PSU	C4-N3	-2.39	1.34	1.38
32	2a	527	7MG	C6-N1	-2.37	1.34	1.38
55	1x	55	PSU	C4-N3	-2.37	1.34	1.38
32	2a	1407	5MC	C6-C5	2.36	1.38	1.34
1	1A	1961	5MU	C6-N1	-2.36	1.34	1.38
1	2A	2552	2MU	C5-C4	2.36	1.48	1.43
43	1l	92	0TD	CB-CA	-2.36	1.54	1.54
1	2A	1915	5MU	C4-N3	-2.36	1.34	1.38
54	1y	55	PSU	C4-N3	-2.36	1.34	1.38
32	1a	527	7MG	C6-N1	-2.36	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.33	1.34	1.38
32	1a	966	M2G	C6-N1	-2.32	1.34	1.37
54	1y	46	7MG	C4-N9	-2.32	1.35	1.37
54	1w	8	4SU	C2-N1	2.32	1.42	1.38
54	2y	32	PSU	C4-N3	-2.30	1.34	1.38
32	2a	1519	MA6	C6-C5	2.29	1.48	1.44
32	2a	1400	5MC	C6-N1	-2.29	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.28	1.34	1.38
54	1y	46	7MG	C6-N1	-2.28	1.34	1.38
1	2A	2605	PSU	C4-N3	-2.27	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	37	MIA	C6-N1	2.27	1.36	1.33
1	1A	1937	5MU	C4-C5	2.27	1.48	1.44
1	1A	1937	5MU	C2-N1	2.26	1.42	1.38
1	2A	1939	5MU	C6-N1	-2.26	1.34	1.38
1	1A	1984	5MC	C6-C5	2.26	1.38	1.34
54	1y	46	7MG	C8-N9	2.25	1.47	1.45
32	2a	527	7MG	C5-C6	2.25	1.49	1.43
32	1a	527	7MG	C8-N9	2.25	1.47	1.45
32	1a	1400	5MC	C6-N1	-2.22	1.34	1.38
1	1A	2564	2MU	C2-N3	-2.22	1.34	1.38
54	1y	32	PSU	C4-N3	-2.22	1.34	1.38
55	2x	54	5MU	C4-N3	-2.20	1.34	1.38
1	1A	1939	PSU	C2-N1	-2.19	1.33	1.36
1	1A	1961	5MU	C2-N3	-2.19	1.34	1.38
32	1a	967	5MC	C6-N1	-2.19	1.34	1.38
32	2a	1498	UR3	C6-C5	2.19	1.40	1.35
54	1y	54	5MU	C2-N3	-2.18	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.17	1.34	1.37
32	2a	1518	MA6	C6-N1	2.17	1.35	1.32
32	2a	516	PSU	C4-N3	-2.17	1.34	1.38
54	2y	55	PSU	C2-N1	-2.16	1.33	1.36
55	1x	54	5MU	C2-N3	-2.16	1.34	1.38
1	1A	1964	5MC	C6-N1	-2.15	1.34	1.38
32	1a	516	PSU	C2-N3	-2.15	1.33	1.37
32	1a	1404	5MC	C6-N1	-2.14	1.34	1.38
1	2A	2251	OMG	C6-N1	-2.14	1.34	1.37
55	1x	54	5MU	C2-N1	2.14	1.41	1.38
54	1w	55	PSU	C4-N3	-2.13	1.34	1.38
1	2A	1939	5MU	C2-N1	2.13	1.41	1.38
1	1A	2617	PSU	C6-C5	2.12	1.37	1.35
1	1A	1937	5MU	C6-N1	-2.12	1.34	1.38
32	2a	1519	MA6	C6-N1	2.12	1.35	1.32
32	1a	1519	MA6	C6-C5	2.11	1.48	1.44
32	1a	1407	5MC	C6-N1	-2.11	1.34	1.38
54	2w	54	5MU	C4-N3	-2.10	1.34	1.38
55	2x	8	4SU	O2-C2	2.10	1.26	1.23
32	1a	1519	MA6	C6-N1	2.09	1.35	1.32
54	1w	54	5MU	C2-N3	-2.08	1.34	1.38
55	2x	8	4SU	C2-N1	2.07	1.41	1.38
1	1A	1939	PSU	C2-N3	-2.07	1.34	1.37
54	2y	46	7MG	C2-N3	2.07	1.38	1.33
55	1x	54	5MU	C6-N1	-2.05	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	8	4SU	C2-N3	-2.04	1.34	1.38
32	2a	1404	5MC	C6-N1	-2.02	1.34	1.38
55	2x	54	5MU	C6-N1	-2.02	1.34	1.38
55	2x	54	5MU	C2-N1	2.02	1.41	1.38
54	1y	54	5MU	C6-N1	-2.02	1.34	1.38
54	1y	32	PSU	C4-C5	2.01	1.49	1.44
1	2A	1915	5MU	C2-N3	-2.01	1.34	1.38
54	1y	8	4SU	C6-C5	2.01	1.39	1.35
32	2a	966	M2G	C6-N1	-2.00	1.34	1.37
55	2x	32	5MC	C6-N1	-2.00	1.34	1.38

All (344) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2y	46	7MG	N9-C4-N3	10.07	140.22	125.46
54	1y	46	7MG	N9-C4-N3	9.11	138.80	125.46
54	1w	37	MIA	C12-C13-C14	-8.83	111.17	127.01
54	1w	46	7MG	N9-C4-N3	8.77	138.32	125.46
32	2a	527	7MG	N9-C4-N3	8.50	137.91	125.46
32	1a	527	7MG	N9-C4-N3	8.37	137.72	125.46
54	2w	46	7MG	N9-C4-N3	7.71	136.76	125.46
54	2w	8	4SU	C4-N3-C2	-7.55	120.08	127.31
43	1l	92	0TD	CB-CA-N	-7.31	94.29	109.10
32	2a	1498	UR3	C4-N3-C2	-7.02	118.93	124.58
1	1A	2515	2MA	C2-N3-C4	6.85	120.99	115.46
32	1a	1498	UR3	C4-N3-C2	-6.78	119.13	124.58
43	1l	92	0TD	CSB-SB-CB	6.71	114.44	102.36
54	1y	55	PSU	N1-C2-N3	6.64	122.17	115.17
1	1A	1939	PSU	N1-C2-N3	6.57	122.10	115.17
1	1A	1961	5MU	O4-C4-C5	-6.45	117.54	124.92
1	1A	2617	PSU	N1-C2-N3	6.42	121.94	115.17
1	1A	1961	5MU	C5-C4-N3	6.41	120.89	115.32
32	1a	1518	MA6	C2-N1-C6	6.41	123.12	116.84
54	2w	8	4SU	C5-C4-N3	6.36	120.67	114.75
55	2x	55	PSU	N1-C2-N3	6.36	121.87	115.17
54	2w	32	PSU	N1-C2-N3	6.32	121.83	115.17
1	2A	1939	5MU	C4-N3-C2	-6.19	119.23	127.34
54	2y	8	4SU	C4-N3-C2	-6.15	121.42	127.31
1	1A	1961	5MU	C4-N3-C2	-6.14	119.29	127.34
1	1A	1933	PSU	N1-C2-N3	6.14	121.64	115.17
55	1x	55	PSU	N1-C2-N3	6.12	121.62	115.17
54	1w	32	PSU	N1-C2-N3	6.12	121.62	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1917	PSU	N1-C2-N3	6.10	121.60	115.17
1	2A	2503	2MA	C2-N3-C4	6.09	120.37	115.46
54	1w	39	PSU	N1-C2-N3	6.08	121.58	115.17
1	2A	2605	PSU	N1-C2-N3	6.05	121.55	115.17
54	2y	8	4SU	C5-C4-N3	6.01	120.34	114.75
32	2a	1518	MA6	C2-N1-C6	5.99	122.71	116.84
54	2y	32	PSU	N1-C2-N3	5.96	121.45	115.17
54	2y	39	PSU	N1-C2-N3	5.94	121.43	115.17
54	2w	55	PSU	N1-C2-N3	5.90	121.39	115.17
54	1y	39	PSU	N1-C2-N3	5.88	121.37	115.17
54	1y	32	PSU	N1-C2-N3	5.83	121.32	115.17
1	2A	1939	5MU	C5-C4-N3	5.82	120.38	115.32
54	1w	55	PSU	N1-C2-N3	5.78	121.27	115.17
54	2y	46	7MG	C5-C4-N3	-5.76	117.31	128.13
1	2A	1911	PSU	N1-C2-N3	5.76	121.24	115.17
32	1a	516	PSU	N1-C2-N3	5.71	121.19	115.17
32	2a	516	PSU	N1-C2-N3	5.67	121.15	115.17
32	2a	527	7MG	N9-C8-N7	-5.62	95.42	103.37
54	1w	8	4SU	C4-N3-C2	-5.55	121.99	127.31
54	1y	8	4SU	C4-N3-C2	-5.55	122.00	127.31
54	2w	39	PSU	N1-C2-N3	5.53	121.00	115.17
32	2a	1519	MA6	C2-N1-C6	5.50	122.23	116.84
55	2x	54	5MU	N3-C2-N1	5.42	121.94	114.89
54	2w	46	7MG	N9-C8-N7	-5.42	95.70	103.37
1	2A	1915	5MU	C4-N3-C2	-5.40	120.26	127.34
55	2x	54	5MU	C4-N3-C2	-5.39	120.28	127.34
54	1w	54	5MU	N3-C2-N1	5.36	121.87	114.89
54	2y	55	PSU	N1-C2-N3	5.36	120.82	115.17
1	2A	1915	5MU	C5-C4-N3	5.36	119.98	115.32
1	1A	1937	5MU	C4-N3-C2	-5.34	120.34	127.34
54	1w	8	4SU	C5-C4-N3	5.30	119.68	114.75
54	1y	46	7MG	N9-C8-N7	-5.26	95.92	103.37
1	2A	1939	5MU	C5-C6-N1	-5.25	117.61	123.31
32	2a	527	7MG	C5-C4-N3	-5.23	118.30	128.13
54	1w	46	7MG	N9-C8-N7	-5.18	96.03	103.37
1	1A	2564	2MU	N3-C2-N1	5.17	121.62	114.89
43	2l	92	0TD	CSB-SB-CB	5.14	111.61	102.36
54	1y	46	7MG	C5-C4-N3	-5.11	118.54	128.13
54	1w	54	5MU	C4-N3-C2	-5.04	120.73	127.34
1	1A	2564	2MU	C4-N3-C2	-5.04	120.36	126.61
1	2A	1939	5MU	N3-C2-N1	5.02	121.42	114.89
1	1A	1937	5MU	N3-C2-N1	5.01	121.42	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	527	7MG	N9-C8-N7	-4.94	96.38	103.37
54	1y	54	5MU	N3-C2-N1	4.92	121.30	114.89
32	1a	527	7MG	C5-C4-N3	-4.90	118.92	128.13
1	2A	2605	PSU	C4-N3-C2	-4.84	119.70	126.37
1	1A	1937	5MU	C5-C4-N3	4.84	119.53	115.32
1	2A	2552	2MU	N3-C2-N1	4.82	121.17	114.89
54	2y	46	7MG	C2-N3-C4	4.81	120.58	112.30
54	1y	54	5MU	C4-N3-C2	-4.81	121.04	127.34
32	1a	1519	MA6	C2-N1-C6	4.72	121.47	116.84
54	2y	46	7MG	N9-C8-N7	-4.71	96.71	103.37
54	2w	46	7MG	C5-C4-N3	-4.70	119.30	128.13
1	1A	1961	5MU	N3-C2-N1	4.70	121.00	114.89
55	1x	54	5MU	N3-C2-N1	4.69	121.00	114.89
1	2A	1915	5MU	N3-C2-N1	4.63	120.92	114.89
1	1A	1961	5MU	C5-C6-N1	-4.61	118.30	123.31
1	2A	1939	5MU	O4-C4-C5	-4.60	119.65	124.92
54	1w	46	7MG	C5-C4-N3	-4.52	119.64	128.13
1	2A	1915	5MU	O4-C4-C5	-4.52	119.75	124.92
54	2y	8	4SU	C5-C4-S4	-4.52	119.15	124.31
1	2A	2552	2MU	C4-N3-C2	-4.51	121.02	126.61
54	2y	54	5MU	C5-C4-N3	4.50	119.23	115.32
32	2a	527	7MG	C2-N3-C4	4.49	120.04	112.30
55	1x	54	5MU	C4-N3-C2	-4.45	121.50	127.34
54	2y	54	5MU	C4-N3-C2	-4.41	121.55	127.34
1	1A	1933	PSU	C4-N3-C2	-4.39	120.32	126.37
1	1A	2617	PSU	C4-N3-C2	-4.39	120.33	126.37
1	1A	1937	5MU	O4-C4-C5	-4.39	119.90	124.92
32	2a	1519	MA6	N1-C6-N6	4.37	121.88	116.83
54	1y	46	7MG	C2-N3-C4	4.34	119.78	112.30
54	1w	54	5MU	C5-C4-N3	4.34	119.10	115.32
54	1y	8	4SU	N3-C2-N1	4.30	120.49	114.89
54	1y	54	5MU	C5-C4-N3	4.29	119.05	115.32
54	2w	54	5MU	O4-C4-C5	-4.27	120.03	124.92
55	2x	54	5MU	C5-C4-N3	4.26	119.02	115.32
55	2x	54	5MU	O4-C4-C5	-4.21	120.10	124.92
54	2y	37	MIA	N3-C2-N1	-4.19	122.98	128.67
54	2w	8	4SU	N3-C2-N1	4.19	120.35	114.89
54	1w	37	MIA	C15-C14-C13	-4.18	110.11	122.66
54	2y	54	5MU	N3-C2-N1	4.16	120.31	114.89
54	2w	54	5MU	C4-N3-C2	-4.15	121.90	127.34
1	1A	1939	PSU	C4-N3-C2	-4.15	120.66	126.37
54	2w	54	5MU	N3-C2-N1	4.12	120.25	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1400	5MC	C5-C6-N1	-4.11	118.84	123.31
55	1x	8	4SU	C6-C5-C4	-4.10	116.40	119.95
54	1y	37	MIA	N3-C2-N1	-4.10	123.11	128.67
54	1w	55	PSU	O2-C2-N1	-4.07	118.59	122.79
54	2w	46	7MG	C2-N3-C4	4.06	119.29	112.30
54	2y	54	5MU	O4-C4-C5	-4.04	120.30	124.92
54	1w	32	PSU	C4-N3-C2	-4.04	120.81	126.37
54	2w	32	PSU	C4-N3-C2	-4.03	120.82	126.37
1	1A	1939	PSU	O2-C2-N1	-4.03	118.64	122.79
54	2w	8	4SU	C5-C4-S4	-4.01	119.73	124.31
54	1y	55	PSU	O2-C2-N1	-3.98	118.69	122.79
55	1x	55	PSU	C4-N3-C2	-3.95	120.93	126.37
32	2a	1518	MA6	N3-C2-N1	-3.95	123.32	128.67
32	1a	1518	MA6	N3-C2-N1	-3.94	123.32	128.67
54	2w	54	5MU	C5-C4-N3	3.94	118.75	115.32
54	1y	8	4SU	C5-C4-N3	3.94	118.41	114.75
32	2a	1519	MA6	N3-C2-N1	-3.94	123.33	128.67
54	1y	55	PSU	C4-N3-C2	-3.92	120.97	126.37
1	1A	1964	5MC	C5-C6-N1	-3.91	119.06	123.31
54	2y	55	PSU	C4-N3-C2	-3.90	120.99	126.37
32	1a	527	7MG	C2-N3-C4	3.88	118.97	112.30
55	2x	55	PSU	C4-N3-C2	-3.84	121.08	126.37
55	2x	8	4SU	C1'-N1-C2	3.84	124.49	117.59
1	2A	1915	5MU	C5-C6-N1	-3.82	119.16	123.31
54	2y	55	PSU	O2-C2-N1	-3.82	118.85	122.79
55	1x	54	5MU	C5-C4-N3	3.82	118.64	115.32
1	2A	1917	PSU	C4-N3-C2	-3.81	121.12	126.37
54	2y	32	PSU	C4-N3-C2	-3.81	121.13	126.37
54	2w	55	PSU	C4-N3-C2	-3.80	121.14	126.37
32	1a	967	5MC	C5-C6-N1	-3.79	119.19	123.31
1	2A	1917	PSU	O2-C2-N1	-3.79	118.88	122.79
54	2y	39	PSU	C4-N3-C2	-3.77	121.17	126.37
32	2a	516	PSU	C4-N3-C2	-3.77	121.18	126.37
54	1w	39	PSU	O2-C2-N1	-3.77	118.91	122.79
32	2a	1518	MA6	C9-N6-C6	-3.75	109.05	119.40
54	1w	32	PSU	O2-C2-N1	-3.75	118.92	122.79
54	1w	54	5MU	O4-C4-C5	-3.74	120.64	124.92
1	2A	1962	5MC	C5-C6-N1	-3.74	119.25	123.31
54	2w	39	PSU	C4-N3-C2	-3.71	121.26	126.37
1	1A	2617	PSU	O2-C2-N1	-3.70	118.97	122.79
55	1x	8	4SU	O2-C2-N1	3.69	127.60	122.80
54	1w	39	PSU	C4-N3-C2	-3.69	121.28	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	516	PSU	C4-N3-C2	-3.63	121.36	126.37
32	2a	1400	5MC	C5-C6-N1	-3.63	119.37	123.31
54	1w	8	4SU	N3-C2-N1	3.62	119.60	114.89
1	1A	2564	2MU	O2-C2-N1	-3.60	118.11	122.80
54	1y	54	5MU	C5-C6-N1	-3.60	119.40	123.31
1	1A	1933	PSU	O2-C2-N1	-3.60	119.08	122.79
54	1w	55	PSU	C4-N3-C2	-3.57	121.45	126.37
54	2y	8	4SU	N3-C2-N1	3.56	119.53	114.89
55	2x	54	5MU	O2-C2-N1	-3.55	118.17	122.80
54	1y	32	PSU	C4-N3-C2	-3.54	121.49	126.37
32	1a	1404	5MC	C5-C6-N1	-3.54	119.47	123.31
54	1w	46	7MG	C2-N3-C4	3.53	118.38	112.30
32	1a	1519	MA6	N1-C6-N6	3.53	120.91	116.83
54	1w	37	MIA	C16-C14-C13	-3.50	112.16	122.66
55	1x	54	5MU	C5-C6-N1	-3.48	119.53	123.31
54	1y	54	5MU	O4-C4-C5	-3.47	120.94	124.92
32	2a	967	5MC	C5-C6-N1	-3.47	119.55	123.31
32	1a	1519	MA6	C9-N6-C6	-3.46	109.85	119.40
54	2y	39	PSU	O2-C2-N1	-3.46	119.22	122.79
32	1a	1518	MA6	C4-C5-N7	-3.45	105.69	109.34
54	1w	8	4SU	C5-C4-S4	-3.44	120.38	124.31
54	2y	54	5MU	C1'-N1-C2	3.43	123.75	117.59
32	1a	1407	5MC	C5-C6-N1	-3.43	119.59	123.31
55	2x	54	5MU	C5-C6-N1	-3.41	119.61	123.31
1	1A	2564	2MU	C5-C4-N3	3.40	119.56	114.80
54	1y	39	PSU	C4-N3-C2	-3.39	121.70	126.37
54	1w	46	7MG	C5-C4-N9	-3.39	102.00	106.33
1	1A	2564	2MU	O4-C4-C5	-3.38	119.33	125.16
1	2A	1942	5MC	C5-C6-N1	-3.38	119.64	123.31
32	2a	516	PSU	O2-C2-N1	-3.36	119.32	122.79
1	2A	1911	PSU	C4-N3-C2	-3.36	121.75	126.37
54	1y	32	PSU	O2-C2-N1	-3.36	119.33	122.79
32	2a	1407	5MC	C5-C4-N3	-3.33	118.34	121.75
32	1a	1518	MA6	C9-N6-C6	-3.33	110.23	119.40
54	1w	54	5MU	C5-C6-N1	-3.31	119.72	123.31
1	2A	2605	PSU	O2-C2-N1	-3.31	119.38	122.79
55	1x	32	5MC	C5-C4-N3	-3.30	118.38	121.75
1	1A	1937	5MU	C5-C6-N1	-3.28	119.75	123.31
54	2w	55	PSU	O2-C2-N1	-3.27	119.42	122.79
54	2w	32	PSU	O2-C2-N1	-3.27	119.42	122.79
32	2a	1519	MA6	C9-N6-C6	-3.25	110.44	119.40
55	1x	55	PSU	O2-C2-N1	-3.24	119.45	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2y	54	5MU	C1'-N1-C6	-3.23	115.83	121.15
55	1x	54	5MU	O4-C4-C5	-3.23	121.23	124.92
32	2a	1207	2MG	C8-N7-C5	3.22	108.03	102.55
55	2x	8	4SU	C5-C4-N3	3.22	117.74	114.75
1	2A	2552	2MU	O2-C2-N1	-3.21	118.61	122.80
54	2y	32	PSU	O2-C2-N1	-3.19	119.50	122.79
1	1A	1961	5MU	O2-C2-N1	-3.16	118.68	122.80
55	1x	32	5MC	C5-C6-N1	-3.15	119.89	123.31
1	2A	2251	OMG	C8-N7-C5	3.15	107.91	102.55
32	2a	1404	5MC	C5-C6-N1	-3.15	119.90	123.31
32	1a	1207	2MG	C8-N7-C5	3.12	107.87	102.55
55	2x	55	PSU	O2-C2-N1	-3.10	119.59	122.79
54	1w	37	MIA	C2-N1-C6	3.06	122.86	117.42
1	1A	1964	5MC	C5-C4-N3	-3.05	118.62	121.75
1	2A	1939	5MU	O2-C2-N1	-3.03	118.85	122.80
54	2w	8	4SU	C1'-N1-C2	3.03	123.04	117.59
32	2a	1518	MA6	C4-C5-N7	-3.03	106.14	109.34
55	1x	8	4SU	C1'-N1-C2	3.03	123.03	117.59
54	2y	46	7MG	C5-C4-N9	-3.03	102.46	106.33
32	1a	1519	MA6	N3-C2-N1	-3.02	124.57	128.67
32	1a	1404	5MC	C5-C4-N3	-3.00	118.68	121.75
32	2a	527	7MG	C5-C6-N1	2.98	116.19	110.94
1	2A	1911	PSU	O2-C2-N1	-2.98	119.72	122.79
32	2a	1404	5MC	C5-C4-N3	-2.97	118.71	121.75
32	2a	1498	UR3	C5-C4-N3	2.96	118.94	115.04
1	1A	1984	5MC	C5-C4-N3	-2.94	118.74	121.75
54	2w	37	MIA	C12-N6-C6	-2.94	120.12	122.85
54	2w	37	MIA	C4-C5-N7	-2.94	106.23	109.34
55	2x	32	5MC	C5-C4-N3	-2.92	118.76	121.75
54	1y	46	7MG	C5-C4-N9	-2.88	102.65	106.33
1	2A	2552	2MU	C5-C4-N3	2.88	118.83	114.80
32	2a	1407	5MC	C5-C6-N1	-2.85	120.22	123.31
32	1a	1498	UR3	C5-C4-N3	2.84	118.78	115.04
1	1A	2515	2MA	C4-C5-N7	-2.84	106.34	109.34
32	1a	1519	MA6	C4-C5-N7	-2.83	106.34	109.34
32	2a	1498	UR3	C6-N1-C2	-2.83	119.49	121.80
1	2A	1942	5MC	C5-C4-N3	-2.83	118.85	121.75
32	1a	1407	5MC	C5-C4-N3	-2.83	118.86	121.75
1	1A	1937	5MU	O2-C2-N1	-2.81	119.14	122.80
32	2a	1400	5MC	C5-C4-N3	-2.81	118.88	121.75
32	1a	966	M2G	C8-N7-C5	2.78	107.29	102.55
32	1a	1498	UR3	C1'-N1-C2	2.76	121.55	117.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1y	37	MIA	C4-C5-N7	-2.75	106.43	109.34
1	2A	1962	5MC	C5-C4-N3	-2.74	118.95	121.75
1	1A	1942	4OC	O2-C2-N3	-2.74	118.02	122.33
32	1a	516	PSU	O2-C2-N1	-2.73	119.97	122.79
32	2a	966	M2G	C8-N7-C5	2.73	107.20	102.55
55	2x	32	5MC	C5-C6-N1	-2.72	120.36	123.31
1	1A	2263	OMG	C8-N7-C5	2.71	107.16	102.55
54	2w	37	MIA	C2-N1-C6	2.70	122.21	117.42
54	2y	54	5MU	C5-C6-N1	-2.69	120.39	123.31
54	1y	8	4SU	C5-C4-S4	-2.68	121.25	124.31
54	2y	54	5MU	O2-C2-N3	-2.61	116.67	121.49
54	1w	37	MIA	N3-C2-N1	-2.60	122.27	127.03
1	2A	2552	2MU	O4-C4-C5	-2.59	120.69	125.16
32	1a	527	7MG	C5-C6-N1	2.59	115.50	110.94
54	2w	46	7MG	C5-C6-N1	2.58	115.49	110.94
55	1x	8	4SU	C4-N3-C2	2.58	129.79	127.31
32	2a	1518	MA6	C10-N6-C9	-2.55	107.98	116.18
1	1A	2617	PSU	C5-C6-N1	-2.55	118.61	122.14
32	2a	967	5MC	C5-C4-N3	-2.54	119.16	121.75
32	2a	1519	MA6	C4-C5-N7	-2.51	106.68	109.34
1	1A	1984	5MC	O2-C2-N3	-2.50	118.39	122.33
1	1A	1984	5MC	C5-C6-N1	-2.50	120.60	123.31
32	1a	516	PSU	C6-C5-C4	-2.50	116.49	118.17
1	2A	2605	PSU	C6-C5-C4	-2.50	116.49	118.17
32	2a	1402	4OC	C6-C5-C4	2.49	120.00	117.00
32	1a	967	5MC	C5-C4-N3	-2.47	119.22	121.75
54	1w	37	MIA	C4-C5-N7	-2.47	106.73	109.34
54	1w	46	7MG	C4-C5-N7	2.46	108.29	105.38
1	1A	2564	2MU	C2'-C1'-N1	-2.45	109.59	114.24
32	2a	1407	5MC	O2-C2-N3	-2.44	118.48	122.33
54	2w	37	MIA	N3-C2-N1	-2.44	122.57	127.03
32	1a	1404	5MC	O2-C2-N3	-2.43	118.50	122.33
32	1a	1518	MA6	C10-N6-C9	-2.43	108.38	116.18
32	1a	1402	4OC	C6-C5-C4	2.42	119.92	117.00
54	2w	54	5MU	C5-C6-N1	-2.42	120.69	123.31
54	2w	54	5MU	C5M-C5-C4	2.42	121.36	118.78
32	1a	1400	5MC	C5-C4-N3	-2.42	119.28	121.75
32	1a	1498	UR3	C3U-N3-C4	2.41	121.21	117.87
55	2x	8	4SU	O2-C2-N1	2.41	125.93	122.80
32	1a	1402	4OC	CM4-N4-C4	-2.38	117.80	122.45
32	1a	1498	UR3	C6-N1-C2	-2.35	119.88	121.80
32	1a	527	7MG	C5-C4-N9	-2.34	103.33	106.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2605	PSU	O4-C4-C5	-2.33	118.21	124.01
54	2w	39	PSU	O2-C2-N1	-2.33	120.38	122.79
1	1A	2263	OMG	C5-C6-N1	2.32	118.49	114.07
54	2y	54	5MU	C5M-C5-C4	2.31	121.25	118.78
55	1x	54	5MU	O2-C2-N1	-2.31	119.79	122.80
54	1y	39	PSU	O2-C2-N1	-2.31	120.41	122.79
55	2x	32	5MC	O2-C2-N3	-2.27	118.75	122.33
32	1a	1407	5MC	O2-C2-N3	-2.27	118.75	122.33
32	2a	1404	5MC	O2-C2-N3	-2.27	118.75	122.33
54	1w	8	4SU	C1'-N1-C2	2.27	121.67	117.59
54	1y	46	7MG	C5-C6-N1	2.27	114.93	110.94
54	2y	8	4SU	C1'-N1-C2	2.24	121.62	117.59
54	1w	54	5MU	O2-C2-N1	-2.22	119.91	122.80
54	2y	37	MIA	C4-C5-N7	-2.22	106.99	109.34
32	2a	967	5MC	CM5-C5-C6	-2.22	119.85	122.85
55	1x	8	4SU	C5-C4-N3	2.21	116.80	114.75
1	1A	1984	5MC	C1'-N1-C6	-2.20	117.52	121.15
32	1a	527	7MG	O6-C6-C5	-2.19	122.23	127.62
54	1y	54	5MU	O2-C2-N3	-2.19	117.45	121.49
32	2a	967	5MC	O2-C2-N3	-2.19	118.89	122.33
1	2A	2251	OMG	O6-C6-C5	-2.18	120.01	124.32
32	1a	967	5MC	O2-C2-N3	-2.17	118.91	122.33
1	1A	1933	PSU	C5-C6-N1	-2.17	119.13	122.14
54	2w	46	7MG	O6-C6-C5	-2.17	122.30	127.62
32	1a	1518	MA6	C10-N6-C6	-2.17	113.43	119.40
1	2A	1911	PSU	C6-C5-C4	-2.14	116.73	118.17
1	1A	1937	5MU	C5M-C5-C4	2.14	121.06	118.78
32	2a	1518	MA6	C10-N6-C6	-2.13	113.52	119.40
54	2y	46	7MG	C5-C6-N1	2.13	114.69	110.94
54	1w	46	7MG	O6-C6-C5	-2.13	122.39	127.62
55	2x	8	4SU	C1'-N1-C6	-2.13	116.23	120.78
1	2A	2251	OMG	C5-C6-N1	2.13	118.13	114.07
1	2A	1962	5MC	N4-C4-N3	2.13	122.36	118.51
1	1A	2515	2MA	C2-N1-C6	2.12	121.36	118.10
55	2x	55	PSU	C5-C6-N1	-2.11	119.21	122.14
54	1y	8	4SU	C1'-N1-C2	2.11	121.38	117.59
54	1y	55	PSU	O4'-C1'-C2'	2.11	108.07	105.15
54	2y	55	PSU	C6-C5-C4	-2.11	116.75	118.17
54	2y	32	PSU	O4'-C1'-C2'	2.10	108.06	105.15
55	2x	8	4SU	C6-C5-C4	-2.10	118.13	119.95
54	2y	55	PSU	O4'-C1'-C2'	2.09	108.05	105.15
32	2a	1207	2MG	N1-C2-N2	2.09	118.69	116.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1x	55	PSU	C5-C6-N1	-2.09	119.25	122.14
32	2a	1407	5MC	CM5-C5-C6	-2.08	120.04	122.85
1	1A	1984	5MC	CM5-C5-C6	-2.07	120.04	122.85
32	2a	516	PSU	O4'-C1'-C2'	2.07	108.02	105.15
55	1x	8	4SU	O2-C2-N3	-2.07	117.67	121.49
32	1a	1518	MA6	C1'-N9-C4	-2.06	123.01	126.64
54	2w	32	PSU	C5-C6-N1	-2.06	119.28	122.14
1	2A	1915	5MU	C5M-C5-C4	2.05	120.98	118.78
54	1y	39	PSU	O2-C2-N3	-2.05	118.22	121.86
1	2A	2605	PSU	C5-C6-N1	-2.05	119.30	122.14
32	1a	516	PSU	O4'-C1'-C2'	2.05	107.98	105.15
1	1A	1939	PSU	C5-C6-N1	-2.03	119.32	122.14
32	1a	1407	5MC	CM5-C5-C6	-2.03	120.10	122.85
43	1l	92	0TD	O-C-CA	-2.03	119.56	124.77
54	1y	8	4SU	C6-N1-C2	-2.02	118.54	121.00
54	2w	39	PSU	C5-C6-N1	-2.02	119.34	122.14
32	2a	1400	5MC	O2-C2-N3	-2.01	119.16	122.33
32	2a	1498	UR3	C3U-N3-C4	2.01	120.66	117.87
55	1x	32	5MC	O2-C2-N3	-2.01	119.16	122.33
32	2a	1518	MA6	C1'-N9-C4	-2.01	123.11	126.64
32	2a	527	7MG	C5-C4-N9	-2.00	103.77	106.33
1	2A	2503	2MA	C4-C5-N7	-2.00	107.22	109.34

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD2
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
54	1w	37	MIA	C12-C13-C14-C16
54	1y	46	7MG	C4'-C5'-O5'-P
54	1y	54	5MU	O4'-C4'-C5'-O5'
54	2y	55	PSU	C2'-C1'-C5-C6
54	2y	55	PSU	O4'-C1'-C5-C6
32	1a	1400	5MC	O4'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
54	2y	37	MIA	C3'-C4'-C5'-O5'
54	1y	8	4SU	C3'-C4'-C5'-O5'
54	1y	8	4SU	O4'-C4'-C5'-O5'
54	2w	46	7MG	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
54	1y	54	5MU	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
54	2w	46	7MG	C3'-C4'-C5'-O5'
32	1a	527	7MG	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	527	7MG	C3'-C4'-C5'-O5'
54	2y	37	MIA	O4'-C4'-C5'-O5'
54	2y	46	7MG	O4'-C1'-N9-C4
32	1a	1402	4OC	C3'-C4'-C5'-O5'
54	2y	32	PSU	O4'-C4'-C5'-O5'
54	2w	46	7MG	C2'-C1'-N9-C8
54	1w	46	7MG	C2'-C1'-N9-C8
54	2y	46	7MG	C2'-C1'-N9-C8
32	1a	527	7MG	O4'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
54	2w	37	MIA	N1-C6-N6-C12
43	1l	92	0TD	SB-CB-CG-OD1
54	1w	39	PSU	O4'-C1'-C5-C4
54	1y	55	PSU	O4'-C1'-C5-C4
32	2a	527	7MG	O4'-C4'-C5'-O5'
54	1y	46	7MG	C2'-C1'-N9-C8
54	2y	46	7MG	O4'-C1'-N9-C8
32	1a	1519	MA6	C4'-C5'-O5'-P
54	1w	46	7MG	C4'-C5'-O5'-P
32	1a	1402	4OC	C3'-C2'-O2'-CM2
54	1y	8	4SU	C4'-C5'-O5'-P
54	2y	37	MIA	C4'-C5'-O5'-P
54	2y	54	5MU	C2'-C1'-N1-C6
32	2a	527	7MG	C4'-C5'-O5'-P
54	2y	54	5MU	C2'-C1'-N1-C2
54	2w	46	7MG	O4'-C1'-N9-C8
1	2A	2503	2MA	O4'-C4'-C5'-O5'
1	1A	2515	2MA	C4'-C5'-O5'-P
54	1w	46	7MG	O4'-C1'-N9-C8
54	2w	37	MIA	C5-C6-N6-C12
55	2x	8	4SU	C2'-C1'-N1-C2
54	1y	54	5MU	C4'-C5'-O5'-P
1	1A	1942	4OC	C2'-C1'-N1-C2
54	2w	8	4SU	C2'-C1'-N1-C2

There are no ring outliers.

44 monomers are involved in 73 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1519	MA6	3	0
54	1y	37	MIA	1	0
1	2A	1915	5MU	1	0
1	2A	1917	PSU	1	0
54	1y	8	4SU	3	0
54	2w	37	MIA	1	0
32	2a	1207	2MG	3	0
1	2A	1911	PSU	1	0
54	2w	39	PSU	3	0
55	1x	8	4SU	2	0
1	2A	2552	2MU	1	0
32	2a	527	7MG	1	0
32	2a	1402	4OC	2	0
32	2a	1407	5MC	1	0
54	2y	55	PSU	8	0
54	2y	8	4SU	1	0
43	2l	92	0TD	4	0
54	2y	39	PSU	2	0
32	1a	1519	MA6	2	0
1	1A	1961	5MU	1	0
32	2a	967	5MC	2	0
1	1A	2515	2MA	1	0
32	2a	966	M2G	1	0
1	1A	1939	PSU	1	0
54	1y	39	PSU	1	0
43	1l	92	0TD	1	0
1	2A	2251	OMG	1	0
54	2y	37	MIA	1	0
54	2w	46	7MG	2	0
1	1A	2564	2MU	2	0
1	2A	1920	4OC	2	0
55	2x	8	4SU	1	0
32	2a	1518	MA6	2	0
54	1y	55	PSU	2	0
32	1a	1402	4OC	2	0
55	2x	32	5MC	1	0
54	2y	46	7MG	1	0
32	1a	1518	MA6	3	0
54	1w	39	PSU	1	0
32	2a	1404	5MC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	2503	2MA	2	0
54	1w	37	MIA	1	0
54	1w	46	7MG	2	0
54	2w	8	4SU	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2853 ligands modelled in this entry, 2851 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
59	SF4	1d	501	35	0,12,12	-	-	-		
59	SF4	2d	501	35	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	SF4	1d	501	35	-	-	0/6/5/5
59	SF4	2d	501	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	2d	501	SF4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	1A	2860/2915 (98%)	-0.03	172 (6%) 29 27	24, 43, 91, 103	0
1	2A	2789/2915 (95%)	0.06	116 (4%) 41 38	28, 48, 89, 106	0
2	1B	120/121 (99%)	0.55	1 (0%) 82 79	39, 61, 72, 90	0
2	2B	120/121 (99%)	1.34	15 (12%) 9 9	45, 68, 77, 91	0
3	1D	275/276 (99%)	0.22	4 (1%) 71 68	25, 42, 58, 80	0
3	2D	275/276 (99%)	0.21	3 (1%) 77 74	28, 45, 61, 78	0
4	1E	204/206 (99%)	0.32	7 (3%) 48 45	23, 46, 66, 80	0
4	2E	204/206 (99%)	0.30	2 (0%) 79 76	26, 50, 67, 80	0
5	1F	203/210 (96%)	0.45	5 (2%) 58 55	22, 51, 76, 91	0
5	2F	203/210 (96%)	0.56	6 (2%) 52 49	27, 56, 76, 91	0
6	1G	181/182 (99%)	1.30	29 (16%) 6 6	48, 69, 80, 92	0
6	2G	181/182 (99%)	2.05	91 (50%) 0 0	54, 73, 81, 93	0
7	1H	174/180 (96%)	1.09	12 (6%) 24 22	47, 64, 74, 83	0
7	2H	174/180 (96%)	1.51	42 (24%) 2 2	54, 70, 78, 83	0
8	1I	146/148 (98%)	1.09	12 (8%) 19 18	49, 73, 82, 85	0
8	2I	146/148 (98%)	1.23	21 (14%) 7 7	50, 73, 82, 86	0
9	1N	140/140 (100%)	0.65	3 (2%) 63 60	31, 48, 67, 77	0
9	2N	140/140 (100%)	0.60	3 (2%) 63 60	37, 53, 71, 80	0
10	1O	122/122 (100%)	-0.02	2 (1%) 70 67	23, 40, 60, 74	0
10	2O	122/122 (100%)	0.78	4 (3%) 49 46	45, 59, 72, 81	0
11	1P	149/150 (99%)	0.74	13 (8%) 17 16	24, 53, 75, 81	0
11	2P	149/150 (99%)	0.75	9 (6%) 29 27	29, 58, 76, 85	0
12	1Q	141/141 (100%)	0.55	2 (1%) 73 70	33, 51, 68, 77	0
12	2Q	141/141 (100%)	1.16	24 (17%) 5 5	37, 56, 73, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	0.06	0 100 100	29, 40, 55, 62	0
13	2R	118/118 (100%)	0.04	0 100 100	31, 43, 58, 65	0
14	1S	110/112 (98%)	1.09	12 (10%) 12 11	49, 62, 72, 77	0
14	2S	110/112 (98%)	1.82	37 (33%) 1 1	55, 66, 75, 79	0
15	1T	131/146 (89%)	0.59	8 (6%) 28 26	38, 50, 72, 77	0
15	2T	131/146 (89%)	0.57	3 (2%) 61 58	43, 53, 74, 78	0
16	1U	116/118 (98%)	0.29	2 (1%) 69 65	26, 39, 55, 73	0
16	2U	116/118 (98%)	0.45	1 (0%) 81 78	33, 46, 61, 73	0
17	1V	101/101 (100%)	0.48	3 (2%) 52 49	28, 51, 67, 76	0
17	2V	101/101 (100%)	0.86	5 (4%) 35 32	33, 57, 70, 76	0
18	1W	112/113 (99%)	0.04	2 (1%) 67 64	26, 37, 55, 88	0
18	2W	112/113 (99%)	0.09	2 (1%) 67 64	30, 41, 57, 88	0
19	1X	95/96 (98%)	0.41	3 (3%) 50 47	30, 44, 63, 75	0
19	2X	95/96 (98%)	0.53	1 (1%) 77 74	34, 49, 65, 76	0
20	1Y	107/110 (97%)	0.94	9 (8%) 18 17	45, 57, 74, 83	0
20	2Y	107/110 (97%)	1.27	13 (12%) 10 9	48, 61, 76, 86	0
21	1Z	154/206 (74%)	0.87	20 (12%) 9 8	38, 64, 86, 96	0
21	2Z	160/206 (77%)	2.24	96 (60%) 0 0	72, 83, 93, 99	0
22	10	83/85 (97%)	0.11	0 100 100	25, 38, 59, 71	0
22	20	83/85 (97%)	1.44	17 (20%) 3 3	41, 66, 78, 82	0
23	11	97/98 (98%)	0.17	1 (1%) 79 76	23, 44, 71, 77	0
23	21	97/98 (98%)	0.93	13 (13%) 8 8	38, 58, 74, 82	0
24	12	70/72 (97%)	0.78	5 (7%) 23 22	40, 57, 66, 79	0
24	22	70/72 (97%)	0.91	3 (4%) 40 37	46, 61, 69, 78	0
25	13	59/60 (98%)	0.48	1 (1%) 69 65	29, 45, 69, 83	0
25	23	59/60 (98%)	0.68	2 (3%) 48 45	36, 51, 72, 87	0
26	14	69/71 (97%)	1.64	22 (31%) 1 1	64, 79, 89, 97	0
26	24	69/71 (97%)	2.16	36 (52%) 0 0	70, 80, 89, 97	0
27	15	59/60 (98%)	0.02	1 (1%) 69 65	25, 36, 57, 72	0
27	25	59/60 (98%)	0.02	1 (1%) 69 65	30, 40, 60, 71	0
28	16	53/54 (98%)	0.44	1 (1%) 66 63	38, 51, 64, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.77	3 (5%) 30 28	42, 54, 65, 71	0
29	17	48/49 (97%)	0.02	5 (10%) 13 12	24, 31, 58, 69	0
29	27	48/49 (97%)	-0.02	2 (4%) 41 38	28, 35, 58, 70	0
30	18	64/65 (98%)	0.40	4 (6%) 27 25	33, 42, 50, 66	0
30	28	64/65 (98%)	0.60	1 (1%) 70 67	38, 46, 53, 67	0
31	19	37/37 (100%)	0.65	0 100 100	37, 50, 67, 68	0
31	29	37/37 (100%)	1.21	5 (13%) 8 7	46, 54, 71, 72	0
32	1a	1488/1521 (97%)	0.82	105 (7%) 23 22	42, 72, 92, 103	0
32	2a	1491/1521 (98%)	1.10	279 (18%) 4 4	44, 74, 93, 103	0
33	1b	231/256 (90%)	1.58	70 (30%) 1 1	69, 82, 89, 94	0
33	2b	231/256 (90%)	2.35	145 (62%) 0 0	72, 83, 89, 94	0
34	1c	206/239 (86%)	1.57	55 (26%) 2 2	67, 80, 86, 92	0
34	2c	206/239 (86%)	2.44	133 (64%) 0 0	69, 82, 88, 93	0
35	1d	208/209 (99%)	1.35	36 (17%) 5 5	56, 72, 80, 87	0
35	2d	208/209 (99%)	1.36	35 (16%) 5 5	58, 71, 80, 88	0
36	1e	148/162 (91%)	1.30	22 (14%) 7 6	56, 72, 80, 86	0
36	2e	148/162 (91%)	1.96	67 (45%) 1 1	59, 74, 83, 87	0
37	1f	100/101 (99%)	1.02	5 (5%) 35 32	50, 66, 76, 78	0
37	2f	100/101 (99%)	1.05	6 (6%) 29 27	60, 72, 80, 86	0
38	1g	155/156 (99%)	1.48	36 (23%) 2 3	62, 74, 83, 100	0
38	2g	155/156 (99%)	1.69	44 (28%) 1 1	65, 76, 84, 102	0
39	1h	137/138 (99%)	1.19	15 (10%) 12 11	60, 72, 78, 83	0
39	2h	137/138 (99%)	1.71	44 (32%) 1 1	64, 74, 80, 84	0
40	1i	127/128 (99%)	1.48	33 (25%) 2 2	51, 75, 83, 87	0
40	2i	127/128 (99%)	2.72	90 (70%) 0 0	71, 85, 91, 92	0
41	1j	97/105 (92%)	1.79	33 (34%) 1 1	59, 78, 90, 95	0
41	2j	96/105 (91%)	2.97	74 (77%) 0 0	74, 87, 94, 98	0
42	1k	114/129 (88%)	1.06	13 (11%) 11 10	52, 69, 80, 83	0
42	2k	114/129 (88%)	1.24	17 (14%) 7 6	55, 71, 81, 87	0
43	1l	121/132 (91%)	0.98	15 (12%) 9 9	53, 64, 74, 77	0
43	2l	121/132 (91%)	1.29	16 (13%) 8 8	55, 67, 75, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	123/126 (97%)	1.04	12 (9%) 14 13	54, 69, 78, 82	0
44	2m	122/126 (96%)	2.51	69 (56%) 0 0	73, 84, 90, 94	0
45	1n	60/61 (98%)	1.37	8 (13%) 8 8	57, 69, 78, 82	0
45	2n	60/61 (98%)	3.14	54 (90%) 0 0	78, 85, 93, 95	0
46	1o	88/89 (98%)	1.14	14 (15%) 6 6	56, 69, 78, 82	0
46	2o	88/89 (98%)	1.29	13 (14%) 7 7	57, 70, 80, 83	0
47	1p	82/88 (93%)	1.69	27 (32%) 1 1	58, 70, 80, 83	0
47	2p	82/88 (93%)	1.53	16 (19%) 4 4	59, 69, 81, 82	0
48	1q	99/105 (94%)	1.23	7 (7%) 23 22	57, 70, 79, 82	0
48	2q	99/105 (94%)	1.44	21 (21%) 3 3	60, 70, 79, 82	0
49	1r	68/88 (77%)	1.08	6 (8%) 17 16	60, 68, 79, 82	0
49	2r	68/88 (77%)	1.20	9 (13%) 8 8	60, 70, 80, 82	0
50	1s	83/93 (89%)	1.50	19 (22%) 2 3	70, 79, 86, 91	0
50	2s	83/93 (89%)	2.73	64 (77%) 0 0	74, 81, 88, 94	0
51	1t	96/106 (90%)	1.44	23 (23%) 2 2	58, 71, 80, 86	0
51	2t	96/106 (90%)	1.15	11 (11%) 11 10	59, 71, 81, 85	0
52	1u	23/27 (85%)	1.77	9 (39%) 1 1	65, 74, 78, 80	0
52	2u	23/27 (85%)	2.85	17 (73%) 0 0	68, 75, 80, 83	0
53	1v	13/24 (54%)	1.84	7 (53%) 0 0	60, 74, 92, 98	0
53	2v	13/24 (54%)	2.44	7 (53%) 0 0	65, 78, 95, 98	0
54	1w	67/76 (88%)	1.51	21 (31%) 1 1	44, 89, 97, 101	0
54	1y	67/76 (88%)	1.50	15 (22%) 3 3	37, 91, 97, 101	0
54	2w	65/76 (85%)	1.79	20 (30%) 1 1	56, 96, 101, 104	0
54	2y	66/76 (86%)	1.66	15 (22%) 3 3	51, 95, 99, 100	0
55	1x	72/77 (93%)	0.54	5 (6%) 24 22	33, 66, 84, 87	0
55	2x	72/77 (93%)	0.99	3 (4%) 41 38	52, 81, 90, 95	0
All	All	20875/21748 (95%)	0.79	2818 (13%) 8 7	22, 63, 88, 106	0

All (2818) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	2m	102	ARG	6.9
38	1g	80	VAL	6.8

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Mol	Chain	Res	Type	RSRZ
41	2j	40	LEU	6.7
45	2n	25	VAL	6.6
45	1n	2	ALA	6.6
38	1g	82	GLY	6.5
33	2b	165	VAL	6.3
50	2s	79	THR	6.2
52	2u	11	GLY	6.1
41	2j	47	PHE	6.0
34	2c	171	GLY	6.0
7	1H	2	SER	5.9
16	1U	117	GLN	5.9
40	2i	14	VAL	5.8
41	2j	55	LYS	5.7
52	2u	14	TRP	5.7
21	2Z	139	VAL	5.6
41	2j	65	LEU	5.6
45	2n	39	LEU	5.6
21	2Z	172	ALA	5.5
44	2m	90	LEU	5.4
44	2m	6	GLY	5.4
38	1g	79	ARG	5.4
3	1D	276	LYS	5.3
40	2i	9	ARG	5.3
1	1A	1140	U	5.3
23	21	2	SER	5.3
44	2m	123	ALA	5.3
33	2b	237	ALA	5.2
1	1A	1104	G	5.2
44	2m	100	GLY	5.2
45	2n	34	TYR	5.2
41	2j	54	PHE	5.1
34	2c	198	VAL	5.1
44	2m	124	PRO	5.1
1	1A	1110	C	5.1
45	2n	7	ILE	5.1
34	1c	2	GLY	5.1
21	2Z	173	ALA	5.0
1	1A	1141	A	5.0
53	2v	14	A	5.0
33	2b	21	ARG	5.0
1	1A	932	C	5.0
40	2i	102	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
6	2G	74	LYS	5.0
33	2b	214	ILE	5.0
34	2c	182	ILE	5.0
6	2G	29	TRP	5.0
41	2j	32	ALA	5.0
40	2i	126	SER	5.0
50	2s	80	TYR	5.0
1	1A	1143	U	5.0
34	2c	2	GLY	4.9
44	2m	78	ILE	4.9
33	2b	161	ALA	4.9
34	2c	189	ALA	4.9
6	1G	139	LEU	4.8
33	2b	187	LEU	4.8
45	2n	2	ALA	4.8
45	2n	5	ALA	4.8
46	1o	87	ILE	4.8
38	2g	82	GLY	4.8
41	2j	37	PRO	4.8
32	1a	1531	A	4.8
44	2m	104	ARG	4.8
44	1m	2	ALA	4.8
44	1m	122	LYS	4.8
41	2j	41	PRO	4.8
34	2c	124	ILE	4.8
44	2m	68	GLY	4.8
26	14	59	PHE	4.8
41	2j	35	SER	4.7
33	2b	200	ILE	4.7
1	1A	2814	C	4.7
40	2i	106	ALA	4.7
1	1A	2906	U	4.7
39	1h	2	LEU	4.7
34	2c	68	VAL	4.7
41	2j	85	LEU	4.6
50	2s	13	ASP	4.6
38	2g	16	LEU	4.6
33	2b	185	ILE	4.6
1	2A	883	G	4.6
34	2c	149	ALA	4.6
52	2u	6	ARG	4.6
6	2G	159	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
40	2i	11	LYS	4.5
44	2m	4	ILE	4.5
33	2b	152	PHE	4.5
1	1A	1144	A	4.5
50	2s	84	GLY	4.5
34	2c	129	ALA	4.5
34	2c	33	LEU	4.5
1	1A	1112	U	4.5
1	1A	1105	G	4.5
1	1A	1103	A	4.5
1	1A	931	C	4.4
32	1a	1023	G	4.4
1	2A	896	A	4.4
41	2j	87	THR	4.4
44	2m	120	LYS	4.4
44	2m	122	LYS	4.4
33	2b	236	TYR	4.4
32	1a	344	A	4.4
54	1w	1	G	4.4
21	2Z	146	ILE	4.4
1	1A	936	C	4.4
34	2c	137	ALA	4.4
41	1j	32	ALA	4.4
44	1m	124	PRO	4.3
6	2G	28	VAL	4.3
44	2m	60	VAL	4.3
50	2s	9	VAL	4.3
45	2n	38	GLY	4.3
34	2c	8	ILE	4.3
41	2j	50	ILE	4.3
34	1c	207	VAL	4.3
1	1A	2141	A	4.3
53	1v	12	A	4.3
32	2a	1150	U	4.3
38	2g	5	ARG	4.3
40	2i	83	ARG	4.3
40	2i	39	GLY	4.3
32	1a	163	C	4.2
32	2a	1149	C	4.2
40	2i	36	TYR	4.2
45	2n	21	TYR	4.2
1	1A	1127	U	4.2

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Mol	Chain	Res	Type	RSRZ
21	1Z	141	VAL	4.2
45	2n	29	ARG	4.2
50	2s	75	ALA	4.2
36	2e	22	GLY	4.2
33	2b	163	PHE	4.2
6	2G	15	VAL	4.2
9	1N	9	VAL	4.2
21	1Z	149	SER	4.2
34	2c	197	GLY	4.2
1	1A	1106	U	4.2
32	2a	1119	C	4.2
34	2c	187	ALA	4.2
44	2m	118	ALA	4.2
50	2s	54	GLY	4.2
44	2m	96	LEU	4.2
24	12	70	GLN	4.2
32	2a	1219	U	4.2
38	2g	84	ASN	4.2
41	2j	78	ASN	4.2
1	1A	933	C	4.2
40	2i	90	PRO	4.1
21	2Z	171	ILE	4.1
41	2j	74	ILE	4.1
32	2a	1222	G	4.1
40	2i	62	TYR	4.1
45	2n	55	GLY	4.1
54	2w	3	C	4.1
45	2n	3	ARG	4.1
40	2i	37	PHE	4.1
7	2H	52	VAL	4.1
21	2Z	86	VAL	4.1
26	14	56	VAL	4.1
38	2g	80	VAL	4.1
32	2a	1033	G	4.1
40	2i	124	GLN	4.1
34	2c	52	LEU	4.1
1	1A	1142	A	4.1
24	12	69	ARG	4.1
40	2i	10	ARG	4.1
54	2y	36	A	4.1
33	2b	39	ILE	4.1
40	2i	125	TYR	4.1

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Mol	Chain	Res	Type	RSRZ
33	2b	61	LEU	4.1
40	2i	19	LEU	4.1
1	2A	229	A	4.1
41	2j	42	THR	4.1
45	2n	13	THR	4.1
27	15	60	VAL	4.1
45	2n	18	VAL	4.1
50	2s	24	ALA	4.1
6	2G	11	TYR	4.0
34	2c	9	GLY	4.0
38	1g	81	GLY	4.0
32	1a	1001(A)	G	4.0
33	2b	91	PRO	4.0
38	1g	8	GLU	4.0
32	2a	1030	C	4.0
40	2i	7	THR	4.0
54	1w	73	A	4.0
41	2j	49	VAL	4.0
38	2g	81	GLY	4.0
41	2j	38	ILE	4.0
1	1A	1102	G	4.0
33	2b	81	VAL	4.0
1	2A	2136	C	4.0
21	2Z	144	LEU	4.0
26	14	58	ARG	4.0
34	2c	48	TYR	4.0
42	2k	25	TYR	4.0
1	1A	2163	G	4.0
1	1A	2813	G	4.0
32	1a	630	G	4.0
32	2a	1127	G	4.0
33	2b	184	VAL	4.0
6	2G	50	ALA	4.0
33	1b	228	GLY	4.0
47	2p	48	TRP	4.0
52	1u	2	GLY	4.0
22	20	84	LEU	4.0
33	2b	11	LEU	4.0
25	23	2	PRO	4.0
26	24	32	TYR	4.0
44	2m	23	TYR	4.0
33	1b	127	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
45	2n	40	CYS	4.0
33	2b	230	VAL	4.0
50	2s	2	PRO	3.9
41	2j	13	HIS	3.9
32	2a	1038	C	3.9
38	2g	85	TYR	3.9
53	2v	12	A	3.9
47	1p	82	GLN	3.9
32	2a	1126	U	3.9
33	1b	120	ALA	3.9
34	2c	188	LEU	3.9
36	2e	12	LEU	3.9
50	2s	82	GLY	3.9
44	2m	67	GLU	3.9
1	2A	2155	G	3.9
32	1a	1036	G	3.9
32	2a	973	G	3.9
32	2a	1220	G	3.9
54	2w	71	G	3.9
34	1c	184	TYR	3.9
32	2a	1183	A	3.9
47	2p	82	GLN	3.9
26	24	49	PHE	3.9
40	2i	27	THR	3.9
7	2H	45	VAL	3.9
45	2n	58	LYS	3.9
38	2g	7	ALA	3.9
45	2n	6	LEU	3.9
1	1A	1145	G	3.9
32	2a	1018	C	3.9
40	2i	67	GLY	3.9
33	2b	101	MET	3.9
34	2c	5	ILE	3.9
44	2m	87	TYR	3.9
38	2g	76	ARG	3.9
6	1G	80	PHE	3.8
1	1A	2136	A	3.8
32	1a	1002	G	3.8
32	1a	1035	A	3.8
32	2a	1224	G	3.8
54	2w	73	A	3.8
1	1A	935	C	3.8

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Mol	Chain	Res	Type	RSRZ
32	2a	1019	C	3.8
33	1b	229	VAL	3.8
26	24	65	ASP	3.8
39	2h	2	LEU	3.8
50	2s	71	LEU	3.8
40	2i	15	ALA	3.8
51	1t	103	GLY	3.8
33	2b	201	ILE	3.8
44	2m	106	ASN	3.8
42	2k	126	ARG	3.8
47	1p	42	ARG	3.8
50	2s	81	ARG	3.8
44	2m	105	THR	3.8
40	2i	99	LEU	3.8
44	2m	54	VAL	3.8
45	2n	53	LEU	3.8
1	1A	1114	G	3.8
1	1A	1116	A	3.8
1	1A	1146	C	3.8
32	1a	1026	G	3.8
33	2b	123	ALA	3.8
53	2v	13	A	3.8
40	2i	49	PRO	3.8
41	1j	86	MET	3.8
1	1A	1111	U	3.8
34	2c	170	GLN	3.8
40	2i	20	ARG	3.8
6	1G	146	TYR	3.8
51	1t	13	LEU	3.8
44	2m	117	VAL	3.8
40	2i	105	ASP	3.8
36	2e	81	GLU	3.8
32	1a	160	A	3.8
32	1a	1005	A	3.8
32	2a	1030(A)	G	3.8
32	2a	1034	G	3.8
32	2a	1036	G	3.8
54	2y	19	G	3.8
21	2Z	137	ILE	3.8
34	1c	39	ILE	3.8
40	2i	81	ILE	3.8
21	2Z	149	SER	3.8

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Mol	Chain	Res	Type	RSRZ
40	2i	5	TYR	3.8
45	1n	34	TYR	3.8
34	2c	53	ALA	3.8
26	24	31	ILE	3.8
32	2a	994	A	3.8
1	2A	1536	C	3.8
32	1a	204	U	3.8
35	1d	194	LEU	3.7
38	1g	85	TYR	3.7
41	2j	8	LEU	3.7
34	2c	195	VAL	3.7
36	1e	10	MET	3.7
33	1b	125	PRO	3.7
15	1T	130	ALA	3.7
26	14	54	GLY	3.7
33	2b	38	GLY	3.7
33	1b	21	ARG	3.7
32	1a	1447	A	3.7
1	2A	1043	C	3.7
32	2a	1030(B)	C	3.7
32	2a	1216	G	3.7
50	2s	10	PHE	3.7
50	2s	22	LEU	3.7
33	2b	199	TYR	3.7
40	2i	61	ALA	3.7
21	1Z	146	ILE	3.7
21	1Z	150	LEU	3.7
45	2n	49	HIS	3.7
54	1w	4	C	3.7
26	14	50	VAL	3.7
33	1b	165	VAL	3.7
44	2m	98	VAL	3.7
1	1A	1221	G	3.7
15	1T	131	ALA	3.7
22	20	5	LYS	3.7
29	17	48	LYS	3.7
32	2a	1058	G	3.7
36	2e	85	GLY	3.7
36	2e	86	ALA	3.7
19	1X	95	LEU	3.7
33	2b	118	LEU	3.7
34	2c	12	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
32	1a	1001	A	3.7
32	2a	1251	A	3.7
53	2v	24	A	3.7
1	1A	2807	C	3.7
5	1F	131	GLY	3.7
6	2G	146	TYR	3.7
33	2b	71	VAL	3.7
35	1d	167	GLY	3.7
40	2i	41	VAL	3.7
36	2e	94	ALA	3.7
38	1g	2	ALA	3.7
33	2b	222	ILE	3.7
54	1w	65	G	3.7
38	2g	12	LEU	3.6
41	2j	88	LEU	3.6
32	1a	1257	U	3.6
41	2j	10	GLY	3.6
32	2a	1092	A	3.6
32	2a	1286	A	3.6
1	1A	1138	C	3.6
1	2A	2803	C	3.6
32	2a	980	C	3.6
32	2a	1260	C	3.6
1	1A	1133	G	3.6
1	1A	1139	G	3.6
41	2j	59	SER	3.6
21	1Z	168	GLU	3.6
7	2H	50	VAL	3.6
21	2Z	26	GLY	3.6
26	24	56	VAL	3.6
45	2n	61	TRP	3.6
32	2a	975	A	3.6
26	24	51	ASP	3.6
1	1A	2905	C	3.6
32	2a	962	C	3.6
19	2X	92	LEU	3.6
1	1A	1108	G	3.6
32	1a	1024	G	3.6
14	2S	29	PHE	3.6
34	2c	151	VAL	3.6
39	1h	93	VAL	3.6
40	2i	44	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
40	2i	66	ARG	3.6
21	2Z	170	THR	3.6
41	1j	34	VAL	3.6
32	2a	1281	U	3.6
51	1t	12	ALA	3.6
34	2c	157	ILE	3.6
1	1A	934	A	3.6
32	2a	983	A	3.6
34	2c	142	MET	3.6
34	2c	176	HIS	3.6
21	2Z	33	LEU	3.6
34	2c	94	LEU	3.6
1	2A	2160	G	3.6
34	2c	41	GLY	3.6
6	1G	50	ALA	3.6
6	2G	57	ALA	3.6
6	2G	12	TYR	3.6
50	1s	13	ASP	3.6
1	1A	2167	C	3.5
33	1b	129	GLU	3.5
52	2u	15	ARG	3.5
40	2i	17	VAL	3.5
40	2i	45	ALA	3.5
1	1A	2174	G	3.5
1	2A	2159	G	3.5
32	1a	1003	G	3.5
32	2a	993	G	3.5
32	2a	1017	G	3.5
50	2s	40	ILE	3.5
54	2y	34	G	3.5
1	1A	271	U	3.5
1	1A	2135	U	3.5
14	2S	58	LEU	3.5
34	2c	178	LEU	3.5
45	2n	44	LEU	3.5
50	2s	20	LEU	3.5
46	1o	88	ARG	3.5
52	2u	24	ARG	3.5
53	1v	24	A	3.5
33	2b	122	PHE	3.5
1	1A	2162	C	3.5
1	2A	2804	C	3.5

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Mol	Chain	Res	Type	RSRZ
20	2Y	80	GLY	3.5
45	2n	28	GLY	3.5
51	2t	47	GLY	3.5
21	2Z	174	VAL	3.5
34	2c	138	VAL	3.5
21	2Z	21	ALA	3.5
44	2m	5	ALA	3.5
45	2n	20	ALA	3.5
41	2j	23	ILE	3.5
41	2j	96	ILE	3.5
1	1A	1124	U	3.5
41	2j	71	LEU	3.5
6	2G	35	GLU	3.5
1	1A	572	A	3.5
1	1A	2195	A	3.5
5	1F	208	GLY	3.5
18	1W	112	GLY	3.5
33	2b	99	GLY	3.5
40	1i	126	SER	3.5
9	1N	140	VAL	3.5
21	2Z	27	VAL	3.5
34	2c	55	VAL	3.5
34	2c	120	VAL	3.5
36	2e	41	VAL	3.5
50	2s	41	VAL	3.5
33	2b	67	THR	3.5
35	1d	169	LYS	3.5
26	14	67	TYR	3.5
33	2b	148	TYR	3.5
40	2i	4	TYR	3.5
33	1b	130	ARG	3.5
34	2c	30	ARG	3.5
1	2A	171	G	3.5
1	2A	2116	G	3.5
32	1a	1030(A)	G	3.5
6	1G	42	GLY	3.5
26	14	66	SER	3.5
38	2g	34	GLY	3.5
44	2m	112	GLY	3.5
33	2b	197	VAL	3.5
40	2i	86	VAL	3.5
41	2j	14	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
32	2a	1531	A	3.5
43	2l	51	ALA	3.5
1	2A	886	C	3.4
32	2a	1066	C	3.4
7	2H	64	LEU	3.4
41	2j	90	LEU	3.4
50	1s	71	LEU	3.4
42	1k	25	TYR	3.4
45	2n	23	ARG	3.4
32	1a	1025	U	3.4
1	1A	1109	G	3.4
20	2Y	57	GLN	3.4
23	21	28	GLY	3.4
32	2a	1048	G	3.4
33	2b	136	VAL	3.4
40	2i	28	VAL	3.4
35	2d	146	ILE	3.4
40	2i	13	ALA	3.4
45	2n	30	ALA	3.4
1	1A	1100	A	3.4
1	1A	1115	A	3.4
1	2A	2119	A	3.4
1	1A	1121	C	3.4
1	1A	2186	C	3.4
32	1a	1028	C	3.4
38	1g	3	ARG	3.4
40	2i	16	ARG	3.4
26	24	59	PHE	3.4
33	1b	133	LYS	3.4
38	2g	109	ASN	3.4
34	2c	155	GLY	3.4
23	11	2	SER	3.4
21	2Z	57	ILE	3.4
34	2c	134	ILE	3.4
34	2c	200	ALA	3.4
40	2i	82	ALA	3.4
41	1j	4	ILE	3.4
1	1A	2806	G	3.4
1	2A	2133	G	3.4
1	2A	2157	G	3.4
32	2a	1272	G	3.4
44	1m	5	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
36	2e	31	LEU	3.4
50	2s	15	LEU	3.4
33	1b	131	PRO	3.4
3	1D	275	LYS	3.4
20	1Y	1	MET	3.4
41	2j	69	ASN	3.4
41	2j	36	GLY	3.4
14	2S	69	VAL	3.4
33	1b	230	VAL	3.4
38	2g	75	VAL	3.4
50	2s	11	VAL	3.4
33	2b	162	ILE	3.4
34	2c	77	ILE	3.4
34	2c	202	ILE	3.4
36	2e	109	ILE	3.4
36	2e	118	ILE	3.4
50	1s	40	ILE	3.4
40	1i	106	ALA	3.4
40	2i	96	LEU	3.4
41	2j	79	ARG	3.4
1	1A	2212	G	3.4
1	2A	2149	G	3.4
32	1a	1034	G	3.4
54	1y	18	G	3.4
36	2e	133	TYR	3.4
32	1a	1030(B)	C	3.4
40	2i	101	PHE	3.4
44	2m	22	ILE	3.4
14	2S	5	THR	3.3
40	1i	15	ALA	3.3
44	2m	88	ARG	3.3
44	2m	121	LYS	3.3
1	2A	882	G	3.3
1	2A	2802	G	3.3
2	2B	23	G	3.3
54	1w	70	G	3.3
1	1A	937	A	3.3
48	2q	95	TYR	3.3
50	2s	52	TYR	3.3
21	2Z	48	PHE	3.3
40	1i	59	PHE	3.3
45	2n	36	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
34	2c	13	GLY	3.3
35	2d	87	GLY	3.3
51	2t	9	ASN	3.3
32	2a	1263	C	3.3
1	1A	1128	U	3.3
44	2m	15	VAL	3.3
8	1I	146	ALA	3.3
21	1Z	170	THR	3.3
38	2g	3	ARG	3.3
41	2j	43	ARG	3.3
44	2m	19	LEU	3.3
41	2j	99	LYS	3.3
1	1A	2137	G	3.3
32	2a	971	G	3.3
32	2a	976	G	3.3
1	1A	2803	A	3.3
1	1A	2812	A	3.3
32	2a	1035	A	3.3
41	2j	68	HIS	3.3
6	2G	160	VAL	3.3
36	2e	33	VAL	3.3
43	1l	43	VAL	3.3
32	1a	1532	U	3.3
44	2m	3	ARG	3.3
50	2s	78	ARG	3.3
33	2b	196	LEU	3.3
33	2b	218	ALA	3.3
49	2r	60	ALA	3.3
26	24	57	GLU	3.3
6	2G	80	PHE	3.3
21	2Z	121	HIS	3.3
37	2f	60	PHE	3.3
41	2j	56	HIS	3.3
50	2s	14	HIS	3.3
39	2h	106	GLY	3.3
40	2i	63	ILE	3.3
1	1A	942	A	3.3
1	2A	2135	A	3.3
32	2a	953	G	3.3
32	2a	1030(D)	A	3.3
32	2a	1110	A	3.3
40	1i	14	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
41	2j	72	VAL	3.3
32	2a	1124	G	3.3
21	2Z	51	ALA	3.3
41	1j	88	LEU	3.3
33	2b	22	LYS	3.3
40	2i	103	THR	3.3
32	1a	1027	C	3.3
32	1a	1037	C	3.3
32	2a	979	C	3.3
54	1w	72	C	3.3
33	2b	86	GLU	3.3
50	2s	31	ILE	3.2
33	2b	69	LEU	3.2
43	2l	52	LEU	3.2
49	2r	66	LEU	3.2
22	20	43	THR	3.2
33	2b	207	ALA	3.2
41	1j	87	THR	3.2
44	2m	72	ALA	3.2
1	1A	2173	G	3.2
6	2G	17	PRO	3.2
32	2a	1182	G	3.2
1	1A	2164	C	3.2
1	2A	885	C	3.2
1	2A	2896	C	3.2
40	2i	18	PHE	3.2
26	24	54	GLY	3.2
31	29	37	GLY	3.2
40	2i	92	TYR	3.2
47	1p	39	TYR	3.2
34	2c	91	LEU	3.2
39	2h	36	LEU	3.2
41	2j	94	VAL	3.2
48	2q	9	VAL	3.2
20	2Y	5	MET	3.2
34	2c	71	ALA	3.2
41	2j	27	ALA	3.2
50	2s	63	THR	3.2
1	1A	218	A	3.2
1	1A	1130	A	3.2
1	1A	1134	A	3.2
1	1A	1147	U	3.2

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Mol	Chain	Res	Type	RSRZ
32	1a	162	A	3.2
1	1A	1135	G	3.2
1	2A	2112	G	3.2
32	1a	1021	G	3.2
36	2e	20	GLN	3.2
32	2a	995	C	3.2
32	2a	1116	C	3.2
40	2i	104	ARG	3.2
52	2u	10	ARG	3.2
41	2j	80	LYS	3.2
41	2j	75	ILE	3.2
21	2Z	30	ASN	3.2
40	2i	29	ASN	3.2
6	2G	5	VAL	3.2
34	2c	153	VAL	3.2
36	2e	61	TYR	3.2
33	2b	173	ALA	3.2
34	2c	168	ALA	3.2
34	2c	109	PRO	3.2
44	2m	64	TRP	3.2
32	1a	1446	U	3.2
32	2a	1085	U	3.2
1	2A	1847	A	3.2
47	1p	76	GLN	3.2
53	2v	15	A	3.2
21	2Z	136	PHE	3.2
32	1a	1033	G	3.2
32	2a	1024	G	3.2
40	2i	91	ASP	3.2
47	1p	27	LYS	3.2
1	1A	1126	C	3.2
1	1A	2160	C	3.2
21	2Z	147	GLY	3.2
32	1a	1008	C	3.2
32	2a	1203	C	3.2
35	2d	167	GLY	3.2
36	2e	74	GLY	3.2
54	2w	2	C	3.2
6	2G	88	ILE	3.2
7	2H	72	ILE	3.2
39	2h	135	CYS	3.2
33	2b	10	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
44	2m	66	LEU	3.2
14	1S	46	VAL	3.2
44	2m	53	VAL	3.2
14	2S	92	TYR	3.2
26	24	63	TYR	3.2
36	2e	17	ALA	3.2
7	2H	2	SER	3.2
34	1c	179	ARG	3.2
38	2g	4	ARG	3.2
32	2a	1357	A	3.2
31	29	21	GLY	3.1
34	2c	205	GLY	3.1
40	2i	115	GLY	3.1
41	1j	31	GLY	3.1
6	2G	82	LEU	3.1
21	2Z	150	LEU	3.1
33	2b	145	LEU	3.1
1	1A	2165	C	3.1
1	1A	2181	G	3.1
1	2A	884	C	3.1
32	1a	102	G	3.1
32	1a	1006	C	3.1
32	2a	1064	G	3.1
32	2a	1114	C	3.1
32	2a	1115	C	3.1
34	2c	141	VAL	3.1
45	2n	33	VAL	3.1
33	2b	31	TYR	3.1
40	1i	2	GLU	3.1
41	2j	61	GLU	3.1
12	2Q	22	LYS	3.1
14	2S	17	ARG	3.1
33	2b	144	ARG	3.1
34	1c	79	ARG	3.1
50	2s	29	ARG	3.1
34	1c	96	GLY	3.1
34	2c	128	PHE	3.1
1	1A	2139	A	3.1
1	2A	2173	A	3.1
6	2G	53	LEU	3.1
36	2e	13	ILE	3.1
46	2o	31	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
52	2u	5	ASP	3.1
32	2a	974	A	3.1
54	1y	35	A	3.1
38	2g	21	VAL	3.1
51	1t	9	ASN	3.1
44	2m	97	PRO	3.1
1	1A	2805	G	3.1
1	2A	2166	G	3.1
32	2a	948	C	3.1
33	1b	107	THR	3.1
34	2c	201	TYR	3.1
39	2h	94	TYR	3.1
50	2s	48	THR	3.1
21	2Z	52	SER	3.1
51	2t	74	LYS	3.1
7	1H	3	ARG	3.1
33	2b	175	ARG	3.1
51	2t	8	ARG	3.1
22	20	69	PHE	3.1
8	2I	68	LEU	3.1
51	2t	103	GLY	3.1
52	1u	16	GLY	3.1
1	2A	2117	A	3.1
33	2b	131	PRO	3.1
50	2s	76	PRO	3.1
54	2y	35	A	3.1
34	2c	146	ALA	3.1
41	2j	48	THR	3.1
51	1t	14	LYS	3.1
52	2u	3	LYS	3.1
32	1a	1354	C	3.1
32	2a	1037	C	3.1
32	2a	1262	C	3.1
34	2c	190	ARG	3.1
11	1P	105	LEU	3.1
33	2b	55	PHE	3.1
34	1c	52	LEU	3.1
34	2c	80	GLY	3.1
43	1l	60	LEU	3.1
39	1h	134	ILE	3.1
52	2u	16	GLY	3.1
8	1I	19	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
10	2O	98	VAL	3.1
33	2b	234	PRO	3.1
20	1Y	92	ASN	3.1
34	2c	60	ALA	3.1
36	1e	86	ALA	3.1
40	2i	76	ALA	3.1
26	14	69	LYS	3.1
32	1a	152	A	3.1
32	1a	1503	A	3.1
47	1p	43	LYS	3.1
50	2s	70	LYS	3.1
6	1G	51	ARG	3.1
14	2S	36	TYR	3.1
33	2b	92	TYR	3.1
40	2i	42	ARG	3.1
52	1u	24	ARG	3.1
32	2a	1277	C	3.1
34	2c	167	TRP	3.1
1	1A	927	G	3.0
1	1A	930	G	3.0
32	1a	346	G	3.0
32	2a	1215	G	3.0
32	2a	1356	G	3.0
35	1d	176	LEU	3.0
40	2i	56	LEU	3.0
6	2G	39	ILE	3.0
34	2c	158	GLY	3.0
40	2i	100	GLY	3.0
41	2j	63	PHE	3.0
50	2s	26	GLY	3.0
26	24	50	VAL	3.0
32	2a	1196	U	3.0
33	2b	112	VAL	3.0
43	2l	18	VAL	3.0
10	1O	108	GLU	3.0
45	1n	59	ALA	3.0
6	2G	161	THR	3.0
36	2e	107	ARG	3.0
1	1A	302	A	3.0
1	2A	2310	A	3.0
33	2b	192	SER	3.0
21	2Z	125	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
41	1j	85	LEU	3.0
32	2a	1128	C	3.0
21	2Z	53	ILE	3.0
33	2b	57	PHE	3.0
34	1c	10	PHE	3.0
36	1e	85	GLY	3.0
41	2j	52	GLY	3.0
41	2j	82	ILE	3.0
1	1A	2187	G	3.0
1	2A	2156	G	3.0
1	2A	2793	G	3.0
32	2a	1002	G	3.0
32	2a	1221	G	3.0
36	2e	5	ASP	3.0
21	2Z	138	GLU	3.0
35	1d	150	GLU	3.0
40	2i	12	GLU	3.0
41	2j	44	VAL	3.0
51	1t	75	ASN	3.0
45	2n	41	ARG	3.0
14	1S	84	GLN	3.0
44	2m	37	THR	3.0
46	1o	69	TYR	3.0
47	2p	38	TYR	3.0
50	2s	61	TYR	3.0
32	1a	1030(D)	A	3.0
32	2a	949	A	3.0
32	2a	1151	A	3.0
5	2F	208	GLY	3.0
6	2G	102	PHE	3.0
23	21	84	GLY	3.0
34	1c	84	ILE	3.0
34	2c	148	GLY	3.0
37	1f	60	PHE	3.0
38	1g	50	ILE	3.0
45	2n	16	PHE	3.0
32	2a	866	C	3.0
52	2u	23	PRO	3.0
1	2A	545	G	3.0
32	2a	1001(A)	G	3.0
32	2a	1117	G	3.0
33	1b	237	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
34	2c	180	ALA	3.0
38	1g	153	HIS	3.0
41	2j	76	ASN	3.0
45	2n	59	ALA	3.0
54	2w	15	G	3.0
55	1x	70	G	3.0
6	2G	41	GLN	3.0
35	1d	181	MET	3.0
6	2G	19	LEU	3.0
6	2G	43	LEU	3.0
33	2b	121	LEU	3.0
50	2s	30	LEU	3.0
1	1A	1119	A	3.0
1	2A	2126	A	3.0
34	2c	57	ILE	3.0
41	1j	6	ILE	3.0
33	1b	106	LYS	3.0
21	2Z	167	PRO	3.0
11	1P	119	GLU	3.0
33	2b	141	GLU	3.0
47	1p	68	ASP	3.0
1	1A	943	C	3.0
7	2H	37	VAL	3.0
40	1i	10	ARG	3.0
32	2a	1129	C	3.0
12	2Q	136	ALA	3.0
14	2S	61	ASN	3.0
44	1m	123	ALA	3.0
36	2e	10	MET	3.0
47	1p	1	MET	3.0
1	1A	1072	U	3.0
1	2A	1026	U	3.0
1	1A	1101	G	3.0
32	2a	1031	G	3.0
32	2a	1190	G	3.0
32	2a	1202	G	3.0
32	2a	1255	G	3.0
40	2i	79	LEU	2.9
44	2m	70	LEU	2.9
41	2j	19	SER	2.9
6	2G	20	ILE	2.9
6	2G	24	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
34	2c	194	GLY	2.9
45	2n	42	ILE	2.9
1	2A	2169	A	2.9
6	2G	2	PRO	2.9
6	2G	87	PRO	2.9
17	2V	50	PRO	2.9
32	2a	1213	A	2.9
32	2a	1280	A	2.9
53	1v	13	A	2.9
23	21	83	GLU	2.9
26	14	55	ARG	2.9
30	18	65	GLU	2.9
33	2b	93	VAL	2.9
41	2j	34	VAL	2.9
42	2k	114	VAL	2.9
26	24	47	GLN	2.9
40	2i	122	ALA	2.9
42	2k	19	ALA	2.9
32	1a	1119	C	2.9
32	2a	990	C	2.9
41	2j	15	THR	2.9
1	2A	2132	U	2.9
33	2b	154	LEU	2.9
34	2c	32	LEU	2.9
34	2c	204	LEU	2.9
39	1h	112	LEU	2.9
40	1i	102	LEU	2.9
6	1G	75	LYS	2.9
1	2A	1171	G	2.9
22	20	26	TYR	2.9
32	1a	1031	G	2.9
32	2a	1156	G	2.9
54	2w	18	G	2.9
34	2c	145	GLY	2.9
44	2m	119	GLY	2.9
7	2H	6	ARG	2.9
14	1S	3	ARG	2.9
44	2m	94	ARG	2.9
25	23	60	GLU	2.9
26	14	57	GLU	2.9
33	1b	126	GLU	2.9
47	1p	48	TRP	2.9

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Mol	Chain	Res	Type	RSRZ
1	1A	945	A	2.9
1	1A	2180	A	2.9
32	2a	1004	A	2.9
32	2a	1016	A	2.9
34	2c	130	VAL	2.9
41	2j	86	MET	2.9
42	1k	14	VAL	2.9
50	1s	9	VAL	2.9
3	2D	2	ALA	2.9
12	2Q	28	ALA	2.9
54	2w	72	C	2.9
1	1A	1129	U	2.9
50	2s	16	LEU	2.9
33	1b	200	ILE	2.9
33	2b	172	ILE	2.9
36	2e	131	ILE	2.9
35	1d	180	GLY	2.9
43	2l	50	SER	2.9
12	2Q	104	PHE	2.9
40	2i	59	PHE	2.9
6	2G	32	PRO	2.9
6	2G	118	ARG	2.9
46	2o	19	PRO	2.9
1	2A	2154	G	2.9
47	1p	16	HIS	2.9
54	1y	19	G	2.9
21	2Z	141	VAL	2.9
33	2b	7	VAL	2.9
34	2c	18	TRP	2.9
34	2c	70	VAL	2.9
36	2e	67	VAL	2.9
32	1a	101	A	2.9
41	1j	78	ASN	2.9
52	2u	17	THR	2.9
8	2I	38	LEU	2.9
14	2S	32	LEU	2.9
33	2b	158	LEU	2.9
39	2h	127	LEU	2.9
1	1A	1122	C	2.9
1	1A	2196	C	2.9
1	2A	2137	C	2.9
1	2A	2146	C	2.9

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Mol	Chain	Res	Type	RSRZ
1	2A	2150	U	2.9
1	2A	2297	C	2.9
2	2B	88	C	2.9
6	2G	140	ILE	2.9
32	2a	950	U	2.9
32	2a	970	C	2.9
33	2b	211	ILE	2.9
41	1j	98	ILE	2.9
52	2u	13	ILE	2.9
54	1y	48	C	2.9
54	2w	4	C	2.9
21	2Z	99	TYR	2.9
21	2Z	166	SER	2.9
34	1c	25	GLY	2.9
34	1c	185	GLY	2.9
34	2c	10	PHE	2.9
35	1d	110	PHE	2.9
38	1g	32	ARG	2.9
50	2s	4	SER	2.9
45	2n	8	GLU	2.9
38	2g	86	GLN	2.9
6	2G	92	VAL	2.9
35	1d	170	VAL	2.9
44	2m	7	VAL	2.9
1	1A	2134	G	2.9
1	1A	2816	G	2.9
21	2Z	164	ALA	2.9
36	1e	95	ALA	2.9
40	2i	84	ALA	2.9
42	2k	89	ALA	2.9
45	2n	10	ALA	2.9
49	1r	24	ALA	2.9
40	2i	64	THR	2.9
44	2m	103	THR	2.9
32	2a	965	A	2.8
32	2a	1001	A	2.8
32	2a	1250	A	2.8
44	2m	34	LEU	2.8
33	2b	32	ILE	2.8
34	1c	14	ILE	2.8
11	2P	118	GLY	2.8
12	2Q	23	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
18	2W	112	GLY	2.8
41	2j	9	ARG	2.8
26	24	29	PRO	2.8
32	2a	1040	U	2.8
32	2a	1532	U	2.8
26	24	66	SER	2.8
35	2d	37	PRO	2.8
34	1c	201	TYR	2.8
34	2c	6	HIS	2.8
38	2g	77	SER	2.8
41	2j	77	PRO	2.8
32	1a	150	C	2.8
32	2a	1029	C	2.8
32	2a	1054	C	2.8
32	2a	1109	C	2.8
32	2a	1112	C	2.8
51	1t	70	SER	2.8
54	1w	2	C	2.8
55	1x	69	C	2.8
7	2H	24	VAL	2.8
8	2I	92	VAL	2.8
14	2S	28	VAL	2.8
21	2Z	90	VAL	2.8
50	2s	45	VAL	2.8
22	20	71	ASP	2.8
39	2h	64	LYS	2.8
41	2j	18	ALA	2.8
1	2A	2115	G	2.8
32	1a	306	G	2.8
32	2a	1061	G	2.8
33	1b	221	LEU	2.8
46	1o	66	LEU	2.8
54	2y	5	G	2.8
32	2a	1130	A	2.8
38	2g	32	ARG	2.8
41	1j	74	ILE	2.8
45	1n	57	ARG	2.8
42	2k	125	PHE	2.8
47	1p	80	PHE	2.8
47	2p	9	PHE	2.8
50	2s	83	HIS	2.8
1	1A	2194	U	2.8

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Mol	Chain	Res	Type	RSRZ
32	2a	952	U	2.8
32	2a	992	U	2.8
36	1e	81	GLU	2.8
54	1y	47	U	2.8
1	1A	34	C	2.8
32	2a	1118	C	2.8
32	2a	1217	C	2.8
21	2Z	78	LYS	2.8
21	2Z	96	VAL	2.8
34	2c	4	LYS	2.8
34	2c	66	VAL	2.8
34	2c	75	VAL	2.8
34	2c	199	LYS	2.8
51	1t	74	LYS	2.8
7	2H	145	ALA	2.8
21	2Z	87	ASP	2.8
33	2b	225	ALA	2.8
36	2e	54	ALA	2.8
42	2k	23	ALA	2.8
35	2d	47	ARG	2.8
41	2j	5	ARG	2.8
41	2j	70	ARG	2.8
1	2A	881	G	2.8
2	2B	24	G	2.8
15	2T	52	ILE	2.8
32	1a	183	G	2.8
32	2a	630	G	2.8
32	2a	1108	G	2.8
32	2a	1171	G	2.8
32	2a	1181	G	2.8
36	1e	13	ILE	2.8
54	1w	69	G	2.8
54	1w	71	G	2.8
54	2w	19	G	2.8
21	1Z	160	GLY	2.8
35	2d	23	GLY	2.8
36	2e	78	HIS	2.8
36	2e	114	GLY	2.8
2	2B	120	A	2.8
32	2a	969	A	2.8
32	2a	1014	A	2.8
32	2a	1261	A	2.8

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Mol	Chain	Res	Type	RSRZ
33	2b	70	PHE	2.8
34	2c	186	PHE	2.8
21	2Z	16	SER	2.8
1	2A	271(L)	U	2.8
1	2A	2113	U	2.8
32	2a	1148	U	2.8
51	1t	18	GLN	2.8
54	2y	33	U	2.8
9	2N	118	LYS	2.8
40	2i	70	LYS	2.8
44	1m	27	LYS	2.8
7	2H	35	VAL	2.8
46	2o	27	VAL	2.8
32	1a	1029	C	2.8
32	2a	1214	C	2.8
32	2a	1223	C	2.8
33	2b	171	ALA	2.8
44	2m	76	ALA	2.8
54	2w	13	C	2.8
34	2c	87	LEU	2.8
36	2e	71	LEU	2.8
36	2e	123	LEU	2.8
45	2n	47	LEU	2.8
48	2q	84	LEU	2.8
33	2b	54	THR	2.8
33	2b	94	ASN	2.8
34	1c	15	THR	2.8
34	2c	3	ASN	2.8
41	1j	46	ARG	2.8
6	1G	88	ILE	2.8
8	2I	88	ILE	2.8
38	2g	27	ILE	2.8
31	29	20	HIS	2.8
21	2Z	143	GLY	2.8
36	2e	99	GLY	2.8
41	1j	77	PRO	2.8
52	2u	2	GLY	2.8
6	2G	48	GLU	2.8
12	2Q	65	PHE	2.8
33	1b	70	PHE	2.8
33	2b	17	PHE	2.8
41	1j	47	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	1A	2176	G	2.8
32	2a	1030(C)	G	2.8
1	2A	652(B)	A	2.8
32	2a	1275	A	2.8
34	2c	147	LYS	2.8
32	2a	1078	U	2.8
34	1c	48	TYR	2.8
54	1w	20	U	2.8
21	2Z	126	VAL	2.8
35	1d	105	VAL	2.8
8	2I	146	ALA	2.8
35	1d	111	ALA	2.8
11	2P	105	LEU	2.7
21	2Z	102	LEU	2.7
26	14	51	ASP	2.7
33	2b	221	LEU	2.7
1	1A	944	C	2.7
14	1S	13	ARG	2.7
32	1a	1533	C	2.7
32	2a	1189	C	2.7
32	2a	1321	C	2.7
32	2a	1322	C	2.7
40	2i	93	ARG	2.7
40	2i	128	ARG	2.7
41	2j	66	ARG	2.7
21	2Z	98	MET	2.7
45	2n	54	PRO	2.7
14	1S	22	GLY	2.7
21	2Z	84	GLU	2.7
33	1b	227	GLY	2.7
50	2s	8	GLY	2.7
50	2s	72	GLY	2.7
50	2s	18	LYS	2.7
1	1A	2155	G	2.7
1	2A	887	A	2.7
1	2A	2125	G	2.7
2	2B	25	A	2.7
2	2B	119	G	2.7
32	1a	1032	G	2.7
32	2a	1088	G	2.7
32	2a	1131	G	2.7
36	2e	90	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
38	2g	151	TYR	2.7
54	1y	15	G	2.7
1	1A	2154	U	2.7
39	2h	93	VAL	2.7
54	2w	66	U	2.7
6	2G	133	LEU	2.7
41	1j	8	LEU	2.7
50	2s	5	LEU	2.7
34	2c	62	ASP	2.7
35	2d	35	ARG	2.7
1	1A	1555	C	2.7
1	1A	2815	C	2.7
32	1a	345	C	2.7
35	2d	29	PRO	2.7
39	2h	35	ILE	2.7
54	2w	67	C	2.7
33	2b	132	LYS	2.7
45	2n	17	LYS	2.7
45	2n	50	LYS	2.7
51	2t	96	GLY	2.7
36	2e	6	PHE	2.7
45	2n	37	PHE	2.7
7	1H	113	VAL	2.7
12	2Q	106	VAL	2.7
36	2e	100	VAL	2.7
39	2h	53	VAL	2.7
39	2h	137	VAL	2.7
40	1i	4	TYR	2.7
47	1p	2	VAL	2.7
47	2p	20	VAL	2.7
48	2q	56	VAL	2.7
6	2G	61	ALA	2.7
11	1P	106	LEU	2.7
33	2b	138	LEU	2.7
34	2c	160	ALA	2.7
40	2i	43	ALA	2.7
45	2n	24	CYS	2.7
49	2r	40	LEU	2.7
50	1s	5	LEU	2.7
26	14	68	ARG	2.7
32	1a	161	A	2.7
32	1a	1286	A	2.7

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Mol	Chain	Res	Type	RSRZ
32	2a	1205	U	2.7
32	2a	1358	U	2.7
51	1t	8	ARG	2.7
1	1A	929	G	2.7
1	1A	2147	G	2.7
1	1A	2184	G	2.7
2	2B	118	G	2.7
21	2Z	154	ASP	2.7
32	2a	1047	G	2.7
32	2a	1120	G	2.7
54	2y	15	G	2.7
26	24	44	THR	2.7
34	2c	192	THR	2.7
6	1G	77	ILE	2.7
21	2Z	15	PRO	2.7
47	1p	19	ILE	2.7
50	2s	42	PRO	2.7
12	2Q	139	GLU	2.7
21	2Z	106	GLY	2.7
26	24	17	GLY	2.7
33	2b	97	TRP	2.7
34	2c	19	GLU	2.7
35	2d	192	GLU	2.7
44	1m	26	GLY	2.7
1	2A	888	C	2.7
26	24	42	PHE	2.7
48	2q	99	SER	2.7
50	2s	38	SER	2.7
6	2G	109	VAL	2.7
7	1H	45	VAL	2.7
7	2H	79	VAL	2.7
14	2S	49	VAL	2.7
14	2S	65	VAL	2.7
21	2Z	128	VAL	2.7
42	2k	14	VAL	2.7
6	2G	115	ARG	2.7
33	2b	142	LEU	2.7
34	1c	178	LEU	2.7
35	1d	162	LEU	2.7
35	2d	122	ARG	2.7
40	1i	19	LEU	2.7
40	2i	40	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
36	2e	21	ALA	2.7
40	1i	55	ALA	2.7
40	2i	119	ALA	2.7
48	1q	95	TYR	2.7
50	1s	24	ALA	2.7
32	2a	1125	U	2.7
1	1A	925	A	2.7
1	2A	2114	A	2.7
26	24	40	HIS	2.7
32	1a	149	A	2.7
32	2a	1152	A	2.7
47	1p	69	THR	2.7
50	1s	14	HIS	2.7
3	1D	38	LYS	2.7
34	2c	150	LYS	2.7
35	1d	154	ASN	2.7
36	1e	118	ILE	2.7
38	2g	37	ASN	2.7
39	2h	32	LYS	2.7
1	1A	2228	G	2.7
32	2a	987	G	2.7
41	2j	53	PRO	2.7
54	1y	24	G	2.7
41	2j	93	GLY	2.7
41	2j	84	GLN	2.7
1	1A	1098	C	2.7
1	2A	2139	C	2.7
1	2A	2174	C	2.7
1	2A	2313	C	2.7
2	2B	27	C	2.7
32	2a	1027	C	2.7
32	2a	1113	C	2.7
32	2a	1254	C	2.7
54	1w	13	C	2.7
6	2G	62	LEU	2.6
7	2H	7	LEU	2.6
11	1P	100	LEU	2.6
26	24	9	LEU	2.6
29	17	46	VAL	2.6
38	1g	5	ARG	2.6
38	1g	10	ARG	2.6
6	2G	163	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
38	1g	154	TYR	2.6
18	2W	111	HIS	2.6
33	2b	60	ASP	2.6
40	2i	95	LYS	2.6
50	2s	28	LYS	2.6
1	1A	1220	U	2.6
1	1A	2166	U	2.6
6	2G	52	ILE	2.6
21	2Z	130	PRO	2.6
42	2k	117	ASN	2.6
1	1A	1149	A	2.6
12	2Q	33	GLY	2.6
45	2n	51	GLY	2.6
14	2S	68	GLN	2.6
1	1A	11	G	2.6
22	20	45	PHE	2.6
32	2a	951	G	2.6
32	2a	1032	G	2.6
32	2a	1276	G	2.6
36	2e	84	PHE	2.6
46	2o	15	PHE	2.6
54	1w	6	G	2.6
21	2Z	81	ARG	2.6
42	1k	126	ARG	2.6
32	2a	985	C	2.6
33	1b	158	LEU	2.6
34	1c	32	LEU	2.6
41	1j	71	LEU	2.6
11	1P	83	VAL	2.6
33	1b	136	VAL	2.6
43	1l	18	VAL	2.6
8	2I	53	ALA	2.6
34	1c	53	ALA	2.6
33	1b	27	LYS	2.6
21	2Z	8	TYR	2.6
38	2g	154	TYR	2.6
42	1k	75	TYR	2.6
47	1p	38	TYR	2.6
21	2Z	140	ASP	2.6
33	2b	223	ILE	2.6
35	1d	189	PRO	2.6
36	2e	135	THR	2.6

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Mol	Chain	Res	Type	RSRZ
39	2h	4	ASP	2.6
40	2i	32	ASP	2.6
33	2b	58	ILE	2.6
1	1A	2189	U	2.6
32	2a	982	U	2.6
32	2a	1121	U	2.6
33	1b	128	GLU	2.6
4	2E	10	GLY	2.6
1	1A	1113	A	2.6
1	1A	2192	A	2.6
32	2a	959	A	2.6
34	1c	128	PHE	2.6
48	1q	71	PHE	2.6
54	2y	14	A	2.6
34	1c	18	TRP	2.6
6	2G	83	ARG	2.6
15	1T	125	ARG	2.6
29	17	47	ARG	2.6
1	1A	2153	G	2.6
1	2A	2153	G	2.6
1	2A	2319	G	2.6
32	2a	963	G	2.6
32	2a	1089	G	2.6
32	2a	1094	G	2.6
33	1b	187	LEU	2.6
33	2b	44	LEU	2.6
47	2p	6	LEU	2.6
49	1r	79	LEU	2.6
7	2H	49	VAL	2.6
35	1d	88	VAL	2.6
40	1i	41	VAL	2.6
43	1l	40	VAL	2.6
43	2l	39	VAL	2.6
50	2s	19	VAL	2.6
40	2i	112	LYS	2.6
45	2n	4	LYS	2.6
1	1A	1908	C	2.6
6	2G	151	ALA	2.6
21	1Z	151	HIS	2.6
32	2a	1282	C	2.6
32	2a	1362	C	2.6
33	2b	29	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
35	2d	164	ALA	2.6
54	1y	13	C	2.6
26	24	25	TYR	2.6
6	2G	49	ASP	2.6
7	2H	128	PRO	2.6
36	2e	60	TYR	2.6
39	2h	67	PRO	2.6
40	2i	114	TYR	2.6
40	1i	75	ASP	2.6
40	2i	75	ASP	2.6
51	2t	98	PRO	2.6
6	2G	101	ILE	2.6
8	2I	86	THR	2.6
33	1b	190	THR	2.6
41	2j	6	ILE	2.6
50	1s	48	THR	2.6
51	1t	100	ILE	2.6
1	1A	12	U	2.6
1	2A	2118	U	2.6
32	2a	1364	U	2.6
33	2b	66	GLY	2.6
35	2d	45	GLN	2.6
33	1b	163	PHE	2.6
33	2b	105	PHE	2.6
7	2H	41	MET	2.6
15	1T	111	ARG	2.6
41	2j	46	ARG	2.6
41	2j	51	ARG	2.6
32	1a	228	A	2.6
33	1b	10	LEU	2.6
33	1b	11	LEU	2.6
33	2b	215	LEU	2.6
36	2e	142	LEU	2.6
41	1j	65	LEU	2.6
47	2p	74	LEU	2.6
29	27	48	LYS	2.6
34	2c	72	LYS	2.6
42	2k	124	LYS	2.6
48	1q	100	LYS	2.6
8	2I	144	VAL	2.6
33	2b	229	VAL	2.6
36	2e	51	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
44	2m	74	VAL	2.6
48	2q	23	VAL	2.6
50	1s	67	VAL	2.6
6	2G	110	ALA	2.6
21	2Z	152	ALA	2.6
22	20	3	HIS	2.6
29	17	45	ALA	2.6
32	2a	947	G	2.6
32	2a	1042	G	2.6
34	2c	163	ALA	2.6
38	2g	83	ALA	2.6
39	1h	7	ALA	2.6
54	1w	44	G	2.6
54	2w	70	G	2.6
5	2F	14	PRO	2.6
41	2j	91	PRO	2.6
1	2A	2164	C	2.6
32	1a	153	C	2.6
32	2a	1039	C	2.6
32	2a	1354	C	2.6
32	2a	1384	C	2.6
8	2I	117	GLU	2.6
21	1Z	69	THR	2.6
21	1Z	169	GLU	2.6
33	2b	12	GLU	2.6
33	2b	80	ILE	2.6
34	1c	56	ASP	2.6
35	1d	179	GLU	2.6
43	1l	7	ILE	2.6
47	1p	4	ILE	2.6
35	1d	87	GLY	2.6
36	1e	72	GLN	2.6
1	1A	2211	U	2.6
32	1a	182	U	2.6
32	1a	1040	U	2.6
54	1w	66	U	2.6
21	2Z	131	ARG	2.6
26	24	58	ARG	2.6
35	2d	115	ARG	2.6
39	2h	104	ARG	2.6
47	1p	5	ARG	2.6
6	2G	34	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
8	1I	140	LEU	2.5
11	2P	106	LEU	2.5
21	2Z	156	LYS	2.5
33	1b	132	LYS	2.5
35	1d	135	LEU	2.5
45	2n	9	LYS	2.5
48	2q	76	LEU	2.5
38	2g	156	TRP	2.5
32	2a	10	A	2.5
32	2a	1225	A	2.5
32	2a	1363(A)	A	2.5
54	1y	36	A	2.5
33	1b	7	VAL	2.5
35	2d	105	VAL	2.5
38	2g	9	VAL	2.5
50	1s	11	VAL	2.5
36	1e	94	ALA	2.5
36	2e	95	ALA	2.5
38	2g	108	ALA	2.5
44	2m	75	ALA	2.5
24	22	66	GLU	2.5
39	2h	134	ILE	2.5
44	1m	4	ILE	2.5
1	1A	926	G	2.5
1	2A	2206	G	2.5
6	2G	156	ASP	2.5
14	2S	7	TYR	2.5
32	2a	1050	G	2.5
32	2a	1253	G	2.5
34	2c	17	ASP	2.5
1	2A	2111	C	2.5
32	2a	1028	C	2.5
40	2i	69	GLY	2.5
41	1j	76	ASN	2.5
50	2s	23	ASN	2.5
50	2s	53	ASN	2.5
54	1y	56	C	2.5
7	2H	60	ARG	2.5
33	2b	63	MET	2.5
33	2b	217	ARG	2.5
35	2d	168	ARG	2.5
44	2m	82	MET	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2144	U	2.5
32	1a	560	U	2.5
6	2G	175	LEU	2.5
14	2S	26	LEU	2.5
19	1X	92	LEU	2.5
35	2d	21	LEU	2.5
46	1o	57	LEU	2.5
21	1Z	121	HIS	2.5
1	1A	2901	A	2.5
32	1a	472	A	2.5
32	1a	609	A	2.5
38	1g	7	ALA	2.5
44	2m	33	ALA	2.5
6	1G	137	GLU	2.5
21	2Z	13	GLU	2.5
22	20	68	GLU	2.5
33	1b	12	GLU	2.5
33	2b	42	ILE	2.5
51	1t	55	ILE	2.5
12	2Q	25	ASP	2.5
33	1b	95	GLN	2.5
33	2b	103	THR	2.5
33	2b	168	THR	2.5
34	2c	15	THR	2.5
41	2j	67	THR	2.5
17	2V	65	GLY	2.5
33	1b	18	GLY	2.5
36	2e	29	GLY	2.5
46	1o	89	GLY	2.5
50	1s	26	GLY	2.5
20	1Y	2	ARG	2.5
30	28	46	ARG	2.5
36	2e	126	ARG	2.5
40	2i	111	ARG	2.5
41	1j	66	ARG	2.5
47	1p	25	ARG	2.5
49	2r	53	ARG	2.5
1	2A	2751	G	2.5
6	2G	141	PHE	2.5
12	2Q	58	PHE	2.5
32	2a	1178	G	2.5
32	2a	1283	G	2.5

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Mol	Chain	Res	Type	RSRZ
33	2b	147	LYS	2.5
54	2w	5	G	2.5
1	1A	270	C	2.5
1	1A	2133	C	2.5
1	1A	2183	C	2.5
1	2A	2794	C	2.5
2	2B	3	C	2.5
55	1x	68	C	2.5
5	2F	24	LEU	2.5
6	2G	172	LEU	2.5
34	2c	42	LEU	2.5
40	1i	56	LEU	2.5
49	1r	31	LEU	2.5
18	1W	111	HIS	2.5
6	1G	5	VAL	2.5
8	2I	142	VAL	2.5
40	1i	86	VAL	2.5
6	1G	76	SER	2.5
6	2G	73	ALA	2.5
21	2Z	129	SER	2.5
34	1c	60	ALA	2.5
34	2c	20	SER	2.5
36	2e	138	ALA	2.5
44	2m	18	ALA	2.5
47	1p	41	PRO	2.5
4	1E	73	GLU	2.5
28	16	4	GLU	2.5
34	2c	152	ILE	2.5
36	2e	7	GLU	2.5
1	2A	2158	A	2.5
32	2a	1179	A	2.5
8	2I	54	GLN	2.5
50	1s	39	THR	2.5
52	1u	17	THR	2.5
7	2H	82	GLY	2.5
33	2b	203	GLY	2.5
40	1i	66	ARG	2.5
44	2m	114	ARG	2.5
45	2n	26	ARG	2.5
33	2b	37	ASN	2.5
40	2i	116	LYS	2.5
40	2i	127	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
6	2G	139	LEU	2.5
21	2Z	76	LEU	2.5
21	2Z	91	LEU	2.5
33	1b	61	LEU	2.5
38	1g	16	LEU	2.5
48	2q	98	LEU	2.5
51	1t	24	LEU	2.5
51	2t	10	LEU	2.5
1	1A	1117	G	2.5
1	1A	2188	G	2.5
1	2A	2145	C	2.5
1	2A	2165	G	2.5
2	1B	88	C	2.5
32	1a	230	G	2.5
32	2a	1009	G	2.5
32	2a	1069	C	2.5
32	2a	1161	C	2.5
32	1a	1020	U	2.5
32	2a	1159	U	2.5
32	2a	1235	U	2.5
6	2G	149	VAL	2.5
39	2h	51	VAL	2.5
49	2r	22	VAL	2.5
12	2Q	53	ALA	2.5
21	1Z	152	ALA	2.5
34	2c	61	ALA	2.5
51	2t	97	ALA	2.5
52	1u	14	TRP	2.5
21	1Z	166	SER	2.5
35	1d	71	SER	2.5
8	2I	109	ILE	2.5
11	1P	117	GLU	2.5
17	1V	43	GLU	2.5
34	1c	5	ILE	2.5
41	1j	83	GLU	2.5
50	2s	49	ILE	2.5
14	2S	38	GLN	2.5
6	2G	91	ARG	2.5
6	2G	93	THR	2.5
6	2G	99	MET	2.5
12	2Q	56	ARG	2.5
14	1S	20	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
29	17	23	ARG	2.5
30	18	46	ARG	2.5
36	2e	27	ARG	2.5
21	2Z	64	GLY	2.5
35	1d	16	GLY	2.5
38	2g	133	GLY	2.5
45	2n	11	LYS	2.5
51	1t	68	LYS	2.5
32	2a	986	A	2.5
32	2a	1105	A	2.5
21	2Z	38	TYR	2.5
40	2i	33	PHE	2.5
43	2l	32	PHE	2.5
6	1G	53	LEU	2.4
6	1G	152	LEU	2.4
9	1N	138	LEU	2.4
21	2Z	155	LEU	2.4
36	2e	112	LEU	2.4
44	2m	48	LEU	2.4
51	1t	10	LEU	2.4
21	2Z	54	HIS	2.4
1	1A	2124	U	2.4
1	2A	897	C	2.4
2	2B	1	U	2.4
34	1c	151	VAL	2.4
38	1g	9	VAL	2.4
48	2q	10	VAL	2.4
32	1a	226	G	2.4
54	1y	20	U	2.4
39	2h	89	PRO	2.4
12	2Q	49	ALA	2.4
44	2m	28	ALA	2.4
20	2Y	44	ILE	2.4
35	2d	158	ILE	2.4
35	2d	165	MET	2.4
39	1h	70	GLN	2.4
44	2m	101	GLN	2.4
14	2S	13	ARG	2.4
38	2g	6	ARG	2.4
40	2i	97	LYS	2.4
43	2l	47	LYS	2.4
22	20	6	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
26	24	64	GLY	2.4
38	1g	34	GLY	2.4
40	1i	67	GLY	2.4
46	2o	20	GLY	2.4
20	1Y	107	ASP	2.4
14	1S	16	ASN	2.4
6	1G	25	TYR	2.4
7	1H	7	LEU	2.4
7	2H	157	TYR	2.4
14	2S	110	LEU	2.4
21	2Z	9	TYR	2.4
21	2Z	70	LEU	2.4
21	2Z	88	PHE	2.4
34	2c	193	TYR	2.4
38	1g	26	PHE	2.4
43	2l	49	ASN	2.4
33	1b	33	TYR	2.4
33	1b	213	LEU	2.4
39	2h	58	TYR	2.4
50	1s	15	LEU	2.4
54	1w	7	A	2.4
34	1c	55	VAL	2.4
34	2c	174	PRO	2.4
35	2d	88	VAL	2.4
40	2i	123	PRO	2.4
22	20	2	ALA	2.4
32	2a	1020	U	2.4
32	2a	1070	U	2.4
33	2b	170	GLU	2.4
34	2c	44	GLU	2.4
34	2c	92	ALA	2.4
38	1g	83	ALA	2.4
1	1A	940	C	2.4
14	2S	40	ILE	2.4
24	22	70	GLN	2.4
32	2a	972	C	2.4
34	1c	124	ILE	2.4
34	2c	135	LYS	2.4
36	2e	66	MET	2.4
50	2s	7	LYS	2.4
1	1A	2143	G	2.4
1	1A	2190	G	2.4

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Mol	Chain	Res	Type	RSRZ
1	2A	2110	G	2.4
1	2A	2168	G	2.4
32	1a	1009	G	2.4
7	2H	106	THR	2.4
12	2Q	19	GLY	2.4
40	1i	39	GLY	2.4
40	2i	68	GLY	2.4
41	2j	31	GLY	2.4
48	2q	7	THR	2.4
49	2r	47	THR	2.4
50	2s	77	THR	2.4
6	2G	97	ASP	2.4
37	1f	55	ASP	2.4
40	1i	105	ASP	2.4
41	2j	17	ASP	2.4
6	2G	27	ASN	2.4
21	2Z	24	LEU	2.4
33	1b	28	PHE	2.4
35	1d	78	LEU	2.4
38	1g	12	LEU	2.4
38	1g	84	ASN	2.4
41	1j	90	LEU	2.4
51	2t	99	LEU	2.4
39	2h	82	HIS	2.4
1	1A	1132	A	2.4
1	1A	2641	A	2.4
1	2A	899	A	2.4
1	2A	2134	A	2.4
2	2B	58	A	2.4
32	2a	958	A	2.4
32	2a	1005	A	2.4
32	2a	1201	A	2.4
32	2a	1289	A	2.4
5	2F	6	VAL	2.4
6	2G	37	VAL	2.4
20	2Y	45	VAL	2.4
21	1Z	100	VAL	2.4
26	14	10	VAL	2.4
35	2d	121	VAL	2.4
39	2h	101	PRO	2.4
44	2m	41	PRO	2.4
44	2m	45	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
45	2n	56	VAL	2.4
4	1E	28	ALA	2.4
23	21	81	LYS	2.4
33	2b	129	GLU	2.4
33	2b	186	ALA	2.4
33	2b	188	ALA	2.4
34	2c	131	ARG	2.4
34	2c	133	ALA	2.4
40	2i	110	GLU	2.4
41	1j	29	ARG	2.4
45	1n	20	ALA	2.4
33	1b	39	ILE	2.4
35	1d	158	ILE	2.4
48	1q	68	ARG	2.4
32	1a	203	U	2.4
1	1A	2150	C	2.4
6	1G	29	TRP	2.4
32	2a	1325	C	2.4
39	2h	138	TRP	2.4
17	1V	101	GLY	2.4
33	1b	38	GLY	2.4
33	2b	107	THR	2.4
38	1g	132	GLY	2.4
40	1i	8	GLY	2.4
43	2l	63	GLY	2.4
43	2l	72	GLY	2.4
1	1A	928	G	2.4
1	2A	2308	G	2.4
3	2D	71	ASP	2.4
6	2G	120	LEU	2.4
7	2H	71	LEU	2.4
7	2H	171	LEU	2.4
10	2O	81	ASP	2.4
32	1a	1010	G	2.4
32	2a	631	G	2.4
32	2a	1355	G	2.4
34	2c	196	LEU	2.4
36	2e	36	ASP	2.4
49	2r	51	LEU	2.4
33	2b	204	ASN	2.4
38	1g	43	PHE	2.4
32	1a	140	A	2.4

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Mol	Chain	Res	Type	RSRZ
32	2a	996	A	2.4
33	2b	159	PRO	2.4
34	2c	73	PRO	2.4
34	1c	86	VAL	2.4
36	1e	67	VAL	2.4
37	1f	54	LYS	2.4
53	1v	14	A	2.4
6	2G	31	VAL	2.4
20	1Y	7	VAL	2.4
21	1Z	105	VAL	2.4
33	2b	83	MET	2.4
33	2b	90	MET	2.4
21	2Z	79	ARG	2.4
26	24	53	GLU	2.4
34	2c	119	ARG	2.4
43	1l	41	ARG	2.4
44	2m	29	ARG	2.4
47	1p	75	ARG	2.4
21	2Z	65	GLN	2.4
39	2h	70	GLN	2.4
42	1k	74	ALA	2.4
47	1p	64	ALA	2.4
1	1A	274	U	2.4
32	2a	961	U	2.4
36	2e	125	SER	2.4
6	2G	100	TRP	2.4
26	24	45	GLY	2.4
26	24	52	THR	2.4
33	1b	24	TRP	2.4
33	2b	24	TRP	2.4
36	1e	29	GLY	2.4
44	1m	49	THR	2.4
44	1m	109	THR	2.4
45	2n	22	THR	2.4
46	2o	89	GLY	2.4
48	2q	80	GLY	2.4
1	1A	2159	C	2.3
8	1I	72	LEU	2.3
32	1a	63	C	2.3
32	1a	103	C	2.3
32	2a	984	C	2.3
32	2a	1060	C	2.3

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Mol	Chain	Res	Type	RSRZ
36	1e	71	LEU	2.3
36	2e	139	LEU	2.3
40	2i	117	HIS	2.3
55	1x	67	C	2.3
8	2I	20	ASP	2.3
10	2O	99	PHE	2.3
20	2Y	89	PHE	2.3
21	2Z	34	ASN	2.3
35	2d	154	ASN	2.3
1	1A	299	G	2.3
1	2A	1533	G	2.3
14	2S	59	LYS	2.3
44	2m	31	LYS	2.3
45	2n	14	PRO	2.3
6	2G	38	VAL	2.3
8	1I	107	VAL	2.3
9	2N	9	VAL	2.3
11	1P	90	ARG	2.3
12	2Q	60	ARG	2.3
14	2S	46	VAL	2.3
33	1b	20	GLU	2.3
33	2b	130	ARG	2.3
34	2c	207	VAL	2.3
36	2e	25	ARG	2.3
39	2h	84	ARG	2.3
40	2i	26	VAL	2.3
43	2l	19	ARG	2.3
44	2m	69	GLU	2.3
45	2n	46	GLU	2.3
1	2A	2320	A	2.3
2	2B	66	A	2.3
6	1G	26	GLN	2.3
8	1I	71	ILE	2.3
14	2S	72	ALA	2.3
32	2a	1180	A	2.3
33	1b	214	ILE	2.3
33	2b	41	ILE	2.3
34	1c	134	ILE	2.3
7	2H	56	SER	2.3
39	2h	29	SER	2.3
11	2P	93	GLY	2.3
12	2Q	61	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
14	2S	45	GLY	2.3
14	2S	104	GLY	2.3
21	2Z	160	GLY	2.3
26	14	52	THR	2.3
32	2a	1062	U	2.3
32	2a	1232	U	2.3
32	2a	1315	U	2.3
4	1E	195	LEU	2.3
6	1G	43	LEU	2.3
14	2S	95	HIS	2.3
33	2b	113	HIS	2.3
33	2b	140	HIS	2.3
34	2c	175	LEU	2.3
35	1d	120	LEU	2.3
36	2e	43	LEU	2.3
36	2e	119	LEU	2.3
51	2t	24	LEU	2.3
6	2G	4	ASP	2.3
33	2b	195	ASP	2.3
36	1e	6	PHE	2.3
38	2g	26	PHE	2.3
44	2m	77	ASN	2.3
1	2A	2789	C	2.3
32	1a	174	C	2.3
32	1a	1039	C	2.3
32	2a	1192	C	2.3
32	2a	1244	C	2.3
54	2y	13	C	2.3
35	1d	166	LYS	2.3
48	1q	87	LYS	2.3
34	2c	184	TYR	2.3
44	2m	59	TYR	2.3
15	1T	129	ARG	2.3
22	20	74	ARG	2.3
1	1A	1584	G	2.3
1	2A	271(M)	G	2.3
1	2A	2131	G	2.3
6	2G	30	GLU	2.3
32	2a	1021	G	2.3
32	2a	1023	G	2.3
32	2a	1084	G	2.3
32	2a	1177	G	2.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1530	G	2.3
54	2w	34	G	2.3
7	2H	43	VAL	2.3
8	2I	17	GLN	2.3
34	1c	99	VAL	2.3
34	1c	170	GLN	2.3
36	2e	105	VAL	2.3
46	1o	71	GLN	2.3
50	2s	51	VAL	2.3
6	2G	171	ALA	2.3
31	29	17	ILE	2.3
33	1b	34	ALA	2.3
33	1b	225	ALA	2.3
33	2b	88	ALA	2.3
34	1c	57	ILE	2.3
40	2i	52	ALA	2.3
42	1k	89	ALA	2.3
45	2n	27	CYS	2.3
50	2s	62	ILE	2.3
1	2A	878	A	2.3
1	2A	2171	A	2.3
32	2a	250	A	2.3
32	2a	1015	A	2.3
54	2y	21	A	2.3
26	24	4	GLY	2.3
41	1j	93	GLY	2.3
42	2k	102	GLY	2.3
6	2G	64	THR	2.3
8	1I	68	LEU	2.3
14	2S	80	LEU	2.3
21	2Z	85	HIS	2.3
34	2c	34	LEU	2.3
35	1d	188	LEU	2.3
39	2h	39	LEU	2.3
47	2p	69	THR	2.3
1	1A	2172	U	2.3
32	1a	723	U	2.3
32	2a	957	U	2.3
40	1i	18	PHE	2.3
33	1b	60	ASP	2.3
39	2h	15	ASN	2.3
42	1k	106	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
43	1l	47	LYS	2.3
1	1A	1118	C	2.3
1	1A	2130	C	2.3
1	1A	2151	C	2.3
1	1A	2168	C	2.3
1	2A	2138	C	2.3
14	1S	17	ARG	2.3
21	2Z	25	PRO	2.3
34	2c	7	PRO	2.3
34	2c	16	ARG	2.3
35	2d	73	ARG	2.3
35	2d	197	PRO	2.3
36	2e	18	ARG	2.3
36	2e	93	PRO	2.3
40	1i	90	PRO	2.3
45	2n	31	ARG	2.3
26	24	30	GLU	2.3
33	1b	236	TYR	2.3
33	2b	33	TYR	2.3
54	2w	56	C	2.3
39	2h	136	GLU	2.3
49	2r	46	GLU	2.3
21	2Z	71	VAL	2.3
33	1b	93	VAL	2.3
34	1c	70	VAL	2.3
47	2p	62	VAL	2.3
36	2e	101	ILE	2.3
39	1h	86	ILE	2.3
39	2h	38	ILE	2.3
39	2h	86	ILE	2.3
46	2o	12	ILE	2.3
35	2d	117	ALA	2.3
38	2g	127	ALA	2.3
47	2p	7	ALA	2.3
1	1A	2122	G	2.3
1	1A	2132	G	2.3
32	1a	148	G	2.3
54	2w	65	G	2.3
7	2H	88	LEU	2.3
14	2S	31	SER	2.3
21	2Z	157	LEU	2.3
28	26	11	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
33	2b	109	SER	2.3
33	2b	149	LEU	2.3
34	1c	13	GLY	2.3
35	2d	208	SER	2.3
37	2f	21	LEU	2.3
39	2h	63	LEU	2.3
39	2h	112	LEU	2.3
39	2h	128	GLY	2.3
41	1j	36	GLY	2.3
49	1r	26	LEU	2.3
1	1A	1878	A	2.3
2	2B	59	A	2.3
12	2Q	21	THR	2.3
32	1a	134	A	2.3
32	1a	608	A	2.3
32	2a	964	A	2.3
32	2a	1245	A	2.3
54	2w	31	A	2.3
1	2A	362	U	2.3
1	2A	614(A)	U	2.3
53	2v	22	U	2.3
15	1T	38	ASN	2.3
35	2d	161	ASN	2.3
33	2b	96	ARG	2.3
34	2c	11	ARG	2.3
35	1d	59	ARG	2.3
38	1g	4	ARG	2.3
41	2j	60	ARG	2.3
48	2q	92	ARG	2.3
51	1t	80	ARG	2.3
33	1b	167	PRO	2.3
43	1l	16	GLU	2.3
50	2s	17	GLU	2.3
33	2b	110	GLN	2.3
34	2c	162	GLN	2.3
48	2q	32	TYR	2.3
1	2A	652(T)	C	2.3
1	2A	2175	C	2.3
8	2I	19	VAL	2.3
8	2I	107	VAL	2.3
29	27	46	VAL	2.3
32	1a	165	C	2.3

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Mol	Chain	Res	Type	RSRZ
32	1a	840	C	2.3
32	1a	1030	C	2.3
32	2a	1200	C	2.3
33	1b	42	ILE	2.3
34	1c	64	VAL	2.3
35	1d	204	ILE	2.3
38	2g	105	VAL	2.3
39	2h	61	VAL	2.3
48	1q	23	VAL	2.3
15	2T	130	ALA	2.3
51	1t	94	ALA	2.3
6	2G	176	LEU	2.2
14	2S	48	LEU	2.2
16	2U	43	GLY	2.2
20	1Y	90	LEU	2.2
21	2Z	5	LEU	2.2
23	21	82	LEU	2.2
33	1b	19	HIS	2.2
34	1c	42	LEU	2.2
34	2c	111	LEU	2.2
1	1A	162	G	2.2
1	2A	2318	G	2.2
5	1F	15	SER	2.2
11	2P	76	LYS	2.2
32	1a	625	G	2.2
32	1a	1022	G	2.2
32	2a	654	G	2.2
32	2a	1271	G	2.2
32	2a	1310	G	2.2
33	2b	190	THR	2.2
34	2c	67	THR	2.2
34	2c	144	SER	2.2
35	2d	22	LYS	2.2
39	1h	3	THR	2.2
44	1m	121	LYS	2.2
14	2S	12	PHE	2.2
22	20	57	PHE	2.2
34	2c	203	PHE	2.2
39	2h	9	MET	2.2
46	1o	18	PHE	2.2
1	1A	1219	A	2.2
21	1Z	154	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
21	2Z	72	ARG	2.2
24	12	55	ARG	2.2
32	1a	1196	U	2.2
32	2a	991	U	2.2
32	2a	997	U	2.2
32	2a	1052	U	2.2
32	2a	1056	U	2.2
33	2b	189	ASP	2.2
34	1c	38	ARG	2.2
34	1c	83	ARG	2.2
38	1g	156	TRP	2.2
40	1i	9	ARG	2.2
47	1p	81	ARG	2.2
33	2b	183	PRO	2.2
41	1j	91	PRO	2.2
33	1b	9	GLU	2.2
6	2G	138	GLN	2.2
6	2G	157	ILE	2.2
21	2Z	29	TYR	2.2
21	2Z	56	VAL	2.2
26	14	35	VAL	2.2
36	1e	82	VAL	2.2
37	2f	40	VAL	2.2
39	2h	109	ILE	2.2
41	2j	98	ILE	2.2
43	2l	55	VAL	2.2
47	1p	21	VAL	2.2
7	2H	75	ALA	2.2
8	2I	100	ALA	2.2
33	1b	13	ALA	2.2
41	2j	26	ALA	2.2
47	2p	77	ALA	2.2
2	2B	5	C	2.2
54	2y	4	C	2.2
11	1P	99	LEU	2.2
34	1c	9	GLY	2.2
34	2c	78	GLY	2.2
36	2e	53	LEU	2.2
39	2h	107	LEU	2.2
42	2k	103	LEU	2.2
3	2D	275	LYS	2.2
20	1Y	88	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
44	2m	46	LYS	2.2
44	2m	95	GLY	2.2
52	2u	20	LYS	2.2
6	2G	71	THR	2.2
4	1E	1	MET	2.2
21	2Z	28	MET	2.2
11	2P	91	PHE	2.2
7	2H	3	ARG	2.2
12	1Q	60	ARG	2.2
21	2Z	20	ARG	2.2
23	21	61	ARG	2.2
26	24	13	ARG	2.2
33	2b	36	ARG	2.2
1	1A	1120	G	2.2
1	1A	1217	G	2.2
1	1A	2178	G	2.2
1	2A	652(U)	G	2.2
32	1a	104	G	2.2
32	1a	631	G	2.2
32	1a	1356	G	2.2
32	2a	867	G	2.2
32	2a	1013	G	2.2
32	2a	1154	G	2.2
32	2a	1258	G	2.2
23	21	68	PRO	2.2
1	1A	9	U	2.2
1	1A	1123	A	2.2
1	2A	157	U	2.2
1	2A	2130	U	2.2
32	2a	938	A	2.2
11	2P	92	GLU	2.2
32	2a	1012	U	2.2
32	2a	1093	A	2.2
33	1b	232	PRO	2.2
39	2h	76	PRO	2.2
40	1i	91	ASP	2.2
35	1d	173	TRP	2.2
40	2i	21	PRO	2.2
33	2b	231	GLU	2.2
34	1c	206	GLU	2.2
41	2j	64	GLU	2.2
34	2c	107	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
6	1G	52	ILE	2.2
22	20	66	VAL	2.2
26	24	33	VAL	2.2
26	24	35	VAL	2.2
34	1c	66	VAL	2.2
34	2c	14	ILE	2.2
35	1d	5	ILE	2.2
46	2o	87	ILE	2.2
50	1s	51	VAL	2.2
20	2Y	35	TYR	2.2
33	2b	120	ALA	2.2
34	1c	189	ALA	2.2
34	2c	50	ALA	2.2
35	2d	20	TYR	2.2
37	2f	53	ALA	2.2
39	1h	62	TYR	2.2
51	1t	67	ALA	2.2
14	2S	33	LYS	2.2
33	2b	19	HIS	2.2
23	21	85	LEU	2.2
34	1c	204	LEU	2.2
39	2h	10	LEU	2.2
41	2j	16	LEU	2.2
50	2s	32	LYS	2.2
6	2G	129	GLY	2.2
33	2b	18	GLY	2.2
36	2e	35	GLY	2.2
40	2i	6	GLY	2.2
40	2i	72	GLY	2.2
45	1n	51	GLY	2.2
1	1A	161	C	2.2
1	1A	670	C	2.2
1	1A	2158	C	2.2
1	2A	277	C	2.2
32	1a	221	C	2.2
32	1a	1019	C	2.2
32	2a	999	C	2.2
5	1F	13	SER	2.2
30	18	6	THR	2.2
21	2Z	19	ARG	2.2
24	12	37	PHE	2.2
33	1b	17	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
38	1g	78	ARG	2.2
45	2n	12	ARG	2.2
46	2o	88	ARG	2.2
6	1G	49	ASP	2.2
7	1H	57	ASP	2.2
8	2I	132	PRO	2.2
37	1f	83	ASP	2.2
38	2g	14	PRO	2.2
5	2F	161	GLU	2.2
38	1g	86	GLN	2.2
1	1A	2131	U	2.2
1	1A	2331	G	2.2
1	1A	2843	G	2.2
1	2A	880	G	2.2
1	2A	1170	G	2.2
1	2A	2167	U	2.2
32	1a	164	U	2.2
32	1a	1353	G	2.2
32	2a	988	G	2.2
32	2a	1080	A	2.2
32	2a	1184	G	2.2
54	1y	33	U	2.2
32	2a	1236	A	2.2
32	2a	1285	A	2.2
32	2a	1349	A	2.2
54	2y	57	G	2.2
7	2H	44	VAL	2.2
7	2H	136	ILE	2.2
33	1b	71	VAL	2.2
34	2c	116	VAL	2.2
38	1g	61	VAL	2.2
40	1i	17	VAL	2.2
40	2i	53	VAL	2.2
47	1p	79	VAL	2.2
48	2q	5	VAL	2.2
14	2S	76	LYS	2.2
20	2Y	55	TYR	2.2
33	1b	22	LYS	2.2
33	1b	31	TYR	2.2
33	2b	75	LYS	2.2
33	2b	133	LYS	2.2
34	2c	23	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
34	2c	29	TYR	2.2
35	1d	20	TYR	2.2
35	1d	195	ALA	2.2
36	1e	132	ALA	2.2
36	2e	132	ALA	2.2
40	1i	125	TYR	2.2
43	1l	91	LYS	2.2
45	1n	5	ALA	2.2
50	2s	50	ALA	2.2
6	1G	82	LEU	2.2
34	1c	188	LEU	2.2
38	1g	124	LEU	2.2
17	1V	1	MET	2.2
26	14	17	GLY	2.2
26	14	64	GLY	2.2
6	1G	93	THR	2.2
7	1H	59	ARG	2.2
20	2Y	23	ARG	2.2
34	2c	79	ARG	2.2
34	2c	165	THR	2.2
34	2c	191	THR	2.2
36	1e	18	ARG	2.2
38	1g	76	ARG	2.2
43	1l	67	THR	2.2
43	1l	89	ARG	2.2
47	2p	45	THR	2.2
52	1u	6	ARG	2.2
1	2A	2163	C	2.2
20	1Y	60	PHE	2.2
33	2b	233	SER	2.2
32	1a	100	C	2.2
32	2a	1045	C	2.2
32	2a	1071	C	2.2
32	2a	1218	C	2.2
6	2G	142	PRO	2.2
7	2H	36	PRO	2.2
43	1l	94	PRO	2.2
6	1G	48	GLU	2.2
19	1X	90	GLU	2.2
39	1h	4	ASP	2.2
50	1s	12	ASP	2.2
1	1A	386	U	2.2

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Mol	Chain	Res	Type	RSRZ
14	2S	39	ILE	2.2
26	24	15	ILE	2.2
21	2Z	165	VAL	2.2
32	2a	960	U	2.2
32	2a	1122	U	2.2
32	2a	1278	U	2.2
39	1h	100	ILE	2.2
39	2h	6	ILE	2.2
33	2b	156	LYS	2.2
35	2d	170	VAL	2.2
36	2e	34	VAL	2.2
39	2h	79	VAL	2.2
43	2l	43	VAL	2.2
43	2l	123	LYS	2.2
47	1p	62	VAL	2.2
48	2q	21	VAL	2.2
48	2q	77	VAL	2.2
50	2s	60	VAL	2.2
53	1v	22	U	2.2
1	1A	273	G	2.2
1	2A	900	A	2.2
1	2A	2894	G	2.2
7	2H	73	ALA	2.2
8	1I	63	ALA	2.2
14	1S	72	ALA	2.2
32	1a	181	G	2.2
32	1a	607	A	2.2
32	1a	1151	A	2.2
32	2a	1155	G	2.2
32	2a	1175	G	2.2
32	2a	1256	A	2.2
32	2a	1365	G	2.2
32	2a	1373	G	2.2
34	2c	24	ALA	2.2
36	2e	30	ALA	2.2
40	2i	94	ALA	2.2
41	1j	27	ALA	2.2
53	1v	23	A	2.2
54	1y	34	G	2.2
54	2y	6	G	2.2
6	2G	90	LEU	2.1
12	2Q	26	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
21	1Z	102	LEU	2.1
23	21	46	LEU	2.1
26	14	63	TYR	2.1
28	26	36	LEU	2.1
34	1c	12	LEU	2.1
38	2g	101	LEU	2.1
40	1i	88	TYR	2.1
50	1s	20	LEU	2.1
8	1I	106	GLY	2.1
15	2T	69	GLY	2.1
44	2m	24	GLY	2.1
6	1G	83	ARG	2.1
6	2G	181	ARG	2.1
10	1O	49	ARG	2.1
52	1u	15	ARG	2.1
36	2e	75	THR	2.1
6	2G	178	PHE	2.1
36	1e	45	PHE	2.1
20	2Y	53	PRO	2.1
26	24	41	PRO	2.1
41	2j	39	PRO	2.1
43	2l	94	PRO	2.1
1	1A	1125	C	2.1
1	1A	2161	C	2.1
1	2A	2108	C	2.1
21	2Z	2	GLU	2.1
3	1D	71	ASP	2.1
20	2Y	107	ASP	2.1
32	1a	1137	C	2.1
32	2a	1007	C	2.1
32	2a	1008	C	2.1
32	2a	1145	C	2.1
32	2a	1153	C	2.1
32	2a	1226	C	2.1
32	2a	1234	C	2.1
32	2a	1389	C	2.1
33	1b	195	ASP	2.1
42	2k	36	ASP	2.1
46	2o	9	GLN	2.1
26	24	5	ILE	2.1
34	1c	77	ILE	2.1
40	2i	118	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
4	1E	47	VAL	2.1
7	2H	26	VAL	2.1
7	2H	76	VAL	2.1
28	26	52	VAL	2.1
34	2c	106	VAL	2.1
50	2s	34	TRP	2.1
47	2p	16	HIS	2.1
1	2A	9	U	2.1
1	2A	2897	U	2.1
5	2F	33	LEU	2.1
6	1G	46	ALA	2.1
6	2G	7	LEU	2.1
26	24	12	ALA	2.1
32	1a	1000	U	2.1
32	2a	1257	U	2.1
33	2b	62	ALA	2.1
33	2b	77	ALA	2.1
35	1d	48	ALA	2.1
38	2g	38	LEU	2.1
38	2g	39	ALA	2.1
38	2g	152	ALA	2.1
45	2n	48	ALA	2.1
55	2x	47	U	2.1
33	2b	48	MET	2.1
39	2h	133	LEU	2.1
47	1p	74	LEU	2.1
50	1s	66	MET	2.1
21	2Z	3	TYR	2.1
26	14	43	TYR	2.1
32	2a	1287	A	2.1
6	1G	113	ARG	2.1
7	2H	174	GLY	2.1
40	1i	6	GLY	2.1
54	2w	14	A	2.1
11	2P	102	ARG	2.1
51	1t	89	ARG	2.1
1	1A	269	G	2.1
1	1A	1137	G	2.1
1	2A	2207	G	2.1
32	1a	69	G	2.1
32	1a	1030(C)	G	2.1
32	1a	1368	G	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1011	G	2.1
32	2a	1087	G	2.1
32	2a	1106	G	2.1
32	2a	1160	G	2.1
7	2H	129	THR	2.1
44	2m	43	THR	2.1
21	2Z	44	PHE	2.1
21	2Z	104	PHE	2.1
50	2s	74	PHE	2.1
5	1F	14	PRO	2.1
7	2H	10	PRO	2.1
21	2Z	159	PRO	2.1
33	2b	194	PRO	2.1
35	1d	83	SER	2.1
44	2m	113	PRO	2.1
4	1E	87	GLU	2.1
20	2Y	91	GLU	2.1
33	1b	231	GLU	2.1
38	1g	56	GLN	2.1
46	2o	71	GLN	2.1
6	2G	75	LYS	2.1
7	1H	175	LYS	2.1
14	1S	44	LYS	2.1
21	1Z	123	ASP	2.1
23	21	78	LYS	2.1
33	2b	166	ASP	2.1
34	2c	93	LYS	2.1
41	2j	7	LYS	2.1
1	2A	889	C	2.1
1	2A	2295	C	2.1
2	2B	4	C	2.1
21	2Z	124	ILE	2.1
32	1a	848	C	2.1
32	2a	1006	C	2.1
36	2e	11	ILE	2.1
41	1j	82	ILE	2.1
54	2y	56	C	2.1
33	1b	16	HIS	2.1
34	1c	69	HIS	2.1
50	2s	47	HIS	2.1
4	1E	33	VAL	2.1
4	2E	75	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
7	1H	17	VAL	2.1
34	2c	99	VAL	2.1
35	1d	121	VAL	2.1
40	1i	65	VAL	2.1
6	2G	6	ALA	2.1
7	2H	67	LEU	2.1
9	2N	1	MET	2.1
11	1P	103	ALA	2.1
17	2V	71	LEU	2.1
21	2Z	1	MET	2.1
8	2I	55	ALA	2.1
33	2b	213	LEU	2.1
34	1c	24	ALA	2.1
34	1c	47	LEU	2.1
34	2c	43	LEU	2.1
34	2c	65	ALA	2.1
36	1e	21	ALA	2.1
42	1k	23	ALA	2.1
46	2o	85	LEU	2.1
51	1t	76	ALA	2.1
7	2H	59	ARG	2.1
26	14	62	ARG	2.1
34	2c	83	ARG	2.1
38	2g	111	ARG	2.1
45	2n	45	ARG	2.1
12	2Q	24	GLY	2.1
17	2V	42	GLY	2.1
34	2c	51	GLY	2.1
50	2s	46	GLY	2.1
6	1G	12	TYR	2.1
26	14	32	TYR	2.1
26	24	67	TYR	2.1
42	2k	75	TYR	2.1
43	2l	69	TYR	2.1
1	1A	2191	A	2.1
1	2A	2176	A	2.1
32	1a	614	A	2.1
32	2a	919	A	2.1
32	2a	968	A	2.1
32	2a	1067	A	2.1
32	2a	1227	A	2.1
32	2a	1252	A	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1447	A	2.1
54	1w	9	A	2.1
54	2y	26	A	2.1
26	24	27	THR	2.1
50	2s	33	THR	2.1
21	1Z	104	PHE	2.1
33	2b	202	PRO	2.1
42	2k	115	PRO	2.1
1	1A	298	G	2.1
1	1A	387	G	2.1
1	1A	639	G	2.1
1	1A	938	G	2.1
1	1A	2903	G	2.1
1	2A	100	G	2.1
1	2A	1042	G	2.1
1	2A	2124	G	2.1
1	2A	2304	G	2.1
1	2A	2807	G	2.1
32	1a	851	G	2.1
32	1a	933	G	2.1
32	2a	1010	G	2.1
32	2a	1053	G	2.1
54	1w	5	G	2.1
54	1w	15	G	2.1
55	2x	70	G	2.1
34	2c	143	GLU	2.1
42	1k	104	GLN	2.1
50	1s	17	GLU	2.1
50	2s	64	GLU	2.1
22	20	49	LYS	2.1
48	2q	100	LYS	2.1
6	2G	114	ILE	2.1
8	1I	11	ASN	2.1
33	2b	220	ASP	2.1
51	1t	64	ASP	2.1
10	2O	86	ILE	2.1
33	1b	32	ILE	2.1
33	1b	40	HIS	2.1
33	1b	222	ILE	2.1
33	2b	208	ILE	2.1
35	2d	123	HIS	2.1
39	1h	6	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
39	1h	111	ILE	2.1
42	1k	29	ILE	2.1
52	1u	13	ILE	2.1
15	1T	1	MET	2.1
6	2G	103	LEU	2.1
7	2H	98	LEU	2.1
22	20	7	LEU	2.1
33	1b	215	LEU	2.1
33	2b	98	LEU	2.1
33	2b	102	LEU	2.1
38	1g	104	LEU	2.1
38	2g	17	VAL	2.1
39	2h	59	LEU	2.1
40	2i	65	VAL	2.1
40	2i	85	LEU	2.1
1	1A	2804	C	2.1
11	1P	134	ALA	2.1
14	1S	74	ALA	2.1
32	1a	1054	C	2.1
32	2a	1096	C	2.1
32	2a	1249	C	2.1
14	2S	10	ARG	2.1
21	2Z	103	ARG	2.1
24	12	13	ALA	2.1
47	2p	59	TRP	2.1
55	2x	34	C	2.1
26	14	61	ARG	2.1
33	1b	30	ARG	2.1
36	1e	15	ARG	2.1
39	1h	30	ARG	2.1
50	2s	3	ARG	2.1
1	1A	2140	U	2.1
1	2A	2109	U	2.1
32	2a	1000	U	2.1
34	1c	81	GLY	2.1
54	1y	60	U	2.1
17	2V	91	TYR	2.1
37	2f	63	TYR	2.1
42	2k	50	TYR	2.1
8	2I	80	PRO	2.1
21	2Z	95	PRO	2.1
27	25	29	THR	2.1

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Mol	Chain	Res	Type	RSRZ
38	1g	112	PRO	2.1
46	2o	4	THR	2.1
1	1A	2148	A	2.1
1	2A	1445	A	2.1
1	2A	2801(A)	A	2.1
7	2H	58	GLU	2.1
7	2H	62	LYS	2.1
11	1P	107	LYS	2.1
14	1S	83	LYS	2.1
20	1Y	91	GLU	2.1
32	1a	1252	A	2.1
34	2c	45	LYS	2.1
34	2c	161	GLU	2.1
35	1d	18	LYS	2.1
35	1d	86	LYS	2.1
36	1e	20	GLN	2.1
36	1e	79	GLU	2.1
36	2e	141	GLN	2.1
38	2g	110	GLN	2.1
40	2i	2	GLU	2.1
42	1k	51	LYS	2.1
46	1o	28	GLN	2.1
53	1v	15	A	2.1
53	2v	23	A	2.1
54	1w	23	A	2.1
34	1c	20	SER	2.1
1	2A	11	G	2.1
1	2A	916	G	2.1
1	2A	2148	G	2.1
32	2a	954	G	2.1
32	2a	998	G	2.1
32	2a	1003	G	2.1
32	2a	1198	G	2.1
32	2a	1233	G	2.1
32	2a	1290	G	2.1
32	2a	1370	G	2.1
6	2G	126	ASP	2.1
8	2I	79	ILE	2.1
14	2S	41	ASP	2.1
6	2G	148	MET	2.1
21	2Z	75	ASN	2.1
33	1b	160	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
33	2b	16	HIS	2.1
33	2b	108	ILE	2.1
34	2c	181	ASN	2.1
42	1k	48	ILE	2.1
44	2m	84	ILE	2.1
46	1o	3	ILE	2.1
6	2G	70	VAL	2.0
6	2G	135	LEU	2.0
7	1H	67	LEU	2.0
12	2Q	37	LEU	2.0
21	2Z	67	LEU	2.0
23	21	62	VAL	2.0
33	2b	15	VAL	2.0
35	2d	128	VAL	2.0
37	2f	43	LEU	2.0
39	1h	118	VAL	2.0
42	2k	66	LEU	2.0
43	1l	55	VAL	2.0
44	2m	81	LEU	2.0
50	2s	58	VAL	2.0
7	1H	149	ARG	2.0
33	1b	36	ARG	2.0
34	1c	172	ARG	2.0
45	2n	19	ARG	2.0
52	2u	9	ARG	2.0
35	2d	149	ALA	2.0
36	2e	108	ALA	2.0
38	2g	25	ALA	2.0
41	1j	26	ALA	2.0
33	1b	97	TRP	2.0
1	2A	271(J)	C	2.0
6	2G	42	GLY	2.0
6	2G	119	GLY	2.0
32	2a	217	C	2.0
32	2a	848	C	2.0
32	2a	1059	C	2.0
32	2a	1210	C	2.0
32	2a	1259	C	2.0
34	2c	81	GLY	2.0
43	1l	63	GLY	2.0
43	1l	95	GLY	2.0
52	2u	4	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
54	1w	67	C	2.0
54	1w	68	C	2.0
32	1a	841	U	2.0
32	2a	981	U	2.0
32	2a	1212	U	2.0
12	2Q	137	TYR	2.0
21	2Z	83	PRO	2.0
33	2b	125	PRO	2.0
34	1c	23	TYR	2.0
47	2p	32	TYR	2.0
48	2q	88	TYR	2.0
49	1r	25	THR	2.0
51	1t	98	PRO	2.0
52	2u	18	TYR	2.0
21	1Z	136	PHE	2.0
40	1i	7	THR	2.0
41	1j	7	LYS	2.0
49	1r	29	PHE	2.0
16	1U	111	GLU	2.0
34	1c	35	GLU	2.0
40	1i	12	GLU	2.0
48	2q	78	GLU	2.0
23	21	86	SER	2.0
41	1j	30	SER	2.0
1	1A	678	A	2.0
1	1A	2193	A	2.0
1	2A	1460	A	2.0
32	2a	978	A	2.0
32	2a	1157	A	2.0
32	2a	1229	A	2.0
12	2Q	1	MET	2.0
14	2S	34	HIS	2.0
36	2e	80	ILE	2.0
38	1g	42	ILE	2.0
38	2g	89	MET	2.0
48	2q	82	MET	2.0
50	2s	57	HIS	2.0
7	2H	9	ILE	2.0
8	1I	109	ILE	2.0
21	2Z	148	ASP	2.0
33	2b	205	ASP	2.0
38	2g	148	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
47	1p	40	ASP	2.0
6	2G	3	LEU	2.0
6	2G	9	ARG	2.0
7	1H	71	LEU	2.0
8	1I	75	LEU	2.0
11	1P	112	LEU	2.0
14	2S	78	LEU	2.0
6	1G	149	VAL	2.0
14	2S	85	VAL	2.0
15	1T	112	ARG	2.0
21	2Z	37	VAL	2.0
22	20	67	VAL	2.0
31	29	25	VAL	2.0
33	2b	56	ARG	2.0
33	2b	137	ARG	2.0
34	1c	94	LEU	2.0
40	1i	47	LEU	2.0
44	2m	71	ARG	2.0
46	1o	65	ARG	2.0
49	2r	85	LEU	2.0
36	2e	115	VAL	2.0
50	2s	36	ARG	2.0
1	1A	2182	G	2.0
1	1A	2213	G	2.0
1	1A	2902	G	2.0
32	2a	945	G	2.0
32	2a	1026	G	2.0
32	2a	1079	G	2.0
32	2a	1138	G	2.0
32	2a	1309	G	2.0
54	2w	57	G	2.0
55	1x	46	G	2.0
33	2b	72	GLY	2.0
50	1s	8	GLY	2.0
45	1n	61	TRP	2.0
6	1G	182	LYS	2.0
1	1A	1985	U	2.0
32	1a	1114	C	2.0
32	1a	1118	C	2.0
32	1a	1452	C	2.0
32	2a	723	U	2.0
32	2a	955	U	2.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1063	C	2.0
32	2a	1095	U	2.0
32	2a	1284	C	2.0
32	2a	1382	C	2.0
40	1i	98	PRO	2.0
41	1j	39	PRO	2.0
52	1u	23	PRO	2.0
11	1P	91	PHE	2.0
12	2Q	32	TYR	2.0
20	2Y	83	THR	2.0
35	2d	75	PHE	2.0
36	2e	45	PHE	2.0
38	1g	151	TYR	2.0
39	2h	65	TYR	2.0
41	1j	100	THR	2.0
44	1m	21	TYR	2.0
54	1y	45	U	2.0
21	2Z	168	GLU	2.0
30	18	56	GLU	2.0
38	2g	11	GLN	2.0
41	2j	33	GLN	2.0
46	1o	62	GLN	2.0
48	1q	24	GLU	2.0
48	2q	86	GLU	2.0
33	1b	210	SER	2.0
33	2b	40	HIS	2.0
35	2d	181	MET	2.0
42	1k	53	SER	2.0
45	2n	60	SER	2.0
46	1o	24	SER	2.0
51	1t	16	HIS	2.0
6	2G	51	ARG	2.0
6	2G	132	ASN	2.0
11	2P	90	ARG	2.0
12	1Q	6	ARG	2.0
24	22	51	ARG	2.0
25	13	29	ARG	2.0
33	2b	178	ARG	2.0
35	2d	132	ARG	2.0
36	1e	73	ASN	2.0
37	1f	46	ARG	2.0
44	2m	91	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
46	1o	68	ARG	2.0
47	2p	5	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
54	7MG	2w	46	24/25	0.51	0.16	83,96,107,134	0
54	4SU	2w	8	20/21	0.58	0.16	81,98,120,128	0
54	7MG	2y	46	24/25	0.61	0.19	68,95,99,128	0
54	PSU	2y	55	20/21	0.61	0.15	80,96,115,118	0
54	5MU	2y	54	21/22	0.63	0.17	79,93,108,123	0
54	PSU	2w	55	20/21	0.65	0.17	80,94,98,113	0
54	7MG	1w	46	24/25	0.66	0.17	76,90,101,124	0
54	7MG	1y	46	24/25	0.67	0.17	76,95,106,115	0
54	5MU	1y	54	21/22	0.68	0.15	76,87,95,116	0
54	4SU	1y	8	20/21	0.70	0.17	80,98,105,114	0
54	MIA	2y	37	22/30	0.70	0.17	72,86,94,120	0
54	PSU	1y	55	20/21	0.72	0.16	72,89,99,120	0
54	4SU	2y	8	20/21	0.74	0.16	87,94,106,113	0
32	2MG	2a	1207	24/25	0.75	0.16	74,85,90,98	0
54	PSU	2y	32	20/21	0.76	0.17	73,89,97,108	0
55	PSU	2x	55	20/21	0.80	0.14	69,84,106,107	0
54	PSU	1y	32	20/21	0.81	0.16	69,87,94,95	0
54	PSU	2y	39	20/21	0.81	0.13	78,84,100,112	0
54	4SU	1w	8	20/21	0.81	0.14	75,86,105,114	0
54	5MU	2w	54	21/22	0.82	0.15	66,85,93,101	0
55	5MU	2x	54	21/22	0.82	0.15	71,87,95,100	0
54	MIA	1y	37	22/30	0.82	0.14	76,83,93,94	0
54	PSU	1w	55	20/21	0.83	0.12	72,81,90,98	0
55	4SU	2x	8	20/21	0.83	0.15	74,85,90,96	0
1	5MU	2A	1915	21/22	0.85	0.16	64,72,79,93	0
54	PSU	2w	39	20/21	0.86	0.14	80,88,96,102	0
54	PSU	2w	32	20/21	0.87	0.13	69,85,94,103	0
32	M2G	2a	966	25/26	0.87	0.18	52,69,95,99	0
54	MIA	2w	37	25/30	0.88	0.13	70,82,91,110	0
54	PSU	1y	39	20/21	0.88	0.12	71,81,89,95	0
43	0TD	2l	92	10/11	0.89	0.14	65,68,73,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	5MC	2x	32	21/22	0.89	0.15	65,78,87,88	0
32	PSU	2a	516	20/21	0.90	0.10	65,72,79,83	0
32	5MC	2a	967	21/22	0.91	0.15	62,71,79,86	0
43	0TD	1l	92	10/11	0.91	0.15	61,64,70,74	0
32	5MC	2a	1400	21/22	0.91	0.16	70,74,80,93	0
54	PSU	1w	32	20/21	0.91	0.12	59,72,79,83	0
32	5MC	2a	1404	21/22	0.91	0.12	47,59,74,77	0
32	7MG	2a	527	24/25	0.91	0.12	61,70,77,88	0
55	PSU	1x	55	20/21	0.91	0.11	56,67,81,87	0
1	PSU	2A	1917	20/21	0.91	0.12	56,65,75,76	0
54	MIA	1w	37	29/30	0.92	0.14	43,62,74,78	0
32	4OC	2a	1402	22/23	0.92	0.12	45,63,71,90	0
55	5MU	1x	54	21/22	0.92	0.11	57,71,79,83	0
1	PSU	2A	1911	20/21	0.93	0.10	56,60,66,70	0
32	PSU	1a	516	20/21	0.93	0.12	63,70,78,78	0
1	5MU	1A	1937	21/22	0.93	0.12	56,67,75,82	0
54	PSU	1w	39	20/21	0.93	0.10	50,70,80,83	0
1	4OC	2A	1920	21/23	0.93	0.12	46,57,62,72	0
32	UR3	2a	1498	21/22	0.93	0.12	48,58,62,68	0
55	5MC	1x	32	21/22	0.94	0.12	44,54,67,73	0
32	2MG	1a	1207	24/25	0.94	0.09	62,72,76,80	0
54	5MU	1w	54	21/22	0.94	0.10	55,67,78,79	0
1	PSU	1A	1939	20/21	0.94	0.13	53,60,71,72	0
1	5MU	2A	1939	21/22	0.94	0.10	24,34,41,46	0
32	MA6	2a	1518	24/25	0.94	0.13	41,63,74,82	0
1	5MC	1A	1964	21/22	0.95	0.10	38,47,52,60	0
1	PSU	1A	1933	20/21	0.95	0.12	49,59,62,66	0
55	4SU	1x	8	20/21	0.95	0.10	46,60,69,73	0
1	5MC	2A	1942	21/22	0.95	0.10	45,50,58,61	0
1	5MC	2A	1962	21/22	0.95	0.10	28,43,52,59	0
32	7MG	1a	527	24/25	0.95	0.10	40,50,60,67	0
32	5MC	2a	1407	21/22	0.95	0.12	48,57,69,76	0
32	M2G	1a	966	25/26	0.95	0.10	41,55,61,77	0
32	5MC	1a	967	21/22	0.95	0.11	51,58,67,70	0
32	MA6	2a	1519	24/25	0.95	0.13	47,65,74,81	0
32	MA6	1a	1519	24/25	0.96	0.10	39,48,57,71	0
1	PSU	2A	2605	20/21	0.96	0.07	25,33,40,42	0
32	5MC	1a	1407	21/22	0.96	0.10	34,42,56,62	0
1	5MU	1A	1961	21/22	0.97	0.08	21,33,38,44	0
32	5MC	1a	1400	21/22	0.97	0.09	39,53,61,67	0
32	4OC	1a	1402	22/23	0.97	0.09	37,47,55,61	0
32	5MC	1a	1404	21/22	0.97	0.08	32,43,50,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	4OC	1A	1942	21/23	0.97	0.10	42,55,61,65	0
1	2MU	1A	2564	21/23	0.97	0.08	26,36,40,46	0
1	PSU	1A	2617	20/21	0.97	0.08	24,31,37,39	0
1	OMG	2A	2251	24/25	0.97	0.07	27,36,44,46	0
1	2MA	2A	2503	23/24	0.97	0.07	25,30,35,37	0
1	2MU	2A	2552	21/23	0.97	0.08	28,38,46,52	0
1	OMG	1A	2263	24/25	0.98	0.07	22,32,39,44	0
32	UR3	1a	1498	21/22	0.98	0.06	38,43,50,54	0
32	MA6	1a	1518	24/25	0.98	0.09	31,47,51,57	0
1	2MA	1A	2515	23/24	0.98	0.08	20,26,31,34	0
1	5MC	1A	1984	21/22	0.98	0.07	31,38,48,57	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
56	MG	1A	3786	1/1	0.27	0.30	81,81,81,81	0
56	MG	1A	4076	1/1	0.55	0.14	75,75,75,75	0
56	MG	2B	3016	1/1	0.60	0.28	81,81,81,81	0
56	MG	1Z	302	1/1	0.63	0.13	67,67,67,67	0
56	MG	1G	3004	1/1	0.63	0.22	92,92,92,92	0
56	MG	1A	3671	1/1	0.65	0.21	67,67,67,67	0
56	MG	2a	3028	1/1	0.66	0.37	84,84,84,84	0
56	MG	2A	3687	1/1	0.68	0.29	63,63,63,63	0
56	MG	2A	3875	1/1	0.68	0.24	76,76,76,76	0
56	MG	2a	3201	1/1	0.68	0.24	79,79,79,79	0
56	MG	1A	3975	1/1	0.70	0.18	93,93,93,93	0
56	MG	1B	3032	1/1	0.70	0.23	80,80,80,80	0
56	MG	2a	3198	1/1	0.70	0.22	83,83,83,83	0
56	MG	1A	4044	1/1	0.70	0.25	79,79,79,79	0
56	MG	1A	3468	1/1	0.71	0.17	68,68,68,68	0
56	MG	1A	3894	1/1	0.71	0.21	73,73,73,73	0
56	MG	1a	1746	1/1	0.71	0.21	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1773	1/1	0.72	0.13	90,90,90,90	0
56	MG	2A	3856	1/1	0.72	0.19	41,41,41,41	0
56	MG	2a	3131	1/1	0.72	0.31	80,80,80,80	0
56	MG	2A	3686	1/1	0.72	0.22	57,57,57,57	0
56	MG	2B	3014	1/1	0.72	0.17	77,77,77,77	0
56	MG	2a	3210	1/1	0.72	0.16	70,70,70,70	0
56	MG	2A	3821	1/1	0.73	0.20	79,79,79,79	0
56	MG	2A	3884	1/1	0.73	0.20	42,42,42,42	0
56	MG	1A	3585	1/1	0.73	0.20	66,66,66,66	0
56	MG	1E	307	1/1	0.74	0.21	70,70,70,70	0
56	MG	1A	3795	1/1	0.74	0.24	51,51,51,51	0
56	MG	1y	3004	1/1	0.74	0.18	86,86,86,86	0
56	MG	2A	3091	1/1	0.74	0.17	60,60,60,60	0
56	MG	2A	3656	1/1	0.74	0.17	77,77,77,77	0
56	MG	1A	3531	1/1	0.74	0.21	67,67,67,67	0
56	MG	2a	3228	1/1	0.74	0.28	86,86,86,86	0
56	MG	2A	3712	1/1	0.75	0.15	63,63,63,63	0
56	MG	2a	3010	1/1	0.75	0.29	76,76,76,76	0
56	MG	2B	3003	1/1	0.75	0.25	74,74,74,74	0
56	MG	1A	3834	1/1	0.75	0.21	69,69,69,69	0
56	MG	2a	3127	1/1	0.76	0.22	85,85,85,85	0
56	MG	1A	3994	1/1	0.76	0.19	76,76,76,76	0
56	MG	2a	3136	1/1	0.76	0.19	73,73,73,73	0
56	MG	2A	3691	1/1	0.76	0.26	68,68,68,68	0
56	MG	2B	3021	1/1	0.76	0.27	75,75,75,75	0
56	MG	1a	1610	1/1	0.76	0.14	79,79,79,79	0
56	MG	1a	1656	1/1	0.76	0.29	75,75,75,75	0
56	MG	2a	3240	1/1	0.76	0.15	63,63,63,63	0
56	MG	2y	3005	1/1	0.76	0.24	82,82,82,82	0
56	MG	1A	3423	1/1	0.77	0.24	67,67,67,67	0
56	MG	2a	3003	1/1	0.77	0.14	64,64,64,64	0
56	MG	1A	3555	1/1	0.77	0.30	60,60,60,60	0
56	MG	1B	3007	1/1	0.77	0.31	85,85,85,85	0
56	MG	2a	3046	1/1	0.77	0.23	64,64,64,64	0
56	MG	1A	3566	1/1	0.77	0.29	72,72,72,72	0
56	MG	2A	3844	1/1	0.77	0.15	50,50,50,50	0
56	MG	1a	1776	1/1	0.77	0.12	91,91,91,91	0
56	MG	2a	3179	1/1	0.77	0.13	100,100,100,100	0
56	MG	2A	3871	1/1	0.77	0.15	70,70,70,70	0
56	MG	1e	201	1/1	0.77	0.14	79,79,79,79	0
56	MG	1A	3319	1/1	0.77	0.24	63,63,63,63	0
56	MG	1A	3641	1/1	0.77	0.24	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1U	202	1/1	0.77	0.36	73,73,73,73	0
56	MG	2v	3002	1/1	0.77	0.23	77,77,77,77	0
56	MG	1A	3530	1/1	0.77	0.22	63,63,63,63	0
56	MG	2A	3865	1/1	0.78	0.13	71,71,71,71	0
56	MG	2a	3090	1/1	0.78	0.12	68,68,68,68	0
56	MG	2a	3117	1/1	0.78	0.27	81,81,81,81	0
56	MG	1A	3912	1/1	0.78	0.19	80,80,80,80	0
56	MG	1A	3962	1/1	0.78	0.14	62,62,62,62	0
56	MG	1x	102	1/1	0.78	0.27	63,63,63,63	0
56	MG	1A	3879	1/1	0.78	0.20	51,51,51,51	0
56	MG	2a	3192	1/1	0.78	0.22	63,63,63,63	0
56	MG	1A	3466	1/1	0.78	0.13	64,64,64,64	0
56	MG	2a	3199	1/1	0.78	0.19	72,72,72,72	0
56	MG	2A	3719	1/1	0.78	0.22	57,57,57,57	0
56	MG	2A	3291	1/1	0.78	0.13	56,56,56,56	0
56	MG	2Z	8001	1/1	0.78	0.17	78,78,78,78	0
56	MG	2A	3839	1/1	0.78	0.13	45,45,45,45	0
56	MG	2A	3362	1/1	0.78	0.21	68,68,68,68	0
56	MG	2x	102	1/1	0.78	0.21	77,77,77,77	0
56	MG	2A	3536	1/1	0.78	0.12	51,51,51,51	0
56	MG	1A	3264	1/1	0.79	0.12	63,63,63,63	0
56	MG	2A	3880	1/1	0.79	0.12	65,65,65,65	0
56	MG	2A	3754	1/1	0.79	0.13	45,45,45,45	0
56	MG	2A	3646	1/1	0.79	0.14	55,55,55,55	0
56	MG	2a	3104	1/1	0.79	0.23	75,75,75,75	0
56	MG	1A	3164	1/1	0.79	0.26	73,73,73,73	0
56	MG	1a	1738	1/1	0.79	0.14	66,66,66,66	0
56	MG	1A	3832	1/1	0.79	0.17	62,62,62,62	0
56	MG	2A	3374	1/1	0.79	0.21	65,65,65,65	0
56	MG	2A	3453	1/1	0.79	0.11	45,45,45,45	0
56	MG	1f	3002	1/1	0.80	0.33	80,80,80,80	0
56	MG	2a	3036	1/1	0.80	0.21	83,83,83,83	0
56	MG	1A	3718	1/1	0.80	0.20	67,67,67,67	0
56	MG	2A	3855	1/1	0.80	0.12	69,69,69,69	0
56	MG	2A	3667	1/1	0.80	0.15	49,49,49,49	0
56	MG	1a	1689	1/1	0.80	0.27	73,73,73,73	0
56	MG	1A	3830	1/1	0.80	0.12	66,66,66,66	0
56	MG	1A	3776	1/1	0.80	0.27	75,75,75,75	0
56	MG	2A	3710	1/1	0.80	0.14	63,63,63,63	0
56	MG	2a	3155	1/1	0.80	0.13	81,81,81,81	0
56	MG	2a	3161	1/1	0.80	0.14	91,91,91,91	0
56	MG	2a	3166	1/1	0.80	0.13	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1750	1/1	0.80	0.29	85,85,85,85	0
56	MG	2A	3716	1/1	0.80	0.19	55,55,55,55	0
56	MG	1A	3694	1/1	0.80	0.16	61,61,61,61	0
56	MG	2A	3722	1/1	0.80	0.20	58,58,58,58	0
56	MG	15	103	1/1	0.80	0.15	61,61,61,61	0
56	MG	2a	3204	1/1	0.80	0.23	86,86,86,86	0
56	MG	2E	307	1/1	0.80	0.20	54,54,54,54	0
56	MG	2E	308	1/1	0.80	0.12	38,38,38,38	0
56	MG	2A	3756	1/1	0.80	0.18	42,42,42,42	0
56	MG	2j	8001	1/1	0.80	0.14	75,75,75,75	0
56	MG	1A	3875	1/1	0.80	0.19	60,60,60,60	0
56	MG	2w	108	1/1	0.80	0.22	66,66,66,66	0
56	MG	2A	3822	1/1	0.80	0.16	66,66,66,66	0
56	MG	2a	3024	1/1	0.80	0.32	72,72,72,72	0
56	MG	1x	114	1/1	0.81	0.21	82,82,82,82	0
56	MG	2A	3748	1/1	0.81	0.13	57,57,57,57	0
56	MG	1A	3829	1/1	0.81	0.11	59,59,59,59	0
56	MG	1A	3073	1/1	0.81	0.29	69,69,69,69	0
56	MG	2a	3034	1/1	0.81	0.23	72,72,72,72	0
56	MG	2A	3773	1/1	0.81	0.16	63,63,63,63	0
56	MG	2A	3808	1/1	0.81	0.15	60,60,60,60	0
56	MG	2a	3062	1/1	0.81	0.28	70,70,70,70	0
56	MG	1A	3272	1/1	0.81	0.14	60,60,60,60	0
56	MG	2a	3206	1/1	0.81	0.17	69,69,69,69	0
56	MG	2a	3103	1/1	0.81	0.22	76,76,76,76	0
56	MG	1A	3913	1/1	0.81	0.15	80,80,80,80	0
56	MG	2a	3108	1/1	0.81	0.26	78,78,78,78	0
56	MG	1B	3029	1/1	0.81	0.23	66,66,66,66	0
56	MG	1A	3646	1/1	0.81	0.10	32,32,32,32	0
56	MG	2a	3128	1/1	0.81	0.21	87,87,87,87	0
56	MG	1a	1672	1/1	0.81	0.12	73,73,73,73	0
56	MG	1A	3824	1/1	0.81	0.23	70,70,70,70	0
56	MG	1w	109	1/1	0.82	0.21	67,67,67,67	0
56	MG	2B	3020	1/1	0.82	0.30	78,78,78,78	0
56	MG	1Y	503	1/1	0.82	0.15	78,78,78,78	0
56	MG	2A	3769	1/1	0.82	0.15	62,62,62,62	0
56	MG	2A	3607	1/1	0.82	0.18	55,55,55,55	0
56	MG	1B	3020	1/1	0.82	0.26	82,82,82,82	0
56	MG	1A	3888	1/1	0.82	0.15	70,70,70,70	0
56	MG	2A	3058	1/1	0.82	0.19	66,66,66,66	0
56	MG	2a	3012	1/1	0.82	0.27	71,71,71,71	0
56	MG	1A	3863	1/1	0.82	0.22	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3200	1/1	0.82	0.26	76,76,76,76	0
56	MG	2A	3128	1/1	0.82	0.13	48,48,48,48	0
56	MG	2A	3138	1/1	0.82	0.20	59,59,59,59	0
56	MG	2A	3699	1/1	0.82	0.10	76,76,76,76	0
56	MG	2A	3256	1/1	0.82	0.18	53,53,53,53	0
56	MG	2A	3266	1/1	0.82	0.15	59,59,59,59	0
56	MG	1A	3871	1/1	0.82	0.23	49,49,49,49	0
56	MG	1A	3800	1/1	0.82	0.15	65,65,65,65	0
56	MG	2A	3364	1/1	0.82	0.29	77,77,77,77	0
56	MG	2w	102	1/1	0.82	0.13	62,62,62,62	0
56	MG	2A	3893	1/1	0.82	0.16	66,66,66,66	0
56	MG	2A	3741	1/1	0.82	0.14	61,61,61,61	0
56	MG	1A	3548	1/1	0.82	0.17	49,49,49,49	0
56	MG	1A	3853	1/1	0.83	0.13	52,52,52,52	0
56	MG	1A	3799	1/1	0.83	0.16	57,57,57,57	0
56	MG	2a	3037	1/1	0.83	0.15	77,77,77,77	0
56	MG	2a	3040	1/1	0.83	0.15	57,57,57,57	0
56	MG	1A	3727	1/1	0.83	0.17	36,36,36,36	0
56	MG	2A	3810	1/1	0.83	0.14	51,51,51,51	0
56	MG	2a	3085	1/1	0.83	0.26	65,65,65,65	0
56	MG	2A	3819	1/1	0.83	0.20	64,64,64,64	0
56	MG	2a	3099	1/1	0.83	0.26	74,74,74,74	0
56	MG	1A	4024	1/1	0.83	0.14	71,71,71,71	0
56	MG	1a	1784	1/1	0.83	0.15	74,74,74,74	0
56	MG	2A	3501	1/1	0.83	0.16	59,59,59,59	0
56	MG	1a	1824	1/1	0.83	0.15	73,73,73,73	0
56	MG	2A	3606	1/1	0.83	0.18	61,61,61,61	0
56	MG	1A	3802	1/1	0.83	0.13	57,57,57,57	0
56	MG	1A	4072	1/1	0.83	0.19	62,62,62,62	0
56	MG	1v	3001	1/1	0.83	0.31	77,77,77,77	0
56	MG	1A	3734	1/1	0.83	0.10	59,59,59,59	0
56	MG	1a	1612	1/1	0.83	0.15	74,74,74,74	0
56	MG	1x	109	1/1	0.83	0.21	82,82,82,82	0
56	MG	1a	1617	1/1	0.83	0.13	63,63,63,63	0
56	MG	2A	3696	1/1	0.83	0.11	58,58,58,58	0
56	MG	2B	3010	1/1	0.83	0.16	73,73,73,73	0
56	MG	1A	3757	1/1	0.83	0.18	27,27,27,27	0
56	MG	1a	1663	1/1	0.83	0.15	76,76,76,76	0
56	MG	1A	3316	1/1	0.83	0.22	58,58,58,58	0
56	MG	2A	3116	1/1	0.83	0.29	68,68,68,68	0
56	MG	2A	3117	1/1	0.83	0.19	63,63,63,63	0
56	MG	1A	3446	1/1	0.83	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
56	MG	2A	3737	1/1	0.83	0.20	72,72,72,72	0
56	MG	2a	3236	1/1	0.83	0.14	75,75,75,75	0
56	MG	1a	1702	1/1	0.83	0.41	73,73,73,73	0
56	MG	2a	3007	1/1	0.83	0.26	71,71,71,71	0
56	MG	2n	502	1/1	0.83	0.11	86,86,86,86	0
56	MG	2A	3744	1/1	0.83	0.18	55,55,55,55	0
56	MG	2w	101	1/1	0.83	0.26	73,73,73,73	0
56	MG	1a	1718	1/1	0.83	0.22	70,70,70,70	0
56	MG	2w	104	1/1	0.83	0.14	69,69,69,69	0
56	MG	2a	3013	1/1	0.83	0.33	78,78,78,78	0
56	MG	2A	3259	1/1	0.83	0.24	61,61,61,61	0
56	MG	1A	3320	1/1	0.83	0.20	60,60,60,60	0
56	MG	1A	4061	1/1	0.84	0.14	72,72,72,72	0
56	MG	2A	3466	1/1	0.84	0.22	65,65,65,65	0
56	MG	1x	103	1/1	0.84	0.14	71,71,71,71	0
56	MG	2a	3071	1/1	0.84	0.18	75,75,75,75	0
56	MG	2a	3083	1/1	0.84	0.20	72,72,72,72	0
56	MG	1A	3521	1/1	0.84	0.20	65,65,65,65	0
56	MG	2A	3829	1/1	0.84	0.12	59,59,59,59	0
56	MG	2a	3095	1/1	0.84	0.22	71,71,71,71	0
56	MG	2A	3568	1/1	0.84	0.13	46,46,46,46	0
56	MG	2A	3577	1/1	0.84	0.22	56,56,56,56	0
56	MG	1A	3937	1/1	0.84	0.15	31,31,31,31	0
56	MG	1a	1744	1/1	0.84	0.22	73,73,73,73	0
56	MG	2A	3039	1/1	0.84	0.12	55,55,55,55	0
56	MG	2A	3649	1/1	0.84	0.14	69,69,69,69	0
56	MG	1B	3002	1/1	0.84	0.19	58,58,58,58	0
56	MG	2A	3876	1/1	0.84	0.14	66,66,66,66	0
56	MG	1A	3948	1/1	0.84	0.15	60,60,60,60	0
56	MG	2A	3883	1/1	0.84	0.16	56,56,56,56	0
56	MG	2A	3101	1/1	0.84	0.22	59,59,59,59	0
56	MG	1A	3630	1/1	0.84	0.11	32,32,32,32	0
56	MG	1B	3024	1/1	0.84	0.10	50,50,50,50	0
56	MG	2A	3126	1/1	0.84	0.19	58,58,58,58	0
56	MG	1A	3794	1/1	0.84	0.18	61,61,61,61	0
56	MG	2A	3700	1/1	0.84	0.19	65,65,65,65	0
56	MG	2B	3019	1/1	0.84	0.16	76,76,76,76	0
56	MG	1a	1795	1/1	0.84	0.14	70,70,70,70	0
56	MG	2A	3169	1/1	0.84	0.45	73,73,73,73	0
56	MG	1A	3890	1/1	0.84	0.15	57,57,57,57	0
56	MG	1a	1665	1/1	0.84	0.18	78,78,78,78	0
56	MG	1A	3257	1/1	0.84	0.12	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3229	1/1	0.84	0.30	69,69,69,69	0
56	MG	28	102	1/1	0.84	0.14	52,52,52,52	0
56	MG	2A	3728	1/1	0.84	0.12	58,58,58,58	0
56	MG	1A	3708	1/1	0.84	0.17	76,76,76,76	0
56	MG	2A	3342	1/1	0.84	0.19	59,59,59,59	0
56	MG	2t	3001	1/1	0.84	0.18	60,60,60,60	0
56	MG	2A	3353	1/1	0.84	0.17	65,65,65,65	0
56	MG	2A	3354	1/1	0.84	0.21	68,68,68,68	0
56	MG	1w	101	1/1	0.84	0.15	64,64,64,64	0
56	MG	1a	1696	1/1	0.84	0.24	71,71,71,71	0
56	MG	1w	110	1/1	0.84	0.16	66,66,66,66	0
56	MG	2A	3406	1/1	0.84	0.19	55,55,55,55	0
56	MG	2A	3447	1/1	0.84	0.25	46,46,46,46	0
56	MG	2y	3007	1/1	0.84	0.17	68,68,68,68	0
56	MG	1A	3895	1/1	0.85	0.13	61,61,61,61	0
56	MG	1a	1829	1/1	0.85	0.19	73,73,73,73	0
56	MG	1A	3478	1/1	0.85	0.32	65,65,65,65	0
56	MG	1A	4000	1/1	0.85	0.14	34,34,34,34	0
56	MG	2a	3110	1/1	0.85	0.24	73,73,73,73	0
56	MG	19	102	1/1	0.85	0.15	51,51,51,51	0
56	MG	2A	3757	1/1	0.85	0.12	52,52,52,52	0
56	MG	2A	3766	1/1	0.85	0.14	52,52,52,52	0
56	MG	2A	3635	1/1	0.85	0.17	43,43,43,43	0
56	MG	2A	3770	1/1	0.85	0.12	57,57,57,57	0
56	MG	2a	3138	1/1	0.85	0.13	79,79,79,79	0
56	MG	2A	3644	1/1	0.85	0.15	64,64,64,64	0
56	MG	2T	3001	1/1	0.85	0.15	53,53,53,53	0
56	MG	2A	3780	1/1	0.85	0.16	80,80,80,80	0
56	MG	2A	3802	1/1	0.85	0.08	56,56,56,56	0
56	MG	1a	1704	1/1	0.85	0.23	63,63,63,63	0
56	MG	1A	3357	1/1	0.85	0.15	56,56,56,56	0
56	MG	2A	3814	1/1	0.85	0.19	55,55,55,55	0
56	MG	1A	4026	1/1	0.85	0.13	51,51,51,51	0
56	MG	1a	1743	1/1	0.85	0.16	73,73,73,73	0
56	MG	2A	3330	1/1	0.85	0.26	63,63,63,63	0
56	MG	1A	3752	1/1	0.85	0.12	41,41,41,41	0
56	MG	2a	3033	1/1	0.85	0.13	63,63,63,63	0
56	MG	1a	1625	1/1	0.85	0.29	63,63,63,63	0
56	MG	1a	1645	1/1	0.85	0.17	80,80,80,80	0
56	MG	2a	3232	1/1	0.85	0.17	77,77,77,77	0
56	MG	2a	3234	1/1	0.85	0.14	66,66,66,66	0
56	MG	1x	115	1/1	0.85	0.15	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1y	3001	1/1	0.85	0.11	64,64,64,64	0
56	MG	1a	1762	1/1	0.85	0.17	78,78,78,78	0
56	MG	2a	3048	1/1	0.85	0.25	67,67,67,67	0
56	MG	2a	3053	1/1	0.85	0.28	66,66,66,66	0
56	MG	2v	3001	1/1	0.85	0.23	69,69,69,69	0
56	MG	1A	3691	1/1	0.85	0.19	41,41,41,41	0
56	MG	2a	3063	1/1	0.85	0.17	74,74,74,74	0
56	MG	1A	3774	1/1	0.85	0.12	55,55,55,55	0
56	MG	1A	3970	1/1	0.85	0.13	70,70,70,70	0
56	MG	1a	1790	1/1	0.85	0.12	73,73,73,73	0
56	MG	1a	1669	1/1	0.85	0.19	73,73,73,73	0
56	MG	2a	3093	1/1	0.85	0.23	64,64,64,64	0
56	MG	2A	3506	1/1	0.85	0.17	31,31,31,31	0
56	MG	2A	3540	1/1	0.86	0.09	47,47,47,47	0
56	MG	1a	1660	1/1	0.86	0.15	74,74,74,74	0
56	MG	2A	3096	1/1	0.86	0.11	59,59,59,59	0
56	MG	2A	3100	1/1	0.86	0.11	57,57,57,57	0
56	MG	2a	3076	1/1	0.86	0.15	73,73,73,73	0
56	MG	1A	3407	1/1	0.86	0.14	65,65,65,65	0
56	MG	2A	3610	1/1	0.86	0.14	67,67,67,67	0
56	MG	2A	3614	1/1	0.86	0.12	36,36,36,36	0
56	MG	2A	3626	1/1	0.86	0.13	53,53,53,53	0
56	MG	2A	3113	1/1	0.86	0.11	52,52,52,52	0
56	MG	2A	3860	1/1	0.86	0.13	59,59,59,59	0
56	MG	1a	1789	1/1	0.86	0.12	72,72,72,72	0
56	MG	1A	3332	1/1	0.86	0.27	56,56,56,56	0
56	MG	2A	3647	1/1	0.86	0.19	51,51,51,51	0
56	MG	1A	4033	1/1	0.86	0.10	76,76,76,76	0
56	MG	1a	1797	1/1	0.86	0.16	64,64,64,64	0
56	MG	2a	3120	1/1	0.86	0.18	72,72,72,72	0
56	MG	2a	3121	1/1	0.86	0.28	75,75,75,75	0
56	MG	1A	3487	1/1	0.86	0.21	70,70,70,70	0
56	MG	1a	1827	1/1	0.86	0.11	58,58,58,58	0
56	MG	2A	3892	1/1	0.86	0.16	78,78,78,78	0
56	MG	2A	3229	1/1	0.86	0.15	41,41,41,41	0
56	MG	1V	203	1/1	0.86	0.16	67,67,67,67	0
56	MG	2a	3148	1/1	0.86	0.11	77,77,77,77	0
56	MG	2B	3004	1/1	0.86	0.15	69,69,69,69	0
56	MG	1A	4060	1/1	0.86	0.09	37,37,37,37	0
56	MG	1A	3488	1/1	0.86	0.21	59,59,59,59	0
56	MG	2a	3171	1/1	0.86	0.14	73,73,73,73	0
56	MG	1A	3432	1/1	0.86	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3295	1/1	0.86	0.15	63,63,63,63	0
56	MG	2A	3711	1/1	0.86	0.20	56,56,56,56	0
56	MG	2A	3326	1/1	0.86	0.27	64,64,64,64	0
56	MG	1A	3440	1/1	0.86	0.16	50,50,50,50	0
56	MG	2A	3341	1/1	0.86	0.17	52,52,52,52	0
56	MG	1a	1721	1/1	0.86	0.11	58,58,58,58	0
56	MG	2U	202	1/1	0.86	0.13	54,54,54,54	0
56	MG	1a	1603	1/1	0.86	0.10	59,59,59,59	0
56	MG	2a	3226	1/1	0.86	0.26	64,64,64,64	0
56	MG	1A	3823	1/1	0.86	0.20	65,65,65,65	0
56	MG	1A	3343	1/1	0.86	0.25	59,59,59,59	0
56	MG	2a	3231	1/1	0.86	0.11	68,68,68,68	0
56	MG	1B	3019	1/1	0.86	0.15	56,56,56,56	0
56	MG	1A	3245	1/1	0.86	0.20	64,64,64,64	0
56	MG	1a	1755	1/1	0.86	0.11	74,74,74,74	0
56	MG	2A	3421	1/1	0.86	0.21	61,61,61,61	0
56	MG	1a	1760	1/1	0.86	0.09	74,74,74,74	0
56	MG	2j	8002	1/1	0.86	0.13	66,66,66,66	0
56	MG	2l	202	1/1	0.86	0.10	70,70,70,70	0
56	MG	1A	3692	1/1	0.86	0.19	64,64,64,64	0
56	MG	2a	3030	1/1	0.86	0.11	61,61,61,61	0
56	MG	1a	1766	1/1	0.86	0.28	76,76,76,76	0
56	MG	2A	3481	1/1	0.86	0.18	56,56,56,56	0
56	MG	2A	3488	1/1	0.86	0.18	65,65,65,65	0
56	MG	2A	3051	1/1	0.86	0.10	43,43,43,43	0
56	MG	2A	3056	1/1	0.86	0.13	60,60,60,60	0
56	MG	2A	3520	1/1	0.86	0.22	65,65,65,65	0
56	MG	1A	4012	1/1	0.86	0.11	34,34,34,34	0
56	MG	2a	3050	1/1	0.86	0.22	61,61,61,61	0
56	MG	2a	3051	1/1	0.86	0.20	69,69,69,69	0
56	MG	2A	3141	1/1	0.87	0.09	51,51,51,51	0
56	MG	2A	3153	1/1	0.87	0.18	52,52,52,52	0
56	MG	1a	1705	1/1	0.87	0.27	63,63,63,63	0
56	MG	2A	3832	1/1	0.87	0.11	54,54,54,54	0
56	MG	1A	3377	1/1	0.87	0.14	54,54,54,54	0
56	MG	2A	3245	1/1	0.87	0.18	59,59,59,59	0
56	MG	1w	105	1/1	0.87	0.15	87,87,87,87	0
56	MG	2A	3615	1/1	0.87	0.10	51,51,51,51	0
56	MG	2A	3625	1/1	0.87	0.21	69,69,69,69	0
56	MG	1A	3744	1/1	0.87	0.21	74,74,74,74	0
56	MG	1a	1730	1/1	0.87	0.13	80,80,80,80	0
56	MG	2A	3271	1/1	0.87	0.15	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3290	1/1	0.87	0.22	50,50,50,50	0
56	MG	1a	1602	1/1	0.87	0.24	72,72,72,72	0
56	MG	1A	3541	1/1	0.87	0.15	73,73,73,73	0
56	MG	2A	3301	1/1	0.87	0.11	60,60,60,60	0
56	MG	2A	3307	1/1	0.87	0.23	68,68,68,68	0
56	MG	1A	3348	1/1	0.87	0.13	62,62,62,62	0
56	MG	1A	3766	1/1	0.87	0.12	47,47,47,47	0
56	MG	2A	3336	1/1	0.87	0.13	53,53,53,53	0
56	MG	2B	3006	1/1	0.87	0.16	59,59,59,59	0
56	MG	1A	3685	1/1	0.87	0.21	60,60,60,60	0
56	MG	1a	1624	1/1	0.87	0.10	50,50,50,50	0
56	MG	2A	3346	1/1	0.87	0.11	54,54,54,54	0
56	MG	2A	3703	1/1	0.87	0.10	47,47,47,47	0
56	MG	1y	3002	1/1	0.87	0.21	75,75,75,75	0
56	MG	1A	3850	1/1	0.87	0.10	53,53,53,53	0
56	MG	2a	3193	1/1	0.87	0.26	73,73,73,73	0
56	MG	2A	3360	1/1	0.87	0.14	63,63,63,63	0
56	MG	1A	3441	1/1	0.87	0.20	56,56,56,56	0
56	MG	1A	3856	1/1	0.87	0.14	47,47,47,47	0
56	MG	1A	3987	1/1	0.87	0.10	32,32,32,32	0
56	MG	1A	3557	1/1	0.87	0.32	60,60,60,60	0
56	MG	2A	3408	1/1	0.87	0.10	51,51,51,51	0
56	MG	2A	3062	1/1	0.87	0.15	61,61,61,61	0
56	MG	2a	3214	1/1	0.87	0.08	91,91,91,91	0
56	MG	2a	3220	1/1	0.87	0.15	66,66,66,66	0
56	MG	2a	3221	1/1	0.87	0.19	60,60,60,60	0
56	MG	2a	3006	1/1	0.87	0.21	74,74,74,74	0
56	MG	2A	3743	1/1	0.87	0.14	75,75,75,75	0
56	MG	2A	3428	1/1	0.87	0.10	52,52,52,52	0
56	MG	2A	3747	1/1	0.87	0.12	51,51,51,51	0
56	MG	1A	3867	1/1	0.87	0.15	69,69,69,69	0
56	MG	2a	3017	1/1	0.87	0.16	66,66,66,66	0
56	MG	1A	3444	1/1	0.87	0.31	63,63,63,63	0
56	MG	2a	3238	1/1	0.87	0.18	62,62,62,62	0
56	MG	2A	3459	1/1	0.87	0.15	62,62,62,62	0
56	MG	1O	206	1/1	0.87	0.17	84,84,84,84	0
56	MG	2A	3470	1/1	0.87	0.17	56,56,56,56	0
56	MG	1a	1674	1/1	0.87	0.29	72,72,72,72	0
56	MG	1a	1676	1/1	0.87	0.29	67,67,67,67	0
56	MG	1a	1677	1/1	0.87	0.19	68,68,68,68	0
56	MG	1A	3312	1/1	0.87	0.30	59,59,59,59	0
56	MG	2A	3799	1/1	0.87	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
56	MG	2A	3507	1/1	0.87	0.19	64,64,64,64	0
56	MG	1A	3623	1/1	0.87	0.16	59,59,59,59	0
56	MG	1A	3723	1/1	0.87	0.09	47,47,47,47	0
56	MG	2A	3812	1/1	0.87	0.10	47,47,47,47	0
56	MG	2a	3058	1/1	0.87	0.36	73,73,73,73	0
56	MG	1A	3428	1/1	0.87	0.11	51,51,51,51	0
56	MG	2A	3553	1/1	0.87	0.13	71,71,71,71	0
56	MG	2A	3119	1/1	0.88	0.13	47,47,47,47	0
56	MG	2A	3795	1/1	0.88	0.12	37,37,37,37	0
56	MG	2A	3123	1/1	0.88	0.13	56,56,56,56	0
56	MG	2A	3500	1/1	0.88	0.16	55,55,55,55	0
56	MG	2A	3805	1/1	0.88	0.17	77,77,77,77	0
56	MG	1A	3821	1/1	0.88	0.13	47,47,47,47	0
56	MG	2a	3064	1/1	0.88	0.18	81,81,81,81	0
56	MG	2a	3069	1/1	0.88	0.12	62,62,62,62	0
56	MG	2A	3505	1/1	0.88	0.14	59,59,59,59	0
56	MG	1B	3035	1/1	0.88	0.10	59,59,59,59	0
56	MG	1E	302	1/1	0.88	0.29	58,58,58,58	0
56	MG	2A	3815	1/1	0.88	0.16	48,48,48,48	0
56	MG	1A	3997	1/1	0.88	0.12	39,39,39,39	0
56	MG	2A	3535	1/1	0.88	0.21	59,59,59,59	0
56	MG	2a	3094	1/1	0.88	0.21	68,68,68,68	0
56	MG	2A	3147	1/1	0.88	0.16	58,58,58,58	0
56	MG	1A	3607	1/1	0.88	0.10	35,35,35,35	0
56	MG	1A	3610	1/1	0.88	0.18	54,54,54,54	0
56	MG	2A	3220	1/1	0.88	0.27	68,68,68,68	0
56	MG	1a	1694	1/1	0.88	0.14	58,58,58,58	0
56	MG	2A	3601	1/1	0.88	0.11	39,39,39,39	0
56	MG	2a	3111	1/1	0.88	0.19	76,76,76,76	0
56	MG	2A	3604	1/1	0.88	0.24	64,64,64,64	0
56	MG	1T	8001	1/1	0.88	0.15	63,63,63,63	0
56	MG	2A	3255	1/1	0.88	0.11	59,59,59,59	0
56	MG	2A	3867	1/1	0.88	0.09	64,64,64,64	0
56	MG	1A	3542	1/1	0.88	0.27	75,75,75,75	0
56	MG	1w	104	1/1	0.88	0.22	69,69,69,69	0
56	MG	1A	3544	1/1	0.88	0.08	47,47,47,47	0
56	MG	1w	106	1/1	0.88	0.26	74,74,74,74	0
56	MG	1A	3512	1/1	0.88	0.10	50,50,50,50	0
56	MG	1a	1709	1/1	0.88	0.13	59,59,59,59	0
56	MG	1A	3472	1/1	0.88	0.13	56,56,56,56	0
56	MG	1A	4049	1/1	0.88	0.11	55,55,55,55	0
56	MG	2B	3002	1/1	0.88	0.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3305	1/1	0.88	0.12	56,56,56,56	0
56	MG	2a	3182	1/1	0.88	0.17	71,71,71,71	0
56	MG	2a	3187	1/1	0.88	0.17	72,72,72,72	0
56	MG	2a	3190	1/1	0.88	0.16	66,66,66,66	0
56	MG	1a	1726	1/1	0.88	0.39	67,67,67,67	0
56	MG	1x	111	1/1	0.88	0.22	66,66,66,66	0
56	MG	1x	113	1/1	0.88	0.18	62,62,62,62	0
56	MG	2A	3333	1/1	0.88	0.13	55,55,55,55	0
56	MG	1A	3897	1/1	0.88	0.18	62,62,62,62	0
56	MG	1A	3836	1/1	0.88	0.19	54,54,54,54	0
56	MG	1A	3424	1/1	0.88	0.22	70,70,70,70	0
56	MG	2A	3345	1/1	0.88	0.14	59,59,59,59	0
56	MG	1A	3308	1/1	0.88	0.17	51,51,51,51	0
56	MG	1A	4084	1/1	0.88	0.10	50,50,50,50	0
56	MG	2O	8001	1/1	0.88	0.18	65,65,65,65	0
56	MG	1a	1613	1/1	0.88	0.09	74,74,74,74	0
56	MG	1a	1752	1/1	0.88	0.13	68,68,68,68	0
56	MG	2a	3227	1/1	0.88	0.17	59,59,59,59	0
56	MG	1A	4113	1/1	0.88	0.15	56,56,56,56	0
56	MG	1A	3855	1/1	0.88	0.18	53,53,53,53	0
56	MG	2a	3230	1/1	0.88	0.12	63,63,63,63	0
56	MG	1A	3951	1/1	0.88	0.16	72,72,72,72	0
56	MG	2a	3005	1/1	0.88	0.37	75,75,75,75	0
56	MG	2A	3397	1/1	0.88	0.15	54,54,54,54	0
56	MG	2A	3066	1/1	0.88	0.10	41,41,41,41	0
56	MG	2a	3008	1/1	0.88	0.28	68,68,68,68	0
56	MG	2A	3080	1/1	0.88	0.14	58,58,58,58	0
56	MG	2A	3738	1/1	0.88	0.15	59,59,59,59	0
56	MG	2A	3413	1/1	0.88	0.12	56,56,56,56	0
56	MG	1B	3012	1/1	0.88	0.16	55,55,55,55	0
56	MG	1A	3350	1/1	0.88	0.26	59,59,59,59	0
56	MG	2A	3429	1/1	0.88	0.09	65,65,65,65	0
56	MG	2A	3437	1/1	0.88	0.12	67,67,67,67	0
56	MG	2A	3439	1/1	0.88	0.13	60,60,60,60	0
56	MG	1A	3754	1/1	0.88	0.14	48,48,48,48	0
56	MG	1a	1779	1/1	0.88	0.11	65,65,65,65	0
56	MG	1A	3866	1/1	0.88	0.17	46,46,46,46	0
56	MG	2a	3039	1/1	0.88	0.36	73,73,73,73	0
56	MG	1A	3805	1/1	0.88	0.12	54,54,54,54	0
56	MG	2y	3002	1/1	0.88	0.15	64,64,64,64	0
56	MG	2A	3468	1/1	0.88	0.33	59,59,59,59	0
56	MG	1a	1666	1/1	0.88	0.13	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3239	1/1	0.89	0.13	52,52,52,52	0
56	MG	1a	1629	1/1	0.89	0.11	57,57,57,57	0
56	MG	1a	1633	1/1	0.89	0.14	60,60,60,60	0
56	MG	1a	1636	1/1	0.89	0.15	67,67,67,67	0
56	MG	2A	3257	1/1	0.89	0.24	65,65,65,65	0
56	MG	1a	1640	1/1	0.89	0.13	58,58,58,58	0
56	MG	1A	4103	1/1	0.89	0.14	67,67,67,67	0
56	MG	2A	3268	1/1	0.89	0.14	63,63,63,63	0
56	MG	1A	3901	1/1	0.89	0.21	43,43,43,43	0
56	MG	2A	3654	1/1	0.89	0.19	62,62,62,62	0
56	MG	2a	3014	1/1	0.89	0.17	64,64,64,64	0
56	MG	2A	3281	1/1	0.89	0.13	63,63,63,63	0
56	MG	2a	3018	1/1	0.89	0.23	65,65,65,65	0
56	MG	2a	3019	1/1	0.89	0.12	57,57,57,57	0
56	MG	2a	3020	1/1	0.89	0.15	71,71,71,71	0
56	MG	2A	3664	1/1	0.89	0.11	54,54,54,54	0
56	MG	2a	3026	1/1	0.89	0.23	64,64,64,64	0
56	MG	2A	3286	1/1	0.89	0.17	55,55,55,55	0
56	MG	2a	3029	1/1	0.89	0.15	67,67,67,67	0
56	MG	1A	3905	1/1	0.89	0.12	46,46,46,46	0
56	MG	2a	3032	1/1	0.89	0.20	60,60,60,60	0
56	MG	1n	102	1/1	0.89	0.29	66,66,66,66	0
56	MG	1a	1661	1/1	0.89	0.20	70,70,70,70	0
56	MG	2A	3693	1/1	0.89	0.09	35,35,35,35	0
56	MG	1A	3703	1/1	0.89	0.11	56,56,56,56	0
56	MG	1A	3315	1/1	0.89	0.25	61,61,61,61	0
56	MG	1B	3016	1/1	0.89	0.13	54,54,54,54	0
56	MG	2A	3702	1/1	0.89	0.07	49,49,49,49	0
56	MG	2A	3322	1/1	0.89	0.14	60,60,60,60	0
56	MG	1A	3926	1/1	0.89	0.17	53,53,53,53	0
56	MG	1A	3344	1/1	0.89	0.22	64,64,64,64	0
56	MG	2A	3332	1/1	0.89	0.13	62,62,62,62	0
56	MG	1A	3571	1/1	0.89	0.10	57,57,57,57	0
56	MG	2a	3059	1/1	0.89	0.21	74,74,74,74	0
56	MG	2A	3718	1/1	0.89	0.16	64,64,64,64	0
56	MG	1B	3025	1/1	0.89	0.16	77,77,77,77	0
56	MG	2A	3340	1/1	0.89	0.11	51,51,51,51	0
56	MG	1B	3028	1/1	0.89	0.07	61,61,61,61	0
56	MG	2a	3070	1/1	0.89	0.14	61,61,61,61	0
56	MG	2A	3733	1/1	0.89	0.13	50,50,50,50	0
56	MG	1a	1683	1/1	0.89	0.13	61,61,61,61	0
56	MG	2a	3081	1/1	0.89	0.12	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1688	1/1	0.89	0.24	74,74,74,74	0
56	MG	1A	3218	1/1	0.89	0.16	62,62,62,62	0
56	MG	2A	3350	1/1	0.89	0.19	61,61,61,61	0
56	MG	1A	3833	1/1	0.89	0.14	60,60,60,60	0
56	MG	2A	3745	1/1	0.89	0.14	56,56,56,56	0
56	MG	1A	3598	1/1	0.89	0.12	51,51,51,51	0
56	MG	1A	3504	1/1	0.89	0.12	44,44,44,44	0
56	MG	1A	3983	1/1	0.89	0.13	48,48,48,48	0
56	MG	1F	302	1/1	0.89	0.13	47,47,47,47	0
56	MG	2a	3106	1/1	0.89	0.17	62,62,62,62	0
56	MG	2A	3023	1/1	0.89	0.09	48,48,48,48	0
56	MG	2A	3758	1/1	0.89	0.12	58,58,58,58	0
56	MG	2A	3765	1/1	0.89	0.10	53,53,53,53	0
56	MG	2A	3380	1/1	0.89	0.11	55,55,55,55	0
56	MG	2A	3386	1/1	0.89	0.19	63,63,63,63	0
56	MG	1A	3299	1/1	0.89	0.28	61,61,61,61	0
56	MG	1a	1712	1/1	0.89	0.23	67,67,67,67	0
56	MG	2A	3053	1/1	0.89	0.14	54,54,54,54	0
56	MG	2A	3410	1/1	0.89	0.17	55,55,55,55	0
56	MG	1A	3143	1/1	0.89	0.20	55,55,55,55	0
56	MG	1R	203	1/1	0.89	0.20	47,47,47,47	0
56	MG	2a	3141	1/1	0.89	0.14	94,94,94,94	0
56	MG	2A	3424	1/1	0.89	0.19	50,50,50,50	0
56	MG	2A	3425	1/1	0.89	0.18	58,58,58,58	0
56	MG	2a	3156	1/1	0.89	0.10	69,69,69,69	0
56	MG	1A	3362	1/1	0.89	0.14	54,54,54,54	0
56	MG	2A	3064	1/1	0.89	0.10	51,51,51,51	0
56	MG	2A	3065	1/1	0.89	0.18	57,57,57,57	0
56	MG	1A	3363	1/1	0.89	0.22	60,60,60,60	0
56	MG	2A	3441	1/1	0.89	0.11	51,51,51,51	0
56	MG	1a	1735	1/1	0.89	0.18	57,57,57,57	0
56	MG	1A	3370	1/1	0.89	0.18	57,57,57,57	0
56	MG	2A	3094	1/1	0.89	0.13	44,44,44,44	0
56	MG	2A	3463	1/1	0.89	0.14	57,57,57,57	0
56	MG	2A	3836	1/1	0.89	0.20	42,42,42,42	0
56	MG	1A	4022	1/1	0.89	0.08	72,72,72,72	0
56	MG	1A	3648	1/1	0.89	0.12	55,55,55,55	0
56	MG	2A	3469	1/1	0.89	0.15	55,55,55,55	0
56	MG	13	103	1/1	0.89	0.12	47,47,47,47	0
56	MG	2A	3474	1/1	0.89	0.14	55,55,55,55	0
56	MG	2A	3104	1/1	0.89	0.10	53,53,53,53	0
56	MG	1A	3783	1/1	0.89	0.14	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1751	1/1	0.89	0.16	70,70,70,70	0
56	MG	1A	3665	1/1	0.89	0.12	60,60,60,60	0
56	MG	1a	1601	1/1	0.89	0.10	53,53,53,53	0
56	MG	1A	3667	1/1	0.89	0.11	61,61,61,61	0
56	MG	1A	3322	1/1	0.89	0.18	59,59,59,59	0
56	MG	1a	1605	1/1	0.89	0.10	65,65,65,65	0
56	MG	2A	3521	1/1	0.89	0.12	51,51,51,51	0
56	MG	2A	3130	1/1	0.89	0.15	53,53,53,53	0
56	MG	2A	3906	1/1	0.89	0.35	62,62,62,62	0
56	MG	2B	3001	1/1	0.89	0.16	62,62,62,62	0
56	MG	1a	1770	1/1	0.89	0.16	60,60,60,60	0
56	MG	2a	3237	1/1	0.89	0.32	66,66,66,66	0
56	MG	1A	3268	1/1	0.89	0.30	59,59,59,59	0
56	MG	2A	3544	1/1	0.89	0.10	42,42,42,42	0
56	MG	2d	502	1/1	0.89	0.16	68,68,68,68	0
56	MG	2A	3546	1/1	0.89	0.10	44,44,44,44	0
56	MG	2B	3007	1/1	0.89	0.13	55,55,55,55	0
56	MG	2B	3008	1/1	0.89	0.14	58,58,58,58	0
56	MG	2A	3549	1/1	0.89	0.16	58,58,58,58	0
56	MG	2q	202	1/1	0.89	0.12	78,78,78,78	0
56	MG	2r	102	1/1	0.89	0.13	73,73,73,73	0
56	MG	1A	3687	1/1	0.89	0.11	31,31,31,31	0
56	MG	1A	4068	1/1	0.89	0.14	48,48,48,48	0
56	MG	1A	3545	1/1	0.89	0.13	67,67,67,67	0
56	MG	2A	3579	1/1	0.89	0.17	60,60,60,60	0
56	MG	2A	3186	1/1	0.89	0.16	54,54,54,54	0
56	MG	2A	3206	1/1	0.89	0.19	56,56,56,56	0
56	MG	2A	3605	1/1	0.89	0.12	51,51,51,51	0
56	MG	1A	3471	1/1	0.89	0.19	57,57,57,57	0
56	MG	2A	3228	1/1	0.89	0.29	65,65,65,65	0
56	MG	2T	3003	1/1	0.89	0.17	63,63,63,63	0
56	MG	1A	3418	1/1	0.89	0.13	54,54,54,54	0
58	ZN	24	501	1/1	0.89	0.11	128,128,128,128	0
56	MG	2B	3017	1/1	0.90	0.12	65,65,65,65	0
56	MG	11	103	1/1	0.90	0.09	65,65,65,65	0
56	MG	2A	3168	1/1	0.90	0.19	52,52,52,52	0
56	MG	1A	4007	1/1	0.90	0.08	86,86,86,86	0
56	MG	2A	3171	1/1	0.90	0.11	38,38,38,38	0
56	MG	2A	3177	1/1	0.90	0.21	63,63,63,63	0
56	MG	2A	3572	1/1	0.90	0.09	44,44,44,44	0
56	MG	2A	3573	1/1	0.90	0.09	42,42,42,42	0
56	MG	2A	3178	1/1	0.90	0.16	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3831	1/1	0.90	0.28	70,70,70,70	0
56	MG	2W	202	1/1	0.90	0.10	58,58,58,58	0
56	MG	2A	3583	1/1	0.90	0.26	69,69,69,69	0
56	MG	23	101	1/1	0.90	0.15	61,61,61,61	0
56	MG	2A	3590	1/1	0.90	0.13	64,64,64,64	0
56	MG	1a	1767	1/1	0.90	0.14	66,66,66,66	0
56	MG	2A	3603	1/1	0.90	0.10	50,50,50,50	0
56	MG	2A	3218	1/1	0.90	0.14	61,61,61,61	0
56	MG	18	103	1/1	0.90	0.12	72,72,72,72	0
56	MG	1A	3458	1/1	0.90	0.15	54,54,54,54	0
56	MG	1A	3203	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3209	1/1	0.90	0.15	68,68,68,68	0
56	MG	1A	3835	1/1	0.90	0.14	59,59,59,59	0
56	MG	1A	3699	1/1	0.90	0.17	64,64,64,64	0
56	MG	2a	3015	1/1	0.90	0.23	62,62,62,62	0
56	MG	2a	3016	1/1	0.90	0.15	66,66,66,66	0
56	MG	2A	3619	1/1	0.90	0.12	37,37,37,37	0
56	MG	1A	3558	1/1	0.90	0.12	52,52,52,52	0
56	MG	1a	1794	1/1	0.90	0.11	52,52,52,52	0
56	MG	1A	4053	1/1	0.90	0.20	37,37,37,37	0
56	MG	2A	3642	1/1	0.90	0.16	47,47,47,47	0
56	MG	2A	3261	1/1	0.90	0.15	59,59,59,59	0
56	MG	2A	3265	1/1	0.90	0.14	59,59,59,59	0
56	MG	1A	3560	1/1	0.90	0.23	55,55,55,55	0
56	MG	1a	1803	1/1	0.90	0.10	73,73,73,73	0
56	MG	2a	3031	1/1	0.90	0.10	49,49,49,49	0
56	MG	1A	3709	1/1	0.90	0.14	52,52,52,52	0
56	MG	2A	3655	1/1	0.90	0.12	65,65,65,65	0
56	MG	2A	3280	1/1	0.90	0.14	54,54,54,54	0
56	MG	2A	3658	1/1	0.90	0.14	55,55,55,55	0
56	MG	1a	1618	1/1	0.90	0.08	48,48,48,48	0
56	MG	2A	3284	1/1	0.90	0.15	59,59,59,59	0
56	MG	2A	3681	1/1	0.90	0.10	50,50,50,50	0
56	MG	2a	3044	1/1	0.90	0.17	57,57,57,57	0
56	MG	2A	3684	1/1	0.90	0.09	44,44,44,44	0
56	MG	2A	3685	1/1	0.90	0.10	53,53,53,53	0
56	MG	1a	1620	1/1	0.90	0.15	66,66,66,66	0
56	MG	1d	502	1/1	0.90	0.28	67,67,67,67	0
56	MG	1a	1623	1/1	0.90	0.11	60,60,60,60	0
56	MG	2a	3056	1/1	0.90	0.21	63,63,63,63	0
56	MG	2a	3057	1/1	0.90	0.19	71,71,71,71	0
56	MG	1A	4065	1/1	0.90	0.09	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1l	203	1/1	0.90	0.12	63,63,63,63	0
56	MG	2A	3304	1/1	0.90	0.15	60,60,60,60	0
56	MG	1A	4066	1/1	0.90	0.11	71,71,71,71	0
56	MG	1A	3711	1/1	0.90	0.10	61,61,61,61	0
56	MG	2a	3065	1/1	0.90	0.09	57,57,57,57	0
56	MG	2a	3067	1/1	0.90	0.36	65,65,65,65	0
56	MG	2A	3313	1/1	0.90	0.25	64,64,64,64	0
56	MG	2A	3709	1/1	0.90	0.10	33,33,33,33	0
56	MG	2A	3314	1/1	0.90	0.11	47,47,47,47	0
56	MG	1a	1630	1/1	0.90	0.09	60,60,60,60	0
56	MG	1A	4071	1/1	0.90	0.07	26,26,26,26	0
56	MG	1A	3564	1/1	0.90	0.07	40,40,40,40	0
56	MG	2A	3717	1/1	0.90	0.11	39,39,39,39	0
56	MG	2a	3088	1/1	0.90	0.17	62,62,62,62	0
56	MG	2A	3331	1/1	0.90	0.08	56,56,56,56	0
56	MG	2a	3091	1/1	0.90	0.18	76,76,76,76	0
56	MG	1A	4074	1/1	0.90	0.12	64,64,64,64	0
56	MG	1w	107	1/1	0.90	0.32	67,67,67,67	0
56	MG	1A	3378	1/1	0.90	0.11	53,53,53,53	0
56	MG	2a	3096	1/1	0.90	0.14	65,65,65,65	0
56	MG	1A	3568	1/1	0.90	0.15	50,50,50,50	0
56	MG	2a	3100	1/1	0.90	0.15	69,69,69,69	0
56	MG	1x	101	1/1	0.90	0.10	56,56,56,56	0
56	MG	1A	3386	1/1	0.90	0.17	54,54,54,54	0
56	MG	2A	3740	1/1	0.90	0.12	53,53,53,53	0
56	MG	1A	4104	1/1	0.90	0.09	30,30,30,30	0
56	MG	1x	104	1/1	0.90	0.23	72,72,72,72	0
56	MG	1A	3737	1/1	0.90	0.13	57,57,57,57	0
56	MG	1A	4116	1/1	0.90	0.11	41,41,41,41	0
56	MG	1A	4120	1/1	0.90	0.13	44,44,44,44	0
56	MG	1A	3581	1/1	0.90	0.17	58,58,58,58	0
56	MG	2A	3753	1/1	0.90	0.19	45,45,45,45	0
56	MG	1B	3006	1/1	0.90	0.23	45,45,45,45	0
56	MG	2a	3130	1/1	0.90	0.38	72,72,72,72	0
56	MG	1A	3745	1/1	0.90	0.14	19,19,19,19	0
56	MG	2a	3135	1/1	0.90	0.13	62,62,62,62	0
56	MG	1A	3406	1/1	0.90	0.16	47,47,47,47	0
56	MG	1y	3003	1/1	0.90	0.25	71,71,71,71	0
56	MG	2A	3759	1/1	0.90	0.09	46,46,46,46	0
56	MG	2a	3145	1/1	0.90	0.08	76,76,76,76	0
56	MG	2a	3146	1/1	0.90	0.13	84,84,84,84	0
56	MG	2A	3764	1/1	0.90	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
56	MG	2A	3381	1/1	0.90	0.11	53,53,53,53	0
56	MG	1A	3595	1/1	0.90	0.12	59,59,59,59	0
56	MG	2A	3387	1/1	0.90	0.18	59,59,59,59	0
56	MG	2A	3393	1/1	0.90	0.09	48,48,48,48	0
56	MG	2A	3008	1/1	0.90	0.11	49,49,49,49	0
56	MG	2a	3174	1/1	0.90	0.13	69,69,69,69	0
56	MG	2a	3178	1/1	0.90	0.12	75,75,75,75	0
56	MG	1a	1682	1/1	0.90	0.09	66,66,66,66	0
56	MG	1A	3323	1/1	0.90	0.14	50,50,50,50	0
56	MG	2A	3798	1/1	0.90	0.14	52,52,52,52	0
56	MG	2A	3042	1/1	0.90	0.12	42,42,42,42	0
56	MG	2A	3412	1/1	0.90	0.19	59,59,59,59	0
56	MG	2A	3045	1/1	0.90	0.11	58,58,58,58	0
56	MG	2a	3197	1/1	0.90	0.10	69,69,69,69	0
56	MG	2A	3050	1/1	0.90	0.08	51,51,51,51	0
56	MG	1A	3412	1/1	0.90	0.17	52,52,52,52	0
56	MG	1B	3021	1/1	0.90	0.12	46,46,46,46	0
56	MG	2A	3426	1/1	0.90	0.17	63,63,63,63	0
56	MG	1a	1691	1/1	0.90	0.23	69,69,69,69	0
56	MG	2a	3205	1/1	0.90	0.26	70,70,70,70	0
56	MG	2A	3818	1/1	0.90	0.18	66,66,66,66	0
56	MG	2a	3209	1/1	0.90	0.21	77,77,77,77	0
56	MG	1A	3770	1/1	0.90	0.09	74,74,74,74	0
56	MG	1A	3325	1/1	0.90	0.22	64,64,64,64	0
56	MG	2a	3219	1/1	0.90	0.11	65,65,65,65	0
56	MG	2A	3438	1/1	0.90	0.25	68,68,68,68	0
56	MG	2A	3827	1/1	0.90	0.14	58,58,58,58	0
56	MG	2a	3224	1/1	0.90	0.19	74,74,74,74	0
56	MG	1A	3618	1/1	0.90	0.14	56,56,56,56	0
56	MG	1A	3215	1/1	0.90	0.14	65,65,65,65	0
56	MG	1A	3918	1/1	0.90	0.12	56,56,56,56	0
56	MG	1A	3513	1/1	0.90	0.13	62,62,62,62	0
56	MG	2A	3458	1/1	0.90	0.17	65,65,65,65	0
56	MG	1A	3304	1/1	0.90	0.27	55,55,55,55	0
56	MG	1A	3643	1/1	0.90	0.08	34,34,34,34	0
56	MG	2a	3233	1/1	0.90	0.14	68,68,68,68	0
56	MG	1a	1719	1/1	0.90	0.28	63,63,63,63	0
56	MG	1a	1720	1/1	0.90	0.20	67,67,67,67	0
56	MG	1A	3645	1/1	0.90	0.10	37,37,37,37	0
56	MG	1a	1722	1/1	0.90	0.15	65,65,65,65	0
56	MG	2A	3471	1/1	0.90	0.22	54,54,54,54	0
56	MG	2a	3242	1/1	0.90	0.17	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3110	1/1	0.90	0.10	58,58,58,58	0
56	MG	2g	8001	1/1	0.90	0.11	75,75,75,75	0
56	MG	2A	3477	1/1	0.90	0.35	56,56,56,56	0
56	MG	1A	3525	1/1	0.90	0.21	58,58,58,58	0
56	MG	1O	201	1/1	0.90	0.17	63,63,63,63	0
56	MG	2A	3888	1/1	0.90	0.11	57,57,57,57	0
56	MG	1A	3305	1/1	0.90	0.26	55,55,55,55	0
56	MG	1O	207	1/1	0.90	0.13	65,65,65,65	0
56	MG	2A	3503	1/1	0.90	0.11	58,58,58,58	0
56	MG	1A	3127	1/1	0.90	0.23	51,51,51,51	0
56	MG	1A	3048	1/1	0.90	0.22	48,48,48,48	0
56	MG	1T	8002	1/1	0.90	0.11	58,58,58,58	0
56	MG	2A	3515	1/1	0.90	0.10	55,55,55,55	0
56	MG	1A	3253	1/1	0.90	0.08	61,61,61,61	0
56	MG	2w	107	1/1	0.90	0.12	75,75,75,75	0
56	MG	2A	3134	1/1	0.90	0.15	72,72,72,72	0
56	MG	1A	3679	1/1	0.90	0.15	39,39,39,39	0
56	MG	1A	3110	1/1	0.90	0.09	42,42,42,42	0
56	MG	2B	3011	1/1	0.90	0.24	67,67,67,67	0
56	MG	1A	3188	1/1	0.90	0.10	49,49,49,49	0
56	MG	2A	3541	1/1	0.90	0.07	30,30,30,30	0
56	MG	1A	3026	1/1	0.91	0.15	60,60,60,60	0
56	MG	1A	3182	1/1	0.91	0.14	55,55,55,55	0
56	MG	2A	3317	1/1	0.91	0.11	55,55,55,55	0
56	MG	2A	3321	1/1	0.91	0.18	54,54,54,54	0
56	MG	1A	3870	1/1	0.91	0.11	39,39,39,39	0
56	MG	1x	106	1/1	0.91	0.14	63,63,63,63	0
56	MG	1x	108	1/1	0.91	0.19	63,63,63,63	0
56	MG	1A	3732	1/1	0.91	0.19	64,64,64,64	0
56	MG	1A	4134	1/1	0.91	0.28	46,46,46,46	0
56	MG	2a	3021	1/1	0.91	0.20	65,65,65,65	0
56	MG	1x	112	1/1	0.91	0.16	71,71,71,71	0
56	MG	2A	3335	1/1	0.91	0.14	59,59,59,59	0
56	MG	1A	3572	1/1	0.91	0.09	55,55,55,55	0
56	MG	1A	3878	1/1	0.91	0.12	33,33,33,33	0
56	MG	2A	3695	1/1	0.91	0.13	38,38,38,38	0
56	MG	1A	3278	1/1	0.91	0.10	51,51,51,51	0
56	MG	2A	3698	1/1	0.91	0.08	51,51,51,51	0
56	MG	1A	3361	1/1	0.91	0.09	49,49,49,49	0
56	MG	1B	3014	1/1	0.91	0.08	63,63,63,63	0
56	MG	1A	3285	1/1	0.91	0.17	39,39,39,39	0
56	MG	2A	3348	1/1	0.91	0.14	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3708	1/1	0.91	0.10	53,53,53,53	0
56	MG	1A	3597	1/1	0.91	0.15	50,50,50,50	0
56	MG	2A	3001	1/1	0.91	0.15	47,47,47,47	0
56	MG	2A	3006	1/1	0.91	0.24	56,56,56,56	0
56	MG	1A	3484	1/1	0.91	0.11	54,54,54,54	0
56	MG	2A	3018	1/1	0.91	0.14	44,44,44,44	0
56	MG	1A	3756	1/1	0.91	0.09	39,39,39,39	0
56	MG	2A	3366	1/1	0.91	0.08	54,54,54,54	0
56	MG	2a	3054	1/1	0.91	0.14	65,65,65,65	0
56	MG	1A	3089	1/1	0.91	0.12	48,48,48,48	0
56	MG	2A	3378	1/1	0.91	0.12	62,62,62,62	0
56	MG	1A	3904	1/1	0.91	0.12	36,36,36,36	0
56	MG	2A	3731	1/1	0.91	0.14	57,57,57,57	0
56	MG	1A	3189	1/1	0.91	0.23	43,43,43,43	0
56	MG	2A	3734	1/1	0.91	0.11	57,57,57,57	0
56	MG	2A	3384	1/1	0.91	0.11	62,62,62,62	0
56	MG	1a	1701	1/1	0.91	0.24	51,51,51,51	0
56	MG	1A	3489	1/1	0.91	0.11	44,44,44,44	0
56	MG	1A	3192	1/1	0.91	0.12	52,52,52,52	0
56	MG	1B	3034	1/1	0.91	0.11	58,58,58,58	0
56	MG	2A	3398	1/1	0.91	0.23	55,55,55,55	0
56	MG	1a	1707	1/1	0.91	0.35	63,63,63,63	0
56	MG	1a	1708	1/1	0.91	0.20	68,68,68,68	0
56	MG	2A	3063	1/1	0.91	0.17	67,67,67,67	0
56	MG	1A	3505	1/1	0.91	0.10	47,47,47,47	0
56	MG	1a	1710	1/1	0.91	0.35	77,77,77,77	0
56	MG	2A	3420	1/1	0.91	0.14	43,43,43,43	0
56	MG	1D	311	1/1	0.91	0.19	56,56,56,56	0
56	MG	1A	3778	1/1	0.91	0.15	57,57,57,57	0
56	MG	1E	304	1/1	0.91	0.14	55,55,55,55	0
56	MG	2A	3762	1/1	0.91	0.10	52,52,52,52	0
56	MG	1A	3936	1/1	0.91	0.09	31,31,31,31	0
56	MG	1A	3639	1/1	0.91	0.12	41,41,41,41	0
56	MG	1G	3002	1/1	0.91	0.13	56,56,56,56	0
56	MG	2a	3101	1/1	0.91	0.15	56,56,56,56	0
56	MG	1A	3307	1/1	0.91	0.21	45,45,45,45	0
56	MG	1a	1727	1/1	0.91	0.14	49,49,49,49	0
56	MG	2A	3771	1/1	0.91	0.10	39,39,39,39	0
56	MG	2A	3772	1/1	0.91	0.11	53,53,53,53	0
56	MG	1a	1729	1/1	0.91	0.26	61,61,61,61	0
56	MG	1G	3005	1/1	0.91	0.15	66,66,66,66	0
56	MG	2a	3114	1/1	0.91	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
56	MG	2A	3783	1/1	0.91	0.14	58,58,58,58	0
56	MG	2a	3119	1/1	0.91	0.24	71,71,71,71	0
56	MG	2A	3442	1/1	0.91	0.24	50,50,50,50	0
56	MG	1a	1733	1/1	0.91	0.09	58,58,58,58	0
56	MG	2a	3122	1/1	0.91	0.26	73,73,73,73	0
56	MG	2a	3126	1/1	0.91	0.25	69,69,69,69	0
56	MG	1N	201	1/1	0.91	0.34	59,59,59,59	0
56	MG	2A	3801	1/1	0.91	0.09	64,64,64,64	0
56	MG	2a	3129	1/1	0.91	0.14	59,59,59,59	0
56	MG	2A	3455	1/1	0.91	0.25	54,54,54,54	0
56	MG	1A	3787	1/1	0.91	0.11	55,55,55,55	0
56	MG	1A	3955	1/1	0.91	0.10	30,30,30,30	0
56	MG	1A	3788	1/1	0.91	0.17	59,59,59,59	0
56	MG	2A	3465	1/1	0.91	0.25	55,55,55,55	0
56	MG	1A	3966	1/1	0.91	0.14	59,59,59,59	0
56	MG	1A	3096	1/1	0.91	0.19	49,49,49,49	0
56	MG	1A	3100	1/1	0.91	0.14	60,60,60,60	0
56	MG	1A	3016	1/1	0.91	0.18	51,51,51,51	0
56	MG	1A	3124	1/1	0.91	0.22	44,44,44,44	0
56	MG	2A	3472	1/1	0.91	0.18	60,60,60,60	0
56	MG	2A	3823	1/1	0.91	0.10	73,73,73,73	0
56	MG	2a	3165	1/1	0.91	0.10	54,54,54,54	0
56	MG	1a	1757	1/1	0.91	0.14	48,48,48,48	0
56	MG	2A	3475	1/1	0.91	0.10	44,44,44,44	0
56	MG	2A	3152	1/1	0.91	0.10	62,62,62,62	0
56	MG	1A	3649	1/1	0.91	0.10	54,54,54,54	0
56	MG	1A	3232	1/1	0.91	0.15	47,47,47,47	0
56	MG	10	106	1/1	0.91	0.09	65,65,65,65	0
56	MG	2A	3854	1/1	0.91	0.10	77,77,77,77	0
56	MG	1A	3539	1/1	0.91	0.07	49,49,49,49	0
56	MG	2A	3172	1/1	0.91	0.09	47,47,47,47	0
56	MG	2A	3174	1/1	0.91	0.10	53,53,53,53	0
56	MG	2a	3194	1/1	0.91	0.16	68,68,68,68	0
56	MG	1A	4002	1/1	0.91	0.17	33,33,33,33	0
56	MG	1A	4006	1/1	0.91	0.08	76,76,76,76	0
56	MG	2A	3183	1/1	0.91	0.11	56,56,56,56	0
56	MG	2A	3518	1/1	0.91	0.12	52,52,52,52	0
56	MG	16	104	1/1	0.91	0.18	53,53,53,53	0
56	MG	2A	3189	1/1	0.91	0.10	52,52,52,52	0
56	MG	2A	3531	1/1	0.91	0.12	51,51,51,51	0
56	MG	2A	3532	1/1	0.91	0.24	65,65,65,65	0
56	MG	2a	3208	1/1	0.91	0.14	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3203	1/1	0.91	0.11	46,46,46,46	0
56	MG	2A	3890	1/1	0.91	0.12	61,61,61,61	0
56	MG	17	101	1/1	0.91	0.13	54,54,54,54	0
56	MG	2a	3215	1/1	0.91	0.17	71,71,71,71	0
56	MG	2a	3218	1/1	0.91	0.16	61,61,61,61	0
56	MG	1A	3822	1/1	0.91	0.10	48,48,48,48	0
56	MG	2A	3894	1/1	0.91	0.12	55,55,55,55	0
56	MG	1A	3420	1/1	0.91	0.21	55,55,55,55	0
56	MG	2A	3910	1/1	0.91	0.18	57,57,57,57	0
56	MG	2A	3224	1/1	0.91	0.12	52,52,52,52	0
56	MG	1A	3053	1/1	0.91	0.12	52,52,52,52	0
56	MG	1A	3247	1/1	0.91	0.12	58,58,58,58	0
56	MG	1A	3425	1/1	0.91	0.10	55,55,55,55	0
56	MG	1A	3058	1/1	0.91	0.11	54,54,54,54	0
56	MG	1A	4036	1/1	0.91	0.09	43,43,43,43	0
56	MG	1a	1813	1/1	0.91	0.14	58,58,58,58	0
56	MG	1A	3552	1/1	0.91	0.14	60,60,60,60	0
56	MG	1A	3148	1/1	0.91	0.23	48,48,48,48	0
56	MG	2a	3235	1/1	0.91	0.12	71,71,71,71	0
56	MG	1a	1828	1/1	0.91	0.12	59,59,59,59	0
56	MG	1A	4052	1/1	0.91	0.10	31,31,31,31	0
56	MG	2A	3592	1/1	0.91	0.20	57,57,57,57	0
56	MG	1A	3696	1/1	0.91	0.11	61,61,61,61	0
56	MG	1A	3698	1/1	0.91	0.11	73,73,73,73	0
56	MG	1A	3328	1/1	0.91	0.16	64,64,64,64	0
56	MG	2e	3001	1/1	0.91	0.11	79,79,79,79	0
56	MG	2D	305	1/1	0.91	0.17	50,50,50,50	0
56	MG	2E	306	1/1	0.91	0.15	67,67,67,67	0
56	MG	1A	3844	1/1	0.91	0.12	54,54,54,54	0
56	MG	1A	3848	1/1	0.91	0.10	56,56,56,56	0
56	MG	1A	3261	1/1	0.91	0.17	55,55,55,55	0
56	MG	1A	3851	1/1	0.91	0.16	62,62,62,62	0
56	MG	2T	3002	1/1	0.91	0.12	58,58,58,58	0
56	MG	2A	3287	1/1	0.91	0.14	55,55,55,55	0
56	MG	1A	3333	1/1	0.91	0.17	52,52,52,52	0
56	MG	1A	3854	1/1	0.91	0.10	51,51,51,51	0
56	MG	2Y	502	1/1	0.91	0.18	54,54,54,54	0
56	MG	2A	3622	1/1	0.91	0.25	63,63,63,63	0
56	MG	1a	1639	1/1	0.91	0.13	62,62,62,62	0
56	MG	1A	3152	1/1	0.91	0.12	55,55,55,55	0
56	MG	1a	1642	1/1	0.91	0.28	67,67,67,67	0
56	MG	1A	3565	1/1	0.91	0.27	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3306	1/1	0.91	0.10	58,58,58,58	0
56	MG	2y	3003	1/1	0.91	0.14	70,70,70,70	0
56	MG	1A	3266	1/1	0.91	0.08	52,52,52,52	0
56	MG	2A	3308	1/1	0.91	0.10	49,49,49,49	0
56	MG	2A	3312	1/1	0.91	0.11	51,51,51,51	0
56	MG	2A	3493	1/1	0.92	0.20	53,53,53,53	0
56	MG	1A	3582	1/1	0.92	0.22	54,54,54,54	0
56	MG	2B	3012	1/1	0.92	0.10	55,55,55,55	0
56	MG	1A	3419	1/1	0.92	0.31	60,60,60,60	0
56	MG	2A	3155	1/1	0.92	0.08	59,59,59,59	0
56	MG	1W	201	1/1	0.92	0.23	57,57,57,57	0
56	MG	1A	3710	1/1	0.92	0.17	68,68,68,68	0
56	MG	1A	4010	1/1	0.92	0.08	26,26,26,26	0
56	MG	2A	3508	1/1	0.92	0.09	60,60,60,60	0
56	MG	2D	301	1/1	0.92	0.10	57,57,57,57	0
56	MG	10	105	1/1	0.92	0.17	70,70,70,70	0
56	MG	2E	302	1/1	0.92	0.09	52,52,52,52	0
56	MG	2E	303	1/1	0.92	0.10	49,49,49,49	0
56	MG	1A	3088	1/1	0.92	0.09	47,47,47,47	0
56	MG	2A	3175	1/1	0.92	0.15	65,65,65,65	0
56	MG	1a	1761	1/1	0.92	0.10	64,64,64,64	0
56	MG	2A	3530	1/1	0.92	0.11	37,37,37,37	0
56	MG	2Q	3001	1/1	0.92	0.09	50,50,50,50	0
56	MG	11	101	1/1	0.92	0.07	38,38,38,38	0
56	MG	2A	3180	1/1	0.92	0.13	51,51,51,51	0
56	MG	2A	3534	1/1	0.92	0.09	40,40,40,40	0
56	MG	1A	4019	1/1	0.92	0.12	42,42,42,42	0
56	MG	2W	201	1/1	0.92	0.14	57,57,57,57	0
56	MG	1A	3712	1/1	0.92	0.06	40,40,40,40	0
56	MG	2W	203	1/1	0.92	0.12	59,59,59,59	0
56	MG	2A	3539	1/1	0.92	0.11	62,62,62,62	0
56	MG	1A	3596	1/1	0.92	0.14	51,51,51,51	0
56	MG	20	3001	1/1	0.92	0.14	59,59,59,59	0
56	MG	2A	3195	1/1	0.92	0.10	56,56,56,56	0
56	MG	25	105	1/1	0.92	0.11	58,58,58,58	0
56	MG	27	101	1/1	0.92	0.15	51,51,51,51	0
56	MG	2A	3197	1/1	0.92	0.27	57,57,57,57	0
56	MG	2A	3198	1/1	0.92	0.09	61,61,61,61	0
56	MG	2a	3004	1/1	0.92	0.21	57,57,57,57	0
56	MG	1a	1771	1/1	0.92	0.10	70,70,70,70	0
56	MG	1A	3840	1/1	0.92	0.11	63,63,63,63	0
56	MG	2A	3555	1/1	0.92	0.10	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3556	1/1	0.92	0.14	43,43,43,43	0
56	MG	2A	3560	1/1	0.92	0.12	63,63,63,63	0
56	MG	2A	3209	1/1	0.92	0.12	61,61,61,61	0
56	MG	2A	3217	1/1	0.92	0.24	64,64,64,64	0
56	MG	1A	3310	1/1	0.92	0.15	40,40,40,40	0
56	MG	18	102	1/1	0.92	0.16	50,50,50,50	0
56	MG	1a	1782	1/1	0.92	0.09	79,79,79,79	0
56	MG	2A	3226	1/1	0.92	0.08	58,58,58,58	0
56	MG	2A	3227	1/1	0.92	0.23	57,57,57,57	0
56	MG	1a	1783	1/1	0.92	0.13	83,83,83,83	0
56	MG	2A	3597	1/1	0.92	0.28	61,61,61,61	0
56	MG	2A	3599	1/1	0.92	0.08	51,51,51,51	0
56	MG	2a	3022	1/1	0.92	0.12	72,72,72,72	0
56	MG	1A	3724	1/1	0.92	0.12	58,58,58,58	0
56	MG	1A	3224	1/1	0.92	0.13	50,50,50,50	0
56	MG	2A	3241	1/1	0.92	0.19	56,56,56,56	0
56	MG	1A	4047	1/1	0.92	0.14	50,50,50,50	0
56	MG	2A	3252	1/1	0.92	0.14	52,52,52,52	0
56	MG	1A	3729	1/1	0.92	0.09	42,42,42,42	0
56	MG	1A	3852	1/1	0.92	0.08	33,33,33,33	0
56	MG	1A	3267	1/1	0.92	0.09	57,57,57,57	0
56	MG	1A	4054	1/1	0.92	0.11	81,81,81,81	0
56	MG	1A	3004	1/1	0.92	0.10	34,34,34,34	0
56	MG	2A	3620	1/1	0.92	0.21	65,65,65,65	0
56	MG	2a	3038	1/1	0.92	0.09	68,68,68,68	0
56	MG	2A	3262	1/1	0.92	0.11	57,57,57,57	0
56	MG	1a	1815	1/1	0.92	0.06	64,64,64,64	0
56	MG	1a	1818	1/1	0.92	0.09	54,54,54,54	0
56	MG	1A	3735	1/1	0.92	0.12	41,41,41,41	0
56	MG	2A	3637	1/1	0.92	0.09	42,42,42,42	0
56	MG	2a	3049	1/1	0.92	0.19	55,55,55,55	0
56	MG	2A	3640	1/1	0.92	0.15	45,45,45,45	0
56	MG	2A	3269	1/1	0.92	0.12	53,53,53,53	0
56	MG	1A	3614	1/1	0.92	0.08	39,39,39,39	0
56	MG	2A	3275	1/1	0.92	0.16	58,58,58,58	0
56	MG	1A	3861	1/1	0.92	0.11	33,33,33,33	0
56	MG	1A	3743	1/1	0.92	0.15	60,60,60,60	0
56	MG	2A	3653	1/1	0.92	0.22	58,58,58,58	0
56	MG	1a	1622	1/1	0.92	0.24	62,62,62,62	0
56	MG	1A	3526	1/1	0.92	0.14	53,53,53,53	0
56	MG	1A	3527	1/1	0.92	0.12	40,40,40,40	0
56	MG	1A	3746	1/1	0.92	0.16	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3661	1/1	0.92	0.11	56,56,56,56	0
56	MG	1a	1628	1/1	0.92	0.16	58,58,58,58	0
56	MG	1s	101	1/1	0.92	0.14	65,65,65,65	0
56	MG	2A	3670	1/1	0.92	0.14	70,70,70,70	0
56	MG	2A	3300	1/1	0.92	0.21	55,55,55,55	0
56	MG	2a	3073	1/1	0.92	0.09	66,66,66,66	0
56	MG	2A	3682	1/1	0.92	0.12	70,70,70,70	0
56	MG	1A	3240	1/1	0.92	0.08	35,35,35,35	0
56	MG	1A	3631	1/1	0.92	0.08	32,32,32,32	0
56	MG	1a	1631	1/1	0.92	0.21	54,54,54,54	0
56	MG	1A	3242	1/1	0.92	0.10	43,43,43,43	0
56	MG	1a	1635	1/1	0.92	0.34	75,75,75,75	0
56	MG	1A	3367	1/1	0.92	0.12	57,57,57,57	0
56	MG	2A	3694	1/1	0.92	0.10	51,51,51,51	0
56	MG	2A	3309	1/1	0.92	0.10	53,53,53,53	0
56	MG	2A	3310	1/1	0.92	0.21	62,62,62,62	0
56	MG	1a	1637	1/1	0.92	0.23	68,68,68,68	0
56	MG	1A	3882	1/1	0.92	0.11	36,36,36,36	0
56	MG	1A	3884	1/1	0.92	0.13	48,48,48,48	0
56	MG	1A	3762	1/1	0.92	0.09	60,60,60,60	0
56	MG	1a	1643	1/1	0.92	0.21	61,61,61,61	0
56	MG	1A	4125	1/1	0.92	0.19	54,54,54,54	0
56	MG	2a	3105	1/1	0.92	0.15	45,45,45,45	0
56	MG	1a	1651	1/1	0.92	0.12	56,56,56,56	0
56	MG	1A	3067	1/1	0.92	0.16	51,51,51,51	0
56	MG	1A	3769	1/1	0.92	0.13	29,29,29,29	0
56	MG	1x	110	1/1	0.92	0.11	52,52,52,52	0
56	MG	1B	3003	1/1	0.92	0.15	56,56,56,56	0
56	MG	2a	3115	1/1	0.92	0.14	57,57,57,57	0
56	MG	2A	3334	1/1	0.92	0.25	64,64,64,64	0
56	MG	1A	3445	1/1	0.92	0.31	62,62,62,62	0
56	MG	1A	3298	1/1	0.92	0.09	43,43,43,43	0
56	MG	2A	3339	1/1	0.92	0.11	51,51,51,51	0
56	MG	1A	3900	1/1	0.92	0.15	44,44,44,44	0
56	MG	2a	3124	1/1	0.92	0.20	61,61,61,61	0
56	MG	1A	3450	1/1	0.92	0.14	57,57,57,57	0
56	MG	1a	1671	1/1	0.92	0.25	66,66,66,66	0
56	MG	1A	3169	1/1	0.92	0.21	55,55,55,55	0
56	MG	1B	3017	1/1	0.92	0.18	50,50,50,50	0
56	MG	1A	3779	1/1	0.92	0.11	56,56,56,56	0
56	MG	1A	3465	1/1	0.92	0.14	60,60,60,60	0
56	MG	2a	3132	1/1	0.92	0.24	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1679	1/1	0.92	0.10	73,73,73,73	0
56	MG	2A	3742	1/1	0.92	0.10	49,49,49,49	0
56	MG	1a	1681	1/1	0.92	0.14	54,54,54,54	0
56	MG	2A	3359	1/1	0.92	0.09	56,56,56,56	0
56	MG	2A	3017	1/1	0.92	0.21	52,52,52,52	0
56	MG	1A	3382	1/1	0.92	0.11	54,54,54,54	0
56	MG	1B	3022	1/1	0.92	0.15	60,60,60,60	0
56	MG	2a	3149	1/1	0.92	0.08	56,56,56,56	0
56	MG	2a	3151	1/1	0.92	0.09	78,78,78,78	0
56	MG	2a	3152	1/1	0.92	0.08	67,67,67,67	0
56	MG	2A	3751	1/1	0.92	0.11	61,61,61,61	0
56	MG	2A	3365	1/1	0.92	0.12	56,56,56,56	0
56	MG	1A	3302	1/1	0.92	0.21	56,56,56,56	0
56	MG	2A	3367	1/1	0.92	0.21	61,61,61,61	0
56	MG	1A	3392	1/1	0.92	0.16	56,56,56,56	0
56	MG	2A	3376	1/1	0.92	0.11	58,58,58,58	0
56	MG	1A	3682	1/1	0.92	0.12	35,35,35,35	0
56	MG	1A	3399	1/1	0.92	0.10	52,52,52,52	0
56	MG	1a	1695	1/1	0.92	0.41	68,68,68,68	0
56	MG	1B	3030	1/1	0.92	0.12	59,59,59,59	0
56	MG	2a	3185	1/1	0.92	0.10	47,47,47,47	0
56	MG	1a	1697	1/1	0.92	0.18	63,63,63,63	0
56	MG	1A	3947	1/1	0.92	0.08	44,44,44,44	0
56	MG	2A	3060	1/1	0.92	0.19	53,53,53,53	0
56	MG	2A	3394	1/1	0.92	0.16	50,50,50,50	0
56	MG	2A	3396	1/1	0.92	0.08	56,56,56,56	0
56	MG	1B	3033	1/1	0.92	0.11	56,56,56,56	0
56	MG	1a	1703	1/1	0.92	0.30	55,55,55,55	0
56	MG	2A	3404	1/1	0.92	0.07	53,53,53,53	0
56	MG	1A	3798	1/1	0.92	0.08	63,63,63,63	0
56	MG	2A	3797	1/1	0.92	0.13	52,52,52,52	0
56	MG	1A	3686	1/1	0.92	0.11	35,35,35,35	0
56	MG	1A	3476	1/1	0.92	0.13	52,52,52,52	0
56	MG	2A	3067	1/1	0.92	0.09	57,57,57,57	0
56	MG	2A	3068	1/1	0.92	0.11	56,56,56,56	0
56	MG	2A	3071	1/1	0.92	0.10	52,52,52,52	0
56	MG	2A	3072	1/1	0.92	0.07	46,46,46,46	0
56	MG	2A	3422	1/1	0.92	0.10	58,58,58,58	0
56	MG	2A	3811	1/1	0.92	0.08	47,47,47,47	0
56	MG	2A	3074	1/1	0.92	0.18	73,73,73,73	0
56	MG	1A	3689	1/1	0.92	0.12	51,51,51,51	0
56	MG	2A	3088	1/1	0.92	0.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3816	1/1	0.92	0.16	57,57,57,57	0
56	MG	2a	3222	1/1	0.92	0.14	63,63,63,63	0
56	MG	2A	3427	1/1	0.92	0.07	45,45,45,45	0
56	MG	1A	3963	1/1	0.92	0.15	60,60,60,60	0
56	MG	1A	3404	1/1	0.92	0.16	59,59,59,59	0
56	MG	2A	3430	1/1	0.92	0.07	51,51,51,51	0
56	MG	2A	3432	1/1	0.92	0.11	60,60,60,60	0
56	MG	2A	3434	1/1	0.92	0.11	59,59,59,59	0
56	MG	1A	3808	1/1	0.92	0.10	36,36,36,36	0
56	MG	2A	3097	1/1	0.92	0.07	56,56,56,56	0
56	MG	1a	1713	1/1	0.92	0.09	68,68,68,68	0
56	MG	1F	308	1/1	0.92	0.14	53,53,53,53	0
56	MG	1A	3483	1/1	0.92	0.09	46,46,46,46	0
56	MG	2A	3106	1/1	0.92	0.14	59,59,59,59	0
56	MG	2A	3448	1/1	0.92	0.17	49,49,49,49	0
56	MG	2A	3450	1/1	0.92	0.21	50,50,50,50	0
56	MG	2A	3108	1/1	0.92	0.18	44,44,44,44	0
56	MG	2A	3864	1/1	0.92	0.08	63,63,63,63	0
56	MG	1A	3980	1/1	0.92	0.10	74,74,74,74	0
56	MG	2A	3456	1/1	0.92	0.26	60,60,60,60	0
56	MG	2A	3457	1/1	0.92	0.23	57,57,57,57	0
56	MG	2A	3111	1/1	0.92	0.14	54,54,54,54	0
56	MG	1A	3982	1/1	0.92	0.12	29,29,29,29	0
56	MG	2A	3461	1/1	0.92	0.25	52,52,52,52	0
56	MG	2A	3115	1/1	0.92	0.22	51,51,51,51	0
56	MG	1A	3206	1/1	0.92	0.15	55,55,55,55	0
56	MG	1a	1723	1/1	0.92	0.26	61,61,61,61	0
56	MG	1A	3181	1/1	0.92	0.18	54,54,54,54	0
56	MG	1O	204	1/1	0.92	0.21	58,58,58,58	0
56	MG	1A	3342	1/1	0.92	0.13	57,57,57,57	0
56	MG	1A	3996	1/1	0.92	0.07	43,43,43,43	0
56	MG	1Q	203	1/1	0.92	0.12	64,64,64,64	0
56	MG	1A	3573	1/1	0.92	0.20	60,60,60,60	0
56	MG	1S	3001	1/1	0.92	0.22	51,51,51,51	0
56	MG	1A	3006	1/1	0.92	0.19	57,57,57,57	0
56	MG	2A	3479	1/1	0.92	0.29	54,54,54,54	0
56	MG	2y	3001	1/1	0.92	0.15	59,59,59,59	0
56	MG	1A	4001	1/1	0.92	0.10	17,17,17,17	0
56	MG	2B	3005	1/1	0.92	0.07	53,53,53,53	0
56	MG	2A	3482	1/1	0.92	0.24	63,63,63,63	0
56	MG	2A	3487	1/1	0.92	0.25	62,62,62,62	0
56	MG	2A	3150	1/1	0.92	0.20	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3446	1/1	0.93	0.21	45,45,45,45	0
56	MG	1A	3733	1/1	0.93	0.07	52,52,52,52	0
56	MG	1A	3047	1/1	0.93	0.05	21,21,21,21	0
56	MG	2A	3449	1/1	0.93	0.24	47,47,47,47	0
56	MG	1A	3885	1/1	0.93	0.10	37,37,37,37	0
56	MG	2A	3452	1/1	0.93	0.19	42,42,42,42	0
56	MG	1A	3886	1/1	0.93	0.11	57,57,57,57	0
56	MG	2A	3454	1/1	0.93	0.14	58,58,58,58	0
56	MG	2A	3908	1/1	0.93	0.15	44,44,44,44	0
56	MG	1a	1706	1/1	0.93	0.26	60,60,60,60	0
56	MG	1A	3251	1/1	0.93	0.08	58,58,58,58	0
56	MG	1A	3589	1/1	0.93	0.11	52,52,52,52	0
56	MG	1A	3892	1/1	0.93	0.09	39,39,39,39	0
56	MG	1A	3590	1/1	0.93	0.15	37,37,37,37	0
56	MG	1a	1711	1/1	0.93	0.17	65,65,65,65	0
56	MG	2A	3462	1/1	0.93	0.23	59,59,59,59	0
56	MG	1A	3592	1/1	0.93	0.13	21,21,21,21	0
56	MG	2A	3127	1/1	0.93	0.07	50,50,50,50	0
56	MG	2B	3009	1/1	0.93	0.19	61,61,61,61	0
56	MG	1A	3594	1/1	0.93	0.10	31,31,31,31	0
56	MG	1A	3473	1/1	0.93	0.19	50,50,50,50	0
56	MG	1A	3094	1/1	0.93	0.14	52,52,52,52	0
56	MG	1A	3753	1/1	0.93	0.15	34,34,34,34	0
56	MG	1A	3385	1/1	0.93	0.18	58,58,58,58	0
56	MG	2A	3143	1/1	0.93	0.17	56,56,56,56	0
56	MG	1A	3906	1/1	0.93	0.11	51,51,51,51	0
56	MG	1D	302	1/1	0.93	0.19	55,55,55,55	0
56	MG	1A	3907	1/1	0.93	0.15	54,54,54,54	0
56	MG	2A	3478	1/1	0.93	0.09	50,50,50,50	0
56	MG	1A	3908	1/1	0.93	0.26	65,65,65,65	0
56	MG	1A	3256	1/1	0.93	0.08	57,57,57,57	0
56	MG	2A	3161	1/1	0.93	0.13	44,44,44,44	0
56	MG	2A	3484	1/1	0.93	0.11	53,53,53,53	0
56	MG	2A	3485	1/1	0.93	0.17	63,63,63,63	0
56	MG	1E	305	1/1	0.93	0.21	57,57,57,57	0
56	MG	2F	302	1/1	0.93	0.12	53,53,53,53	0
56	MG	1A	3190	1/1	0.93	0.15	39,39,39,39	0
56	MG	2A	3492	1/1	0.93	0.10	54,54,54,54	0
56	MG	2A	3170	1/1	0.93	0.23	54,54,54,54	0
56	MG	2A	3494	1/1	0.93	0.22	50,50,50,50	0
56	MG	1A	3759	1/1	0.93	0.11	24,24,24,24	0
56	MG	1a	1737	1/1	0.93	0.12	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2V	201	1/1	0.93	0.08	53,53,53,53	0
56	MG	1F	307	1/1	0.93	0.09	50,50,50,50	0
56	MG	1A	3923	1/1	0.93	0.07	47,47,47,47	0
56	MG	1A	3095	1/1	0.93	0.12	55,55,55,55	0
56	MG	1G	3003	1/1	0.93	0.09	66,66,66,66	0
56	MG	2A	3179	1/1	0.93	0.10	59,59,59,59	0
56	MG	1A	3613	1/1	0.93	0.07	33,33,33,33	0
56	MG	2A	3516	1/1	0.93	0.17	56,56,56,56	0
56	MG	2A	3182	1/1	0.93	0.11	42,42,42,42	0
56	MG	1A	3197	1/1	0.93	0.08	52,52,52,52	0
56	MG	28	101	1/1	0.93	0.10	53,53,53,53	0
56	MG	1I	3001	1/1	0.93	0.12	70,70,70,70	0
56	MG	2a	3001	1/1	0.93	0.11	57,57,57,57	0
56	MG	2A	3528	1/1	0.93	0.15	57,57,57,57	0
56	MG	1A	3943	1/1	0.93	0.08	81,81,81,81	0
56	MG	2A	3194	1/1	0.93	0.23	67,67,67,67	0
56	MG	1N	204	1/1	0.93	0.20	64,64,64,64	0
56	MG	1a	1758	1/1	0.93	0.08	56,56,56,56	0
56	MG	1a	1759	1/1	0.93	0.14	64,64,64,64	0
56	MG	2A	3202	1/1	0.93	0.17	56,56,56,56	0
56	MG	1N	205	1/1	0.93	0.18	57,57,57,57	0
56	MG	2A	3205	1/1	0.93	0.23	52,52,52,52	0
56	MG	1A	3944	1/1	0.93	0.08	60,60,60,60	0
56	MG	1O	202	1/1	0.93	0.13	67,67,67,67	0
56	MG	2A	3210	1/1	0.93	0.09	47,47,47,47	0
56	MG	1A	3616	1/1	0.93	0.10	40,40,40,40	0
56	MG	2A	3552	1/1	0.93	0.10	59,59,59,59	0
56	MG	1A	3265	1/1	0.93	0.21	63,63,63,63	0
56	MG	1A	3494	1/1	0.93	0.09	39,39,39,39	0
56	MG	1A	3625	1/1	0.93	0.07	19,19,19,19	0
56	MG	2A	3225	1/1	0.93	0.13	62,62,62,62	0
56	MG	2A	3561	1/1	0.93	0.09	62,62,62,62	0
56	MG	1Q	205	1/1	0.93	0.12	39,39,39,39	0
56	MG	2a	3027	1/1	0.93	0.09	61,61,61,61	0
56	MG	1a	1774	1/1	0.93	0.09	60,60,60,60	0
56	MG	1A	3959	1/1	0.93	0.12	56,56,56,56	0
56	MG	1a	1777	1/1	0.93	0.16	55,55,55,55	0
56	MG	2A	3231	1/1	0.93	0.10	49,49,49,49	0
56	MG	2A	3235	1/1	0.93	0.15	50,50,50,50	0
56	MG	2A	3588	1/1	0.93	0.06	47,47,47,47	0
56	MG	2A	3238	1/1	0.93	0.17	56,56,56,56	0
56	MG	1A	3146	1/1	0.93	0.13	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1S	3002	1/1	0.93	0.08	49,49,49,49	0
56	MG	2A	3244	1/1	0.93	0.10	54,54,54,54	0
56	MG	1A	3782	1/1	0.93	0.15	25,25,25,25	0
56	MG	2A	3247	1/1	0.93	0.10	51,51,51,51	0
56	MG	2a	3042	1/1	0.93	0.26	58,58,58,58	0
56	MG	1A	3409	1/1	0.93	0.27	60,60,60,60	0
56	MG	2a	3045	1/1	0.93	0.12	65,65,65,65	0
56	MG	2A	3254	1/1	0.93	0.17	53,53,53,53	0
56	MG	1a	1788	1/1	0.93	0.08	69,69,69,69	0
56	MG	1A	3969	1/1	0.93	0.09	66,66,66,66	0
56	MG	1U	203	1/1	0.93	0.24	42,42,42,42	0
56	MG	2A	3258	1/1	0.93	0.20	58,58,58,58	0
56	MG	2a	3052	1/1	0.93	0.11	62,62,62,62	0
56	MG	1a	1793	1/1	0.93	0.09	82,82,82,82	0
56	MG	1A	3784	1/1	0.93	0.07	39,39,39,39	0
56	MG	1A	3506	1/1	0.93	0.07	42,42,42,42	0
56	MG	1X	105	1/1	0.93	0.07	47,47,47,47	0
56	MG	2A	3623	1/1	0.93	0.11	48,48,48,48	0
56	MG	1a	1798	1/1	0.93	0.12	56,56,56,56	0
56	MG	2a	3060	1/1	0.93	0.08	63,63,63,63	0
56	MG	2a	3061	1/1	0.93	0.16	54,54,54,54	0
56	MG	2A	3267	1/1	0.93	0.18	58,58,58,58	0
56	MG	2A	3630	1/1	0.93	0.13	69,69,69,69	0
56	MG	1A	3509	1/1	0.93	0.09	45,45,45,45	0
56	MG	1A	3410	1/1	0.93	0.09	57,57,57,57	0
56	MG	2A	3270	1/1	0.93	0.10	53,53,53,53	0
56	MG	1A	3002	1/1	0.93	0.10	59,59,59,59	0
56	MG	2A	3643	1/1	0.93	0.08	34,34,34,34	0
56	MG	2A	3272	1/1	0.93	0.12	51,51,51,51	0
56	MG	1A	3087	1/1	0.93	0.15	32,32,32,32	0
56	MG	2a	3075	1/1	0.93	0.17	49,49,49,49	0
56	MG	2A	3278	1/1	0.93	0.10	57,57,57,57	0
56	MG	2a	3078	1/1	0.93	0.22	74,74,74,74	0
56	MG	2a	3080	1/1	0.93	0.08	50,50,50,50	0
56	MG	1a	1823	1/1	0.93	0.12	68,68,68,68	0
56	MG	1A	3330	1/1	0.93	0.11	50,50,50,50	0
56	MG	2A	3282	1/1	0.93	0.12	63,63,63,63	0
56	MG	2a	3087	1/1	0.93	0.16	63,63,63,63	0
56	MG	1A	3995	1/1	0.93	0.10	73,73,73,73	0
56	MG	13	101	1/1	0.93	0.11	55,55,55,55	0
56	MG	1A	3270	1/1	0.93	0.15	59,59,59,59	0
56	MG	2A	3659	1/1	0.93	0.08	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3288	1/1	0.93	0.07	49,49,49,49	0
56	MG	1b	3001	1/1	0.93	0.07	83,83,83,83	0
56	MG	1b	3002	1/1	0.93	0.13	61,61,61,61	0
56	MG	2a	3097	1/1	0.93	0.14	72,72,72,72	0
56	MG	2A	3294	1/1	0.93	0.09	52,52,52,52	0
56	MG	2A	3671	1/1	0.93	0.07	46,46,46,46	0
56	MG	2A	3672	1/1	0.93	0.14	45,45,45,45	0
56	MG	2A	3673	1/1	0.93	0.13	64,64,64,64	0
56	MG	2A	3674	1/1	0.93	0.13	55,55,55,55	0
56	MG	1A	3659	1/1	0.93	0.06	23,23,23,23	0
56	MG	2A	3299	1/1	0.93	0.10	51,51,51,51	0
56	MG	1A	3999	1/1	0.93	0.12	55,55,55,55	0
56	MG	2a	3109	1/1	0.93	0.27	67,67,67,67	0
56	MG	1A	3422	1/1	0.93	0.14	38,38,38,38	0
56	MG	2A	3303	1/1	0.93	0.09	60,60,60,60	0
56	MG	1A	3666	1/1	0.93	0.10	34,34,34,34	0
56	MG	1A	3154	1/1	0.93	0.20	51,51,51,51	0
56	MG	2a	3116	1/1	0.93	0.18	67,67,67,67	0
56	MG	1A	3810	1/1	0.93	0.14	45,45,45,45	0
56	MG	1A	3813	1/1	0.93	0.14	56,56,56,56	0
56	MG	1A	3814	1/1	0.93	0.15	45,45,45,45	0
56	MG	1w	103	1/1	0.93	0.07	57,57,57,57	0
56	MG	1A	3818	1/1	0.93	0.14	57,57,57,57	0
56	MG	2A	3311	1/1	0.93	0.18	63,63,63,63	0
56	MG	2a	3125	1/1	0.93	0.08	65,65,65,65	0
56	MG	1A	3334	1/1	0.93	0.20	56,56,56,56	0
56	MG	1a	1606	1/1	0.93	0.11	65,65,65,65	0
56	MG	1A	3537	1/1	0.93	0.11	49,49,49,49	0
56	MG	2A	3705	1/1	0.93	0.12	57,57,57,57	0
56	MG	1A	3538	1/1	0.93	0.12	54,54,54,54	0
56	MG	1A	3684	1/1	0.93	0.10	32,32,32,32	0
56	MG	1a	1615	1/1	0.93	0.09	67,67,67,67	0
56	MG	2A	3325	1/1	0.93	0.10	63,63,63,63	0
56	MG	1A	3340	1/1	0.93	0.19	58,58,58,58	0
56	MG	2a	3137	1/1	0.93	0.08	79,79,79,79	0
56	MG	2A	3327	1/1	0.93	0.10	50,50,50,50	0
56	MG	1A	3426	1/1	0.93	0.14	50,50,50,50	0
56	MG	2a	3142	1/1	0.93	0.10	74,74,74,74	0
56	MG	1A	3101	1/1	0.93	0.11	44,44,44,44	0
56	MG	1A	4046	1/1	0.93	0.07	30,30,30,30	0
56	MG	1A	3431	1/1	0.93	0.14	52,52,52,52	0
56	MG	1A	3690	1/1	0.93	0.06	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3281	1/1	0.93	0.11	50,50,50,50	0
56	MG	1a	1626	1/1	0.93	0.15	61,61,61,61	0
56	MG	2a	3153	1/1	0.93	0.09	74,74,74,74	0
56	MG	2A	3337	1/1	0.93	0.10	47,47,47,47	0
56	MG	1A	3436	1/1	0.93	0.10	45,45,45,45	0
56	MG	2a	3158	1/1	0.93	0.08	52,52,52,52	0
56	MG	1A	3438	1/1	0.93	0.13	50,50,50,50	0
56	MG	1A	3839	1/1	0.93	0.09	66,66,66,66	0
56	MG	1A	3219	1/1	0.93	0.09	37,37,37,37	0
56	MG	2A	3343	1/1	0.93	0.09	57,57,57,57	0
56	MG	2A	3344	1/1	0.93	0.12	55,55,55,55	0
56	MG	1A	3064	1/1	0.93	0.14	53,53,53,53	0
56	MG	1A	3231	1/1	0.93	0.19	51,51,51,51	0
56	MG	1A	4067	1/1	0.93	0.08	56,56,56,56	0
56	MG	2A	3349	1/1	0.93	0.12	58,58,58,58	0
56	MG	1A	3352	1/1	0.93	0.18	64,64,64,64	0
56	MG	1A	3301	1/1	0.93	0.10	54,54,54,54	0
56	MG	2A	3004	1/1	0.93	0.14	48,48,48,48	0
56	MG	1A	3448	1/1	0.93	0.19	59,59,59,59	0
56	MG	1A	3114	1/1	0.93	0.16	57,57,57,57	0
56	MG	2A	3010	1/1	0.93	0.14	51,51,51,51	0
56	MG	1A	3454	1/1	0.93	0.08	59,59,59,59	0
56	MG	2A	3760	1/1	0.93	0.19	58,58,58,58	0
56	MG	2A	3761	1/1	0.93	0.17	46,46,46,46	0
56	MG	1A	3570	1/1	0.93	0.08	54,54,54,54	0
56	MG	2a	3202	1/1	0.93	0.14	64,64,64,64	0
56	MG	1a	1648	1/1	0.93	0.11	59,59,59,59	0
56	MG	2A	3024	1/1	0.93	0.11	49,49,49,49	0
56	MG	2A	3369	1/1	0.93	0.10	47,47,47,47	0
56	MG	2a	3207	1/1	0.93	0.12	74,74,74,74	0
56	MG	2A	3768	1/1	0.93	0.10	62,62,62,62	0
56	MG	2A	3370	1/1	0.93	0.15	50,50,50,50	0
56	MG	2A	3372	1/1	0.93	0.17	41,41,41,41	0
56	MG	2a	3211	1/1	0.93	0.17	61,61,61,61	0
56	MG	2A	3029	1/1	0.93	0.11	44,44,44,44	0
56	MG	2A	3035	1/1	0.93	0.07	31,31,31,31	0
56	MG	1A	4087	1/1	0.93	0.18	54,54,54,54	0
56	MG	2A	3774	1/1	0.93	0.09	51,51,51,51	0
56	MG	2A	3777	1/1	0.93	0.10	41,41,41,41	0
56	MG	1A	4092	1/1	0.93	0.18	37,37,37,37	0
56	MG	2A	3781	1/1	0.93	0.10	55,55,55,55	0
56	MG	2A	3043	1/1	0.93	0.08	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3794	1/1	0.93	0.08	67,67,67,67	0
56	MG	1A	4093	1/1	0.93	0.31	35,35,35,35	0
56	MG	1A	4095	1/1	0.93	0.08	67,67,67,67	0
56	MG	1a	1662	1/1	0.93	0.09	67,67,67,67	0
56	MG	2A	3392	1/1	0.93	0.07	55,55,55,55	0
56	MG	1A	3715	1/1	0.93	0.12	54,54,54,54	0
56	MG	1A	3859	1/1	0.93	0.14	44,44,44,44	0
56	MG	1A	4109	1/1	0.93	0.14	49,49,49,49	0
56	MG	1A	3116	1/1	0.93	0.13	47,47,47,47	0
56	MG	2A	3809	1/1	0.93	0.08	59,59,59,59	0
56	MG	1A	3719	1/1	0.93	0.10	50,50,50,50	0
56	MG	1A	3722	1/1	0.93	0.14	39,39,39,39	0
56	MG	1A	4123	1/1	0.93	0.12	35,35,35,35	0
56	MG	2a	3239	1/1	0.93	0.10	65,65,65,65	0
56	MG	2A	3407	1/1	0.93	0.15	61,61,61,61	0
56	MG	1A	3183	1/1	0.93	0.08	54,54,54,54	0
56	MG	1A	4131	1/1	0.93	0.13	58,58,58,58	0
56	MG	1A	3306	1/1	0.93	0.24	38,38,38,38	0
56	MG	1A	4137	1/1	0.93	0.07	44,44,44,44	0
56	MG	2A	3414	1/1	0.93	0.15	59,59,59,59	0
56	MG	2A	3419	1/1	0.93	0.09	51,51,51,51	0
56	MG	1A	3576	1/1	0.93	0.21	57,57,57,57	0
56	MG	1A	3872	1/1	0.93	0.11	33,33,33,33	0
56	MG	2q	201	1/1	0.93	0.09	76,76,76,76	0
56	MG	2A	3073	1/1	0.93	0.07	36,36,36,36	0
56	MG	1a	1686	1/1	0.93	0.21	54,54,54,54	0
56	MG	2A	3077	1/1	0.93	0.09	45,45,45,45	0
56	MG	2A	3079	1/1	0.93	0.07	41,41,41,41	0
56	MG	1B	3005	1/1	0.93	0.08	55,55,55,55	0
56	MG	1A	3874	1/1	0.93	0.12	40,40,40,40	0
56	MG	2A	3090	1/1	0.93	0.11	60,60,60,60	0
56	MG	1a	1690	1/1	0.93	0.18	70,70,70,70	0
56	MG	2A	3857	1/1	0.93	0.09	47,47,47,47	0
56	MG	1A	3728	1/1	0.93	0.10	26,26,26,26	0
56	MG	2A	3095	1/1	0.93	0.08	39,39,39,39	0
56	MG	2x	103	1/1	0.93	0.09	64,64,64,64	0
56	MG	2x	104	1/1	0.93	0.17	60,60,60,60	0
56	MG	2A	3436	1/1	0.93	0.10	49,49,49,49	0
56	MG	1B	3009	1/1	0.93	0.14	43,43,43,43	0
56	MG	1B	3010	1/1	0.93	0.24	73,73,73,73	0
56	MG	2y	3004	1/1	0.93	0.13	59,59,59,59	0
56	MG	1B	3011	1/1	0.93	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3580	1/1	0.93	0.15	39,39,39,39	0
56	MG	1A	3185	1/1	0.93	0.12	47,47,47,47	0
56	MG	2A	3907	1/1	0.94	0.09	57,57,57,57	0
56	MG	1A	3452	1/1	0.94	0.21	58,58,58,58	0
56	MG	2A	3909	1/1	0.94	0.11	43,43,43,43	0
56	MG	1A	3971	1/1	0.94	0.11	44,44,44,44	0
56	MG	1A	3453	1/1	0.94	0.11	57,57,57,57	0
56	MG	2A	3486	1/1	0.94	0.35	55,55,55,55	0
56	MG	1A	3976	1/1	0.94	0.09	72,72,72,72	0
56	MG	1a	1775	1/1	0.94	0.10	76,76,76,76	0
56	MG	2A	3490	1/1	0.94	0.09	61,61,61,61	0
56	MG	1A	3979	1/1	0.94	0.10	73,73,73,73	0
56	MG	2A	3213	1/1	0.94	0.10	45,45,45,45	0
56	MG	1A	3023	1/1	0.94	0.18	59,59,59,59	0
56	MG	2A	3498	1/1	0.94	0.08	55,55,55,55	0
56	MG	1A	3455	1/1	0.94	0.08	47,47,47,47	0
56	MG	2A	3219	1/1	0.94	0.10	51,51,51,51	0
56	MG	1a	1781	1/1	0.94	0.08	71,71,71,71	0
56	MG	2B	3013	1/1	0.94	0.12	61,61,61,61	0
56	MG	1A	3129	1/1	0.94	0.18	51,51,51,51	0
56	MG	2B	3015	1/1	0.94	0.11	50,50,50,50	0
56	MG	1A	3459	1/1	0.94	0.12	47,47,47,47	0
56	MG	1A	3990	1/1	0.94	0.12	52,52,52,52	0
56	MG	1A	3346	1/1	0.94	0.16	48,48,48,48	0
56	MG	2A	3510	1/1	0.94	0.12	46,46,46,46	0
56	MG	1A	3131	1/1	0.94	0.10	72,72,72,72	0
56	MG	1A	3790	1/1	0.94	0.07	25,25,25,25	0
56	MG	2D	302	1/1	0.94	0.13	51,51,51,51	0
56	MG	2D	304	1/1	0.94	0.22	45,45,45,45	0
56	MG	1A	3467	1/1	0.94	0.08	45,45,45,45	0
56	MG	1A	3194	1/1	0.94	0.20	43,43,43,43	0
56	MG	1Y	502	1/1	0.94	0.17	59,59,59,59	0
56	MG	2A	3522	1/1	0.94	0.09	59,59,59,59	0
56	MG	1A	3627	1/1	0.94	0.15	62,62,62,62	0
56	MG	2A	3529	1/1	0.94	0.07	43,43,43,43	0
56	MG	1Z	301	1/1	0.94	0.11	56,56,56,56	0
56	MG	2G	3001	1/1	0.94	0.11	51,51,51,51	0
56	MG	2A	3242	1/1	0.94	0.11	52,52,52,52	0
56	MG	1A	3351	1/1	0.94	0.19	49,49,49,49	0
56	MG	1a	1804	1/1	0.94	0.08	77,77,77,77	0
56	MG	2A	3246	1/1	0.94	0.08	65,65,65,65	0
56	MG	1a	1806	1/1	0.94	0.09	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3196	1/1	0.94	0.12	59,59,59,59	0
56	MG	2U	203	1/1	0.94	0.20	46,46,46,46	0
56	MG	1A	4003	1/1	0.94	0.08	20,20,20,20	0
56	MG	1A	3637	1/1	0.94	0.11	50,50,50,50	0
56	MG	2A	3543	1/1	0.94	0.06	34,34,34,34	0
56	MG	1A	3353	1/1	0.94	0.25	64,64,64,64	0
56	MG	2X	102	1/1	0.94	0.09	56,56,56,56	0
56	MG	12	101	1/1	0.94	0.11	60,60,60,60	0
56	MG	1A	3134	1/1	0.94	0.10	54,54,54,54	0
56	MG	2A	3550	1/1	0.94	0.15	44,44,44,44	0
56	MG	13	102	1/1	0.94	0.14	53,53,53,53	0
56	MG	23	102	1/1	0.94	0.09	48,48,48,48	0
56	MG	1A	3273	1/1	0.94	0.23	53,53,53,53	0
56	MG	2A	3554	1/1	0.94	0.07	39,39,39,39	0
56	MG	1A	3811	1/1	0.94	0.08	45,45,45,45	0
56	MG	2A	3263	1/1	0.94	0.08	55,55,55,55	0
56	MG	2A	3558	1/1	0.94	0.08	31,31,31,31	0
56	MG	1A	4021	1/1	0.94	0.19	66,66,66,66	0
56	MG	1A	3812	1/1	0.94	0.07	45,45,45,45	0
56	MG	2A	3563	1/1	0.94	0.08	49,49,49,49	0
56	MG	1A	3480	1/1	0.94	0.08	52,52,52,52	0
56	MG	1A	4025	1/1	0.94	0.07	77,77,77,77	0
56	MG	1A	3137	1/1	0.94	0.09	33,33,33,33	0
56	MG	2A	3574	1/1	0.94	0.08	44,44,44,44	0
56	MG	2a	3011	1/1	0.94	0.22	64,64,64,64	0
56	MG	2A	3576	1/1	0.94	0.12	39,39,39,39	0
56	MG	1A	4029	1/1	0.94	0.07	53,53,53,53	0
56	MG	1A	4032	1/1	0.94	0.09	68,68,68,68	0
56	MG	2A	3580	1/1	0.94	0.12	49,49,49,49	0
56	MG	1A	3647	1/1	0.94	0.08	29,29,29,29	0
56	MG	2A	3586	1/1	0.94	0.12	53,53,53,53	0
56	MG	2A	3274	1/1	0.94	0.20	53,53,53,53	0
56	MG	1a	1604	1/1	0.94	0.10	58,58,58,58	0
56	MG	2A	3591	1/1	0.94	0.07	50,50,50,50	0
56	MG	2A	3276	1/1	0.94	0.10	55,55,55,55	0
56	MG	1A	3280	1/1	0.94	0.10	50,50,50,50	0
56	MG	1A	3076	1/1	0.94	0.19	53,53,53,53	0
56	MG	1a	1607	1/1	0.94	0.22	67,67,67,67	0
56	MG	1A	3652	1/1	0.94	0.08	31,31,31,31	0
56	MG	1A	3658	1/1	0.94	0.12	37,37,37,37	0
56	MG	1A	3825	1/1	0.94	0.11	57,57,57,57	0
56	MG	1A	4051	1/1	0.94	0.09	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3369	1/1	0.94	0.13	57,57,57,57	0
56	MG	2A	3289	1/1	0.94	0.09	47,47,47,47	0
56	MG	2A	3611	1/1	0.94	0.11	62,62,62,62	0
56	MG	1A	3660	1/1	0.94	0.17	31,31,31,31	0
56	MG	1A	3207	1/1	0.94	0.13	54,54,54,54	0
56	MG	2A	3616	1/1	0.94	0.08	46,46,46,46	0
56	MG	2A	3617	1/1	0.94	0.10	38,38,38,38	0
56	MG	2A	3292	1/1	0.94	0.09	54,54,54,54	0
56	MG	1A	3491	1/1	0.94	0.12	59,59,59,59	0
56	MG	2a	3041	1/1	0.94	0.19	50,50,50,50	0
56	MG	1x	105	1/1	0.94	0.10	62,62,62,62	0
56	MG	2a	3043	1/1	0.94	0.10	64,64,64,64	0
56	MG	1A	3493	1/1	0.94	0.09	36,36,36,36	0
56	MG	1x	107	1/1	0.94	0.07	61,61,61,61	0
56	MG	1A	4062	1/1	0.94	0.06	14,14,14,14	0
56	MG	2A	3628	1/1	0.94	0.09	52,52,52,52	0
56	MG	2A	3629	1/1	0.94	0.07	43,43,43,43	0
56	MG	2A	3302	1/1	0.94	0.10	66,66,66,66	0
56	MG	2A	3631	1/1	0.94	0.09	39,39,39,39	0
56	MG	1A	3669	1/1	0.94	0.07	34,34,34,34	0
56	MG	1A	3373	1/1	0.94	0.11	52,52,52,52	0
56	MG	1a	1627	1/1	0.94	0.20	55,55,55,55	0
56	MG	1A	3674	1/1	0.94	0.10	39,39,39,39	0
56	MG	1A	3501	1/1	0.94	0.10	51,51,51,51	0
56	MG	1A	4069	1/1	0.94	0.13	42,42,42,42	0
56	MG	1A	4070	1/1	0.94	0.13	56,56,56,56	0
56	MG	1A	3681	1/1	0.94	0.06	34,34,34,34	0
56	MG	1A	3291	1/1	0.94	0.09	59,59,59,59	0
56	MG	1A	4073	1/1	0.94	0.06	42,42,42,42	0
56	MG	1A	3846	1/1	0.94	0.08	53,53,53,53	0
56	MG	1a	1638	1/1	0.94	0.10	58,58,58,58	0
56	MG	1A	3293	1/1	0.94	0.19	50,50,50,50	0
56	MG	2A	3318	1/1	0.94	0.13	48,48,48,48	0
56	MG	1A	4083	1/1	0.94	0.10	44,44,44,44	0
56	MG	1A	3380	1/1	0.94	0.18	48,48,48,48	0
56	MG	2A	3324	1/1	0.94	0.07	41,41,41,41	0
56	MG	2a	3072	1/1	0.94	0.09	53,53,53,53	0
56	MG	1A	3507	1/1	0.94	0.18	51,51,51,51	0
56	MG	2a	3074	1/1	0.94	0.15	63,63,63,63	0
56	MG	2A	3012	1/1	0.94	0.07	39,39,39,39	0
56	MG	2A	3016	1/1	0.94	0.13	61,61,61,61	0
56	MG	2a	3077	1/1	0.94	0.09	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4091	1/1	0.94	0.14	49,49,49,49	0
56	MG	1a	1647	1/1	0.94	0.13	65,65,65,65	0
56	MG	1A	3079	1/1	0.94	0.09	57,57,57,57	0
56	MG	2A	3675	1/1	0.94	0.13	55,55,55,55	0
56	MG	2A	3680	1/1	0.94	0.10	62,62,62,62	0
56	MG	1A	3061	1/1	0.94	0.31	62,62,62,62	0
56	MG	1a	1652	1/1	0.94	0.20	63,63,63,63	0
56	MG	2A	3683	1/1	0.94	0.10	62,62,62,62	0
56	MG	2A	3033	1/1	0.94	0.10	42,42,42,42	0
56	MG	1A	3300	1/1	0.94	0.23	61,61,61,61	0
56	MG	1a	1657	1/1	0.94	0.13	57,57,57,57	0
56	MG	1A	4101	1/1	0.94	0.10	39,39,39,39	0
56	MG	1A	4102	1/1	0.94	0.10	45,45,45,45	0
56	MG	1A	3519	1/1	0.94	0.06	49,49,49,49	0
56	MG	1A	3387	1/1	0.94	0.12	54,54,54,54	0
56	MG	1a	1664	1/1	0.94	0.23	62,62,62,62	0
56	MG	2A	3052	1/1	0.94	0.11	58,58,58,58	0
56	MG	1A	4108	1/1	0.94	0.20	48,48,48,48	0
56	MG	2A	3055	1/1	0.94	0.07	46,46,46,46	0
56	MG	1A	3857	1/1	0.94	0.14	48,48,48,48	0
56	MG	1a	1668	1/1	0.94	0.20	67,67,67,67	0
56	MG	1A	3391	1/1	0.94	0.09	41,41,41,41	0
56	MG	1A	3103	1/1	0.94	0.06	38,38,38,38	0
56	MG	1A	3697	1/1	0.94	0.10	51,51,51,51	0
56	MG	2A	3358	1/1	0.94	0.07	65,65,65,65	0
56	MG	1a	1673	1/1	0.94	0.21	67,67,67,67	0
56	MG	1A	3398	1/1	0.94	0.17	58,58,58,58	0
56	MG	1a	1675	1/1	0.94	0.10	60,60,60,60	0
56	MG	2A	3363	1/1	0.94	0.29	65,65,65,65	0
56	MG	2a	3118	1/1	0.94	0.10	65,65,65,65	0
56	MG	1A	3104	1/1	0.94	0.16	40,40,40,40	0
56	MG	1A	3400	1/1	0.94	0.14	54,54,54,54	0
56	MG	1A	3705	1/1	0.94	0.09	42,42,42,42	0
56	MG	2A	3721	1/1	0.94	0.07	46,46,46,46	0
56	MG	1A	4135	1/1	0.94	0.11	44,44,44,44	0
56	MG	1A	3402	1/1	0.94	0.17	54,54,54,54	0
56	MG	2A	3730	1/1	0.94	0.09	43,43,43,43	0
56	MG	1A	3221	1/1	0.94	0.15	55,55,55,55	0
56	MG	1a	1684	1/1	0.94	0.19	60,60,60,60	0
56	MG	1A	3155	1/1	0.94	0.15	47,47,47,47	0
56	MG	2A	3736	1/1	0.94	0.16	67,67,67,67	0
56	MG	2A	3375	1/1	0.94	0.10	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1687	1/1	0.94	0.11	50,50,50,50	0
56	MG	2A	3082	1/1	0.94	0.09	50,50,50,50	0
56	MG	2A	3379	1/1	0.94	0.07	53,53,53,53	0
56	MG	2A	3085	1/1	0.94	0.10	44,44,44,44	0
56	MG	1A	3877	1/1	0.94	0.06	39,39,39,39	0
56	MG	1A	3540	1/1	0.94	0.18	52,52,52,52	0
56	MG	1A	3226	1/1	0.94	0.10	47,47,47,47	0
56	MG	1A	3227	1/1	0.94	0.10	42,42,42,42	0
56	MG	2A	3388	1/1	0.94	0.10	56,56,56,56	0
56	MG	2A	3749	1/1	0.94	0.08	48,48,48,48	0
56	MG	1A	3543	1/1	0.94	0.16	73,73,73,73	0
56	MG	2A	3752	1/1	0.94	0.17	61,61,61,61	0
56	MG	1A	3163	1/1	0.94	0.23	52,52,52,52	0
56	MG	1A	3028	1/1	0.94	0.09	34,34,34,34	0
56	MG	2A	3098	1/1	0.94	0.07	49,49,49,49	0
56	MG	1B	3013	1/1	0.94	0.07	55,55,55,55	0
56	MG	1A	3416	1/1	0.94	0.10	47,47,47,47	0
56	MG	2A	3399	1/1	0.94	0.13	60,60,60,60	0
56	MG	2a	3164	1/1	0.94	0.09	73,73,73,73	0
56	MG	2A	3402	1/1	0.94	0.11	50,50,50,50	0
56	MG	2A	3403	1/1	0.94	0.22	60,60,60,60	0
56	MG	2a	3170	1/1	0.94	0.07	80,80,80,80	0
56	MG	2A	3103	1/1	0.94	0.20	42,42,42,42	0
56	MG	2a	3172	1/1	0.94	0.07	66,66,66,66	0
56	MG	1A	3417	1/1	0.94	0.12	51,51,51,51	0
56	MG	2a	3176	1/1	0.94	0.08	62,62,62,62	0
56	MG	2a	3177	1/1	0.94	0.07	67,67,67,67	0
56	MG	2A	3105	1/1	0.94	0.09	51,51,51,51	0
56	MG	1A	3236	1/1	0.94	0.21	37,37,37,37	0
56	MG	2a	3180	1/1	0.94	0.07	73,73,73,73	0
56	MG	2A	3767	1/1	0.94	0.09	56,56,56,56	0
56	MG	1A	3165	1/1	0.94	0.15	48,48,48,48	0
56	MG	1A	3166	1/1	0.94	0.19	38,38,38,38	0
56	MG	1A	3730	1/1	0.94	0.10	43,43,43,43	0
56	MG	1A	3421	1/1	0.94	0.08	46,46,46,46	0
56	MG	1A	3034	1/1	0.94	0.13	45,45,45,45	0
56	MG	1A	3246	1/1	0.94	0.11	58,58,58,58	0
56	MG	2a	3196	1/1	0.94	0.11	64,64,64,64	0
56	MG	1A	3180	1/1	0.94	0.11	36,36,36,36	0
56	MG	1A	3250	1/1	0.94	0.09	49,49,49,49	0
56	MG	1A	3742	1/1	0.94	0.08	64,64,64,64	0
56	MG	1A	3115	1/1	0.94	0.17	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3782	1/1	0.94	0.05	51,51,51,51	0
56	MG	1a	1715	1/1	0.94	0.12	49,49,49,49	0
56	MG	2A	3784	1/1	0.94	0.06	47,47,47,47	0
56	MG	2A	3786	1/1	0.94	0.06	48,48,48,48	0
56	MG	2A	3788	1/1	0.94	0.07	53,53,53,53	0
56	MG	2A	3790	1/1	0.94	0.15	65,65,65,65	0
56	MG	1a	1717	1/1	0.94	0.12	64,64,64,64	0
56	MG	1A	3909	1/1	0.94	0.08	40,40,40,40	0
56	MG	2A	3796	1/1	0.94	0.09	49,49,49,49	0
56	MG	1A	3326	1/1	0.94	0.14	41,41,41,41	0
56	MG	1A	3430	1/1	0.94	0.08	47,47,47,47	0
56	MG	2A	3431	1/1	0.94	0.14	62,62,62,62	0
56	MG	1A	3090	1/1	0.94	0.19	54,54,54,54	0
56	MG	1D	305	1/1	0.94	0.09	42,42,42,42	0
56	MG	2A	3435	1/1	0.94	0.06	49,49,49,49	0
56	MG	1D	309	1/1	0.94	0.07	46,46,46,46	0
56	MG	2A	3148	1/1	0.94	0.14	52,52,52,52	0
56	MG	2A	3149	1/1	0.94	0.25	54,54,54,54	0
56	MG	1A	3920	1/1	0.94	0.09	44,44,44,44	0
56	MG	2A	3151	1/1	0.94	0.11	40,40,40,40	0
56	MG	2A	3813	1/1	0.94	0.12	48,48,48,48	0
56	MG	1A	3921	1/1	0.94	0.10	50,50,50,50	0
56	MG	2A	3444	1/1	0.94	0.16	49,49,49,49	0
56	MG	1A	3748	1/1	0.94	0.14	25,25,25,25	0
56	MG	1A	3329	1/1	0.94	0.10	43,43,43,43	0
56	MG	2A	3158	1/1	0.94	0.07	41,41,41,41	0
56	MG	2A	3159	1/1	0.94	0.18	53,53,53,53	0
56	MG	1E	306	1/1	0.94	0.09	31,31,31,31	0
56	MG	2A	3167	1/1	0.94	0.14	52,52,52,52	0
56	MG	1A	3435	1/1	0.94	0.09	53,53,53,53	0
56	MG	1E	311	1/1	0.94	0.14	42,42,42,42	0
56	MG	1A	3254	1/1	0.94	0.14	53,53,53,53	0
56	MG	2A	3834	1/1	0.94	0.07	40,40,40,40	0
56	MG	1F	303	1/1	0.94	0.10	38,38,38,38	0
56	MG	2a	3243	1/1	0.94	0.16	64,64,64,64	0
56	MG	1F	306	1/1	0.94	0.12	53,53,53,53	0
56	MG	2A	3842	1/1	0.94	0.09	59,59,59,59	0
56	MG	2A	3843	1/1	0.94	0.13	58,58,58,58	0
56	MG	2i	8001	1/1	0.94	0.06	51,51,51,51	0
56	MG	2A	3173	1/1	0.94	0.07	51,51,51,51	0
56	MG	1A	3939	1/1	0.94	0.11	53,53,53,53	0
56	MG	2A	3460	1/1	0.94	0.25	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3117	1/1	0.94	0.21	39,39,39,39	0
56	MG	1A	3583	1/1	0.94	0.16	42,42,42,42	0
56	MG	1A	3184	1/1	0.94	0.14	62,62,62,62	0
56	MG	2r	101	1/1	0.94	0.09	68,68,68,68	0
56	MG	1A	3760	1/1	0.94	0.12	35,35,35,35	0
56	MG	1a	1756	1/1	0.94	0.22	72,72,72,72	0
56	MG	2A	3866	1/1	0.94	0.09	42,42,42,42	0
56	MG	1A	3260	1/1	0.94	0.09	39,39,39,39	0
56	MG	1A	3335	1/1	0.94	0.32	62,62,62,62	0
56	MG	2A	3185	1/1	0.94	0.07	45,45,45,45	0
56	MG	1A	3337	1/1	0.94	0.14	48,48,48,48	0
56	MG	1N	202	1/1	0.94	0.09	48,48,48,48	0
56	MG	2A	3191	1/1	0.94	0.15	50,50,50,50	0
56	MG	1A	3338	1/1	0.94	0.12	49,49,49,49	0
56	MG	2A	3886	1/1	0.94	0.18	45,45,45,45	0
56	MG	2A	3476	1/1	0.94	0.10	41,41,41,41	0
56	MG	1A	3772	1/1	0.94	0.07	36,36,36,36	0
56	MG	2A	3196	1/1	0.94	0.10	56,56,56,56	0
56	MG	1A	3119	1/1	0.94	0.09	51,51,51,51	0
56	MG	2A	3480	1/1	0.94	0.28	65,65,65,65	0
56	MG	2A	3899	1/1	0.94	0.12	45,45,45,45	0
56	MG	2A	3903	1/1	0.94	0.11	58,58,58,58	0
56	MG	1A	3070	1/1	0.94	0.15	41,41,41,41	0
58	ZN	2n	501	1/1	0.94	0.08	107,107,107,107	0
56	MG	2A	3208	1/1	0.95	0.16	57,57,57,57	0
56	MG	2A	3885	1/1	0.95	0.18	54,54,54,54	0
56	MG	1A	3992	1/1	0.95	0.12	75,75,75,75	0
56	MG	1Q	204	1/1	0.95	0.08	51,51,51,51	0
56	MG	2A	3889	1/1	0.95	0.10	49,49,49,49	0
56	MG	1A	3993	1/1	0.95	0.07	37,37,37,37	0
56	MG	2A	3891	1/1	0.95	0.12	71,71,71,71	0
56	MG	2A	3214	1/1	0.95	0.07	56,56,56,56	0
56	MG	2A	3216	1/1	0.95	0.12	56,56,56,56	0
56	MG	1Q	206	1/1	0.95	0.06	54,54,54,54	0
56	MG	2A	3495	1/1	0.95	0.07	51,51,51,51	0
56	MG	2A	3900	1/1	0.95	0.15	44,44,44,44	0
56	MG	1A	3208	1/1	0.95	0.08	55,55,55,55	0
56	MG	1a	1778	1/1	0.95	0.08	64,64,64,64	0
56	MG	1A	3655	1/1	0.95	0.07	39,39,39,39	0
56	MG	1A	3514	1/1	0.95	0.12	53,53,53,53	0
56	MG	1S	3003	1/1	0.95	0.08	59,59,59,59	0
56	MG	1A	3158	1/1	0.95	0.11	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3210	1/1	0.95	0.08	42,42,42,42	0
56	MG	1A	3809	1/1	0.95	0.15	51,51,51,51	0
56	MG	2A	3509	1/1	0.95	0.10	38,38,38,38	0
56	MG	1A	3664	1/1	0.95	0.07	48,48,48,48	0
56	MG	2A	3230	1/1	0.95	0.11	48,48,48,48	0
56	MG	1V	202	1/1	0.95	0.18	53,53,53,53	0
56	MG	2A	3232	1/1	0.95	0.14	64,64,64,64	0
56	MG	2A	3234	1/1	0.95	0.09	52,52,52,52	0
56	MG	1A	3339	1/1	0.95	0.11	51,51,51,51	0
56	MG	2A	3236	1/1	0.95	0.08	53,53,53,53	0
56	MG	2A	3527	1/1	0.95	0.06	31,31,31,31	0
56	MG	1A	3121	1/1	0.95	0.13	43,43,43,43	0
56	MG	1W	204	1/1	0.95	0.10	40,40,40,40	0
56	MG	1A	3216	1/1	0.95	0.20	50,50,50,50	0
56	MG	1A	3529	1/1	0.95	0.15	43,43,43,43	0
56	MG	2A	3243	1/1	0.95	0.11	52,52,52,52	0
56	MG	2A	3533	1/1	0.95	0.10	48,48,48,48	0
56	MG	2B	3018	1/1	0.95	0.08	65,65,65,65	0
56	MG	1A	3816	1/1	0.95	0.10	49,49,49,49	0
56	MG	1Y	504	1/1	0.95	0.18	48,48,48,48	0
56	MG	1A	3123	1/1	0.95	0.12	54,54,54,54	0
56	MG	2A	3537	1/1	0.95	0.06	35,35,35,35	0
56	MG	1a	1812	1/1	0.95	0.09	70,70,70,70	0
56	MG	2A	3249	1/1	0.95	0.10	57,57,57,57	0
56	MG	1A	3025	1/1	0.95	0.09	41,41,41,41	0
56	MG	1Z	303	1/1	0.95	0.06	56,56,56,56	0
56	MG	10	101	1/1	0.95	0.11	63,63,63,63	0
56	MG	2E	304	1/1	0.95	0.17	46,46,46,46	0
56	MG	2E	305	1/1	0.95	0.10	40,40,40,40	0
56	MG	2A	3545	1/1	0.95	0.11	52,52,52,52	0
56	MG	10	104	1/1	0.95	0.20	64,64,64,64	0
56	MG	1A	3675	1/1	0.95	0.15	32,32,32,32	0
56	MG	2E	309	1/1	0.95	0.10	60,60,60,60	0
56	MG	2F	301	1/1	0.95	0.15	58,58,58,58	0
56	MG	1A	3676	1/1	0.95	0.12	24,24,24,24	0
56	MG	1A	3677	1/1	0.95	0.10	29,29,29,29	0
56	MG	2N	8001	1/1	0.95	0.05	47,47,47,47	0
56	MG	1A	3678	1/1	0.95	0.07	61,61,61,61	0
56	MG	1A	3102	1/1	0.95	0.09	54,54,54,54	0
56	MG	2Q	3002	1/1	0.95	0.08	44,44,44,44	0
56	MG	2R	201	1/1	0.95	0.09	48,48,48,48	0
56	MG	1A	3680	1/1	0.95	0.14	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3427	1/1	0.95	0.09	44,44,44,44	0
56	MG	2A	3557	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	3167	1/1	0.95	0.09	41,41,41,41	0
56	MG	2A	3559	1/1	0.95	0.10	39,39,39,39	0
56	MG	2U	204	1/1	0.95	0.14	45,45,45,45	0
56	MG	15	102	1/1	0.95	0.08	39,39,39,39	0
56	MG	1A	3225	1/1	0.95	0.17	52,52,52,52	0
56	MG	16	101	1/1	0.95	0.09	45,45,45,45	0
56	MG	2A	3565	1/1	0.95	0.07	36,36,36,36	0
56	MG	1A	4037	1/1	0.95	0.10	62,62,62,62	0
56	MG	2X	103	1/1	0.95	0.10	46,46,46,46	0
56	MG	2A	3569	1/1	0.95	0.09	49,49,49,49	0
56	MG	2A	3571	1/1	0.95	0.07	35,35,35,35	0
56	MG	1t	3001	1/1	0.95	0.12	58,58,58,58	0
56	MG	20	3003	1/1	0.95	0.10	58,58,58,58	0
56	MG	1A	4043	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3273	1/1	0.95	0.07	51,51,51,51	0
56	MG	25	101	1/1	0.95	0.23	55,55,55,55	0
56	MG	18	101	1/1	0.95	0.16	47,47,47,47	0
56	MG	1A	3128	1/1	0.95	0.21	41,41,41,41	0
56	MG	1A	4045	1/1	0.95	0.07	38,38,38,38	0
56	MG	1A	3171	1/1	0.95	0.23	53,53,53,53	0
56	MG	2A	3582	1/1	0.95	0.06	51,51,51,51	0
56	MG	2a	3002	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3279	1/1	0.95	0.10	53,53,53,53	0
56	MG	1A	3294	1/1	0.95	0.16	52,52,52,52	0
56	MG	1A	4048	1/1	0.95	0.07	48,48,48,48	0
56	MG	1A	3354	1/1	0.95	0.15	68,68,68,68	0
56	MG	2A	3283	1/1	0.95	0.10	61,61,61,61	0
56	MG	1A	3437	1/1	0.95	0.07	52,52,52,52	0
56	MG	2A	3596	1/1	0.95	0.08	47,47,47,47	0
56	MG	2A	3285	1/1	0.95	0.06	49,49,49,49	0
56	MG	1A	3841	1/1	0.95	0.09	27,27,27,27	0
56	MG	1A	3842	1/1	0.95	0.11	26,26,26,26	0
56	MG	1A	3546	1/1	0.95	0.11	45,45,45,45	0
56	MG	1a	1608	1/1	0.95	0.12	60,60,60,60	0
56	MG	1A	4055	1/1	0.95	0.05	33,33,33,33	0
56	MG	1A	4059	1/1	0.95	0.06	21,21,21,21	0
56	MG	1A	3230	1/1	0.95	0.17	60,60,60,60	0
56	MG	1A	3847	1/1	0.95	0.08	48,48,48,48	0
56	MG	1a	1616	1/1	0.95	0.09	55,55,55,55	0
56	MG	2A	3612	1/1	0.95	0.08	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3613	1/1	0.95	0.09	33,33,33,33	0
56	MG	2A	3297	1/1	0.95	0.16	51,51,51,51	0
56	MG	1A	3693	1/1	0.95	0.13	40,40,40,40	0
56	MG	1A	4063	1/1	0.95	0.07	57,57,57,57	0
56	MG	1A	4064	1/1	0.95	0.08	66,66,66,66	0
56	MG	1A	3062	1/1	0.95	0.27	59,59,59,59	0
56	MG	1A	3130	1/1	0.95	0.10	41,41,41,41	0
56	MG	1A	3442	1/1	0.95	0.09	56,56,56,56	0
56	MG	1A	3235	1/1	0.95	0.14	66,66,66,66	0
56	MG	1A	3364	1/1	0.95	0.16	64,64,64,64	0
56	MG	1A	3700	1/1	0.95	0.07	16,16,16,16	0
56	MG	2a	3035	1/1	0.95	0.25	63,63,63,63	0
56	MG	2A	3627	1/1	0.95	0.10	50,50,50,50	0
56	MG	1A	3563	1/1	0.95	0.13	43,43,43,43	0
56	MG	1A	3704	1/1	0.95	0.10	49,49,49,49	0
56	MG	1A	3858	1/1	0.95	0.04	30,30,30,30	0
56	MG	1A	3029	1/1	0.95	0.10	38,38,38,38	0
56	MG	1A	3447	1/1	0.95	0.06	46,46,46,46	0
56	MG	1A	4078	1/1	0.95	0.10	41,41,41,41	0
56	MG	2A	3638	1/1	0.95	0.12	43,43,43,43	0
56	MG	1A	3238	1/1	0.95	0.14	57,57,57,57	0
56	MG	2A	3641	1/1	0.95	0.10	57,57,57,57	0
56	MG	2A	3315	1/1	0.95	0.11	54,54,54,54	0
56	MG	2a	3047	1/1	0.95	0.12	52,52,52,52	0
56	MG	1A	3865	1/1	0.95	0.33	43,43,43,43	0
56	MG	1A	3567	1/1	0.95	0.10	54,54,54,54	0
56	MG	2A	3645	1/1	0.95	0.07	40,40,40,40	0
56	MG	2A	3320	1/1	0.95	0.20	54,54,54,54	0
56	MG	1A	4088	1/1	0.95	0.10	57,57,57,57	0
56	MG	1A	4090	1/1	0.95	0.14	37,37,37,37	0
56	MG	2A	3651	1/1	0.95	0.15	44,44,44,44	0
56	MG	1a	1641	1/1	0.95	0.14	58,58,58,58	0
56	MG	2A	3028	1/1	0.95	0.07	54,54,54,54	0
56	MG	1A	3132	1/1	0.95	0.09	40,40,40,40	0
56	MG	2A	3030	1/1	0.95	0.07	51,51,51,51	0
56	MG	2A	3329	1/1	0.95	0.11	56,56,56,56	0
56	MG	1A	3869	1/1	0.95	0.08	56,56,56,56	0
56	MG	2A	3034	1/1	0.95	0.08	45,45,45,45	0
56	MG	2A	3662	1/1	0.95	0.10	48,48,48,48	0
56	MG	2A	3663	1/1	0.95	0.10	64,64,64,64	0
56	MG	1a	1644	1/1	0.95	0.14	66,66,66,66	0
56	MG	2A	3665	1/1	0.95	0.07	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3068	1/1	0.95	0.18	72,72,72,72	0
56	MG	2A	3036	1/1	0.95	0.09	54,54,54,54	0
56	MG	1A	3569	1/1	0.95	0.10	54,54,54,54	0
56	MG	1a	1646	1/1	0.95	0.07	51,51,51,51	0
56	MG	1A	3451	1/1	0.95	0.09	47,47,47,47	0
56	MG	1A	4097	1/1	0.95	0.07	47,47,47,47	0
56	MG	2A	3338	1/1	0.95	0.24	62,62,62,62	0
56	MG	1a	1649	1/1	0.95	0.13	45,45,45,45	0
56	MG	2A	3676	1/1	0.95	0.11	48,48,48,48	0
56	MG	2A	3678	1/1	0.95	0.07	49,49,49,49	0
56	MG	1A	4100	1/1	0.95	0.07	47,47,47,47	0
56	MG	2a	3079	1/1	0.95	0.17	59,59,59,59	0
56	MG	1A	3133	1/1	0.95	0.08	44,44,44,44	0
56	MG	1A	3374	1/1	0.95	0.17	55,55,55,55	0
56	MG	2A	3054	1/1	0.95	0.09	54,54,54,54	0
56	MG	2a	3084	1/1	0.95	0.07	44,44,44,44	0
56	MG	1A	3721	1/1	0.95	0.09	57,57,57,57	0
56	MG	1a	1659	1/1	0.95	0.21	62,62,62,62	0
56	MG	2A	3057	1/1	0.95	0.07	46,46,46,46	0
56	MG	1A	3376	1/1	0.95	0.10	51,51,51,51	0
56	MG	2A	3688	1/1	0.95	0.06	38,38,38,38	0
56	MG	2A	3689	1/1	0.95	0.16	71,71,71,71	0
56	MG	2A	3059	1/1	0.95	0.10	46,46,46,46	0
56	MG	1A	4105	1/1	0.95	0.11	44,44,44,44	0
56	MG	2A	3351	1/1	0.95	0.16	54,54,54,54	0
56	MG	2A	3061	1/1	0.95	0.07	49,49,49,49	0
56	MG	1A	3244	1/1	0.95	0.07	49,49,49,49	0
56	MG	2A	3355	1/1	0.95	0.10	51,51,51,51	0
56	MG	2A	3356	1/1	0.95	0.12	55,55,55,55	0
56	MG	1A	3579	1/1	0.95	0.16	44,44,44,44	0
56	MG	1A	3457	1/1	0.95	0.11	59,59,59,59	0
56	MG	1A	3883	1/1	0.95	0.11	68,68,68,68	0
56	MG	2A	3704	1/1	0.95	0.06	56,56,56,56	0
56	MG	2a	3107	1/1	0.95	0.12	57,57,57,57	0
56	MG	1A	3052	1/1	0.95	0.07	56,56,56,56	0
56	MG	1a	1667	1/1	0.95	0.16	65,65,65,65	0
56	MG	1A	3112	1/1	0.95	0.10	49,49,49,49	0
56	MG	2A	3070	1/1	0.95	0.21	42,42,42,42	0
56	MG	2a	3112	1/1	0.95	0.12	54,54,54,54	0
56	MG	1A	3464	1/1	0.95	0.11	45,45,45,45	0
56	MG	1A	4129	1/1	0.95	0.09	42,42,42,42	0
56	MG	2A	3713	1/1	0.95	0.13	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3091	1/1	0.95	0.14	43,43,43,43	0
56	MG	1A	3586	1/1	0.95	0.15	49,49,49,49	0
56	MG	2A	3371	1/1	0.95	0.09	48,48,48,48	0
56	MG	1A	3588	1/1	0.95	0.10	46,46,46,46	0
56	MG	2A	3720	1/1	0.95	0.06	41,41,41,41	0
56	MG	1A	3384	1/1	0.95	0.12	57,57,57,57	0
56	MG	1A	4142	1/1	0.95	0.10	42,42,42,42	0
56	MG	2A	3726	1/1	0.95	0.13	56,56,56,56	0
56	MG	2A	3727	1/1	0.95	0.09	51,51,51,51	0
56	MG	1A	3249	1/1	0.95	0.21	56,56,56,56	0
56	MG	1A	3741	1/1	0.95	0.10	45,45,45,45	0
56	MG	1a	1680	1/1	0.95	0.15	64,64,64,64	0
56	MG	1B	3004	1/1	0.95	0.16	50,50,50,50	0
56	MG	1A	3898	1/1	0.95	0.10	50,50,50,50	0
56	MG	2A	3382	1/1	0.95	0.08	50,50,50,50	0
56	MG	2a	3134	1/1	0.95	0.18	64,64,64,64	0
56	MG	1A	3899	1/1	0.95	0.10	52,52,52,52	0
56	MG	1A	3001	1/1	0.95	0.09	42,42,42,42	0
56	MG	2A	3739	1/1	0.95	0.12	59,59,59,59	0
56	MG	1B	3008	1/1	0.95	0.13	57,57,57,57	0
56	MG	2a	3139	1/1	0.95	0.08	73,73,73,73	0
56	MG	1A	3318	1/1	0.95	0.07	46,46,46,46	0
56	MG	2A	3389	1/1	0.95	0.12	58,58,58,58	0
56	MG	2A	3391	1/1	0.95	0.12	58,58,58,58	0
56	MG	1A	3147	1/1	0.95	0.15	54,54,54,54	0
56	MG	2A	3099	1/1	0.95	0.10	42,42,42,42	0
56	MG	1A	3252	1/1	0.95	0.11	52,52,52,52	0
56	MG	2A	3395	1/1	0.95	0.09	50,50,50,50	0
56	MG	1A	3393	1/1	0.95	0.10	50,50,50,50	0
56	MG	2A	3750	1/1	0.95	0.13	47,47,47,47	0
56	MG	1A	3395	1/1	0.95	0.11	42,42,42,42	0
56	MG	1a	1692	1/1	0.95	0.25	69,69,69,69	0
56	MG	1a	1693	1/1	0.95	0.10	58,58,58,58	0
56	MG	2a	3159	1/1	0.95	0.19	71,71,71,71	0
56	MG	1A	3750	1/1	0.95	0.09	29,29,29,29	0
56	MG	2a	3163	1/1	0.95	0.06	72,72,72,72	0
56	MG	1A	3751	1/1	0.95	0.10	48,48,48,48	0
56	MG	1A	3600	1/1	0.95	0.07	46,46,46,46	0
56	MG	1A	3601	1/1	0.95	0.09	11,11,11,11	0
56	MG	2a	3168	1/1	0.95	0.07	78,78,78,78	0
56	MG	2A	3112	1/1	0.95	0.10	42,42,42,42	0
56	MG	1A	3916	1/1	0.95	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3114	1/1	0.95	0.10	55,55,55,55	0
56	MG	2A	3411	1/1	0.95	0.09	53,53,53,53	0
56	MG	2A	3763	1/1	0.95	0.09	52,52,52,52	0
56	MG	1A	3193	1/1	0.95	0.13	34,34,34,34	0
56	MG	1A	3919	1/1	0.95	0.12	38,38,38,38	0
56	MG	1B	3023	1/1	0.95	0.07	54,54,54,54	0
56	MG	2A	3415	1/1	0.95	0.09	50,50,50,50	0
56	MG	2A	3416	1/1	0.95	0.18	59,59,59,59	0
56	MG	2A	3418	1/1	0.95	0.08	61,61,61,61	0
56	MG	2a	3186	1/1	0.95	0.13	53,53,53,53	0
56	MG	1A	3044	1/1	0.95	0.08	37,37,37,37	0
56	MG	2a	3189	1/1	0.95	0.11	48,48,48,48	0
56	MG	1A	3324	1/1	0.95	0.20	55,55,55,55	0
56	MG	1A	3758	1/1	0.95	0.09	71,71,71,71	0
56	MG	1A	3486	1/1	0.95	0.06	42,42,42,42	0
56	MG	1A	3255	1/1	0.95	0.13	47,47,47,47	0
56	MG	2A	3776	1/1	0.95	0.10	44,44,44,44	0
56	MG	1A	3403	1/1	0.95	0.10	27,27,27,27	0
56	MG	2A	3778	1/1	0.95	0.06	52,52,52,52	0
56	MG	2A	3131	1/1	0.95	0.08	42,42,42,42	0
56	MG	2A	3133	1/1	0.95	0.07	49,49,49,49	0
56	MG	1A	3938	1/1	0.95	0.05	55,55,55,55	0
56	MG	1A	3765	1/1	0.95	0.06	25,25,25,25	0
56	MG	2a	3203	1/1	0.95	0.16	62,62,62,62	0
56	MG	1A	3195	1/1	0.95	0.23	40,40,40,40	0
56	MG	1A	3768	1/1	0.95	0.10	61,61,61,61	0
56	MG	2A	3146	1/1	0.95	0.07	43,43,43,43	0
56	MG	1A	3624	1/1	0.95	0.09	28,28,28,28	0
56	MG	2A	3791	1/1	0.95	0.09	46,46,46,46	0
56	MG	2A	3792	1/1	0.95	0.15	51,51,51,51	0
56	MG	1D	307	1/1	0.95	0.10	45,45,45,45	0
56	MG	1A	3490	1/1	0.95	0.07	50,50,50,50	0
56	MG	2a	3213	1/1	0.95	0.14	69,69,69,69	0
56	MG	1A	3949	1/1	0.95	0.09	63,63,63,63	0
56	MG	1E	301	1/1	0.95	0.10	37,37,37,37	0
56	MG	2a	3216	1/1	0.95	0.18	65,65,65,65	0
56	MG	1A	3950	1/1	0.95	0.07	41,41,41,41	0
56	MG	2A	3440	1/1	0.95	0.15	43,43,43,43	0
56	MG	1A	3626	1/1	0.95	0.09	44,44,44,44	0
56	MG	1A	3953	1/1	0.95	0.07	46,46,46,46	0
56	MG	2A	3803	1/1	0.95	0.06	42,42,42,42	0
56	MG	2a	3223	1/1	0.95	0.23	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3443	1/1	0.95	0.20	50,50,50,50	0
56	MG	2a	3225	1/1	0.95	0.10	57,57,57,57	0
56	MG	1A	3954	1/1	0.95	0.08	58,58,58,58	0
56	MG	1A	3327	1/1	0.95	0.13	28,28,28,28	0
56	MG	1A	3957	1/1	0.95	0.06	55,55,55,55	0
56	MG	1a	1731	1/1	0.95	0.13	50,50,50,50	0
56	MG	1F	301	1/1	0.95	0.10	40,40,40,40	0
56	MG	1a	1734	1/1	0.95	0.13	67,67,67,67	0
56	MG	1A	3151	1/1	0.95	0.14	47,47,47,47	0
56	MG	1a	1736	1/1	0.95	0.09	57,57,57,57	0
56	MG	1A	3961	1/1	0.95	0.08	38,38,38,38	0
56	MG	1A	3408	1/1	0.95	0.14	60,60,60,60	0
56	MG	1a	1742	1/1	0.95	0.06	51,51,51,51	0
56	MG	1A	3636	1/1	0.95	0.09	38,38,38,38	0
56	MG	1A	3780	1/1	0.95	0.06	21,21,21,21	0
56	MG	1A	3495	1/1	0.95	0.10	42,42,42,42	0
56	MG	1a	1747	1/1	0.95	0.10	49,49,49,49	0
56	MG	2A	3828	1/1	0.95	0.07	80,80,80,80	0
56	MG	1A	3638	1/1	0.95	0.07	53,53,53,53	0
56	MG	2A	3830	1/1	0.95	0.15	48,48,48,48	0
56	MG	1A	3259	1/1	0.95	0.06	40,40,40,40	0
56	MG	1A	3973	1/1	0.95	0.06	85,85,85,85	0
56	MG	1A	3502	1/1	0.95	0.13	49,49,49,49	0
56	MG	2A	3837	1/1	0.95	0.08	37,37,37,37	0
56	MG	1A	3059	1/1	0.95	0.11	48,48,48,48	0
56	MG	2A	3187	1/1	0.95	0.10	50,50,50,50	0
56	MG	2A	3188	1/1	0.95	0.06	36,36,36,36	0
56	MG	1A	3153	1/1	0.95	0.11	37,37,37,37	0
56	MG	2A	3848	1/1	0.95	0.06	36,36,36,36	0
56	MG	2A	3850	1/1	0.95	0.07	59,59,59,59	0
56	MG	2A	3190	1/1	0.95	0.09	45,45,45,45	0
56	MG	1A	3413	1/1	0.95	0.10	36,36,36,36	0
56	MG	2A	3473	1/1	0.95	0.13	57,57,57,57	0
56	MG	2A	3193	1/1	0.95	0.07	55,55,55,55	0
56	MG	2A	3858	1/1	0.95	0.07	43,43,43,43	0
56	MG	1A	3981	1/1	0.95	0.06	52,52,52,52	0
56	MG	2w	103	1/1	0.95	0.10	56,56,56,56	0
56	MG	1N	206	1/1	0.95	0.12	42,42,42,42	0
56	MG	2w	105	1/1	0.95	0.15	70,70,70,70	0
56	MG	1A	3415	1/1	0.95	0.12	59,59,59,59	0
56	MG	1A	3060	1/1	0.95	0.06	45,45,45,45	0
56	MG	1A	3985	1/1	0.95	0.09	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3868	1/1	0.95	0.08	69,69,69,69	0
56	MG	2A	3869	1/1	0.95	0.05	56,56,56,56	0
56	MG	2x	105	1/1	0.95	0.16	57,57,57,57	0
56	MG	2A	3199	1/1	0.95	0.08	50,50,50,50	0
56	MG	2A	3872	1/1	0.95	0.07	44,44,44,44	0
56	MG	2A	3874	1/1	0.95	0.07	53,53,53,53	0
56	MG	1A	3796	1/1	0.95	0.06	34,34,34,34	0
56	MG	1a	1769	1/1	0.95	0.08	55,55,55,55	0
56	MG	2A	3878	1/1	0.95	0.08	49,49,49,49	0
57	K	1A	3584	1/1	0.95	0.09	58,58,58,58	0
56	MG	1A	3120	1/1	0.95	0.09	42,42,42,42	0
56	MG	1P	204	1/1	0.95	0.15	47,47,47,47	0
56	MG	1A	3396	1/1	0.96	0.06	47,47,47,47	0
56	MG	2D	303	1/1	0.96	0.05	35,35,35,35	0
56	MG	1A	3198	1/1	0.96	0.12	41,41,41,41	0
56	MG	1A	3474	1/1	0.96	0.22	60,60,60,60	0
56	MG	2E	301	1/1	0.96	0.11	50,50,50,50	0
56	MG	2A	3014	1/1	0.96	0.18	43,43,43,43	0
56	MG	1A	4094	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3725	1/1	0.96	0.07	52,52,52,52	0
56	MG	1A	3201	1/1	0.96	0.08	45,45,45,45	0
56	MG	1A	3587	1/1	0.96	0.14	38,38,38,38	0
56	MG	2A	3598	1/1	0.96	0.07	48,48,48,48	0
56	MG	1A	3477	1/1	0.96	0.09	48,48,48,48	0
56	MG	2A	3025	1/1	0.96	0.14	42,42,42,42	0
56	MG	2A	3026	1/1	0.96	0.08	36,36,36,36	0
56	MG	1A	3202	1/1	0.96	0.06	32,32,32,32	0
56	MG	1A	3479	1/1	0.96	0.05	38,38,38,38	0
56	MG	1A	3591	1/1	0.96	0.14	52,52,52,52	0
56	MG	2A	3031	1/1	0.96	0.07	45,45,45,45	0
56	MG	2P	201	1/1	0.96	0.05	45,45,45,45	0
56	MG	2A	3608	1/1	0.96	0.05	61,61,61,61	0
56	MG	2A	3609	1/1	0.96	0.12	42,42,42,42	0
56	MG	2A	3032	1/1	0.96	0.06	38,38,38,38	0
56	MG	1A	3889	1/1	0.96	0.13	60,60,60,60	0
56	MG	1A	3017	1/1	0.96	0.12	54,54,54,54	0
56	MG	1A	3482	1/1	0.96	0.08	50,50,50,50	0
56	MG	2U	201	1/1	0.96	0.09	40,40,40,40	0
56	MG	1A	4112	1/1	0.96	0.11	42,42,42,42	0
56	MG	2A	3038	1/1	0.96	0.07	31,31,31,31	0
56	MG	1A	3093	1/1	0.96	0.16	33,33,33,33	0
56	MG	2A	3040	1/1	0.96	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3316	1/1	0.96	0.10	54,54,54,54	0
56	MG	2A	3041	1/1	0.96	0.12	49,49,49,49	0
56	MG	1a	1650	1/1	0.96	0.11	53,53,53,53	0
56	MG	1A	3066	1/1	0.96	0.07	35,35,35,35	0
56	MG	2A	3044	1/1	0.96	0.09	48,48,48,48	0
56	MG	1A	4117	1/1	0.96	0.21	39,39,39,39	0
56	MG	2A	3323	1/1	0.96	0.12	56,56,56,56	0
56	MG	2A	3046	1/1	0.96	0.07	48,48,48,48	0
56	MG	2A	3048	1/1	0.96	0.09	41,41,41,41	0
56	MG	1A	3485	1/1	0.96	0.10	48,48,48,48	0
56	MG	1A	3018	1/1	0.96	0.13	33,33,33,33	0
56	MG	2A	3328	1/1	0.96	0.13	39,39,39,39	0
56	MG	25	103	1/1	0.96	0.10	52,52,52,52	0
56	MG	25	104	1/1	0.96	0.07	43,43,43,43	0
56	MG	2A	3636	1/1	0.96	0.23	59,59,59,59	0
56	MG	1A	4124	1/1	0.96	0.29	46,46,46,46	0
56	MG	1A	3019	1/1	0.96	0.14	37,37,37,37	0
56	MG	2A	3639	1/1	0.96	0.11	34,34,34,34	0
56	MG	1A	4127	1/1	0.96	0.09	34,34,34,34	0
56	MG	1A	4128	1/1	0.96	0.22	43,43,43,43	0
56	MG	1A	3331	1/1	0.96	0.11	54,54,54,54	0
56	MG	1A	4130	1/1	0.96	0.05	38,38,38,38	0
56	MG	1A	3604	1/1	0.96	0.11	65,65,65,65	0
56	MG	1A	4132	1/1	0.96	0.17	39,39,39,39	0
56	MG	1A	3605	1/1	0.96	0.08	32,32,32,32	0
56	MG	1A	3159	1/1	0.96	0.08	39,39,39,39	0
56	MG	2A	3648	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	3608	1/1	0.96	0.10	51,51,51,51	0
56	MG	1A	4138	1/1	0.96	0.09	43,43,43,43	0
56	MG	1A	4140	1/1	0.96	0.06	31,31,31,31	0
56	MG	1A	3609	1/1	0.96	0.10	50,50,50,50	0
56	MG	1A	3212	1/1	0.96	0.21	32,32,32,32	0
56	MG	1A	3411	1/1	0.96	0.10	43,43,43,43	0
56	MG	1A	3911	1/1	0.96	0.09	65,65,65,65	0
56	MG	1A	3755	1/1	0.96	0.11	36,36,36,36	0
56	MG	2A	3660	1/1	0.96	0.06	45,45,45,45	0
56	MG	1a	1678	1/1	0.96	0.23	63,63,63,63	0
56	MG	1A	3492	1/1	0.96	0.12	52,52,52,52	0
56	MG	1A	3615	1/1	0.96	0.08	25,25,25,25	0
56	MG	1A	3917	1/1	0.96	0.05	80,80,80,80	0
56	MG	2a	3025	1/1	0.96	0.14	57,57,57,57	0
56	MG	2A	3352	1/1	0.96	0.09	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3666	1/1	0.96	0.07	34,34,34,34	0
56	MG	2A	3076	1/1	0.96	0.11	35,35,35,35	0
56	MG	2A	3669	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3213	1/1	0.96	0.09	42,42,42,42	0
56	MG	1A	3160	1/1	0.96	0.13	41,41,41,41	0
56	MG	1A	3621	1/1	0.96	0.10	48,48,48,48	0
56	MG	2A	3081	1/1	0.96	0.12	45,45,45,45	0
56	MG	1a	1685	1/1	0.96	0.16	51,51,51,51	0
56	MG	2A	3083	1/1	0.96	0.16	49,49,49,49	0
56	MG	2A	3361	1/1	0.96	0.11	51,51,51,51	0
56	MG	1A	3622	1/1	0.96	0.07	36,36,36,36	0
56	MG	2A	3679	1/1	0.96	0.07	41,41,41,41	0
56	MG	2A	3086	1/1	0.96	0.10	44,44,44,44	0
56	MG	2A	3087	1/1	0.96	0.10	53,53,53,53	0
56	MG	1A	3922	1/1	0.96	0.08	57,57,57,57	0
56	MG	2A	3089	1/1	0.96	0.06	46,46,46,46	0
56	MG	1A	3763	1/1	0.96	0.09	52,52,52,52	0
56	MG	1A	3336	1/1	0.96	0.11	41,41,41,41	0
56	MG	1A	3931	1/1	0.96	0.08	55,55,55,55	0
56	MG	1A	3497	1/1	0.96	0.14	33,33,33,33	0
56	MG	1A	3498	1/1	0.96	0.08	46,46,46,46	0
56	MG	2A	3373	1/1	0.96	0.07	52,52,52,52	0
56	MG	1A	3499	1/1	0.96	0.09	49,49,49,49	0
56	MG	2A	3692	1/1	0.96	0.09	56,56,56,56	0
56	MG	1A	3500	1/1	0.96	0.05	38,38,38,38	0
56	MG	1A	3628	1/1	0.96	0.09	28,28,28,28	0
56	MG	2A	3377	1/1	0.96	0.07	57,57,57,57	0
56	MG	1A	3162	1/1	0.96	0.31	44,44,44,44	0
56	MG	2a	3055	1/1	0.96	0.05	51,51,51,51	0
56	MG	1A	3945	1/1	0.96	0.09	41,41,41,41	0
56	MG	1a	1700	1/1	0.96	0.23	50,50,50,50	0
56	MG	1A	3269	1/1	0.96	0.12	52,52,52,52	0
56	MG	1A	3777	1/1	0.96	0.10	55,55,55,55	0
56	MG	2A	3383	1/1	0.96	0.20	60,60,60,60	0
56	MG	1A	3633	1/1	0.96	0.08	58,58,58,58	0
56	MG	1B	3031	1/1	0.96	0.06	67,67,67,67	0
56	MG	2A	3706	1/1	0.96	0.05	47,47,47,47	0
56	MG	2A	3707	1/1	0.96	0.06	61,61,61,61	0
56	MG	1A	3503	1/1	0.96	0.08	32,32,32,32	0
56	MG	1A	3217	1/1	0.96	0.15	47,47,47,47	0
56	MG	1A	3952	1/1	0.96	0.08	46,46,46,46	0
56	MG	2A	3390	1/1	0.96	0.08	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3781	1/1	0.96	0.09	32,32,32,32	0
56	MG	1B	3037	1/1	0.96	0.06	40,40,40,40	0
56	MG	1A	3126	1/1	0.96	0.09	41,41,41,41	0
56	MG	1A	3099	1/1	0.96	0.08	44,44,44,44	0
56	MG	1A	3956	1/1	0.96	0.06	61,61,61,61	0
56	MG	2A	3118	1/1	0.96	0.15	50,50,50,50	0
56	MG	1A	3021	1/1	0.96	0.10	45,45,45,45	0
56	MG	2A	3120	1/1	0.96	0.10	51,51,51,51	0
56	MG	2A	3122	1/1	0.96	0.06	39,39,39,39	0
56	MG	2A	3724	1/1	0.96	0.06	57,57,57,57	0
56	MG	2A	3725	1/1	0.96	0.09	49,49,49,49	0
56	MG	1a	1714	1/1	0.96	0.16	66,66,66,66	0
56	MG	2a	3082	1/1	0.96	0.16	54,54,54,54	0
56	MG	2A	3124	1/1	0.96	0.10	48,48,48,48	0
56	MG	1D	310	1/1	0.96	0.14	39,39,39,39	0
56	MG	2A	3405	1/1	0.96	0.14	33,33,33,33	0
56	MG	2a	3086	1/1	0.96	0.10	57,57,57,57	0
56	MG	1A	3958	1/1	0.96	0.12	44,44,44,44	0
56	MG	1D	312	1/1	0.96	0.17	42,42,42,42	0
56	MG	2A	3129	1/1	0.96	0.10	50,50,50,50	0
56	MG	2A	3409	1/1	0.96	0.17	47,47,47,47	0
56	MG	2a	3092	1/1	0.96	0.13	51,51,51,51	0
56	MG	1A	3785	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	3960	1/1	0.96	0.08	23,23,23,23	0
56	MG	1A	3642	1/1	0.96	0.06	40,40,40,40	0
56	MG	1A	3222	1/1	0.96	0.12	56,56,56,56	0
56	MG	1A	3345	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	3964	1/1	0.96	0.08	45,45,45,45	0
56	MG	1E	308	1/1	0.96	0.13	34,34,34,34	0
56	MG	2A	3417	1/1	0.96	0.10	41,41,41,41	0
56	MG	2a	3102	1/1	0.96	0.19	58,58,58,58	0
56	MG	2A	3144	1/1	0.96	0.14	45,45,45,45	0
56	MG	1A	3074	1/1	0.96	0.06	27,27,27,27	0
56	MG	1A	3968	1/1	0.96	0.06	62,62,62,62	0
56	MG	1A	3791	1/1	0.96	0.07	43,43,43,43	0
56	MG	1A	3793	1/1	0.96	0.27	37,37,37,37	0
56	MG	1F	305	1/1	0.96	0.07	48,48,48,48	0
56	MG	1A	3347	1/1	0.96	0.08	44,44,44,44	0
56	MG	1A	3517	1/1	0.96	0.08	37,37,37,37	0
56	MG	1A	3518	1/1	0.96	0.10	48,48,48,48	0
56	MG	1A	3651	1/1	0.96	0.12	32,32,32,32	0
56	MG	2A	3156	1/1	0.96	0.07	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3977	1/1	0.96	0.09	56,56,56,56	0
56	MG	1A	3978	1/1	0.96	0.06	65,65,65,65	0
56	MG	2A	3160	1/1	0.96	0.17	44,44,44,44	0
56	MG	2A	3433	1/1	0.96	0.05	64,64,64,64	0
56	MG	1A	3283	1/1	0.96	0.14	40,40,40,40	0
56	MG	2A	3162	1/1	0.96	0.12	53,53,53,53	0
56	MG	2A	3166	1/1	0.96	0.11	47,47,47,47	0
56	MG	1A	3284	1/1	0.96	0.21	56,56,56,56	0
56	MG	2a	3123	1/1	0.96	0.13	54,54,54,54	0
56	MG	1A	3657	1/1	0.96	0.10	27,27,27,27	0
56	MG	1A	3803	1/1	0.96	0.25	44,44,44,44	0
56	MG	1A	3804	1/1	0.96	0.06	40,40,40,40	0
56	MG	1A	3522	1/1	0.96	0.06	49,49,49,49	0
56	MG	1a	1753	1/1	0.96	0.09	59,59,59,59	0
56	MG	1a	1754	1/1	0.96	0.06	51,51,51,51	0
56	MG	1A	3806	1/1	0.96	0.06	34,34,34,34	0
56	MG	2A	3445	1/1	0.96	0.21	55,55,55,55	0
56	MG	1A	3989	1/1	0.96	0.06	60,60,60,60	0
56	MG	2A	3775	1/1	0.96	0.06	38,38,38,38	0
56	MG	2A	3176	1/1	0.96	0.09	46,46,46,46	0
56	MG	1A	3075	1/1	0.96	0.06	28,28,28,28	0
56	MG	1O	203	1/1	0.96	0.11	63,63,63,63	0
56	MG	2A	3779	1/1	0.96	0.08	56,56,56,56	0
56	MG	1A	3429	1/1	0.96	0.07	48,48,48,48	0
56	MG	1A	3057	1/1	0.96	0.10	54,54,54,54	0
56	MG	1A	3528	1/1	0.96	0.05	45,45,45,45	0
56	MG	2a	3144	1/1	0.96	0.11	83,83,83,83	0
56	MG	1A	3292	1/1	0.96	0.07	56,56,56,56	0
56	MG	1A	3031	1/1	0.96	0.12	31,31,31,31	0
56	MG	1A	3356	1/1	0.96	0.09	39,39,39,39	0
56	MG	1a	1768	1/1	0.96	0.09	53,53,53,53	0
56	MG	2a	3150	1/1	0.96	0.06	78,78,78,78	0
56	MG	1A	3998	1/1	0.96	0.09	65,65,65,65	0
56	MG	1A	3815	1/1	0.96	0.21	44,44,44,44	0
56	MG	1A	3533	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3817	1/1	0.96	0.14	45,45,45,45	0
56	MG	2A	3192	1/1	0.96	0.09	44,44,44,44	0
56	MG	1A	3672	1/1	0.96	0.06	31,31,31,31	0
56	MG	2A	3464	1/1	0.96	0.23	54,54,54,54	0
56	MG	1A	3819	1/1	0.96	0.12	48,48,48,48	0
56	MG	1A	3534	1/1	0.96	0.19	33,33,33,33	0
56	MG	2A	3800	1/1	0.96	0.05	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3467	1/1	0.96	0.17	60,60,60,60	0
56	MG	1A	3179	1/1	0.96	0.07	36,36,36,36	0
56	MG	1U	201	1/1	0.96	0.09	52,52,52,52	0
56	MG	1A	3105	1/1	0.96	0.10	40,40,40,40	0
56	MG	1A	4011	1/1	0.96	0.07	43,43,43,43	0
56	MG	2A	3201	1/1	0.96	0.06	51,51,51,51	0
56	MG	2a	3173	1/1	0.96	0.07	62,62,62,62	0
56	MG	1U	204	1/1	0.96	0.13	38,38,38,38	0
56	MG	1U	205	1/1	0.96	0.10	35,35,35,35	0
56	MG	1V	201	1/1	0.96	0.08	49,49,49,49	0
56	MG	1a	1786	1/1	0.96	0.08	64,64,64,64	0
56	MG	2A	3207	1/1	0.96	0.08	44,44,44,44	0
56	MG	1A	3082	1/1	0.96	0.15	49,49,49,49	0
56	MG	1A	4016	1/1	0.96	0.06	46,46,46,46	0
56	MG	2a	3183	1/1	0.96	0.06	76,76,76,76	0
56	MG	2a	3184	1/1	0.96	0.13	54,54,54,54	0
56	MG	1A	3233	1/1	0.96	0.07	49,49,49,49	0
56	MG	2A	3212	1/1	0.96	0.06	52,52,52,52	0
56	MG	1A	4020	1/1	0.96	0.06	53,53,53,53	0
56	MG	2a	3188	1/1	0.96	0.08	68,68,68,68	0
56	MG	2A	3483	1/1	0.96	0.16	55,55,55,55	0
56	MG	1A	3826	1/1	0.96	0.06	42,42,42,42	0
56	MG	2a	3191	1/1	0.96	0.06	63,63,63,63	0
56	MG	2A	3824	1/1	0.96	0.08	78,78,78,78	0
56	MG	1A	3827	1/1	0.96	0.14	50,50,50,50	0
56	MG	1A	3234	1/1	0.96	0.20	54,54,54,54	0
56	MG	2a	3195	1/1	0.96	0.06	41,41,41,41	0
56	MG	1A	3135	1/1	0.96	0.06	32,32,32,32	0
56	MG	1A	3368	1/1	0.96	0.17	47,47,47,47	0
56	MG	1A	4028	1/1	0.96	0.09	69,69,69,69	0
56	MG	2A	3833	1/1	0.96	0.11	55,55,55,55	0
56	MG	2A	3223	1/1	0.96	0.13	44,44,44,44	0
56	MG	1A	3136	1/1	0.96	0.10	52,52,52,52	0
56	MG	1a	1811	1/1	0.96	0.08	77,77,77,77	0
56	MG	1A	3683	1/1	0.96	0.12	40,40,40,40	0
56	MG	10	102	1/1	0.96	0.07	44,44,44,44	0
56	MG	10	103	1/1	0.96	0.07	45,45,45,45	0
56	MG	1A	3086	1/1	0.96	0.12	50,50,50,50	0
56	MG	1A	3239	1/1	0.96	0.10	30,30,30,30	0
56	MG	2A	3504	1/1	0.96	0.05	36,36,36,36	0
56	MG	1A	3140	1/1	0.96	0.16	43,43,43,43	0
56	MG	1a	1826	1/1	0.96	0.06	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4040	1/1	0.96	0.05	60,60,60,60	0
56	MG	1A	4041	1/1	0.96	0.18	36,36,36,36	0
56	MG	1A	3838	1/1	0.96	0.15	45,45,45,45	0
56	MG	2A	3237	1/1	0.96	0.09	39,39,39,39	0
56	MG	2A	3511	1/1	0.96	0.08	24,24,24,24	0
56	MG	1A	3142	1/1	0.96	0.10	23,23,23,23	0
56	MG	1A	3553	1/1	0.96	0.25	49,49,49,49	0
56	MG	2A	3517	1/1	0.96	0.06	42,42,42,42	0
56	MG	1A	3554	1/1	0.96	0.17	47,47,47,47	0
56	MG	1A	3113	1/1	0.96	0.07	35,35,35,35	0
56	MG	1A	3843	1/1	0.96	0.08	31,31,31,31	0
56	MG	1l	202	1/1	0.96	0.09	69,69,69,69	0
56	MG	2A	3873	1/1	0.96	0.10	40,40,40,40	0
56	MG	1A	3556	1/1	0.96	0.21	42,42,42,42	0
56	MG	1A	3845	1/1	0.96	0.10	38,38,38,38	0
56	MG	1A	3311	1/1	0.96	0.14	48,48,48,48	0
56	MG	2A	3248	1/1	0.96	0.09	42,42,42,42	0
56	MG	1A	3144	1/1	0.96	0.09	52,52,52,52	0
56	MG	2A	3881	1/1	0.96	0.07	48,48,48,48	0
56	MG	1A	3695	1/1	0.96	0.07	57,57,57,57	0
56	MG	2A	3253	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	3849	1/1	0.96	0.10	44,44,44,44	0
56	MG	19	101	1/1	0.96	0.17	49,49,49,49	0
56	MG	2A	3887	1/1	0.96	0.07	48,48,48,48	0
56	MG	1A	4056	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	4058	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	3313	1/1	0.96	0.26	49,49,49,49	0
56	MG	1A	3383	1/1	0.96	0.09	55,55,55,55	0
56	MG	2A	3260	1/1	0.96	0.09	53,53,53,53	0
56	MG	1A	3456	1/1	0.96	0.13	48,48,48,48	0
56	MG	1A	3005	1/1	0.96	0.09	41,41,41,41	0
56	MG	2A	3897	1/1	0.96	0.14	57,57,57,57	0
56	MG	2A	3898	1/1	0.96	0.07	28,28,28,28	0
56	MG	1w	111	1/1	0.96	0.07	41,41,41,41	0
56	MG	2A	3264	1/1	0.96	0.05	62,62,62,62	0
56	MG	2A	3902	1/1	0.96	0.15	43,43,43,43	0
56	MG	2A	3547	1/1	0.96	0.04	37,37,37,37	0
56	MG	2A	3905	1/1	0.96	0.13	38,38,38,38	0
56	MG	1A	3040	1/1	0.96	0.07	36,36,36,36	0
56	MG	1A	3317	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3461	1/1	0.96	0.15	44,44,44,44	0
56	MG	1A	3462	1/1	0.96	0.10	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3706	1/1	0.96	0.10	40,40,40,40	0
56	MG	1A	3463	1/1	0.96	0.06	53,53,53,53	0
56	MG	1A	3860	1/1	0.96	0.11	47,47,47,47	0
56	MG	1A	3042	1/1	0.96	0.13	40,40,40,40	0
56	MG	1A	3862	1/1	0.96	0.16	43,43,43,43	0
56	MG	1A	3388	1/1	0.96	0.10	42,42,42,42	0
56	MG	1A	3149	1/1	0.96	0.10	33,33,33,33	0
56	MG	1A	3575	1/1	0.96	0.14	33,33,33,33	0
56	MG	2w	106	1/1	0.96	0.12	60,60,60,60	0
56	MG	2A	3277	1/1	0.96	0.14	50,50,50,50	0
56	MG	1A	3150	1/1	0.96	0.14	50,50,50,50	0
56	MG	1A	3868	1/1	0.96	0.08	47,47,47,47	0
56	MG	1A	4079	1/1	0.96	0.13	46,46,46,46	0
56	MG	2A	3570	1/1	0.96	0.08	53,53,53,53	0
56	MG	1A	3716	1/1	0.96	0.08	28,28,28,28	0
56	MG	1A	3321	1/1	0.96	0.20	51,51,51,51	0
56	MG	1A	4085	1/1	0.96	0.08	21,21,21,21	0
56	MG	1A	3469	1/1	0.96	0.12	53,53,53,53	0
56	MG	1A	3720	1/1	0.96	0.07	53,53,53,53	0
56	MG	1A	3024	1/1	0.96	0.09	43,43,43,43	0
56	MG	2A	3578	1/1	0.96	0.07	39,39,39,39	0
56	MG	2A	3005	1/1	0.96	0.15	48,48,48,48	0
56	MG	1a	1632	1/1	0.96	0.15	52,52,52,52	0
56	MG	2A	3007	1/1	0.96	0.06	43,43,43,43	0
56	MG	2A	3003	1/1	0.97	0.12	43,43,43,43	0
56	MG	1A	3173	1/1	0.97	0.13	42,42,42,42	0
56	MG	1A	3175	1/1	0.97	0.17	40,40,40,40	0
56	MG	1A	3876	1/1	0.97	0.08	49,49,49,49	0
56	MG	2a	3009	1/1	0.97	0.06	60,60,60,60	0
56	MG	1A	3764	1/1	0.97	0.09	31,31,31,31	0
56	MG	1A	4027	1/1	0.97	0.12	50,50,50,50	0
56	MG	2A	3451	1/1	0.97	0.29	56,56,56,56	0
56	MG	1A	3460	1/1	0.97	0.08	48,48,48,48	0
56	MG	2A	3011	1/1	0.97	0.04	48,48,48,48	0
56	MG	1A	3389	1/1	0.97	0.11	53,53,53,53	0
56	MG	2A	3013	1/1	0.97	0.11	44,44,44,44	0
56	MG	1A	4031	1/1	0.97	0.06	54,54,54,54	0
56	MG	2A	3015	1/1	0.97	0.10	43,43,43,43	0
56	MG	2A	3240	1/1	0.97	0.10	40,40,40,40	0
56	MG	1E	309	1/1	0.97	0.05	50,50,50,50	0
56	MG	1A	3880	1/1	0.97	0.11	30,30,30,30	0
56	MG	1A	3881	1/1	0.97	0.08	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3023	1/1	0.97	0.05	47,47,47,47	0
56	MG	2A	3019	1/1	0.97	0.06	38,38,38,38	0
56	MG	2A	3022	1/1	0.97	0.12	47,47,47,47	0
56	MG	1A	3390	1/1	0.97	0.12	35,35,35,35	0
56	MG	1A	3007	1/1	0.97	0.06	38,38,38,38	0
56	MG	1A	4038	1/1	0.97	0.04	45,45,45,45	0
56	MG	1A	3654	1/1	0.97	0.12	36,36,36,36	0
56	MG	1A	3550	1/1	0.97	0.16	38,38,38,38	0
56	MG	1A	4042	1/1	0.97	0.07	46,46,46,46	0
56	MG	2A	3735	1/1	0.97	0.06	55,55,55,55	0
56	MG	1G	3001	1/1	0.97	0.10	41,41,41,41	0
56	MG	1A	3220	1/1	0.97	0.08	41,41,41,41	0
56	MG	1A	3775	1/1	0.97	0.11	27,27,27,27	0
56	MG	1A	3045	1/1	0.97	0.07	36,36,36,36	0
56	MG	1A	3022	1/1	0.97	0.07	21,21,21,21	0
56	MG	1A	3008	1/1	0.97	0.10	26,26,26,26	0
56	MG	1A	3893	1/1	0.97	0.11	17,17,17,17	0
56	MG	1A	3397	1/1	0.97	0.07	47,47,47,47	0
56	MG	1A	3271	1/1	0.97	0.09	50,50,50,50	0
56	MG	1a	1698	1/1	0.97	0.04	52,52,52,52	0
56	MG	2A	3746	1/1	0.97	0.04	68,68,68,68	0
56	MG	1a	1699	1/1	0.97	0.17	40,40,40,40	0
56	MG	1A	3049	1/1	0.97	0.11	26,26,26,26	0
56	MG	1A	3559	1/1	0.97	0.17	34,34,34,34	0
56	MG	1A	3092	1/1	0.97	0.07	50,50,50,50	0
56	MG	1A	3670	1/1	0.97	0.07	32,32,32,32	0
56	MG	1A	3562	1/1	0.97	0.05	24,24,24,24	0
56	MG	2A	3047	1/1	0.97	0.09	46,46,46,46	0
56	MG	1A	3401	1/1	0.97	0.14	35,35,35,35	0
56	MG	2A	3755	1/1	0.97	0.08	50,50,50,50	0
56	MG	1O	205	1/1	0.97	0.05	44,44,44,44	0
56	MG	2A	3489	1/1	0.97	0.06	41,41,41,41	0
56	MG	1A	3274	1/1	0.97	0.11	36,36,36,36	0
56	MG	1A	3475	1/1	0.97	0.08	42,42,42,42	0
56	MG	1A	3789	1/1	0.97	0.05	29,29,29,29	0
56	MG	1A	3277	1/1	0.97	0.11	38,38,38,38	0
56	MG	1A	3051	1/1	0.97	0.06	50,50,50,50	0
56	MG	2A	3497	1/1	0.97	0.06	63,63,63,63	0
56	MG	1A	3792	1/1	0.97	0.07	35,35,35,35	0
56	MG	2A	3499	1/1	0.97	0.05	46,46,46,46	0
56	MG	1A	3405	1/1	0.97	0.16	42,42,42,42	0
56	MG	1R	202	1/1	0.97	0.11	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3502	1/1	0.97	0.05	43,43,43,43	0
56	MG	2a	3066	1/1	0.97	0.12	54,54,54,54	0
56	MG	1A	3228	1/1	0.97	0.08	41,41,41,41	0
56	MG	1A	3187	1/1	0.97	0.14	47,47,47,47	0
56	MG	1A	3282	1/1	0.97	0.05	30,30,30,30	0
56	MG	1A	3797	1/1	0.97	0.10	53,53,53,53	0
56	MG	1A	3341	1/1	0.97	0.14	55,55,55,55	0
56	MG	1A	3033	1/1	0.97	0.17	36,36,36,36	0
56	MG	1A	3574	1/1	0.97	0.19	43,43,43,43	0
56	MG	1A	3012	1/1	0.97	0.05	30,30,30,30	0
56	MG	1a	1725	1/1	0.97	0.26	55,55,55,55	0
56	MG	1A	3054	1/1	0.97	0.11	39,39,39,39	0
56	MG	1A	3288	1/1	0.97	0.08	43,43,43,43	0
56	MG	1a	1728	1/1	0.97	0.22	48,48,48,48	0
56	MG	2A	3293	1/1	0.97	0.07	50,50,50,50	0
56	MG	1A	3929	1/1	0.97	0.07	42,42,42,42	0
56	MG	1U	208	1/1	0.97	0.10	38,38,38,38	0
56	MG	2A	3296	1/1	0.97	0.11	45,45,45,45	0
56	MG	2A	3523	1/1	0.97	0.08	27,27,27,27	0
56	MG	2A	3524	1/1	0.97	0.06	48,48,48,48	0
56	MG	2A	3789	1/1	0.97	0.09	49,49,49,49	0
56	MG	2A	3526	1/1	0.97	0.04	41,41,41,41	0
56	MG	1A	3688	1/1	0.97	0.06	15,15,15,15	0
56	MG	2A	3298	1/1	0.97	0.08	41,41,41,41	0
56	MG	2A	3793	1/1	0.97	0.13	56,56,56,56	0
56	MG	1A	4082	1/1	0.97	0.11	38,38,38,38	0
56	MG	1A	3934	1/1	0.97	0.06	44,44,44,44	0
56	MG	2A	3078	1/1	0.97	0.09	25,25,25,25	0
56	MG	1A	3191	1/1	0.97	0.16	42,42,42,42	0
56	MG	1A	3807	1/1	0.97	0.06	38,38,38,38	0
56	MG	1X	101	1/1	0.97	0.08	40,40,40,40	0
56	MG	1X	102	1/1	0.97	0.08	46,46,46,46	0
56	MG	2a	3098	1/1	0.97	0.08	46,46,46,46	0
56	MG	1a	1740	1/1	0.97	0.10	35,35,35,35	0
56	MG	1X	103	1/1	0.97	0.11	40,40,40,40	0
56	MG	1X	104	1/1	0.97	0.06	52,52,52,52	0
56	MG	1A	4086	1/1	0.97	0.20	43,43,43,43	0
56	MG	2A	3806	1/1	0.97	0.08	66,66,66,66	0
56	MG	1a	1745	1/1	0.97	0.10	55,55,55,55	0
56	MG	2A	3542	1/1	0.97	0.04	39,39,39,39	0
56	MG	1A	3125	1/1	0.97	0.15	41,41,41,41	0
56	MG	1A	3039	1/1	0.97	0.09	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1748	1/1	0.97	0.06	43,43,43,43	0
56	MG	2A	3092	1/1	0.97	0.10	43,43,43,43	0
56	MG	1A	4089	1/1	0.97	0.05	36,36,36,36	0
56	MG	2A	3548	1/1	0.97	0.09	38,38,38,38	0
56	MG	1A	3940	1/1	0.97	0.05	48,48,48,48	0
56	MG	1A	3942	1/1	0.97	0.05	56,56,56,56	0
56	MG	1A	3349	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	3077	1/1	0.97	0.14	35,35,35,35	0
56	MG	1A	3078	1/1	0.97	0.10	31,31,31,31	0
56	MG	1A	3156	1/1	0.97	0.15	40,40,40,40	0
56	MG	1A	3157	1/1	0.97	0.11	53,53,53,53	0
56	MG	2A	3825	1/1	0.97	0.09	58,58,58,58	0
56	MG	2A	3102	1/1	0.97	0.09	56,56,56,56	0
56	MG	1A	4099	1/1	0.97	0.09	41,41,41,41	0
56	MG	1A	3496	1/1	0.97	0.10	38,38,38,38	0
56	MG	1A	3243	1/1	0.97	0.08	53,53,53,53	0
56	MG	2A	3831	1/1	0.97	0.05	45,45,45,45	0
56	MG	1A	3013	1/1	0.97	0.17	35,35,35,35	0
56	MG	2A	3562	1/1	0.97	0.04	37,37,37,37	0
56	MG	2A	3107	1/1	0.97	0.06	46,46,46,46	0
56	MG	1A	3199	1/1	0.97	0.11	45,45,45,45	0
56	MG	2A	3566	1/1	0.97	0.09	33,33,33,33	0
56	MG	2A	3838	1/1	0.97	0.06	47,47,47,47	0
56	MG	2A	3109	1/1	0.97	0.05	37,37,37,37	0
56	MG	2A	3840	1/1	0.97	0.11	43,43,43,43	0
56	MG	1a	1764	1/1	0.97	0.04	59,59,59,59	0
56	MG	1a	1765	1/1	0.97	0.06	49,49,49,49	0
56	MG	1A	3593	1/1	0.97	0.10	56,56,56,56	0
56	MG	2A	3845	1/1	0.97	0.08	42,42,42,42	0
56	MG	1A	3820	1/1	0.97	0.09	41,41,41,41	0
56	MG	2A	3849	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	4106	1/1	0.97	0.07	29,29,29,29	0
56	MG	2A	3852	1/1	0.97	0.05	49,49,49,49	0
56	MG	1A	4107	1/1	0.97	0.08	42,42,42,42	0
56	MG	2A	3575	1/1	0.97	0.06	39,39,39,39	0
56	MG	1A	3358	1/1	0.97	0.12	33,33,33,33	0
56	MG	1A	3360	1/1	0.97	0.20	31,31,31,31	0
56	MG	1a	1772	1/1	0.97	0.05	39,39,39,39	0
56	MG	2A	3859	1/1	0.97	0.06	53,53,53,53	0
56	MG	16	103	1/1	0.97	0.08	54,54,54,54	0
56	MG	1A	4110	1/1	0.97	0.06	56,56,56,56	0
56	MG	2a	3154	1/1	0.97	0.11	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3581	1/1	0.97	0.07	25,25,25,25	0
56	MG	1A	4111	1/1	0.97	0.08	34,34,34,34	0
56	MG	1A	3080	1/1	0.97	0.14	42,42,42,42	0
56	MG	1A	3081	1/1	0.97	0.15	34,34,34,34	0
56	MG	1A	3248	1/1	0.97	0.16	47,47,47,47	0
56	MG	2A	3589	1/1	0.97	0.05	45,45,45,45	0
56	MG	2A	3347	1/1	0.97	0.12	51,51,51,51	0
56	MG	1A	3599	1/1	0.97	0.08	21,21,21,21	0
56	MG	1a	1780	1/1	0.97	0.06	74,74,74,74	0
56	MG	2A	3595	1/1	0.97	0.08	49,49,49,49	0
56	MG	2a	3169	1/1	0.97	0.07	51,51,51,51	0
56	MG	1A	3161	1/1	0.97	0.16	38,38,38,38	0
56	MG	1A	3365	1/1	0.97	0.09	53,53,53,53	0
56	MG	2A	3879	1/1	0.97	0.07	37,37,37,37	0
56	MG	1A	3713	1/1	0.97	0.14	62,62,62,62	0
56	MG	2A	3132	1/1	0.97	0.14	56,56,56,56	0
56	MG	2a	3175	1/1	0.97	0.06	46,46,46,46	0
56	MG	1A	3714	1/1	0.97	0.08	46,46,46,46	0
56	MG	2A	3602	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	3965	1/1	0.97	0.13	67,67,67,67	0
56	MG	2A	3135	1/1	0.97	0.07	43,43,43,43	0
56	MG	1A	3603	1/1	0.97	0.14	39,39,39,39	0
56	MG	2a	3181	1/1	0.97	0.06	69,69,69,69	0
56	MG	1A	3433	1/1	0.97	0.13	47,47,47,47	0
56	MG	2A	3142	1/1	0.97	0.16	41,41,41,41	0
56	MG	1A	3434	1/1	0.97	0.08	48,48,48,48	0
56	MG	1a	1792	1/1	0.97	0.06	59,59,59,59	0
56	MG	2A	3145	1/1	0.97	0.09	36,36,36,36	0
56	MG	1A	3606	1/1	0.97	0.10	36,36,36,36	0
56	MG	1a	1609	1/1	0.97	0.15	54,54,54,54	0
56	MG	1A	3510	1/1	0.97	0.05	45,45,45,45	0
56	MG	1A	4133	1/1	0.97	0.14	45,45,45,45	0
56	MG	1A	3972	1/1	0.97	0.06	60,60,60,60	0
56	MG	1a	1800	1/1	0.97	0.10	70,70,70,70	0
56	MG	1a	1614	1/1	0.97	0.11	45,45,45,45	0
56	MG	1A	3511	1/1	0.97	0.06	45,45,45,45	0
56	MG	2A	3904	1/1	0.97	0.16	41,41,41,41	0
56	MG	2A	3154	1/1	0.97	0.16	48,48,48,48	0
56	MG	2A	3621	1/1	0.97	0.08	51,51,51,51	0
56	MG	1A	4136	1/1	0.97	0.07	40,40,40,40	0
56	MG	1A	3366	1/1	0.97	0.05	38,38,38,38	0
56	MG	1A	3309	1/1	0.97	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
56	MG	1A	3611	1/1	0.97	0.06	25,25,25,25	0
56	MG	1a	1814	1/1	0.97	0.09	55,55,55,55	0
56	MG	1a	1621	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	4141	1/1	0.97	0.24	50,50,50,50	0
56	MG	2A	3163	1/1	0.97	0.10	56,56,56,56	0
56	MG	2A	3164	1/1	0.97	0.20	53,53,53,53	0
56	MG	2A	3633	1/1	0.97	0.11	55,55,55,55	0
56	MG	2A	3634	1/1	0.97	0.07	34,34,34,34	0
56	MG	2A	3165	1/1	0.97	0.20	49,49,49,49	0
56	MG	1a	1819	1/1	0.97	0.05	48,48,48,48	0
56	MG	2A	3385	1/1	0.97	0.13	52,52,52,52	0
56	MG	1a	1820	1/1	0.97	0.05	57,57,57,57	0
56	MG	1a	1821	1/1	0.97	0.05	62,62,62,62	0
56	MG	1A	3020	1/1	0.97	0.05	25,25,25,25	0
56	MG	1B	3001	1/1	0.97	0.20	48,48,48,48	0
56	MG	2a	3217	1/1	0.97	0.07	61,61,61,61	0
56	MG	1A	3515	1/1	0.97	0.09	29,29,29,29	0
56	MG	1A	3107	1/1	0.97	0.14	35,35,35,35	0
56	MG	1A	3108	1/1	0.97	0.29	43,43,43,43	0
56	MG	1A	3371	1/1	0.97	0.07	45,45,45,45	0
56	MG	1A	3620	1/1	0.97	0.12	25,25,25,25	0
56	MG	1A	3520	1/1	0.97	0.09	41,41,41,41	0
56	MG	1A	3372	1/1	0.97	0.12	58,58,58,58	0
56	MG	1A	3443	1/1	0.97	0.07	54,54,54,54	0
56	MG	1f	3001	1/1	0.97	0.12	34,34,34,34	0
56	MG	2A	3652	1/1	0.97	0.13	41,41,41,41	0
56	MG	1A	3524	1/1	0.97	0.05	47,47,47,47	0
56	MG	2A	3400	1/1	0.97	0.06	56,56,56,56	0
56	MG	2A	3401	1/1	0.97	0.12	52,52,52,52	0
56	MG	2A	3181	1/1	0.97	0.13	40,40,40,40	0
56	MG	2A	3657	1/1	0.97	0.16	39,39,39,39	0
56	MG	1A	3991	1/1	0.97	0.12	48,48,48,48	0
56	MG	1A	3083	1/1	0.97	0.15	44,44,44,44	0
56	MG	1A	3111	1/1	0.97	0.06	40,40,40,40	0
56	MG	1n	103	1/1	0.97	0.16	48,48,48,48	0
56	MG	1A	3211	1/1	0.97	0.07	49,49,49,49	0
56	MG	1B	3015	1/1	0.97	0.09	58,58,58,58	0
56	MG	1A	3043	1/1	0.97	0.06	39,39,39,39	0
56	MG	1A	3629	1/1	0.97	0.08	32,32,32,32	0
56	MG	1w	102	1/1	0.97	0.13	61,61,61,61	0
56	MG	1A	3138	1/1	0.97	0.25	36,36,36,36	0
56	MG	2a	3244	1/1	0.97	0.07	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3449	1/1	0.97	0.06	41,41,41,41	0
56	MG	1A	3749	1/1	0.97	0.07	41,41,41,41	0
56	MG	1A	3379	1/1	0.97	0.09	37,37,37,37	0
56	MG	1A	3634	1/1	0.97	0.08	44,44,44,44	0
56	MG	2Q	3003	1/1	0.97	0.06	51,51,51,51	0
56	MG	1A	3532	1/1	0.97	0.16	36,36,36,36	0
56	MG	1A	3258	1/1	0.97	0.07	33,33,33,33	0
56	MG	1B	3027	1/1	0.97	0.04	35,35,35,35	0
56	MG	2A	3200	1/1	0.97	0.10	42,42,42,42	0
56	MG	2A	3677	1/1	0.97	0.27	35,35,35,35	0
56	MG	1A	4005	1/1	0.97	0.05	50,50,50,50	0
56	MG	1A	3864	1/1	0.97	0.13	35,35,35,35	0
56	MG	2A	3423	1/1	0.97	0.07	58,58,58,58	0
56	MG	1A	3381	1/1	0.97	0.07	43,43,43,43	0
56	MG	1a	1654	1/1	0.97	0.17	49,49,49,49	0
56	MG	1A	4008	1/1	0.97	0.06	56,56,56,56	0
56	MG	1A	4009	1/1	0.97	0.09	27,27,27,27	0
56	MG	1a	1658	1/1	0.97	0.12	57,57,57,57	0
56	MG	1A	3214	1/1	0.97	0.10	42,42,42,42	0
56	MG	1A	3640	1/1	0.97	0.09	53,53,53,53	0
56	MG	1A	3170	1/1	0.97	0.11	39,39,39,39	0
56	MG	1A	4013	1/1	0.97	0.04	33,33,33,33	0
56	MG	2A	3690	1/1	0.97	0.12	61,61,61,61	0
56	MG	2x	101	1/1	0.97	0.10	42,42,42,42	0
56	MG	1D	301	1/1	0.97	0.17	46,46,46,46	0
56	MG	2A	3215	1/1	0.97	0.09	37,37,37,37	0
56	MG	1A	4015	1/1	0.97	0.04	37,37,37,37	0
56	MG	1D	304	1/1	0.97	0.12	30,30,30,30	0
56	MG	1A	3139	1/1	0.97	0.08	48,48,48,48	0
56	MG	1A	4018	1/1	0.97	0.13	67,67,67,67	0
56	MG	2A	3697	1/1	0.97	0.06	34,34,34,34	0
56	MG	1A	3262	1/1	0.97	0.06	49,49,49,49	0
56	MG	2A	3222	1/1	0.97	0.10	38,38,38,38	0
56	MG	2y	3006	1/1	0.97	0.05	86,86,86,86	0
56	MG	1A	3263	1/1	0.97	0.13	52,52,52,52	0
56	MG	1a	1670	1/1	0.97	0.09	59,59,59,59	0
57	K	2A	3496	1/1	0.97	0.10	73,73,73,73	0
56	MG	1A	3761	1/1	0.97	0.09	51,51,51,51	0
56	MG	2A	3002	1/1	0.97	0.26	57,57,57,57	0
56	MG	1A	3663	1/1	0.98	0.05	28,28,28,28	0
56	MG	1A	3470	1/1	0.98	0.07	47,47,47,47	0
56	MG	2A	3846	1/1	0.98	0.05	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3847	1/1	0.98	0.09	42,42,42,42	0
56	MG	1w	108	1/1	0.98	0.05	63,63,63,63	0
56	MG	2A	3650	1/1	0.98	0.11	41,41,41,41	0
56	MG	1A	3915	1/1	0.98	0.05	39,39,39,39	0
56	MG	1A	3106	1/1	0.98	0.06	25,25,25,25	0
56	MG	2A	3853	1/1	0.98	0.05	50,50,50,50	0
56	MG	1A	3237	1/1	0.98	0.19	38,38,38,38	0
56	MG	2A	3136	1/1	0.98	0.12	45,45,45,45	0
56	MG	2A	3137	1/1	0.98	0.04	42,42,42,42	0
56	MG	1A	3828	1/1	0.98	0.07	34,34,34,34	0
56	MG	2A	3139	1/1	0.98	0.15	32,32,32,32	0
56	MG	2A	3140	1/1	0.98	0.14	50,50,50,50	0
56	MG	1A	4139	1/1	0.98	0.05	35,35,35,35	0
56	MG	2A	3861	1/1	0.98	0.06	36,36,36,36	0
56	MG	2A	3862	1/1	0.98	0.07	71,71,71,71	0
56	MG	2A	3863	1/1	0.98	0.06	58,58,58,58	0
56	MG	1A	3204	1/1	0.98	0.12	26,26,26,26	0
56	MG	1A	3668	1/1	0.98	0.11	28,28,28,28	0
56	MG	2a	3089	1/1	0.98	0.18	65,65,65,65	0
56	MG	1A	3205	1/1	0.98	0.08	42,42,42,42	0
56	MG	1A	3275	1/1	0.98	0.07	44,44,44,44	0
56	MG	1A	3276	1/1	0.98	0.08	49,49,49,49	0
56	MG	1A	4030	1/1	0.98	0.05	44,44,44,44	0
56	MG	1A	3174	1/1	0.98	0.20	38,38,38,38	0
56	MG	1A	3927	1/1	0.98	0.04	47,47,47,47	0
56	MG	2A	3668	1/1	0.98	0.06	45,45,45,45	0
56	MG	1A	3673	1/1	0.98	0.09	29,29,29,29	0
56	MG	1A	4034	1/1	0.98	0.05	51,51,51,51	0
56	MG	1A	4035	1/1	0.98	0.04	46,46,46,46	0
56	MG	2A	3877	1/1	0.98	0.14	28,28,28,28	0
56	MG	1A	3930	1/1	0.98	0.04	30,30,30,30	0
56	MG	1a	1716	1/1	0.98	0.06	53,53,53,53	0
56	MG	1x	116	1/1	0.98	0.04	59,59,59,59	0
56	MG	1A	3241	1/1	0.98	0.07	44,44,44,44	0
56	MG	2A	3882	1/1	0.98	0.06	44,44,44,44	0
56	MG	2A	3157	1/1	0.98	0.09	58,58,58,58	0
56	MG	1A	3933	1/1	0.98	0.05	47,47,47,47	0
56	MG	2A	3491	1/1	0.98	0.16	55,55,55,55	0
56	MG	1A	3837	1/1	0.98	0.10	21,21,21,21	0
56	MG	1A	3535	1/1	0.98	0.18	45,45,45,45	0
56	MG	1A	3536	1/1	0.98	0.15	37,37,37,37	0
56	MG	1A	3279	1/1	0.98	0.05	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3113	1/1	0.98	0.13	46,46,46,46	0
56	MG	1A	3014	1/1	0.98	0.05	31,31,31,31	0
56	MG	1a	1724	1/1	0.98	0.06	36,36,36,36	0
56	MG	1A	3481	1/1	0.98	0.09	39,39,39,39	0
56	MG	1B	3018	1/1	0.98	0.04	37,37,37,37	0
56	MG	1A	3941	1/1	0.98	0.04	46,46,46,46	0
56	MG	2A	3896	1/1	0.98	0.19	39,39,39,39	0
56	MG	1A	3176	1/1	0.98	0.05	37,37,37,37	0
56	MG	2A	3009	1/1	0.98	0.06	31,31,31,31	0
56	MG	1A	3177	1/1	0.98	0.14	38,38,38,38	0
56	MG	1A	3178	1/1	0.98	0.10	21,21,21,21	0
56	MG	1A	4050	1/1	0.98	0.12	32,32,32,32	0
56	MG	1a	1732	1/1	0.98	0.08	48,48,48,48	0
56	MG	1A	3071	1/1	0.98	0.10	38,38,38,38	0
56	MG	1A	3072	1/1	0.98	0.07	19,19,19,19	0
56	MG	1B	3026	1/1	0.98	0.04	42,42,42,42	0
56	MG	1A	3286	1/1	0.98	0.31	49,49,49,49	0
56	MG	2A	3512	1/1	0.98	0.04	53,53,53,53	0
56	MG	2A	3513	1/1	0.98	0.08	34,34,34,34	0
56	MG	1A	3767	1/1	0.98	0.07	41,41,41,41	0
56	MG	2a	3133	1/1	0.98	0.07	54,54,54,54	0
56	MG	2A	3701	1/1	0.98	0.08	64,64,64,64	0
56	MG	1A	3287	1/1	0.98	0.13	30,30,30,30	0
56	MG	2A	3020	1/1	0.98	0.17	49,49,49,49	0
56	MG	2A	3021	1/1	0.98	0.07	28,28,28,28	0
56	MG	2A	3519	1/1	0.98	0.06	33,33,33,33	0
56	MG	1A	3547	1/1	0.98	0.06	53,53,53,53	0
56	MG	2a	3140	1/1	0.98	0.04	57,57,57,57	0
56	MG	1a	1741	1/1	0.98	0.06	34,34,34,34	0
56	MG	2A	3184	1/1	0.98	0.13	48,48,48,48	0
56	MG	2a	3143	1/1	0.98	0.05	73,73,73,73	0
56	MG	1A	4057	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	3015	1/1	0.98	0.07	40,40,40,40	0
56	MG	2A	3525	1/1	0.98	0.07	34,34,34,34	0
56	MG	2a	3147	1/1	0.98	0.10	49,49,49,49	0
56	MG	1A	3771	1/1	0.98	0.08	49,49,49,49	0
56	MG	2A	3027	1/1	0.98	0.16	48,48,48,48	0
56	MG	2A	3714	1/1	0.98	0.07	39,39,39,39	0
56	MG	1A	3549	1/1	0.98	0.05	38,38,38,38	0
56	MG	2A	3357	1/1	0.98	0.05	39,39,39,39	0
56	MG	1a	1611	1/1	0.98	0.06	22,22,22,22	0
56	MG	1A	3289	1/1	0.98	0.07	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3617	1/1	0.98	0.07	33,33,33,33	0
56	MG	1a	1749	1/1	0.98	0.10	45,45,45,45	0
56	MG	2a	3157	1/1	0.98	0.06	64,64,64,64	0
56	MG	1A	3290	1/1	0.98	0.08	46,46,46,46	0
56	MG	2A	3723	1/1	0.98	0.05	50,50,50,50	0
56	MG	1A	3619	1/1	0.98	0.13	31,31,31,31	0
56	MG	2a	3162	1/1	0.98	0.03	62,62,62,62	0
56	MG	1D	303	1/1	0.98	0.13	37,37,37,37	0
56	MG	1A	3439	1/1	0.98	0.09	40,40,40,40	0
56	MG	2A	3037	1/1	0.98	0.05	35,35,35,35	0
56	MG	1A	3056	1/1	0.98	0.10	28,28,28,28	0
56	MG	2A	3729	1/1	0.98	0.05	41,41,41,41	0
56	MG	2A	3368	1/1	0.98	0.06	47,47,47,47	0
56	MG	1a	1619	1/1	0.98	0.06	62,62,62,62	0
56	MG	1A	3011	1/1	0.98	0.12	46,46,46,46	0
56	MG	1A	3035	1/1	0.98	0.09	20,20,20,20	0
56	MG	1A	3046	1/1	0.98	0.12	32,32,32,32	0
56	MG	2A	3204	1/1	0.98	0.13	48,48,48,48	0
56	MG	1A	3295	1/1	0.98	0.05	48,48,48,48	0
56	MG	1A	3296	1/1	0.98	0.08	58,58,58,58	0
56	MG	1A	3701	1/1	0.98	0.08	48,48,48,48	0
56	MG	2F	303	1/1	0.98	0.04	48,48,48,48	0
56	MG	2F	304	1/1	0.98	0.17	53,53,53,53	0
56	MG	1A	3702	1/1	0.98	0.07	34,34,34,34	0
56	MG	2A	3551	1/1	0.98	0.07	39,39,39,39	0
56	MG	1E	303	1/1	0.98	0.08	26,26,26,26	0
56	MG	1A	3394	1/1	0.98	0.05	35,35,35,35	0
56	MG	2A	3211	1/1	0.98	0.06	43,43,43,43	0
56	MG	1A	3561	1/1	0.98	0.28	48,48,48,48	0
56	MG	1A	4077	1/1	0.98	0.10	11,11,11,11	0
56	MG	1A	3297	1/1	0.98	0.13	32,32,32,32	0
56	MG	1A	3186	1/1	0.98	0.08	39,39,39,39	0
56	MG	1A	4080	1/1	0.98	0.10	23,23,23,23	0
56	MG	1a	1634	1/1	0.98	0.05	27,27,27,27	0
56	MG	1E	310	1/1	0.98	0.03	42,42,42,42	0
56	MG	1A	3036	1/1	0.98	0.12	31,31,31,31	0
56	MG	1A	3974	1/1	0.98	0.06	45,45,45,45	0
56	MG	2A	3564	1/1	0.98	0.06	31,31,31,31	0
56	MG	1A	3098	1/1	0.98	0.11	25,25,25,25	0
56	MG	1A	3118	1/1	0.98	0.09	38,38,38,38	0
56	MG	2A	3567	1/1	0.98	0.04	50,50,50,50	0
56	MG	1F	304	1/1	0.98	0.17	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2X	101	1/1	0.98	0.03	37,37,37,37	0
56	MG	1A	3037	1/1	0.98	0.11	40,40,40,40	0
56	MG	1A	3303	1/1	0.98	0.08	33,33,33,33	0
56	MG	1A	3223	1/1	0.98	0.08	32,32,32,32	0
56	MG	1A	3038	1/1	0.98	0.07	50,50,50,50	0
56	MG	1A	3141	1/1	0.98	0.06	35,35,35,35	0
56	MG	1A	3063	1/1	0.98	0.08	38,38,38,38	0
56	MG	1A	3717	1/1	0.98	0.08	22,22,22,22	0
56	MG	2A	3069	1/1	0.98	0.06	40,40,40,40	0
56	MG	1a	1785	1/1	0.98	0.04	55,55,55,55	0
56	MG	1A	3984	1/1	0.98	0.09	34,34,34,34	0
56	MG	1a	1787	1/1	0.98	0.05	72,72,72,72	0
56	MG	1A	3801	1/1	0.98	0.04	28,28,28,28	0
56	MG	2a	3212	1/1	0.98	0.10	51,51,51,51	0
56	MG	1A	3986	1/1	0.98	0.08	22,22,22,22	0
56	MG	2A	3075	1/1	0.98	0.08	37,37,37,37	0
56	MG	1A	3355	1/1	0.98	0.18	47,47,47,47	0
56	MG	2A	3584	1/1	0.98	0.12	37,37,37,37	0
56	MG	2A	3585	1/1	0.98	0.05	43,43,43,43	0
56	MG	1a	1791	1/1	0.98	0.05	54,54,54,54	0
56	MG	2A	3587	1/1	0.98	0.05	37,37,37,37	0
56	MG	1A	4098	1/1	0.98	0.06	45,45,45,45	0
56	MG	1N	203	1/1	0.98	0.05	48,48,48,48	0
56	MG	1A	3988	1/1	0.98	0.04	68,68,68,68	0
56	MG	1A	3122	1/1	0.98	0.06	44,44,44,44	0
56	MG	1A	3644	1/1	0.98	0.04	33,33,33,33	0
56	MG	2A	3594	1/1	0.98	0.04	38,38,38,38	0
56	MG	1A	3887	1/1	0.98	0.09	31,31,31,31	0
56	MG	2A	3785	1/1	0.98	0.16	45,45,45,45	0
56	MG	2A	3084	1/1	0.98	0.04	45,45,45,45	0
56	MG	2A	3787	1/1	0.98	0.04	64,64,64,64	0
56	MG	1a	1799	1/1	0.98	0.05	49,49,49,49	0
56	MG	2A	3250	1/1	0.98	0.06	41,41,41,41	0
56	MG	1A	3050	1/1	0.98	0.14	32,32,32,32	0
56	MG	2A	3600	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	3229	1/1	0.98	0.17	33,33,33,33	0
56	MG	1A	3578	1/1	0.98	0.14	33,33,33,33	0
56	MG	1a	1805	1/1	0.98	0.05	47,47,47,47	0
56	MG	1A	3891	1/1	0.98	0.04	41,41,41,41	0
56	MG	1a	1808	1/1	0.98	0.05	53,53,53,53	0
56	MG	1a	1809	1/1	0.98	0.05	56,56,56,56	0
56	MG	2A	3093	1/1	0.98	0.09	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3241	1/1	0.98	0.04	41,41,41,41	0
56	MG	1A	3516	1/1	0.98	0.15	25,25,25,25	0
56	MG	1A	3359	1/1	0.98	0.09	38,38,38,38	0
56	MG	1P	201	1/1	0.98	0.04	26,26,26,26	0
56	MG	1P	202	1/1	0.98	0.06	31,31,31,31	0
56	MG	1P	203	1/1	0.98	0.15	30,30,30,30	0
56	MG	2f	3001	1/1	0.98	0.08	41,41,41,41	0
56	MG	2A	3804	1/1	0.98	0.12	31,31,31,31	0
56	MG	1A	3145	1/1	0.98	0.13	32,32,32,32	0
56	MG	1Q	201	1/1	0.98	0.08	36,36,36,36	0
56	MG	2A	3807	1/1	0.98	0.06	61,61,61,61	0
56	MG	2l	201	1/1	0.98	0.04	66,66,66,66	0
56	MG	1Q	202	1/1	0.98	0.04	46,46,46,46	0
56	MG	1A	3168	1/1	0.98	0.08	42,42,42,42	0
56	MG	1a	1822	1/1	0.98	0.10	54,54,54,54	0
56	MG	2A	3618	1/1	0.98	0.06	39,39,39,39	0
56	MG	1A	3653	1/1	0.98	0.08	27,27,27,27	0
56	MG	1A	3009	1/1	0.98	0.04	24,24,24,24	0
56	MG	1A	3731	1/1	0.98	0.04	17,17,17,17	0
56	MG	1R	201	1/1	0.98	0.17	30,30,30,30	0
56	MG	1A	4114	1/1	0.98	0.04	34,34,34,34	0
56	MG	2A	3624	1/1	0.98	0.04	32,32,32,32	0
56	MG	1A	4115	1/1	0.98	0.15	51,51,51,51	0
56	MG	1A	3314	1/1	0.98	0.05	33,33,33,33	0
56	MG	1A	3656	1/1	0.98	0.05	46,46,46,46	0
56	MG	1A	4118	1/1	0.98	0.10	36,36,36,36	0
56	MG	1A	4119	1/1	0.98	0.07	34,34,34,34	0
56	MG	1A	3902	1/1	0.98	0.08	33,33,33,33	0
56	MG	2A	3826	1/1	0.98	0.14	54,54,54,54	0
56	MG	1A	4122	1/1	0.98	0.04	41,41,41,41	0
56	MG	1A	3903	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	3010	1/1	0.98	0.14	39,39,39,39	0
56	MG	1A	3523	1/1	0.98	0.07	44,44,44,44	0
56	MG	1A	4126	1/1	0.98	0.12	45,45,45,45	0
56	MG	1U	206	1/1	0.98	0.14	32,32,32,32	0
56	MG	2A	3121	1/1	0.98	0.12	42,42,42,42	0
56	MG	1A	3736	1/1	0.98	0.09	46,46,46,46	0
56	MG	1A	3069	1/1	0.98	0.12	20,20,20,20	0
56	MG	1A	3738	1/1	0.98	0.04	43,43,43,43	0
56	MG	2A	3125	1/1	0.98	0.14	44,44,44,44	0
56	MG	1A	3172	1/1	0.98	0.05	43,43,43,43	0
56	MG	1A	3910	1/1	0.98	0.04	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3841	1/1	0.98	0.04	30,30,30,30	0
58	ZN	14	501	1/1	0.98	0.05	99,99,99,99	0
58	ZN	2Y	501	1/1	0.98	0.04	81,81,81,81	0
56	MG	1A	3662	1/1	0.98	0.07	30,30,30,30	0
58	ZN	25	102	1/1	0.98	0.15	68,68,68,68	0
56	MG	1W	205	1/1	0.98	0.05	39,39,39,39	0
59	SF4	1d	501	8/8	0.98	0.05	59,71,76,86	0
59	SF4	2d	501	8/8	0.98	0.05	61,71,85,99	0
56	MG	1D	306	1/1	0.99	0.10	32,32,32,32	0
56	MG	1A	3739	1/1	0.99	0.04	39,39,39,39	0
56	MG	1l	201	1/1	0.99	0.11	43,43,43,43	0
56	MG	1D	308	1/1	0.99	0.06	48,48,48,48	0
56	MG	1A	3740	1/1	0.99	0.09	28,28,28,28	0
56	MG	1a	1653	1/1	0.99	0.04	54,54,54,54	0
56	MG	1A	3032	1/1	0.99	0.17	31,31,31,31	0
56	MG	1a	1655	1/1	0.99	0.03	43,43,43,43	0
56	MG	2A	3851	1/1	0.99	0.04	46,46,46,46	0
56	MG	2A	3538	1/1	0.99	0.04	35,35,35,35	0
56	MG	1A	3924	1/1	0.99	0.03	50,50,50,50	0
56	MG	1A	3925	1/1	0.99	0.04	14,14,14,14	0
56	MG	2A	3319	1/1	0.99	0.04	49,49,49,49	0
56	MG	1A	3041	1/1	0.99	0.20	38,38,38,38	0
56	MG	1A	4004	1/1	0.99	0.04	29,29,29,29	0
56	MG	1A	3027	1/1	0.99	0.04	33,33,33,33	0
56	MG	1A	4096	1/1	0.99	0.05	30,30,30,30	0
56	MG	2A	3251	1/1	0.99	0.06	42,42,42,42	0
56	MG	1A	3928	1/1	0.99	0.11	31,31,31,31	0
56	MG	1A	3967	1/1	0.99	0.05	65,65,65,65	0
56	MG	1A	3773	1/1	0.99	0.04	41,41,41,41	0
56	MG	1A	3065	1/1	0.99	0.13	33,33,33,33	0
56	MG	1A	3896	1/1	0.99	0.12	47,47,47,47	0
56	MG	1A	3932	1/1	0.99	0.06	45,45,45,45	0
56	MG	1A	3602	1/1	0.99	0.08	25,25,25,25	0
56	MG	2A	3049	1/1	0.99	0.07	23,23,23,23	0
56	MG	1U	207	1/1	0.99	0.13	31,31,31,31	0
56	MG	2A	3870	1/1	0.99	0.05	33,33,33,33	0
56	MG	2A	3632	1/1	0.99	0.03	41,41,41,41	0
56	MG	1A	3030	1/1	0.99	0.04	34,34,34,34	0
56	MG	1A	4014	1/1	0.99	0.03	34,34,34,34	0
56	MG	1A	3935	1/1	0.99	0.05	50,50,50,50	0
56	MG	1A	3747	1/1	0.99	0.09	53,53,53,53	0
56	MG	1A	4017	1/1	0.99	0.05	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1W	202	1/1	0.99	0.13	50,50,50,50	0
56	MG	1W	203	1/1	0.99	0.05	30,30,30,30	0
56	MG	1A	3200	1/1	0.99	0.15	23,23,23,23	0
56	MG	1a	1796	1/1	0.99	0.03	59,59,59,59	0
56	MG	1A	3003	1/1	0.99	0.05	27,27,27,27	0
56	MG	1A	3551	1/1	0.99	0.14	37,37,37,37	0
56	MG	1A	3084	1/1	0.99	0.04	34,34,34,34	0
56	MG	1a	1739	1/1	0.99	0.03	36,36,36,36	0
56	MG	1a	1801	1/1	0.99	0.03	53,53,53,53	0
56	MG	1a	1802	1/1	0.99	0.06	52,52,52,52	0
56	MG	1A	3650	1/1	0.99	0.07	35,35,35,35	0
56	MG	2a	3160	1/1	0.99	0.04	49,49,49,49	0
56	MG	1A	4023	1/1	0.99	0.04	47,47,47,47	0
56	MG	1A	3414	1/1	0.99	0.04	39,39,39,39	0
56	MG	20	3002	1/1	0.99	0.03	63,63,63,63	0
56	MG	1X	106	1/1	0.99	0.06	29,29,29,29	0
56	MG	1a	1807	1/1	0.99	0.04	67,67,67,67	0
56	MG	1A	3085	1/1	0.99	0.10	30,30,30,30	0
56	MG	2a	3167	1/1	0.99	0.03	69,69,69,69	0
56	MG	2A	3732	1/1	0.99	0.07	42,42,42,42	0
56	MG	1A	3726	1/1	0.99	0.04	48,48,48,48	0
56	MG	2A	3895	1/1	0.99	0.09	46,46,46,46	0
56	MG	1a	1810	1/1	0.99	0.03	51,51,51,51	0
56	MG	1A	3068	1/1	0.99	0.10	38,38,38,38	0
56	MG	1A	3946	1/1	0.99	0.03	49,49,49,49	0
56	MG	1A	3097	1/1	0.99	0.03	35,35,35,35	0
56	MG	1A	4121	1/1	0.99	0.09	34,34,34,34	0
56	MG	2A	3901	1/1	0.99	0.12	59,59,59,59	0
56	MG	2A	3817	1/1	0.99	0.03	56,56,56,56	0
56	MG	1A	3632	1/1	0.99	0.03	34,34,34,34	0
56	MG	1a	1816	1/1	0.99	0.04	48,48,48,48	0
56	MG	2A	3820	1/1	0.99	0.06	49,49,49,49	0
56	MG	1a	1817	1/1	0.99	0.04	79,79,79,79	0
56	MG	1A	4075	1/1	0.99	0.03	42,42,42,42	0
56	MG	1A	3612	1/1	0.99	0.05	41,41,41,41	0
56	MG	2A	3221	1/1	0.99	0.08	48,48,48,48	0
56	MG	2A	3514	1/1	0.99	0.04	32,32,32,32	0
56	MG	1A	3508	1/1	0.99	0.11	36,36,36,36	0
56	MG	1A	3635	1/1	0.99	0.05	32,32,32,32	0
56	MG	1A	3914	1/1	0.99	0.07	53,53,53,53	0
56	MG	2A	3593	1/1	0.99	0.05	30,30,30,30	0
56	MG	1A	3707	1/1	0.99	0.09	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	11	102	1/1	0.99	0.04	36,36,36,36	0
56	MG	1a	1825	1/1	0.99	0.14	37,37,37,37	0
56	MG	1A	4081	1/1	0.99	0.08	44,44,44,44	0
56	MG	1B	3036	1/1	0.99	0.03	36,36,36,36	0
56	MG	2A	3835	1/1	0.99	0.03	43,43,43,43	0
56	MG	1A	3375	1/1	0.99	0.08	43,43,43,43	0
58	ZN	15	101	1/1	0.99	0.09	37,37,37,37	0
58	ZN	19	103	1/1	0.99	0.04	44,44,44,44	0
58	ZN	1n	101	1/1	0.99	0.04	71,71,71,71	0
56	MG	1A	3109	1/1	0.99	0.13	35,35,35,35	0
56	MG	1A	3661	1/1	0.99	0.07	32,32,32,32	0
56	MG	2A	3233	1/1	0.99	0.10	32,32,32,32	0
58	ZN	26	501	1/1	0.99	0.03	60,60,60,60	0
58	ZN	29	101	1/1	0.99	0.04	73,73,73,73	0
56	MG	1A	4039	1/1	0.99	0.02	21,21,21,21	0
56	MG	1A	3577	1/1	0.99	0.09	27,27,27,27	0
56	MG	1A	3055	1/1	0.99	0.11	43,43,43,43	0
56	MG	1A	3873	1/1	1.00	0.07	35,35,35,35	0
58	ZN	1Y	501	1/1	1.00	0.03	60,60,60,60	0
56	MG	1a	1763	1/1	1.00	0.09	55,55,55,55	0
56	MG	2A	3715	1/1	1.00	0.04	46,46,46,46	0
58	ZN	16	102	1/1	1.00	0.04	44,44,44,44	0

6.5 Other polymers (i)

There are no such residues in this entry.