Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 11:04 AM UTC

PDB ID	:	8T8C / pdb_00008t8c
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with protein Y, A-site aminoacyl-tRNA analog ACC-PMN, and P-site formyl-MFI -tripeptidyl-tRNA analog ACCA-IFMf at 2.60A resolution
Authors	:	Thaler, J.; Syroegin, E.A.; Breuker, K.; Polikanov, Y.S.; Micura, R.
Deposited on	:	2023-06-22
Resolution	:	2.60 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:

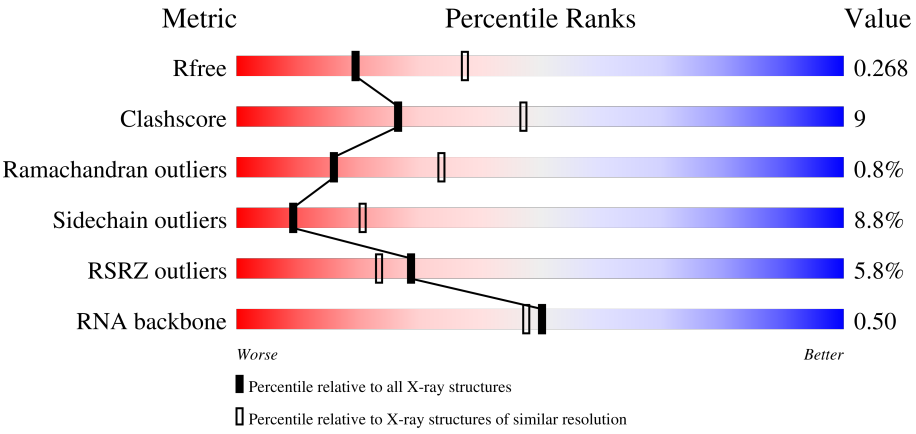
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)
RNA backbone	3983	1014 (2.84-2.36)

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

Mol	Chain	Length	Quality of chain
1	1A	2915	4% 64% 29% 6%
1	2A	2915	5% 57% 34% 7%
2	1B	121	% 64% 31%
2	2B	121	16% 53% 41% 5%

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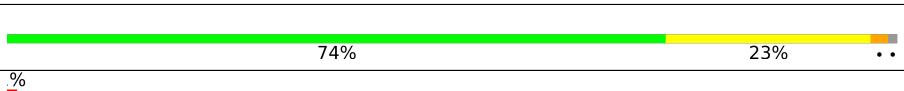
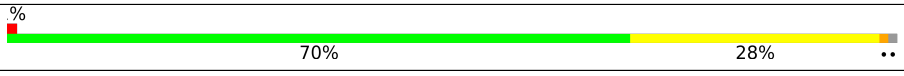
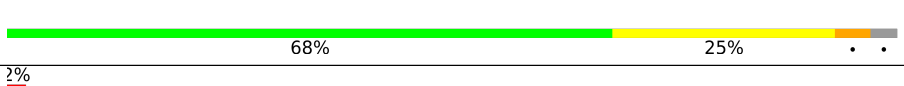
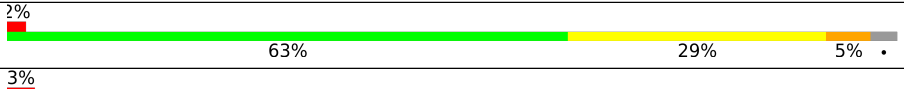
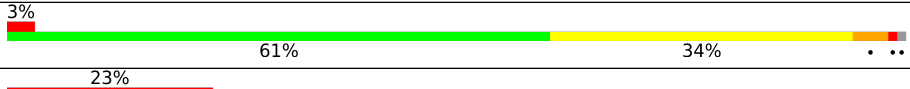
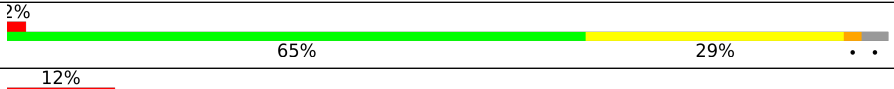
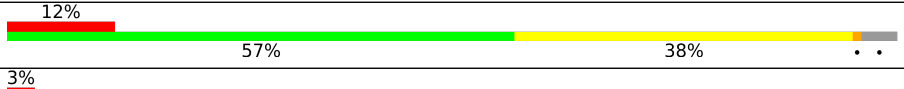
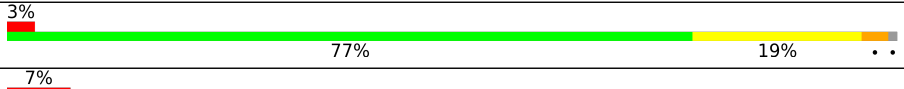
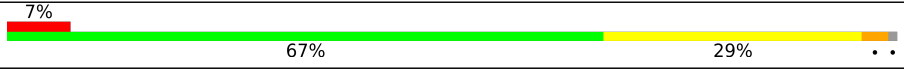
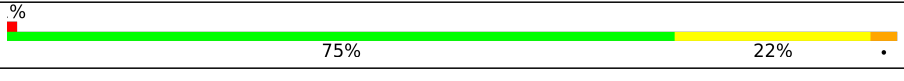
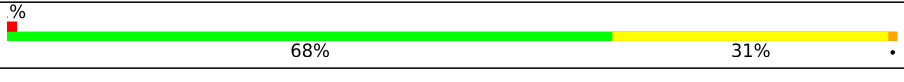
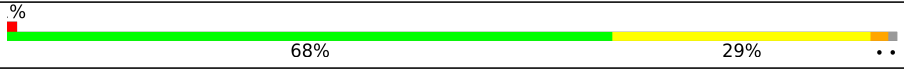
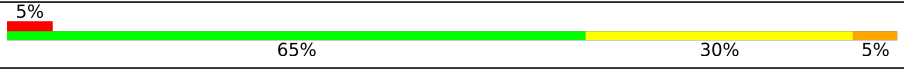
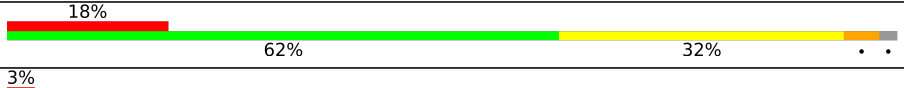
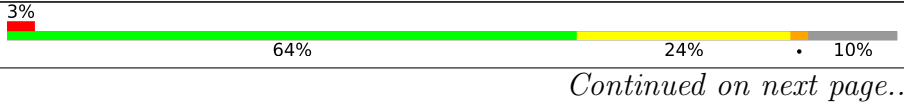
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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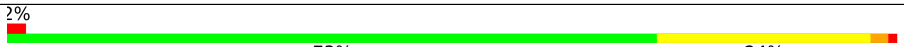
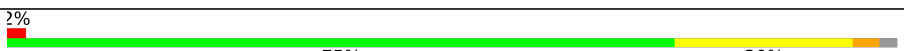
Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	
27	25	60	

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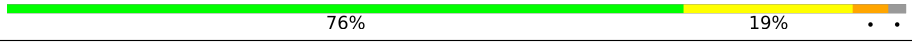
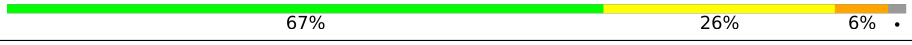
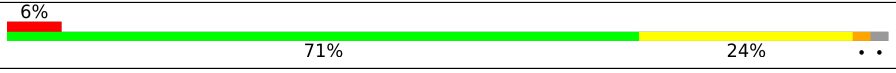
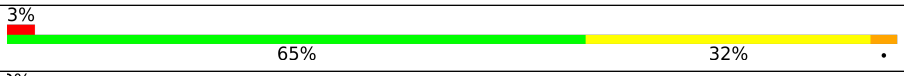
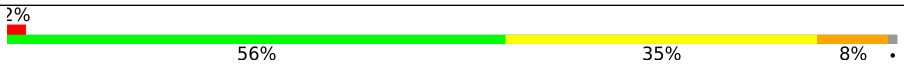
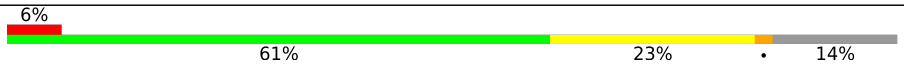
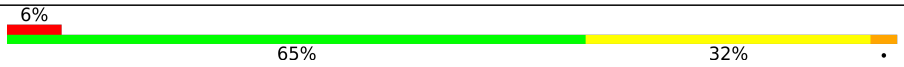
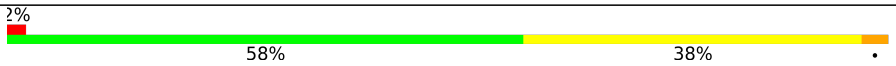
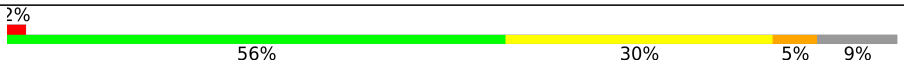
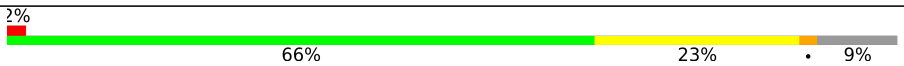
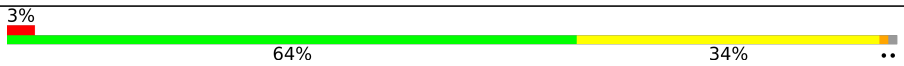
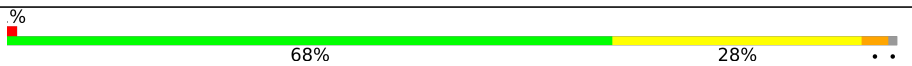
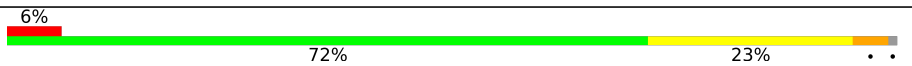
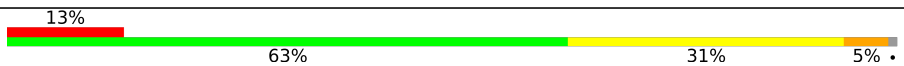
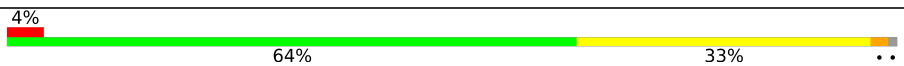
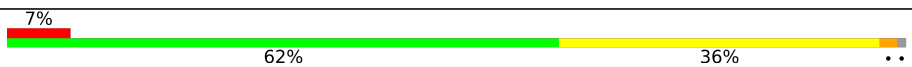
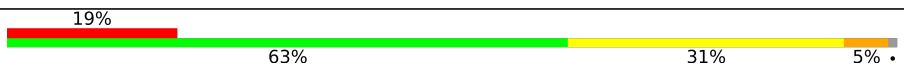
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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Mol	Chain	Length	Quality of chain
40	2i	128	41% 52% 40% 7%
41	1j	105	12% 59% 30% 8%
41	2j	105	41% 54% 33% 9%
42	1k	129	2% 73% 14% 12%
42	2k	129	5% 70% 16% 12%
43	1l	132	2% 71% 19% 8%
43	2l	132	2% 74% 17% 8%
44	1m	126	6% 49% 38% 5% 8%
44	2m	126	21% 63% 24% 10%
45	1n	61	8% 61% 36%
45	2n	61	54% 69% 30%
46	1o	89	7% 66% 28%
46	2o	89	6% 69% 27%
47	1p	88	13% 61% 26% 6% 7%
47	2p	88	7% 57% 33% 7%
48	1q	105	5% 71% 20% 6%
48	2q	105	3% 57% 36% 6%
49	1r	88	% 60% 14% 23%
49	2r	88	% 57% 20% 23%
50	1s	93	4% 52% 34% 11%
50	2s	93	26% 48% 38% 11%
51	1t	106	10% 60% 26% 9%
51	2t	106	8% 67% 25% 8%
52	1u	27	19% 56% 30% 15%
52	2u	27	37% 56% 30% 15%

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Mol	Chain	Length	Quality of chain
53	1y	113	6% 60% 24% 14%
53	2y	113	23% 57% 26% 15%
54	1w	4	50% 50%
54	2w	4	50% 25% 25%
55	1x	4	75% 25%
55	2x	4	25% 75% 25%
56	1v	3	33% 67%
56	2v	3	33% 67%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	1a	1871	-	-	-	X
57	MG	2A	3090	-	-	-	X
57	MG	2A	3291	-	-	-	X
61	SF4	2d	501	-	-	X	-

2 Entry composition (i)

There are 62 unique types of molecules in this entry. The entry contains 296459 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	2872	Total	C	N	O	P	0	0	0
			61869	27540	11574	19884	2871			
1	2A	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

- 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
			2572	1145	476	832	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- 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
			2131	1346	422	360	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
			1426	916	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	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	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	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
			1121	722	208	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 877	C 553	N 175	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
			775	498	141	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
			810	520	153	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			
21	2Z	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	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
			650	401	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
			754	475	148	130	1			
23	21	97	Total	C	N	O	S	0	0	0
			759	478	149	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
			592	368	119	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
			546	346	96	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			536	342	98	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
			459	288	90	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	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			

- 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
			1842	1175	330	332	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
			1558	979	305	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
			1665	1043	329	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1668	1047	330	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
			1133	716	214	199	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
			814	516	144	151	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
			1235	769	244	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1229	766	241	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
			1098	694	210	192	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
			986	625	193	168			
40	2i	126	Total	C	N	O	0	0	0
			966	613	186	167			

- 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
			719	446	142	131			
41	2j	96	Total	C	N	O	0	0	0
			710	442	137	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
			834	520	156	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	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			
44	2m	114	Total	C	N	O	S	0	0	0
			895	550	186	157	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
			648	415	120	111	2			
50	2s	83	Total	C	N	O	S	0	0	0
			645	410	118	115	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
			732	449	157	124	2			
51	2t	98	Total	C	N	O	S	0	0	0
			733	451	154	126	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 protein called Ribosome-associated inhibitor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1y	97	Total	C	N	O	S	0	0	0
			764	478	144	139	3			
53	2y	96	Total	C	N	O	S	0	0	0
			749	468	141	137	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	4	Total	C	N	O	P	0	0	1
			78	40	13	22	3			
54	2w	4	Total	C	N	O	P	0	0	1
			78	40	13	22	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	1x	4	Total	C	N	O	P	0	0	1
			63	28	12	20	3			
55	2x	4	Total	C	N	O	P	0	0	1
			63	28	12	20	3			

- Molecule 56 is a protein called P-site Peptidyl-tRNA Analog Peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	1v	3	Total	C	N	O	S	0	0	0
			29	21	3	4	1			
56	2v	3	Total	C	N	O	S	0	0	0
			29	21	3	4	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1029	Total	Mg	0	0
			1029	1029		
57	1B	29	Total	Mg	0	0
			29	29		
57	1D	16	Total	Mg	0	0
			16	16		
57	1E	9	Total	Mg	0	0
			9	9		
57	1F	15	Total	Mg	0	0
			15	15		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1G	4	Total Mg 4 4	0	0
57	1H	2	Total Mg 2 2	0	0
57	1N	4	Total Mg 4 4	0	0
57	1O	2	Total Mg 2 2	0	0
57	1P	3	Total Mg 3 3	0	0
57	1Q	5	Total Mg 5 5	0	0
57	1R	5	Total Mg 5 5	0	0
57	1T	5	Total Mg 5 5	0	0
57	1U	7	Total Mg 7 7	0	0
57	1V	6	Total Mg 6 6	0	0
57	1W	4	Total Mg 4 4	0	0
57	1Y	1	Total Mg 1 1	0	0
57	1Z	1	Total Mg 1 1	0	0
57	10	10	Total Mg 10 10	0	0
57	11	3	Total Mg 3 3	0	0
57	13	4	Total Mg 4 4	0	0
57	15	9	Total Mg 9 9	0	0
57	17	5	Total Mg 5 5	0	0
57	18	2	Total Mg 2 2	0	0
57	19	3	Total Mg 3 3	0	0
57	1a	272	Total Mg 272 272	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1b	1	Total Mg 1 1	0	0
57	1d	5	Total Mg 5 5	0	0
57	1e	3	Total Mg 3 3	0	0
57	1f	2	Total Mg 2 2	0	0
57	1g	2	Total Mg 2 2	0	0
57	1h	2	Total Mg 2 2	0	0
57	1i	1	Total Mg 1 1	0	0
57	1l	2	Total Mg 2 2	0	0
57	1m	1	Total Mg 1 1	0	0
57	1n	3	Total Mg 3 3	0	0
57	1o	1	Total Mg 1 1	0	0
57	1t	1	Total Mg 1 1	0	0
57	1u	1	Total Mg 1 1	0	0
57	1y	3	Total Mg 3 3	0	0
57	1w	1	Total Mg 1 1	0	0
57	1x	2	Total Mg 2 2	0	0
57	2A	734	Total Mg 734 734	0	0
57	2B	17	Total Mg 17 17	0	0
57	2D	11	Total Mg 11 11	0	0
57	2E	8	Total Mg 8 8	0	0
57	2F	4	Total Mg 4 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2G	2	Total Mg 2 2	0	0
57	2I	1	Total Mg 1 1	0	0
57	2N	1	Total Mg 1 1	0	0
57	2P	2	Total Mg 2 2	0	0
57	2Q	2	Total Mg 2 2	0	0
57	2R	2	Total Mg 2 2	0	0
57	2T	4	Total Mg 4 4	0	0
57	2V	2	Total Mg 2 2	0	0
57	2W	3	Total Mg 3 3	0	0
57	2X	1	Total Mg 1 1	0	0
57	2Y	1	Total Mg 1 1	0	0
57	20	1	Total Mg 1 1	0	0
57	21	4	Total Mg 4 4	0	0
57	23	1	Total Mg 1 1	0	0
57	25	4	Total Mg 4 4	0	0
57	27	1	Total Mg 1 1	0	0
57	28	1	Total Mg 1 1	0	0
57	29	1	Total Mg 1 1	0	0
57	2a	188	Total Mg 188 188	0	0
57	2e	2	Total Mg 2 2	0	0
57	2f	1	Total Mg 1 1	0	0

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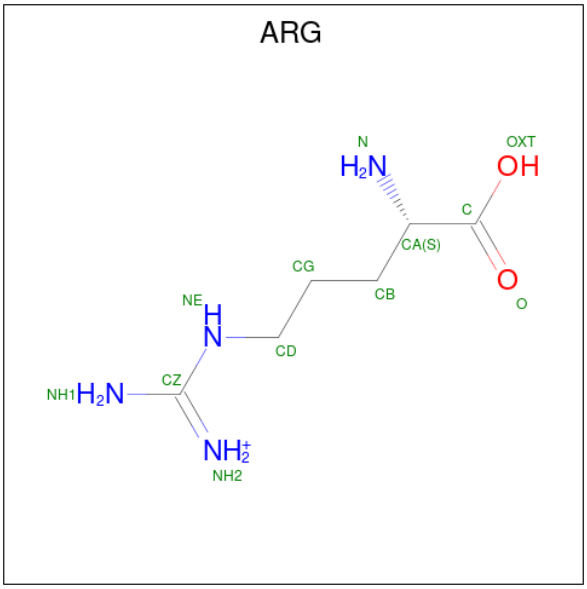
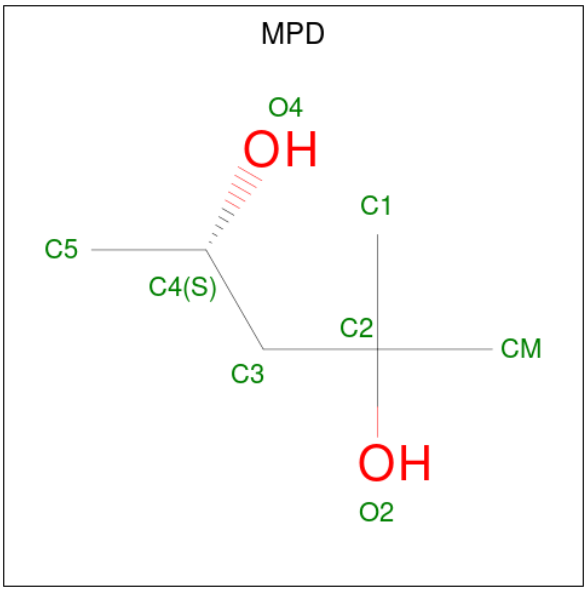
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2j	1	Total Mg 1 1	0	0
57	2n	1	Total Mg 1 1	0	0
57	2p	1	Total Mg 1 1	0	0
57	2t	1	Total Mg 1 1	0	0
57	2x	1	Total Mg 1 1	0	0

- Molecule 58 is ARGININE (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1A	1	Total C N O 12 6 4 2	0	0
58	1B	1	Total C N O 12 6 4 2	0	0

- Molecule 59 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	1	Total C O 8 6 2	0	0
59	18	1	Total C O 8 6 2	0	0
59	1a	1	Total C O 8 6 2	0	0
59	1a	1	Total C O 8 6 2	0	0
59	2A	1	Total C O 8 6 2	0	0
59	2A	1	Total C O 8 6 2	0	0
59	2A	1	Total C O 8 6 2	0	0

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

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

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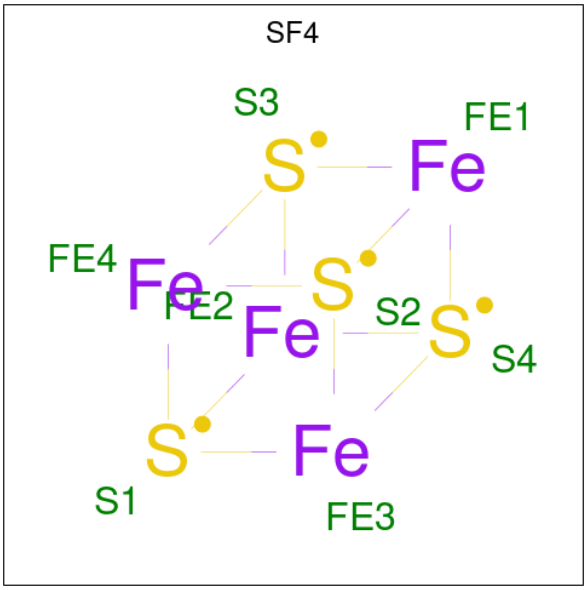
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1n	1	Total Zn 1 1	0	0
60	2Y	1	Total Zn 1 1	0	0
60	24	1	Total Zn 1 1	0	0
60	25	1	Total Zn 1 1	0	0
60	26	1	Total Zn 1 1	0	0
60	29	1	Total Zn 1 1	0	0
60	2n	1	Total Zn 1 1	0	0

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



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

- Molecule 62 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1A	3560	Total O 3560 3560	0	0
62	1B	89	Total O 89 89	0	0
62	1D	98	Total O 98 98	0	0
62	1E	69	Total O 69 69	0	0
62	1F	51	Total O 51 51	0	0
62	1G	15	Total O 15 15	0	0
62	1H	6	Total O 6 6	0	0
62	1I	4	Total O 4 4	0	0
62	1N	43	Total O 43 43	0	0
62	1O	22	Total O 22 22	0	0
62	1P	63	Total O 63 63	0	0
62	1Q	33	Total O 33 33	0	0
62	1R	30	Total O 30 30	0	0
62	1S	8	Total O 8 8	0	0
62	1T	24	Total O 24 24	0	0
62	1U	45	Total O 45 45	0	0
62	1V	30	Total O 30 30	0	0
62	1W	26	Total O 26 26	0	0
62	1X	23	Total O 23 23	0	0
62	1Y	12	Total O 12 12	0	0
62	1Z	9	Total O 9 9	0	0
62	10	22	Total O 22 22	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	11	24	Total O 24 24	0	0
62	12	10	Total O 10 10	0	0
62	13	19	Total O 19 19	0	0
62	14	2	Total O 2 2	0	0
62	15	24	Total O 24 24	0	0
62	16	15	Total O 15 15	0	0
62	17	14	Total O 14 14	0	0
62	18	21	Total O 21 21	0	0
62	19	7	Total O 7 7	0	0
62	1a	382	Total O 382 382	0	0
62	1d	5	Total O 5 5	0	0
62	1e	3	Total O 3 3	0	0
62	1f	2	Total O 2 2	0	0
62	1h	1	Total O 1 1	0	0
62	1i	1	Total O 1 1	0	0
62	1j	1	Total O 1 1	0	0
62	1l	3	Total O 3 3	0	0
62	1o	3	Total O 3 3	0	0
62	1p	2	Total O 2 2	0	0
62	1u	1	Total O 1 1	0	0
62	1y	3	Total O 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1w	4	Total O 4 4	0	0
62	1x	4	Total O 4 4	0	0
62	2A	1737	Total O 1737 1737	0	0
62	2B	33	Total O 33 33	0	0
62	2D	32	Total O 32 32	0	0
62	2E	22	Total O 22 22	0	0
62	2F	20	Total O 20 20	0	0
62	2G	2	Total O 2 2	0	0
62	2I	2	Total O 2 2	0	0
62	2N	3	Total O 3 3	0	0
62	2O	11	Total O 11 11	0	0
62	2P	18	Total O 18 18	0	0
62	2Q	7	Total O 7 7	0	0
62	2R	14	Total O 14 14	0	0
62	2S	2	Total O 2 2	0	0
62	2T	6	Total O 6 6	0	0
62	2U	7	Total O 7 7	0	0
62	2V	5	Total O 5 5	0	0
62	2W	7	Total O 7 7	0	0
62	2X	4	Total O 4 4	0	0
62	2Y	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	2Z	9	Total O 9 9	0	0
62	20	7	Total O 7 7	0	0
62	21	17	Total O 17 17	0	0
62	25	7	Total O 7 7	0	0
62	26	1	Total O 1 1	0	0
62	27	4	Total O 4 4	0	0
62	28	12	Total O 12 12	0	0
62	2a	224	Total O 224 224	0	0
62	2d	3	Total O 3 3	0	0
62	2e	2	Total O 2 2	0	0
62	2f	1	Total O 1 1	0	0
62	2j	1	Total O 1 1	0	0
62	2l	3	Total O 3 3	0	0
62	2o	3	Total O 3 3	0	0
62	2p	1	Total O 1 1	0	0
62	2q	1	Total O 1 1	0	0
62	2r	2	Total O 2 2	0	0
62	2t	1	Total O 1 1	0	0
62	2y	1	Total O 1 1	0	0
62	2w	3	Total O 3 3	0	0
62	2x	2	Total O 2 2	0	0

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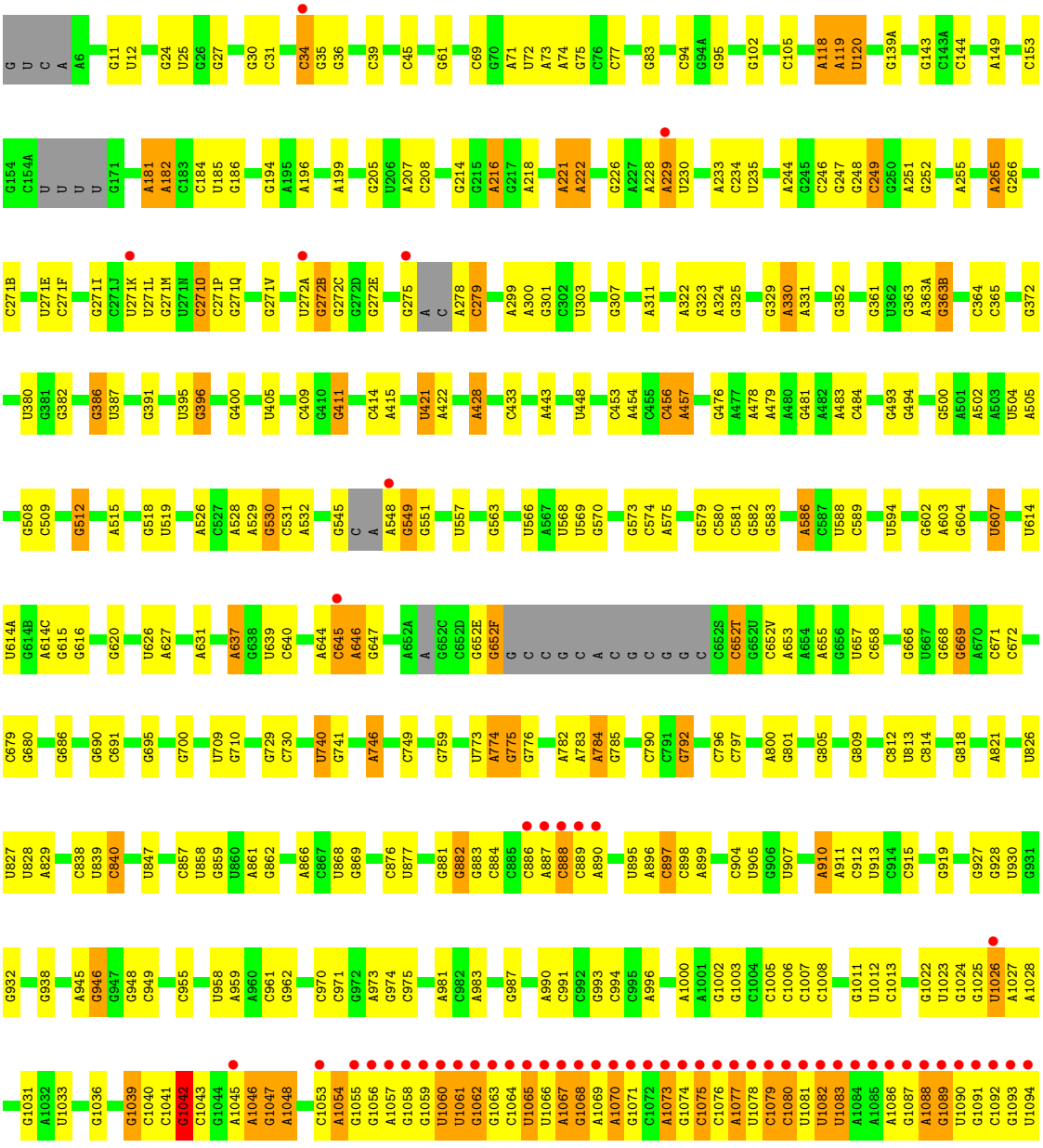
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	2v	1	Total O 1 1	0	0

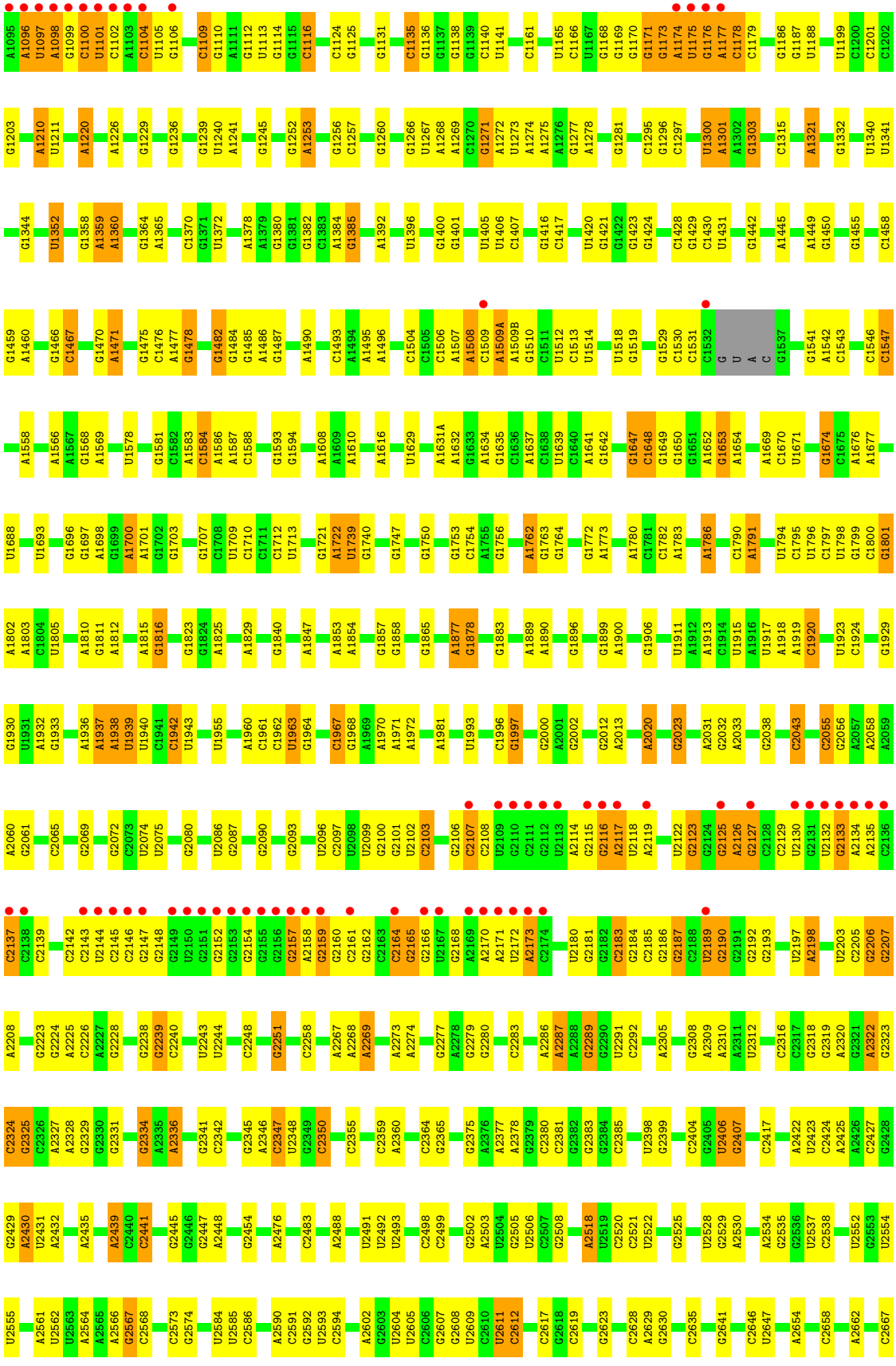
3 Residue-property plots (i)

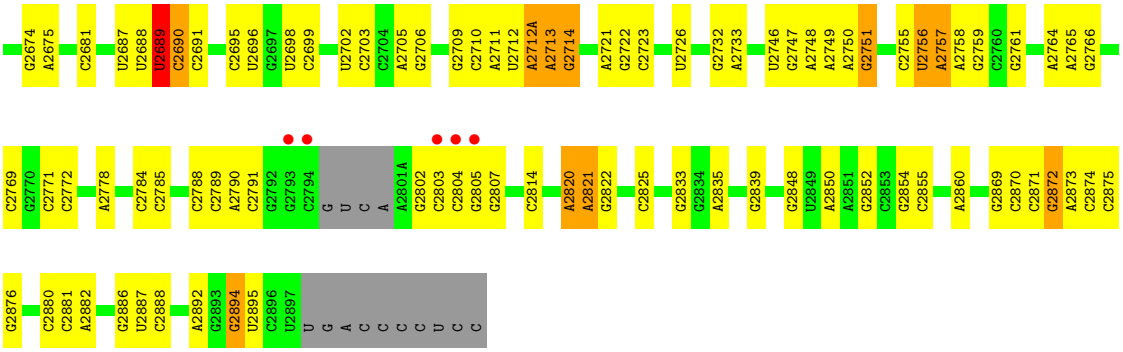
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

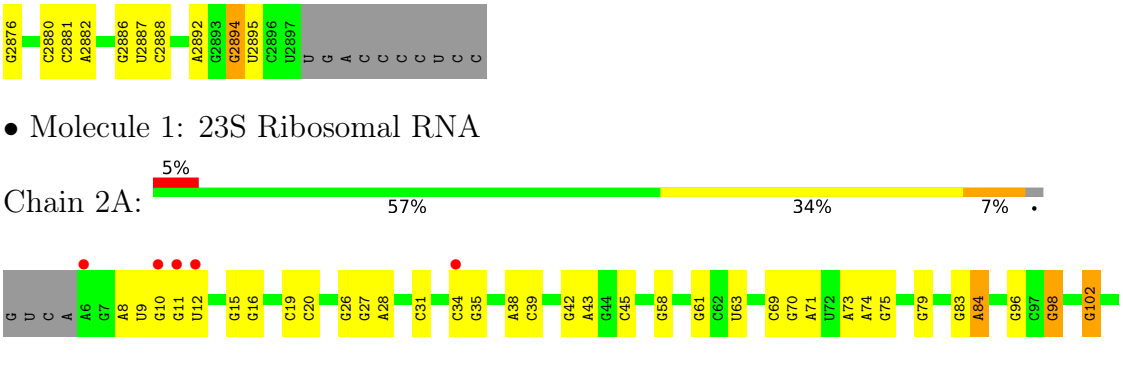
• Molecule 1: 23S Ribosomal RNA

Chain 1A:



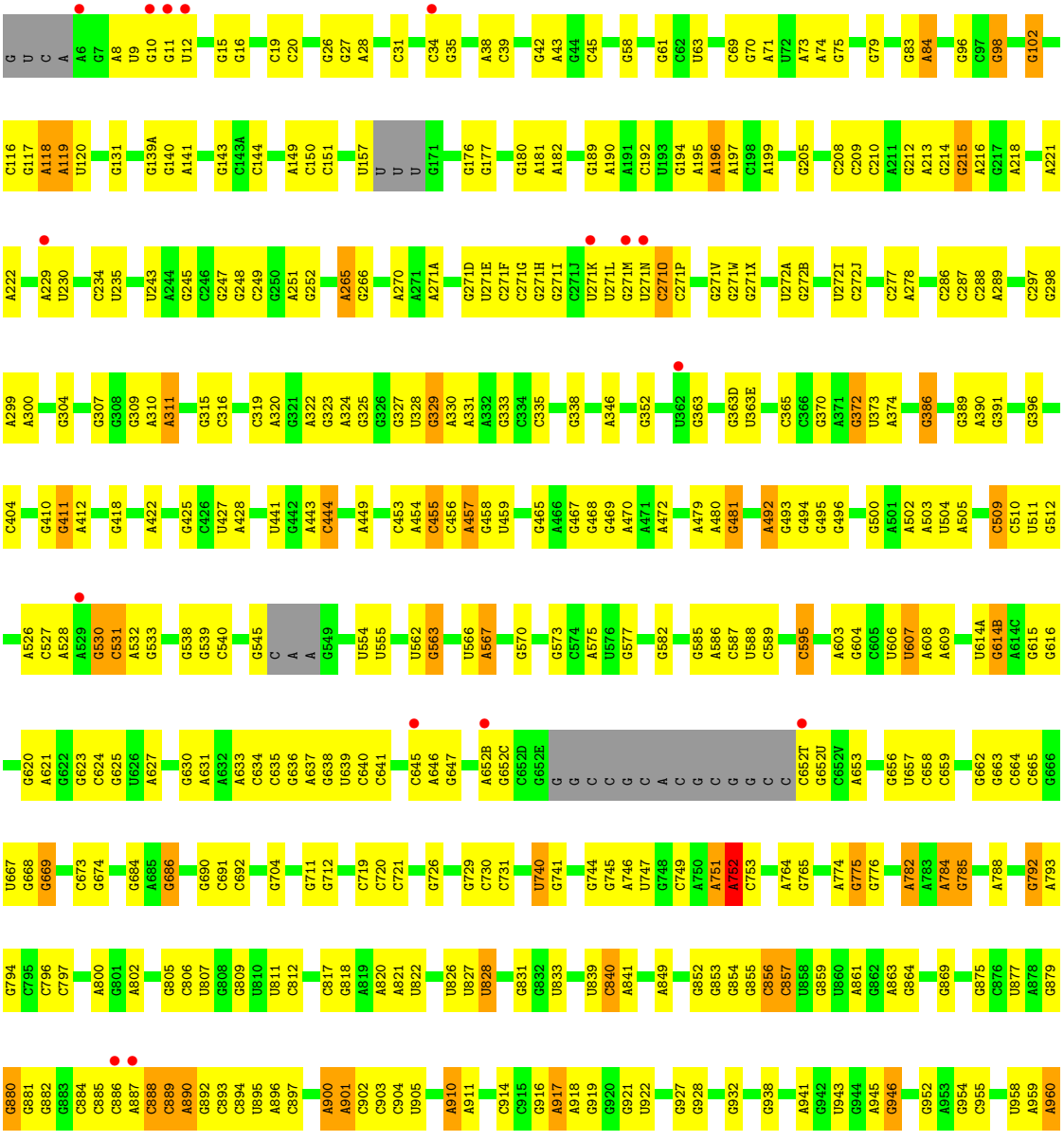


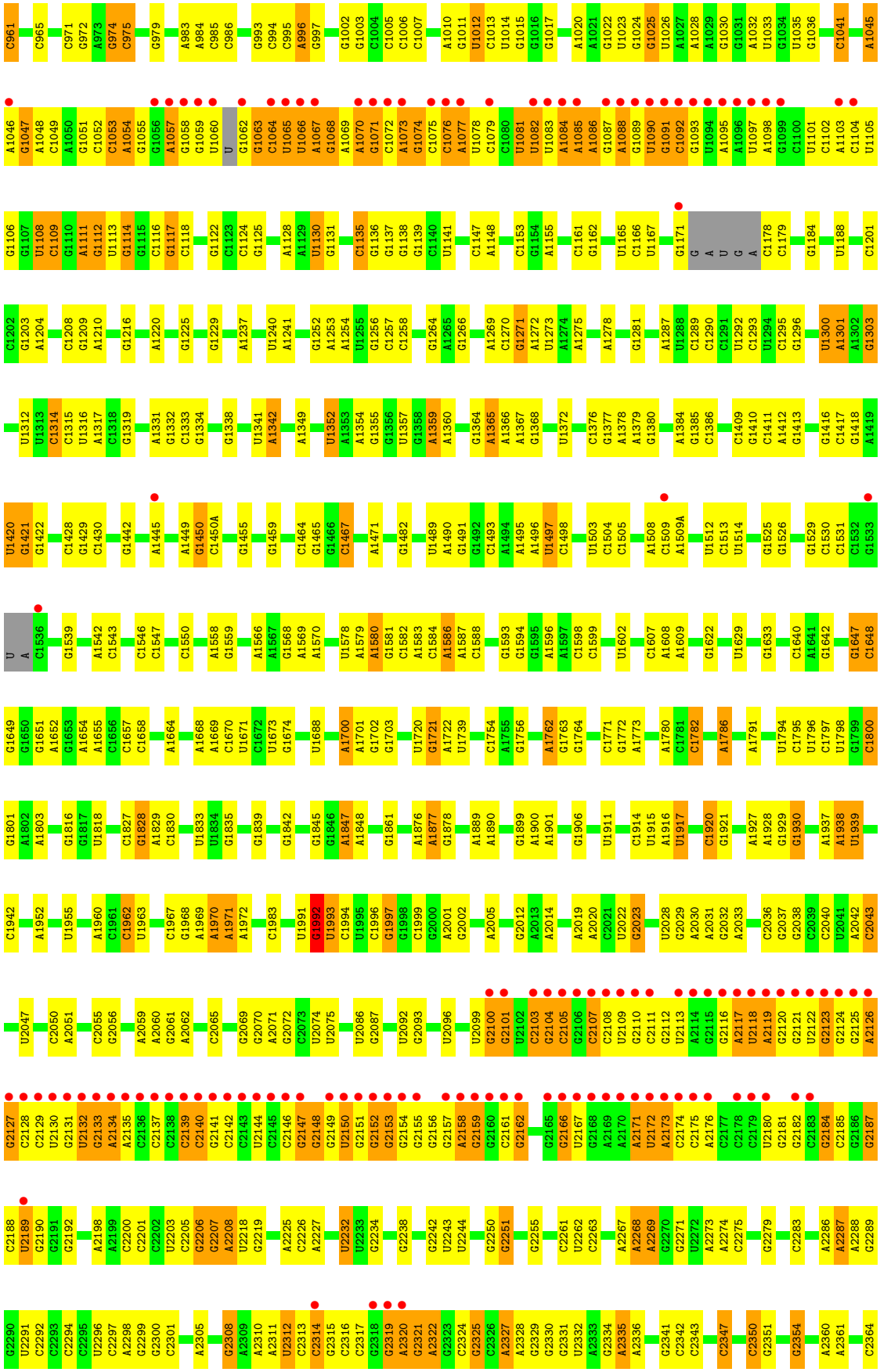


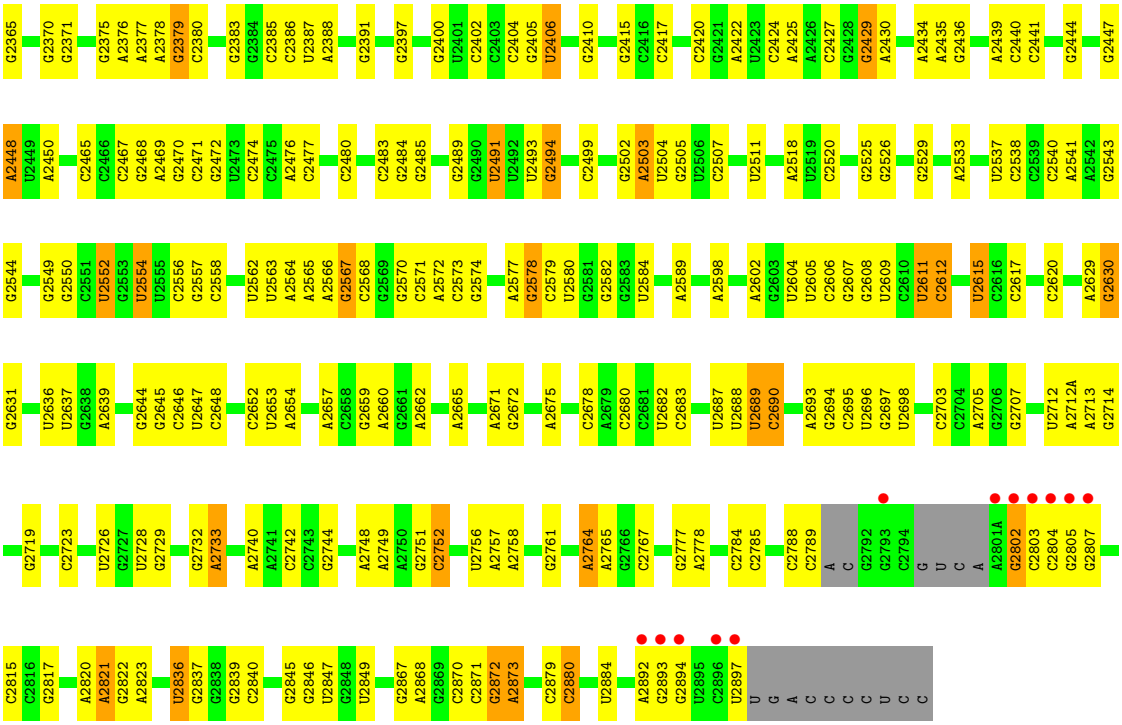


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

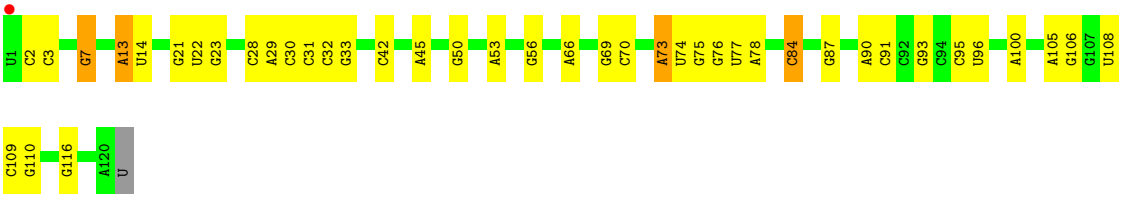






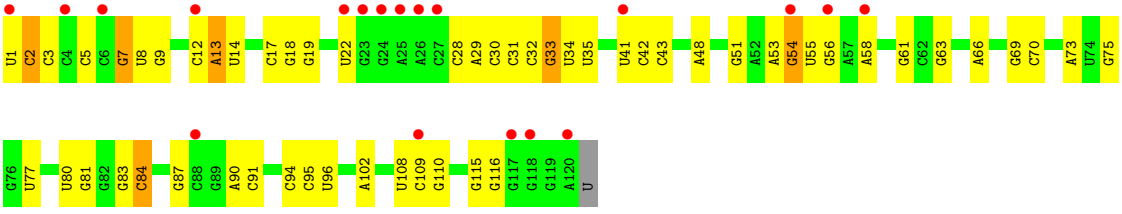
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



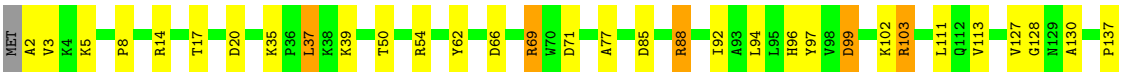
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



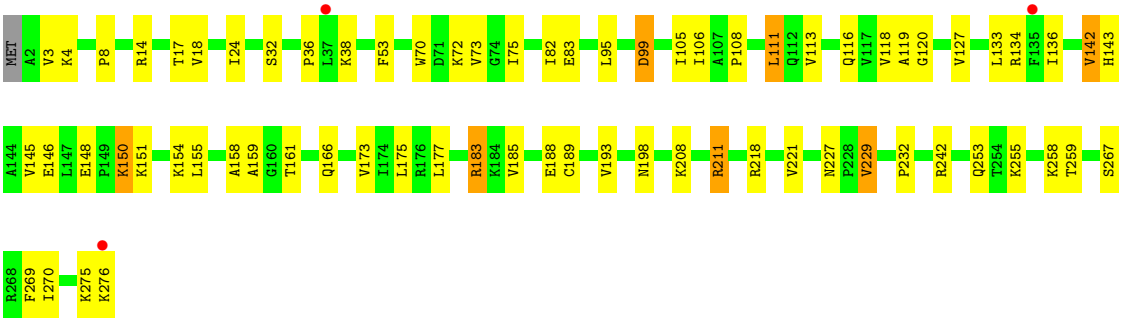
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



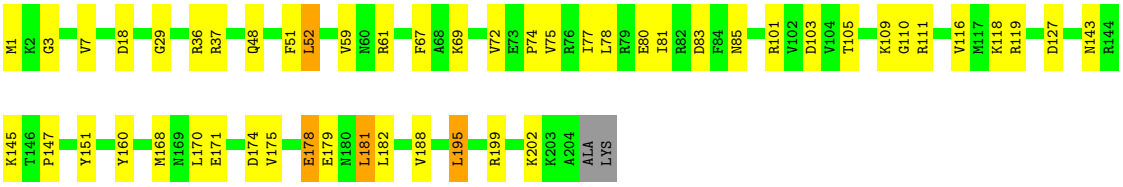
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



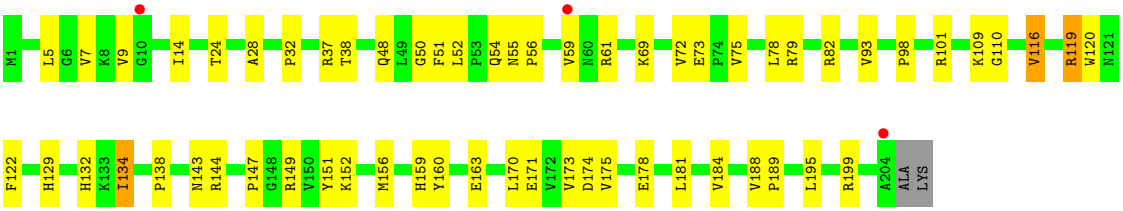
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



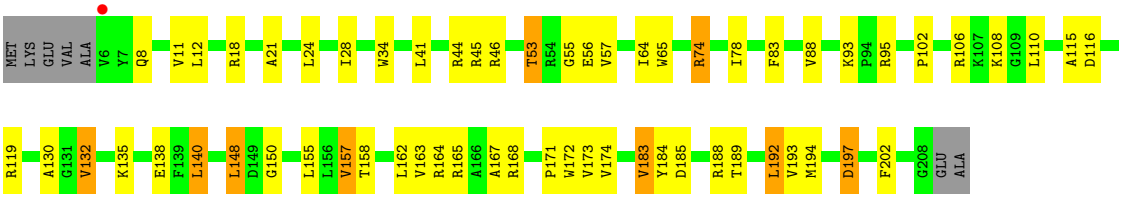
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



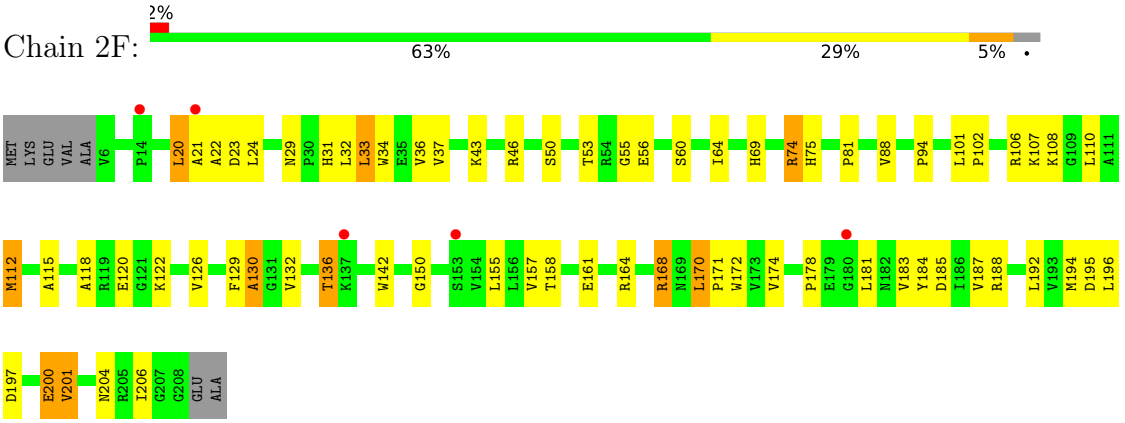
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



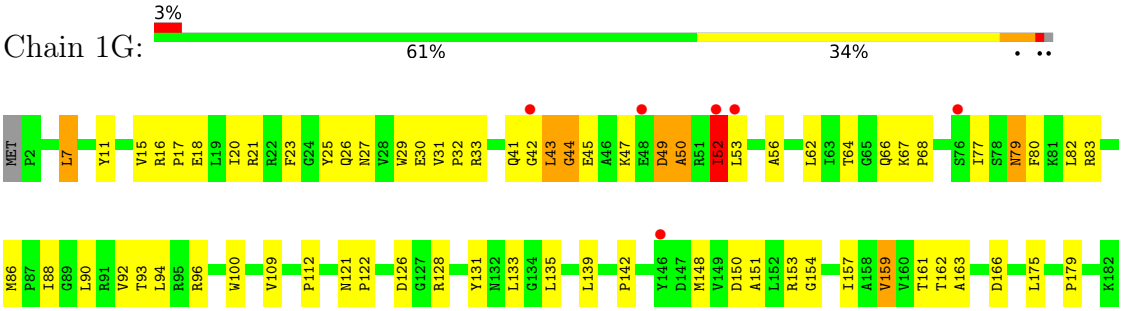
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



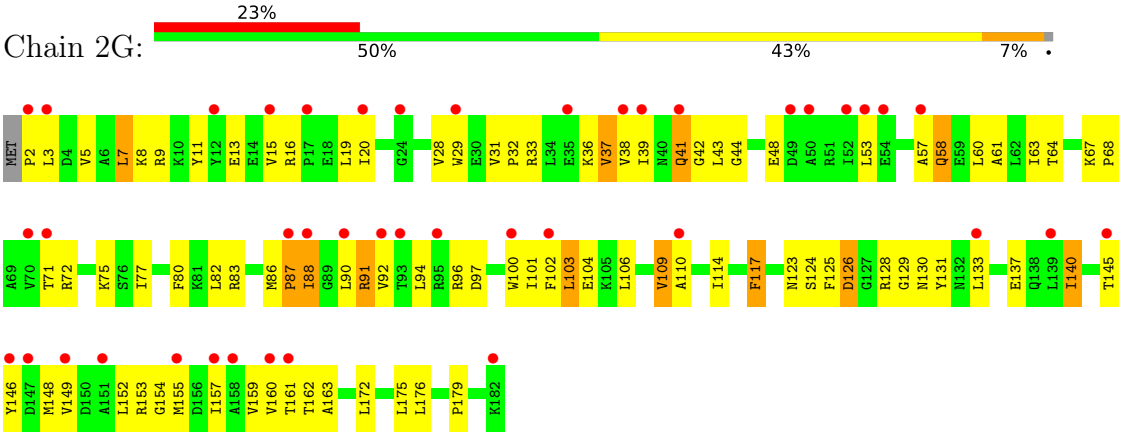
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



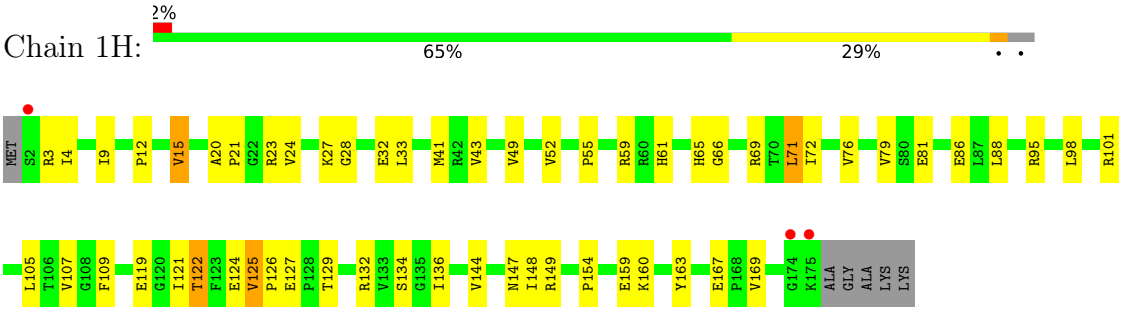
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



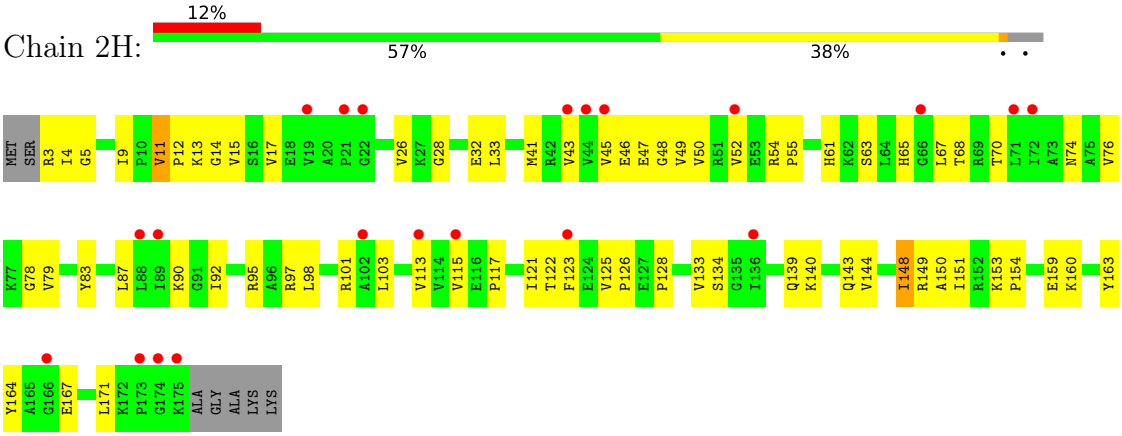
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



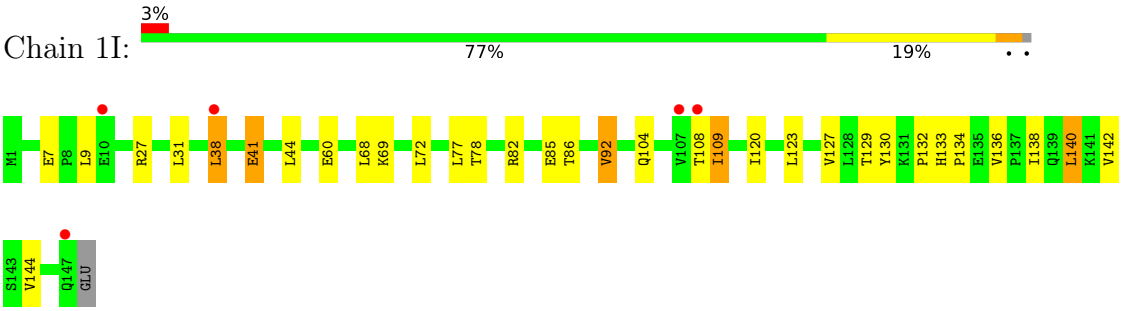
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



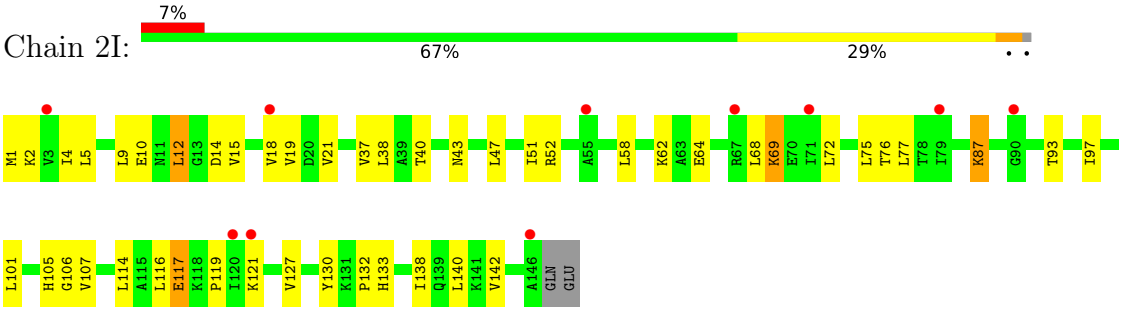
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



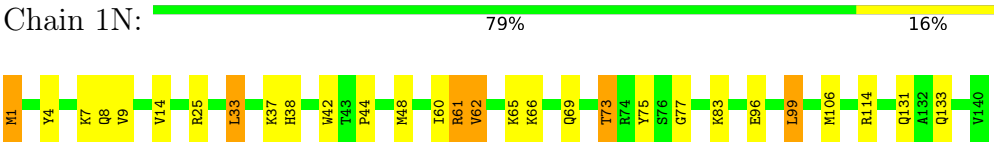
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



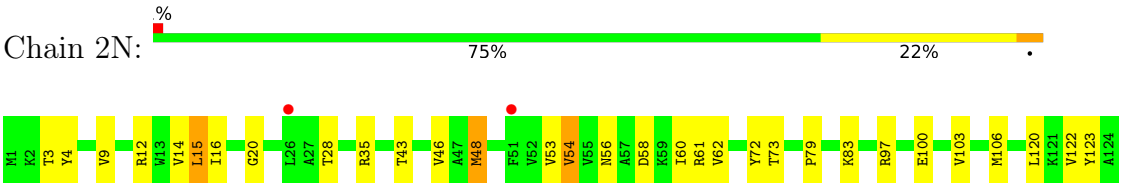
• Molecule 9: 50S ribosomal protein L13

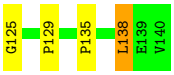
Chain 1N:



• Molecule 9: 50S ribosomal protein L13

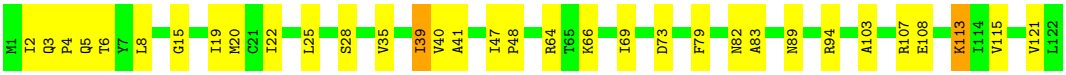
Chain 2N:





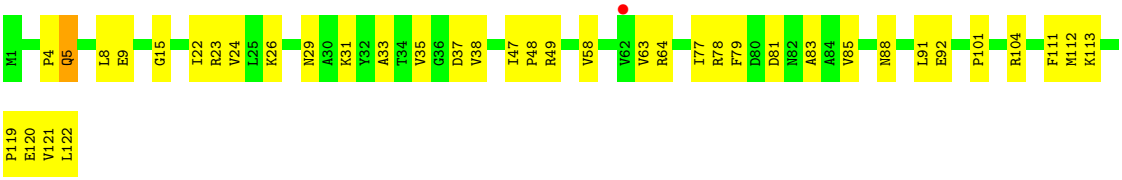
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



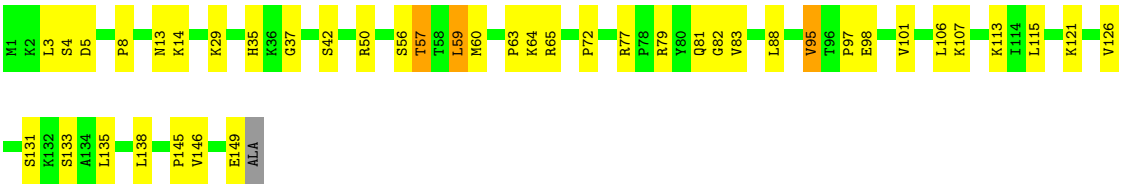
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



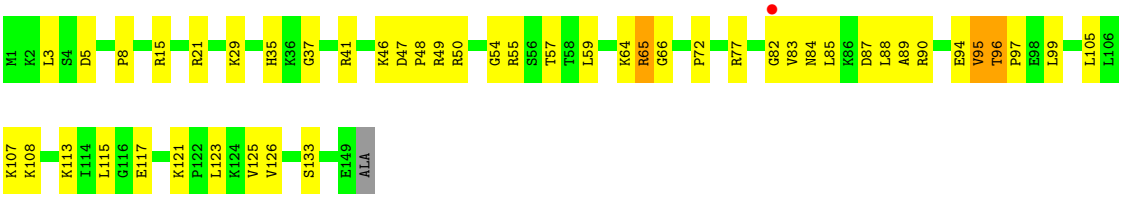
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



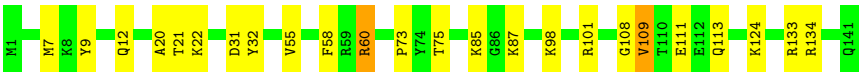
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



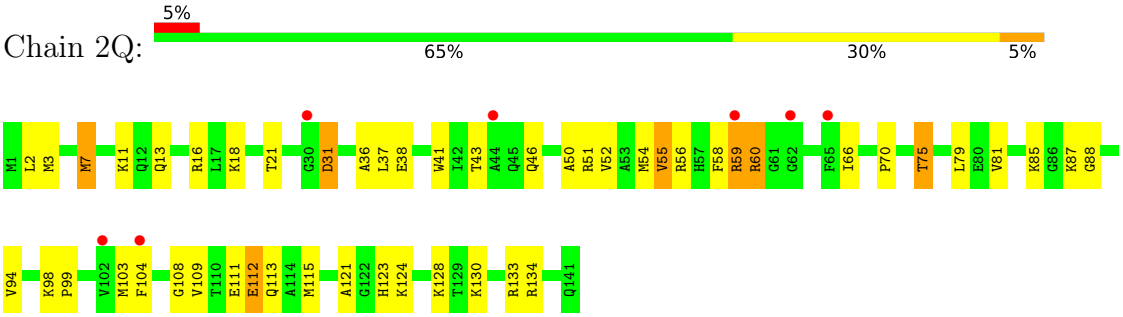
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



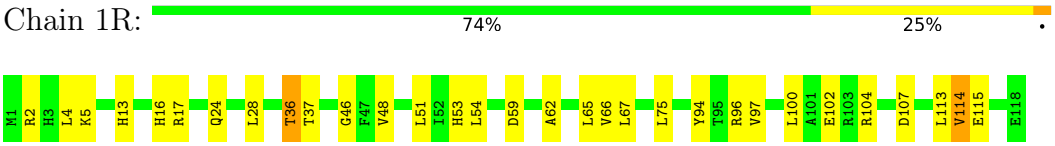
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



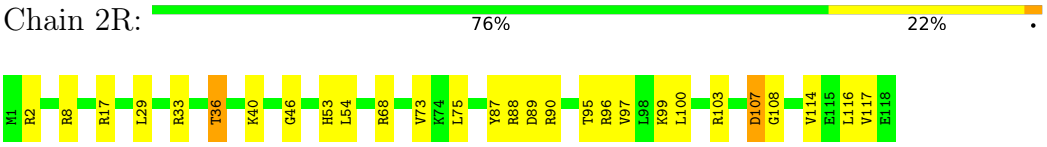
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



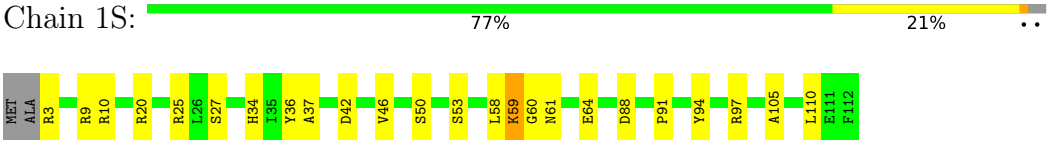
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



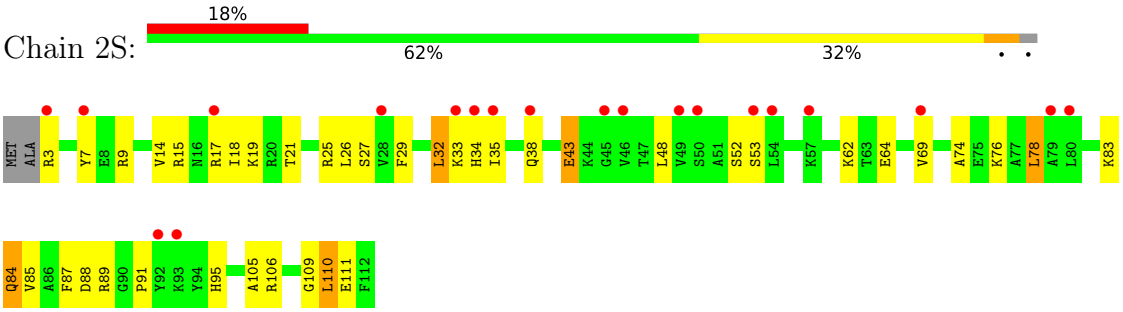
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



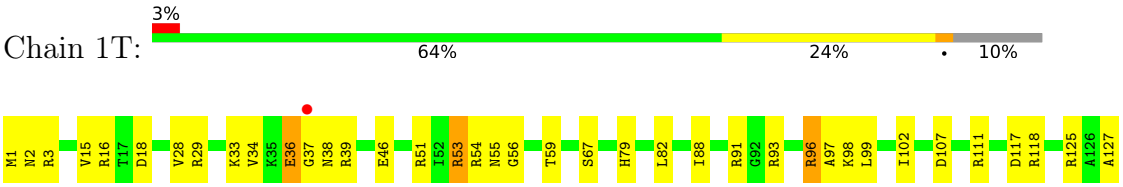
• Molecule 14: 50S ribosomal protein L18

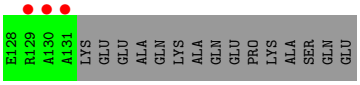
Chain 2S:



• Molecule 15: 50S ribosomal protein L19

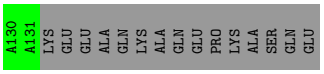
Chain 1T:





• Molecule 15: 50S ribosomal protein L19

Chain 2T:

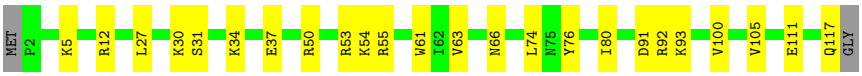


• Molecule 16: 50S ribosomal protein L20

Chain 1U:

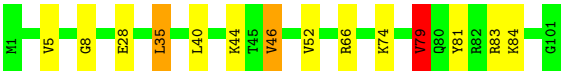
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



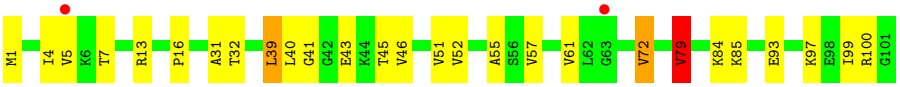
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



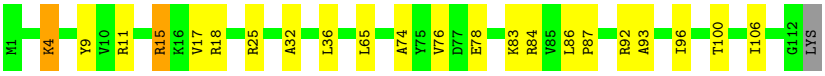
• Molecule 17: 50S ribosomal protein L21

Chain 2V:



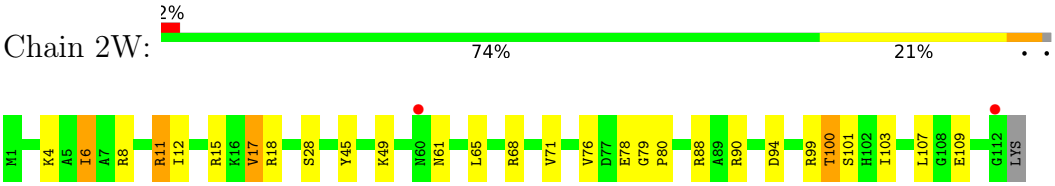
• Molecule 18: 50S ribosomal protein L22

Chain 1W:



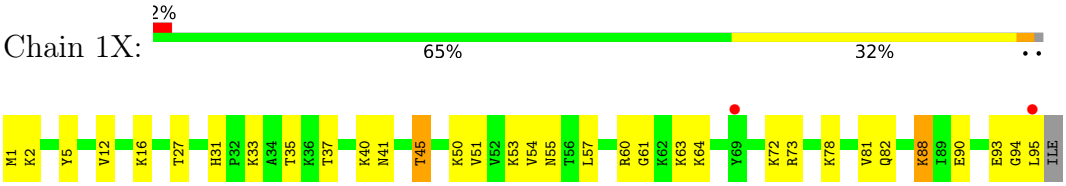
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



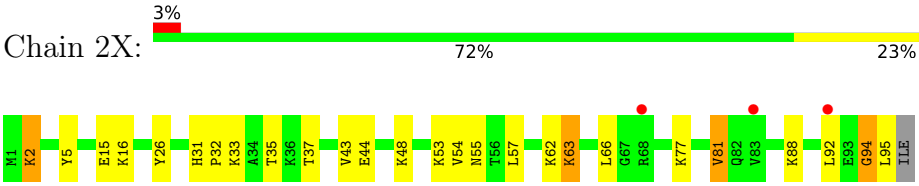
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



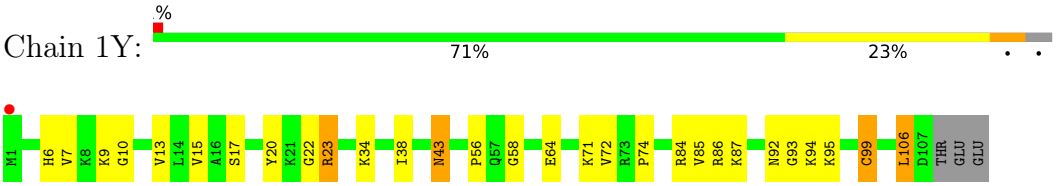
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



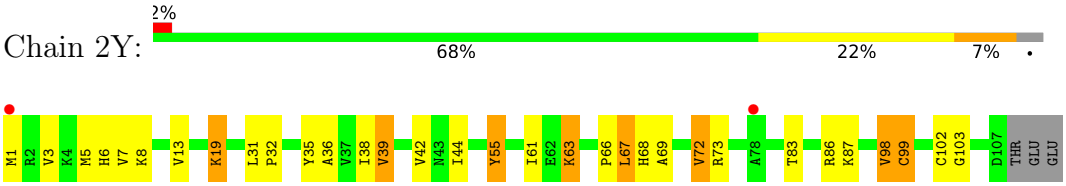
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



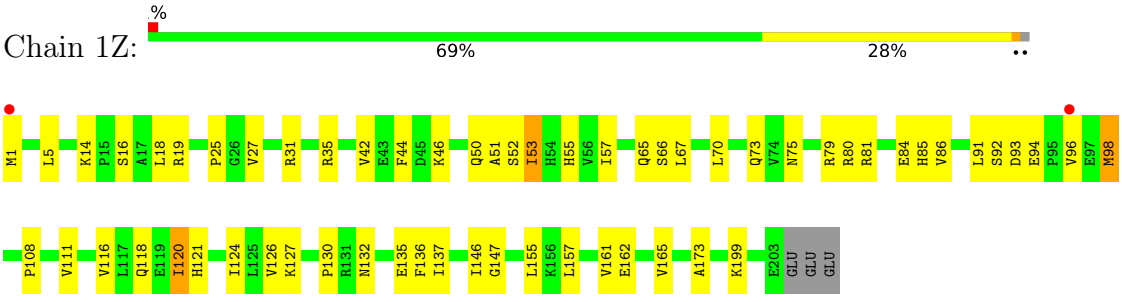
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



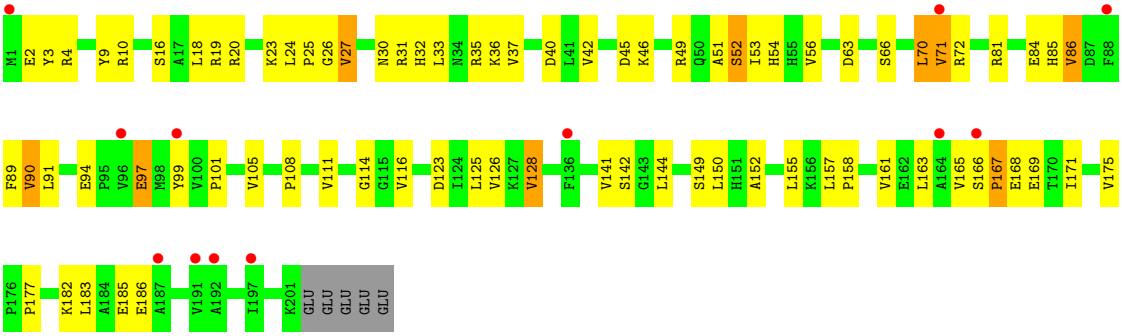
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:

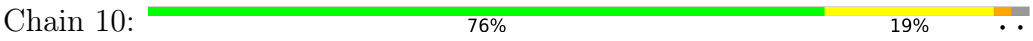


• Molecule 21: 50S ribosomal protein L25

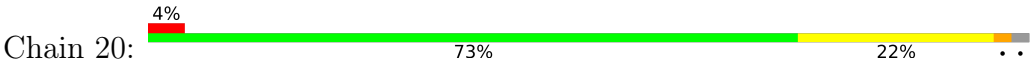
Chain 2Z:



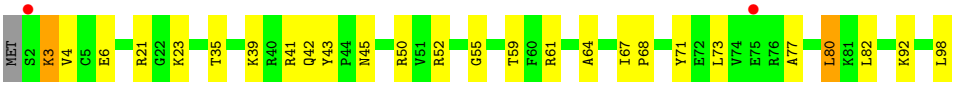
• Molecule 22: 50S ribosomal protein L27



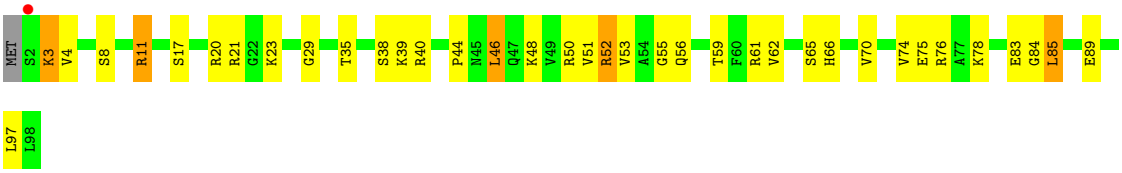
• Molecule 22: 50S ribosomal protein L27



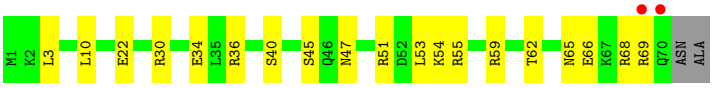
• Molecule 23: 50S ribosomal protein L28



• Molecule 23: 50S ribosomal protein L28

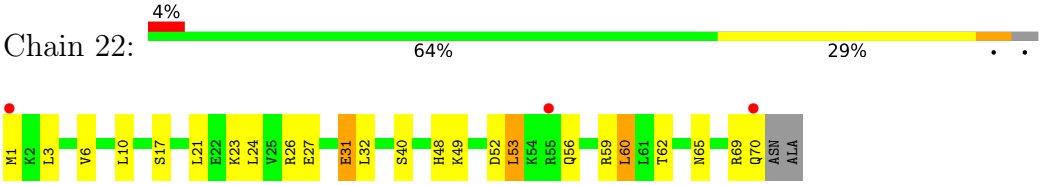


• Molecule 24: 50S ribosomal protein L29



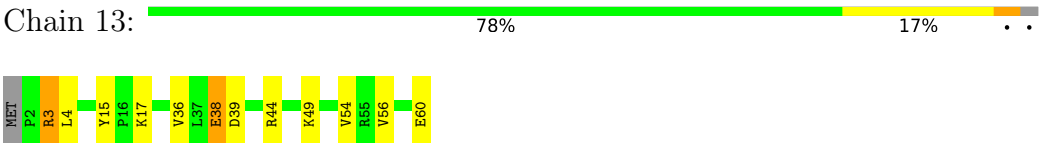
• Molecule 24: 50S ribosomal protein L29

Chain 22:



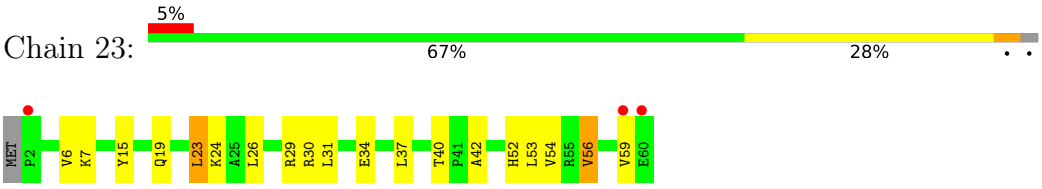
• Molecule 25: 50S ribosomal protein L30

Chain 13:



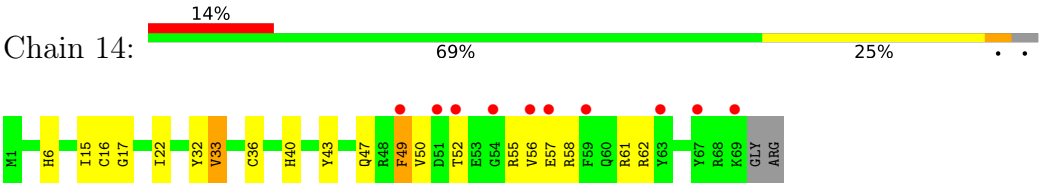
• Molecule 25: 50S ribosomal protein L30

Chain 23:



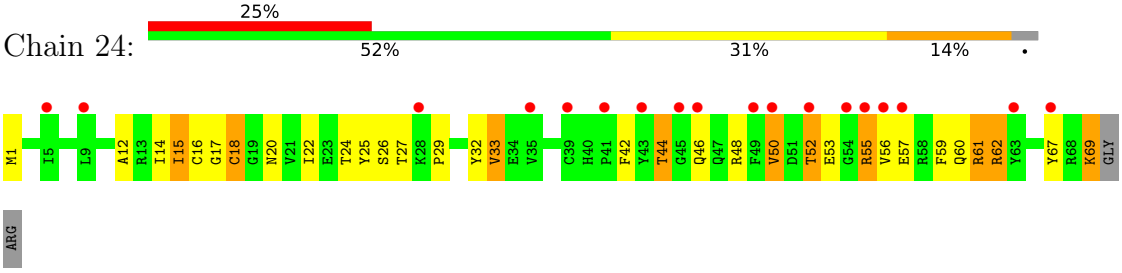
• Molecule 26: 50S ribosomal protein L31

Chain 14:



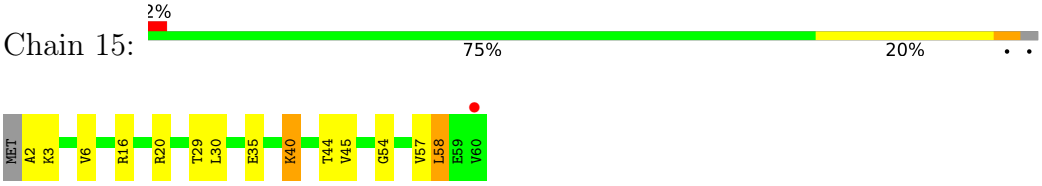
• Molecule 26: 50S ribosomal protein L31

Chain 24:



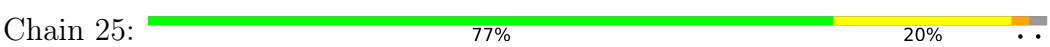
• Molecule 27: 50S ribosomal protein L32

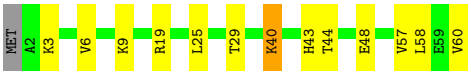
Chain 15:



• Molecule 27: 50S ribosomal protein L32

Chain 25:



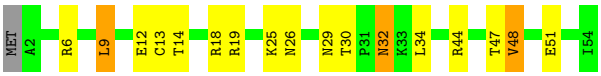


• Molecule 28: 50S ribosomal protein L33

Chain 16:

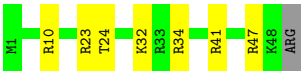
• Molecule 28: 50S ribosomal protein L33

Chain 26:



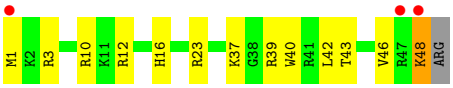
• Molecule 29: 50S ribosomal protein L34

Chain 17:



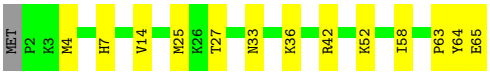
• Molecule 29: 50S ribosomal protein L34

Chain 27:



• Molecule 30: 50S ribosomal protein L35

Chain 18:

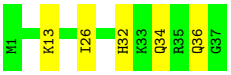


• Molecule 30: 50S ribosomal protein L35

Chain 28:

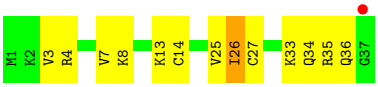
• Molecule 31: 50S ribosomal protein L36

Chain 19:



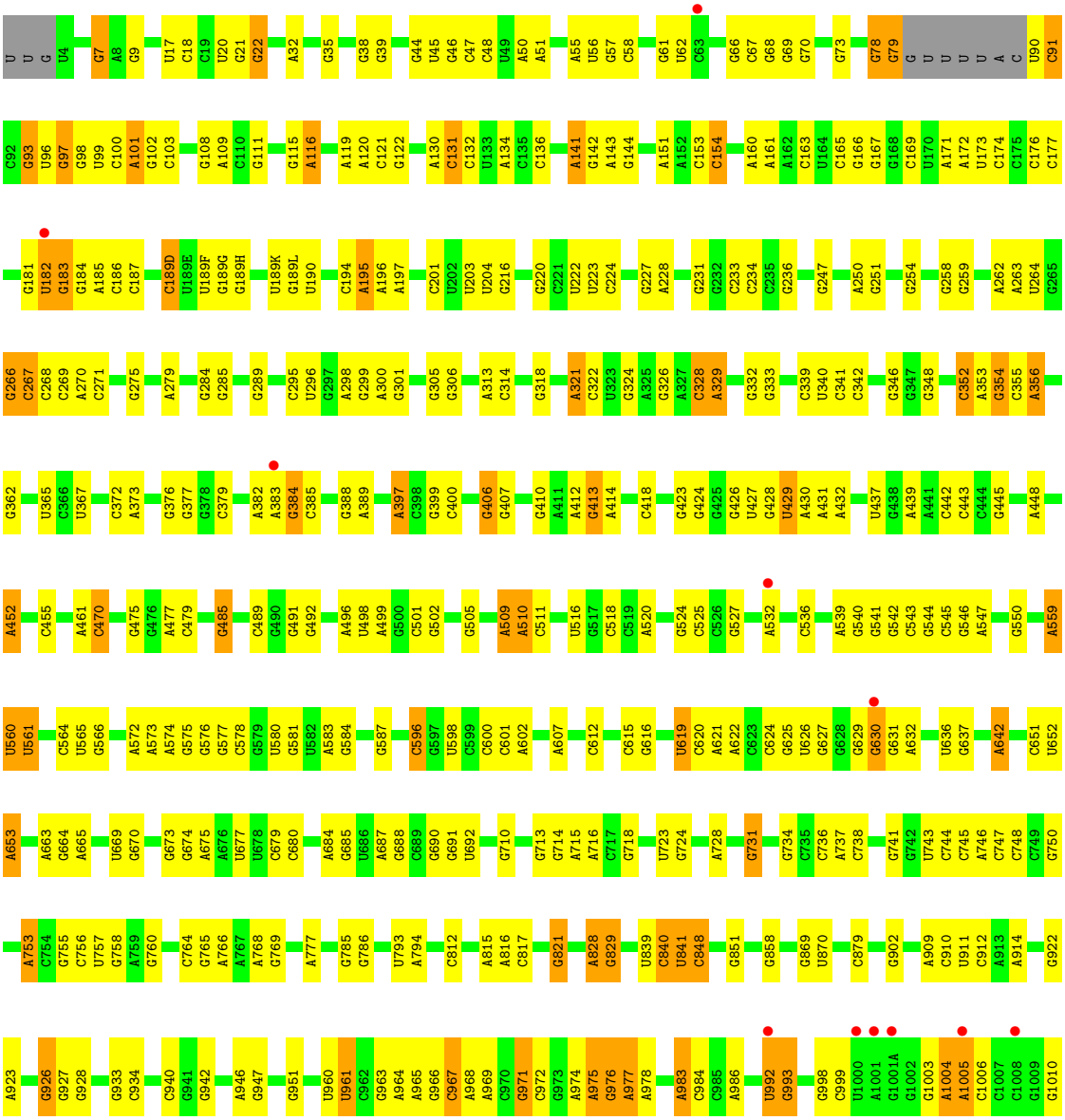
• Molecule 31: 50S ribosomal protein L36

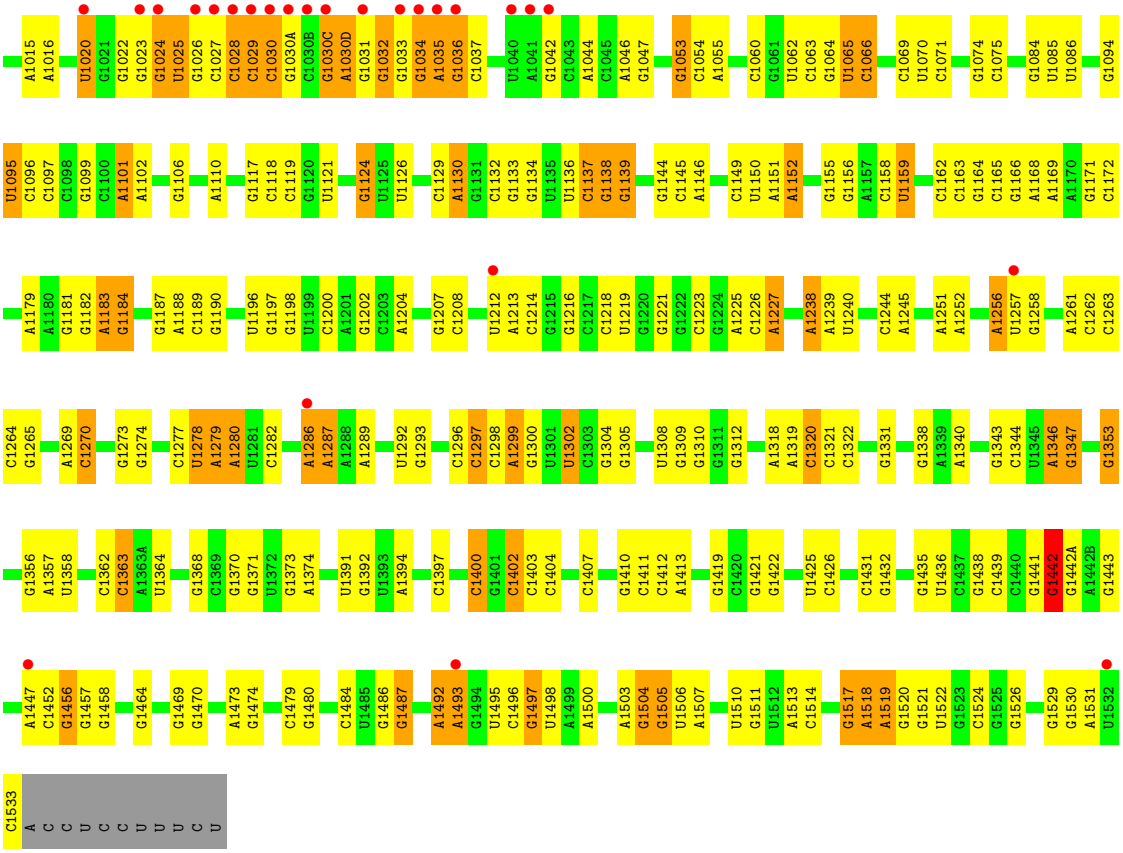
Chain 29:



• Molecule 32: 16S Ribosomal RNA

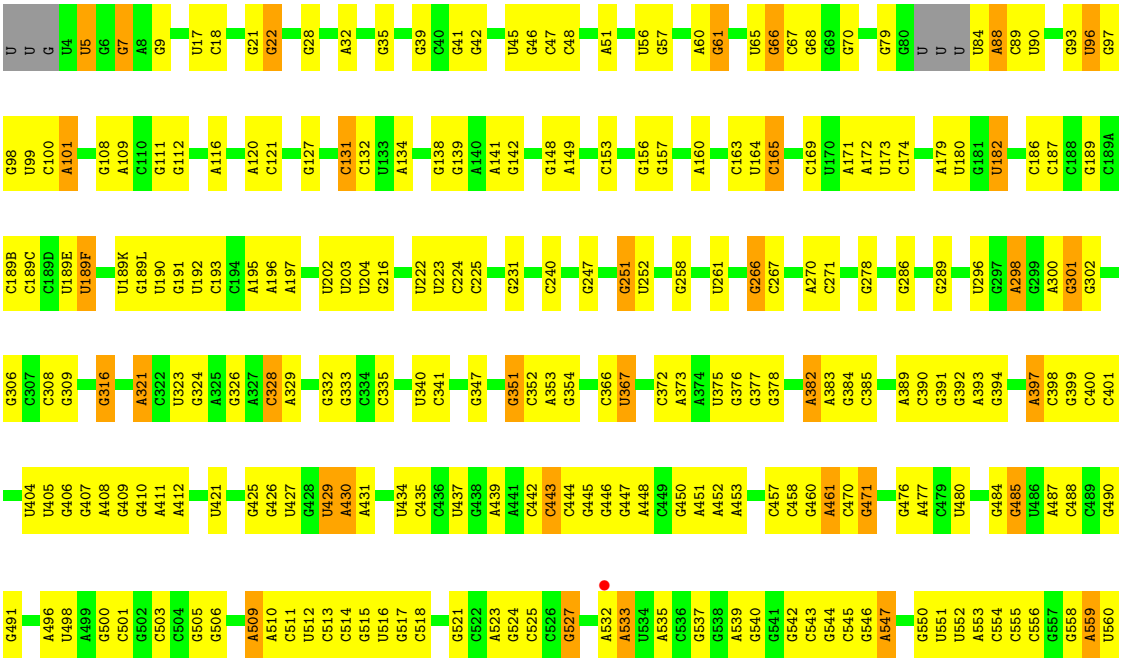
Chain 1a:

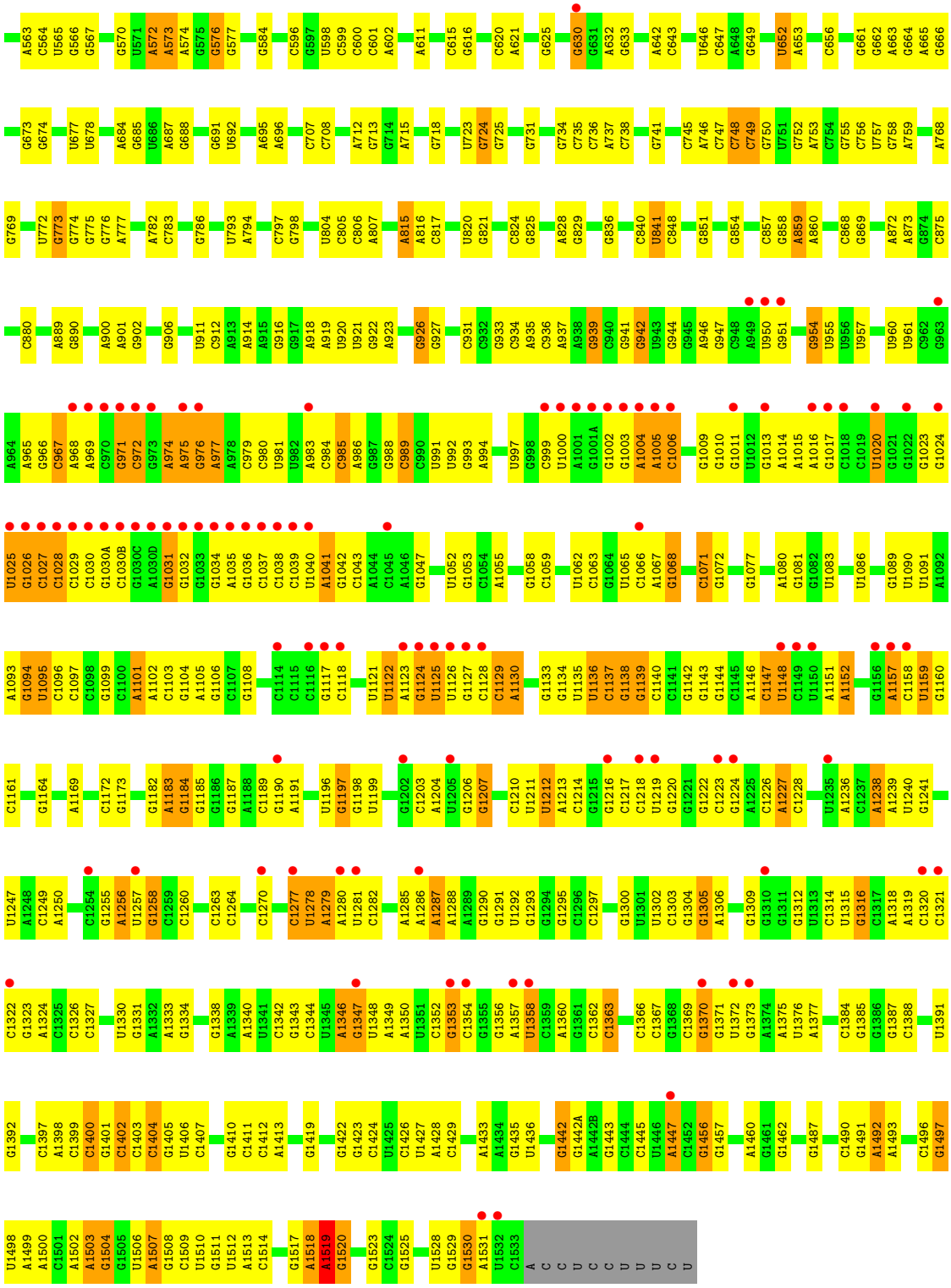




• Molecule 32: 16S Ribosomal RNA

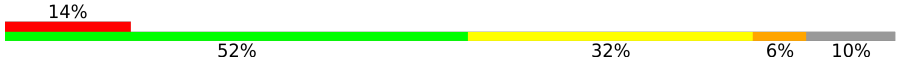
Chain 2a:

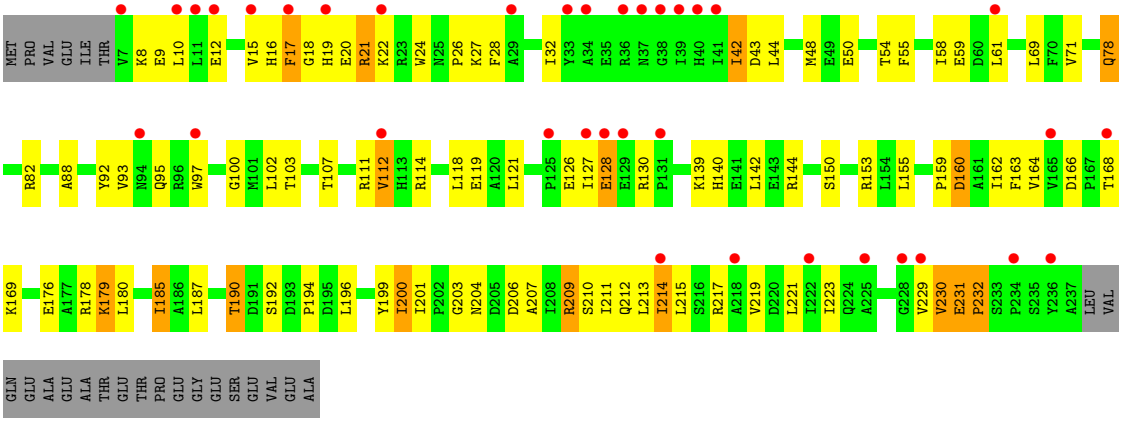




• Molecule 33: 30S ribosomal protein S2

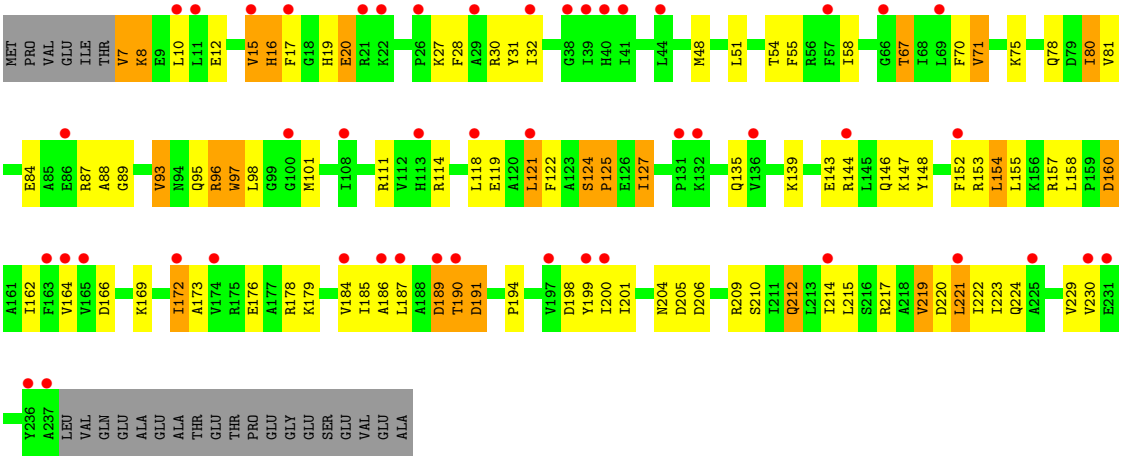
Chain 1b:





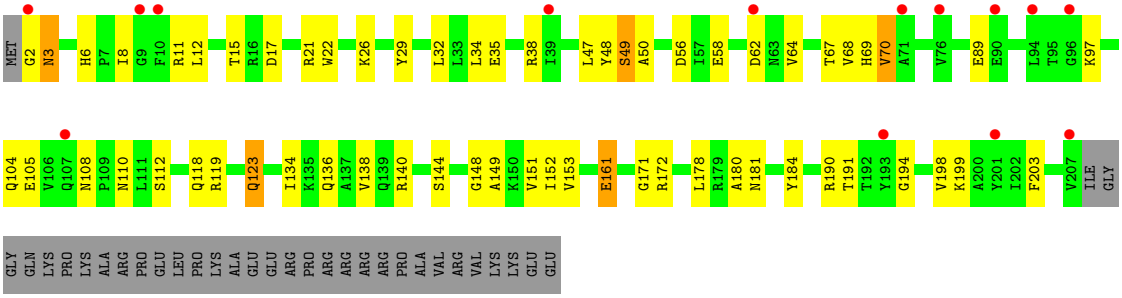
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



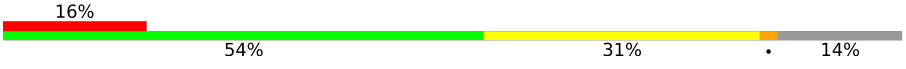
• Molecule 34: 30S ribosomal protein S3

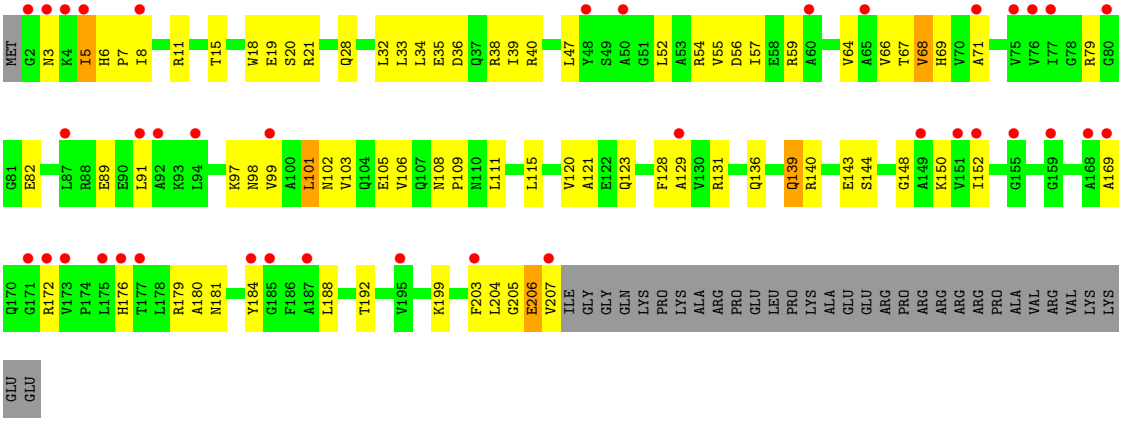
Chain 1c:



• Molecule 34: 30S ribosomal protein S3

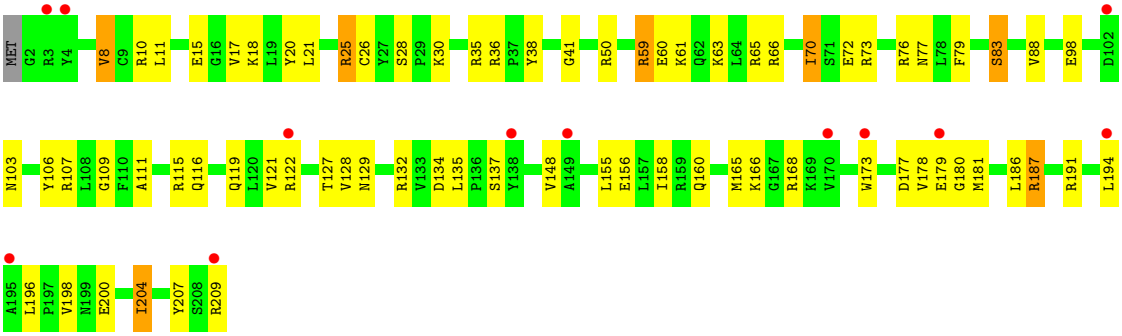
Chain 2c:





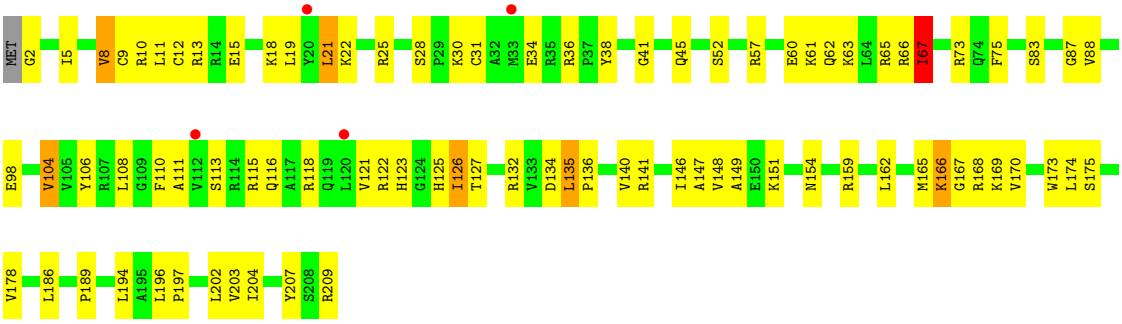
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



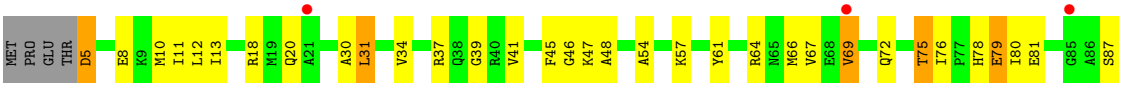
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



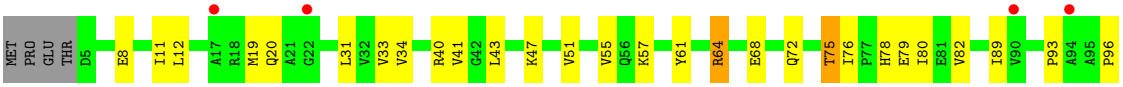
• Molecule 36: 30S ribosomal protein S5

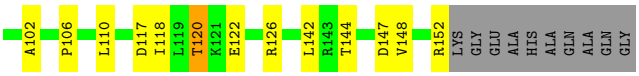
Chain 1e:



• Molecule 36: 30S ribosomal protein S5

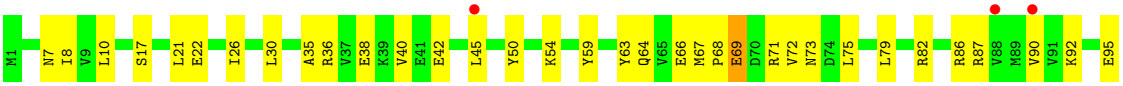
Chain 2e:





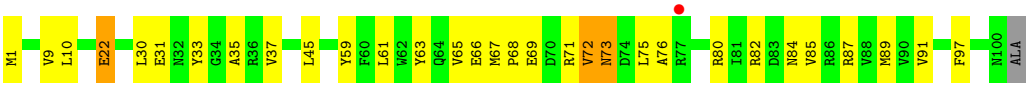
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



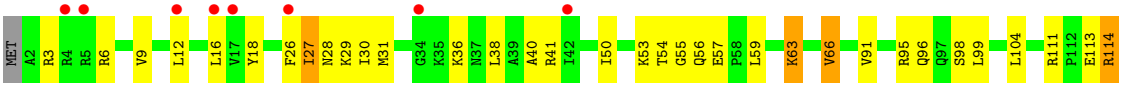
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



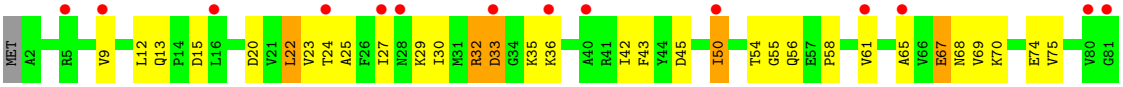
• Molecule 38: 30S ribosomal protein S7

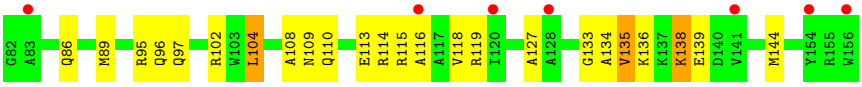
Chain 1g:



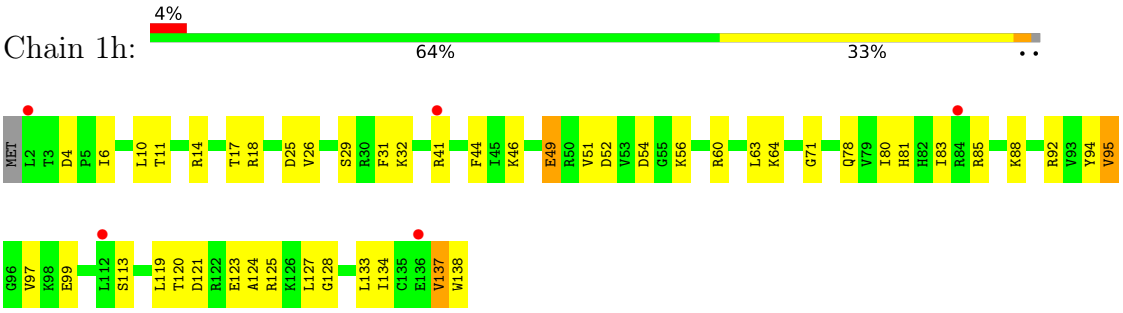
• Molecule 38: 30S ribosomal protein S7

Chain 2g:

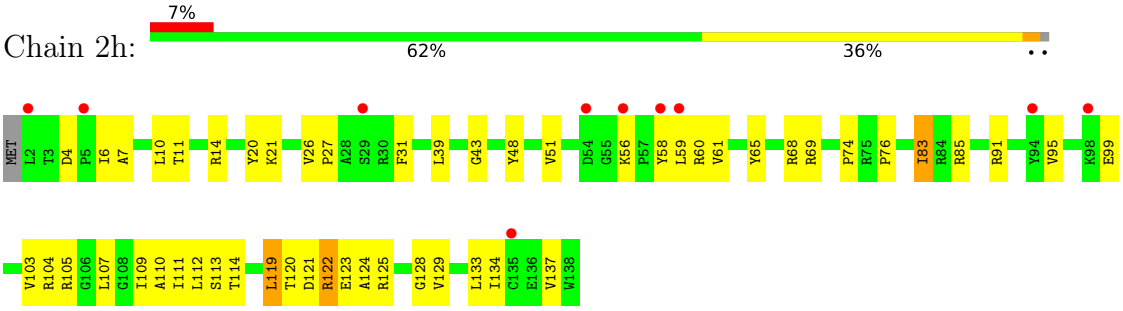




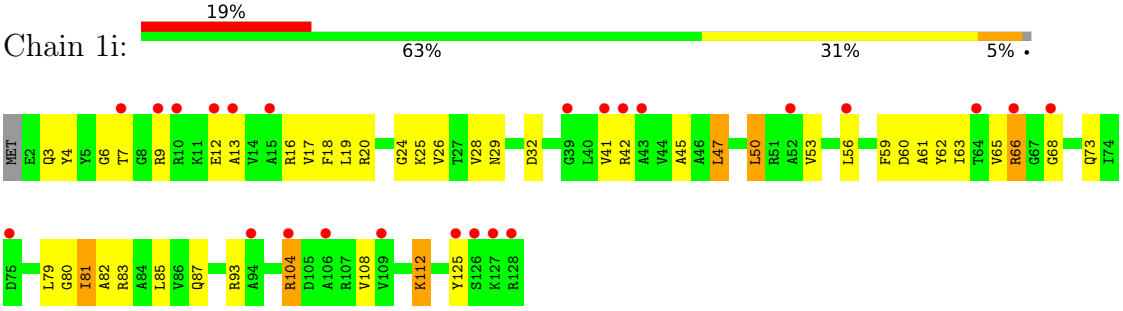
• Molecule 39: 30S ribosomal protein S8



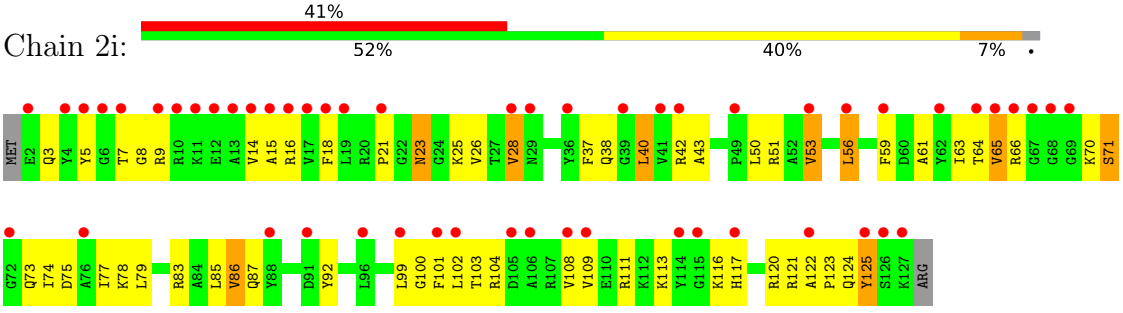
• Molecule 39: 30S ribosomal protein S8



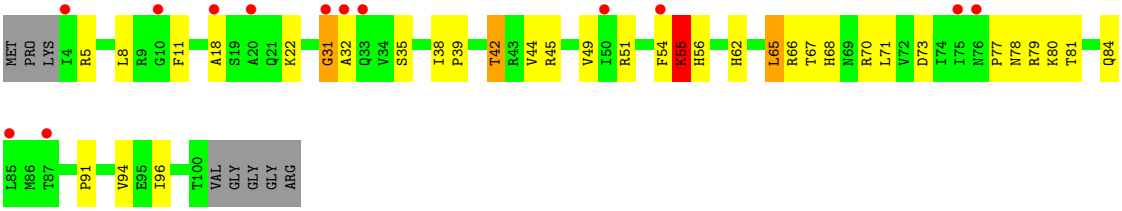
• Molecule 40: 30S ribosomal protein S9



• Molecule 40: 30S ribosomal protein S9

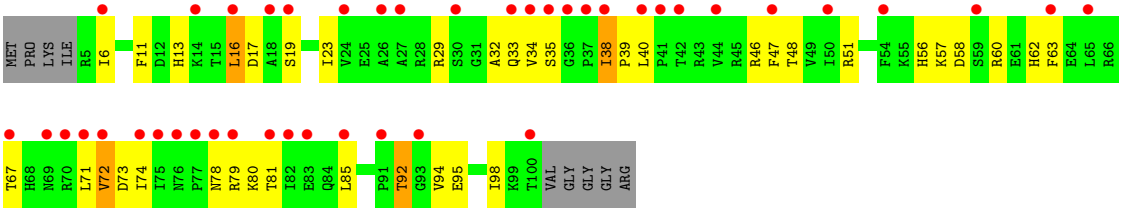


• Molecule 41: 30S ribosomal protein S10



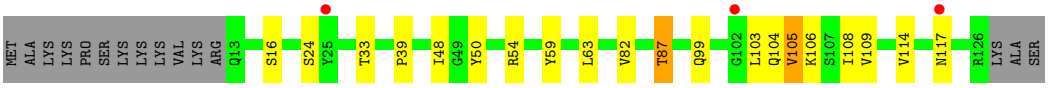
• Molecule 41: 30S ribosomal protein S10

Chain 2j:



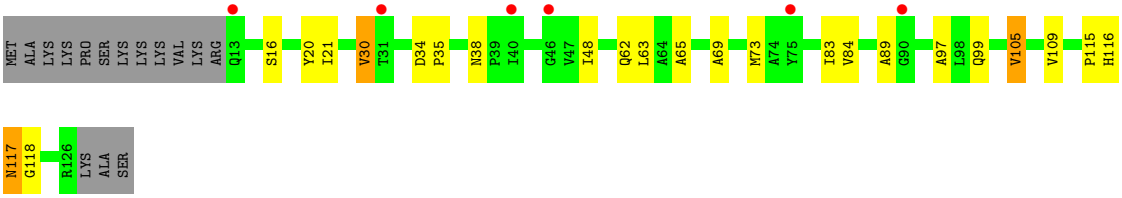
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



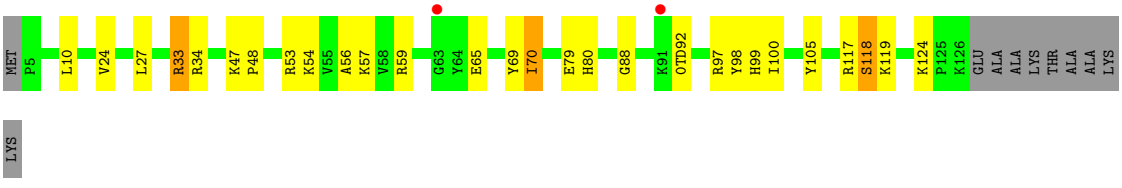
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



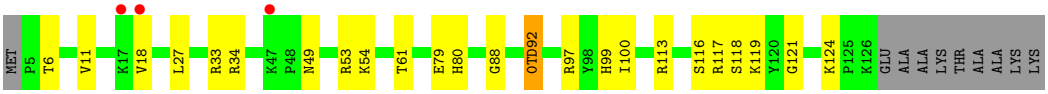
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



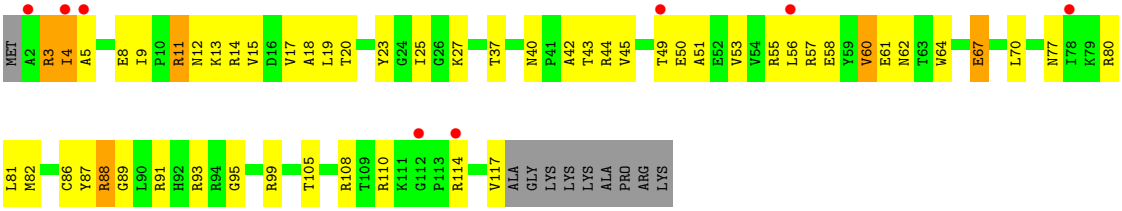
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



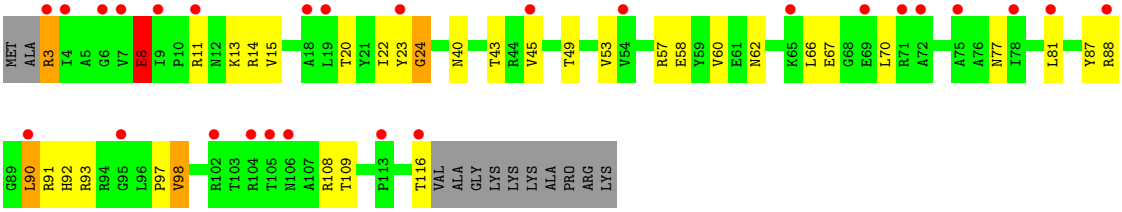
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



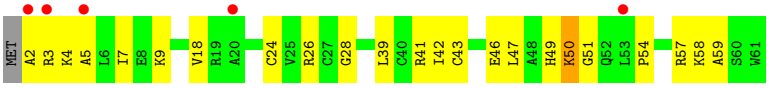
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



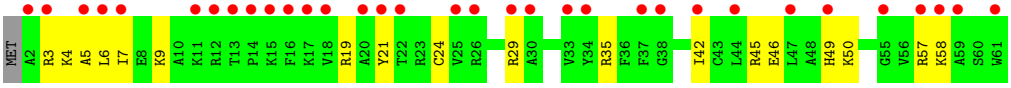
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



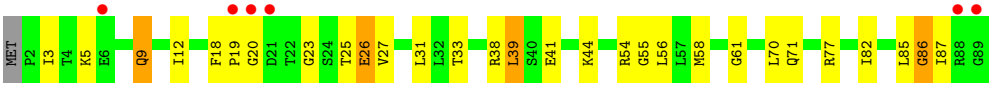
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:



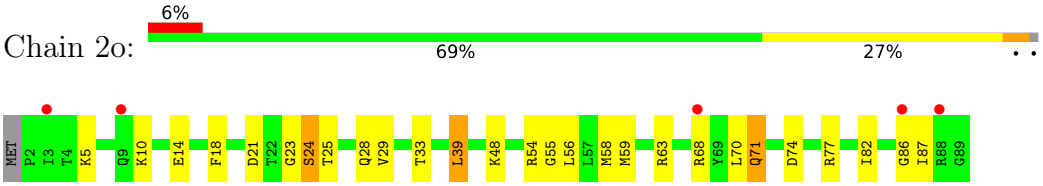
• Molecule 46: 30S ribosomal protein S15

Chain 1o:



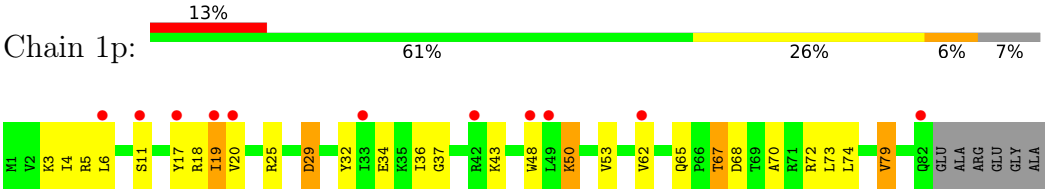
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



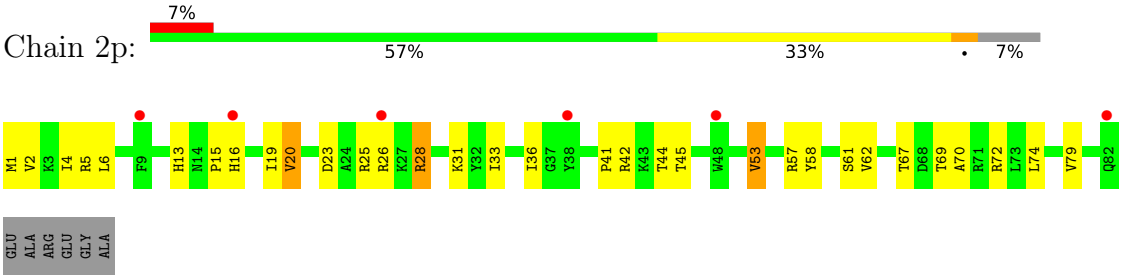
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



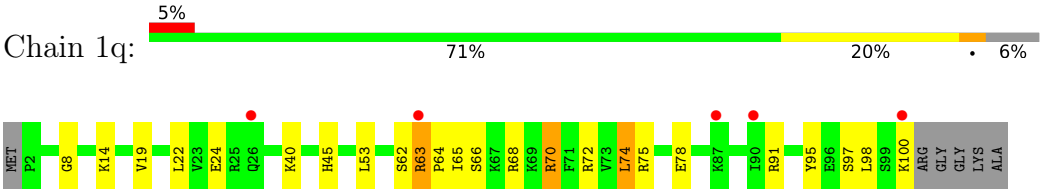
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



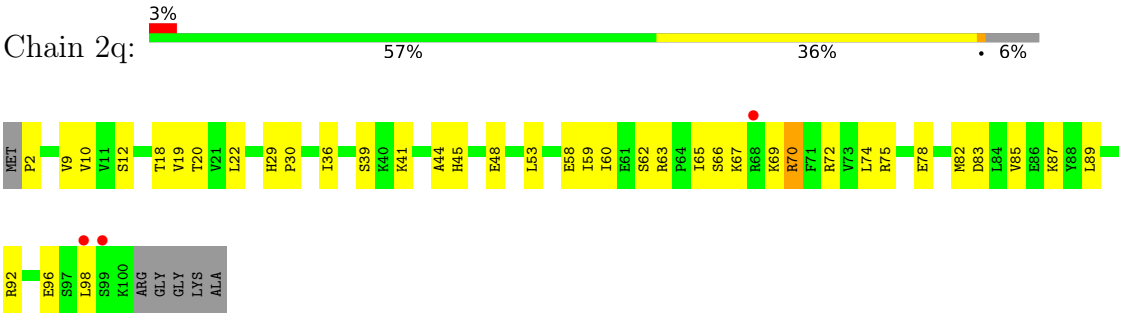
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



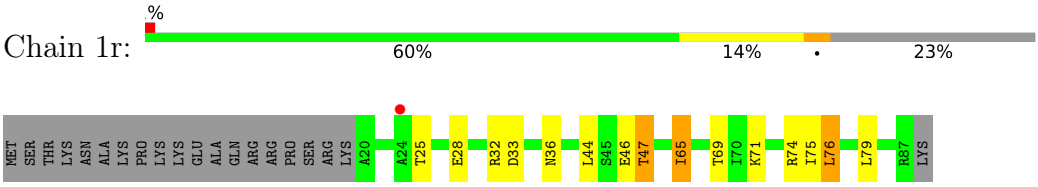
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



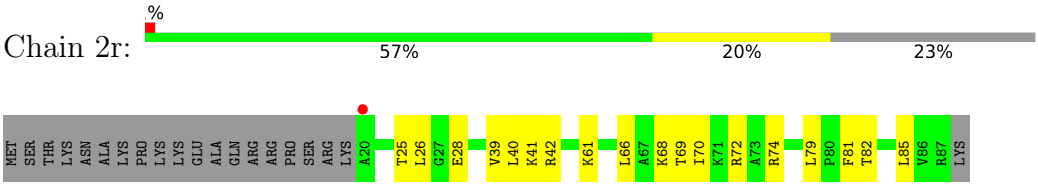
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



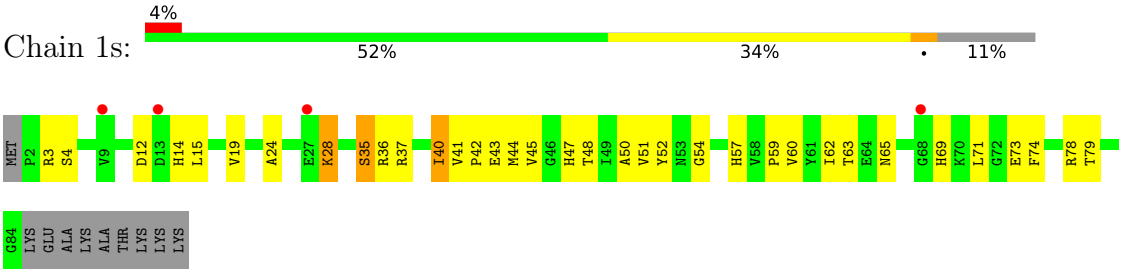
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



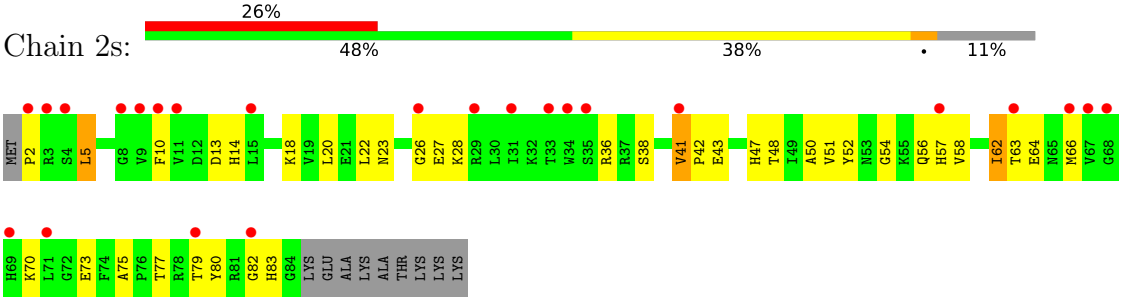
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



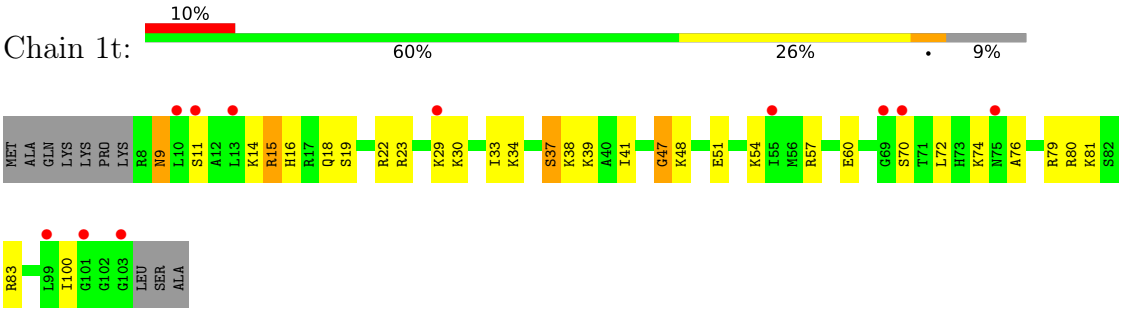
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



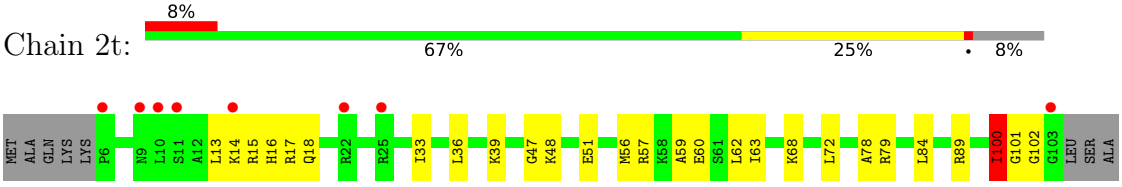
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



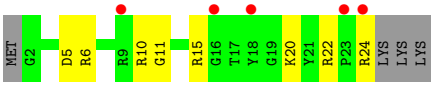
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



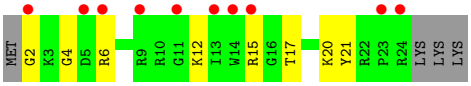
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



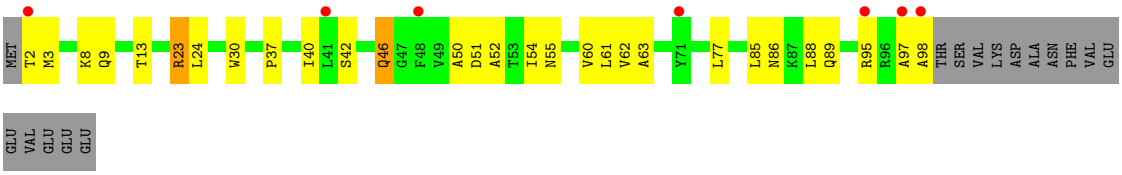
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



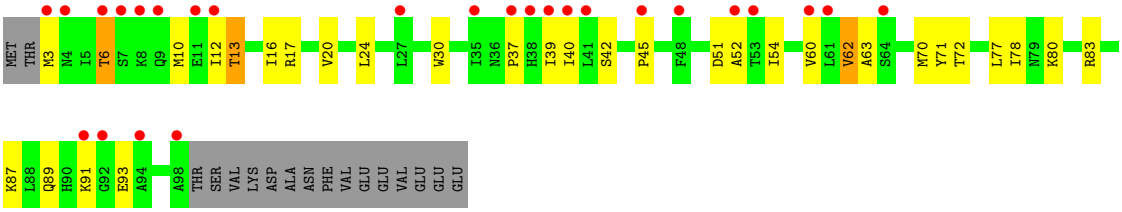
• Molecule 53: Ribosome-associated inhibitor A

Chain 1y:



• Molecule 53: Ribosome-associated inhibitor A

Chain 2y:



• Molecule 54: A-site Aminoacyl-tRNA Analog

Chain 1w:

• Molecule 54: A-site Aminoacyl-tRNA Analog

Chain 2w:

• Molecule 55: P-site Peptidyl-tRNA Analog RNA

Chain 1x:

• Molecule 55: P-site Peptidyl-tRNA Analog RNA

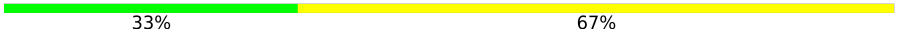
Chain 2x:

• Molecule 56: P-site Peptidyl-tRNA Analog Peptide

Chain 1v:

• Molecule 56: P-site Peptidyl-tRNA Analog Peptide

Chain 2v:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.83Å 450.39Å 621.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	122.10 – 2.60 122.10 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (122.10-2.60) 99.5 (122.10-2.60)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.25 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.220 , 0.269 0.221 , 0.268	Depositor DCC
R_{free} test set	88928 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	51.1	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 56.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	296459	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

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

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1A	0.28	0/69030	0.47	3/107750 (0.0%)
1	2A	0.22	0/68902	0.41	2/107548 (0.0%)
2	1B	0.24	0/2876	0.42	0/4486
2	2B	0.20	0/2878	0.37	0/4490
3	1D	0.28	0/2181	0.51	0/2940
3	2D	0.22	0/2186	0.47	0/2944
4	1E	0.26	0/1592	0.51	0/2149
4	2E	0.21	0/1592	0.43	0/2149
5	1F	0.26	0/1619	0.48	0/2193
5	2F	0.21	0/1615	0.46	0/2188
6	1G	0.22	0/1451	0.48	1/1961 (0.1%)
6	2G	0.22	0/1449	0.47	0/1957
7	1H	0.22	0/1356	0.41	0/1834
7	2H	0.20	0/1350	0.40	0/1826
8	1I	0.20	0/1109	0.44	0/1512
8	2I	0.19	0/1091	0.41	0/1490
9	1N	0.25	0/1148	0.48	0/1547
9	2N	0.20	0/1144	0.39	0/1543
10	1O	0.26	0/943	0.46	0/1269
10	2O	0.21	0/943	0.43	0/1269
11	1P	0.27	0/1152	0.50	0/1533
11	2P	0.20	0/1152	0.46	0/1533
12	1Q	0.26	0/1143	0.48	0/1527
12	2Q	0.19	0/1143	0.42	0/1527
13	1R	0.28	0/982	0.50	0/1312
13	2R	0.21	0/982	0.46	0/1312
14	1S	0.22	0/887	0.49	0/1180
14	2S	0.20	0/880	0.44	0/1172
15	1T	0.24	0/1105	0.47	0/1477
15	2T	0.21	0/1097	0.44	0/1468
16	1U	0.28	0/977	0.47	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
16	2U	0.20	0/977	0.38	0/1301
17	1V	0.27	0/786	0.48	0/1053
17	2V	0.20	0/782	0.41	0/1049
18	1W	0.27	0/897	0.50	0/1205
18	2W	0.20	0/897	0.42	0/1205
19	1X	0.27	0/764	0.49	0/1025
19	2X	0.20	0/764	0.42	0/1025
20	1Y	0.23	0/823	0.47	0/1099
20	2Y	0.20	0/823	0.43	0/1100
21	1Z	0.24	0/1620	0.48	1/2200 (0.0%)
21	2Z	0.21	0/1590	0.43	0/2162
22	10	0.27	0/662	0.50	0/881
22	20	0.22	0/659	0.49	0/877
23	11	0.25	0/761	0.46	0/1013
23	21	0.22	0/766	0.42	0/1018
24	12	0.22	0/590	0.43	0/781
24	22	0.20	0/594	0.38	0/785
25	13	0.28	0/474	0.53	0/635
25	23	0.19	0/469	0.39	0/630
26	14	0.25	0/559	0.58	0/754
26	24	0.27	0/549	0.59	0/741
27	15	0.28	0/473	0.52	0/639
27	25	0.24	0/469	0.49	0/635
28	16	0.25	0/460	0.46	0/613
28	26	0.20	0/456	0.42	0/608
29	17	0.31	0/426	0.54	0/561
29	27	0.24	0/426	0.50	0/561
30	18	0.27	0/525	0.50	0/691
30	28	0.20	0/525	0.39	0/691
31	19	0.29	0/310	0.46	0/407
31	29	0.20	0/310	0.40	0/407
32	1a	0.20	0/35795	0.39	1/55864 (0.0%)
32	2a	0.20	0/35890	0.38	0/56012
33	1b	0.21	0/1876	0.49	0/2533
33	2b	0.23	0/1860	0.48	0/2518
34	1c	0.19	0/1582	0.42	0/2137
34	2c	0.21	0/1566	0.43	0/2119
35	1d	0.20	0/1695	0.43	0/2274
35	2d	0.19	0/1698	0.48	1/2277 (0.0%)
36	1e	0.20	0/1149	0.45	0/1548
36	2e	0.20	0/1149	0.44	0/1548
37	1f	0.21	0/827	0.40	0/1120
37	2f	0.19	0/829	0.41	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.18	0/1254	0.37	0/1683
38	2g	0.20	0/1248	0.41	0/1676
39	1h	0.19	0/1118	0.41	0/1506
39	2h	0.19	0/1108	0.41	0/1494
40	1i	0.20	0/1005	0.42	0/1351
40	2i	0.21	0/985	0.46	0/1329
41	1j	0.20	0/732	0.43	0/993
41	2j	0.22	0/723	0.45	0/984
42	1k	0.19	0/849	0.40	0/1150
42	2k	0.18	0/848	0.44	1/1149 (0.1%)
43	1l	0.20	0/937	0.42	0/1260
43	2l	0.22	0/937	0.42	0/1260
44	1m	0.19	0/924	0.45	0/1242
44	2m	0.23	0/905	0.46	0/1217
45	1n	0.20	0/501	0.45	0/664
45	2n	0.22	0/501	0.43	0/664
46	1o	0.19	0/739	0.38	0/985
46	2o	0.19	0/739	0.39	0/985
47	1p	0.21	0/697	0.47	0/939
47	2p	0.19	0/693	0.45	1/935 (0.1%)
48	1q	0.20	0/836	0.43	0/1117
48	2q	0.19	0/836	0.42	0/1117
49	1r	0.20	0/560	0.42	0/746
49	2r	0.20	0/560	0.38	0/746
50	1s	0.17	0/663	0.44	0/895
50	2s	0.23	0/660	0.42	0/893
51	1t	0.21	0/734	0.45	0/969
51	2t	0.19	0/736	0.45	0/976
52	1u	0.20	0/203	0.45	0/266
52	2u	0.23	0/203	0.44	0/266
53	1y	0.20	0/776	0.40	0/1048
53	2y	0.21	0/761	0.40	0/1030
54	1w	1.86	2/44 (4.5%)	1.54	1/67 (1.5%)
54	2w	1.56	1/44 (2.3%)	1.06	0/67
55	1x	0.44	0/44	0.52	0/67
55	2x	0.29	0/44	0.44	0/67
56	1v	0.29	0/19	0.37	0/24
56	2v	0.24	0/19	0.41	0/24
All	All	0.23	3/310242 (0.0%)	0.43	12/463663 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
11	1P	0	1
11	2P	0	1
14	1S	0	1
26	24	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	74	C	O3'-P	-5.64	1.52	1.61
54	2w	74	C	O3'-P	-5.44	1.52	1.61
54	1w	75	C	P-OP1	-5.43	1.38	1.49

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1w	75	C	C3'-C2'-O2'	-9.42	96.56	110.70
1	1A	1042	G	OP1-P-O3'	-9.31	80.08	108.00
35	2d	67	ILE	N-CA-C	-7.06	105.90	112.96
1	1A	1042	G	OP2-P-O3'	-6.86	87.42	108.00
6	1G	96	ARG	CB-CA-C	-5.96	109.69	116.54
47	2p	33	ILE	N-CA-C	-5.70	107.26	112.96
1	2A	1992	G	C2'-C3'-O3'	5.69	118.03	109.50
1	2A	752	A	C2'-C3'-O3'	5.59	117.88	109.50
1	1A	2689	U	C4'-C3'-O3'	5.42	117.54	109.40
32	1a	1442	G	P-O3'-C3'	5.28	126.04	119.70
21	1Z	53	ILE	N-CA-C	-5.19	107.41	112.29
42	2k	118	GLY	N-CA-C	5.14	120.70	110.77

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	1P	35	HIS	Peptide
14	1S	58	LEU	Peptide
26	24	18	CYS	Peptide
11	2P	35	HIS	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61869	0	31204	647	0
1	2A	61758	0	31152	789	0
2	1B	2572	0	1305	29	0
2	2B	2573	0	1306	34	0
3	1D	2131	0	2207	45	0
3	2D	2136	0	2218	48	0
4	1E	1559	0	1618	33	0
4	2E	1559	0	1617	38	0
5	1F	1584	0	1625	37	0
5	2F	1580	0	1619	46	0
6	1G	1426	0	1445	52	0
6	2G	1424	0	1441	67	0
7	1H	1330	0	1407	33	0
7	2H	1324	0	1402	37	0
8	1I	1094	0	1127	16	0
8	2I	1076	0	1094	19	0
9	1N	1121	0	1195	25	0
9	2N	1117	0	1184	21	0
10	1O	933	0	996	25	0
10	2O	933	0	996	29	0
11	1P	1135	0	1212	30	0
11	2P	1135	0	1212	37	0
12	1Q	1122	0	1179	20	0
12	2Q	1122	0	1179	35	0
13	1R	968	0	1033	22	0
13	2R	968	0	1033	19	0
14	1S	877	0	938	17	0
14	2S	870	0	923	30	0
15	1T	1091	0	1151	31	0
15	2T	1083	0	1136	28	0
16	1U	959	0	1019	14	0
16	2U	959	0	1019	20	0
17	1V	775	0	841	8	0
17	2V	771	0	830	14	0
18	1W	886	0	940	11	0
18	2W	886	0	940	16	0
19	1X	750	0	814	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	15	0
20	1Y	810	0	892	18	0
20	2Y	810	0	887	25	0
21	1Z	1587	0	1598	31	0
21	2Z	1557	0	1564	55	0
22	10	653	0	674	13	0
22	20	650	0	665	20	0
23	11	754	0	823	20	0
23	21	759	0	837	28	0
24	12	588	0	643	13	0
24	22	592	0	654	11	0
25	13	469	0	518	6	0
25	23	464	0	514	9	0
26	14	546	0	522	14	0
26	24	536	0	514	22	0
27	15	459	0	476	12	0
27	25	455	0	465	10	0
28	16	453	0	473	7	0
28	26	449	0	469	10	0
29	17	418	0	467	5	0
29	27	418	0	467	12	0
30	18	517	0	582	10	0
30	28	517	0	582	8	0
31	19	307	0	335	2	0
31	29	307	0	335	7	0
32	1a	32246	0	16295	430	0
32	2a	32331	0	16338	508	0
33	1b	1842	0	1862	63	0
33	2b	1825	0	1828	69	0
34	1c	1558	0	1557	36	0
34	2c	1542	0	1517	53	0
35	1d	1665	0	1687	56	0
35	2d	1668	0	1703	64	0
36	1e	1133	0	1191	35	0
36	2e	1133	0	1191	29	0
37	1f	814	0	808	20	0
37	2f	816	0	808	18	0
38	1g	1235	0	1249	24	0
38	2g	1229	0	1238	36	0
39	1h	1098	0	1143	29	0
39	2h	1088	0	1126	36	0
40	1i	986	0	990	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	966	0	953	50	0
41	1j	719	0	672	26	0
41	2j	710	0	661	25	0
42	1k	834	0	838	11	0
42	2k	833	0	836	14	0
43	1l	932	0	981	20	0
43	2l	932	0	981	17	0
44	1m	914	0	954	37	0
44	2m	895	0	920	28	0
45	1n	492	0	529	19	0
45	2n	492	0	529	16	0
46	1o	728	0	760	17	0
46	2o	728	0	760	19	0
47	1p	681	0	697	22	0
47	2p	677	0	686	19	0
48	1q	823	0	891	15	0
48	2q	823	0	891	23	0
49	1r	555	0	618	9	0
49	2r	555	0	618	9	0
50	1s	648	0	658	22	0
50	2s	645	0	635	34	0
51	1t	732	0	809	22	0
51	2t	733	0	795	19	0
52	1u	199	0	208	8	0
52	2u	199	0	208	10	0
53	1y	764	0	786	20	0
53	2y	749	0	757	22	0
54	1w	78	0	50	3	0
54	2w	78	0	49	4	0
55	1x	63	0	33	0	0
55	2x	63	0	33	2	0
56	1v	29	0	30	1	0
56	2v	29	0	30	3	0
57	10	10	0	0	0	0
57	11	3	0	0	0	0
57	13	4	0	0	0	0
57	15	9	0	0	0	0
57	17	5	0	0	0	0
57	18	2	0	0	0	0
57	19	3	0	0	0	0
57	1A	1029	0	0	0	0
57	1B	29	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1D	16	0	0	0	0
57	1E	9	0	0	0	0
57	1F	15	0	0	0	0
57	1G	4	0	0	0	0
57	1H	2	0	0	0	0
57	1N	4	0	0	0	0
57	1O	2	0	0	0	0
57	1P	3	0	0	0	0
57	1Q	5	0	0	0	0
57	1R	5	0	0	0	0
57	1T	5	0	0	0	0
57	1U	7	0	0	0	0
57	1V	6	0	0	0	0
57	1W	4	0	0	0	0
57	1Y	1	0	0	0	0
57	1Z	1	0	0	0	0
57	1a	272	0	0	0	0
57	1b	1	0	0	0	0
57	1d	5	0	0	0	0
57	1e	3	0	0	0	0
57	1f	2	0	0	0	0
57	1g	2	0	0	0	0
57	1h	2	0	0	0	0
57	1i	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	3	0	0	0	0
57	1o	1	0	0	0	0
57	1t	1	0	0	0	0
57	1u	1	0	0	0	0
57	1w	1	0	0	0	0
57	1x	2	0	0	0	0
57	1y	3	0	0	0	0
57	20	1	0	0	0	0
57	21	4	0	0	0	0
57	23	1	0	0	0	0
57	25	4	0	0	0	0
57	27	1	0	0	0	0
57	28	1	0	0	0	0
57	29	1	0	0	0	0
57	2A	734	0	0	0	0
57	2B	17	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2D	11	0	0	0	0
57	2E	8	0	0	0	0
57	2F	4	0	0	0	0
57	2G	2	0	0	0	0
57	2I	1	0	0	0	0
57	2N	1	0	0	0	0
57	2P	2	0	0	0	0
57	2Q	2	0	0	0	0
57	2R	2	0	0	0	0
57	2T	4	0	0	0	0
57	2V	2	0	0	0	0
57	2W	3	0	0	0	0
57	2X	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2a	188	0	0	0	0
57	2e	2	0	0	0	0
57	2f	1	0	0	0	0
57	2j	1	0	0	0	0
57	2n	1	0	0	0	0
57	2p	1	0	0	0	0
57	2t	1	0	0	0	0
57	2x	1	0	0	0	0
58	1A	12	0	12	4	0
58	1B	12	0	12	0	0
59	18	8	0	14	0	0
59	1A	8	0	14	1	0
59	1a	16	0	28	4	0
59	2A	24	0	42	1	0
60	14	1	0	0	0	0
60	15	1	0	0	0	0
60	16	1	0	0	0	0
60	19	1	0	0	0	0
60	1Y	1	0	0	0	0
60	1n	1	0	0	0	0
60	24	1	0	0	0	0
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	29	1	0	0	0	0
60	2Y	1	0	0	0	0
60	2n	1	0	0	0	0
61	1d	8	0	0	0	0
61	2d	8	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	10	22	0	0	1	0
62	11	24	0	0	2	0
62	12	10	0	0	3	0
62	13	19	0	0	1	0
62	14	2	0	0	0	0
62	15	24	0	0	0	0
62	16	15	0	0	1	0
62	17	14	0	0	1	0
62	18	21	0	0	2	0
62	19	7	0	0	0	0
62	1A	3560	0	0	122	0
62	1B	89	0	0	3	0
62	1D	98	0	0	4	0
62	1E	69	0	0	2	0
62	1F	51	0	0	1	0
62	1G	15	0	0	1	0
62	1H	6	0	0	1	0
62	1I	4	0	0	0	0
62	1N	43	0	0	3	0
62	1O	22	0	0	3	0
62	1P	63	0	0	4	0
62	1Q	33	0	0	3	0
62	1R	30	0	0	2	0
62	1S	8	0	0	1	0
62	1T	24	0	0	4	0
62	1U	45	0	0	3	0
62	1V	30	0	0	1	0
62	1W	26	0	0	1	0
62	1X	23	0	0	1	0
62	1Y	12	0	0	1	0
62	1Z	9	0	0	2	0
62	1a	382	0	0	27	0
62	1d	5	0	0	1	0
62	1e	3	0	0	0	0
62	1f	2	0	0	0	0
62	1h	1	0	0	0	0
62	1i	1	0	0	0	0
62	1j	1	0	0	0	0
62	1l	3	0	0	1	0
62	1o	3	0	0	0	0
62	1p	2	0	0	0	0
62	1u	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	1w	4	0	0	1	0
62	1x	4	0	0	0	0
62	1y	3	0	0	0	0
62	20	7	0	0	0	0
62	21	17	0	0	4	0
62	25	7	0	0	0	0
62	26	1	0	0	0	0
62	27	4	0	0	0	0
62	28	12	0	0	0	0
62	2A	1737	0	0	121	0
62	2B	33	0	0	4	0
62	2D	32	0	0	1	0
62	2E	22	0	0	1	0
62	2F	20	0	0	1	0
62	2G	2	0	0	0	0
62	2I	2	0	0	0	0
62	2N	3	0	0	1	0
62	2O	11	0	0	1	0
62	2P	18	0	0	2	0
62	2Q	7	0	0	0	0
62	2R	14	0	0	2	0
62	2S	2	0	0	0	0
62	2T	6	0	0	0	0
62	2U	7	0	0	1	0
62	2V	5	0	0	0	0
62	2W	7	0	0	0	0
62	2X	4	0	0	0	0
62	2Y	2	0	0	0	0
62	2Z	9	0	0	2	0
62	2a	224	0	0	19	0
62	2d	3	0	0	0	0
62	2e	2	0	0	0	0
62	2f	1	0	0	0	0
62	2j	1	0	0	0	0
62	2l	3	0	0	1	0
62	2o	3	0	0	0	0
62	2p	1	0	0	0	0
62	2q	1	0	0	0	0
62	2r	2	0	0	0	0
62	2t	1	0	0	0	0
62	2v	1	0	0	0	0
62	2w	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	2x	2	0	0	0	0
62	2y	1	0	0	0	0
All	All	296459	0	194836	4310	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (4310) 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)
54:1w:73:A:O3'	62:1w:201:HOH:O	1.60	1.20
1:1A:1082:U:H3	1:1A:1086:A:N6	1.41	1.17
1:2A:2139:C:N4	1:2A:2152:G:H1	1.44	1.14
1:1A:2137:C:N4	1:1A:2154:G:H1	1.56	1.04
1:1A:1082:U:O4	1:1A:1086:A:N1	1.92	1.01
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.23	1.01
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.25	1.00
1:2A:2122:U:H3	1:2A:2176:A:H61	1.08	0.99
1:2A:2107:C:H42	1:2A:2182:G:H1	1.10	0.98
1:2A:2144:U:HO2'	1:2A:2147:G:H1	1.01	0.98
22:10:10:THR:HG22	22:10:12:ASN:H	1.28	0.94
1:1A:1082:U:H3	1:1A:1086:A:H61	1.07	0.94
1:2A:2139:C:N3	1:2A:2152:G:N2	2.17	0.92
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.50	0.90
1:1A:1082:U:N3	1:1A:1086:A:N6	2.15	0.90
33:2b:80:ILE:HD11	33:2b:212:GLN:HG2	1.53	0.90
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.54	0.90
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.52	0.89
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.37	0.89
1:2A:1970:A:OP1	62:2A:3804:HOH:O	1.91	0.88
26:14:16:CYS:SG	26:14:17:GLY:N	2.48	0.87
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.56	0.87
4:2E:110:GLY:O	62:2R:301:HOH:O	1.92	0.87
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.57	0.86
1:2A:2427:C:OP1	62:2A:3805:HOH:O	1.92	0.86
1:2A:511:U:OP2	62:2A:3806:HOH:O	1.94	0.85
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.08	0.85
1:1A:962:G:OP1	62:1A:4103:HOH:O	1.93	0.85
1:1A:1059:G:H1	1:1A:1079:C:H42	1.21	0.85
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.59	0.85
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2427:C:OP1	62:1A:4104:HOH:O	1.94	0.85
1:2A:2122:U:H3	1:2A:2176:A:N6	1.75	0.84
34:2c:108:ASN:HD21	34:2c:144:SER:HB3	1.42	0.84
11:1P:42:SER:O	62:1P:301:HOH:O	1.95	0.83
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.11	0.83
1:2A:2107:C:N4	1:2A:2182:G:H1	1.75	0.83
1:2A:826:U:OP1	62:2A:3805:HOH:O	1.96	0.83
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.60	0.83
32:2a:79:G:H1	32:2a:90:U:H3	1.23	0.83
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.44	0.82
1:1A:826:U:OP1	62:1A:4104:HOH:O	1.95	0.82
6:1G:43:LEU:O	6:1G:45:GLU:N	2.12	0.82
11:1P:57:THR:HG22	11:1P:60:MET:H	1.44	0.82
20:1Y:92:ASN:H	20:1Y:93:GLY:HA2	1.42	0.82
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.12	0.82
32:1a:975:A:H4'	32:1a:976:G:H5"	1.61	0.82
33:1b:178:ARG:NH1	39:1h:71:GLY:O	2.12	0.82
1:2A:731:C:OP1	62:2A:3807:HOH:O	1.95	0.81
1:2A:194:G:OP2	62:2A:3808:HOH:O	1.96	0.81
1:1A:991:C:OP2	62:1A:4105:HOH:O	1.97	0.81
1:1A:1332:G:OP1	62:1A:4106:HOH:O	1.98	0.81
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	1.63	0.81
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.63	0.80
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.46	0.80
26:14:57:GLU:HB3	26:14:58:ARG:HA	1.62	0.80
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.14	0.80
1:1A:2137:C:N3	1:1A:2154:G:N2	2.28	0.80
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.17	0.80
1:1A:990:A:OP2	62:1A:4105:HOH:O	1.99	0.80
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.13	0.80
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.64	0.79
32:1a:612:C:O2	32:1a:629:G:N2	2.15	0.79
1:1A:120:U:OP2	62:1A:4107:HOH:O	2.00	0.79
4:1E:110:GLY:O	62:1R:301:HOH:O	1.99	0.79
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.63	0.79
32:1a:559:A:H4'	32:1a:560:U:H3'	1.63	0.79
1:2A:1064:C:N4	1:2A:1074:G:O6	2.14	0.79
32:2a:677:U:H3	32:2a:713:G:H22	1.28	0.79
32:2a:1403:C:O2	32:2a:1499:A:N6	2.15	0.79
22:20:10:THR:HG22	22:20:12:ASN:H	1.45	0.78
14:1S:59:LYS:HD2	14:1S:60:GLY:H	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1158:C:H5	32:1a:1181:G:H1	1.31	0.78
1:2A:2615:U:OP1	62:2A:3809:HOH:O	2.00	0.78
1:1A:1315:C:OP2	62:1A:4106:HOH:O	2.01	0.78
1:2A:512:G:N7	62:2A:3806:HOH:O	2.14	0.78
32:2a:1456:G:N1	51:2t:51:GLU:OE2	2.15	0.78
1:1A:1024:G:OP2	62:1A:4108:HOH:O	2.01	0.77
32:1a:664:G:H22	32:1a:741:G:H1	1.28	0.77
1:2A:1890:A:OP2	62:2A:3810:HOH:O	2.01	0.77
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.15	0.77
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.17	0.77
1:2A:1315:C:OP2	62:2A:3812:HOH:O	2.01	0.77
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.67	0.77
1:2A:510:C:OP1	62:2A:3806:HOH:O	2.02	0.77
34:2c:35:GLU:HA	34:2c:38:ARG:HD2	1.65	0.77
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.67	0.77
33:1b:15:VAL:HG11	33:1b:213:LEU:HD13	1.66	0.77
1:2A:370:G:OP2	62:2A:3811:HOH:O	2.01	0.77
7:1H:124:GLU:HG3	7:1H:132:ARG:HB3	1.65	0.77
1:1A:1648:C:OP1	62:1A:4109:HOH:O	2.02	0.76
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.68	0.76
1:2A:98:G:H5'	24:22:3:LEU:HD23	1.68	0.76
26:14:40:HIS:HB3	26:14:43:TYR:HD2	1.49	0.76
1:1A:1054:A:N6	1:1A:1105:U:H3	1.84	0.76
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.18	0.76
32:2a:664:G:H22	32:2a:741:G:H1	1.31	0.76
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.49	0.76
1:2A:1041:C:H42	1:2A:1114:G:H1	1.30	0.76
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.68	0.76
1:1A:1981:A:OP1	62:1A:4110:HOH:O	2.03	0.76
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.16	0.76
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.19	0.75
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD13	1.68	0.75
10:1O:121:VAL:HG23	59:1a:1874:MPD:H13	1.68	0.75
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	1.68	0.75
33:2b:7:VAL:O	33:2b:217:ARG:NH1	2.20	0.75
1:1A:2534:A:N7	62:1A:4182:HOH:O	2.20	0.75
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.03	0.75
1:1A:1865:G:OP1	62:1A:4112:HOH:O	2.05	0.75
1:2A:1055:G:H21	1:2A:1086:A:H8	1.35	0.75
33:2b:19:HIS:HE1	33:2b:206:ASP:HB2	1.52	0.75
1:1A:1634:A:OP2	62:1A:4111:HOH:O	2.04	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2137:C:H42	1:1A:2154:G:H1	0.81	0.74
1:1A:530:G:N1	1:1A:2023:G:OP1	2.18	0.74
32:1a:1054:C:N4	53:1y:46:GLN:OE1	2.18	0.74
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.03	0.74
17:1V:66:ARG:NH1	62:1V:301:HOH:O	2.13	0.74
39:2h:103:VAL:HG21	39:2h:110:ALA:HB2	1.70	0.74
1:1A:1568:G:N7	62:1A:4169:HOH:O	2.18	0.74
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.18	0.74
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.69	0.74
33:2b:184:VAL:HG23	33:2b:198:ASP:H	1.51	0.74
1:1A:1060:U:H4'	1:1A:1061:U:H5'	1.70	0.74
26:24:16:CYS:SG	26:24:17:GLY:N	2.61	0.74
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.68	0.74
33:2b:119:GLU:HG3	33:2b:153:ARG:HH22	1.52	0.74
1:1A:1054:A:H61	1:1A:1105:U:H3	1.33	0.73
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.06	0.73
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.51	0.73
1:2A:1209:G:OP2	62:2A:3813:HOH:O	2.05	0.73
5:2F:200:GLU:O	5:2F:204:ASN:ND2	2.20	0.73
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.70	0.73
1:1A:330:A:H2	1:1A:1210:A:HO2'	1.33	0.73
1:1A:1671:U:O4	62:1A:4115:HOH:O	2.06	0.73
32:1a:1441:G:H5"	32:1a:1442:G:H5'	1.71	0.73
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.54	0.73
4:1E:127:ASP:OD2	62:1E:402:HOH:O	2.05	0.73
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.54	0.73
1:2A:1602:U:O4	62:2A:3814:HOH:O	2.06	0.73
1:1A:568:U:O4	62:1A:4113:HOH:O	2.06	0.73
1:2A:2807:G:N1	1:2A:2893:G:O6	2.19	0.73
32:2a:954:G:H21	32:2a:1227:A:H62	1.36	0.73
16:1U:36:ARG:NH2	62:1U:302:HOH:O	2.21	0.73
1:2A:792:G:O6	62:2A:3816:HOH:O	2.06	0.73
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.21	0.73
1:2A:1648:C:OP1	62:2A:3815:HOH:O	2.06	0.72
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.71	0.72
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.24	0.72
4:1E:77:ILE:HD13	4:1E:195:LEU:HD13	1.69	0.72
1:2A:854:G:H2'	1:2A:855:G:H8	1.54	0.72
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.22	0.72
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.21	0.72
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:38:G:H22	32:1a:397:A:H5'	1.52	0.72
32:1a:1069:C:OP2	62:1a:4601:HOH:O	2.07	0.72
1:2A:2319:G:H22	14:2S:3:ARG:HH11	1.36	0.72
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.07	0.72
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.22	0.72
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.22	0.72
5:2F:188:ARG:HA	11:2P:3:LEU:HD11	1.72	0.72
34:2c:35:GLU:OE2	34:2c:59:ARG:NH2	2.23	0.72
1:1A:2499:C:OP1	62:1A:4114:HOH:O	2.06	0.72
36:1e:5:ASP:OD1	36:1e:5:ASP:N	2.18	0.72
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.72	0.72
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.53	0.72
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.70	0.72
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.23	0.72
1:2A:2499:C:OP1	62:2A:3817:HOH:O	2.06	0.72
4:2E:119:ARG:HD3	4:2E:160:TYR:HB2	1.70	0.72
32:2a:662:G:O2'	32:2a:836:G:OP1	2.07	0.72
44:2m:24:GLY:HA3	44:2m:66:LEU:HD22	1.72	0.72
32:1a:1030(C):G:N7	32:1a:1031:G:N2	2.38	0.71
1:2A:422:A:OP2	62:2A:3811:HOH:O	2.07	0.71
1:2A:2250:G:OP1	12:2Q:85:LYS:NZ	2.21	0.71
32:2a:1004:A:H5"	32:2a:1025:U:C5	2.24	0.71
32:2a:1222:G:O6	62:2a:3202:HOH:O	2.07	0.71
1:1A:2821:A:OP2	62:1A:4116:HOH:O	2.08	0.71
1:2A:531:C:OP2	62:2A:3818:HOH:O	2.08	0.71
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.23	0.71
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.55	0.71
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.55	0.71
1:1A:1094:U:N3	1:1A:1097:U:OP2	2.22	0.71
32:1a:73:G:H1	32:1a:96:U:H3	1.38	0.71
1:2A:1568:G:N7	62:2A:3885:HOH:O	2.21	0.71
32:2a:35:G:O2'	43:2l:118:SER:O	2.09	0.71
33:2b:201:ILE:HG21	33:2b:214:ILE:HG21	1.71	0.71
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.72	0.71
44:1m:80:ARG:HH22	50:1s:69:HIS:HE1	1.39	0.71
1:1A:679:C:OP1	62:1A:4118:HOH:O	2.09	0.71
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.24	0.71
1:2A:1314:C:OP1	62:2A:3812:HOH:O	2.08	0.71
1:1A:1102:C:OP2	1:1A:1104:C:N4	2.24	0.71
1:1A:2096:U:H3	1:1A:2193:G:H1	1.37	0.71
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.73	0.71
1:1A:400:G:N7	62:1A:4216:HOH:O	2.24	0.70
1:1A:1669:A:OP2	62:1A:4115:HOH:O	2.07	0.70
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.73	0.70
32:1a:1264:C:H2'	32:1a:1265:G:H8	1.56	0.70
1:2A:1090:U:H2'	1:2A:1091:G:C8	2.26	0.70
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.24	0.70
1:1A:1295:C:OP2	62:1A:4119:HOH:O	2.09	0.70
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.74	0.70
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.09	0.70
51:1t:60:GLU:HG3	51:1t:81:LYS:HE3	1.73	0.70
1:2A:1023:U:OP2	62:2A:3824:HOH:O	2.10	0.70
3:1D:88:ARG:NH1	62:1D:402:HOH:O	2.23	0.70
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.71	0.70
1:1A:105:C:OP1	62:1A:4117:HOH:O	2.08	0.70
1:2A:2036:C:OP2	62:2A:3825:HOH:O	2.10	0.70
3:2D:108:PRO:HD2	3:2D:111:LEU:HD12	1.74	0.70
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.72	0.70
58:1A:4030:ARG:HH11	5:1F:164:ARG:HE	1.39	0.70
35:2d:13:ARG:NH1	35:2d:38:TYR:O	2.24	0.70
1:1A:2258:C:OP1	62:1A:4123:HOH:O	2.09	0.70
1:2A:586:A:N1	1:2A:809:G:O2'	2.25	0.70
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	1.73	0.70
32:1a:324:G:N7	62:1a:4620:HOH:O	2.24	0.70
32:1a:1075:C:H5"	33:1b:179:LYS:HE3	1.74	0.70
1:2A:404:C:OP1	62:2A:3820:HOH:O	2.09	0.70
1:1A:1968:G:OP1	62:1A:4120:HOH:O	2.09	0.69
32:1a:21:G:OP1	62:1a:4602:HOH:O	2.10	0.69
35:2d:12:CYS:HB2	61:2d:501:SF4:S2	2.30	0.69
42:2k:117:ASN:N	42:2k:117:ASN:OD1	2.22	0.69
3:1D:71:ASP:HB2	3:1D:103:ARG:HH22	1.55	0.69
35:1d:109:GLY:HA3	35:1d:165:MET:HG3	1.72	0.69
1:2A:1365:A:O2'	23:21:11:ARG:NH1	2.25	0.69
32:2a:1009:G:H1	32:2a:1020:U:H3	1.40	0.69
1:2A:83:G:H1	1:2A:102:G:HO2'	1.37	0.69
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.74	0.69
32:2a:427:U:OP1	35:2d:13:ARG:NH2	2.24	0.69
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	1.74	0.69
5:2F:24:LEU:HD13	5:2F:115:ALA:HA	1.75	0.69
32:2a:574:A:OP2	62:2a:3203:HOH:O	2.10	0.69
33:2b:95:GLN:HG3	33:2b:147:LYS:HB2	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:595:C:N4	62:2A:3830:HOH:O	2.23	0.69
1:2A:2434:A:N7	62:2A:3915:HOH:O	2.25	0.69
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.58	0.69
1:1A:948:G:OP1	62:1A:4103:HOH:O	2.10	0.69
1:1A:2058:A:OP1	62:1A:4126:HOH:O	2.10	0.69
1:2A:1495:A:OP2	62:2A:3826:HOH:O	2.10	0.69
1:2A:1647:G:OP1	62:2A:3815:HOH:O	2.11	0.69
1:2A:1971:A:OP1	62:2A:3804:HOH:O	2.09	0.69
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.25	0.69
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.75	0.69
1:2A:527:C:OP1	62:2A:3819:HOH:O	2.08	0.69
1:2A:818:G:OP2	62:2A:3823:HOH:O	2.09	0.69
1:2A:952:G:OP1	12:2Q:16:ARG:NH2	2.26	0.69
1:1A:1890:A:OP2	62:1A:4124:HOH:O	2.10	0.69
1:1A:2406:U:OP1	62:1A:4127:HOH:O	2.11	0.69
25:13:49:LYS:O	62:13:201:HOH:O	2.10	0.69
32:1a:1297:C:O2	38:1g:114:ARG:NH1	2.26	0.69
33:1b:9:GLU:OE2	33:1b:217:ARG:NH1	2.26	0.69
50:1s:36:ARG:NH1	50:1s:52:TYR:O	2.26	0.69
51:1t:33:ILE:O	51:1t:37:SER:OG	2.11	0.69
1:2A:84:A:N1	1:2A:98:G:O2'	2.26	0.69
23:21:17:SER:O	62:21:201:HOH:O	2.10	0.69
1:1A:1271:G:OP2	62:1A:4109:HOH:O	2.09	0.69
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.73	0.69
1:1A:2447:G:OP2	62:1A:4128:HOH:O	2.11	0.69
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.75	0.69
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.73	0.69
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.26	0.68
23:11:41:ARG:O	62:11:201:HOH:O	2.10	0.68
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	1.74	0.68
32:2a:405:U:O4	35:2d:2:GLY:N	2.25	0.68
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.66	0.68
8:1I:77:LEU:HD12	8:1I:104:GLN:HE21	1.58	0.68
32:1a:1129:C:H5"	40:1i:16:ARG:HH12	1.58	0.68
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.26	0.68
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.28	0.68
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.56	0.68
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.20	0.68
1:1A:2822:G:OP2	62:1A:4116:HOH:O	2.12	0.68
33:1b:119:GLU:OE2	33:1b:153:ARG:NH1	2.25	0.68
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:981:U:O4	62:2a:3202:HOH:O	2.10	0.68
43:2l:49:ASN:ND2	43:2l:92:0TD:SB	2.67	0.68
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.76	0.68
27:25:40:LYS:NZ	27:25:44:THR:O	2.27	0.68
35:2d:189:PRO:HB2	35:2d:194:LEU:HD11	1.75	0.68
32:2a:1083:U:OP2	62:2a:3204:HOH:O	2.11	0.68
32:2a:1104:G:H4'	33:2b:111:ARG:HH11	1.58	0.68
1:1A:1199:U:OP2	62:1A:4132:HOH:O	2.12	0.68
1:1A:2789:C:O2	1:1A:2894:G:N1	2.19	0.68
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.76	0.68
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.75	0.68
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HB	1.74	0.68
32:2a:429:U:OP2	35:2d:36:ARG:NH2	2.24	0.68
1:1A:1059:G:H1	1:1A:1079:C:N4	1.91	0.68
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.26	0.68
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.75	0.68
40:1i:3:GLN:HE21	40:1i:20:ARG:HH21	1.42	0.68
2:2B:58:A:OP2	62:2B:301:HOH:O	2.12	0.68
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.75	0.68
44:1m:50:GLU:HA	44:1m:53:VAL:HG22	1.76	0.68
1:2A:530:G:O6	62:2A:3822:HOH:O	2.09	0.68
40:2i:28:VAL:HG13	40:2i:63:ILE:HB	1.76	0.68
1:1A:2623:G:OP1	62:1A:4134:HOH:O	2.12	0.67
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.17	0.67
1:2A:2123:G:H2'	1:2A:2124:G:H8	1.58	0.67
18:1W:4:LYS:NZ	62:1W:301:HOH:O	2.26	0.67
34:1c:34:LEU:HG	34:1c:38:ARG:HD2	1.74	0.67
34:2c:148:GLY:HA3	34:2c:203:PHE:HB3	1.77	0.67
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.75	0.67
42:2k:21:ILE:HB	42:2k:84:VAL:HG12	1.76	0.67
1:1A:1358:G:OP2	62:1A:4133:HOH:O	2.12	0.67
32:1a:1500:A:OP1	62:1a:4603:HOH:O	2.12	0.67
36:1e:96:PRO:O	36:1e:98:THR:N	2.26	0.67
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.75	0.67
1:1A:981:A:OP1	62:1A:4131:HOH:O	2.12	0.67
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.40	0.67
47:1p:53:VAL:HG13	47:1p:79:VAL:HG12	1.76	0.67
5:2F:120:GLU:HB2	5:2F:122:LYS:HG2	1.75	0.67
1:1A:2145:C:O2'	1:1A:2147:G:N2	2.27	0.67
35:2d:98:GLU:HG3	35:2d:194:LEU:HD21	1.75	0.67
32:1a:596:C:OP2	62:1a:4604:HOH:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:955:C:OP1	12:2Q:87:LYS:NZ	2.27	0.67
32:2a:1388:C:O2'	62:2a:3206:HOH:O	2.12	0.67
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.76	0.67
32:2a:1457:G:OP1	51:2t:39:LYS:NZ	2.27	0.67
32:1a:352:C:O2'	32:1a:354:G:OP1	2.11	0.67
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.18	0.67
32:1a:452:A:OP1	47:1p:43:LYS:NZ	2.27	0.67
32:1a:1031:G:H2'	32:1a:1032:G:H8	1.59	0.67
40:1i:79:LEU:HD22	40:1i:104:ARG:HB2	1.77	0.67
44:2m:3:ARG:HH12	44:2m:11:ARG:HG2	1.60	0.67
12:2Q:51:ARG:NH2	21:2Z:186:GLU:OE1	2.27	0.67
53:2y:20:VAL:HG11	53:2y:39:ILE:HG21	1.76	0.67
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.27	0.67
1:1A:1352:U:OP1	62:1A:4135:HOH:O	2.13	0.67
1:1A:2130:U:O2'	1:1A:2133:G:O2'	2.12	0.67
1:1A:2875:C:O2'	15:1T:2:ASN:OD1	2.12	0.67
32:1a:176:C:H2'	32:1a:177:C:H6	1.60	0.67
32:2a:393:A:OP1	62:2a:3205:HOH:O	2.12	0.67
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.60	0.67
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.76	0.67
1:2A:2657:A:O3'	7:2H:160:LYS:NZ	2.28	0.66
19:2X:26:TYR:HB3	19:2X:92:LEU:HD22	1.78	0.66
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.29	0.66
33:1b:27:LYS:HB2	33:1b:194:PRO:HD2	1.76	0.66
36:1e:69:VAL:HG21	36:1e:113:ALA:HB1	1.76	0.66
1:2A:2371:G:O6	62:2A:3828:HOH:O	2.12	0.66
32:2a:1004:A:H5"	32:2a:1025:U:H5	1.60	0.66
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.28	0.66
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.75	0.66
32:1a:130:A:N3	32:1a:263:A:O2'	2.28	0.66
1:2A:2255:G:OP2	62:2A:3833:HOH:O	2.13	0.66
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.58	0.66
14:2S:84:GLN:HA	14:2S:111:GLU:HB2	1.78	0.66
32:2a:1503:A:H5'	32:2a:1531:A:H1'	1.76	0.66
36:2e:152:ARG:HB3	39:2h:43:GLY:HA3	1.75	0.66
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.12	0.66
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.31	0.66
1:1A:72:U:OP1	62:1A:4136:HOH:O	2.13	0.66
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	1.94	0.66
1:1A:1772:G:OP2	62:1A:4129:HOH:O	2.11	0.66
1:1A:2038:G:O6	62:1A:4122:HOH:O	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2506:U:OP2	62:1A:4130:HOH:O	2.11	0.66
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.77	0.66
9:2N:72:TYR:OH	62:2N:301:HOH:O	2.10	0.66
1:1A:1647:G:OP1	62:1A:4109:HOH:O	2.12	0.66
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.31	0.66
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.31	0.66
1:2A:2639:A:OP2	62:2A:3834:HOH:O	2.13	0.66
32:2a:1500:A:OP1	62:2a:3207:HOH:O	2.13	0.66
1:1A:1629:U:O4	62:1A:4125:HOH:O	2.10	0.66
1:2A:585:G:OP2	62:2A:3827:HOH:O	2.12	0.66
1:2A:745:G:O6	62:2A:3821:HOH:O	2.09	0.66
1:2A:2161:C:O2'	1:2A:2173:A:O2'	2.12	0.66
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.60	0.66
32:2a:410:G:OP1	35:2d:30:LYS:NZ	2.24	0.66
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.78	0.66
1:1A:2407:G:OP1	62:1A:4142:HOH:O	2.14	0.66
29:17:34:ARG:NH2	62:17:201:HOH:O	2.23	0.66
1:2A:2313:C:H4'	6:2G:91:ARG:HD3	1.77	0.66
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.28	0.66
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.78	0.66
32:1a:437:U:H5'	35:1d:155:LEU:HD11	1.78	0.66
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.31	0.65
8:1I:133:HIS:ND1	8:1I:134:PRO:O	2.29	0.65
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.08	0.65
24:12:47:ASN:O	62:12:101:HOH:O	2.13	0.65
32:1a:300:A:O2'	32:1a:564:C:N3	2.28	0.65
32:1a:642:A:N3	39:1h:113:SER:OG	2.27	0.65
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.78	0.65
1:2A:1237:A:OP1	62:2A:3837:HOH:O	2.14	0.65
1:1A:1252:G:OP1	62:1A:4141:HOH:O	2.14	0.65
32:1a:768:A:OP2	62:1a:4605:HOH:O	2.14	0.65
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.14	0.65
1:2A:2092:U:OP1	62:2A:3831:HOH:O	2.13	0.65
32:2a:98:G:N7	62:2a:3229:HOH:O	2.30	0.65
1:1A:1321:A:N1	62:1A:4270:HOH:O	2.30	0.65
35:1d:65:ARG:HG3	35:1d:70:ILE:HG22	1.78	0.65
1:2A:1066:U:O2'	1:2A:1067:A:O5'	2.14	0.65
7:2H:101:ARG:HG2	7:2H:117:PRO:HG2	1.77	0.65
1:1A:1186:G:OP2	62:1A:4105:HOH:O	2.12	0.65
43:1l:59:ARG:NH1	43:1l:65:GLU:OE1	2.29	0.65
1:2A:2123:G:H1	1:2A:2175:C:H42	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.29	0.65
1:1A:801:G:OP2	62:1A:4138:HOH:O	2.13	0.65
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.77	0.65
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.30	0.65
1:2A:338:G:N7	62:2A:3948:HOH:O	2.29	0.65
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.43	0.65
16:2U:5:LYS:NZ	62:2U:202:HOH:O	2.29	0.65
1:1A:246:C:OP1	62:1A:4139:HOH:O	2.14	0.65
6:1G:18:GLU:OE2	6:1G:21:ARG:NH1	2.30	0.65
1:2A:1771:C:OP1	62:2A:3840:HOH:O	2.14	0.65
40:1i:18:PHE:HD2	40:1i:62:TYR:HD2	1.43	0.65
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.14	0.65
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.61	0.65
22:20:26:TYR:N	22:20:29:GLN:OE1	2.29	0.65
1:1A:1175:U:OP1	1:1A:1177:A:N6	2.30	0.65
16:1U:56:ASP:OD2	62:1U:301:HOH:O	2.13	0.65
32:1a:78:G:H1	32:1a:91:C:H42	1.42	0.65
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.30	0.65
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.30	0.65
1:2A:493:G:OP2	62:2A:3836:HOH:O	2.14	0.65
1:2A:2029:G:OP2	62:2A:3839:HOH:O	2.14	0.65
4:2E:199:ARG:NH1	62:2E:402:HOH:O	2.29	0.65
1:1A:2239:G:OP2	62:1A:4146:HOH:O	2.15	0.65
1:1A:2628:C:O2	62:1A:4121:HOH:O	2.09	0.65
2:1B:87:G:N2	2:1B:90:A:OP2	2.28	0.65
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.78	0.65
33:1b:230:VAL:HG13	33:1b:232:PRO:HD2	1.79	0.65
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.26	0.65
48:1q:45:HIS:HB2	48:1q:65:ILE:HD13	1.79	0.65
1:2A:2589:A:OP1	62:2A:3841:HOH:O	2.15	0.65
32:2a:1005:A:H5"	32:2a:1006:C:C5	2.32	0.65
1:1A:387:U:OP1	62:1A:4150:HOH:O	2.15	0.64
1:1A:987:G:O2'	1:1A:1000:A:N3	2.28	0.64
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.29	0.64
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.60	0.64
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.78	0.64
1:2A:1830:C:OP2	62:2A:3844:HOH:O	2.15	0.64
1:1A:847:U:OP2	62:1A:4144:HOH:O	2.14	0.64
4:1E:29:GLY:HA3	62:1E:405:HOH:O	1.97	0.64
32:1a:1505:G:OP1	62:1a:4603:HOH:O	2.15	0.64
44:2m:92:HIS:CD2	44:2m:98:VAL:HG21	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.97	0.64
2:1B:23:G:O6	62:1B:301:HOH:O	2.08	0.64
3:2D:232:PRO:O	62:2D:401:HOH:O	2.15	0.64
20:2Y:86:ARG:HB2	20:2Y:98:VAL:HG22	1.79	0.64
32:2a:1508:G:OP1	62:2a:3207:HOH:O	2.14	0.64
1:1A:749:C:OP2	62:1A:4145:HOH:O	2.15	0.64
32:1a:1130:A:O2'	40:1i:3:GLN:NE2	2.23	0.64
1:2A:752:A:H3'	29:27:1:MET:HE1	1.80	0.64
1:2A:1108:U:O2'	1:2A:1109:C:OP1	2.16	0.64
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.33	0.64
1:1A:973:A:OP2	62:1A:4113:HOH:O	2.13	0.64
32:2a:986:A:N3	50:2s:52:TYR:OH	2.26	0.64
1:1A:512:G:OP2	62:1A:4143:HOH:O	2.14	0.64
1:1A:888:C:N3	44:1m:93:ARG:NH1	2.44	0.64
39:1h:124:ALA:O	39:1h:128:GLY:N	2.30	0.64
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.22	0.64
1:1A:380:U:OP1	62:1A:4148:HOH:O	2.15	0.64
1:1A:2116:G:OP2	1:1A:2166:G:N2	2.30	0.64
14:1S:10:ARG:HG2	14:1S:91:PRO:HA	1.79	0.64
19:1X:50:LYS:NZ	62:1X:103:HOH:O	2.29	0.64
47:1p:6:LEU:HD13	47:1p:19:ILE:HD13	1.80	0.64
1:2A:131:G:OP1	62:2A:3838:HOH:O	2.14	0.64
1:2A:1901:A:OP2	3:2D:255:LYS:NZ	2.31	0.64
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.33	0.64
1:2A:2723:C:OP2	4:2E:109:LYS:NZ	2.31	0.64
1:2A:2141:G:O6	1:2A:2150:U:O2	2.15	0.64
32:2a:1129:C:N4	32:2a:1143:G:H1	1.95	0.64
7:1H:121:ILE:HG13	7:1H:144:VAL:HG21	1.80	0.64
34:1c:191:THR:OG1	34:1c:194:GLY:O	2.15	0.64
1:2A:494:G:OP1	18:2W:8:ARG:NH1	2.31	0.64
1:2A:995:C:OP2	16:2U:54:LYS:NZ	2.30	0.64
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.30	0.64
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.78	0.64
1:1A:1064:C:H3'	1:1A:1065:U:H5"	1.78	0.64
1:1A:2147:G:H2'	1:1A:2148:G:H4'	1.80	0.64
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.26	0.64
1:2A:492:A:OP2	62:2A:3843:HOH:O	2.15	0.64
1:2A:2099:U:H3	1:2A:2190:G:H1	1.44	0.64
1:1A:1063:G:H5"	1:1A:1065:U:H5	1.62	0.63
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.13	0.63
26:14:61:ARG:HG3	26:14:62:ARG:H	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.32	0.63
1:2A:1671:U:OP2	62:2A:3842:HOH:O	2.15	0.63
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.13	0.63
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	1.80	0.63
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.31	0.63
25:23:40:THR:HG22	25:23:42:ALA:H	1.62	0.63
33:2b:67:THR:H	33:2b:160:ASP:HB2	1.62	0.63
3:1D:96:HIS:CD2	3:1D:102:LYS:HD3	2.32	0.63
28:26:25:LYS:NZ	28:26:30:THR:O	2.26	0.63
32:2a:573:A:OP2	62:2a:3203:HOH:O	2.15	0.63
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.63	0.63
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.80	0.63
1:1A:365:C:OP2	62:1A:4153:HOH:O	2.15	0.63
1:1A:1840:G:N7	62:1A:4276:HOH:O	2.30	0.63
2:1B:14:U:OP2	2:1B:70:C:O2'	2.14	0.63
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.79	0.63
41:2j:35:SER:HB2	41:2j:73:ASP:HB2	1.79	0.63
1:1A:1092:C:N3	1:1A:1099:G:O6	2.32	0.63
1:1A:2814:C:OP2	62:1A:4152:HOH:O	2.15	0.63
35:1d:166:LYS:HA	35:1d:178:VAL:HG11	1.79	0.63
1:2A:2286:A:H4'	1:2A:2287:A:O4'	1.98	0.63
6:2G:43:LEU:HD11	6:2G:153:ARG:HD2	1.78	0.63
32:2a:278:G:OP2	48:2q:41:LYS:NZ	2.30	0.63
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.47	0.63
40:2i:42:ARG:NH1	40:2i:71:SER:O	2.32	0.63
1:1A:2825:C:OP2	62:1A:4151:HOH:O	2.15	0.63
4:1E:119:ARG:HD3	4:1E:160:TYR:HB2	1.81	0.63
32:1a:1309:G:OP2	44:1m:99:ARG:NH2	2.26	0.63
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.30	0.63
1:2A:2400:G:H4'	28:26:18:ARG:HG2	1.80	0.63
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.31	0.63
6:1G:166:ASP:OD2	62:1G:301:HOH:O	2.15	0.63
32:1a:673:G:H2'	32:1a:674:G:C8	2.34	0.63
32:2a:70:G:H1	32:2a:99:U:H3	1.47	0.63
33:2b:15:VAL:O	33:2b:16:HIS:HB3	1.99	0.63
40:2i:23:ASN:N	40:2i:23:ASN:OD1	2.32	0.63
1:2A:2107:C:N3	1:2A:2182:G:N2	2.47	0.63
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.34	0.63
32:2a:1129:C:H42	32:2a:1143:G:H1	1.44	0.63
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.32	0.63
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:20:ARG:NH1	62:1S:201:HOH:O	2.30	0.63
32:1a:1028:C:H2'	32:1a:1029:C:H4'	1.80	0.63
1:2A:2580:U:O4	62:2A:3847:HOH:O	2.16	0.63
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.29	0.63
32:2a:1348:U:H2'	32:2a:1349:A:H8	1.64	0.63
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.64	0.63
6:1G:16:ARG:HE	6:1G:31:VAL:HG21	1.64	0.63
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.81	0.63
1:2A:271(W):G:O6	62:2A:3829:HOH:O	2.12	0.63
1:2A:674:G:OP2	62:2A:3848:HOH:O	2.16	0.63
1:2A:2131:G:OP1	1:2A:2132:U:H5'	1.99	0.63
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.80	0.63
38:2g:135:VAL:HA	38:2g:138:LYS:HB3	1.81	0.63
32:1a:35:G:O2'	43:1l:118:SER:O	2.16	0.62
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.31	0.62
1:1A:194:G:N3	62:1A:4280:HOH:O	2.31	0.62
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.81	0.62
40:1i:20:ARG:O	40:1i:60:ASP:N	2.30	0.62
21:2Z:26:GLY:HA3	21:2Z:86:VAL:HG23	1.81	0.62
26:24:59:PHE:HA	26:24:60:GLN:C	2.24	0.62
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.99	0.62
1:1A:2114:A:H1'	1:1A:2168:G:H5'	1.81	0.62
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.34	0.62
8:2I:69:LYS:HB2	8:2I:138:ILE:HG12	1.82	0.62
20:2Y:83:THR:HG21	20:2Y:99:CYS:HB2	1.81	0.62
34:2c:66:VAL:HB	34:2c:101:LEU:HD12	1.80	0.62
1:2A:995:C:O2	9:2N:3:THR:OG1	2.15	0.62
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.34	0.62
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.15	0.62
58:1A:4030:ARG:NH1	5:1F:164:ARG:HE	1.98	0.62
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.18	0.62
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.35	0.62
33:1b:10:LEU:HA	33:1b:48:MET:HE1	1.81	0.62
46:1o:26:GLU:OE2	46:1o:77:ARG:NH2	2.31	0.62
1:2A:2022:U:O2	62:2A:3832:HOH:O	2.13	0.62
32:2a:944:G:N1	32:2a:1338:G:OP2	2.33	0.62
40:2i:5:TYR:HE1	40:2i:16:ARG:HB3	1.63	0.62
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.82	0.62
1:2A:1754:C:P	15:2T:96:ARG:HH12	2.22	0.62
7:2H:11:VAL:HG23	7:2H:15:VAL:HG23	1.81	0.62
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:53:VAL:HG13	47:2p:79:VAL:HG12	1.80	0.62
1:1A:639:U:H2'	1:1A:640:C:C6	2.35	0.62
1:2A:2125:G:N2	1:2A:2172:U:OP2	2.32	0.62
1:2A:2821:A:OP2	62:2R:301:HOH:O	2.16	0.62
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.79	0.62
46:2o:39:LEU:HB3	46:2o:56:LEU:HD12	1.80	0.62
1:1A:1175:U:O2'	1:1A:1176:G:O5'	2.17	0.62
3:1D:206:LEU:O	3:1D:211:ARG:HD3	2.00	0.62
12:1Q:98:LYS:NZ	62:1Q:302:HOH:O	2.31	0.62
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.17	0.62
1:2A:1971:A:N1	62:2A:3963:HOH:O	2.31	0.62
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.33	0.62
32:2a:737:A:H2'	32:2a:738:C:C6	2.35	0.62
56:1v:1:FME:HG2	56:1v:3:ILE:HD12	1.81	0.62
1:2A:2705:A:OP2	62:2A:3851:HOH:O	2.16	0.62
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.33	0.62
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.33	0.62
1:2A:775:G:O3'	62:2A:3849:HOH:O	2.16	0.62
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.32	0.62
33:2b:55:PHE:HD1	33:2b:221:LEU:HD22	1.65	0.62
39:2h:112:LEU:HA	39:2h:134:ILE:HG12	1.81	0.62
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.82	0.62
32:1a:17:U:H2'	32:1a:18:C:C6	2.35	0.61
1:2A:662:G:O6	62:2A:3830:HOH:O	2.12	0.61
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.82	0.61
32:2a:662:G:H2'	32:2a:663:A:H8	1.63	0.61
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.33	0.61
35:2d:166:LYS:HA	35:2d:178:VAL:HG21	1.82	0.61
1:1A:1670:C:OP2	62:1A:4115:HOH:O	2.16	0.61
32:1a:1318:A:OP1	50:1s:3:ARG:NH1	2.33	0.61
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.81	0.61
38:2g:113:GLU:HB2	38:2g:115:ARG:HH12	1.65	0.61
1:1A:955:C:OP1	12:1Q:87:LYS:NZ	2.30	0.61
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.34	0.61
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.35	0.61
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	1.82	0.61
21:2Z:126:VAL:HG11	21:2Z:161:VAL:HB	1.82	0.61
30:28:33:ASN:OD1	30:28:36:LYS:NZ	2.23	0.61
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	1.81	0.61
38:2g:15:ASP:OD1	38:2g:20:ASP:N	2.32	0.61
1:1A:2424:C:OP1	62:1A:4155:HOH:O	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.33	0.61
15:1T:33:LYS:HE3	15:1T:82:LEU:HD23	1.82	0.61
32:1a:757:U:O2'	32:1a:879:C:O2	2.19	0.61
3:2D:8:PRO:HB3	3:2D:14:ARG:HG3	1.82	0.61
6:2G:37:VAL:HG21	6:2G:103:LEU:HD21	1.81	0.61
33:2b:114:ARG:HD2	33:2b:118:LEU:HG	1.81	0.61
41:2j:6:ILE:HB	41:2j:72:VAL:HG22	1.83	0.61
1:1A:1070:A:O2'	1:1A:1098:A:OP1	2.16	0.61
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.82	0.61
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.33	0.61
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.35	0.61
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.64	0.61
8:2I:75:LEU:HD11	8:2I:105:HIS:HD2	1.65	0.61
32:2a:696:A:N1	32:2a:797:C:O2'	2.30	0.61
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.34	0.61
35:2d:104:VAL:HG11	35:2d:140:VAL:HG21	1.83	0.61
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.32	0.61
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.82	0.61
1:2A:459:U:H5"	29:27:40:TRP:CD2	2.36	0.61
1:2A:2105:C:H42	1:2A:2184:G:H1	1.48	0.61
26:24:48:ARG:HD2	26:24:52:THR:HA	1.82	0.61
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.01	0.61
32:1a:1270:C:OP2	52:1u:24:ARG:NH2	2.33	0.61
33:2b:162:ILE:HD11	33:2b:184:VAL:HG12	1.81	0.61
1:1A:796:C:H2'	1:1A:797:C:C6	2.36	0.61
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.34	0.61
2:2B:102:A:OP2	62:2B:302:HOH:O	2.16	0.61
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.83	0.61
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.82	0.61
1:1A:588:U:H2'	1:1A:589:C:C6	2.36	0.61
1:2A:8:A:H2'	1:2A:9:U:H6	1.65	0.61
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.48	0.61
32:2a:56:U:H2'	32:2a:57:G:H8	1.65	0.61
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.19	0.61
33:2b:27:LYS:O	33:2b:30:ARG:NH1	2.34	0.61
48:2q:45:HIS:HB2	48:2q:65:ILE:HD13	1.82	0.61
53:1y:55:ASN:HA	53:1y:60:VAL:HA	1.83	0.60
1:2A:500:G:N1	1:2A:503:A:OP2	2.34	0.60
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.34	0.60
35:2d:111:ALA:HB1	35:2d:116:GLN:HG2	1.82	0.60
49:2r:26:LEU:HD13	49:2r:39:VAL:HG13	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:376:G:H5”	47:2p:5:ARG:HD2	1.83	0.60
40:2i:14:VAL:HG23	40:2i:66:ARG:HB2	1.82	0.60
40:2i:86:VAL:HG21	40:2i:102:LEU:HD21	1.82	0.60
1:2A:1058:G:H1’	1:2A:1082:U:H3	1.66	0.60
1:2A:2682:U:OP2	62:2A:3853:HOH:O	2.16	0.60
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.82	0.60
22:20:27:GLU:HB2	22:20:69:PHE:HD1	1.65	0.60
32:2a:1090:U:H2’	32:2a:1091:U:H6	1.66	0.60
32:2a:1197:G:OP2	62:2a:3208:HOH:O	2.17	0.60
32:2a:1321:C:H4’	44:2m:87:TYR:HE2	1.66	0.60
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.37	0.60
1:2A:2504:U:OP2	62:2A:3850:HOH:O	2.16	0.60
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.36	0.60
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.82	0.60
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.67	0.60
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.83	0.60
32:2a:980:C:OP2	62:2a:3202:HOH:O	2.16	0.60
34:2c:128:PHE:HD1	34:2c:129:ALA:H	1.49	0.60
12:1Q:32:TYR:OH	12:1Q:111:GLU:HG3	2.02	0.60
32:1a:1356:G:H2’	32:1a:1357:A:C8	2.37	0.60
21:2Z:126:VAL:HG22	21:2Z:163:LEU:HA	1.83	0.60
32:2a:1190:G:H5’	34:2c:176:HIS:CE1	2.37	0.60
1:1A:1027:A:N3	62:1A:4292:HOH:O	2.31	0.60
1:1A:1188:U:H4’	17:1V:79:VAL:HG22	1.81	0.60
30:18:65:GLU:OXT	62:18:201:HOH:O	2.16	0.60
32:1a:1518:MA6:OP2	62:1a:4607:HOH:O	2.17	0.60
1:2A:577:G:O2’	1:2A:1254:A:OP1	2.17	0.60
32:2a:1323:G:H4’	32:2a:1363:C:C2	2.37	0.60
40:2i:40:LEU:HD13	40:2i:74:ILE:HD11	1.84	0.60
1:1A:2882:A:OP1	13:1R:96:ARG:NH1	2.32	0.60
32:1a:1055:A:O2’	34:1c:161:GLU:O	2.10	0.60
1:2A:195:A:OP1	11:2P:46:LYS:NZ	2.32	0.60
4:2E:14:ILE:HD11	4:2E:173:VAL:HG11	1.84	0.60
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	1.82	0.60
6:2G:145:THR:HG22	6:2G:146:TYR:H	1.66	0.60
32:1a:328:C:H4’	32:1a:329:A:H5”	1.84	0.60
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.75	0.60
26:24:55:ARG:O	26:24:57:GLU:N	2.35	0.60
32:2a:1086:U:H3	32:2a:1099:G:H22	1.48	0.60
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.83	0.60
35:2d:166:LYS:HE3	35:2d:166:LYS:H	1.64	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1226:A:OP1	17:1V:84:LYS:NZ	2.31	0.60
1:1A:1300:U:H4'	1:1A:1301:A:H5"	1.84	0.60
1:2A:668:G:H5'	1:2A:669:G:OP2	2.01	0.60
1:2A:1087:G:H1	1:2A:1102:C:H42	1.50	0.60
7:2H:45:VAL:HG12	7:2H:50:VAL:HG13	1.84	0.60
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.32	0.60
1:1A:1175:U:H3'	1:1A:1177:A:OP2	2.01	0.60
32:1a:1439:C:OP1	51:1t:38:LYS:NZ	2.34	0.60
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.35	0.60
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.84	0.60
32:2a:975:A:H4'	32:2a:976:G:H5"	1.84	0.60
32:2a:1312:G:H5"	50:2s:5:LEU:HD21	1.84	0.60
32:1a:651:C:N4	32:1a:753:A:OP2	2.35	0.59
6:2G:137:GLU:HA	6:2G:152:LEU:HD21	1.84	0.59
32:2a:673:G:H2'	32:2a:674:G:C8	2.36	0.59
33:2b:12:GLU:HA	33:2b:15:VAL:HG23	1.84	0.59
1:1A:307:G:H21	1:1A:330:A:H62	1.49	0.59
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.37	0.59
1:2A:2065:C:H4'	1:2A:2251:OMG:HM22	1.84	0.59
12:2Q:18:LYS:O	12:2Q:98:LYS:NZ	2.24	0.59
21:2Z:3:TYR:CD2	21:2Z:51:ALA:HB2	2.37	0.59
32:2a:533:A:O2'	32:2a:535:A:OP2	2.19	0.59
32:2a:1320:C:N3	50:2s:36:ARG:NH2	2.50	0.59
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.37	0.59
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.32	0.59
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.67	0.59
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.84	0.59
32:1a:38:G:N2	32:1a:397:A:H5'	2.17	0.59
32:1a:1029:C:N3	32:1a:1032:G:O6	2.35	0.59
21:2Z:157:LEU:HD11	21:2Z:163:LEU:HB2	1.84	0.59
1:1A:1486:A:H2'	1:1A:1487:G:H8	1.67	0.59
1:1A:2126:A:N3	1:1A:2162:G:N2	2.48	0.59
15:1T:39:ARG:NH2	62:1T:302:HOH:O	2.35	0.59
32:1a:1095:U:OP2	62:1a:4606:HOH:O	2.15	0.59
32:2a:189(F):U:O2	48:2q:63:ARG:NH2	2.34	0.59
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.18	0.59
23:11:39:LYS:NZ	62:11:202:HOH:O	2.34	0.59
1:2A:79:G:O2'	1:2A:346:A:N3	2.28	0.59
1:2A:881:G:H1	1:2A:895:U:H3	1.50	0.59
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.37	0.59
32:2a:890:G:O2'	32:2a:906:G:O6	2.13	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1057:A:H62	1:1A:1087:G:P	2.25	0.59
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.36	0.59
1:1A:2020:A:OP2	62:1A:4154:HOH:O	2.16	0.59
46:1o:82:ILE:O	46:1o:86:GLY:N	2.35	0.59
52:1u:6:ARG:HE	52:1u:15:ARG:HE	1.49	0.59
1:2A:854:G:H2'	1:2A:855:G:C8	2.38	0.59
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.37	0.59
1:2A:2584:U:H5'	54:2w:76:PPU:H103	1.83	0.59
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.84	0.59
7:2H:98:LEU:HD11	7:2H:125:VAL:H	1.67	0.59
1:1A:1650:G:OP2	62:1A:4158:HOH:O	2.17	0.59
7:1H:159:GLU:HG3	7:1H:169:VAL:HG11	1.85	0.59
32:1a:79:G:N1	32:1a:90:U:N3	2.50	0.59
32:2a:153:C:N3	32:2a:169:C:N4	2.50	0.59
38:2g:69:VAL:HG22	38:2g:135:VAL:HG13	1.85	0.59
53:2y:3:MET:HE3	53:2y:37:PRO:HG2	1.84	0.59
6:1G:53:LEU:O	6:1G:56:ALA:N	2.32	0.59
6:1G:133:LEU:HD11	6:1G:157:ILE:HD12	1.85	0.59
8:1I:77:LEU:HB3	8:1I:142:VAL:HG13	1.84	0.59
32:1a:1110:A:OP2	62:1a:4608:HOH:O	2.17	0.59
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.83	0.59
1:2A:365:C:OP2	62:2A:3854:HOH:O	2.17	0.59
1:1A:1344:G:O6	62:1A:4149:HOH:O	2.15	0.59
1:2A:2126:A:H4'	1:2A:2127:G:O5'	2.03	0.59
1:1A:2147:G:H2'	1:1A:2148:G:C4'	2.33	0.58
1:2A:1010:A:OP2	62:2A:3856:HOH:O	2.17	0.58
44:2m:91:ARG:HB2	44:2m:98:VAL:HG13	1.85	0.58
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.37	0.58
39:1h:18:ARG:NH2	39:1h:81:HIS:O	2.36	0.58
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.36	0.58
1:2A:2472:G:N1	1:2A:2477:C:OP1	2.26	0.58
32:2a:1005:A:H1'	32:2a:1025:U:C2	2.38	0.58
32:2a:1326:C:OP1	52:2u:17:THR:OG1	2.20	0.58
39:2h:56:LYS:HE3	39:2h:58:TYR:HE2	1.67	0.58
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.17	0.58
7:1H:27:LYS:HG2	7:1H:32:GLU:HG2	1.86	0.58
36:1e:78:HIS:HE1	36:1e:80:ILE:HD13	1.67	0.58
1:2A:822:U:OP2	62:2A:3852:HOH:O	2.16	0.58
1:2A:1377:G:N7	62:2A:3973:HOH:O	2.32	0.58
1:2A:1651:G:OP1	13:2R:40:LYS:NZ	2.37	0.58
1:2A:2206:G:H8	1:2A:2207:G:N7	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:55:U:HO2'	6:2G:29:TRP:CD1	2.21	0.58
12:2Q:75:THR:HG21	12:2Q:87:LYS:HE3	1.84	0.58
14:2S:35:ILE:H	14:2S:53:SER:HB3	1.67	0.58
14:2S:43:GLU:OE2	22:20:49:LYS:NZ	2.35	0.58
32:2a:1373:G:H5"	38:2g:36:LYS:HB2	1.85	0.58
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.85	0.58
1:1A:279:C:H42	1:1A:361:G:H1	1.52	0.58
1:1A:2522:U:O2'	1:1A:2647:U:OP1	2.18	0.58
32:1a:142:G:O2'	32:1a:196:A:N1	2.36	0.58
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.37	0.58
1:2A:2232:U:O4	62:2A:3846:HOH:O	2.16	0.58
2:2B:84:C:OP1	25:23:15:TYR:OH	2.21	0.58
9:2N:120:LEU:HG	9:2N:122:VAL:HG23	1.85	0.58
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.68	0.58
34:1c:190:ARG:HB2	34:1c:190:ARG:HH21	1.67	0.58
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.03	0.58
1:2A:889:C:O2'	1:2A:890:A:O5'	2.20	0.58
24:22:1:MET:SD	24:22:56:GLN:NE2	2.77	0.58
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.85	0.58
1:1A:39:C:O2	5:1F:46:ARG:NH2	2.34	0.58
9:1N:77:GLY:O	62:1N:301:HOH:O	2.17	0.58
12:1Q:31:ASP:OD1	12:1Q:134:ARG:NH1	2.37	0.58
32:1a:224:C:OP1	51:1t:74:LYS:NZ	2.36	0.58
32:1a:677:U:H3	32:1a:713:G:H22	1.50	0.58
33:1b:12:GLU:HA	33:1b:15:VAL:HG12	1.86	0.58
12:2Q:58:PHE:C	12:2Q:60:ARG:H	2.12	0.58
32:2a:5:U:H5	35:2d:87:GLY:H	1.49	0.58
32:1a:601:C:H2'	32:1a:602:A:H8	1.67	0.58
1:2A:796:C:H2'	1:2A:797:C:C6	2.38	0.58
1:2A:1071:G:H21	1:2A:1072:C:H41	1.52	0.58
5:2F:29:ASN:H	5:2F:112:MET:HE3	1.68	0.58
6:2G:72:ARG:HE	6:2G:87:PRO:HG3	1.68	0.58
32:2a:192:U:H2'	32:2a:193:C:H6	1.69	0.58
32:2a:662:G:H2'	32:2a:663:A:C8	2.38	0.58
32:2a:1016:A:HO2'	32:2a:1217:C:HO2'	1.50	0.58
35:2d:8:VAL:HG22	35:2d:21:LEU:HD23	1.85	0.58
1:1A:548:A:O2'	1:1A:549:G:OP1	2.21	0.58
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.34	0.58
21:1Z:199:LYS:NZ	62:1Z:402:HOH:O	2.36	0.58
46:1o:9:GLN:HA	46:1o:12:ILE:HD12	1.85	0.58
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:60:LEU:O	6:2G:64:THR:HG22	2.04	0.58
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.67	0.58
50:1s:51:VAL:HG21	50:1s:71:LEU:HB3	1.84	0.58
1:2A:309:G:N3	1:2A:329:G:O2'	2.37	0.58
1:2A:1281:G:N7	62:2A:3971:HOH:O	2.32	0.58
11:2P:95:VAL:HG23	11:2P:125:VAL:HA	1.84	0.58
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.38	0.58
34:2c:55:VAL:HG12	34:2c:57:ILE:HD11	1.85	0.58
3:1D:183:ARG:NH2	62:1D:411:HOH:O	2.36	0.58
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.86	0.58
32:2a:1346:A:H5"	40:2i:120:ARG:HH12	1.68	0.58
34:2c:57:ILE:HG13	34:2c:66:VAL:HG13	1.86	0.58
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.37	0.58
44:2m:92:HIS:HD2	44:2m:98:VAL:HG21	1.67	0.58
1:1A:759:G:N7	62:1A:4304:HOH:O	2.32	0.57
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.36	0.57
34:1c:12:LEU:HD11	45:1n:51:GLY:HA2	1.86	0.57
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.04	0.57
1:2A:2127:G:O6	1:2A:2161:C:N3	2.37	0.57
6:2G:7:LEU:N	6:2G:104:GLU:OE2	2.36	0.57
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.86	0.57
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.85	0.57
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.87	0.57
32:1a:79:G:C2	32:1a:90:U:O2	2.57	0.57
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.39	0.57
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.36	0.57
12:2Q:43:THR:N	12:2Q:46:GLN:OE1	2.35	0.57
32:2a:1292:U:H5'	40:2i:38:GLN:HE22	1.68	0.57
34:2c:20:SER:HB2	34:2c:40:ARG:HH21	1.69	0.57
2:1B:76:G:N7	62:1B:305:HOH:O	2.33	0.57
32:1a:78:G:H1	32:1a:91:C:N4	2.01	0.57
32:1a:399:G:H2'	32:1a:400:C:C6	2.39	0.57
32:1a:840:C:H4'	32:1a:841:U:OP2	2.04	0.57
1:2A:1376:C:OP2	62:2A:3859:HOH:O	2.17	0.57
40:2i:5:TYR:CE1	40:2i:16:ARG:HB3	2.39	0.57
1:1A:1825:A:OP1	3:1D:249:PRO:HD3	2.05	0.57
1:1A:2129:C:N3	1:1A:2159:G:O6	2.37	0.57
32:1a:1179:A:OP2	40:1i:93:ARG:NH2	2.37	0.57
1:2A:299:A:N1	1:2A:322:A:O2'	2.36	0.57
1:2A:1063:G:H1	1:2A:1075:C:H42	1.52	0.57
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:57:THR:HG22	11:2P:59:LEU:H	1.68	0.57
33:2b:204:ASN:OD1	33:2b:205:ASP:N	2.37	0.57
34:2c:40:ARG:NH1	34:2c:55:VAL:O	2.37	0.57
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.23	0.57
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	1.85	0.57
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.02	0.57
32:1a:536:C:OP2	62:1a:4609:HOH:O	2.18	0.57
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.40	0.57
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.37	0.57
32:2a:1321:C:H4'	44:2m:87:TYR:CE2	2.40	0.57
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.39	0.57
1:1A:1967:C:OP1	62:1A:4159:HOH:O	2.17	0.57
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.86	0.57
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.39	0.57
38:1g:27:ILE:HD13	38:1g:40:ALA:HA	1.86	0.57
11:2P:85:LEU:HA	11:2P:88:LEU:HD12	1.86	0.57
38:2g:68:ASN:ND2	38:2g:127:ALA:O	2.34	0.57
48:2q:12:SER:HB3	48:2q:20:THR:HB	1.86	0.57
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.49	0.57
21:1Z:108:PRO:HB2	21:1Z:111:VAL:H	1.69	0.57
32:1a:413:G:N7	35:1d:35:ARG:NH1	2.53	0.57
34:1c:134:ILE:HG23	34:1c:151:VAL:HB	1.86	0.57
43:1l:34:ARG:NH2	62:1l:301:HOH:O	2.36	0.57
21:2Z:10:ARG:NH1	21:2Z:37:VAL:O	2.38	0.57
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.87	0.57
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.86	0.57
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.38	0.57
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.40	0.57
1:1A:1932:A:OP2	62:1A:4165:HOH:O	2.18	0.57
32:1a:1518:MA6:O5'	32:1a:1518:MA6:H8	2.04	0.57
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.33	0.57
8:2I:72:LEU:HD21	8:2I:107:VAL:HG21	1.86	0.57
32:2a:757:U:H2'	32:2a:758:G:O4'	2.05	0.57
1:1A:574:C:N3	4:1E:145:LYS:NZ	2.48	0.57
1:1A:1203:G:O6	62:1A:4156:HOH:O	2.16	0.57
1:1A:1340:U:OP1	19:1X:16:LYS:NZ	2.34	0.57
25:13:39:ASP:CG	25:13:44:ARG:HH21	2.13	0.57
32:1a:1047:G:H5"	45:1n:4:LYS:HD2	1.86	0.57
1:2A:140:G:N2	1:2A:1596:A:H4'	2.19	0.57
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.38	0.57
16:2U:34:LYS:NZ	16:2U:37:GLU:OE1	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.40	0.57
46:2o:33:THR:HG23	46:2o:63:ARG:NH1	2.20	0.57
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.40	0.57
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.05	0.57
26:14:55:ARG:H	26:14:56:VAL:HA	1.69	0.57
32:1a:428:G:OP2	35:1d:10:ARG:NH1	2.37	0.57
34:1c:108:ASN:ND2	34:1c:144:SER:OG	2.38	0.57
37:1f:42:GLU:OE2	37:1f:59:TYR:OH	2.21	0.57
8:2I:97:ILE:HD12	8:2I:114:LEU:HD21	1.87	0.57
2:1B:42:C:OP1	6:1G:67:LYS:NZ	2.37	0.56
6:1G:62:LEU:HD12	6:1G:148:MET:HE1	1.86	0.56
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.40	0.56
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.87	0.56
1:1A:580:C:OP1	62:1A:4162:HOH:O	2.18	0.56
1:1A:1486:A:H2'	1:1A:1487:G:C8	2.40	0.56
1:2A:625:G:N7	11:2P:107:LYS:NZ	2.42	0.56
1:2A:2122:U:O2	1:2A:2176:A:N1	2.39	0.56
1:2A:2173:A:OP2	1:2A:2174:C:N4	2.38	0.56
1:2A:2489:G:N2	1:2A:2491:U:O4	2.37	0.56
1:2A:2815:C:C5'	27:25:29:THR:HG21	2.36	0.56
14:2S:33:LYS:HA	14:2S:62:LYS:HE2	1.87	0.56
30:28:21:LYS:HE2	30:28:49:VAL:HG11	1.85	0.56
1:1A:303:U:O4	62:1A:4163:HOH:O	2.18	0.56
1:1A:1091:G:H2'	1:1A:1092:C:C6	2.40	0.56
1:1A:1124:C:OP1	62:1A:4164:HOH:O	2.18	0.56
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.21	0.56
1:1A:1674:G:N2	1:1A:1677:A:N1	2.43	0.56
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.39	0.56
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.37	0.56
21:1Z:1:MET:N	21:1Z:135:GLU:OE2	2.24	0.56
30:18:42:ARG:NH1	62:18:202:HOH:O	2.19	0.56
32:1a:79:G:N1	32:1a:90:U:C2	2.72	0.56
32:1a:262:A:H2'	32:1a:263:A:C8	2.40	0.56
32:1a:540:G:H2'	32:1a:541:G:O4'	2.05	0.56
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.38	0.56
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.40	0.56
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	1.87	0.56
1:2A:140:G:H22	1:2A:1596:A:H4'	1.70	0.56
1:2A:587:C:OP1	62:2A:3858:HOH:O	2.17	0.56
10:2O:120:GLU:HG2	10:2O:122:LEU:HG	1.86	0.56
11:2P:89:ALA:HA	11:2P:121:LYS:HE2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:707:C:H2'	32:2a:708:C:C6	2.41	0.56
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.39	0.56
48:2q:58:GLU:OE1	48:2q:75:ARG:NE	2.37	0.56
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.41	0.56
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.40	0.56
37:1f:36:ARG:NH2	37:1f:66:GLU:OE1	2.38	0.56
39:1h:17:THR:O	39:1h:78:GLN:NE2	2.34	0.56
1:2A:2127:G:N1	1:2A:2161:C:O2	2.39	0.56
6:2G:16:ARG:NH2	6:2G:28:VAL:HB	2.20	0.56
28:26:12:GLU:OE1	28:26:19:ARG:NH1	2.38	0.56
32:2a:404:U:H2'	32:2a:405:U:H6	1.70	0.56
32:2a:1247:U:H1'	32:2a:1291:G:N2	2.20	0.56
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.88	0.56
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.06	0.56
39:1h:119:LEU:HB3	39:1h:123:GLU:HB2	1.88	0.56
1:2A:212:G:H2'	1:2A:213:A:O4'	2.06	0.56
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	1.89	0.56
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.88	0.56
6:2G:109:VAL:HG21	26:24:14:ILE:HG21	1.87	0.56
32:2a:17:U:H2'	32:2a:18:C:C6	2.41	0.56
32:2a:737:A:H1'	37:2f:73:ASN:HD21	1.71	0.56
32:2a:1024:G:H2'	32:2a:1025:U:H5"	1.87	0.56
36:2e:75:THR:HG22	36:2e:76:ILE:H	1.71	0.56
38:2g:54:THR:O	38:2g:56:GLN:N	2.37	0.56
32:1a:718:G:H5'	42:1k:117:ASN:HB2	1.87	0.56
1:2A:1271:G:OP2	62:2A:3815:HOH:O	2.17	0.56
62:2A:3908:HOH:O	11:2P:37:GLY:HA3	2.04	0.56
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.38	0.56
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.40	0.56
35:2d:122:ARG:HH11	35:2d:122:ARG:HA	1.71	0.56
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.41	0.56
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.87	0.56
32:1a:946:A:H2'	32:1a:947:G:C8	2.41	0.56
4:2E:54:GLN:OE1	4:2E:55:ASN:N	2.37	0.56
10:2O:77:ILE:HB	15:2T:74:ARG:HD3	1.86	0.56
15:2T:23:ARG:HD3	15:2T:120:ARG:NH1	2.21	0.56
32:2a:1159:U:O4'	32:2a:1182:G:N2	2.39	0.56
8:1I:41:GLU:HA	8:1I:44:LEU:HD12	1.88	0.56
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.21	0.56
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.71	0.56
7:2H:103:LEU:HB3	7:2H:115:VAL:HB	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:75:LEU:HD11	8:2I:105:HIS:CD2	2.40	0.56
32:2a:490:G:H2'	32:2a:491:G:C8	2.41	0.56
33:2b:71:VAL:HG23	33:2b:164:VAL:HA	1.86	0.56
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.38	0.56
39:2h:21:LYS:O	39:2h:65:TYR:OH	2.21	0.56
5:1F:102:PRO:O	5:1F:106:ARG:HG3	2.06	0.56
32:1a:79:G:C6	32:1a:90:U:N3	2.73	0.56
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.41	0.56
42:1k:48:ILE:HD13	42:1k:63:LEU:HD12	1.87	0.56
1:2A:2153:G:H2'	1:2A:2154:G:H8	1.70	0.56
1:2A:2644:G:O6	62:2A:3857:HOH:O	2.17	0.56
32:2a:164:U:H2'	32:2a:165:C:C6	2.40	0.56
32:2a:1349:A:H5"	40:2i:121:ARG:HB2	1.86	0.56
1:1A:1721:G:H5'	1:1A:1722:A:OP2	2.06	0.56
1:1A:2228:G:OP1	3:1D:261:LYS:NZ	2.33	0.56
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	1.86	0.56
23:11:3:LYS:HG2	23:11:4:VAL:HG23	1.87	0.56
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.40	0.56
32:1a:1118:C:N3	32:1a:1156:G:N2	2.54	0.56
32:1a:1137:C:H5'	32:1a:1138:G:C5	2.41	0.56
33:1b:160:ASP:N	33:1b:160:ASP:OD1	2.39	0.56
39:1h:83:ILE:HB	39:1h:137:VAL:HG13	1.87	0.56
1:2A:11:G:H2'	1:2A:12:U:H5'	1.88	0.56
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.88	0.56
9:2N:103:VAL:HG11	9:2N:120:LEU:HD22	1.88	0.56
24:22:1:MET:N	24:22:52:ASP:OD1	2.37	0.56
32:2a:111:G:OP2	62:2a:3209:HOH:O	2.18	0.56
32:2a:979:C:O2	45:2n:19:ARG:NE	2.39	0.56
1:1A:414:C:H2'	1:1A:415:A:C8	2.40	0.55
2:1B:75:G:N7	62:1B:306:HOH:O	2.33	0.55
35:1d:72:GLU:OE2	35:1d:207:TYR:OH	2.19	0.55
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.42	0.55
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.86	0.55
1:1A:2417:C:OP1	11:1P:65:ARG:NH2	2.39	0.55
32:1a:1412:C:H2'	32:1a:1413:A:H8	1.71	0.55
36:1e:137:GLU:HG3	36:1e:141:GLN:HE21	1.71	0.55
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.36	0.55
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.07	0.55
8:2I:2:LYS:HD2	8:2I:18:VAL:HG12	1.87	0.55
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.39	0.55
32:2a:815:A:N7	32:2a:1509:C:O2'	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:181:ASN:HB3	34:2c:205:GLY:H	1.71	0.55
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.71	0.55
1:1A:821:A:H2'	1:1A:946:G:H5"	1.87	0.55
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.36	0.55
37:1f:35:ALA:HA	37:1f:67:MET:HB3	1.88	0.55
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.06	0.55
1:2A:1497:U:H5"	1:2A:1498:C:H5	1.72	0.55
1:1A:620:G:N3	1:1A:620:G:H5'	2.21	0.55
1:1A:2129:C:C2	1:1A:2159:G:N1	2.74	0.55
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.40	0.55
24:12:54:LYS:NZ	62:12:103:HOH:O	2.35	0.55
32:1a:601:C:H2'	32:1a:602:A:C8	2.42	0.55
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.72	0.55
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.71	0.55
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.21	0.55
53:2y:12:ILE:HG23	53:2y:16:ILE:HG23	1.87	0.55
1:1A:668:G:H5'	1:1A:669:G:OP2	2.07	0.55
1:1A:1056:G:H5"	1:1A:1057:A:O4'	2.06	0.55
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.87	0.55
10:1O:28:SER:OG	62:1O:301:HOH:O	2.15	0.55
41:1j:78:ASN:O	41:1j:80:LYS:N	2.39	0.55
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.88	0.55
1:2A:1064:C:H3'	1:2A:1065:U:H5'	1.89	0.55
1:2A:1155:A:H5"	16:2U:55:ARG:HD3	1.89	0.55
1:2A:1642:G:N7	62:2A:3980:HOH:O	2.33	0.55
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.41	0.55
2:2B:55:U:OP2	62:2B:303:HOH:O	2.18	0.55
32:2a:1342:C:H2'	32:2a:1343:G:H8	1.70	0.55
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.42	0.55
1:1A:1698:A:N1	62:1A:4320:HOH:O	2.33	0.55
1:1A:2814:C:HO2'	27:15:29:THR:HG1	1.54	0.55
21:1Z:14:LYS:HD3	21:1Z:16:SER:H	1.72	0.55
34:1c:119:ARG:O	34:1c:123:GLN:HB2	2.07	0.55
1:2A:2153:G:H2'	1:2A:2154:G:C8	2.42	0.55
2:2B:66:A:H61	2:2B:109:C:H5"	1.71	0.55
32:2a:1249:C:O2'	40:2i:73:GLN:NE2	2.39	0.55
1:1A:1637:A:OP1	62:1A:4168:HOH:O	2.18	0.55
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.89	0.55
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.88	0.55
44:1m:40:ASN:HD21	44:1m:42:ALA:HB3	1.71	0.55
49:1r:44:LEU:HD11	49:1r:79:LEU:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.70	0.55
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.42	0.55
33:2b:124:SER:HB2	33:2b:125:PRO:HD3	1.88	0.55
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.71	0.55
47:2p:15:PRO:HD2	47:2p:42:ARG:HD3	1.89	0.55
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.41	0.55
32:1a:284:G:H2'	32:1a:285:G:H8	1.72	0.55
32:1a:714:G:H2'	32:1a:715:A:C8	2.41	0.55
32:1a:1256:A:N6	32:1a:1278:U:O4'	2.39	0.55
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.89	0.55
39:1h:113:SER:HB2	39:1h:134:ILE:HD11	1.89	0.55
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.72	0.55
32:2a:601:C:H2'	32:2a:602:A:C8	2.42	0.55
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.41	0.55
44:2m:81:LEU:HD22	44:2m:88:ARG:HD2	1.87	0.55
48:2q:41:LYS:HZ2	48:2q:92:ARG:HH21	1.54	0.55
1:1A:1485:G:H1	1:1A:1504:C:H42	1.55	0.55
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.88	0.55
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.33	0.55
33:1b:17:PHE:HA	33:1b:44:LEU:HD21	1.89	0.55
35:1d:178:VAL:C	35:1d:180:GLY:H	2.14	0.55
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.23	0.55
4:2E:119:ARG:HG2	4:2E:120:TRP:CD1	2.42	0.55
6:2G:57:ALA:HB2	6:2G:90:LEU:HD22	1.89	0.55
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.89	0.55
32:2a:404:U:H2'	32:2a:405:U:C6	2.42	0.55
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	1.89	0.55
1:1A:2129:C:O2	1:1A:2159:G:N1	2.40	0.55
21:1Z:42:VAL:O	21:1Z:46:LYS:HG2	2.06	0.55
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.42	0.55
11:2P:15:ARG:NH1	62:2P:303:HOH:O	2.40	0.55
26:24:59:PHE:HB2	26:24:62:ARG:HH21	1.71	0.55
1:1A:1097:U:H3'	1:1A:1098:A:H8	1.72	0.54
1:1A:2115:G:N3	1:1A:2117:A:N6	2.55	0.54
1:1A:2712:U:OP1	1:1A:2714:G:H4'	2.07	0.54
3:1D:71:ASP:CB	3:1D:103:ARG:HH22	2.19	0.54
28:16:10:LEU:HB2	28:16:52:VAL:HG12	1.87	0.54
32:1a:1189:C:OP1	45:1n:58:LYS:NZ	2.39	0.54
41:1j:5:ARG:HE	41:1j:73:ASP:CG	2.14	0.54
41:1j:5:ARG:NH2	41:1j:73:ASP:OD2	2.32	0.54
1:2A:658:C:H2'	1:2A:659:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.06	0.54
1:2A:1412:A:H2'	1:2A:1413:G:H8	1.72	0.54
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.08	0.54
18:2W:80:PRO:O	18:2W:100:THR:HB	2.06	0.54
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.42	0.54
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.89	0.54
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.89	0.54
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.42	0.54
10:1O:3:GLN:NE2	62:1O:302:HOH:O	2.38	0.54
12:1Q:21:THR:HG21	12:1Q:101:ARG:HB2	1.88	0.54
39:1h:81:HIS:N	39:1h:138:TRP:O	2.41	0.54
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.22	0.54
10:2O:101:PRO:HB3	10:2O:120:GLU:HB3	1.88	0.54
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.08	0.54
1:1A:143:G:H4'	19:1X:35:THR:HG21	1.89	0.54
1:1A:2055:C:O2	62:1A:4160:HOH:O	2.17	0.54
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.42	0.54
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.89	0.54
14:1S:105:ALA:HB1	14:1S:110:LEU:HD12	1.89	0.54
19:1X:53:LYS:NZ	19:1X:55:ASN:OD1	2.41	0.54
32:1a:266:G:H5"	32:1a:267:C:C5	2.42	0.54
32:1a:1273:G:H3'	32:1a:1274:G:H8	1.73	0.54
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.07	0.54
6:2G:42:GLY:O	6:2G:44:GLY:N	2.38	0.54
32:2a:984:C:H2'	32:2a:985:C:H6	1.72	0.54
1:1A:1053:C:N3	1:1A:1106:G:O6	2.40	0.54
5:2F:53:THR:H	5:2F:56:GLU:HB2	1.73	0.54
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.89	0.54
1:1A:1877:A:H5'	1:1A:1878:G:OP2	2.07	0.54
1:1A:2142:C:H2'	1:1A:2143:C:C6	2.41	0.54
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.41	0.54
8:1I:69:LYS:HG3	8:1I:138:ILE:HG12	1.88	0.54
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.90	0.54
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.43	0.54
36:1e:39:GLY:HA2	36:1e:69:VAL:HG23	1.89	0.54
43:1l:56:ALA:HB3	43:1l:100:ILE:HD11	1.88	0.54
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.39	0.54
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.08	0.54
1:2A:2125:G:N2	1:2A:2172:U:H3'	2.22	0.54
32:2a:192:U:O2'	51:2t:60:GLU:OE1	2.22	0.54
32:2a:946:A:H2'	32:2a:947:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2751:G:H4'	7:1H:4:ILE:HD11	1.88	0.54
1:1A:2759:G:N7	62:1A:4326:HOH:O	2.34	0.54
2:1B:66:A:H61	2:1B:108:U:H2'	1.72	0.54
32:1a:100:C:H2'	32:1a:101:A:C8	2.43	0.54
1:2A:1075:C:OP1	12:2Q:59:ARG:NH1	2.41	0.54
1:2A:2157:G:H5"	1:2A:2158:A:H5'	1.90	0.54
2:2B:43:C:H5"	26:24:1:MET:HG3	1.90	0.54
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.26	0.54
32:2a:1255:G:O2'	32:2a:1258:G:O2'	2.22	0.54
37:2f:1:MET:HE3	37:2f:66:GLU:HG2	1.89	0.54
40:2i:23:ASN:HB2	40:2i:25:LYS:HZ2	1.73	0.54
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.42	0.54
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.17	0.54
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.42	0.54
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD11	1.89	0.54
32:1a:445:G:H1	32:1a:489:C:H42	1.56	0.54
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.43	0.54
32:2a:544:G:OP1	35:2d:62:GLN:NE2	2.29	0.54
32:2a:745:C:H4'	32:2a:836:G:H21	1.73	0.54
1:1A:1101:U:H2'	1:1A:1102:C:H6	1.73	0.54
1:1A:1652:A:O2'	1:1A:1653:G:H5'	2.08	0.54
1:2A:479:A:N3	1:2A:481:G:H5"	2.23	0.54
1:2A:663:G:O6	62:2A:3830:HOH:O	2.16	0.54
1:2A:2572:A:C8	4:2E:144:ARG:HD3	2.43	0.54
10:2O:64:ARG:HG2	10:2O:83:ALA:HB3	1.89	0.54
32:2a:335:C:O2'	32:2a:1433:A:N3	2.35	0.54
32:2a:1104:G:H4'	33:2b:111:ARG:NH1	2.22	0.54
42:2k:48:ILE:HG21	42:2k:63:LEU:HD13	1.90	0.54
50:2s:22:LEU:HD13	50:2s:28:LYS:H	1.72	0.54
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.08	0.54
3:1D:242:ARG:NH1	62:1D:413:HOH:O	2.40	0.54
32:1a:1400:5MC:C2	53:1y:63:ALA:HA	2.43	0.54
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.73	0.54
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.42	0.54
7:2H:121:ILE:HD11	7:2H:140:LYS:HG2	1.90	0.54
35:2d:154:ASN:HA	35:2d:159:ARG:HH21	1.72	0.54
39:2h:69:ARG:HD3	39:2h:76:PRO:HA	1.90	0.54
1:1A:1023:U:OP2	62:1A:4108:HOH:O	2.19	0.54
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.89	0.54
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.33	0.54
1:2A:1055:G:N2	1:2A:1086:A:H8	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2134:A:H5"	1:2A:2156:G:H22	1.72	0.54
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.21	0.54
21:2Z:167:PRO:O	21:2Z:169:GLU:N	2.41	0.54
34:2c:136:GLN:HG3	34:2c:140:ARG:HH21	1.72	0.54
2:1B:74:U:H2'	2:1B:75:G:O4'	2.07	0.53
3:1D:66:ASP:OD2	62:1D:401:HOH:O	2.19	0.53
15:1T:96:ARG:NH2	62:1T:301:HOH:O	2.35	0.53
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.43	0.53
32:1a:1239:A:H62	32:1a:1299:A:N6	2.06	0.53
40:1i:50:LEU:HA	40:1i:53:VAL:HG22	1.90	0.53
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.89	0.53
1:2A:1216:G:P	16:2U:12:ARG:HH21	2.30	0.53
1:2A:1490:A:O2'	3:2D:99:ASP:OD1	2.26	0.53
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.21	0.53
5:2F:64:ILE:HD11	5:2F:75:HIS:HB2	1.90	0.53
26:24:14:ILE:HB	26:24:22:ILE:HB	1.90	0.53
7:1H:3:ARG:HH11	7:1H:3:ARG:HA	1.73	0.53
7:1H:125:VAL:HG12	7:1H:127:GLU:O	2.08	0.53
32:1a:1310:G:OP2	44:1m:88:ARG:NH2	2.41	0.53
34:1c:110:ASN:HD22	34:1c:140:ARG:HB3	1.73	0.53
1:2A:774:A:H2'	1:2A:774:A:N3	2.23	0.53
1:2A:979:G:O6	62:2A:3861:HOH:O	2.18	0.53
1:2A:2511:U:O2'	4:2E:138:PRO:O	2.24	0.53
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.91	0.53
32:2a:1172:C:H2'	32:2a:1173:G:C8	2.39	0.53
52:2u:6:ARG:HE	52:2u:15:ARG:HH21	1.56	0.53
1:1A:251:A:C5	1:1A:252:G:H1'	2.44	0.53
3:1D:166:GLN:HB2	3:1D:174:ILE:HG22	1.90	0.53
33:1b:9:GLU:HG3	33:1b:217:ARG:HH22	1.72	0.53
33:1b:54:THR:HG22	33:1b:58:ILE:HD11	1.90	0.53
34:1c:69:HIS:CD2	34:1c:104:GLN:HG2	2.43	0.53
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.40	0.53
1:2A:1410:G:H2'	1:2A:1411:C:H6	1.74	0.53
6:2G:61:ALA:HB2	6:2G:67:LYS:HG3	1.91	0.53
26:24:48:ARG:O	26:24:50:VAL:N	2.40	0.53
32:2a:1370:G:N7	40:2i:109:VAL:HG11	2.23	0.53
41:2j:63:PHE:HE1	45:2n:58:LYS:HG2	1.74	0.53
1:1A:185:U:H2'	1:1A:186:G:C8	2.44	0.53
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.43	0.53
1:1A:813:U:H2'	1:1A:814:C:C6	2.44	0.53
4:1E:7:VAL:HG23	4:1E:51:PHE:HE2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.43	0.53
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.74	0.53
1:2A:27:G:O2'	1:2A:28:A:OP2	2.25	0.53
1:2A:1203:G:C6	1:2A:1204:A:N6	2.77	0.53
32:2a:967:5MC:H4'	40:2i:125:TYR:HE1	1.73	0.53
32:2a:1375:A:H4'	38:2g:29:LYS:HD3	1.91	0.53
32:2a:1490:C:H2'	32:2a:1491:G:C8	2.43	0.53
1:1A:1053:C:O2	1:1A:1106:G:N1	2.42	0.53
10:1O:3:GLN:NE2	62:1O:304:HOH:O	2.42	0.53
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.89	0.53
1:2A:902:C:H2'	1:2A:903:C:C6	2.44	0.53
1:2A:1063:G:N2	1:2A:1076:C:O2'	2.42	0.53
1:2A:2042:A:OP1	62:2A:3862:HOH:O	2.18	0.53
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.08	0.53
2:2B:14:U:OP2	2:2B:70:C:O2'	2.23	0.53
2:2B:95:C:H2'	2:2B:96:U:C6	2.44	0.53
26:24:26:SER:OG	26:24:27:THR:N	2.38	0.53
32:2a:513:C:H2'	32:2a:514:C:C6	2.43	0.53
32:2a:600:C:H2'	32:2a:601:C:C6	2.43	0.53
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.44	0.53
32:2a:1314:C:N4	50:2s:2:PRO:O	2.41	0.53
33:2b:96:ARG:HG3	33:2b:97:TRP:N	2.22	0.53
33:2b:96:ARG:HB3	33:2b:148:TYR:CD1	2.44	0.53
51:2t:56:MET:HG3	51:2t:84:LEU:HD22	1.89	0.53
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.43	0.53
32:1a:56:U:H2'	32:1a:57:G:C8	2.43	0.53
33:1b:71:VAL:HB	33:1b:164:VAL:HG22	1.90	0.53
1:2A:562:U:O2'	1:2A:563:G:OP2	2.19	0.53
32:2a:134:A:N6	47:2p:25:ARG:HH22	2.07	0.53
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	1.91	0.53
35:2d:196:LEU:H	35:2d:196:LEU:HD12	1.72	0.53
36:2e:8:GLU:HG2	36:2e:34:VAL:HG12	1.90	0.53
1:1A:428:A:OP1	62:1A:4172:HOH:O	2.19	0.53
1:1A:1065:U:H3	1:1A:1073:A:H62	1.56	0.53
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.44	0.53
1:1A:2316:C:O2'	6:1G:128:ARG:NH2	2.41	0.53
20:1Y:17:SER:OG	20:1Y:71:LYS:NZ	2.34	0.53
32:1a:186:C:H2'	32:1a:187:C:C6	2.43	0.53
1:2A:411:G:C5	11:2P:72:PRO:HB3	2.44	0.53
1:2A:720:C:H2'	1:2A:721:C:H6	1.74	0.53
1:2A:1084:A:N6	1:2A:1086:A:N7	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.41	0.53
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.08	0.53
54:2w:76:PPU:H8	54:2w:76:PPU:H5"	1.90	0.53
32:1a:501:C:H2'	32:1a:502:G:C8	2.43	0.53
1:2A:1113:U:H2'	1:2A:1114:G:C8	2.44	0.53
1:2A:2062:A:H2	56:2v:3:ILE:HD11	1.74	0.53
3:2D:53:PHE:HA	3:2D:218:ARG:HB2	1.90	0.53
3:2D:145:VAL:HB	3:2D:155:LEU:HB2	1.89	0.53
14:2S:14:VAL:HG11	14:2S:89:ARG:HG2	1.91	0.53
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.44	0.53
32:2a:1138:G:H2'	32:2a:1140:C:H5"	1.89	0.53
45:2n:4:LYS:HA	45:2n:7:ILE:HG12	1.91	0.53
47:2p:13:HIS:C	47:2p:15:PRO:HD3	2.34	0.53
1:1A:330:A:H2	1:1A:1210:A:O2'	1.91	0.53
1:1A:1541:G:O6	62:1A:4161:HOH:O	2.18	0.53
1:1A:2096:U:H2'	1:1A:2097:C:C6	2.43	0.53
1:1A:2115:G:H2'	1:1A:2117:A:N6	2.23	0.53
1:1A:2162:G:H1'	1:1A:2173:A:C8	2.44	0.53
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.44	0.53
2:1B:93:G:OP1	21:1Z:80:ARG:NH2	2.42	0.53
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.90	0.53
32:1a:184:G:H2'	32:1a:185:A:H8	1.74	0.53
32:1a:384:G:H2'	32:1a:385:C:C6	2.44	0.53
32:1a:992:U:H4'	32:1a:993:G:H5'	1.90	0.53
33:1b:93:VAL:HG11	33:1b:97:TRP:CD1	2.44	0.53
46:1o:33:THR:HG21	46:1o:85:LEU:HD22	1.91	0.53
1:2A:785:G:OP2	62:2A:3865:HOH:O	2.19	0.53
1:2A:954:G:H5"	12:2Q:13:GLN:HB3	1.91	0.53
1:2A:2139:C:H42	1:2A:2152:G:H1	0.67	0.53
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.43	0.53
2:2B:8:U:H5'	14:2S:15:ARG:NH1	2.24	0.53
32:2a:196:A:OP1	51:2t:68:LYS:NZ	2.29	0.53
38:2g:22:LEU:HA	38:2g:25:ALA:HB3	1.91	0.53
40:2i:53:VAL:HG11	40:2i:92:TYR:CE1	2.44	0.53
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.90	0.53
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.74	0.53
1:1A:247:G:H4'	1:1A:386:G:C5	2.44	0.53
1:1A:774:A:HO2'	1:1A:775:G:H8	1.55	0.53
1:1A:1858:G:O6	62:1A:4166:HOH:O	2.18	0.53
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.44	0.53
5:1F:150:GLY:HA2	5:1F:172:TRP:CD2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.44	0.53
12:1Q:31:ASP:OD2	62:1Q:301:HOH:O	2.19	0.53
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.90	0.53
1:2A:863:A:H2'	1:2A:864:G:C8	2.44	0.53
12:2Q:54:MET:HE1	12:2Q:104:PHE:HB3	1.90	0.53
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.23	0.53
32:2a:748:C:H4'	32:2a:749:C:O5'	2.09	0.53
32:2a:1123:A:O2'	32:2a:1124:G:H5'	2.09	0.53
1:1A:913:U:OP1	62:1A:4174:HOH:O	2.19	0.52
1:1A:2277:G:OP2	22:10:10:THR:HG21	2.09	0.52
35:1d:173:TRP:HB3	35:1d:187:ARG:HE	1.74	0.52
1:2A:320:A:H2'	5:2F:136:THR:HG21	1.92	0.52
1:2A:404:C:OP2	62:2A:3867:HOH:O	2.19	0.52
1:2A:1058:G:N1	1:2A:1059:G:O6	2.42	0.52
1:2A:2134:A:H2	1:2A:2159:G:H4'	1.74	0.52
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.45	0.52
23:21:83:GLU:N	23:21:83:GLU:OE2	2.41	0.52
32:2a:576:G:O6	32:2a:880:C:O2'	2.25	0.52
1:1A:1296:G:OP1	1:1A:2709:G:O2'	2.19	0.52
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.09	0.52
5:1F:165:ARG:HA	5:1F:168:ARG:HD3	1.90	0.52
32:1a:346:G:N2	59:1a:1874:MPD:O4	2.33	0.52
32:1a:1521:G:H2'	32:1a:1522:U:C6	2.44	0.52
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.27	0.52
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	1.90	0.52
47:1p:43:LYS:HG2	47:1p:48:TRP:CE2	2.44	0.52
1:2A:849:A:H2	25:23:24:LYS:HB3	1.74	0.52
1:2A:2124:G:H1	1:2A:2174:C:N4	2.07	0.52
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE3	1.90	0.52
32:2a:316:G:OP2	32:2a:351:G:O2'	2.27	0.52
32:2a:991:U:H2'	32:2a:1212:U:C4	2.44	0.52
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.24	0.52
38:2g:75:VAL:HB	38:2g:86:GLN:HB3	1.91	0.52
40:2i:51:ARG:HG2	40:2i:56:LEU:HD11	1.91	0.52
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.09	0.52
2:1B:28:C:OP1	14:1S:36:TYR:OH	2.27	0.52
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.27	0.52
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.40	0.52
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.41	0.52
1:2A:657:U:O4	62:2A:3863:HOH:O	2.19	0.52
1:2A:1257:C:OP2	62:2A:3866:HOH:O	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2884:U:P	27:25:43:HIS:HE2	2.32	0.52
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	1.92	0.52
20:2Y:7:VAL:HG12	20:2Y:8:LYS:H	1.75	0.52
32:2a:457:C:H2'	32:2a:458:C:H6	1.74	0.52
35:2d:122:ARG:HH12	35:2d:134:ASP:CG	2.17	0.52
36:2e:89:ILE:HD11	36:2e:120:THR:HG22	1.91	0.52
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.44	0.52
1:1A:2790:A:H2'	1:1A:2790:A:N3	2.25	0.52
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.45	0.52
32:1a:141:A:H1'	32:1a:182:U:O2	2.09	0.52
32:1a:407:G:OP1	35:1d:115:ARG:HD3	2.10	0.52
32:1a:1053:G:N7	32:1a:1200:C:H5"	2.24	0.52
32:1a:1183:A:H3'	32:1a:1184:G:C5'	2.40	0.52
32:1a:1347:G:HO2'	32:1a:1373:G:H1	1.57	0.52
33:1b:59:GLU:HB3	33:1b:221:LEU:HD11	1.91	0.52
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.10	0.52
1:2A:918:A:N3	2:2B:80:U:O2'	2.43	0.52
1:2A:1258:C:OP2	62:2A:3864:HOH:O	2.19	0.52
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.43	0.52
9:2N:20:GLY:HA2	9:2N:61:ARG:HG3	1.91	0.52
32:2a:93:G:H2'	32:2a:96:U:O4'	2.08	0.52
3:1D:8:PRO:HB3	3:1D:14:ARG:HG3	1.92	0.52
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.92	0.52
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.42	0.52
44:1m:9:ILE:HB	44:1m:18:ALA:HB1	1.92	0.52
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.91	0.52
53:1y:85:LEU:O	53:1y:89:GLN:HG2	2.10	0.52
1:2A:1124:C:OP1	62:2A:3869:HOH:O	2.19	0.52
1:2A:2589:A:N3	62:2A:4001:HOH:O	2.34	0.52
16:2U:105:VAL:HG13	17:2V:45:THR:HG23	1.92	0.52
32:2a:539:A:H2'	32:2a:540:G:C8	2.44	0.52
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.35	0.52
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.25	0.52
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.90	0.52
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.44	0.52
1:1A:1712:C:H2'	1:1A:1713:U:O4'	2.09	0.52
27:15:40:LYS:NZ	27:15:44:THR:O	2.43	0.52
28:16:13:CYS:SG	28:16:47:THR:HG21	2.50	0.52
30:18:63:PRO:HG2	30:18:64:TYR:CE2	2.45	0.52
32:1a:79:G:C2	32:1a:90:U:C2	2.97	0.52
32:1a:620:C:H2'	32:1a:621:A:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:909:A:H2'	32:1a:910:C:O4'	2.09	0.52
32:1a:1373:G:H5"	38:1g:36:LYS:HB2	1.92	0.52
35:1d:50:ARG:HH22	36:1e:10:MET:HE3	1.75	0.52
51:1t:14:LYS:HG2	51:1t:18:GLN:HE21	1.75	0.52
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.75	0.52
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.75	0.52
20:2Y:6:HIS:CD2	20:2Y:7:VAL:HG23	2.44	0.52
32:2a:333:G:H4'	51:2t:16:HIS:CE1	2.45	0.52
47:2p:58:TYR:O	47:2p:61:SER:OG	2.24	0.52
47:2p:74:LEU:HB3	47:2p:79:VAL:HG21	1.91	0.52
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.10	0.52
35:1d:60:GLU:OE2	35:1d:63:LYS:NZ	2.32	0.52
1:2A:1300:U:H4'	1:2A:1301:A:H5'	1.92	0.52
32:2a:131:C:H2'	32:2a:132:C:C6	2.44	0.52
15:1T:29:ARG:HG3	15:1T:46:GLU:HB2	1.91	0.52
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	1.91	0.52
32:1a:299:G:H2'	32:1a:300:A:C8	2.45	0.52
1:2A:2526:G:O3'	31:29:33:LYS:NZ	2.43	0.52
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.45	0.52
23:21:62:VAL:HG21	23:21:70:VAL:HG21	1.90	0.52
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.45	0.52
32:2a:1099:G:OP2	33:2b:144:ARG:NH2	2.43	0.52
32:2a:1143:G:H2'	32:2a:1144:G:H8	1.75	0.52
33:2b:71:VAL:HA	33:2b:93:VAL:HG22	1.90	0.52
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.91	0.52
1:1A:330:A:HO2'	1:1A:331:A:H8	1.56	0.52
1:1A:1823:G:OP1	3:1D:54:ARG:NH1	2.43	0.52
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.40	0.52
1:1A:2498:C:OP1	62:1A:4176:HOH:O	2.19	0.52
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	1.92	0.52
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.43	0.52
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	1.92	0.52
12:1Q:12:GLN:HE21	12:1Q:73:PRO:HD2	1.75	0.52
26:14:55:ARG:N	26:14:56:VAL:HA	2.25	0.52
1:2A:811:U:O4	62:2A:3845:HOH:O	2.15	0.52
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.43	0.52
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.39	0.52
32:2a:148:G:H2'	32:2a:149:A:H8	1.75	0.52
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.21	0.52
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.25	0.52
1:1A:2848:G:H8	15:1T:97:ALA:HB2	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:1Q:22:LYS:NZ	62:1Q:303:HOH:O	2.35	0.52
32:1a:448:A:P	32:1a:485:G:H22	2.33	0.52
32:1a:1003:G:C2	32:1a:1004:A:H1'	2.45	0.52
32:1a:1003:G:O6	32:1a:1035:A:N6	2.41	0.52
51:1t:19:SER:O	51:1t:23:ARG:HB2	2.10	0.52
2:2B:22:U:H3	2:2B:61:G:H1	1.58	0.52
23:21:38:SER:N	62:21:201:HOH:O	2.42	0.52
32:2a:509:A:N3	32:2a:543:C:O2'	2.36	0.52
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.10	0.52
39:2h:124:ALA:O	39:2h:128:GLY:N	2.42	0.52
1:1A:2690:C:H5"	1:1A:2872:G:N2	2.25	0.51
32:1a:222:U:H2'	32:1a:223:U:C6	2.45	0.51
32:1a:266:G:H2'	32:1a:266:G:N3	2.24	0.51
1:2A:39:C:O2	5:2F:46:ARG:NH2	2.43	0.51
1:2A:975:C:O2	62:2A:3860:HOH:O	2.18	0.51
1:2A:1669:A:OP2	62:2A:3870:HOH:O	2.19	0.51
1:2A:2386:C:H2'	1:2A:2387:U:C6	2.45	0.51
8:2I:1:MET:N	8:2I:21:VAL:O	2.35	0.51
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	1.92	0.51
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.41	0.51
23:21:59:THR:HG23	62:21:211:HOH:O	2.09	0.51
32:2a:1240:U:H2'	38:2g:32:ARG:HH21	1.76	0.51
32:2a:1297:C:OP1	44:2m:13:LYS:NZ	2.44	0.51
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.10	0.51
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.56	0.51
45:2n:6:LEU:HA	45:2n:9:LYS:HB3	1.92	0.51
1:1A:2100:G:H1	1:1A:2189:U:H3	1.58	0.51
1:1A:2398:U:H2'	1:1A:2399:G:H8	1.75	0.51
9:1N:33:LEU:HD12	9:1N:38:HIS:CE1	2.45	0.51
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.43	0.51
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.75	0.51
32:2a:1041:A:H2'	32:2a:1042:G:O4'	2.10	0.51
32:2a:1238:A:H2	32:2a:1241:G:N3	2.09	0.51
38:2g:12:LEU:HD13	38:2g:25:ALA:HB2	1.91	0.51
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.41	0.51
40:2i:50:LEU:HD13	40:2i:56:LEU:HA	1.92	0.51
43:2l:54:LYS:NZ	62:2l:201:HOH:O	2.42	0.51
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.41	0.51
1:1A:614(A):U:OP1	58:1A:4030:ARG:NH2	2.44	0.51
1:1A:1047:G:O2'	1:1A:1048:A:H8	1.93	0.51
1:1A:1100:C:H2'	1:1A:1101:U:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1341:U:O4'	19:1X:57:LEU:HD23	2.10	0.51
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.46	0.51
13:1R:51:LEU:HD22	13:1R:66:VAL:HG13	1.93	0.51
32:1a:67:C:H2'	32:1a:68:G:C8	2.44	0.51
32:1a:136:C:O2'	47:1p:65:GLN:NE2	2.37	0.51
36:1e:101:ILE:O	36:1e:120:THR:OG1	2.22	0.51
1:2A:8:A:H2'	1:2A:9:U:C6	2.45	0.51
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.45	0.51
1:2A:974:G:N2	62:2A:3835:HOH:O	2.14	0.51
1:2A:2050:C:H1'	4:2E:156:MET:HE2	1.93	0.51
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.45	0.51
6:2G:126:ASP:HB3	6:2G:130:ASN:HB2	1.93	0.51
22:20:53:MET:HA	22:20:58:THR:O	2.11	0.51
30:28:52:LYS:O	30:28:56:GLU:HG2	2.10	0.51
32:2a:1426:C:H2'	32:2a:1427:U:H6	1.76	0.51
38:2g:70:LYS:HE2	38:2g:96:GLN:OE1	2.10	0.51
52:2u:6:ARG:HH21	52:2u:15:ARG:HH21	1.59	0.51
1:1A:1173:G:C2	1:1A:1175:U:H4'	2.45	0.51
1:1A:2133:G:H3'	1:1A:2157:G:H21	1.75	0.51
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.91	0.51
1:2A:1216:G:OP2	16:2U:12:ARG:NH2	2.37	0.51
1:2A:1409:C:H2'	1:2A:1410:G:C8	2.46	0.51
6:2G:114:ILE:HD13	6:2G:140:ILE:HG12	1.91	0.51
32:2a:1123:A:C2	41:2j:39:PRO:HD2	2.45	0.51
34:2c:181:ASN:HB3	34:2c:204:LEU:HB2	1.92	0.51
1:1A:1057:A:N7	1:1A:1086:A:H2'	2.26	0.51
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.45	0.51
6:1G:33:ARG:H	6:1G:162:THR:HG1	1.58	0.51
32:1a:266:G:H5'	32:1a:268:C:H41	1.76	0.51
32:1a:407:G:H5"	35:1d:115:ARG:HB3	1.91	0.51
32:1a:1273:G:H3'	32:1a:1274:G:C8	2.45	0.51
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.76	0.51
49:1r:47:THR:O	49:1r:47:THR:OG1	2.26	0.51
1:2A:711:G:H1	1:2A:720:C:H42	1.59	0.51
1:2A:2840:C:O3'	13:2R:53:HIS:NE2	2.44	0.51
4:2E:151:TYR:HB3	9:2N:79:PRO:HD3	1.93	0.51
19:2X:44:GLU:O	19:2X:48:LYS:N	2.43	0.51
32:2a:328:C:H4'	32:2a:329:A:H5'	1.93	0.51
32:2a:503:C:OP2	43:2l:116:SER:OG	2.19	0.51
32:2a:1314:C:H2'	32:2a:1315:U:C6	2.46	0.51
44:2m:81:LEU:HD13	44:2m:88:ARG:HD3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2y:12:ILE:HG22	53:2y:17:ARG:HG3	1.92	0.51
32:1a:279:A:OP2	48:1q:95:TYR:OH	2.15	0.51
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.10	0.51
32:1a:1441:G:H4'	32:1a:1442:G:C4	2.46	0.51
36:1e:8:GLU:HG2	36:1e:34:VAL:HG12	1.92	0.51
1:2A:271(A):A:N7	1:2A:271(W):G:N2	2.55	0.51
1:2A:1014:U:H2'	1:2A:1015:G:C8	2.46	0.51
1:2A:1032:A:H2	1:2A:1122:G:H22	1.59	0.51
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.76	0.51
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.43	0.51
3:2D:127:VAL:HA	3:2D:193:VAL:HG23	1.93	0.51
24:22:10:LEU:HD21	24:22:59:ARG:HD2	1.92	0.51
32:2a:21:G:H2'	32:2a:22:G:C8	2.46	0.51
32:2a:971:G:OP1	32:2a:972:C:H5"	2.10	0.51
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.45	0.51
32:2a:1401:G:OP1	53:2y:80:LYS:HE3	2.09	0.51
33:2b:16:HIS:CD2	33:2b:210:SER:HB3	2.46	0.51
34:2c:181:ASN:CG	34:2c:204:LEU:HD12	2.36	0.51
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.93	0.51
40:2i:7:THR:OG1	40:2i:83:ARG:NH1	2.44	0.51
1:1A:2346:A:N1	62:1A:4335:HOH:O	2.34	0.51
1:1A:2658:C:OP1	7:1H:160:LYS:NZ	2.42	0.51
26:14:16:CYS:HA	26:14:33:VAL:HG23	1.93	0.51
32:1a:757:U:H2'	32:1a:758:G:O4'	2.10	0.51
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.25	0.51
41:1j:42:THR:HG23	41:1j:68:HIS:HA	1.92	0.51
1:2A:265:A:N1	1:2A:427:U:O2'	2.44	0.51
1:2A:1105:U:H2'	1:2A:1106:G:O4'	2.10	0.51
1:2A:1409:C:H2'	1:2A:1410:G:H8	1.76	0.51
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.92	0.51
10:2O:64:ARG:HB2	10:2O:79:PHE:CG	2.46	0.51
21:2Z:99:TYR:CE1	21:2Z:125:LEU:HB2	2.46	0.51
32:2a:1106:G:H5"	34:2c:172:ARG:HG2	1.93	0.51
32:2a:1295:G:O3'	44:2m:14:ARG:NH1	2.44	0.51
34:2c:179:ARG:CZ	34:2c:206:GLU:HB2	2.41	0.51
52:2u:20:LYS:HD2	52:2u:21:TYR:CE1	2.45	0.51
1:1A:118:A:C8	1:1A:119:A:C8	2.99	0.51
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.92	0.51
21:1Z:55:HIS:ND1	21:1Z:135:GLU:OE2	2.40	0.51
32:1a:620:C:C2	35:1d:135:LEU:HD13	2.45	0.51
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:48:GLN:HE21	4:2E:78:LEU:HD22	1.75	0.51
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.92	0.51
8:2I:101:LEU:O	8:2I:106:GLY:N	2.44	0.51
32:2a:28:G:O2'	32:2a:296:U:OP1	2.22	0.51
32:2a:67:C:H2'	32:2a:68:G:C8	2.46	0.51
32:2a:308:C:H2'	32:2a:309:G:H8	1.76	0.51
32:2a:965:A:C2	53:2y:6:THR:HG21	2.46	0.51
32:2a:1030:C:H42	32:2a:1031:G:H1	1.59	0.51
32:2a:1191:A:OP2	34:2c:3:ASN:ND2	2.44	0.51
32:2a:1372:U:H5"	40:2i:71:SER:HB3	1.93	0.51
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.93	0.51
41:2j:78:ASN:O	41:2j:80:LYS:N	2.44	0.51
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.26	0.51
1:1A:1056:G:O3'	1:1A:1057:A:H8	1.93	0.51
1:1A:1082:U:C4	1:1A:1086:A:N1	2.75	0.51
1:1A:1508:A:H4'	1:1A:1509(A):A:C5	2.46	0.51
1:1A:2144:U:H2'	1:1A:2147:G:O6	2.11	0.51
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.93	0.51
50:1s:45:VAL:HA	50:1s:62:ILE:HG22	1.92	0.51
1:2A:2577:A:O4'	27:25:3:LYS:HB2	2.10	0.51
18:2W:79:GLY:HA3	18:2W:100:THR:HG22	1.92	0.51
32:2a:988:G:C2	32:2a:989:C:H1'	2.46	0.51
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.26	0.51
33:2b:51:LEU:HD23	33:2b:201:ILE:HD12	1.92	0.51
1:1A:695:G:OP1	1:1A:1380:G:O2'	2.27	0.51
12:1Q:108:GLY:HA3	21:1Z:116:VAL:HG13	1.92	0.51
32:1a:1524:C:OP1	62:1a:4611:HOH:O	2.19	0.51
1:2A:821:A:N1	62:2A:4000:HOH:O	2.34	0.51
1:2A:890:A:H2'	1:2A:892:G:O4'	2.11	0.51
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.46	0.51
1:2A:2297:C:O2	1:2A:2321:G:N2	2.44	0.51
8:2I:77:LEU:HD22	8:2I:101:LEU:HG	1.92	0.51
32:2a:517:G:N2	32:2a:533:A:OP2	2.42	0.51
32:2a:1327:C:P	52:2u:12:LYS:HZ1	2.33	0.51
1:1A:1359:A:H61	1:1A:1372:U:H3	1.59	0.50
32:1a:259:G:OP2	51:1t:83:ARG:NH1	2.44	0.50
32:1a:578:C:O2'	32:1a:728:A:N3	2.31	0.50
32:1a:1457:G:H2'	32:1a:1458:G:C8	2.46	0.50
33:1b:114:ARG:O	33:1b:118:LEU:HG	2.11	0.50
40:1i:4:TYR:HA	40:1i:87:GLN:NE2	2.25	0.50
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:56:ASN:N	9:2N:125:GLY:O	2.42	0.50
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.11	0.50
32:2a:56:U:H2'	32:2a:57:G:C8	2.45	0.50
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.46	0.50
32:2a:1426:C:H2'	32:2a:1427:U:C6	2.46	0.50
1:1A:614(C):A:OP2	62:1A:4177:HOH:O	2.19	0.50
1:1A:1490:A:O2'	3:1D:99:ASP:OD1	2.29	0.50
19:1X:60:ARG:NH1	29:17:47:ARG:HH22	2.09	0.50
32:1a:376:G:H5"	47:1p:5:ARG:HB2	1.93	0.50
1:2A:639:U:H2'	1:2A:640:C:C6	2.47	0.50
1:2A:985:C:H2'	1:2A:986:C:H6	1.75	0.50
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.46	0.50
2:2B:13:A:N1	2:2B:69:G:O2'	2.42	0.50
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.43	0.50
6:2G:129:GLY:O	6:2G:161:THR:HB	2.11	0.50
19:2X:54:VAL:HG22	19:2X:81:VAL:HG12	1.93	0.50
21:2Z:9:TYR:OH	21:2Z:63:ASP:OD2	2.28	0.50
32:2a:141:A:H1'	32:2a:182:U:O2	2.10	0.50
32:2a:523:A:N1	43:2l:92:0TD:H6	2.26	0.50
32:2a:983:A:N1	32:2a:1222:G:N2	2.59	0.50
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.76	0.50
41:2j:19:SER:O	41:2j:23:ILE:HG12	2.11	0.50
1:1A:876:C:H2'	1:1A:877:U:O4'	2.11	0.50
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.44	0.50
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.12	0.50
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.11	0.50
5:1F:183:VAL:HG13	62:1F:428:HOH:O	2.11	0.50
32:1a:176:C:H2'	32:1a:177:C:C6	2.43	0.50
62:1a:4610:HOH:O	38:1g:29:LYS:NZ	2.45	0.50
34:1c:17:ASP:OD2	34:1c:21:ARG:HD3	2.12	0.50
34:1c:190:ARG:HB2	34:1c:190:ARG:NH2	2.26	0.50
37:1f:36:ARG:O	37:1f:66:GLU:N	2.32	0.50
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.11	0.50
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.46	0.50
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.92	0.50
10:2O:31:LYS:NZ	62:2O:201:HOH:O	2.32	0.50
21:2Z:81:ARG:NH1	62:2Z:302:HOH:O	2.43	0.50
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.43	0.50
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.46	0.50
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.11	0.50
34:1c:138:VAL:HG13	34:1c:149:ALA:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:7:THR:O	40:1i:83:ARG:NH1	2.44	0.50
1:2A:234:C:H2'	1:2A:235:U:C6	2.46	0.50
1:2A:2712:U:H2'	1:2A:2714:G:H5"	1.92	0.50
32:2a:500:G:H2'	32:2a:501:C:C6	2.47	0.50
50:2s:70:LYS:HB2	50:2s:73:GLU:HG3	1.93	0.50
1:1A:1378:A:OP1	29:17:10:ARG:NH2	2.44	0.50
1:1A:2336:A:H61	22:10:43:THR:CG2	2.25	0.50
32:1a:1456:G:H1	51:1t:51:GLU:CD	2.20	0.50
32:1a:1492:A:H4'	32:1a:1493:A:N1	2.26	0.50
1:2A:1670:C:OP1	62:2A:3842:HOH:O	2.20	0.50
21:2Z:158:PRO:O	21:2Z:161:VAL:HG22	2.11	0.50
34:2c:15:THR:HG21	34:2c:181:ASN:HA	1.93	0.50
35:2d:19:LEU:HD22	35:2d:67:ILE:HD11	1.93	0.50
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.94	0.50
40:2i:15:ALA:HB2	40:2i:65:VAL:HG23	1.94	0.50
47:2p:42:ARG:HB3	47:2p:44:THR:HG23	1.93	0.50
48:2q:22:LEU:HD11	48:2q:39:SER:HB2	1.94	0.50
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.12	0.50
1:1A:709:U:H2'	1:1A:710:G:C8	2.46	0.50
1:1A:1087:G:H1	1:1A:1102:C:H42	1.57	0.50
1:1A:2189:U:C2'	1:1A:2190:G:H5'	2.42	0.50
1:1A:2607:G:H2'	1:1A:2608:G:O4'	2.11	0.50
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.93	0.50
23:11:41:ARG:NH1	23:11:43:TYR:OH	2.45	0.50
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.26	0.50
50:1s:50:ALA:HA	50:1s:59:PRO:HA	1.91	0.50
1:2A:192:C:O2'	1:2A:802:A:N3	2.39	0.50
1:2A:856:C:O2'	1:2A:857:C:OP1	2.27	0.50
1:2A:863:A:H2'	1:2A:864:G:H8	1.76	0.50
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.94	0.50
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.12	0.50
32:2a:384:G:H2'	32:2a:385:C:C6	2.47	0.50
33:2b:144:ARG:NH1	33:2b:148:TYR:OH	2.45	0.50
1:1A:1942:5MC:OP2	1:1A:1943:U:O2'	2.29	0.50
1:1A:2206:G:H2'	1:1A:2207:G:C2	2.46	0.50
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.46	0.50
1:1A:2324:C:H5"	1:1A:2325:G:H5'	1.93	0.50
1:1A:2820:A:P	13:1R:2:ARG:HH22	2.35	0.50
8:1I:72:LEU:HB3	8:1I:140:LEU:HD23	1.93	0.50
1:2A:509:C:O3'	62:2A:3868:HOH:O	2.19	0.50
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.46	0.50
1:2A:2188:C:H2'	1:2A:2189:U:O4'	2.11	0.50
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.93	0.50
32:2a:514:C:H2'	32:2a:515:G:H8	1.77	0.50
32:2a:572:A:OP2	62:2a:3203:HOH:O	2.20	0.50
42:2k:115:PRO:C	42:2k:117:ASN:HA	2.36	0.50
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.77	0.50
1:1A:644:A:H4'	1:1A:645:C:C5	2.47	0.50
1:1A:2032:G:OP2	1:1A:2454:G:O2'	2.25	0.50
1:1A:2143:C:N3	1:1A:2148:G:O6	2.45	0.50
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.27	0.50
6:1G:42:GLY:O	6:1G:44:GLY:N	2.41	0.50
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.93	0.50
32:1a:587:G:N7	62:1a:4649:HOH:O	2.35	0.50
36:1e:87:SER:OG	36:1e:125:SER:O	2.27	0.50
1:2A:196:A:N3	1:2A:196:A:H2'	2.26	0.50
1:2A:298:G:N7	62:2A:3991:HOH:O	2.33	0.50
1:2A:800:A:H8	1:2A:800:A:OP1	1.95	0.50
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.12	0.50
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.45	0.50
4:2E:56:PRO:HA	4:2E:59:VAL:HG22	1.94	0.50
32:2a:460:G:H2'	32:2a:461:A:H2'	1.93	0.50
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.12	0.50
43:2l:53:ARG:NH1	43:2l:92:0TD:OD1	2.44	0.50
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.47	0.50
1:1A:2002:G:H1'	62:1A:4382:HOH:O	2.11	0.50
3:1D:102:LYS:C	3:1D:103:ARG:HG2	2.37	0.50
10:1O:8:LEU:HB2	10:1O:19:ILE:HG13	1.93	0.50
32:1a:153:C:H2'	32:1a:154:C:C6	2.47	0.50
32:1a:520:A:N1	32:1a:536:C:H1'	2.26	0.50
32:1a:1158:C:H5	32:1a:1181:G:N1	2.04	0.50
34:1c:11:ARG:HB3	34:1c:15:THR:HB	1.94	0.50
1:2A:363(D):G:H2'	1:2A:363(E):U:O4'	2.12	0.50
1:2A:1962:5MC:N4	62:2A:4003:HOH:O	2.34	0.50
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.12	0.50
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.30	0.50
12:2Q:52:VAL:HG13	21:2Z:183:LEU:HD13	1.93	0.50
32:2a:547:A:OP2	35:2d:2:GLY:HA2	2.12	0.50
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.47	0.49
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.46	0.49
1:1A:2350:C:OP2	62:1A:4171:HOH:O	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:940:C:OP1	62:1a:4610:HOH:O	2.18	0.49
34:1c:35:GLU:HA	34:1c:38:ARG:HB2	1.93	0.49
1:2A:500:G:N2	1:2A:502:A:H3'	2.26	0.49
1:2A:1449:A:O2'	1:2A:1529:G:N2	2.29	0.49
1:2A:1464:C:H2'	1:2A:1465:G:C8	2.46	0.49
1:2A:2550:G:OP1	62:2A:3870:HOH:O	2.20	0.49
32:2a:35:G:N2	43:2l:118:SER:OG	2.40	0.49
32:2a:642:A:N3	39:2h:113:SER:OG	2.44	0.49
32:2a:1256:A:H61	32:2a:1278:U:C1'	2.24	0.49
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.45	0.49
32:2a:1490:C:H2'	32:2a:1491:G:H8	1.75	0.49
41:2j:38:ILE:HD13	41:2j:71:LEU:HB3	1.94	0.49
42:2k:34:ASP:OD1	42:2k:38:ASN:N	2.45	0.49
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.27	0.49
1:1A:930:U:OP1	62:1A:4175:HOH:O	2.19	0.49
6:1G:109:VAL:HG11	6:1G:142:PRO:HB3	1.94	0.49
32:1a:270:A:H2'	32:1a:271:C:C6	2.47	0.49
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.47	0.49
1:2A:657:U:H2'	1:2A:658:C:C6	2.47	0.49
1:2A:888:C:H2'	1:2A:889:C:C4	2.47	0.49
1:2A:919:G:N2	1:2A:2269:A:OP2	2.45	0.49
19:2X:94:GLY:HA3	19:2X:95:LEU:C	2.37	0.49
32:2a:192:U:H2'	32:2a:193:C:C6	2.47	0.49
32:2a:923:A:O2'	32:2a:1399:C:OP2	2.29	0.49
32:2a:1036:G:H3'	32:2a:1037:C:C6	2.47	0.49
32:2a:1094:G:O2'	32:2a:1108:G:N2	2.45	0.49
32:2a:1323:G:H4'	32:2a:1363:C:N3	2.26	0.49
34:2c:19:GLU:HB3	34:2c:40:ARG:HH12	1.77	0.49
36:2e:78:HIS:CE1	36:2e:142:LEU:HD23	2.47	0.49
1:1A:1405:U:H2'	1:1A:1406:U:H6	1.76	0.49
32:1a:341:C:H2'	32:1a:342:C:C6	2.47	0.49
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.94	0.49
33:1b:93:VAL:HG11	33:1b:97:TRP:HD1	1.76	0.49
1:2A:307:G:N1	1:2A:310:A:OP2	2.40	0.49
1:2A:588:U:H2'	1:2A:589:C:C6	2.47	0.49
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.11	0.49
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.12	0.49
32:2a:615:C:H2'	32:2a:616:G:O4'	2.12	0.49
33:2b:19:HIS:CD2	33:2b:20:GLU:H	2.31	0.49
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.26	0.49
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:166:LYS:HE3	35:2d:166:LYS:N	2.26	0.49
36:2e:122:GLU:HB2	36:2e:126:ARG:HD3	1.95	0.49
38:2g:69:VAL:HA	38:2g:138:LYS:HD2	1.93	0.49
1:1A:882:G:H2'	1:1A:883:G:H8	1.77	0.49
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.12	0.49
1:1A:2159:G:H2'	1:1A:2160:G:C8	2.47	0.49
1:1A:2287:A:O2'	1:1A:2289:G:N7	2.43	0.49
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.94	0.49
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.94	0.49
32:1a:111:G:HO2'	32:1a:389:A:HO2'	1.60	0.49
32:1a:1457:G:H2'	32:1a:1458:G:H8	1.77	0.49
45:1n:39:LEU:HD11	45:1n:47:LEU:HD12	1.94	0.49
48:1q:74:LEU:HD23	48:1q:75:ARG:HG2	1.94	0.49
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.48	0.49
1:2A:2128:C:H1'	1:2A:2173:A:H2	1.77	0.49
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.47	0.49
7:2H:26:VAL:HG12	7:2H:79:VAL:HG11	1.94	0.49
18:2W:4:LYS:HE2	18:2W:6:ILE:HD11	1.95	0.49
32:2a:542:G:OP1	35:2d:10:ARG:NH1	2.36	0.49
32:2a:1304:G:O2'	32:2a:1333:A:N6	2.32	0.49
48:2q:85:VAL:HG12	48:2q:89:LEU:HD11	1.93	0.49
1:1A:1026:U:OP1	62:1A:4108:HOH:O	2.20	0.49
1:1A:1583:A:H5'	1:1A:1584:C:OP1	2.13	0.49
2:1B:21:G:H2'	2:1B:22:U:C6	2.48	0.49
8:1I:134:PRO:C	8:1I:136:VAL:H	2.20	0.49
32:1a:130:A:C8	48:1q:63:ARG:HD3	2.47	0.49
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.12	0.49
32:1a:1368:G:H5"	40:1i:112:LYS:HB3	1.94	0.49
38:1g:18:TYR:HB3	38:1g:59:LEU:HD12	1.94	0.49
44:1m:13:LYS:C	44:1m:44:ARG:HD3	2.37	0.49
1:2A:2689:U:P	1:2A:2719:G:H22	2.36	0.49
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.77	0.49
41:2j:63:PHE:CE1	45:2n:58:LYS:HG2	2.48	0.49
50:2s:63:THR:HG22	50:2s:64:GLU:H	1.77	0.49
1:1A:2492:U:H2'	1:1A:2493:U:C6	2.47	0.49
5:1F:148:LEU:HD21	5:1F:193:VAL:HG21	1.94	0.49
5:1F:197:ASP:N	5:1F:197:ASP:OD1	2.43	0.49
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.13	0.49
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.12	0.49
32:1a:975:A:H4'	32:1a:976:G:C5'	2.39	0.49
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.47	0.49
36:1e:45:PHE:CD2	36:1e:47:LYS:HE2	2.48	0.49
41:1j:44:VAL:HG22	41:1j:66:ARG:HD2	1.94	0.49
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.48	0.49
1:2A:751:A:H5'	18:2W:90:ARG:HA	1.92	0.49
1:2A:2133:G:N2	1:2A:2157:G:H2'	2.28	0.49
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.12	0.49
7:2H:103:LEU:HB2	7:2H:123:PHE:CD2	2.48	0.49
32:2a:457:C:H2'	32:2a:458:C:C6	2.47	0.49
32:2a:1035:A:O2'	32:2a:1036:G:H8	1.95	0.49
38:2g:74:GLU:OE2	38:2g:95:ARG:NE	2.43	0.49
38:2g:114:ARG:H	38:2g:115:ARG:NH2	2.11	0.49
1:1A:1466:G:H2'	1:1A:1547:C:H41	1.77	0.49
1:1A:1753:G:N1	1:1A:1756:G:OP2	2.44	0.49
3:1D:130:ALA:HA	3:1D:191:ALA:O	2.13	0.49
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.95	0.49
11:1P:59:LEU:HD23	30:18:58:ILE:HD13	1.94	0.49
32:1a:581:G:OP1	46:1o:61:GLY:HA3	2.13	0.49
41:1j:78:ASN:O	41:1j:81:THR:HG23	2.12	0.49
1:2A:479:A:H4'	1:2A:480:A:OP1	2.12	0.49
3:2D:95:LEU:HD11	3:2D:105:ILE:HD13	1.95	0.49
21:2Z:108:PRO:HA	21:2Z:142:SER:O	2.12	0.49
32:2a:302:G:N3	32:2a:556:C:H4'	2.27	0.49
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.27	0.49
35:2d:165:MET:SD	35:2d:168:ARG:NH1	2.67	0.49
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.95	0.49
1:1A:526:A:O2'	1:1A:2043:C:O2	2.26	0.49
1:1A:1637:A:N3	62:1A:4346:HOH:O	2.35	0.49
19:1X:5:TYR:CZ	24:12:30:ARG:HB2	2.47	0.49
20:1Y:23:ARG:NH1	62:1Y:303:HOH:O	2.46	0.49
21:1Z:51:ALA:HB1	21:1Z:57:ILE:HD11	1.95	0.49
32:1a:56:U:H2'	32:1a:57:G:H8	1.78	0.49
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.28	0.49
40:1i:28:VAL:HA	40:1i:63:ILE:O	2.12	0.49
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.47	0.49
4:2E:178:GLU:CD	4:2E:178:GLU:H	2.21	0.49
20:2Y:7:VAL:HG11	20:2Y:13:VAL:HG11	1.95	0.49
21:2Z:23:LYS:NZ	21:2Z:40:ASP:OD2	2.46	0.49
50:2s:62:ILE:HA	50:2s:66:MET:SD	2.53	0.49
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.45	0.49
1:1A:1392:A:N6	62:1A:4547:HOH:O	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2115:G:H2'	1:1A:2117:A:H62	1.78	0.49
32:1a:58:C:O2'	32:1a:388:G:N7	2.39	0.49
32:1a:600:C:H2'	32:1a:601:C:H6	1.78	0.49
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.95	0.49
35:1d:107:ARG:HH21	35:1d:194:LEU:HD21	1.78	0.49
38:1g:116:ALA:O	38:1g:120:ILE:HG12	2.13	0.49
1:2A:286:C:H2'	1:2A:287:C:C6	2.47	0.49
1:2A:1983:C:H4'	1:2A:2606:C:H4'	1.94	0.49
1:2A:2312:U:H4'	6:2G:71:THR:HB	1.94	0.49
1:2A:2324:C:H5"	1:2A:2325:G:H5'	1.95	0.49
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.48	0.49
1:2A:2647:U:H2'	1:2A:2648:C:C6	2.48	0.49
9:2N:15:LEU:HD22	9:2N:16:ILE:H	1.78	0.49
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.46	0.49
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.47	0.49
32:2a:1312:G:H5'	50:2s:5:LEU:HD11	1.94	0.49
32:2a:1318:A:H4'	50:2s:10:PHE:CZ	2.47	0.49
36:2e:78:HIS:HD2	39:2h:107:LEU:HD12	1.78	0.49
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.28	0.49
1:1A:2820:A:C5	13:1R:4:LEU:HD11	2.47	0.49
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.45	0.49
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.28	0.49
32:1a:1086:U:H3	32:1a:1099:G:H22	1.61	0.49
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.48	0.49
36:1e:96:PRO:C	36:1e:98:THR:H	2.20	0.49
38:1g:54:THR:O	38:1g:56:GLN:N	2.42	0.49
1:2A:2103:C:H2'	1:2A:2104:G:H8	1.78	0.49
21:2Z:52:SER:HB3	21:2Z:54:HIS:HD1	1.77	0.49
22:20:47:PRO:HG3	22:20:53:MET:HE2	1.95	0.49
32:2a:1198:G:H2'	32:2a:1199:U:C6	2.47	0.49
48:2q:19:VAL:HG23	48:2q:44:ALA:HB3	1.95	0.49
1:1A:1071:G:O2'	1:1A:1089:G:OP2	2.30	0.48
1:1A:1802:A:H2'	1:1A:1803:A:C8	2.48	0.48
1:1A:2322:A:H2'	1:1A:2323:G:O4'	2.12	0.48
1:1A:2404:C:O3'	11:1P:77:ARG:NH2	2.46	0.48
1:1A:2674:G:H2'	1:1A:2675:A:C8	2.47	0.48
32:1a:978:A:O2'	32:1a:1322:C:N3	2.44	0.48
37:1f:50:TYR:OH	49:1r:74:ARG:O	2.20	0.48
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.47	0.48
32:2a:1030:C:N3	32:2a:1031:G:N2	2.61	0.48
32:2a:1134:G:H2'	32:2a:1135:U:H5'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:13:LYS:O	44:2m:45:VAL:N	2.46	0.48
49:2r:74:ARG:HB3	49:2r:81:PHE:CE1	2.48	0.48
1:1A:184:C:H2'	1:1A:185:U:C6	2.47	0.48
1:1A:1039:G:H1	1:1A:1116:C:H42	1.59	0.48
1:1A:1176:G:H1'	1:1A:1177:A:H5"	1.95	0.48
15:1T:55:ASN:N	15:1T:59:THR:HG22	2.08	0.48
32:1a:160:A:H2'	32:1a:161:A:O4'	2.13	0.48
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.94	0.48
33:1b:207:ALA:O	33:1b:210:SER:N	2.46	0.48
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.94	0.48
43:1l:79:GLU:HG2	43:1l:80:HIS:CD2	2.48	0.48
1:2A:746:A:H2'	1:2A:2612:C:H5"	1.95	0.48
1:2A:1058:G:H8	1:2A:1058:G:O5'	1.96	0.48
1:2A:2123:G:H1	1:2A:2175:C:N4	2.10	0.48
6:2G:83:ARG:O	6:2G:86:MET:HB2	2.13	0.48
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.30	0.48
34:2c:97:LYS:O	34:2c:99:VAL:N	2.46	0.48
41:2j:33:GLN:O	41:2j:74:ILE:HD12	2.13	0.48
44:2m:87:TYR:HD1	44:2m:90:LEU:HD12	1.77	0.48
1:1A:144:C:H5'	19:1X:2:LYS:HD3	1.94	0.48
1:1A:557:U:OP1	62:1A:4183:HOH:O	2.20	0.48
1:1A:652(V):C:H2'	1:1A:653:A:O4'	2.12	0.48
1:1A:1175:U:H1'	1:1A:1176:G:OP1	2.14	0.48
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.43	0.48
4:1E:111:ARG:HG2	4:1E:118:LYS:HD3	1.95	0.48
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.44	0.48
31:19:32:HIS:O	31:19:34:GLN:HG3	2.13	0.48
32:1a:266:G:H5"	32:1a:267:C:H5	1.78	0.48
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.95	0.48
32:1a:858:G:O6	32:1a:869:G:H3'	2.14	0.48
41:1j:5:ARG:NE	41:1j:73:ASP:OD1	2.40	0.48
1:2A:1062:G:C5	1:2A:1070:A:H1'	2.48	0.48
1:2A:2207:G:H3'	1:2A:2208:A:H5"	1.95	0.48
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.48	0.48
32:2a:458:C:H2'	32:2a:460:G:O4'	2.13	0.48
32:2a:746:A:H2'	32:2a:747:C:C6	2.49	0.48
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.47	0.48
43:2l:79:GLU:HG2	43:2l:80:HIS:CD2	2.49	0.48
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.14	0.48
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.48	0.48
1:1A:2584:U:H5'	54:1w:76:PPU:H103	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:83:SER:O	62:1d:401:HOH:O	2.19	0.48
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.28	0.48
44:1m:3:ARG:HG2	44:1m:8:GLU:HG3	1.95	0.48
1:2A:251:A:C5	1:2A:252:G:H1'	2.49	0.48
1:2A:331:A:N1	62:2A:4017:HOH:O	2.35	0.48
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.45	0.48
6:2G:11:TYR:O	6:2G:16:ARG:N	2.43	0.48
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.47	0.48
22:20:27:GLU:HB2	22:20:69:PHE:CD1	2.47	0.48
32:2a:45:U:H2'	32:2a:46:G:C8	2.48	0.48
32:2a:160:A:H61	32:2a:347:G:H1'	1.79	0.48
34:2c:120:VAL:HG13	34:2c:140:ARG:HH22	1.79	0.48
36:2e:110:LEU:HD13	36:2e:118:ILE:HD13	1.94	0.48
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.49	0.48
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.94	0.48
12:1Q:7:MET:HE3	12:1Q:7:MET:HB2	1.71	0.48
32:1a:1003:G:N2	32:1a:1004:A:H1'	2.29	0.48
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.12	0.48
1:2A:218:A:C2	1:2A:235:U:H4'	2.48	0.48
1:2A:1930:G:N2	1:2A:1968:G:H2'	2.29	0.48
14:2S:15:ARG:O	14:2S:19:LYS:HG3	2.13	0.48
14:2S:34:HIS:CG	14:2S:53:SER:HG	2.27	0.48
26:24:24:THR:OG1	26:24:25:TYR:N	2.39	0.48
32:2a:190:U:H2'	32:2a:191:G:O4'	2.14	0.48
32:2a:1036:G:H3'	32:2a:1037:C:H6	1.78	0.48
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.14	0.48
36:2e:93:PRO:HG2	39:2h:105:ARG:HE	1.79	0.48
50:2s:22:LEU:HB3	50:2s:27:GLU:HA	1.95	0.48
1:1A:602:G:O2'	1:1A:655:A:N6	2.46	0.48
1:1A:1940:U:OP1	62:1A:4185:HOH:O	2.20	0.48
5:1F:34:TRP:NE1	11:1P:8:PRO:HD3	2.28	0.48
5:1F:93:LYS:O	5:1F:95:ARG:HG3	2.13	0.48
6:1G:16:ARG:NE	6:1G:31:VAL:HG21	2.28	0.48
32:1a:584:G:H5'	48:1q:91:ARG:HH22	1.77	0.48
36:1e:75:THR:HG22	36:1e:76:ILE:H	1.79	0.48
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.13	0.48
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.96	0.48
1:2A:1147:C:H2'	1:2A:1148:A:C8	2.49	0.48
1:2A:1827:C:C2'	1:2A:1828:G:H5'	2.44	0.48
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.48	0.48
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:31:HIS:O	5:2F:34:TRP:N	2.47	0.48
15:2T:1:MET:HE2	15:2T:3:ARG:HG3	1.95	0.48
26:24:59:PHE:CE2	50:2s:64:GLU:HB2	2.49	0.48
32:2a:1122:U:N3	32:2a:1123:A:N7	2.60	0.48
32:2a:1319:A:OP1	50:2s:70:LYS:NZ	2.46	0.48
44:2m:57:ARG:HA	44:2m:60:VAL:HG12	1.96	0.48
7:1H:24:VAL:HG21	7:1H:72:ILE:HG12	1.95	0.48
15:1T:93:ARG:HB2	15:1T:117:ASP:HB2	1.96	0.48
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.14	0.48
27:15:35:GLU:OE1	27:15:35:GLU:N	2.46	0.48
32:1a:1261:A:H3'	32:1a:1262:C:C6	2.48	0.48
32:1a:1289:A:OP1	52:1u:10:ARG:NH2	2.47	0.48
32:1a:1421:G:H5'	62:1a:4839:HOH:O	2.14	0.48
36:1e:10:MET:SD	36:1e:13:ILE:HD11	2.53	0.48
32:2a:308:C:H2'	32:2a:309:G:C8	2.49	0.48
32:2a:447:G:O6	32:2a:485:G:O2'	2.31	0.48
32:2a:461:A:O2'	32:2a:471:G:N7	2.45	0.48
32:2a:611:A:H2	32:2a:630:G:H22	1.60	0.48
32:2a:691:G:H2'	32:2a:692:U:C6	2.49	0.48
32:2a:926:G:C6	53:2y:87:LYS:HG3	2.49	0.48
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.78	0.48
32:2a:1224:G:C6	32:2a:1322:C:O4'	2.67	0.48
32:2a:1330:U:H2'	32:2a:1331:G:H5'	1.95	0.48
34:2c:11:ARG:HB3	34:2c:15:THR:HB	1.95	0.48
40:2i:5:TYR:H	40:2i:87:GLN:NE2	2.12	0.48
48:2q:62:SER:HB3	48:2q:72:ARG:HH11	1.79	0.48
52:2u:6:ARG:HE	52:2u:15:ARG:HE	1.61	0.48
1:1A:1512:U:H2'	1:1A:1513:C:H6	1.79	0.48
9:1N:42:TRP:HA	9:1N:48:MET:SD	2.54	0.48
41:1j:62:HIS:O	45:1n:59:ALA:N	2.44	0.48
44:1m:11:ARG:O	44:1m:13:LYS:N	2.47	0.48
1:2A:538:G:H2'	1:2A:539:G:H8	1.78	0.48
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.47	0.48
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.14	0.48
1:2A:2312:U:H5'	6:2G:88:ILE:HD11	1.95	0.48
1:2A:2397:G:N2	1:2A:2420:C:H1'	2.28	0.48
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.44	0.48
1:2A:2751:G:H3'	1:2A:2752:C:H6	1.79	0.48
21:2Z:72:ARG:HG2	21:2Z:89:PHE:HB2	1.94	0.48
32:2a:1184:G:H2'	32:2a:1185:G:C8	2.48	0.48
33:2b:19:HIS:CE1	33:2b:206:ASP:HB2	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:594:U:OP2	62:1A:4186:HOH:O	2.20	0.48
1:1A:1174:A:H4'	1:1A:1177:A:H61	1.79	0.48
1:1A:2375:G:O2'	1:1A:2377:A:N7	2.31	0.48
1:1A:2593:U:H2'	1:1A:2594:C:C6	2.49	0.48
21:1Z:137:ILE:HD13	21:1Z:157:LEU:HD22	1.94	0.48
32:1a:971:G:OP1	32:1a:972:C:H5"	2.14	0.48
32:1a:1223:C:OP2	50:1s:78:ARG:NH2	2.44	0.48
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.49	0.48
1:2A:118:A:C8	1:2A:119:A:C8	3.02	0.48
1:2A:840:C:H2'	1:2A:841:A:C8	2.49	0.48
1:2A:1130:U:O2	4:2E:149:ARG:NH2	2.38	0.48
10:2O:119:PRO:HB2	15:2T:68:TYR:CE2	2.49	0.48
19:2X:35:THR:HG22	19:2X:37:THR:H	1.79	0.48
20:2Y:39:VAL:HB	20:2Y:42:VAL:HB	1.95	0.48
32:2a:390:C:H2'	32:2a:391:G:C8	2.49	0.48
32:2a:1002:G:H2'	32:2a:1003:G:C8	2.49	0.48
35:2d:148:VAL:HG12	35:2d:149:ALA:H	1.79	0.48
49:2r:66:LEU:O	49:2r:70:ILE:HG13	2.14	0.48
50:2s:27:GLU:OE1	50:2s:47:HIS:NE2	2.27	0.48
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.13	0.48
4:1E:67:PHE:HB3	4:1E:72:VAL:O	2.14	0.48
5:1F:110:LEU:HG	5:1F:202:PHE:HE1	1.79	0.48
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.96	0.48
32:1a:674:G:H2'	32:1a:675:A:H8	1.79	0.48
32:1a:1164:G:H2'	32:1a:1165:C:C6	2.48	0.48
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.42	0.48
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.78	0.48
1:2A:1598:C:H2'	1:2A:1599:C:C6	2.48	0.48
1:2A:2845:G:H2'	1:2A:2846:G:C8	2.49	0.48
32:2a:376:G:H2'	32:2a:377:G:C8	2.48	0.48
33:2b:30:ARG:HH22	33:2b:194:PRO:HB2	1.79	0.48
34:2c:79:ARG:H	34:2c:82:GLU:HB2	1.79	0.48
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.14	0.48
42:2k:65:ALA:HB3	42:2k:97:ALA:HB3	1.95	0.48
48:2q:60:ILE:HB	48:2q:74:LEU:HD12	1.96	0.48
1:1A:27:G:C2	1:1A:512:G:N3	2.82	0.47
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.14	0.47
1:1A:2133:G:H3'	1:1A:2157:G:N2	2.29	0.47
4:1E:52:LEU:HD12	4:1E:77:ILE:HD12	1.95	0.47
15:1T:99:LEU:O	15:1T:102:ILE:HG12	2.14	0.47
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:100:GLY:N	33:1b:176:GLU:OE2	2.36	0.47
39:1h:11:THR:OG1	39:1h:14:ARG:NH2	2.47	0.47
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	1.96	0.47
53:1y:95:ARG:HD3	53:1y:95:ARG:HA	1.62	0.47
1:2A:1010:A:H1'	1:2A:1153:C:H1'	1.95	0.47
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.49	0.47
1:2A:2707:G:H5'	13:2R:68:ARG:HH21	1.79	0.47
7:2H:54:ARG:HB3	7:2H:65:HIS:CD2	2.49	0.47
32:2a:409:G:H2'	32:2a:410:G:O4'	2.14	0.47
32:2a:1304:G:OP1	52:2u:2:GLY:N	2.46	0.47
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.49	0.47
35:2d:159:ARG:HA	35:2d:162:LEU:HD12	1.96	0.47
1:1A:329:G:OP1	20:1Y:71:LYS:NZ	2.46	0.47
1:1A:476:G:H4'	1:1A:502:A:N1	2.29	0.47
32:1a:62:U:H1'	32:1a:379:C:H1'	1.96	0.47
32:1a:815:A:O2'	32:1a:1526:G:N2	2.37	0.47
38:1g:140:ASP:HA	38:1g:143:ARG:HG2	1.97	0.47
1:2A:271(W):G:O6	1:2A:271(X):G:N1	2.47	0.47
1:2A:623:G:H2'	1:2A:624:C:C6	2.49	0.47
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.41	0.47
1:2A:1798:U:H5'	3:2D:259:THR:HG23	1.96	0.47
23:21:51:VAL:HG12	23:21:53:VAL:HG23	1.94	0.47
33:2b:143:GLU:O	33:2b:146:GLN:HB2	2.15	0.47
36:2e:148:VAL:HG21	39:2h:107:LEU:HD22	1.96	0.47
1:1A:652(F):G:N2	1:1A:652(T):C:O2	2.47	0.47
1:1A:1041:C:H5'	1:1A:1042:G:OP2	2.14	0.47
1:1A:1260:G:OP1	62:1A:4180:HOH:O	2.20	0.47
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.95	0.47
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.45	0.47
11:1P:98:GLU:O	11:1P:101:VAL:HG22	2.14	0.47
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.49	0.47
32:1a:62:U:O2'	32:1a:379:C:O2	2.25	0.47
35:1d:106:TYR:CD2	35:1d:107:ARG:HD3	2.49	0.47
37:1f:69:GLU:O	37:1f:72:VAL:HG12	2.13	0.47
45:1n:3:ARG:O	45:1n:7:ILE:HG23	2.14	0.47
1:2A:449:A:OP2	62:2A:3871:HOH:O	2.20	0.47
1:2A:453:C:O2	1:2A:457:A:O2'	2.33	0.47
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.47	0.47
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.14	0.47
23:21:52:ARG:NH1	23:21:55:GLY:O	2.47	0.47
32:2a:999:C:H2'	32:2a:1000:U:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.14	0.47
32:2a:1101:A:H4'	32:2a:1102:A:O5'	2.14	0.47
33:2b:30:ARG:NH2	33:2b:194:PRO:HB2	2.29	0.47
34:2c:121:ALA:HB1	34:2c:188:LEU:O	2.14	0.47
38:2g:42:ILE:HD12	38:2g:116:ALA:HB3	1.95	0.47
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.47	0.47
44:2m:23:TYR:HE2	44:2m:70:LEU:HD22	1.79	0.47
46:2o:74:ASP:HB3	46:2o:77:ARG:HB2	1.97	0.47
1:1A:83:G:N2	1:1A:102:G:H1'	2.29	0.47
1:1A:1677:A:OP1	62:1A:4181:HOH:O	2.20	0.47
1:1A:2000:G:OP1	13:1R:5:LYS:NZ	2.47	0.47
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.49	0.47
6:1G:150:ASP:CG	6:1G:151:ALA:H	2.22	0.47
28:16:6:ARG:HD3	28:16:24:GLU:OE2	2.14	0.47
32:1a:651:C:H2'	32:1a:652:U:C6	2.50	0.47
32:1a:1060:C:H5"	41:1j:51:ARG:HG2	1.96	0.47
32:1a:1129:C:H4'	40:1i:16:ARG:HH22	1.79	0.47
1:2A:468:G:N7	29:27:39:ARG:NH2	2.59	0.47
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.29	0.47
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.50	0.47
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.30	0.47
1:2A:2327:A:H2'	1:2A:2328:A:H8	1.77	0.47
1:2A:2370:G:O2'	28:26:44:ARG:NH2	2.44	0.47
1:2A:2544:G:H1'	1:2A:2646:C:H4'	1.96	0.47
6:2G:123:ASN:O	6:2G:125:PHE:N	2.40	0.47
12:2Q:112:GLU:HG3	12:2Q:113:GLN:N	2.29	0.47
21:2Z:25:PRO:O	21:2Z:85:HIS:HA	2.14	0.47
32:2a:270:A:H2'	32:2a:271:C:C6	2.49	0.47
32:2a:977:A:O3'	32:2a:980:C:N4	2.48	0.47
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.49	0.47
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	1.96	0.47
1:1A:792:G:N3	1:1A:2072:G:O2'	2.43	0.47
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.49	0.47
1:1A:2705:A:H2'	1:1A:2706:G:O4'	2.15	0.47
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.15	0.47
1:1A:2876:G:OP2	62:1A:4187:HOH:O	2.20	0.47
59:1A:4031:MPD:H4	59:1A:4031:MPD:HM2	1.71	0.47
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.21	0.47
13:1R:36:THR:HG22	13:1R:37:THR:H	1.79	0.47
15:1T:1:MET:HE2	15:1T:3:ARG:HG2	1.96	0.47
23:11:77:ALA:HA	23:11:80:LEU:HD22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:119:A:H4'	32:1a:120:A:C8	2.48	0.47
32:1a:377:G:OP1	47:1p:3:LYS:NZ	2.31	0.47
33:1b:78:GLN:HE21	33:1b:95:GLN:HA	1.80	0.47
33:1b:140:HIS:O	33:1b:144:ARG:HB2	2.15	0.47
1:2A:2788:C:N3	1:2A:2789:C:N4	2.62	0.47
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.48	0.47
24:22:6:VAL:O	24:22:10:LEU:HG	2.15	0.47
32:2a:768:A:OP2	62:2a:3211:HOH:O	2.20	0.47
32:2a:857:C:H2'	32:2a:858:G:O4'	2.14	0.47
32:2a:939:G:H5'	38:2g:102:ARG:NH1	2.29	0.47
34:2c:139:GLN:HA	34:2c:139:GLN:HE21	1.79	0.47
46:2o:21:ASP:OD2	46:2o:24:SER:HB3	2.12	0.47
48:2q:83:ASP:OD1	48:2q:83:ASP:N	2.47	0.47
1:1A:581:C:H2'	1:1A:582:G:C8	2.50	0.47
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.80	0.47
6:1G:83:ARG:H	6:1G:86:MET:CE	2.27	0.47
13:1R:53:HIS:ND1	13:1R:94:TYR:OH	2.37	0.47
14:1S:25:ARG:HD3	14:1S:42:ASP:OD1	2.15	0.47
32:1a:574:A:OP2	62:1a:4612:HOH:O	2.21	0.47
32:1a:663:A:H2'	32:1a:664:G:O4'	2.14	0.47
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.14	0.47
35:1d:17:VAL:HG22	35:1d:18:LYS:H	1.79	0.47
37:1f:36:ARG:N	37:1f:66:GLU:O	2.44	0.47
1:2A:606:U:H4'	1:2A:658:C:H4'	1.96	0.47
3:2D:158:ALA:O	3:2D:161:THR:OG1	2.25	0.47
32:2a:512:U:H2'	32:2a:513:C:C6	2.49	0.47
33:2b:15:VAL:O	33:2b:209:ARG:HB3	2.14	0.47
33:2b:84:GLU:HB3	33:2b:219:VAL:HG11	1.96	0.47
34:2c:91:LEU:HD11	34:2c:101:LEU:HD13	1.95	0.47
40:2i:53:VAL:HG11	40:2i:92:TYR:HE1	1.80	0.47
42:2k:116:HIS:N	42:2k:117:ASN:HA	2.29	0.47
50:2s:27:GLU:CD	50:2s:47:HIS:HE2	2.19	0.47
51:2t:33:ILE:HD13	51:2t:63:ILE:HG12	1.96	0.47
1:1A:666:G:H1'	30:18:4:MET:HE3	1.96	0.47
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.28	0.47
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.96	0.47
1:1A:2398:U:H2'	1:1A:2399:G:C8	2.49	0.47
1:1A:2746:U:OP2	62:1A:4184:HOH:O	2.20	0.47
1:1A:2748:A:H5'	7:1H:4:ILE:HD13	1.97	0.47
2:1B:75:G:H22	21:1Z:73:GLN:NE2	2.13	0.47
32:1a:295:C:H2'	32:1a:296:U:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:426:G:OP1	35:1d:36:ARG:NH1	2.47	0.47
32:1a:539:A:H2'	32:1a:540:G:C8	2.50	0.47
32:1a:624:C:H2'	32:1a:625:G:C8	2.50	0.47
35:1d:196:LEU:O	35:1d:198:VAL:N	2.44	0.47
38:1g:53:LYS:HB2	38:1g:125:MET:HE1	1.97	0.47
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.97	0.47
40:1i:4:TYR:HA	40:1i:87:GLN:HE22	1.80	0.47
46:1o:3:ILE:HD11	46:1o:38:ARG:HG3	1.95	0.47
48:1q:8:GLY:HA3	48:1q:22:LEU:O	2.15	0.47
1:2A:390:A:H4'	1:2A:391:G:H5'	1.97	0.47
1:2A:444:C:H5"	62:2F:402:HOH:O	2.14	0.47
1:2A:900:A:H2'	1:2A:901:A:O4'	2.14	0.47
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.49	0.47
1:2A:1342:A:OP2	62:2A:3814:HOH:O	2.19	0.47
1:2A:1352:U:OP2	62:2A:3873:HOH:O	2.21	0.47
1:2A:1828:G:OP2	1:2A:1828:G:H8	1.98	0.47
1:2A:2117:A:H5'	1:2A:2147:G:O2'	2.14	0.47
1:2A:2125:G:O2'	1:2A:2173:A:N6	2.48	0.47
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.79	0.47
1:2A:2424:C:O2	1:2A:2429:G:O2'	2.29	0.47
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.48	0.47
2:2B:5:C:OP1	2:2B:61:G:O2'	2.25	0.47
26:24:59:PHE:HB3	26:24:61:ARG:HG2	1.96	0.47
32:2a:84:U:H2'	32:2a:88:A:C8	2.50	0.47
32:2a:131:C:H2'	32:2a:132:C:H6	1.80	0.47
32:2a:261:U:OP2	51:2t:79:ARG:NH2	2.47	0.47
32:2a:382:A:H2'	32:2a:383:A:H8	1.79	0.47
32:2a:537:G:H5"	43:2l:113:ARG:NH1	2.28	0.47
32:2a:551:U:H2'	32:2a:552:U:C6	2.49	0.47
32:2a:576:G:N1	32:2a:759:A:OP1	2.40	0.47
32:2a:920:U:H2'	32:2a:921:U:C6	2.49	0.47
32:2a:1004:A:H5'	32:2a:1024:G:H22	1.80	0.47
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.95	0.47
35:2d:11:LEU:O	35:2d:15:GLU:HG2	2.15	0.47
38:2g:23:VAL:HG13	38:2g:43:PHE:CE2	2.50	0.47
46:2o:33:THR:HG23	46:2o:63:ARG:HH11	1.77	0.47
50:2s:80:TYR:CZ	50:2s:82:GLY:HA2	2.50	0.47
1:1A:1131:G:H21	9:1N:73:THR:HG21	1.79	0.47
1:1A:1467:C:C5	1:1A:1546:C:H2'	2.50	0.47
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.49	0.47
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:131:C:H2'	32:1a:132:C:C6	2.50	0.47
32:1a:165:C:H2'	32:1a:166:G:H8	1.78	0.47
32:1a:583:A:H2'	32:1a:584:G:O4'	2.15	0.47
32:1a:629:G:H2'	32:1a:630:G:O4'	2.15	0.47
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	1.97	0.47
1:2A:247:G:H4'	1:2A:386:G:C5	2.50	0.47
1:2A:624:C:OP1	62:2A:3872:HOH:O	2.20	0.47
1:2A:1669:A:H5"	1:2A:2550:G:OP1	2.14	0.47
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.15	0.47
1:2A:2817:G:OP1	13:2R:99:LYS:NZ	2.47	0.47
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.29	0.47
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.96	0.47
32:2a:514:C:H2'	32:2a:515:G:C8	2.50	0.47
32:2a:1143:G:H2'	32:2a:1144:G:C8	2.50	0.47
37:2f:69:GLU:O	37:2f:72:VAL:HG13	2.15	0.47
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.50	0.47
1:1A:1364:G:N7	23:11:3:LYS:HE2	2.29	0.47
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.29	0.47
1:1A:2641:G:OP2	9:1N:83:LYS:NZ	2.48	0.47
32:1a:189(D):C:O2	32:1a:189(H):G:N1	2.48	0.47
32:1a:339:C:H2'	32:1a:340:U:C6	2.50	0.47
32:1a:524:G:H2'	32:1a:525:C:C6	2.50	0.47
32:1a:575:G:O2'	32:1a:821:G:H5'	2.14	0.47
35:1d:36:ARG:HD2	35:1d:38:TYR:OH	2.14	0.47
48:1q:62:SER:OG	48:1q:72:ARG:HG3	2.15	0.47
49:1r:33:ASP:OD2	49:1r:36:ASN:N	2.48	0.47
53:1y:23:ARG:HA	53:1y:23:ARG:HD2	1.67	0.47
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.29	0.47
11:2P:3:LEU:H	11:2P:3:LEU:HD12	1.80	0.47
32:2a:222:U:H2'	32:2a:223:U:C6	2.49	0.47
32:2a:376:G:H2'	32:2a:377:G:H8	1.78	0.47
32:2a:975:A:N1	41:2j:48:THR:HB	2.30	0.47
32:2a:1210:C:H2'	32:2a:1211:U:H5"	1.96	0.47
32:2a:1512:U:H2'	32:2a:1513:A:H8	1.79	0.47
37:2f:10:LEU:HB2	37:2f:59:TYR:HB3	1.97	0.47
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.50	0.47
1:1A:1529:G:O6	1:1A:1530:C:N4	2.46	0.47
1:1A:2206:G:H5'	1:1A:2207:G:C5	2.50	0.47
32:1a:7:G:H21	36:1e:121:LYS:HG2	1.80	0.47
32:1a:67:C:O2'	32:1a:171:A:H1'	2.14	0.47
33:1b:187:LEU:HD12	33:1b:201:ILE:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:11:ARG:C	44:1m:13:LYS:H	2.23	0.47
1:2A:35:G:H1'	1:2A:454:A:C4	2.49	0.47
1:2A:784:A:C5	3:2D:229:VAL:HG21	2.49	0.47
1:2A:2314:C:H4'	6:2G:38:VAL:HG21	1.96	0.47
21:2Z:27:VAL:HG23	21:2Z:36:LYS:HA	1.95	0.47
32:2a:1530:G:H2'	32:2a:1531:A:C8	2.49	0.47
35:2d:111:ALA:HA	35:2d:116:GLN:HE21	1.79	0.47
1:1A:897:C:H2'	1:1A:898:C:C6	2.50	0.46
1:1A:1257:C:H4'	5:1F:83:PHE:CD1	2.50	0.46
1:1A:2721:A:O2'	1:1A:2874:C:H5'	2.15	0.46
1:1A:2803:C:H2'	1:1A:2804:C:C6	2.50	0.46
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.13	0.46
19:1X:72:LYS:HE3	19:1X:72:LYS:HB3	1.75	0.46
20:1Y:15:VAL:O	20:1Y:22:GLY:N	2.37	0.46
32:1a:691:G:H2'	32:1a:692:U:C6	2.49	0.46
36:1e:81:GLU:HG2	36:1e:90:VAL:HG13	1.96	0.46
38:1g:28:ASN:HD21	38:1g:36:LYS:HE2	1.80	0.46
41:1j:54:PHE:CD2	41:1j:55:LYS:HG3	2.51	0.46
50:1s:28:LYS:HB3	50:1s:47:HIS:HD2	1.79	0.46
1:2A:9:U:O4	1:2A:2629:A:H2	1.98	0.46
1:2A:577:G:N3	62:2A:4013:HOH:O	2.35	0.46
1:2A:784:A:C8	1:2A:792:G:C5	3.03	0.46
1:2A:1073:A:C8	1:2A:1073:A:H3'	2.50	0.46
1:2A:2189:U:H2'	1:2A:2190:G:H8	1.80	0.46
1:2A:2308:G:O2'	1:2A:2310:A:N7	2.46	0.46
1:2A:2572:A:OP1	1:2A:2574:G:O2'	2.29	0.46
7:2H:74:ASN:O	7:2H:78:GLY:N	2.47	0.46
18:2W:45:TYR:CZ	18:2W:49:LYS:HE2	2.50	0.46
21:2Z:24:LEU:HD21	21:2Z:86:VAL:HG13	1.96	0.46
21:2Z:157:LEU:HD22	21:2Z:161:VAL:HG23	1.97	0.46
32:2a:382:A:H2'	32:2a:383:A:C8	2.50	0.46
32:2a:775:G:N2	32:2a:804:U:O4	2.47	0.46
32:2a:918:A:H2'	32:2a:919:A:C8	2.50	0.46
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.80	0.46
54:2w:76:PPU:O	54:2w:76:PPU:H5'	2.15	0.46
1:1A:324:A:H2'	1:1A:325:G:O4'	2.15	0.46
1:1A:1087:G:H2'	1:1A:1089:G:O4'	2.15	0.46
1:1A:1091:G:C5	1:1A:1092:C:C4	3.03	0.46
1:1A:1918:A:O2'	1:1A:1920:OMC:N4	2.48	0.46
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.50	0.46
32:1a:341:C:H2'	32:1a:342:C:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:542:G:P	35:1d:10:ARG:HH22	2.37	0.46
32:1a:684:A:H2'	32:1a:685:G:O4'	2.15	0.46
33:1b:19:HIS:NE2	33:1b:206:ASP:HB2	2.31	0.46
1:2A:1331:A:H2'	1:2A:1333:C:C5	2.51	0.46
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.50	0.46
1:2A:2375:G:N2	1:2A:2378:A:OP2	2.46	0.46
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.50	0.46
6:2G:16:ARG:CZ	6:2G:31:VAL:HG21	2.45	0.46
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.50	0.46
11:2P:94:GLU:HG2	11:2P:96:THR:HG22	1.97	0.46
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.28	0.46
21:2Z:108:PRO:HB2	21:2Z:111:VAL:HG23	1.97	0.46
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.16	0.46
33:2b:20:GLU:HG3	33:2b:189:ASP:HB2	1.97	0.46
33:2b:88:ALA:HB1	33:2b:222:ILE:HD11	1.96	0.46
35:2d:146:ILE:HD12	35:2d:146:ILE:H	1.79	0.46
43:2l:27:LEU:O	43:2l:33:ARG:NH1	2.44	0.46
50:2s:14:HIS:O	50:2s:18:LYS:HG3	2.15	0.46
1:1A:645:C:O2	1:1A:645:C:H2'	2.15	0.46
1:1A:740:U:H2'	1:1A:741:G:C8	2.49	0.46
1:1A:2162:G:H4'	1:1A:2172:U:O2'	2.14	0.46
4:1E:7:VAL:HG23	4:1E:51:PHE:CE2	2.50	0.46
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.96	0.46
32:1a:499:A:N1	32:1a:546:G:O2'	2.44	0.46
32:1a:967:5MC:H4'	40:1i:125:TYR:HE1	1.79	0.46
32:1a:1162:C:H2'	32:1a:1163:C:H6	1.80	0.46
33:1b:231:GLU:H	33:1b:232:PRO:HD3	1.81	0.46
38:1g:27:ILE:HA	38:1g:30:ILE:HD12	1.95	0.46
42:1k:87:THR:O	42:1k:87:THR:OG1	2.32	0.46
1:2A:566:U:H2'	1:2A:567:A:O4'	2.15	0.46
1:2A:1649:G:O2'	13:2R:107:ASP:OD2	2.30	0.46
1:2A:2336:A:H61	22:20:43:THR:CG2	2.27	0.46
3:2D:159:ALA:HB1	3:2D:198:ASN:O	2.15	0.46
6:2G:39:ILE:O	6:2G:91:ARG:HA	2.15	0.46
14:2S:7:TYR:CZ	14:2S:91:PRO:HG3	2.50	0.46
18:2W:71:VAL:HA	18:2W:107:LEU:HD23	1.98	0.46
29:27:46:VAL:HB	29:27:48:LYS:NZ	2.30	0.46
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	1.97	0.46
50:2s:23:ASN:HA	50:2s:27:GLU:OE2	2.16	0.46
1:1A:221:A:N1	1:1A:265:A:O2'	2.46	0.46
1:1A:2243:U:H2'	1:1A:2244:U:H6	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.49	0.46
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.38	0.46
24:12:65:ASN:O	24:12:69:ARG:HG3	2.15	0.46
32:1a:284:G:H2'	32:1a:285:G:C8	2.50	0.46
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.32	0.46
38:1g:50:ILE:HG23	38:1g:121:ALA:HB1	1.98	0.46
39:1h:51:VAL:HG11	39:1h:60:ARG:NH1	2.31	0.46
1:2A:526:A:HO2'	1:2A:2043:C:HO2'	1.64	0.46
1:2A:527:C:N4	1:2A:2777:G:O2'	2.45	0.46
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.15	0.46
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.46	0.46
1:2A:2047:U:O2'	1:2A:2823:A:N1	2.45	0.46
6:2G:72:ARG:HA	6:2G:86:MET:O	2.16	0.46
15:2T:16:ARG:HH11	15:2T:19:LEU:HD11	1.80	0.46
21:2Z:19:ARG:NH1	21:2Z:25:PRO:HG2	2.31	0.46
22:20:69:PHE:CE2	22:20:79:VAL:HG22	2.50	0.46
32:2a:1493:A:H4'	53:2y:72:THR:HG23	1.97	0.46
39:2h:48:TYR:HB3	39:2h:61:VAL:HG12	1.97	0.46
40:2i:37:PHE:HB3	40:2i:43:ALA:HB2	1.98	0.46
1:1A:579:G:H2'	1:1A:580:C:C6	2.50	0.46
1:1A:1067:A:H2'	1:1A:1068:G:C8	2.50	0.46
2:1B:13:A:N1	2:1B:69:G:O2'	2.45	0.46
5:1F:155:LEU:HD12	5:1F:174:VAL:O	2.15	0.46
32:1a:736:C:O2'	37:1f:90:VAL:O	2.31	0.46
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.98	0.46
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.50	0.46
1:2A:315:G:H2'	1:2A:316:C:C6	2.50	0.46
1:2A:455:C:N3	1:2A:472:A:H2'	2.31	0.46
1:2A:833:U:O2	11:2P:55:ARG:NH1	2.48	0.46
1:2A:861:A:C2	1:2A:917:A:C4	3.04	0.46
7:2H:95:ARG:HB2	7:2H:128:PRO:HB3	1.97	0.46
11:2P:3:LEU:C	11:2P:5:ASP:H	2.24	0.46
20:2Y:55:TYR:CZ	20:2Y:61:ILE:HG21	2.50	0.46
28:26:44:ARG:HE	28:26:44:ARG:HB3	1.38	0.46
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.51	0.46
33:2b:135:GLN:O	33:2b:139:LYS:HB2	2.15	0.46
38:2g:67:GLU:HA	38:2g:70:LYS:HD3	1.96	0.46
1:1A:912:C:OP1	12:1Q:9:TYR:OH	2.32	0.46
1:1A:1040:C:H2'	1:1A:1041:C:O4'	2.16	0.46
1:1A:2101:G:H2'	1:1A:2102:U:C6	2.50	0.46
10:1O:107:ARG:CZ	15:1T:36:GLU:HG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1W:4:LYS:HB2	18:1W:106:ILE:HG12	1.98	0.46
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.39	0.46
32:1a:1431:C:H2'	32:1a:1432:G:O4'	2.16	0.46
33:1b:59:GLU:HB3	33:1b:221:LEU:HD21	1.98	0.46
34:1c:8:ILE:HD11	34:1c:184:TYR:H	1.81	0.46
34:1c:48:TYR:C	34:1c:50:ALA:H	2.23	0.46
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.81	0.46
40:1i:3:GLN:NE2	40:1i:20:ARG:HH21	2.11	0.46
1:2A:150:C:H2'	1:2A:151:C:C6	2.50	0.46
1:2A:391:G:O2'	1:2A:410:G:OP1	2.29	0.46
1:2A:1058:G:C1'	1:2A:1082:U:H3	2.28	0.46
3:2D:267:SER:C	3:2D:269:PHE:H	2.24	0.46
7:2H:70:THR:O	7:2H:74:ASN:N	2.44	0.46
8:2I:62:LYS:HG2	8:2I:133:HIS:NE2	2.31	0.46
8:2I:87:LYS:HE3	8:2I:87:LYS:HB2	1.70	0.46
11:2P:87:ASP:HB3	11:2P:105:LEU:HD13	1.96	0.46
1:1A:185:U:H2'	1:1A:186:G:H8	1.80	0.46
4:1E:101:ARG:NH2	4:1E:171:GLU:HB2	2.31	0.46
6:1G:83:ARG:H	6:1G:86:MET:HE2	1.80	0.46
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.97	0.46
22:10:32:ARG:H	22:10:35:ASN:ND2	2.13	0.46
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.16	0.46
32:1a:1356:G:H2'	32:1a:1357:A:H8	1.81	0.46
32:1a:1473:A:H2'	32:1a:1474:G:C8	2.50	0.46
45:1n:46:GLU:O	45:1n:50:LYS:HG3	2.15	0.46
47:1p:4:ILE:HA	47:1p:20:VAL:O	2.15	0.46
1:2A:539:G:H2'	1:2A:540:C:C6	2.51	0.46
1:2A:620:G:N3	1:2A:620:G:H5'	2.30	0.46
1:2A:712:G:H1	1:2A:719:C:H42	1.63	0.46
2:2B:14:U:H1'	2:2B:108:U:O2'	2.15	0.46
4:2E:5:LEU:HD21	4:2E:79:ARG:HB2	1.98	0.46
6:2G:2:PRO:HB2	6:2G:3:LEU:H	1.55	0.46
6:2G:94:LEU:HD23	6:2G:94:LEU:HA	1.82	0.46
7:2H:150:ALA:HA	7:2H:153:LYS:HG3	1.98	0.46
10:2O:91:LEU:HD23	10:2O:111:PHE:CZ	2.50	0.46
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.41	0.46
26:24:18:CYS:HB2	26:24:20:ASN:HB2	1.97	0.46
31:29:26:ILE:H	31:29:26:ILE:HG13	1.65	0.46
32:2a:127:G:HO2'	48:2q:2:PRO:N	2.14	0.46
32:2a:664:G:N2	32:2a:741:G:H1	2.05	0.46
32:2a:900:A:H2'	32:2a:901:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:166:LYS:NZ	35:2d:167:GLY:H	2.13	0.46
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.16	0.46
39:2h:26:VAL:HG23	39:2h:27:PRO:O	2.16	0.46
40:2i:117:HIS:CE1	40:2i:123:PRO:HB3	2.51	0.46
43:2l:34:ARG:O	43:2l:61:THR:HG23	2.16	0.46
1:1A:272(B):G:H2'	1:1A:272(C):G:C8	2.50	0.46
1:1A:1096:A:H8	1:1A:1096:A:OP2	1.98	0.46
1:1A:2341:G:H2'	1:1A:2342:C:C6	2.51	0.46
1:1A:2555:U:O2	54:1w:74:C:C2	2.69	0.46
1:1A:2612:C:OP2	27:15:2:ALA:N	2.48	0.46
3:1D:3:VAL:HG22	3:1D:17:THR:HB	1.96	0.46
7:1H:9:ILE:HD11	7:1H:69:ARG:HG2	1.98	0.46
9:1N:65:LYS:HE2	9:1N:69:GLN:NE2	2.31	0.46
10:1O:25:LEU:HG	10:1O:40:VAL:HG23	1.98	0.46
15:1T:54:ARG:HA	15:1T:59:THR:HB	1.98	0.46
18:1W:9:TYR:HA	18:1W:100:THR:CG2	2.45	0.46
32:1a:62:U:OP1	32:1a:385:C:O2'	2.32	0.46
32:1a:1027:C:H2'	32:1a:1028:C:C6	2.50	0.46
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.84	0.46
36:1e:75:THR:CG2	36:1e:94:ALA:H	2.29	0.46
37:1f:86:ARG:O	37:1f:87:ARG:HG2	2.16	0.46
39:1h:120:THR:OG1	39:1h:123:GLU:HG3	2.15	0.46
43:1l:97:ARG:HB2	43:1l:98:TYR:CE2	2.51	0.46
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.79	0.46
1:2A:1035:U:H2'	1:2A:1036:G:H8	1.78	0.46
1:2A:1081:U:C3'	1:2A:1082:U:H5"	2.44	0.46
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.81	0.46
1:2A:2099:U:O2	1:2A:2190:G:N2	2.47	0.46
1:2A:2552:2MU:H2'	1:2A:2554:U:OP2	2.16	0.46
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.46	0.46
3:2D:133:LEU:HD23	3:2D:136:ILE:HD12	1.97	0.46
5:2F:118:ALA:C	5:2F:120:GLU:H	2.24	0.46
7:2H:115:VAL:HG11	7:2H:148:ILE:HD12	1.98	0.46
9:2N:123:TYR:CZ	9:2N:129:PRO:HD2	2.50	0.46
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.97	0.46
21:2Z:30:ASN:ND2	21:2Z:90:VAL:HB	2.30	0.46
32:2a:189(B):C:H2'	32:2a:189(C):C:H6	1.80	0.46
32:2a:1519:MA6:H92	32:2a:1520:G:O2'	2.16	0.46
35:2d:63:LYS:NZ	35:2d:197:PRO:O	2.44	0.46
1:1A:1359:A:N6	1:1A:1372:U:H3	2.13	0.46
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:747:C:H3'	32:1a:748:C:C6	2.51	0.46
32:1a:1302:U:H5	44:1m:17:VAL:HG21	1.81	0.46
35:1d:106:TYR:HD2	35:1d:107:ARG:HD3	1.79	0.46
39:1h:97:VAL:HG21	39:1h:128:GLY:HA2	1.96	0.46
46:1o:85:LEU:HB3	46:1o:87:ILE:HG13	1.98	0.46
50:1s:12:ASP:OD2	50:1s:35:SER:HB3	2.16	0.46
1:2A:1422:G:H1'	1:2A:1496:A:N1	2.31	0.46
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.16	0.46
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.98	0.46
9:2N:54:VAL:HG13	9:2N:122:VAL:HG22	1.98	0.46
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.98	0.46
23:21:76:ARG:NH1	23:21:97:LEU:O	2.48	0.46
34:2c:28:GLN:HG2	34:2c:32:LEU:HD13	1.98	0.46
47:2p:19:ILE:HG22	47:2p:36:ILE:HG13	1.97	0.46
1:1A:185:U:H4'	1:1A:218:A:H4'	1.98	0.46
1:1A:2122:U:H2'	1:1A:2123:G:O4'	2.16	0.46
1:1A:2749:A:H3'	1:1A:2750:A:H2'	1.98	0.46
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.34	0.46
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.55	0.46
24:12:34:GLU:OE1	62:12:102:HOH:O	2.21	0.46
32:1a:97:G:H2'	32:1a:98:G:O4'	2.16	0.46
32:1a:189(F):U:H1'	48:1q:63:ARG:HH21	1.81	0.46
32:1a:426:G:H2'	32:1a:427:U:C6	2.51	0.46
32:1a:977:A:H2'	32:1a:978:A:H5"	1.98	0.46
32:1a:1003:G:H8	32:1a:1003:G:O5'	1.99	0.46
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.50	0.46
33:1b:54:THR:O	33:1b:58:ILE:HG13	2.15	0.46
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.43	0.46
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.31	0.46
46:1o:18:PHE:O	46:1o:20:GLY:N	2.49	0.46
47:1p:70:ALA:O	47:1p:74:LEU:N	2.46	0.46
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.81	0.46
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.48	0.46
1:2A:1654:A:OP1	13:2R:2:ARG:HB2	2.15	0.46
1:2A:1818:U:O4	3:2D:154:LYS:HD3	2.16	0.46
1:2A:1845:G:OP1	3:2D:258:LYS:NZ	2.36	0.46
1:2A:2804:C:H2'	1:2A:2805:G:O4'	2.16	0.46
2:2B:87:G:N2	2:2B:90:A:OP2	2.37	0.46
5:2F:107:LYS:HG3	5:2F:206:ILE:HA	1.96	0.46
10:2O:9:GLU:O	10:2O:83:ALA:HA	2.16	0.46
32:2a:401:C:O2'	32:2a:621:A:N3	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:620:C:C2	35:2d:135:LEU:HG	2.51	0.46
32:2a:620:C:H2'	32:2a:621:A:O4'	2.16	0.46
32:2a:984:C:H2'	32:2a:985:C:C6	2.50	0.46
32:2a:1315:U:H2'	32:2a:1316:G:O4'	2.15	0.46
34:2c:6:HIS:NE2	34:2c:8:ILE:HB	2.31	0.46
39:2h:95:VAL:HB	39:2h:99:GLU:HG3	1.97	0.46
1:1A:143:G:H1'	19:1X:37:THR:HG21	1.96	0.45
1:1A:647:G:H8	1:1A:647:G:O5'	1.98	0.45
1:1A:1754:C:H5	15:1T:96:ARG:NH2	2.15	0.45
1:1A:1762:A:H2'	62:1A:6376:HOH:O	2.16	0.45
1:1A:2139:C:H42	1:1A:2152:G:H1	1.65	0.45
1:1A:2667:C:H1'	7:1H:109:PHE:CD1	2.51	0.45
6:1G:43:LEU:HD11	6:1G:153:ARG:HD2	1.98	0.45
9:1N:60:ILE:HG13	9:1N:61:ARG:H	1.81	0.45
10:1O:73:ASP:HB2	15:1T:82:LEU:CD1	2.46	0.45
10:1O:107:ARG:NH2	15:1T:36:GLU:HG2	2.31	0.45
32:1a:461:A:O2'	32:1a:470:C:H5'	2.15	0.45
32:1a:911:U:H2'	32:1a:912:C:C6	2.51	0.45
32:1a:1029:C:O2	32:1a:1032:G:N1	2.43	0.45
33:1b:200:ILE:HD12	33:1b:200:ILE:H	1.80	0.45
36:1e:135:THR:O	36:1e:139:LEU:HG	2.16	0.45
1:2A:288:C:H2'	1:2A:289:A:H8	1.81	0.45
1:2A:656:G:H2'	1:2A:657:U:O4'	2.16	0.45
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.41	0.45
1:2A:1087:G:H22	1:2A:1102:C:N4	2.14	0.45
1:2A:1252:G:N2	16:2U:37:GLU:OE2	2.41	0.45
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.16	0.45
1:2A:1999:C:H5"	1:2A:2723:C:O2'	2.17	0.45
1:2A:2867:G:OP2	15:2T:119:LYS:NZ	2.35	0.45
2:2B:33:G:C6	2:2B:34:U:C4	3.04	0.45
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.58	0.45
15:2T:61:PHE:CE2	15:2T:76:PHE:HB2	2.51	0.45
20:2Y:7:VAL:HG12	20:2Y:8:LYS:N	2.30	0.45
21:2Z:70:LEU:HD23	21:2Z:70:LEU:HA	1.74	0.45
26:24:15:ILE:HB	26:24:32:TYR:CD2	2.51	0.45
32:2a:41:G:H2'	32:2a:42:G:H8	1.80	0.45
32:2a:399:G:H2'	32:2a:400:C:C6	2.51	0.45
33:2b:121:LEU:O	33:2b:127:ILE:HG23	2.16	0.45
43:2l:119:LYS:C	43:2l:121:GLY:H	2.24	0.45
56:2v:1:FME:C	56:2v:3:ILE:HD12	2.46	0.45
1:1A:626:U:O4	11:1P:107:LYS:HE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:800:A:H8	1:1A:800:A:OP1	1.99	0.45
2:1B:108:U:H2'	2:1B:109:C:H5"	1.98	0.45
5:1F:41:LEU:O	5:1F:44:ARG:HG2	2.16	0.45
6:1G:77:ILE:HB	6:1G:82:LEU:HB2	1.98	0.45
7:1H:28:GLY:HA3	7:1H:79:VAL:HB	1.98	0.45
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.50	0.45
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.15	0.45
24:12:36:ARG:O	24:12:40:SER:N	2.47	0.45
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.81	0.45
32:1a:1151:A:O2'	32:1a:1152:A:H8	1.99	0.45
33:1b:128:GLU:C	33:1b:130:ARG:H	2.24	0.45
34:1c:22:TRP:CH2	34:1c:32:LEU:HB2	2.51	0.45
34:1c:136:GLN:O	34:1c:140:ARG:HG3	2.16	0.45
34:1c:153:VAL:HG22	34:1c:198:VAL:HG22	1.99	0.45
1:2A:272(I):U:H2'	1:2A:272(J):C:C6	2.51	0.45
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.59	0.45
1:2A:1064:C:H5	1:2A:1065:U:C6	2.35	0.45
1:2A:1209:G:N2	1:2A:1210:A:N1	2.64	0.45
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.16	0.45
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.15	0.45
1:2A:1762:A:N1	62:2A:4028:HOH:O	2.36	0.45
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.52	0.45
62:2A:4364:HOH:O	5:2F:74:ARG:HD2	2.15	0.45
32:2a:490:G:H2'	32:2a:491:G:H8	1.80	0.45
32:2a:523:A:H61	43:2l:92:0TD:CG	2.29	0.45
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.51	0.45
47:2p:23:ASP:OD1	47:2p:25:ARG:HG2	2.16	0.45
1:1A:1919:A:N1	32:1a:1495:U:O2'	2.37	0.45
1:1A:2681:C:OP2	4:1E:109:LYS:NZ	2.40	0.45
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.24	0.45
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.45	0.45
32:1a:109:A:C6	32:1a:326:G:C6	3.04	0.45
32:1a:165:C:H2'	32:1a:166:G:C8	2.52	0.45
32:1a:545:C:OP2	35:1d:65:ARG:NH2	2.49	0.45
59:1a:1873:MPD:H12	59:1a:1873:MPD:H4	1.67	0.45
37:1f:92:LYS:HE3	37:1f:92:LYS:HB2	1.72	0.45
41:1j:49:VAL:HG21	45:1n:41:ARG:O	2.17	0.45
47:1p:18:ARG:NH1	47:1p:32:TYR:OH	2.49	0.45
53:1y:2:THR:OG1	53:1y:3:MET:N	2.48	0.45
1:2A:1076:C:H1'	1:2A:1077:A:H5'	1.98	0.45
1:2A:2100:G:C2	1:2A:2101:G:H1'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.51	0.45
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.51	0.45
2:2B:2:C:H2'	2:2B:3:C:C6	2.52	0.45
18:2W:18:ARG:HG3	18:2W:76:VAL:HB	1.98	0.45
31:29:3:VAL:HA	31:29:35:ARG:O	2.17	0.45
32:2a:138:G:H2'	32:2a:139:G:H8	1.81	0.45
32:2a:407:G:H2'	32:2a:408:A:C8	2.51	0.45
32:2a:1369:C:H2'	32:2a:1370:G:O4'	2.17	0.45
33:2b:48:MET:HA	33:2b:51:LEU:HB2	1.98	0.45
39:2h:51:VAL:HG11	39:2h:60:ARG:HH12	1.81	0.45
1:1A:222:A:H3'	1:1A:421:U:H5'	1.98	0.45
1:1A:515:A:H2	1:1A:1260:G:N3	2.15	0.45
1:1A:746:A:H2'	1:1A:2612:C:H5"	1.99	0.45
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.51	0.45
19:1X:57:LEU:HD11	19:1X:78:LYS:HE3	1.98	0.45
29:17:34:ARG:NH1	29:17:41:ARG:O	2.50	0.45
32:1a:313:A:H2'	32:1a:314:C:C6	2.52	0.45
32:1a:406:G:N3	35:1d:119:GLN:NE2	2.62	0.45
38:1g:95:ARG:CZ	38:1g:99:LEU:HD11	2.46	0.45
39:1h:6:ILE:HD11	39:1h:31:PHE:CD2	2.51	0.45
43:1l:57:LYS:HZ2	43:1l:65:GLU:HG2	1.80	0.45
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.81	0.45
11:2P:54:GLY:O	62:2P:301:HOH:O	2.21	0.45
16:2U:76:TYR:CE2	16:2U:80:ILE:HG13	2.51	0.45
21:2Z:42:VAL:O	21:2Z:46:LYS:HG2	2.15	0.45
32:2a:560:U:H5'	32:2a:566:G:N2	2.31	0.45
32:2a:715:A:H5"	32:2a:805:C:H1'	1.99	0.45
41:2j:81:THR:O	41:2j:85:LEU:HG	2.16	0.45
1:1A:581:C:H2'	1:1A:582:G:H8	1.82	0.45
1:1A:839:U:H2'	1:1A:840:C:C6	2.51	0.45
1:1A:1031:G:N3	31:19:36:GLN:NE2	2.59	0.45
1:1A:1168:G:H2'	1:1A:1169:G:O4'	2.17	0.45
1:1A:2492:U:H2'	1:1A:2493:U:H6	1.81	0.45
6:1G:43:LEU:C	6:1G:45:GLU:H	2.17	0.45
10:1O:66:LYS:N	10:1O:82:ASN:OD1	2.48	0.45
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.17	0.45
21:1Z:98:MET:HE3	21:1Z:98:MET:HB2	1.85	0.45
25:13:3:ARG:HG3	25:13:38:GLU:OE1	2.17	0.45
32:1a:166:G:H2'	32:1a:167:G:H8	1.82	0.45
32:1a:429:U:H2'	35:1d:25:ARG:NH1	2.31	0.45
32:1a:1256:A:H2	32:1a:1277:C:C4	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.99	0.45
40:1i:66:ARG:HB2	40:1i:66:ARG:NH2	2.31	0.45
42:1k:50:TYR:CG	42:1k:54:ARG:HD3	2.52	0.45
51:1t:54:LYS:HE2	51:1t:54:LYS:HB3	1.66	0.45
1:2A:69:C:H2'	1:2A:70:G:C8	2.52	0.45
1:2A:1071:G:N2	1:2A:1072:C:H41	2.13	0.45
1:2A:1117:G:H2'	1:2A:1118:C:C6	2.52	0.45
1:2A:2298:A:H2'	1:2A:2299:G:O4'	2.17	0.45
1:2A:2579:C:OP1	62:2A:3875:HOH:O	2.21	0.45
62:2A:3983:HOH:O	11:2P:55:ARG:NH2	2.50	0.45
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.50	0.45
32:2a:445:G:H2'	32:2a:446:G:O4'	2.16	0.45
32:2a:539:A:C6	32:2a:540:G:C6	3.05	0.45
32:2a:1125:U:O2'	32:2a:1126:U:H2'	2.17	0.45
32:2a:1146:A:H5'	32:2a:1147:C:OP2	2.16	0.45
35:2d:62:GLN:HB3	35:2d:66:ARG:HD2	1.99	0.45
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.50	0.45
50:2s:51:VAL:O	50:2s:57:HIS:HA	2.16	0.45
1:1A:382:G:OP2	62:1A:4188:HOH:O	2.21	0.45
1:1A:1693:U:H1'	3:1D:14:ARG:NH1	2.31	0.45
1:1A:2239:G:H5'	3:1D:251:GLY:HA3	1.98	0.45
12:1Q:85:LYS:HD3	22:10:7:LEU:HG	1.97	0.45
35:1d:73:ARG:HD2	35:1d:73:ARG:HA	1.70	0.45
43:1l:117:ARG:NH2	43:1l:124:LYS:HD2	2.31	0.45
50:1s:41:VAL:HG22	50:1s:44:MET:HE3	1.98	0.45
6:2G:125:PHE:CE1	6:2G:131:TYR:HB2	2.52	0.45
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.13	0.45
11:2P:57:THR:HG22	11:2P:59:LEU:N	2.30	0.45
13:2R:88:ARG:NH2	13:2R:89:ASP:OD1	2.49	0.45
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.37	0.45
32:2a:112:G:H4'	32:2a:389:A:H4'	1.98	0.45
32:2a:500:G:C6	32:2a:546:G:C2	3.04	0.45
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.52	0.45
39:2h:104:ARG:O	39:2h:107:LEU:HB2	2.17	0.45
41:2j:32:ALA:HB1	41:2j:33:GLN:HG2	1.99	0.45
44:2m:20:THR:C	44:2m:22:ILE:H	2.24	0.45
56:2v:1:FME:HE2	56:2v:3:ILE:HD13	1.99	0.45
2:1B:2:C:H2'	2:1B:3:C:C6	2.52	0.45
7:1H:101:ARG:NH1	7:1H:121:ILE:O	2.44	0.45
9:1N:1:MET:HE3	9:1N:1:MET:HB2	1.76	0.45
15:1T:53:ARG:HB3	15:1T:53:ARG:HH11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1W:86:LEU:HD12	18:1W:87:PRO:HD2	1.98	0.45
32:1a:926:G:C6	32:1a:1505:G:C6	3.05	0.45
32:1a:1292:U:H2'	32:1a:1293:G:C8	2.51	0.45
33:1b:97:TRP:HH2	33:1b:176:GLU:CD	2.24	0.45
53:1y:3:MET:HE2	53:1y:3:MET:HB3	1.71	0.45
1:2A:749:C:OP1	62:2A:3878:HOH:O	2.21	0.45
1:2A:875:G:H5"	21:2Z:149:SER:CB	2.46	0.45
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.52	0.45
1:2A:1670:C:O2	4:2E:129:HIS:NE2	2.49	0.45
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.51	0.45
62:2A:4287:HOH:O	29:27:43:THR:HB	2.17	0.45
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.16	0.45
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.97	0.45
9:2N:15:LEU:HD23	9:2N:53:VAL:HB	1.99	0.45
17:2V:5:VAL:HG11	17:2V:57:VAL:HG21	1.97	0.45
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.50	0.45
31:29:8:LYS:HB2	31:29:8:LYS:HE3	1.81	0.45
32:2a:430:A:OP1	35:2d:9:CYS:HB2	2.16	0.45
32:2a:1206:G:C2	32:2a:1207:2MG:C4	3.05	0.45
32:2a:1399:C:H4'	32:2a:1400:5MC:O5'	2.17	0.45
33:2b:122:PHE:HA	33:2b:127:ILE:HG21	1.99	0.45
49:2r:41:LYS:HE3	49:2r:42:ARG:HD3	1.98	0.45
50:2s:58:VAL:HG21	50:2s:75:ALA:HA	1.99	0.45
1:1A:226:G:H21	1:1A:228:A:H62	1.65	0.45
1:1A:301:G:OP2	20:1Y:84:ARG:NH2	2.50	0.45
1:1A:476:G:OP1	62:1A:4189:HOH:O	2.21	0.45
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.17	0.45
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.52	0.45
2:1B:7:G:H5"	2:1B:7:G:H8	1.81	0.45
2:1B:66:A:H61	2:1B:109:C:H5"	1.80	0.45
9:1N:99:LEU:HB2	62:1N:307:HOH:O	2.17	0.45
19:1X:12:VAL:HG21	19:1X:27:THR:HG22	1.98	0.45
45:1n:9:LYS:HB2	45:1n:9:LYS:HE3	1.81	0.45
46:1o:41:GLU:OE2	46:1o:44:LYS:NZ	2.32	0.45
1:2A:38:A:H2'	1:2A:39:C:C6	2.52	0.45
1:2A:287:C:H2'	1:2A:288:C:C6	2.52	0.45
1:2A:297:C:H2'	1:2A:298:G:O4'	2.16	0.45
1:2A:527:C:H4'	1:2A:528:A:O5'	2.17	0.45
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.52	0.45
1:2A:1512:U:H2'	1:2A:1513:C:H6	1.82	0.45
6:2G:8:LYS:HB3	6:2G:8:LYS:HE2	1.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:140:LYS:HB2	7:2H:140:LYS:HE3	1.79	0.45
8:2I:4:ILE:HB	8:2I:37:VAL:HG23	1.99	0.45
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.98	0.45
15:2T:127:ALA:C	15:2T:129:ARG:H	2.25	0.45
20:2Y:19:LYS:HB3	20:2Y:19:LYS:HE2	1.86	0.45
32:2a:646:U:H2'	32:2a:647:C:C6	2.51	0.45
32:2a:1164:G:H1	32:2a:1172:C:H42	1.64	0.45
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.98	0.45
32:2a:1320:C:H1'	50:2s:73:GLU:HG2	1.98	0.45
33:2b:97:TRP:NE1	33:2b:173:ALA:HB2	2.31	0.45
37:2f:22:GLU:OE1	37:2f:84:ASN:HB2	2.17	0.45
37:2f:68:PRO:HB2	37:2f:71:ARG:HD2	1.98	0.45
40:2i:65:VAL:HG21	40:2i:73:GLN:HB3	1.99	0.45
48:2q:58:GLU:OE2	48:2q:75:ARG:NH2	2.49	0.45
1:1A:24:G:H2'	1:1A:25:U:O4'	2.17	0.45
1:1A:34:C:O2'	1:1A:35:G:H5'	2.17	0.45
1:1A:2406:U:C2	11:1P:72:PRO:HG2	2.52	0.45
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.17	0.45
1:1A:2691:C:O3'	1:1A:2871:C:H4'	2.17	0.45
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.99	0.45
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HD3	1.98	0.45
32:1a:328:C:OP1	62:1a:4613:HOH:O	2.21	0.45
32:1a:615:C:H2'	32:1a:616:G:H8	1.82	0.45
32:1a:1226:C:H4'	32:1a:1227:A:OP1	2.17	0.45
32:1a:1263:C:H2'	32:1a:1264:C:H6	1.82	0.45
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.32	0.45
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.51	0.45
40:1i:16:ARG:HD3	40:1i:66:ARG:HH12	1.82	0.45
43:1l:119:LYS:H	43:1l:119:LYS:HG3	1.56	0.45
45:1n:58:LYS:HB3	45:1n:58:LYS:HE2	1.70	0.45
1:2A:271(F):C:H2'	1:2A:271(G):C:C6	2.52	0.45
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.50	0.45
7:2H:15:VAL:HG12	7:2H:28:GLY:HA2	1.98	0.45
32:2a:186:C:H5'	51:2t:78:ALA:HB1	1.99	0.45
32:2a:189(B):C:H2'	32:2a:189(C):C:C6	2.51	0.45
32:2a:429:U:H1'	32:2a:430:A:H5"	1.98	0.45
32:2a:450:G:H4'	47:2p:41:PRO:HB2	1.98	0.45
32:2a:524:G:H2'	32:2a:525:C:C6	2.52	0.45
32:2a:555:C:H2'	32:2a:556:C:C6	2.52	0.45
32:2a:724:G:C2	32:2a:725:G:C8	3.05	0.45
33:2b:172:ILE:O	33:2b:176:GLU:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:58:TYR:O	39:2h:59:LEU:HD23	2.17	0.45
1:1A:861:A:H2'	1:1A:862:G:O4'	2.17	0.45
1:1A:1482:G:H2'	1:1A:1484:G:H8	1.81	0.45
1:1A:1790:C:H5"	1:1A:1791:A:OP1	2.17	0.45
1:1A:2065:C:H4'	1:1A:2251:OMG:HM22	1.98	0.45
5:1F:8:GLN:NE2	5:1F:21:ALA:HB2	2.32	0.45
6:1G:45:GLU:O	6:1G:49:ASP:HB2	2.17	0.45
32:1a:130:A:OP2	48:1q:63:ARG:NE	2.45	0.45
32:1a:166:G:H2'	32:1a:167:G:C8	2.51	0.45
32:1a:710:G:H5"	37:1f:54:LYS:NZ	2.32	0.45
32:1a:1438:G:H2'	32:1a:1439:C:H6	1.82	0.45
35:1d:155:LEU:HB3	35:1d:158:ILE:HG12	1.99	0.45
36:1e:30:ALA:N	36:1e:46:GLY:O	2.41	0.45
1:2A:245:G:O6	30:28:8:LYS:NZ	2.45	0.45
1:2A:2271:G:OP1	22:20:18:ALA:HB1	2.17	0.45
1:2A:2354:G:H21	22:20:36:ILE:CD1	2.30	0.45
4:2E:98:PRO:HG3	4:2E:174:ASP:HA	1.99	0.45
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.77	0.45
11:2P:121:LYS:O	11:2P:123:LEU:N	2.49	0.45
15:2T:109:GLU:HG3	15:2T:112:ARG:NH2	2.32	0.45
24:22:31:GLU:HB3	24:22:53:LEU:HD11	1.97	0.45
51:2t:100:ILE:HG13	51:2t:101:GLY:H	1.82	0.45
1:1A:229:A:H5"	1:1A:230:U:H5'	1.99	0.44
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.52	0.44
1:1A:1141:U:OP1	9:1N:25:ARG:NH1	2.50	0.44
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.52	0.44
32:1a:743:U:H2'	32:1a:744:C:C6	2.53	0.44
36:1e:79:GLU:H	36:1e:79:GLU:CD	2.24	0.44
40:1i:24:GLY:N	40:1i:59:PHE:O	2.38	0.44
1:2A:31:C:OP1	62:2A:3874:HOH:O	2.21	0.44
1:2A:1002:G:H2'	1:2A:1003:G:O4'	2.17	0.44
1:2A:1074:G:C2	1:2A:1075:C:H1'	2.52	0.44
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.17	0.44
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.52	0.44
1:2A:2678:C:O3'	62:2A:3879:HOH:O	2.21	0.44
32:2a:7:G:H5'	32:2a:298:A:O4'	2.17	0.44
32:2a:825:G:H21	39:2h:11:THR:HG21	1.81	0.44
32:2a:1223:C:H5"	32:2a:1224:G:H5"	1.99	0.44
36:2e:78:HIS:HA	39:2h:105:ARG:HG3	1.99	0.44
38:2g:69:VAL:HG11	38:2g:134:ALA:HB1	1.98	0.44
53:2y:10:MET:HE2	53:2y:12:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2y:87:LYS:O	53:2y:91:LYS:HB2	2.16	0.44
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.17	0.44
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.44	0.44
10:1O:39:ILE:HD12	10:1O:41:ALA:HB2	1.98	0.44
11:1P:115:LEU:HD23	11:1P:131:SER:HB3	1.98	0.44
32:1a:745:C:H2'	32:1a:746:A:C8	2.51	0.44
32:1a:828:A:H2'	32:1a:829:G:O4'	2.18	0.44
32:1a:1470:G:N7	62:1a:4654:HOH:O	2.35	0.44
35:1d:111:ALA:HB1	35:1d:116:GLN:HB3	1.99	0.44
43:1l:57:LYS:NZ	43:1l:65:GLU:HG2	2.32	0.44
46:1o:39:LEU:HD23	46:1o:39:LEU:HA	1.85	0.44
1:2A:190:A:OP2	23:21:39:LYS:HE3	2.18	0.44
1:2A:210:C:H4'	1:2A:1367:A:H1'	1.99	0.44
1:2A:271(O):C:H2'	1:2A:271(P):C:C6	2.52	0.44
1:2A:747:U:O2	1:2A:2014:A:H1'	2.17	0.44
1:2A:821:A:H2'	1:2A:946:G:H5"	1.97	0.44
1:2A:1090:U:H2'	1:2A:1091:G:H8	1.81	0.44
1:2A:2130:U:H2'	1:2A:2158:A:N6	2.22	0.44
1:2A:2570:G:H2'	1:2A:2571:C:O4'	2.17	0.44
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.17	0.44
21:2Z:16:SER:O	21:2Z:20:ARG:HB2	2.16	0.44
21:2Z:114:GLY:O	21:2Z:177:PRO:HG3	2.17	0.44
26:24:16:CYS:HA	26:24:33:VAL:HG22	1.97	0.44
28:26:9:LEU:HD13	28:26:51:GLU:HG3	1.98	0.44
32:2a:684:A:H2'	32:2a:685:G:C8	2.53	0.44
32:2a:782:A:H2'	32:2a:783:C:O4'	2.18	0.44
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.82	0.44
32:2a:1203:C:H2'	32:2a:1204:A:O4'	2.17	0.44
34:2c:59:ARG:H	41:2j:92:THR:HG23	1.82	0.44
35:2d:118:ARG:HG2	35:2d:136:PRO:HB3	1.99	0.44
39:2h:120:THR:OG1	39:2h:122:ARG:HB3	2.18	0.44
1:1A:69:C:O2	1:1A:73:A:O2'	2.31	0.44
7:1H:101:ARG:NH1	7:1H:122:THR:HA	2.31	0.44
8:1I:140:LEU:HD22	8:1I:140:LEU:HA	1.78	0.44
9:1N:62:VAL:HG13	9:1N:66:LYS:HD2	1.98	0.44
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	1.99	0.44
32:1a:96:U:H2'	32:1a:97:G:C8	2.53	0.44
32:1a:765:G:H5"	32:1a:766:A:OP1	2.17	0.44
39:1h:95:VAL:HG12	39:1h:99:GLU:HG3	1.98	0.44
40:1i:12:GLU:O	40:1i:68:GLY:N	2.50	0.44
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	1.98	0.44
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.82	0.44
45:1n:26:ARG:HD3	45:1n:43:CYS:HB3	1.98	0.44
47:1p:50:LYS:HA	47:1p:50:LYS:NZ	2.32	0.44
1:2A:84:A:H5'	20:2Y:8:LYS:HB3	2.00	0.44
1:2A:1782:C:H1'	1:2A:2609:U:H5"	1.98	0.44
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.99	0.44
1:2A:2310:A:O5'	1:2A:2310:A:H8	2.00	0.44
1:2A:2493:U:H2'	1:2A:2494:G:O4'	2.18	0.44
5:2F:37:VAL:HG13	5:2F:184:TYR:HD1	1.82	0.44
7:2H:12:PRO:O	7:2H:15:VAL:HG22	2.16	0.44
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.99	0.44
23:21:51:VAL:HG11	23:21:74:VAL:HG21	2.00	0.44
32:2a:735:C:H2'	32:2a:736:C:H6	1.83	0.44
32:2a:1122:U:C2	32:2a:1123:A:C8	3.06	0.44
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.82	0.44
35:2d:108:LEU:HD23	35:2d:108:LEU:HA	1.81	0.44
35:2d:166:LYS:H	35:2d:166:LYS:HG3	1.50	0.44
40:2i:42:ARG:NH1	40:2i:75:ASP:OD2	2.50	0.44
47:2p:4:ILE:HA	47:2p:20:VAL:O	2.17	0.44
50:2s:52:TYR:HA	50:2s:56:GLN:O	2.17	0.44
1:1A:244:A:C2	1:1A:255:A:C4	3.05	0.44
1:1A:518:G:H2'	1:1A:519:U:C6	2.52	0.44
1:1A:551:G:O2'	1:1A:1220:A:N3	2.44	0.44
1:1A:881:G:H2'	1:1A:882:G:O4'	2.17	0.44
1:1A:2291:U:OP1	1:1A:2380:C:O2'	2.29	0.44
1:1A:2756:U:H1'	1:1A:2757:A:H5"	1.98	0.44
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	2.00	0.44
9:1N:62:VAL:HG11	9:1N:66:LYS:HB2	1.98	0.44
11:1P:79:ARG:NH2	62:1P:310:HOH:O	2.50	0.44
16:1U:17:ILE:HG13	16:1U:32:PHE:HE1	1.82	0.44
32:1a:181:G:H4'	32:1a:182:U:H5'	1.99	0.44
44:1m:86:CYS:HB2	50:1s:73:GLU:HB3	1.99	0.44
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.41	0.44
53:1y:46:GLN:HE21	53:1y:46:GLN:HB3	1.62	0.44
1:2A:335:C:H4'	20:2Y:73:ARG:HD2	1.98	0.44
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.51	0.44
1:2A:2019:A:N7	27:25:9:LYS:HE2	2.31	0.44
1:2A:2103:C:O2	1:2A:2187:G:N1	2.50	0.44
1:2A:2316:C:H2'	1:2A:2317:C:C6	2.53	0.44
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:178:PRO:HB2	5:2F:201:VAL:CG2	2.48	0.44
5:2F:195:ASP:OD1	5:2F:196:LEU:N	2.50	0.44
6:2G:80:PHE:O	6:2G:82:LEU:N	2.48	0.44
6:2G:137:GLU:HG2	6:2G:152:LEU:HD11	1.99	0.44
23:21:44:PRO:HB2	23:21:46:LEU:HD23	1.98	0.44
32:2a:1349:A:C4	32:2a:1350:A:C8	3.05	0.44
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.98	0.44
47:2p:69:THR:HG23	47:2p:72:ARG:NH1	2.33	0.44
1:1A:1057:A:N6	1:1A:1087:G:OP1	2.51	0.44
1:1A:2508:G:O3'	1:1A:2555:U:H5'	2.17	0.44
11:1P:3:LEU:O	11:1P:5:ASP:N	2.50	0.44
12:1Q:21:THR:HG21	12:1Q:101:ARG:N	2.33	0.44
14:1S:59:LYS:H	14:1S:59:LYS:HG3	1.53	0.44
15:1T:16:ARG:NH2	15:1T:18:ASP:OD2	2.51	0.44
28:16:38:LYS:HE3	28:16:38:LYS:HB3	1.86	0.44
32:1a:103:C:O2'	32:1a:172:A:N1	2.43	0.44
32:1a:598:U:H4'	39:1h:94:TYR:CG	2.53	0.44
34:1c:47:LEU:HD13	34:1c:68:VAL:HG11	2.00	0.44
39:1h:49:GLU:O	39:1h:51:VAL:HG23	2.17	0.44
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	1.98	0.44
49:1r:65:ILE:O	49:1r:69:THR:HG23	2.17	0.44
1:2A:300:A:N3	1:2A:319:C:H1'	2.33	0.44
1:2A:465:G:OP1	29:27:12:ARG:NH2	2.45	0.44
1:2A:582:G:OP2	62:2A:3882:HOH:O	2.21	0.44
1:2A:647:G:H8	1:2A:647:G:O5'	2.01	0.44
1:2A:664:C:H2'	1:2A:665:C:C6	2.52	0.44
1:2A:686:G:N2	1:2A:788:A:H61	2.15	0.44
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.00	0.44
1:2A:1952:A:N3	10:2O:22:ILE:HD12	2.32	0.44
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	2.00	0.44
12:2Q:50:ALA:HB1	12:2Q:121:ALA:HB1	2.00	0.44
32:2a:563:A:H2'	32:2a:567:G:C8	2.53	0.44
32:2a:1292:U:H2'	32:2a:1293:G:H8	1.82	0.44
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.51	0.44
37:2f:89:MET:HE1	49:2r:72:ARG:HB3	1.99	0.44
53:2y:13:THR:OG1	53:2y:16:ILE:HG22	2.18	0.44
1:1A:207:A:H2'	1:1A:208:C:O4'	2.17	0.44
1:1A:645:C:H5'	1:1A:646:A:OP2	2.18	0.44
1:1A:1382:G:N7	62:1A:4367:HOH:O	2.36	0.44
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.25	0.44
6:1G:67:LYS:HE3	6:1G:68:PRO:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:88:LEU:HD22	11:1P:95:VAL:HG11	1.99	0.44
32:1a:131:C:H2'	32:1a:132:C:H6	1.82	0.44
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.41	0.44
32:1a:1308:U:H2'	32:1a:1309:G:H8	1.81	0.44
39:1h:44:PHE:HB3	39:1h:80:ILE:HD11	2.00	0.44
40:1i:47:LEU:H	40:1i:47:LEU:HG	1.55	0.44
40:1i:81:ILE:HG13	40:1i:82:ALA:N	2.31	0.44
49:1r:71:LYS:O	49:1r:75:ILE:HG13	2.18	0.44
1:2A:875:G:H5"	21:2Z:149:SER:HB3	2.00	0.44
1:2A:1024:G:C6	1:2A:1025:G:C6	3.06	0.44
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.52	0.44
1:2A:1450:G:H2'	1:2A:1450(A):C:C6	2.53	0.44
1:2A:2201:C:OP1	23:21:48:LYS:NZ	2.40	0.44
2:2B:116:G:OP2	2:2B:116:G:H8	2.00	0.44
32:2a:981:U:H5'	45:2n:21:TYR:CE2	2.53	0.44
32:2a:983:A:H2	32:2a:984:C:C6	2.35	0.44
36:2e:78:HIS:HA	39:2h:105:ARG:CG	2.48	0.44
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.52	0.44
1:1A:2134:A:N6	1:1A:2157:G:H4'	2.33	0.44
1:1A:2240:C:OP2	62:1A:4191:HOH:O	2.21	0.44
1:1A:2506:U:C2	1:1A:2585:U:O4	2.71	0.44
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.16	0.44
7:1H:55:PRO:HG2	7:1H:61:HIS:CE1	2.53	0.44
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.18	0.44
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.56	0.44
32:1a:45:U:H2'	32:1a:46:G:C8	2.53	0.44
32:1a:108:G:C6	51:1t:15:ARG:HG2	2.53	0.44
32:1a:321:A:H2'	32:1a:322:C:C6	2.52	0.44
33:1b:55:PHE:HA	33:1b:58:ILE:HD12	1.99	0.44
34:1c:8:ILE:HG13	34:1c:184:TYR:HB3	1.99	0.44
36:1e:137:GLU:HG3	36:1e:141:GLN:NE2	2.32	0.44
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.67	0.44
45:1n:24:CYS:HB3	45:1n:28:GLY:H	1.82	0.44
51:1t:9:ASN:N	51:1t:9:ASN:OD1	2.50	0.44
1:2A:884:C:H42	1:2A:892:G:H1	1.66	0.44
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.33	0.44
1:2A:2261:C:C6	22:20:16:SER:HB3	2.52	0.44
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.17	0.44
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	1.99	0.44
12:2Q:7:MET:HB2	12:2Q:7:MET:HE3	1.62	0.44
21:2Z:105:VAL:O	21:2Z:141:VAL:HG22	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:167:PRO:C	21:2Z:169:GLU:H	2.25	0.44
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.59	0.44
32:2a:109:A:C6	32:2a:326:G:C6	3.06	0.44
32:2a:1068:G:H8	32:2a:1068:G:OP2	2.00	0.44
33:2b:189:ASP:O	33:2b:191:ASP:N	2.51	0.44
44:2m:108:ARG:HA	44:2m:108:ARG:HD3	1.73	0.44
46:2o:18:PHE:CZ	46:2o:21:ASP:HB2	2.53	0.44
1:1A:30:G:OP1	62:1A:4190:HOH:O	2.21	0.44
1:1A:249:C:O2'	11:1P:64:LYS:NZ	2.20	0.44
1:1A:1083:U:H1'	1:1A:1086:A:H61	1.83	0.44
1:1A:1177:A:O2'	1:1A:1178:C:O4'	2.30	0.44
1:1A:1509(B):A:H2'	1:1A:1510:G:O4'	2.18	0.44
1:1A:2319:G:N2	14:1S:3:ARG:HD3	2.10	0.44
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.83	0.44
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.51	0.44
15:1T:15:VAL:HG13	15:1T:79:HIS:CE1	2.53	0.44
22:10:3:HIS:HB3	62:10:220:HOH:O	2.18	0.44
32:1a:233:C:H2'	32:1a:234:C:H6	1.82	0.44
32:1a:690:G:C6	32:1a:691:G:C6	3.06	0.44
32:1a:1096:C:H2'	32:1a:1097:C:H6	1.83	0.44
32:1a:1310:G:H5'	44:1m:77:ASN:ND2	2.32	0.44
42:1k:50:TYR:CD1	42:1k:54:ARG:HD3	2.53	0.44
42:1k:59:TYR:CZ	42:1k:63:LEU:HD21	2.53	0.44
1:2A:271(E):U:H2'	1:2A:271(F):C:H6	1.82	0.44
1:2A:1069:A:H2'	1:2A:1073:A:N7	2.32	0.44
1:2A:1359:A:H61	1:2A:1372:U:H3	1.66	0.44
1:2A:1655:A:N6	1:2A:2005:A:O2'	2.51	0.44
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.82	0.44
1:2A:2166:G:H2'	1:2A:2167:U:O4'	2.17	0.44
2:2B:17:C:H2'	2:2B:18:G:O4'	2.18	0.44
5:2F:50:SER:HB2	5:2F:94:PRO:HD3	1.99	0.44
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HG	2.00	0.44
23:21:75:GLU:HA	23:21:78:LYS:HE2	1.99	0.44
32:2a:84:U:H2'	32:2a:88:A:N7	2.33	0.44
32:2a:392:G:H2'	32:2a:393:A:H8	1.83	0.44
32:2a:736:C:H2'	32:2a:737:A:C8	2.53	0.44
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.48	0.44
32:2a:1342:C:H1'	40:2i:124:GLN:OE1	2.18	0.44
32:2a:1348:U:H2'	32:2a:1349:A:C8	2.49	0.44
33:2b:152:PHE:CE1	33:2b:155:LEU:HD23	2.52	0.44
39:2h:104:ARG:HD3	39:2h:104:ARG:HA	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.99	0.44
53:2y:93:GLU:H	53:2y:93:GLU:HG3	1.68	0.44
1:1A:453:C:O2	1:1A:457:A:O2'	2.34	0.44
1:1A:773:U:H2'	1:1A:774:A:H5'	1.99	0.44
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.33	0.44
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.18	0.44
1:1A:2590:A:O2'	1:1A:2591:C:H5'	2.18	0.44
1:1A:2619:C:H4'	4:1E:151:TYR:O	2.18	0.44
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	2.00	0.44
62:1N:306:HOH:O	16:1U:101:ARG:NH1	2.51	0.44
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	2.00	0.44
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	2.00	0.44
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.33	0.44
32:1a:812:C:N3	62:1a:4648:HOH:O	2.34	0.44
32:1a:926:G:O3'	53:1y:95:ARG:NH2	2.51	0.44
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.83	0.44
32:1a:1304:G:C6	32:1a:1305:G:N1	2.86	0.44
39:1h:46:LYS:HG3	39:1h:64:LYS:HB2	2.00	0.44
43:1l:33:ARG:HA	43:1l:33:ARG:HD2	1.70	0.44
1:2A:144:C:H5'	19:2X:2:LYS:HE2	2.00	0.44
1:2A:189:G:OP2	23:21:39:LYS:NZ	2.51	0.44
1:2A:286:C:H2'	1:2A:287:C:H6	1.83	0.44
1:2A:1292:U:H2'	1:2A:1293:C:H6	1.83	0.44
1:2A:1312:U:OP2	19:2X:63:LYS:NZ	2.43	0.44
1:2A:1338:G:N7	19:2X:62:LYS:NZ	2.56	0.44
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.32	0.44
1:2A:2351:G:H8	1:2A:2351:G:O5'	2.01	0.44
9:2N:14:VAL:CG1	9:2N:138:LEU:HB2	2.48	0.44
10:2O:113:LYS:HE2	10:2O:113:LYS:HB2	1.77	0.44
12:2Q:58:PHE:O	12:2Q:60:ARG:N	2.44	0.44
22:20:56:ASP:OD1	22:20:58:THR:OG1	2.36	0.44
32:2a:1103:C:H5"	33:2b:98:LEU:HD22	2.00	0.44
32:2a:1126:U:H3	41:2j:40:LEU:HD11	1.83	0.44
35:2d:126:ILE:HG23	35:2d:147:ALA:O	2.18	0.44
38:2g:13:GLN:O	38:2g:24:THR:HG21	2.18	0.44
1:1A:27:G:N2	1:1A:512:G:H1'	2.32	0.43
1:1A:299:A:N1	1:1A:322:A:O2'	2.42	0.43
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.33	0.43
1:1A:1635:G:N2	62:1A:4652:HOH:O	2.50	0.43
1:1A:2359:C:H2'	1:1A:2360:A:O4'	2.18	0.43
19:1X:63:LYS:O	19:1X:64:LYS:HD3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1256:A:H2	32:1a:1277:C:N4	2.16	0.43
33:1b:28:PHE:O	33:1b:32:ILE:HG13	2.18	0.43
33:1b:112:VAL:C	33:1b:114:ARG:H	2.26	0.43
37:1f:75:LEU:O	37:1f:79:LEU:HG	2.18	0.43
40:1i:18:PHE:HD2	40:1i:62:TYR:CD2	2.30	0.43
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.19	0.43
1:2A:2484:G:C2	1:2A:2485:G:C8	3.06	0.43
1:2A:2751:G:H3'	1:2A:2752:C:C6	2.53	0.43
2:2B:8:U:H5'	14:2S:15:ARG:HH12	1.82	0.43
6:2G:58:GLN:C	6:2G:60:LEU:H	2.25	0.43
11:2P:90:ARG:CZ	11:2P:105:LEU:HD11	2.48	0.43
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.58	0.43
21:2Z:128:VAL:HG21	21:2Z:161:VAL:HG12	2.00	0.43
32:2a:164:U:H2'	32:2a:165:C:H6	1.83	0.43
32:2a:437:U:O2'	35:2d:123:HIS:HD2	2.01	0.43
32:2a:772:U:H2'	32:2a:773:G:O4'	2.18	0.43
32:2a:859:A:H2'	32:2a:860:A:O4'	2.19	0.43
32:2a:1220:G:N3	50:2s:54:GLY:HA2	2.33	0.43
33:2b:97:TRP:HE1	33:2b:173:ALA:HB2	1.83	0.43
34:2c:54:ARG:HB2	34:2c:69:HIS:HB2	2.00	0.43
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.18	0.43
40:2i:100:GLY:O	40:2i:103:THR:HG22	2.18	0.43
42:2k:16:SER:O	42:2k:35:PRO:HG3	2.17	0.43
51:2t:39:LYS:HE3	51:2t:39:LYS:HB2	1.77	0.43
1:1A:904:C:H2'	1:1A:905:U:C6	2.53	0.43
1:1A:1045:A:H5'	1:1A:1046:A:H5"	2.00	0.43
1:1A:1086:A:H3'	1:1A:1086:A:N3	2.33	0.43
1:1A:1529:G:C6	1:1A:1530:C:N4	2.86	0.43
1:1A:1963:U:H4'	1:1A:1964:G:OP1	2.17	0.43
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.18	0.43
15:1T:125:ARG:NH1	32:1a:1443:G:H5'	2.34	0.43
18:1W:9:TYR:HA	18:1W:100:THR:HG23	1.99	0.43
32:1a:181:G:O2'	32:1a:183:G:O6	2.33	0.43
32:1a:715:A:H2'	32:1a:716:A:C8	2.54	0.43
32:1a:983:A:H5"	32:1a:984:C:OP2	2.19	0.43
32:1a:1151:A:N3	41:1j:39:PRO:HG3	2.33	0.43
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.99	0.43
37:1f:30:LEU:HB3	37:1f:35:ALA:HB3	1.99	0.43
1:2A:83:G:N1	1:2A:102:G:O2'	2.36	0.43
1:2A:1047:G:H21	1:2A:1111:A:H62	1.66	0.43
1:2A:1065:U:H3	1:2A:1073:A:H61	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2298:A:C2	1:2A:2299:G:H1'	2.53	0.43
1:2A:2330:G:H2'	1:2A:2331:G:O4'	2.19	0.43
1:2A:2429:G:OP1	62:2A:3805:HOH:O	2.21	0.43
6:2G:5:VAL:HG21	6:2G:101:ILE:HG12	1.99	0.43
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.18	0.43
6:2G:97:ASP:HA	6:2G:100:TRP:CD1	2.46	0.43
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.18	0.43
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.47	0.43
32:2a:286:G:O6	62:2a:3212:HOH:O	2.21	0.43
32:2a:397:A:N7	32:2a:547:A:O2'	2.50	0.43
35:2d:65:ARG:HB2	35:2d:75:PHE:CE2	2.53	0.43
39:2h:39:LEU:HD21	39:2h:111:ILE:HD11	1.99	0.43
39:2h:121:ASP:HB2	39:2h:125:ARG:NH2	2.34	0.43
46:2o:21:ASP:CG	46:2o:24:SER:HB3	2.43	0.43
48:2q:29:HIS:CG	48:2q:30:PRO:HD2	2.53	0.43
51:2t:59:ALA:O	51:2t:63:ILE:HG13	2.17	0.43
1:1A:1423:G:H2'	1:1A:1424:G:H8	1.83	0.43
1:1A:2756:U:O2'	62:1A:4179:HOH:O	2.20	0.43
1:1A:2814:C:O2'	27:15:29:THR:OG1	2.27	0.43
4:1E:48:GLN:HE21	4:1E:78:LEU:HD22	1.83	0.43
7:1H:41:MET:HE3	7:1H:41:MET:HB3	1.81	0.43
16:1U:5:LYS:NZ	62:1U:307:HOH:O	2.52	0.43
17:1V:5:VAL:HG21	17:1V:35:LEU:HD23	2.00	0.43
32:1a:961:U:OP2	32:1a:1223:C:O2'	2.19	0.43
53:1y:97:ALA:HA	53:1y:98:ALA:HA	1.59	0.43
1:2A:667:U:O2	30:28:2:PRO:HD2	2.19	0.43
1:2A:1225:G:H4'	17:2V:84:LYS:HG2	2.00	0.43
1:2A:2267:A:H5"	1:2A:2268:A:H5'	2.00	0.43
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.18	0.43
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	2.01	0.43
6:2G:33:ARG:HE	6:2G:162:THR:HG21	1.84	0.43
6:2G:41:GLN:NE2	6:2G:154:GLY:O	2.28	0.43
12:2Q:3:MET:HE2	12:2Q:3:MET:HB3	1.86	0.43
32:2a:41:G:H2'	32:2a:42:G:C8	2.53	0.43
1:1A:456:C:H4'	62:1A:5142:HOH:O	2.18	0.43
1:1A:1229:G:N3	62:1A:4368:HOH:O	2.36	0.43
1:1A:1277:G:O2'	13:1R:24:GLN:HG2	2.18	0.43
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.82	0.43
1:1A:2096:U:H2'	1:1A:2097:C:H6	1.83	0.43
1:1A:2099:U:H3	1:1A:2190:G:H1	1.66	0.43
4:1E:103:ASP:CG	4:1E:168:MET:HE2	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:68:PRO:HB2	6:1G:90:LEU:HB3	1.99	0.43
6:1G:135:LEU:O	6:1G:154:GLY:HA3	2.18	0.43
6:1G:139:LEU:H	6:1G:139:LEU:HD12	1.83	0.43
19:1X:72:LYS:HG2	19:1X:73:ARG:O	2.19	0.43
23:11:52:ARG:HE	23:11:52:ARG:HB3	1.71	0.43
32:1a:841:U:C5	32:1a:848:C:H1'	2.54	0.43
32:1a:986:A:H1'	50:1s:54:GLY:O	2.18	0.43
32:1a:1171:G:H2'	32:1a:1172:C:C6	2.53	0.43
1:2A:180:G:N2	1:2A:215:G:O6	2.52	0.43
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.18	0.43
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.17	0.43
1:2A:2728:U:H2'	1:2A:2729:G:C8	2.54	0.43
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.53	0.43
6:2G:63:ILE:HG22	6:2G:102:PHE:HE1	1.83	0.43
18:2W:12:ILE:O	18:2W:101:SER:OG	2.32	0.43
24:22:24:LEU:HD23	24:22:60:LEU:HD11	1.99	0.43
27:25:48:GLU:O	27:25:60:VAL:HG11	2.18	0.43
32:2a:171:A:H2'	32:2a:172:A:C8	2.52	0.43
32:2a:584:G:OP2	48:2q:87:LYS:HE3	2.19	0.43
32:2a:1121:U:C2'	32:2a:1122:U:H5'	2.48	0.43
32:2a:1288:A:H2	32:2a:1352:C:O2	2.01	0.43
37:2f:97:PHE:CZ	49:2r:61:LYS:HE2	2.53	0.43
40:2i:73:GLN:O	40:2i:77:ILE:HG13	2.18	0.43
47:2p:70:ALA:O	47:2p:74:LEU:HG	2.18	0.43
1:1A:526:A:H2'	62:1A:4566:HOH:O	2.17	0.43
1:1A:657:U:H2'	1:1A:658:C:C6	2.53	0.43
1:1A:2710:C:H2'	1:1A:2711:A:C8	2.53	0.43
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.19	0.43
11:1P:14:LYS:O	62:1P:302:HOH:O	2.21	0.43
15:1T:59:THR:HG21	62:1T:316:HOH:O	2.18	0.43
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.27	0.43
32:1a:626:U:H2'	32:1a:627:G:H8	1.84	0.43
32:1a:1106:G:H5"	34:1c:172:ARG:HG3	2.01	0.43
32:1a:1441:G:HO2'	32:1a:1442:G:N2	2.15	0.43
35:1d:103:ASN:O	35:1d:107:ARG:HG2	2.19	0.43
35:1d:168:ARG:HA	35:1d:168:ARG:HH11	1.82	0.43
35:1d:204:ILE:H	35:1d:204:ILE:HG12	1.48	0.43
44:1m:20:THR:HA	44:1m:25:ILE:O	2.19	0.43
1:2A:910:A:C5	12:2Q:13:GLN:HG3	2.54	0.43
1:2A:911:A:N6	12:2Q:11:LYS:O	2.47	0.43
1:2A:1357:U:H5'	29:27:23:ARG:HH12	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2354:G:H21	22:20:36:ILE:HD11	1.82	0.43
1:2A:2471:C:H2'	1:2A:2472:G:O4'	2.18	0.43
1:2A:2564:A:OP1	1:2A:2648:C:H4'	2.19	0.43
1:2A:2671:A:H2'	1:2A:2672:G:O4'	2.19	0.43
1:2A:2680:C:H5'	4:2E:189:PRO:HA	2.00	0.43
3:2D:166:GLN:NE2	32:2a:712:A:H5"	2.33	0.43
10:2O:88:ASN:HD21	10:2O:92:GLU:HB2	1.84	0.43
20:2Y:13:VAL:HB	20:2Y:72:VAL:HG13	2.00	0.43
32:2a:677:U:H2'	32:2a:678:U:C6	2.54	0.43
32:2a:974:A:H8	32:2a:974:A:OP1	2.01	0.43
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	2.01	0.43
38:2g:113:GLU:HG3	38:2g:118:VAL:HG12	2.00	0.43
1:1A:234:C:H2'	1:1A:235:U:C6	2.53	0.43
1:1A:271(P):C:H2'	1:1A:271(Q):G:O4'	2.19	0.43
1:1A:528:A:O2'	1:1A:529:A:H5'	2.19	0.43
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.18	0.43
1:1A:2114:A:H3'	1:1A:2115:G:H8	1.83	0.43
1:1A:2528:U:H2'	1:1A:2530:A:O5'	2.19	0.43
6:1G:23:PHE:HB2	6:1G:25:TYR:CE2	2.53	0.43
7:1H:72:ILE:O	7:1H:76:VAL:HG23	2.19	0.43
8:1I:27:ARG:HD2	23:11:71:TYR:CE2	2.53	0.43
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.66	0.43
29:17:23:ARG:HG3	29:17:24:THR:HG23	1.99	0.43
32:1a:679:C:H2'	32:1a:680:C:C6	2.54	0.43
32:1a:731:G:H5'	32:1a:766:A:H4'	2.00	0.43
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.47	0.43
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.54	0.43
43:1l:34:ARG:HD3	43:1l:105:TYR:CE2	2.53	0.43
47:1p:19:ILE:HD12	47:1p:19:ILE:HA	1.69	0.43
1:2A:58:G:O2'	1:2A:73:A:N1	2.39	0.43
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.17	0.43
1:2A:2436:G:N3	1:2A:2598:A:H2	2.16	0.43
12:2Q:41:TRP:HB3	12:2Q:94:VAL:HB	2.00	0.43
16:2U:61:TRP:CZ2	16:2U:93:LYS:HG3	2.54	0.43
26:24:44:THR:C	26:24:46:GLN:H	2.25	0.43
28:26:13:CYS:SG	28:26:47:THR:HG21	2.59	0.43
32:2a:300:A:H2'	32:2a:301:G:O4'	2.18	0.43
32:2a:460:G:H3'	32:2a:461:A:H5"	1.99	0.43
32:2a:718:G:H5'	42:2k:117:ASN:OD1	2.18	0.43
32:2a:768:A:H4'	32:2a:1523:G:N2	2.34	0.43
32:2a:786:G:C2	32:2a:797:C:C2	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1039:C:H2'	32:2a:1040:U:O4'	2.19	0.43
35:2d:22:LYS:HD2	61:2d:501:SF4:S3	2.59	0.43
35:2d:170:VAL:HG12	35:2d:174:LEU:HB2	2.01	0.43
37:2f:22:GLU:OE1	37:2f:84:ASN:ND2	2.33	0.43
1:1A:919:G:N2	1:1A:2269:A:OP2	2.51	0.43
1:1A:1171:G:H3'	1:1A:1173:G:H5'	2.00	0.43
1:1A:1801:G:OP2	3:1D:154:LYS:HE2	2.18	0.43
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.54	0.43
1:1A:2521:C:C4	1:1A:2522:U:C4	3.06	0.43
3:1D:37:LEU:HD12	3:1D:62:TYR:HB2	1.99	0.43
4:1E:178:GLU:H	4:1E:178:GLU:CD	2.27	0.43
12:1Q:109:VAL:HG22	12:1Q:113:GLN:CD	2.44	0.43
13:1R:24:GLN:NE2	62:1R:309:HOH:O	2.51	0.43
32:1a:227:G:H2'	32:1a:228:A:O4'	2.18	0.43
32:1a:501:C:H2'	32:1a:502:G:H8	1.83	0.43
32:1a:922:G:C6	32:1a:923:A:C6	3.07	0.43
32:1a:928:G:O2'	32:1a:1533:C:OP1	2.34	0.43
32:1a:1244:C:H2'	32:1a:1245:A:C8	2.52	0.43
40:1i:13:ALA:HB2	40:1i:68:GLY:HA3	2.01	0.43
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.19	0.43
47:1p:19:ILE:HG22	47:1p:37:GLY:O	2.19	0.43
53:1y:52:ALA:HB2	53:1y:77:LEU:HD21	2.01	0.43
1:2A:692:C:O2'	3:2D:38:LYS:NZ	2.51	0.43
1:2A:817:C:O2'	1:2A:839:U:H5"	2.19	0.43
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.51	0.43
1:2A:2695:C:H2'	1:2A:2696:U:H6	1.83	0.43
3:2D:133:LEU:HB3	3:2D:173:VAL:HG21	2.00	0.43
6:2G:9:ARG:O	6:2G:13:GLU:HB2	2.18	0.43
10:2O:29:ASN:N	10:2O:29:ASN:OD1	2.50	0.43
15:2T:28:VAL:HG22	15:2T:88:ILE:HD13	2.00	0.43
17:2V:31:ALA:O	17:2V:61:VAL:HG22	2.19	0.43
20:2Y:35:TYR:CE2	20:2Y:69:ALA:HB3	2.54	0.43
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.18	0.43
20:2Y:67:LEU:HD23	20:2Y:67:LEU:HA	1.77	0.43
36:2e:40:ARG:HG2	36:2e:68:GLU:OE1	2.19	0.43
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	2.00	0.43
1:1A:1006:C:O2'	9:1N:106:MET:HB3	2.19	0.43
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.99	0.43
1:1A:1721:G:C2	1:1A:1739:U:OP2	2.72	0.43
1:1A:1721:G:H2'	1:1A:1740:G:O6	2.19	0.43
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:146:GLU:HB2	3:1D:189:CYS:HB3	2.00	0.43
5:1F:135:LYS:HB2	5:1F:138:GLU:CD	2.44	0.43
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.38	0.43
15:1T:88:ILE:HG21	15:1T:91:ARG:CZ	2.49	0.43
16:1U:79:PHE:CE2	16:1U:83:LEU:HD11	2.54	0.43
19:1X:95:LEU:H	19:1X:95:LEU:HD12	1.82	0.43
27:15:57:VAL:HG12	27:15:58:LEU:HD23	1.99	0.43
32:1a:747:C:H3'	32:1a:748:C:H6	1.82	0.43
32:1a:1289:A:P	52:1u:10:ARG:HH22	2.42	0.43
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.18	0.43
36:1e:94:ALA:HB1	36:1e:98:THR:HG21	2.00	0.43
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.56	0.43
42:1k:103:LEU:HD23	42:1k:103:LEU:HA	1.89	0.43
44:1m:27:LYS:HE3	44:1m:27:LYS:HB3	1.85	0.43
44:1m:60:VAL:HG22	44:1m:64:TRP:HZ3	1.83	0.43
50:1s:40:ILE:H	50:1s:40:ILE:HG12	1.30	0.43
50:1s:60:VAL:HG21	50:1s:74:PHE:HB3	2.00	0.43
1:2A:1364:G:N7	23:21:3:LYS:HD2	2.33	0.43
1:2A:2028:U:H2'	1:2A:2029:G:O4'	2.19	0.43
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.54	0.43
1:2A:2503:2MA:H4'	1:2A:2504:U:OP1	2.19	0.43
3:2D:142:VAL:HG23	3:2D:193:VAL:HA	2.01	0.43
10:2O:64:ARG:HB2	10:2O:79:PHE:CD2	2.54	0.43
21:2Z:4:ARG:NH2	21:2Z:66:SER:HB2	2.33	0.43
23:21:20:ARG:NH1	62:21:202:HOH:O	2.24	0.43
32:2a:187:C:O2'	51:2t:89:ARG:HD3	2.18	0.43
32:2a:448:A:OP2	32:2a:485:G:N2	2.29	0.43
32:2a:735:C:H2'	32:2a:736:C:C6	2.54	0.43
34:2c:5:ILE:HG12	34:2c:6:HIS:N	2.34	0.43
53:2y:78:ILE:H	53:2y:78:ILE:HD12	1.84	0.43
1:1A:77:C:OP1	24:12:59:ARG:HD3	2.19	0.43
1:1A:396:G:H1'	23:11:42:GLN:HB3	2.00	0.43
1:1A:671:C:O2'	1:1A:672:C:H5'	2.19	0.43
2:1B:78:A:C2	2:1B:100:A:C4	3.07	0.43
2:1B:84:C:OP1	25:13:15:TYR:OH	2.26	0.43
2:1B:90:A:C5	2:1B:91:C:H1'	2.54	0.43
3:1D:2:ALA:O	3:1D:20:ASP:HB3	2.19	0.43
5:1F:150:GLY:HA2	5:1F:172:TRP:CE3	2.54	0.43
21:1Z:118:GLN:N	21:1Z:173:ALA:O	2.50	0.43
26:14:49:PHE:HD1	26:14:49:PHE:HA	1.74	0.43
32:1a:275:G:H5'	48:1q:14:LYS:HD2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:587:G:OP1	39:1h:92:ARG:NH2	2.52	0.43
32:1a:630:G:H2'	32:1a:631:G:O4'	2.18	0.43
32:1a:1004:A:H8	32:1a:1005:A:H1'	1.84	0.43
32:1a:1289:A:N1	32:1a:1371:G:O2'	2.41	0.43
32:1a:1362:C:H2'	32:1a:1363:C:H5"	2.00	0.43
41:1j:45:ARG:HB3	41:1j:65:LEU:HB3	1.99	0.43
47:1p:74:LEU:O	47:1p:79:VAL:HG13	2.19	0.43
1:2A:631:A:H1'	11:2P:66:GLY:HA2	2.00	0.43
1:2A:636:G:C4	11:2P:115:LEU:HD21	2.54	0.43
1:2A:882:G:H1	1:2A:894:C:H42	1.66	0.43
1:2A:1332:G:OP1	62:2A:3812:HOH:O	2.22	0.43
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.54	0.43
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.31	0.43
6:2G:64:THR:OG1	6:2G:94:LEU:HD21	2.19	0.43
6:2G:133:LEU:HD11	6:2G:157:ILE:HD12	2.01	0.43
23:21:21:ARG:HD3	23:21:35:THR:HG21	2.00	0.43
32:2a:397:A:H3'	32:2a:397:A:N3	2.33	0.43
32:2a:565:U:H3'	32:2a:566:G:H2'	2.01	0.43
32:2a:875:C:O2'	39:2h:14:ARG:NE	2.41	0.43
32:2a:1040:U:H2'	32:2a:1041:A:O4'	2.19	0.43
42:2k:20:TYR:CE1	42:2k:83:ILE:HD12	2.54	0.43
45:2n:3:ARG:O	45:2n:7:ILE:HG23	2.19	0.43
46:2o:29:VAL:O	46:2o:33:THR:OG1	2.32	0.43
50:2s:20:LEU:HA	50:2s:23:ASN:HB2	2.00	0.43
1:1A:1140:C:O3'	9:1N:25:ARG:NH1	2.52	0.43
58:1A:4030:ARG:HG2	62:1A:6979:HOH:O	2.18	0.43
6:1G:50:ALA:C	6:1G:52:ILE:H	2.27	0.43
7:1H:147:ASN:OD1	62:1H:301:HOH:O	2.21	0.43
26:14:15:ILE:HB	26:14:32:TYR:CD1	2.53	0.43
32:1a:963:G:H5'	62:1a:4814:HOH:O	2.18	0.43
32:1a:1029:C:H5'	32:1a:1030:C:OP2	2.19	0.43
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.53	0.43
32:1a:1198:G:OP1	62:1a:4614:HOH:O	2.21	0.43
33:1b:162:ILE:HD12	33:1b:164:VAL:HG23	2.00	0.43
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	2.00	0.43
42:1k:33:THR:HG22	42:1k:39:PRO:HA	1.99	0.43
50:1s:12:ASP:HB3	50:1s:14:HIS:CD2	2.54	0.43
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.53	0.43
1:2A:116:C:H2'	1:2A:117:G:O4'	2.19	0.43
1:2A:208:C:H2'	1:2A:209:C:C6	2.54	0.43
1:2A:493:G:H2'	1:2A:494:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.41	0.43
1:2A:1449:A:H2'	1:2A:1450:G:O4'	2.18	0.43
1:2A:1587:A:H2'	1:2A:1588:C:C6	2.53	0.43
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.41	0.43
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.19	0.43
7:2H:47:GLU:H	7:2H:47:GLU:HG2	1.71	0.43
28:26:14:THR:OG1	28:26:48:VAL:O	2.30	0.43
32:2a:189:G:C6	32:2a:189(L):G:C6	3.07	0.43
32:2a:321:A:C2	32:2a:333:G:C2	3.07	0.43
32:2a:451:A:N6	32:2a:480:U:H2'	2.34	0.43
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.54	0.43
32:2a:1238:A:OP2	62:2a:3213:HOH:O	2.21	0.43
35:2d:108:LEU:HD23	35:2d:170:VAL:HG11	2.01	0.43
38:2g:108:ALA:C	38:2g:110:GLN:H	2.27	0.43
44:2m:13:LYS:HE3	44:2m:13:LYS:HB3	1.87	0.43
1:1A:483:A:H3'	1:1A:484:C:C6	2.54	0.42
1:1A:1080:C:H2'	1:1A:1081:U:C6	2.54	0.42
1:1A:1267:U:OP2	1:1A:2012:G:N1	2.28	0.42
1:1A:1301:A:C8	1:1A:1303:G:C8	3.07	0.42
1:1A:2090:G:N2	23:11:45:ASN:OD1	2.42	0.42
1:1A:2103:C:H1'	1:1A:2187:G:N2	2.34	0.42
1:1A:2125:G:O2'	1:1A:2126:A:H5'	2.18	0.42
1:1A:2206:G:O2'	1:1A:2207:G:OP1	2.35	0.42
1:1A:2518:A:N3	1:1A:2518:A:H2'	2.34	0.42
1:1A:2695:C:O2'	1:1A:2696:U:H5'	2.18	0.42
5:1F:132:VAL:HG22	5:1F:163:VAL:HG22	2.01	0.42
21:1Z:124:ILE:HD12	21:1Z:124:ILE:HA	1.93	0.42
24:12:10:LEU:HD23	24:12:10:LEU:HA	1.84	0.42
26:14:16:CYS:HB2	26:14:36:CYS:HB3	2.01	0.42
32:1a:142:G:H2'	32:1a:143:A:H8	1.83	0.42
35:1d:8:VAL:HG22	35:1d:21:LEU:HD13	2.00	0.42
35:1d:20:TYR:HA	35:1d:26:CYS:SG	2.59	0.42
44:1m:81:LEU:O	44:1m:89:GLY:HA3	2.19	0.42
46:1o:31:LEU:HD23	46:1o:31:LEU:HA	1.74	0.42
53:1y:55:ASN:OD1	53:1y:60:VAL:HG12	2.19	0.42
1:2A:176:G:O2'	1:2A:177:G:H5'	2.19	0.42
1:2A:249:C:HO2'	11:2P:64:LYS:HZ2	1.57	0.42
1:2A:740:U:H2'	1:2A:741:G:C8	2.54	0.42
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.54	0.42
1:2A:1289:C:H2'	1:2A:1290:C:H6	1.84	0.42
1:2A:1341:U:O4'	19:2X:57:LEU:HD23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.54	0.42
1:2A:2370:G:C6	1:2A:2371:G:C6	3.07	0.42
2:2B:63:G:OP1	62:2B:304:HOH:O	2.22	0.42
2:2B:83:G:H4'	25:23:52:HIS:CG	2.54	0.42
3:2D:118:VAL:HG22	3:2D:119:ALA:H	1.84	0.42
3:2D:166:GLN:HE22	32:2a:712:A:H5"	1.84	0.42
32:2a:542:G:H5'	35:2d:41:GLY:HA3	2.00	0.42
32:2a:868:C:H2'	32:2a:869:G:O4'	2.19	0.42
32:2a:1067:A:O2'	32:2a:1093:A:O3'	2.34	0.42
35:2d:57:ARG:HG2	35:2d:202:LEU:O	2.19	0.42
36:2e:51:VAL:O	36:2e:55:VAL:HG23	2.19	0.42
38:2g:74:GLU:O	38:2g:89:MET:N	2.51	0.42
1:1A:391:G:H1'	1:1A:411:G:O4'	2.19	0.42
1:1A:566:U:H5"	11:1P:29:LYS:HE3	2.02	0.42
1:1A:868:U:C4	1:1A:869:G:N7	2.87	0.42
2:1B:31:C:H4'	6:1G:29:TRP:CH2	2.53	0.42
3:1D:137:PRO:O	3:1D:140:THR:HG23	2.19	0.42
16:1U:59:ARG:O	16:1U:63:VAL:HG23	2.19	0.42
23:11:23:LYS:HE3	23:11:23:LYS:HB2	1.86	0.42
32:1a:21:G:H2'	32:1a:22:G:C8	2.54	0.42
32:1a:756:C:H2'	32:1a:757:U:O4'	2.19	0.42
32:1a:1036:G:H2'	32:1a:1036:G:N3	2.34	0.42
34:1c:15:THR:OG1	34:1c:178:LEU:O	2.37	0.42
34:1c:62:ASP:O	34:1c:97:LYS:HB2	2.20	0.42
45:1n:4:LYS:O	45:1n:7:ILE:HG12	2.18	0.42
53:1y:54:ILE:O	53:1y:61:LEU:N	2.38	0.42
1:2A:42:G:H2'	1:2A:43:A:O4'	2.20	0.42
6:2G:5:VAL:HG12	6:2G:8:LYS:HE2	2.01	0.42
7:2H:90:LYS:HD2	7:2H:163:TYR:CD2	2.54	0.42
12:2Q:55:VAL:HG22	21:2Z:183:LEU:HD11	2.01	0.42
20:2Y:31:LEU:HB2	20:2Y:36:ALA:HB3	2.01	0.42
21:2Z:2:GLU:HG2	21:2Z:56:VAL:HB	2.01	0.42
21:2Z:45:ASP:O	21:2Z:49:ARG:HG3	2.19	0.42
21:2Z:182:LYS:HB3	21:2Z:182:LYS:HE2	1.88	0.42
32:2a:1117:G:H5"	40:2i:104:ARG:CZ	2.49	0.42
32:2a:1277:C:HO2'	32:2a:1279:A:H8	1.59	0.42
32:2a:1286:A:N6	32:2a:1354:C:H5"	2.34	0.42
32:2a:1326:C:H5"	52:2u:12:LYS:NZ	2.34	0.42
32:2a:1509:C:H2'	32:2a:1510:U:O4'	2.19	0.42
32:2a:1531:A:H8	32:2a:1531:A:O5'	2.02	0.42
34:2c:6:HIS:HD2	34:2c:7:PRO:HD2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.34	0.42
41:2j:56:HIS:CD2	41:2j:56:HIS:N	2.87	0.42
41:2j:57:LYS:HE3	41:2j:60:ARG:NH2	2.34	0.42
44:2m:40:ASN:HB3	44:2m:43:THR:HG23	2.00	0.42
1:1A:218:A:C2	1:1A:235:U:H4'	2.55	0.42
1:1A:478:A:N1	1:1A:500:G:H4'	2.34	0.42
1:1A:1062:G:H8	1:1A:1062:G:OP2	2.02	0.42
1:1A:1857:G:C6	1:1A:1858:G:C6	3.07	0.42
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.54	0.42
1:1A:2635:C:O2'	4:1E:80:GLU:OE2	2.36	0.42
19:1X:90:GLU:HA	19:1X:93:GLU:HB2	2.01	0.42
33:1b:209:ARG:HD3	33:1b:209:ARG:HA	1.76	0.42
42:1k:104:GLN:O	42:1k:106:LYS:N	2.51	0.42
44:1m:57:ARG:O	44:1m:61:GLU:HG3	2.19	0.42
47:1p:67:THR:HG22	47:1p:68:ASP:H	1.84	0.42
1:2A:328:U:H4'	20:2Y:68:HIS:CE1	2.54	0.42
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.20	0.42
1:2A:608:A:H2'	1:2A:609:A:C8	2.54	0.42
1:2A:673:C:H5"	5:2F:81:PRO:HD2	2.01	0.42
1:2A:1137:G:H2'	1:2A:1138:G:O4'	2.20	0.42
1:2A:2200:C:O2	1:2A:2226:C:N4	2.52	0.42
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	2.01	0.42
2:2B:29:A:OP2	14:2S:32:LEU:HB2	2.19	0.42
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.19	0.42
7:2H:90:LYS:NZ	7:2H:159:GLU:OE2	2.52	0.42
8:2I:77:LEU:HD13	8:2I:101:LEU:HD23	2.02	0.42
12:2Q:51:ARG:HD3	12:2Q:66:ILE:HD11	2.02	0.42
15:2T:125:ARG:NH1	32:2a:1443:G:H5'	2.35	0.42
23:21:52:ARG:HA	23:21:56:GLN:O	2.18	0.42
32:2a:340:U:H2'	32:2a:341:C:C6	2.53	0.42
32:2a:841:U:H6	32:2a:841:U:P	2.43	0.42
32:2a:1068:G:N7	32:2a:1094:G:C8	2.87	0.42
32:2a:1320:C:C1'	50:2s:73:GLU:HG2	2.49	0.42
34:2c:47:LEU:HD22	34:2c:68:VAL:HG11	2.01	0.42
35:2d:110:PHE:N	35:2d:110:PHE:CD1	2.87	0.42
37:2f:73:ASN:HD22	37:2f:73:ASN:HA	1.64	0.42
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	2.00	0.42
47:2p:26:ARG:NH1	47:2p:31:LYS:HB3	2.35	0.42
51:2t:47:GLY:HA2	51:2t:48:LYS:CB	2.49	0.42
53:2y:60:VAL:HG22	53:2y:62:VAL:HG12	2.01	0.42
1:1A:637:A:OP1	11:1P:133:SER:OG	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1006:C:C2	1:1A:1138:G:N2	2.87	0.42
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.54	0.42
14:1S:27:SER:O	14:1S:37:ALA:HA	2.19	0.42
22:10:47:PRO:HD3	22:10:59:LEU:HD11	2.02	0.42
32:1a:840:C:OP2	32:1a:840:C:H6	2.02	0.42
32:1a:1292:U:H2'	32:1a:1293:G:H8	1.84	0.42
33:1b:121:LEU:HA	33:1b:126:GLU:HG3	2.01	0.42
37:1f:8:ILE:HD13	37:1f:26:ILE:HD13	2.02	0.42
37:1f:36:ARG:HB3	37:1f:36:ARG:NH1	2.34	0.42
50:1s:3:ARG:HG3	50:1s:4:SER:N	2.33	0.42
51:1t:38:LYS:HB2	51:1t:38:LYS:HE3	1.91	0.42
53:1y:3:MET:HG3	53:1y:37:PRO:HG2	2.01	0.42
1:2A:458:G:C8	29:27:37:LYS:HG2	2.54	0.42
1:2A:921:G:C6	1:2A:922:U:C4	3.07	0.42
1:2A:1269:A:H2'	1:2A:1270:C:C6	2.55	0.42
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.54	0.42
1:2A:2379:G:HO2'	14:2S:17:ARG:HH12	1.57	0.42
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.19	0.42
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.85	0.42
5:2F:164:ARG:O	5:2F:168:ARG:HG3	2.18	0.42
20:2Y:44:ILE:H	20:2Y:44:ILE:HD12	1.84	0.42
32:2a:437:U:O2'	35:2d:125:HIS:HE1	2.02	0.42
32:2a:570:G:H1'	32:2a:820:U:C4	2.54	0.42
32:2a:922:G:C6	32:2a:923:A:C6	3.07	0.42
32:2a:1343:G:C2	32:2a:1344:C:C2	3.07	0.42
33:2b:70:PHE:HB3	33:2b:81:VAL:CG2	2.50	0.42
37:2f:33:TYR:CE2	37:2f:75:LEU:HA	2.55	0.42
38:2g:24:THR:O	38:2g:27:ILE:HG13	2.19	0.42
40:2i:70:LYS:O	40:2i:74:ILE:HG13	2.19	0.42
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.55	0.42
1:1A:784:A:C8	1:1A:792:G:C5	3.08	0.42
1:1A:1131:G:H21	9:1N:73:THR:CG2	2.32	0.42
1:1A:1423:G:H2'	1:1A:1424:G:C8	2.54	0.42
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.42	0.42
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.18	0.42
3:1D:85:ASP:HB2	3:1D:92:ILE:HG12	2.01	0.42
9:1N:7:LYS:O	9:1N:8:GLN:C	2.63	0.42
32:1a:102:G:O2'	32:1a:151:A:N3	2.50	0.42
32:1a:509:A:N3	32:1a:543:C:O2'	2.44	0.42
34:1c:6:HIS:HB3	45:1n:49:HIS:ND1	2.35	0.42
39:1h:29:SER:HB3	39:1h:32:LYS:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	2.00	0.42
44:1m:82:MET:HE3	44:1m:93:ARG:HG3	2.00	0.42
1:2A:856:C:H2'	1:2A:857:C:C6	2.55	0.42
1:2A:960:A:H5"	1:2A:961:C:OP2	2.19	0.42
1:2A:2051:A:H8	1:2A:2051:A:OP2	2.01	0.42
6:2G:32:PRO:HB2	6:2G:172:LEU:HD22	2.01	0.42
10:2O:26:LYS:NZ	10:2O:37:ASP:OD2	2.44	0.42
11:2P:47:ASP:OD2	11:2P:49:ARG:NH2	2.53	0.42
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.54	0.42
17:2V:52:VAL:CG2	17:2V:55:ALA:HB3	2.50	0.42
21:2Z:31:ARG:HB2	21:2Z:32:HIS:CD2	2.55	0.42
31:29:7:VAL:HG21	31:29:36:GLN:HB2	2.01	0.42
32:2a:66:G:H8	32:2a:66:G:OP1	2.02	0.42
32:2a:824:C:H2'	32:2a:825:G:C8	2.54	0.42
32:2a:950:U:H2'	32:2a:951:G:H8	1.85	0.42
32:2a:1058:G:H2'	32:2a:1059:C:C6	2.54	0.42
32:2a:1117:G:H5"	40:2i:104:ARG:NH1	2.34	0.42
32:2a:1136:U:OP2	32:2a:1137:C:N4	2.52	0.42
38:2g:69:VAL:HG21	38:2g:104:LEU:HD11	2.00	0.42
40:2i:116:LYS:HA	40:2i:123:PRO:HD3	2.02	0.42
49:2r:68:LYS:HE2	49:2r:68:LYS:HB2	1.93	0.42
53:2y:3:MET:HB2	53:2y:37:PRO:HG2	2.01	0.42
1:1A:493:G:H2'	1:1A:494:G:O4'	2.20	0.42
1:1A:690:G:H2'	1:1A:691:C:C6	2.55	0.42
1:1A:1025:G:O2'	62:1A:4108:HOH:O	2.12	0.42
1:1A:1750:G:O2'	1:1A:2860:A:N1	2.49	0.42
12:1Q:12:GLN:NE2	12:1Q:73:PRO:HD2	2.35	0.42
15:1T:98:LYS:N	62:1T:304:HOH:O	2.44	0.42
32:1a:194:C:H2'	32:1a:195:A:H5"	2.01	0.42
32:1a:621:A:H2'	32:1a:622:A:C8	2.55	0.42
32:1a:636:U:H2'	32:1a:637:G:C8	2.54	0.42
32:1a:1411:C:H2'	32:1a:1412:C:C6	2.54	0.42
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.55	0.42
47:1p:6:LEU:HB3	47:1p:17:TYR:HB3	2.01	0.42
53:1y:30:TRP:CZ2	53:1y:86:ASN:HB2	2.55	0.42
53:1y:50:ALA:HB1	53:1y:77:LEU:HD22	2.01	0.42
1:2A:270:A:OP2	1:2A:271(X):G:N1	2.43	0.42
1:2A:971:C:H2'	1:2A:972:G:O4'	2.20	0.42
1:2A:997:G:OP1	16:2U:92:ARG:NH1	2.49	0.42
1:2A:1702:G:H2'	1:2A:1703:G:O4'	2.19	0.42
1:2A:2147:G:C8	1:2A:2147:G:H3'	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:53:ARG:HB3	15:2T:53:ARG:NH1	2.34	0.42
21:2Z:16:SER:HA	62:2Z:301:HOH:O	2.19	0.42
23:21:85:LEU:HG	23:21:89:GLU:HB3	2.02	0.42
32:2a:179:A:H2'	32:2a:180:U:H6	1.85	0.42
32:2a:367:U:O4'	32:2a:394:G:N2	2.53	0.42
32:2a:553:A:H2'	32:2a:554:C:C6	2.54	0.42
32:2a:565:U:OP2	32:2a:566:G:O2'	2.27	0.42
32:2a:986:A:H1'	50:2s:54:GLY:O	2.19	0.42
32:2a:1038:C:O5'	32:2a:1038:C:H6	2.02	0.42
44:2m:90:LEU:HD23	44:2m:93:ARG:HH21	1.85	0.42
48:2q:10:VAL:HG13	48:2q:19:VAL:HB	2.02	0.42
1:1A:1039:G:H1	1:1A:1116:C:N4	2.18	0.42
1:1A:1079:C:N4	1:1A:1080:C:N3	2.67	0.42
1:1A:2197:U:H1'	1:1A:2198:A:C8	2.54	0.42
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.52	0.42
5:1F:140:LEU:HD12	5:1F:140:LEU:HA	1.71	0.42
9:1N:131:GLN:H	9:1N:131:GLN:HG2	1.65	0.42
11:1P:81:GLN:NE2	11:1P:106:LEU:HA	2.34	0.42
21:1Z:79:ARG:NE	62:1Z:401:HOH:O	2.27	0.42
21:1Z:135:GLU:O	21:1Z:136:PHE:HB3	2.20	0.42
24:12:3:LEU:HD23	24:12:3:LEU:HA	1.82	0.42
24:12:51:ARG:O	24:12:55:ARG:HG2	2.20	0.42
25:13:4:LEU:O	25:13:36:VAL:HA	2.20	0.42
27:15:45:VAL:HG11	27:15:58:LEU:CD2	2.49	0.42
32:1a:1053:G:H4'	32:1a:1054:C:H3'	2.01	0.42
32:1a:1132:C:H2'	32:1a:1133:G:C8	2.55	0.42
32:1a:1256:A:H62	32:1a:1278:U:C1'	2.33	0.42
38:1g:16:LEU:HD11	40:1i:45:ALA:HB2	2.02	0.42
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.52	0.42
1:2A:630:G:N2	1:2A:633:A:OP2	2.46	0.42
1:2A:690:G:H2'	1:2A:691:C:C6	2.54	0.42
1:2A:806:C:O2	1:2A:2444:G:O2'	2.37	0.42
1:2A:927:G:H2'	1:2A:928:G:O4'	2.19	0.42
1:2A:958:U:OP2	62:2A:3887:HOH:O	2.22	0.42
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.35	0.42
1:2A:1772:G:O6	59:2A:3735:MPD:H32	2.19	0.42
1:2A:1993:U:H2'	1:2A:1994:C:O4'	2.20	0.42
1:2A:2184:G:H2'	1:2A:2185:C:O4'	2.19	0.42
1:2A:2652:C:H2'	1:2A:2653:U:O4'	2.19	0.42
1:2A:2675:A:H5"	10:2O:31:LYS:HE2	2.00	0.42
2:2B:1:U:H2'	2:2B:2:C:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:30:C:H2'	2:2B:31:C:O4'	2.19	0.42
5:2F:118:ALA:O	5:2F:120:GLU:N	2.53	0.42
6:2G:155:MET:HE2	6:2G:155:MET:HB3	1.86	0.42
7:2H:9:ILE:N	7:2H:50:VAL:O	2.37	0.42
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	2.00	0.42
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	2.01	0.42
10:2O:64:ARG:HD2	10:2O:81:ASP:OD1	2.19	0.42
18:2W:11:ARG:NH1	18:2W:99:ARG:O	2.52	0.42
25:23:7:LYS:HG3	25:23:34:GLU:HG2	2.02	0.42
32:2a:560:U:OP2	32:2a:566:G:N2	2.47	0.42
37:2f:82:ARG:HB2	37:2f:85:VAL:HG23	2.01	0.42
1:1A:214:G:H1'	1:1A:216:A:O2'	2.19	0.42
1:1A:1027:A:C2	1:1A:2488:A:H5'	2.55	0.42
1:1A:1275:A:N1	1:1A:1295:C:O2'	2.50	0.42
1:1A:2164:C:H5	1:1A:2165:G:C4	2.38	0.42
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.19	0.42
1:1A:2886:G:H2'	1:1A:2887:U:C6	2.55	0.42
4:1E:18:ASP:HB3	15:1T:82:LEU:HD21	2.01	0.42
32:1a:20:U:H2'	32:1a:21:G:O4'	2.19	0.42
32:1a:1032:G:H2'	32:1a:1033:G:O4'	2.20	0.42
32:1a:1400:5MC:N3	53:1y:63:ALA:HA	2.35	0.42
1:2A:324:A:H2'	1:2A:325:G:O4'	2.18	0.42
1:2A:530:G:N1	1:2A:2023:G:OP1	2.45	0.42
1:2A:631:A:N3	1:2A:2415:G:O2'	2.52	0.42
1:2A:904:C:H2'	1:2A:905:U:C6	2.55	0.42
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.33	0.42
1:2A:2072:G:N2	62:2A:4222:HOH:O	2.53	0.42
1:2A:2112:G:H2'	1:2A:2113:U:H6	1.85	0.42
1:2A:2784:C:H2'	1:2A:2785:C:H6	1.85	0.42
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.53	0.42
4:2E:9:VAL:HG13	15:2T:3:ARG:HG2	2.01	0.42
5:2F:187:VAL:HG12	11:2P:3:LEU:HG	2.01	0.42
6:2G:16:ARG:HH21	6:2G:28:VAL:HB	1.85	0.42
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.85	0.42
10:2O:88:ASN:ND2	10:2O:92:GLU:HB2	2.34	0.42
13:2R:29:LEU:HD23	13:2R:29:LEU:HA	1.81	0.42
24:22:23:LYS:HD3	24:22:26:ARG:HH12	1.85	0.42
32:2a:46:G:H2'	32:2a:366:C:C5	2.54	0.42
32:2a:601:C:H2'	32:2a:602:A:H8	1.81	0.42
32:2a:1027:C:H5"	32:2a:1028:C:C5	2.55	0.42
32:2a:1286:A:H2'	32:2a:1287:A:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	2.02	0.42
46:2o:39:LEU:HD12	46:2o:59:MET:HE2	2.01	0.42
46:2o:71:GLN:HE21	46:2o:71:GLN:HB3	1.64	0.42
50:2s:36:ARG:NH1	50:2s:75:ALA:HB3	2.35	0.42
1:1A:1858:G:N2	1:1A:1883:G:H2'	2.34	0.42
1:1A:2102:U:O2	1:1A:2187:G:O6	2.38	0.42
1:1A:2590:A:H2'	1:1A:2591:C:H6	1.84	0.42
2:1B:66:A:N6	2:1B:108:U:H2'	2.33	0.42
5:1F:28:ILE:HD11	5:1F:115:ALA:HB3	2.02	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.50	0.42
6:1G:150:ASP:OD1	6:1G:150:ASP:N	2.53	0.42
32:1a:1159:U:O4	62:1a:4615:HOH:O	2.22	0.42
32:1a:1456:G:O3'	51:1t:39:LYS:NZ	2.51	0.42
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	2.02	0.42
34:1c:15:THR:CG2	34:1c:181:ASN:HA	2.50	0.42
1:2A:879:G:H2'	1:2A:880:G:O4'	2.20	0.42
1:2A:1334:G:OP2	62:2A:3891:HOH:O	2.22	0.42
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.55	0.42
1:2A:2316:C:H2'	1:2A:2317:C:H6	1.85	0.42
22:20:2:ALA:HB3	55:2x:76:8AN:N6	2.34	0.42
32:2a:551:U:H2'	32:2a:552:U:H6	1.84	0.42
32:2a:598:U:H2'	32:2a:599:C:C6	2.55	0.42
32:2a:1103:C:H2'	32:2a:1104:G:O4'	2.20	0.42
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.84	0.42
32:2a:1290:G:OP1	38:2g:35:LYS:NZ	2.53	0.42
34:2c:59:ARG:HG2	34:2c:64:VAL:HA	2.01	0.42
35:2d:22:LYS:O	35:2d:113:SER:HB3	2.19	0.42
1:1A:11:G:H2'	1:1A:12:U:H5'	2.02	0.42
1:1A:139(A):G:O6	62:1A:4192:HOH:O	2.21	0.42
1:1A:234:C:H2'	1:1A:235:U:H6	1.85	0.42
1:1A:582:G:H2'	1:1A:583:G:C8	2.55	0.42
1:1A:586:A:N1	1:1A:809:G:O2'	2.45	0.42
1:1A:1079:C:C4	1:1A:1088:A:C2	3.08	0.42
8:1I:130:TYR:N	8:1I:138:ILE:O	2.48	0.42
27:15:29:THR:O	27:15:30:LEU:HD23	2.20	0.42
32:1a:764:C:H2'	32:1a:765:G:O4'	2.20	0.42
32:1a:1117:G:H4'	40:1i:104:ARG:NH1	2.35	0.42
32:1a:1118:C:H2'	32:1a:1119:C:C6	2.55	0.42
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.20	0.42
36:1e:90:VAL:O	36:1e:120:THR:HA	2.20	0.42
41:1j:78:ASN:C	41:1j:80:LYS:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:1l:24:VAL:HB	43:1l:27:LEU:HD12	2.01	0.42
51:1t:11:SER:O	51:1t:11:SER:OG	2.37	0.42
1:2A:563:G:H21	16:2U:37:GLU:CD	2.28	0.42
1:2A:720:C:H2'	1:2A:721:C:C6	2.54	0.42
1:2A:782:A:OP2	62:2A:3892:HOH:O	2.22	0.42
1:2A:984:A:H5"	1:2A:985:C:H5	1.85	0.42
1:2A:1045:A:H5'	1:2A:1047:G:O4'	2.20	0.42
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.35	0.42
1:2A:1354:A:H3'	1:2A:1355:G:H8	1.84	0.42
1:2A:1489:U:O2'	1:2A:1490:A:H8	2.03	0.42
1:2A:2847:U:OP1	15:2T:98:LYS:NZ	2.47	0.42
2:2B:48:A:H4'	14:2S:95:HIS:CE1	2.55	0.42
2:2B:80:U:H2'	2:2B:81:G:C8	2.55	0.42
3:2D:70:TRP:CZ2	3:2D:150:LYS:HD3	2.55	0.42
5:2F:129:PHE:HA	5:2F:142:TRP:NE1	2.35	0.42
6:2G:126:ASP:OD2	6:2G:128:ARG:N	2.46	0.42
8:2I:52:ARG:HE	8:2I:52:ARG:HB2	1.61	0.42
12:2Q:58:PHE:C	12:2Q:60:ARG:N	2.78	0.42
21:2Z:144:LEU:HD23	21:2Z:144:LEU:HA	1.81	0.42
32:2a:674:G:H8	32:2a:674:G:O5'	2.03	0.42
32:2a:955:U:O2'	50:2s:83:HIS:HD2	2.03	0.42
32:2a:976:G:C8	32:2a:1358:U:C2	3.08	0.42
32:2a:1343:G:O2'	40:2i:121:ARG:HD2	2.20	0.42
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.35	0.42
34:2c:120:VAL:HA	34:2c:123:GLN:HG3	2.01	0.42
39:2h:7:ALA:O	39:2h:11:THR:OG1	2.18	0.42
53:2y:39:ILE:HD13	53:2y:39:ILE:HA	1.87	0.42
1:1A:30:G:H2'	1:1A:31:C:C6	2.55	0.41
1:1A:272(E):G:C2	1:1A:364:C:C2	3.08	0.41
1:1A:614:U:H5'	1:1A:614(C):A:N6	2.35	0.41
1:1A:1268:A:C2	1:1A:2013:A:C4	3.08	0.41
1:1A:1274:A:N3	1:1A:1297:C:H1'	2.35	0.41
1:1A:1799:G:OP1	3:1D:260:ARG:NE	2.40	0.41
1:1A:2189:U:H2'	1:1A:2190:G:H5'	2.01	0.41
2:1B:73:A:C4	2:1B:105:A:C2	3.08	0.41
8:1I:123:LEU:HD23	8:1I:144:VAL:HG12	2.02	0.41
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.53	0.41
23:1l:80:LEU:HB3	23:1l:82:LEU:HG	2.01	0.41
32:1a:1084:G:C5	32:1a:1085:U:C4	3.08	0.41
32:1a:1239:A:H62	32:1a:1299:A:H61	1.67	0.41
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:15:VAL:HG23	33:1b:209:ARG:HD2	2.02	0.41
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.19	0.41
40:1i:53:VAL:HG21	40:1i:85:LEU:HD13	2.02	0.41
1:2A:310:A:H1'	1:2A:311:A:H2'	2.02	0.41
1:2A:852:G:H2'	1:2A:853:G:C8	2.55	0.41
1:2A:2124:G:H1	1:2A:2174:C:H42	1.66	0.41
1:2A:2227:A:O2'	62:2A:3883:HOH:O	2.21	0.41
1:2A:2242:G:H2'	1:2A:2243:U:O4'	2.19	0.41
1:2A:2300:G:C6	1:2A:2301:C:C4	3.08	0.41
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.54	0.41
3:2D:75:ILE:HD13	3:2D:99:ASP:OD2	2.20	0.41
3:2D:155:LEU:HD13	3:2D:177:LEU:HD21	2.02	0.41
6:2G:91:ARG:HG2	6:2G:92:VAL:N	2.35	0.41
12:2Q:38:GLU:HA	12:2Q:99:PRO:HG3	2.02	0.41
20:2Y:7:VAL:HG11	20:2Y:13:VAL:CG1	2.50	0.41
32:2a:148:G:H2'	32:2a:149:A:C8	2.53	0.41
32:2a:1316:G:H2'	32:2a:1318:A:OP2	2.20	0.41
38:2g:33:ASP:OD1	38:2g:33:ASP:N	2.53	0.41
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	2.02	0.41
46:2o:24:SER:O	46:2o:28:GLN:HG3	2.20	0.41
48:2q:53:LEU:HD21	48:2q:85:VAL:HG11	2.01	0.41
49:2r:40:LEU:HB3	49:2r:79:LEU:HD11	2.01	0.41
1:1A:569:U:C4	1:1A:570:G:C6	3.08	0.41
1:1A:1482:G:H2'	1:1A:1484:G:C8	2.55	0.41
1:1A:1649:G:O2'	13:1R:107:ASP:OD2	2.26	0.41
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.20	0.41
1:1A:2171:A:N3	1:1A:2172:U:N3	2.69	0.41
1:1A:2309:A:H2'	1:1A:2310:A:O4'	2.20	0.41
1:1A:2591:C:H2'	1:1A:2592:G:H8	1.83	0.41
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.19	0.41
2:1B:21:G:H2'	2:1B:22:U:H6	1.84	0.41
2:1B:42:C:O2'	6:1G:66:GLN:HG2	2.20	0.41
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.20	0.41
6:1G:112:PRO:HG3	26:14:43:TYR:CE2	2.55	0.41
11:1P:126:VAL:HG22	11:1P:146:VAL:HB	2.02	0.41
18:1W:32:ALA:O	18:1W:36:LEU:HG	2.20	0.41
18:1W:92:ARG:HG2	18:1W:93:ALA:N	2.35	0.41
22:10:55:ARG:CZ	22:10:55:ARG:HB2	2.50	0.41
23:11:6:GLU:HG3	23:11:61:ARG:O	2.19	0.41
23:11:73:LEU:HD11	23:11:98:LEU:HG	2.03	0.41
28:16:33:LYS:HA	28:16:33:LYS:HD3	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1025:U:O2	32:1a:1036:G:O6	2.39	0.41
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.46	0.41
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.42	0.41
32:1a:1166:G:N2	32:1a:1169:A:H3'	2.34	0.41
33:1b:196:LEU:HD12	33:1b:196:LEU:HA	1.92	0.41
39:1h:4:ASP:OD2	39:1h:85:ARG:NH1	2.53	0.41
43:1l:47:LYS:HA	43:1l:48:PRO:HA	1.80	0.41
47:1p:29:ASP:OD1	47:1p:29:ASP:N	2.54	0.41
52:1u:6:ARG:NE	52:1u:15:ARG:HE	2.17	0.41
1:2A:820:A:N3	1:2A:943:U:H4'	2.35	0.41
1:2A:1053:C:H4'	1:2A:1054:A:OP1	2.20	0.41
1:2A:1153:C:OP2	62:2A:3890:HOH:O	2.22	0.41
1:2A:1155:A:OP1	16:2U:55:ARG:HD3	2.20	0.41
1:2A:2133:G:H21	1:2A:2157:G:H2'	1.84	0.41
1:2A:2147:G:H3'	1:2A:2147:G:H8	1.84	0.41
1:2A:2162:G:H4'	1:2A:2172:U:O2'	2.19	0.41
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	2.01	0.41
4:2E:24:THR:HG21	4:2E:188:VAL:HB	2.01	0.41
4:2E:32:PRO:HD2	4:2E:50:GLY:O	2.20	0.41
7:2H:87:LEU:HD23	7:2H:164:TYR:HA	2.01	0.41
14:2S:83:LYS:HB3	14:2S:111:GLU:HG3	2.02	0.41
32:2a:643:C:H5'	39:2h:31:PHE:CE1	2.55	0.41
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.35	0.41
32:2a:1148:U:O4'	40:2i:16:ARG:HD2	2.19	0.41
32:2a:1423:G:H2'	32:2a:1424:C:C6	2.55	0.41
32:2a:1428:A:H2'	32:2a:1429:C:O4'	2.19	0.41
33:2b:179:LYS:HE3	33:2b:179:LYS:HB3	1.84	0.41
48:2q:82:MET:HA	48:2q:85:VAL:HG23	2.02	0.41
53:2y:30:TRP:HD1	53:2y:89:GLN:HG3	1.85	0.41
1:1A:228:A:H8	1:1A:229:A:H5'	1.85	0.41
1:1A:271(B):C:H42	1:1A:271(V):G:H1	1.69	0.41
1:1A:272(B):G:H2'	1:1A:272(C):G:H8	1.84	0.41
1:1A:1495:A:H2'	1:1A:1496:A:C8	2.55	0.41
1:1A:2355:C:H1'	22:10:39:ARG:HH21	1.85	0.41
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.55	0.41
1:1A:2712(A):A:N3	62:1A:4382:HOH:O	2.37	0.41
10:1O:89:ASN:OD1	10:1O:89:ASN:N	2.53	0.41
14:1S:61:ASN:OD1	14:1S:64:GLU:HG3	2.21	0.41
15:1T:107:ASP:O	15:1T:111:ARG:HG3	2.21	0.41
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.55	0.41
18:1W:83:LYS:O	18:1W:84:ARG:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:16:2:ALA:N	62:16:602:HOH:O	2.53	0.41
32:1a:983:A:H2	32:1a:984:C:C6	2.38	0.41
32:1a:1438:G:H2'	32:1a:1439:C:C6	2.55	0.41
32:1a:1496:C:H2'	32:1a:1497:G:O4'	2.21	0.41
33:1b:21:ARG:HB2	33:1b:22:LYS:H	1.73	0.41
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.21	0.41
40:1i:6:GLY:O	40:1i:17:VAL:HG12	2.21	0.41
1:2A:373:U:H2'	1:2A:374:A:H8	1.85	0.41
1:2A:458:G:O2'	1:2A:469:G:O6	2.33	0.41
1:2A:1081:U:H5"	1:2A:1082:U:OP2	2.20	0.41
1:2A:1270:C:H5"	1:2A:1271:G:O5'	2.21	0.41
1:2A:1570:A:H5'	3:2D:36:PRO:HD3	2.01	0.41
3:2D:275:LYS:HA	3:2D:276:LYS:C	2.45	0.41
5:2F:126:VAL:HG11	5:2F:142:TRP:HH2	1.85	0.41
6:2G:19:LEU:HD23	6:2G:19:LEU:HA	1.85	0.41
15:2T:113:LYS:O	15:2T:114:LEU:HD23	2.19	0.41
17:2V:57:VAL:HG12	17:2V:99:ILE:HG23	2.02	0.41
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	2.03	0.41
24:22:21:LEU:HA	24:22:21:LEU:HD23	1.81	0.41
25:23:19:GLN:O	25:23:23:LEU:HD22	2.20	0.41
32:2a:179:A:H2'	32:2a:180:U:C6	2.55	0.41
32:2a:1058:G:C5	32:2a:1059:C:C4	3.09	0.41
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.55	0.41
32:2a:1343:G:HO2'	40:2i:121:ARG:HD2	1.85	0.41
34:2c:21:ARG:NH2	34:2c:56:ASP:HB3	2.36	0.41
38:2g:135:VAL:O	38:2g:139:GLU:N	2.45	0.41
39:2h:109:ILE:HG12	39:2h:137:VAL:HB	2.01	0.41
1:1A:414:C:H2'	1:1A:415:A:H8	1.85	0.41
1:1A:910:A:N1	1:1A:2277:G:H1'	2.35	0.41
1:1A:1245:G:OP1	11:1P:13:ASN:ND2	2.37	0.41
1:1A:1495:A:C6	1:1A:1496:A:C6	3.08	0.41
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.21	0.41
62:1A:4248:HOH:O	11:1P:37:GLY:HA3	2.21	0.41
6:1G:7:LEU:HD13	6:1G:100:TRP:HE3	1.85	0.41
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	2.00	0.41
10:1O:15:GLY:O	10:1O:47:ILE:HG12	2.21	0.41
13:1R:13:HIS:CE1	13:1R:16:HIS:HB2	2.55	0.41
13:1R:96:ARG:HG2	13:1R:115:GLU:HG2	2.02	0.41
32:1a:636:U:H2'	32:1a:637:G:H8	1.85	0.41
32:1a:785:G:C2'	32:1a:786:G:H5'	2.50	0.41
33:1b:119:GLU:C	33:1b:121:LEU:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:148:VAL:HB	35:1d:181:MET:HB3	2.03	0.41
36:1e:150:ARG:HE	36:1e:150:ARG:HB2	1.73	0.41
39:1h:92:ARG:HA	39:1h:92:ARG:HD3	1.94	0.41
40:1i:16:ARG:HD3	40:1i:66:ARG:NH1	2.34	0.41
1:2A:704:G:H1'	1:2A:726:G:N2	2.36	0.41
1:2A:885:C:H2'	1:2A:886:C:O4'	2.20	0.41
1:2A:1354:A:H3'	1:2A:1355:G:C8	2.55	0.41
1:2A:1586:A:H8	1:2A:1586:A:O5'	2.03	0.41
1:2A:2336:A:H61	22:20:43:THR:HG21	1.84	0.41
2:2B:53:A:H2'	2:2B:54:G:O4'	2.20	0.41
6:2G:75:LYS:NZ	6:2G:77:ILE:HD11	2.35	0.41
7:2H:83:TYR:O	7:2H:134:SER:HA	2.20	0.41
10:2O:119:PRO:HB2	15:2T:68:TYR:CZ	2.56	0.41
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.19	0.41
17:2V:4:ILE:HD12	17:2V:39:LEU:HD22	2.02	0.41
18:2W:6:ILE:HA	18:2W:103:ILE:O	2.20	0.41
32:2a:1059:C:OP1	34:2c:199:LYS:NZ	2.53	0.41
32:2a:1318:A:H4'	50:2s:10:PHE:CE2	2.56	0.41
32:2a:1410:G:H2'	32:2a:1411:C:C6	2.55	0.41
33:2b:75:LYS:HA	33:2b:78:GLN:HB2	2.03	0.41
34:2c:67:THR:HG23	34:2c:102:ASN:HB2	2.03	0.41
34:2c:109:PRO:HB3	34:2c:115:LEU:HD23	2.03	0.41
40:2i:16:ARG:NH1	40:2i:64:THR:HG21	2.35	0.41
46:2o:82:ILE:O	46:2o:86:GLY:N	2.53	0.41
47:2p:5:ARG:HH21	47:2p:28:ARG:HA	1.85	0.41
52:2u:2:GLY:C	52:2u:4:GLY:H	2.28	0.41
1:1A:409:C:H6	1:1A:409:C:O5'	2.03	0.41
1:1A:679:C:H2'	1:1A:680:G:H8	1.85	0.41
1:1A:818:G:H4'	1:1A:838:C:O3'	2.19	0.41
1:1A:829:A:N7	1:1A:2248:C:H5'	2.35	0.41
1:1A:970:C:H2'	1:1A:971:C:C6	2.55	0.41
1:1A:1007:C:OP1	9:1N:37:LYS:NZ	2.53	0.41
1:1A:1075:C:H42	1:1A:1077:A:N6	2.19	0.41
1:1A:1805:U:O2	3:1D:50:THR:HB	2.20	0.41
1:1A:2562:U:H4'	10:1O:25:LEU:HD21	2.02	0.41
1:1A:2593:U:H2'	1:1A:2594:C:H6	1.85	0.41
1:1A:2881:C:O2'	13:1R:96:ARG:HA	2.21	0.41
2:1B:29:A:C2	2:1B:30:C:C2	3.08	0.41
2:1B:95:C:H2'	2:1B:96:U:C6	2.56	0.41
4:1E:1:MET:HB3	4:1E:83:ASP:O	2.20	0.41
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:105:LEU:HD11	7:1H:148:ILE:HG23	2.03	0.41
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.56	0.41
10:1O:20:MET:HE3	10:1O:22:ILE:HG22	2.02	0.41
15:1T:51:ARG:HG3	15:1T:98:LYS:CE	2.50	0.41
30:18:52:LYS:HB2	30:18:52:LYS:HE3	1.88	0.41
32:1a:93:G:H2'	32:1a:96:U:O4'	2.19	0.41
32:1a:362:G:N1	32:1a:365:U:OP2	2.51	0.41
32:1a:580:U:H2'	32:1a:581:G:O4'	2.21	0.41
32:1a:737:A:H2'	32:1a:738:C:C6	2.55	0.41
32:1a:1144:G:N2	32:1a:1146:A:H62	2.18	0.41
32:1a:1238:A:OP2	62:1a:4616:HOH:O	2.22	0.41
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.21	0.41
34:1c:148:GLY:HA2	34:1c:171:GLY:HA3	2.02	0.41
44:1m:11:ARG:HA	44:1m:45:VAL:HB	2.02	0.41
44:1m:19:LEU:HD11	44:1m:56:LEU:HD21	2.02	0.41
44:1m:49:THR:HG22	44:1m:51:ALA:H	1.86	0.41
46:1o:12:ILE:HG23	46:1o:27:VAL:HG11	2.03	0.41
50:1s:43:GLU:OE1	50:1s:43:GLU:N	2.53	0.41
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.43	0.41
1:2A:425:G:OP2	62:2A:3888:HOH:O	2.22	0.41
1:2A:903:C:H2'	1:2A:904:C:H6	1.85	0.41
1:2A:1301:A:C8	1:2A:1303:G:C8	3.08	0.41
1:2A:1529:G:O6	1:2A:1530:C:N4	2.53	0.41
1:2A:1633:G:OP2	62:2A:3894:HOH:O	2.22	0.41
1:2A:2347:C:OP1	1:2A:2347:C:H4'	2.20	0.41
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.85	0.41
2:2B:7:G:H4'	14:2S:29:PHE:CD2	2.55	0.41
3:2D:24:ILE:HA	3:2D:82:ILE:O	2.21	0.41
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	2.01	0.41
5:2F:155:LEU:HD12	5:2F:174:VAL:O	2.21	0.41
12:2Q:31:ASP:O	12:2Q:134:ARG:N	2.47	0.41
15:2T:15:VAL:HG13	15:2T:79:HIS:CE1	2.55	0.41
32:2a:157:G:H1	32:2a:164:U:H3	1.69	0.41
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.56	0.41
32:2a:266:G:H3'	48:2q:67:LYS:HB2	2.02	0.41
32:2a:911:U:H2'	32:2a:912:C:C6	2.56	0.41
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.20	0.41
32:2a:1401:G:N7	53:2y:83:ARG:NH1	2.56	0.41
1:1A:583:G:OP2	16:1U:10:ARG:HD2	2.20	0.41
1:1A:1470:G:H5"	1:1A:1471:A:OP1	2.21	0.41
1:1A:1477:A:H2'	1:1A:1478:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2106:G:C6	1:1A:2107:C:C2	3.08	0.41
6:1G:66:GLN:HB3	6:1G:92:VAL:HG21	2.01	0.41
10:1O:113:LYS:HE2	10:1O:113:LYS:HB2	1.66	0.41
20:1Y:95:LYS:HB3	20:1Y:95:LYS:HE2	1.80	0.41
27:15:35:GLU:OE2	27:15:54:GLY:HA2	2.20	0.41
32:1a:70:G:H1	32:1a:99:U:H3	1.69	0.41
32:1a:120:A:C6	32:1a:122:G:C2	3.08	0.41
32:1a:615:C:H2'	32:1a:616:G:C8	2.56	0.41
32:1a:669:U:H2'	32:1a:670:G:C8	2.55	0.41
32:1a:1456:G:O6	51:1t:54:LYS:NZ	2.33	0.41
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	2.02	0.41
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.21	0.41
1:2A:213:A:N6	1:2A:214:G:C6	2.88	0.41
1:2A:784:A:O4'	3:2D:227:ASN:ND2	2.54	0.41
1:2A:1111:A:N3	1:2A:1111:A:H2'	2.36	0.41
1:2A:1927:A:C6	1:2A:1928:A:C6	3.09	0.41
1:2A:2134:A:H5"	1:2A:2156:G:N2	2.35	0.41
1:2A:2137:C:N3	1:2A:2154:G:O6	2.54	0.41
1:2A:2499:C:OP2	62:2A:3886:HOH:O	2.21	0.41
1:2A:2562:U:H1'	10:2O:23:ARG:NE	2.36	0.41
1:2A:2563:U:O2	1:2A:2565:A:H8	2.03	0.41
1:2A:2636:U:H2'	1:2A:2637:U:C6	2.55	0.41
4:2E:7:VAL:HG23	4:2E:51:PHE:CE2	2.56	0.41
5:2F:101:LEU:O	5:2F:106:ARG:NH2	2.51	0.41
6:2G:16:ARG:HD2	6:2G:16:ARG:HA	1.77	0.41
9:2N:73:THR:HA	9:2N:83:LYS:O	2.21	0.41
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.95	0.41
15:2T:24:PRO:HD3	15:2T:52:ILE:HD12	2.02	0.41
21:2Z:10:ARG:HB3	21:2Z:36:LYS:HB3	2.03	0.41
22:20:2:ALA:HB3	55:2x:76:8AN:HN6A	1.86	0.41
23:21:23:LYS:HB3	23:21:29:GLY:HA3	2.02	0.41
32:2a:60:A:H4'	32:2a:61:G:O5'	2.20	0.41
32:2a:652:U:O4	32:2a:752:G:O2'	2.36	0.41
32:2a:756:C:H2'	32:2a:757:U:O4'	2.21	0.41
32:2a:1405:G:H2'	32:2a:1406:U:C6	2.56	0.41
34:2c:20:SER:HB2	34:2c:40:ARG:NH2	2.36	0.41
44:2m:3:ARG:N	44:2m:8:GLU:HA	2.35	0.41
51:2t:14:LYS:HE3	51:2t:18:GLN:HE21	1.85	0.41
1:1A:300:A:OP1	20:1Y:86:ARG:NH2	2.54	0.41
1:1A:1961:C:H5'	32:1a:1484:C:O2'	2.21	0.41
1:1A:2223:G:OP1	3:1D:172:TYR:OH	2.26	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:71:LEU:HD12	7:1H:71:LEU:HA	1.90	0.41
13:1R:62:ALA:HA	13:1R:65:LEU:HD12	2.02	0.41
32:1a:491:G:H2'	32:1a:492:G:O4'	2.21	0.41
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.42	0.41
32:1a:565:U:H3'	32:1a:566:G:H2'	2.03	0.41
32:1a:1004:A:C8	32:1a:1005:A:H1'	2.55	0.41
32:1a:1065:U:H1'	32:1a:1066:C:OP2	2.21	0.41
32:1a:1152:A:OP1	41:1j:68:HIS:ND1	2.48	0.41
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.55	0.41
35:1d:76:ARG:HA	35:1d:79:PHE:HB3	2.03	0.41
35:1d:122:ARG:HA	35:1d:122:ARG:HD2	1.63	0.41
36:1e:80:ILE:HG21	36:1e:138:ALA:HB1	2.03	0.41
44:1m:95:GLY:O	44:1m:110:ARG:HB3	2.21	0.41
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.55	0.41
1:2A:322:A:OP1	5:2F:168:ARG:HD3	2.20	0.41
1:2A:638:G:C5	1:2A:639:U:C4	3.08	0.41
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.54	0.41
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.55	0.41
1:2A:1587:A:H2'	1:2A:1588:C:H6	1.85	0.41
1:2A:2341:G:H2'	1:2A:2342:C:C6	2.56	0.41
1:2A:2620:C:O2'	4:2E:119:ARG:NH2	2.54	0.41
1:2A:2840:C:H4'	13:2R:53:HIS:CE1	2.55	0.41
2:2B:28:C:H2'	2:2B:29:A:O4'	2.21	0.41
6:2G:36:LYS:HE2	6:2G:160:VAL:HG21	2.03	0.41
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.49	0.41
11:2P:48:PRO:O	30:28:57:ARG:NH2	2.49	0.41
32:2a:138:G:C4	32:2a:139:G:C8	3.08	0.41
32:2a:224:C:H2'	32:2a:225:C:C6	2.55	0.41
32:2a:443:C:H2'	32:2a:444:C:C6	2.56	0.41
32:2a:487:A:H2'	32:2a:488:C:O4'	2.20	0.41
32:2a:806:C:H2'	32:2a:807:A:C8	2.56	0.41
32:2a:922:G:H1'	36:2e:19:MET:HB2	2.03	0.41
32:2a:1496:C:H2'	32:2a:1497:G:O4'	2.20	0.41
33:2b:15:VAL:HG12	33:2b:209:ARG:HD2	2.02	0.41
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.21	0.41
54:2w:76:PPU:N7	54:2w:76:PPU:C9	2.82	0.41
1:1A:700:G:O2'	1:1A:1632:A:N3	2.45	0.41
1:1A:1036:G:OP2	7:1H:59:ARG:NH2	2.53	0.41
1:1A:1124:C:H2'	1:1A:1125:G:O4'	2.21	0.41
1:1A:1709:U:H2'	1:1A:1710:C:C6	2.56	0.41
1:1A:2854:G:H2'	1:1A:2855:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:64:ALA:HA	23:11:67:ILE:HG13	2.02	0.41
35:1d:59:ARG:NH1	35:1d:59:ARG:HA	2.36	0.41
36:1e:131:ILE:HA	36:1e:131:ILE:HD13	1.82	0.41
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	2.01	0.41
1:2A:855:G:H2'	1:2A:856:C:C6	2.56	0.41
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.20	0.41
1:2A:1208:C:C4	1:2A:1209:G:N7	2.89	0.41
1:2A:1359:A:N6	1:2A:1372:U:H3	2.19	0.41
1:2A:2332:U:O2'	1:2A:2335:A:N3	2.53	0.41
1:2A:2448:A:OP1	62:2A:3817:HOH:O	2.21	0.41
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.36	0.41
1:2A:2749:A:H1'	7:2H:63:SER:OG	2.20	0.41
11:2P:84:ASN:HB3	11:2P:117:GLU:HB3	2.02	0.41
19:2X:32:PRO:O	19:2X:77:LYS:HD2	2.21	0.41
32:2a:100:C:H2'	32:2a:101:A:C8	2.56	0.41
32:2a:490:G:P	35:2d:132:ARG:HH22	2.43	0.41
32:2a:550:G:C6	32:2a:551:U:C4	3.09	0.41
32:2a:1305:G:H5"	52:2u:4:GLY:C	2.45	0.41
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.28	0.41
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.20	0.41
34:2c:59:ARG:H	41:2j:92:THR:CG2	2.34	0.41
38:2g:27:ILE:HA	38:2g:30:ILE:HD13	2.02	0.41
51:2t:13:LEU:O	51:2t:17:ARG:HG3	2.20	0.41
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.21	0.41
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.36	0.41
1:1A:1080:C:H2'	1:1A:1081:U:H6	1.85	0.41
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.36	0.41
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.56	0.41
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.55	0.41
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.56	0.41
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.80	0.41
5:1F:11:VAL:HB	5:1F:18:ARG:HB2	2.02	0.41
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.51	0.41
10:1O:20:MET:HE2	10:1O:20:MET:HB3	1.94	0.41
12:1Q:20:ALA:HB2	21:1Z:79:ARG:HB2	2.02	0.41
19:1X:1:MET:HE3	19:1X:1:MET:HB2	1.94	0.41
22:10:43:THR:O	22:10:43:THR:HG23	2.21	0.41
32:1a:7:G:H5'	32:1a:298:A:O4'	2.20	0.41
32:1a:348:G:OP1	59:1a:1873:MPD:HM3	2.21	0.41
32:1a:626:U:H2'	32:1a:627:G:C8	2.56	0.41
32:1a:653:A:O4'	39:1h:56:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:951:G:O6	44:1m:105:THR:HG21	2.20	0.41
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.21	0.41
32:1a:1164:G:H2'	32:1a:1165:C:H6	1.86	0.41
32:1a:1216:G:H5"	45:1n:5:ALA:CB	2.51	0.41
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.21	0.41
32:1a:1308:U:OP2	44:1m:99:ARG:HG3	2.21	0.41
32:1a:1518:MA6:H93	32:1a:1519:MA6:C9	2.47	0.41
33:1b:155:LEU:HD21	33:1b:159:PRO:HD3	2.02	0.41
33:1b:214:ILE:HD13	33:1b:214:ILE:HA	1.82	0.41
35:1d:18:LYS:HE3	35:1d:26:CYS:O	2.21	0.41
35:1d:186:LEU:HD13	35:1d:186:LEU:HA	1.89	0.41
37:1f:7:ASN:HB3	49:1r:76:LEU:HD11	2.02	0.41
37:1f:22:GLU:CD	37:1f:82:ARG:HH21	2.28	0.41
38:1g:63:LYS:O	38:1g:66:VAL:HB	2.21	0.41
38:1g:126:ASP:O	38:1g:131:LYS:N	2.54	0.41
41:1j:49:VAL:CG2	45:1n:41:ARG:HB2	2.49	0.41
43:1l:88:GLY:O	43:1l:99:HIS:HD2	2.03	0.41
53:1y:40:ILE:HB	53:1y:51:ASP:HB2	2.02	0.41
1:2A:26:G:C6	1:2A:27:G:N1	2.88	0.41
1:2A:554:U:C4	1:2A:555:U:C4	3.09	0.41
1:2A:614(A):U:H4'	1:2A:614(B):G:H5"	2.02	0.41
1:2A:635:C:H2'	1:2A:636:G:O4'	2.20	0.41
1:2A:635:C:O2'	1:2A:639:U:OP1	2.26	0.41
1:2A:674:G:H1'	5:2F:74:ARG:HD3	2.03	0.41
1:2A:1418:G:H8	1:2A:1418:G:O5'	2.04	0.41
1:2A:1657:C:H2'	1:2A:1658:C:H6	1.86	0.41
1:2A:1671:U:O2'	1:2A:1673:U:H5	2.04	0.41
1:2A:2036:C:OP1	62:2A:3818:HOH:O	2.21	0.41
1:2A:2051:A:OP2	62:2A:3895:HOH:O	2.22	0.41
1:2A:2070:G:H2'	1:2A:2071:A:H8	1.85	0.41
1:2A:2112:G:H2'	1:2A:2113:U:C6	2.56	0.41
1:2A:2172:U:H4'	1:2A:2173:A:OP1	2.21	0.41
1:2A:2263:C:N4	22:20:15:ASP:OD1	2.54	0.41
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.21	0.41
1:2A:2607:G:H2'	1:2A:2608:G:O4'	2.21	0.41
1:2A:2802:G:C2	1:2A:2803:C:H1'	2.56	0.41
6:2G:19:LEU:HD13	6:2G:32:PRO:HD2	2.03	0.41
6:2G:126:ASP:CG	6:2G:130:ASN:HD22	2.29	0.41
10:2O:104:ARG:NH2	10:2O:121:VAL:O	2.54	0.41
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.21	0.41
14:2S:74:ALA:HB2	14:2S:105:ALA:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:76:LYS:HB3	14:2S:76:LYS:HE2	1.77	0.41
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.53	0.41
21:2Z:40:ASP:OD1	21:2Z:42:VAL:HG12	2.20	0.41
28:26:32:ASN:C	28:26:32:ASN:HD22	2.29	0.41
29:27:46:VAL:HB	29:27:48:LYS:HZ2	1.85	0.41
32:2a:251:G:H4'	32:2a:252:U:O5'	2.21	0.41
32:2a:513:C:H2'	32:2a:514:C:H6	1.84	0.41
32:2a:745:C:H4'	32:2a:836:G:N2	2.34	0.41
32:2a:1130:A:H5'	40:2i:18:PHE:CE2	2.56	0.41
32:2a:1287:A:N6	32:2a:1371:G:O4'	2.47	0.41
32:2a:1309:G:O3'	44:2m:77:ASN:ND2	2.53	0.41
32:2a:1518:MA6:H8	32:2a:1518:MA6:O5'	2.21	0.41
33:2b:10:LEU:HD12	33:2b:48:MET:HE1	2.02	0.41
33:2b:28:PHE:CD2	33:2b:31:TYR:HB2	2.56	0.41
33:2b:98:LEU:H	33:2b:101:MET:HE3	1.86	0.41
35:2d:194:LEU:HD23	35:2d:196:LEU:HD11	2.03	0.41
40:2i:99:LEU:HD23	40:2i:101:PHE:CZ	2.56	0.41
41:2j:16:LEU:HD23	41:2j:94:VAL:HG22	2.03	0.41
41:2j:46:ARG:HD3	41:2j:62:HIS:ND1	2.36	0.41
42:2k:69:ALA:O	42:2k:73:MET:HG3	2.21	0.41
1:1A:857:C:N4	1:1A:858:U:O4	2.54	0.41
1:1A:1506:C:H2'	1:1A:1507:A:H8	1.85	0.41
1:1A:1529:G:C6	1:1A:1530:C:C4	3.09	0.41
1:1A:1923:U:H2'	1:1A:1924:C:C6	2.56	0.41
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.56	0.41
1:1A:2805:G:H2'	1:1A:2807:G:H8	1.86	0.41
62:1A:5754:HOH:O	16:1U:59:ARG:HD2	2.21	0.41
4:1E:179:GLU:HB3	4:1E:181:LEU:HD22	2.03	0.41
5:1F:56:GLU:OE1	5:1F:93:LYS:NZ	2.45	0.41
5:1F:64:ILE:HD12	5:1F:65:TRP:CZ3	2.56	0.41
27:15:16:ARG:O	27:15:20:ARG:HG3	2.20	0.41
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.56	0.41
32:1a:509:A:H2'	32:1a:510:A:C8	2.56	0.41
32:1a:560:U:H4'	32:1a:561:U:O5'	2.21	0.41
32:1a:964:A:OP1	62:1a:4617:HOH:O	2.22	0.41
32:1a:1003:G:N2	32:1a:1004:A:N3	2.69	0.41
33:1b:118:LEU:HB2	33:1b:142:LEU:HD13	2.03	0.41
33:1b:163:PHE:HA	33:1b:185:ILE:O	2.21	0.41
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.86	0.41
35:1d:155:LEU:HD12	35:1d:156:GLU:H	1.86	0.41
36:1e:66:MET:HE3	36:1e:66:MET:HB3	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:91:VAL:HB	38:1g:96:GLN:HE21	1.86	0.41
40:1i:65:VAL:HG21	40:1i:73:GLN:HB3	2.02	0.41
51:1t:72:LEU:HD23	51:1t:72:LEU:HA	1.86	0.41
1:2A:297:C:OP1	20:2Y:87:LYS:HG3	2.20	0.41
1:2A:372:G:H8	23:21:65:SER:O	2.04	0.41
1:2A:861:A:N6	1:2A:916:G:O2'	2.53	0.41
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.56	0.41
1:2A:2155:G:H2'	1:2A:2156:G:O4'	2.21	0.41
10:2O:112:MET:HE2	10:2O:112:MET:HB2	1.90	0.41
19:2X:53:LYS:NZ	19:2X:55:ASN:OD1	2.52	0.41
32:2a:88:A:H8	32:2a:88:A:OP2	2.03	0.41
32:2a:649:G:N7	62:2a:3237:HOH:O	2.37	0.41
32:2a:775:G:C6	32:2a:776:G:C5	3.09	0.41
32:2a:858:G:O6	32:2a:869:G:H3'	2.21	0.41
32:2a:1015:A:N3	32:2a:1218:C:O2'	2.46	0.41
32:2a:1025:U:H2'	32:2a:1027:C:N4	2.36	0.41
32:2a:1400:5MC:N3	53:2y:63:ALA:HA	2.36	0.41
36:2e:75:THR:HG23	36:2e:117:ASP:O	2.21	0.41
42:2k:20:TYR:O	42:2k:30:VAL:HA	2.21	0.41
43:2l:11:VAL:HG11	48:2q:36:ILE:HG21	2.03	0.41
45:2n:46:GLU:O	45:2n:50:LYS:HG3	2.21	0.41
46:2o:28:GLN:HE21	46:2o:28:GLN:HB3	1.67	0.41
1:1A:181:A:OP2	62:1A:4195:HOH:O	2.22	0.40
1:1A:1161:C:O2'	17:1V:8:GLY:HA2	2.21	0.40
1:1A:2267:A:OP1	62:1A:4197:HOH:O	2.22	0.40
1:1A:2590:A:H2'	1:1A:2591:C:C6	2.57	0.40
6:1G:82:LEU:HD23	6:1G:82:LEU:HA	1.94	0.40
6:1G:121:ASN:HA	6:1G:122:PRO:HD3	1.94	0.40
19:1X:88:LYS:HB3	19:1X:88:LYS:HE2	1.91	0.40
32:1a:264:U:O2'	48:1q:64:PRO:O	2.32	0.40
32:1a:355:C:H2'	32:1a:356:A:O4'	2.20	0.40
32:1a:455:C:O5'	32:1a:455:C:H6	2.04	0.40
32:1a:1286:A:H2	52:1u:22:ARG:HH22	1.67	0.40
33:1b:50:GLU:O	33:1b:54:THR:OG1	2.31	0.40
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	2.03	0.40
38:1g:31:MET:HE2	38:1g:36:LYS:HG3	2.04	0.40
38:1g:121:ALA:O	38:1g:125:MET:HB2	2.21	0.40
41:1j:55:LYS:HB2	41:1j:56:HIS:H	1.60	0.40
44:1m:15:VAL:HG13	44:1m:43:THR:O	2.21	0.40
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.56	0.40
1:2A:329:G:H8	1:2A:329:G:OP1	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.56	0.40
1:2A:2872:G:C2	1:2A:2873:A:N6	2.88	0.40
2:2B:90:A:N7	2:2B:91:C:H1'	2.35	0.40
5:2F:130:ALA:H	5:2F:142:TRP:CD1	2.39	0.40
6:2G:60:LEU:HD12	6:2G:60:LEU:HA	1.95	0.40
17:2V:1:MET:HG3	17:2V:41:GLY:O	2.21	0.40
18:2W:68:ARG:O	18:2W:109:GLU:HA	2.21	0.40
25:23:6:VAL:HG22	25:23:56:VAL:HG13	2.03	0.40
26:24:59:PHE:HA	26:24:61:ARG:N	2.36	0.40
32:2a:558:G:OP1	62:2a:3215:HOH:O	2.22	0.40
32:2a:677:U:H3	32:2a:713:G:N2	2.08	0.40
32:2a:936:C:H2'	32:2a:937:A:H8	1.86	0.40
32:2a:1220:G:H1'	50:2s:52:TYR:CD2	2.56	0.40
33:2b:157:ARG:HG2	33:2b:158:LEU:N	2.36	0.40
34:2c:54:ARG:HD3	34:2c:69:HIS:CD2	2.56	0.40
45:2n:58:LYS:HE2	45:2n:58:LYS:HB3	1.85	0.40
48:2q:18:THR:HG23	48:2q:69:LYS:HD2	2.03	0.40
1:1A:428:A:OP2	1:1A:428:A:H8	2.04	0.40
1:1A:1252:G:C2	1:1A:1253:A:C2	3.10	0.40
1:1A:1676:A:H2'	1:1A:1677:A:O4'	2.21	0.40
1:1A:1697:G:OP2	1:1A:1698:A:O2'	2.31	0.40
1:1A:2561:A:H2'	1:1A:2562:U:O4'	2.21	0.40
2:1B:33:G:C2	2:1B:50:G:C2	3.09	0.40
3:1D:5:LYS:HE3	3:1D:5:LYS:HB3	1.87	0.40
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.50	0.40
5:1F:34:TRP:CE2	11:1P:8:PRO:HD3	2.56	0.40
6:1G:41:GLN:HG2	6:1G:154:GLY:O	2.21	0.40
23:11:52:ARG:NH2	23:11:55:GLY:O	2.54	0.40
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.53	0.40
32:1a:382:A:H2'	32:1a:383:A:H8	1.84	0.40
32:1a:509:A:H3'	62:1a:4775:HOH:O	2.21	0.40
32:1a:1187:G:H2'	32:1a:1188:A:C8	2.56	0.40
33:1b:92:TYR:OH	33:1b:150:SER:OG	2.18	0.40
40:1i:25:LYS:HD2	40:1i:32:ASP:OD1	2.21	0.40
43:1l:10:LEU:HD23	43:1l:10:LEU:HA	1.80	0.40
47:1p:72:ARG:HG2	47:1p:73:LEU:N	2.36	0.40
1:2A:19:C:H2'	1:2A:20:C:H6	1.86	0.40
1:2A:1077:A:H2	1:2A:1088:A:C8	2.40	0.40
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.56	0.40
1:2A:1138:G:N3	9:2N:106:MET:HE2	2.36	0.40
1:2A:1341:U:O4	19:2X:16:LYS:HE2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1800:C:P	3:2D:183:ARG:HH12	2.44	0.40
1:2A:1842:G:O2'	3:2D:253:GLN:NE2	2.53	0.40
1:2A:2118:U:C3'	1:2A:2119:A:H5"	2.50	0.40
2:2B:83:G:H1	2:2B:94:C:H42	1.69	0.40
5:2F:32:LEU:HD22	5:2F:112:MET:HE2	2.03	0.40
5:2F:170:LEU:HD12	5:2F:170:LEU:HA	1.88	0.40
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	2.03	0.40
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	2.03	0.40
12:2Q:2:LEU:O	12:2Q:70:PRO:HG2	2.20	0.40
21:2Z:54:HIS:CD2	21:2Z:101:PRO:HG3	2.57	0.40
26:24:12:ALA:CB	26:24:29:PRO:HA	2.51	0.40
26:24:69:LYS:HB3	26:24:69:LYS:NZ	2.36	0.40
32:2a:323:U:H2'	32:2a:324:G:O4'	2.21	0.40
32:2a:375:U:O3'	47:2p:6:LEU:HB2	2.20	0.40
32:2a:957:U:H4'	50:2s:79:THR:OG1	2.22	0.40
32:2a:1123:A:N3	41:2j:39:PRO:HD2	2.36	0.40
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.03	0.40
32:2a:1292:U:H2'	32:2a:1293:G:C8	2.55	0.40
32:2a:1353:G:H2'	32:2a:1354:C:C6	2.56	0.40
32:2a:1384:C:H2'	32:2a:1385:G:C8	2.56	0.40
32:2a:1445:C:O2'	32:2a:1447:A:N6	2.53	0.40
33:2b:32:ILE:HD11	33:2b:190:THR:HB	2.02	0.40
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	2.02	0.40
36:2e:80:ILE:HD12	39:2h:104:ARG:NH2	2.36	0.40
1:1A:1002:G:H2'	1:1A:1003:G:O4'	2.21	0.40
1:1A:1382:G:N2	62:1A:4771:HOH:O	2.54	0.40
1:1A:1400:G:H2'	1:1A:1401:G:C8	2.55	0.40
1:1A:1707:G:C5	1:1A:1756:G:C6	3.10	0.40
1:1A:1790:C:H2'	1:1A:1791:A:C4	2.56	0.40
1:1A:1853:A:H2'	1:1A:1854:A:C8	2.56	0.40
1:1A:2336:A:H61	22:10:43:THR:HG22	1.86	0.40
8:1I:31:LEU:HD21	8:1I:38:LEU:HD13	2.04	0.40
11:1P:56:SER:N	62:1P:304:HOH:O	2.35	0.40
23:11:67:ILE:N	23:11:68:PRO:HD2	2.37	0.40
24:12:62:THR:O	24:12:66:GLU:HG3	2.22	0.40
32:1a:545:C:OP1	35:1d:61:LYS:NZ	2.54	0.40
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.47	0.40
32:1a:1269:A:H2	32:1a:1312:G:N3	2.19	0.40
1:2A:150:C:H2'	1:2A:151:C:H6	1.87	0.40
1:2A:391:G:H1'	1:2A:411:G:O4'	2.21	0.40
1:2A:1075:C:H2'	1:2A:1076:C:H5'	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1138:G:C5	1:2A:1139:G:H1'	2.57	0.40
1:2A:1504:C:H2'	1:2A:1505:C:H6	1.87	0.40
1:2A:2507:C:OP1	62:2A:3889:HOH:O	2.22	0.40
1:2A:2740:A:C6	1:2A:2764:A:C8	3.09	0.40
1:2A:2872:G:O2'	1:2A:2873:A:H5'	2.21	0.40
3:2D:183:ARG:HG3	3:2D:270:ILE:HG12	2.03	0.40
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.56	0.40
14:2S:78:LEU:HD11	14:2S:109:GLY:HA3	2.03	0.40
17:2V:97:LYS:HA	17:2V:97:LYS:HD2	1.83	0.40
20:2Y:1:MET:HE2	20:2Y:1:MET:HB3	1.94	0.40
21:2Z:165:VAL:HG23	21:2Z:166:SER:O	2.21	0.40
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.56	0.40
29:27:1:MET:HE3	29:27:3:ARG:NH2	2.36	0.40
32:2a:434:U:H2'	32:2a:435:C:C6	2.57	0.40
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.32	0.40
33:2b:89:GLY:O	33:2b:154:LEU:HD21	2.22	0.40
33:2b:96:ARG:CZ	33:2b:98:LEU:HD23	2.51	0.40
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.21	0.40
43:2l:88:GLY:O	43:2l:99:HIS:HD2	2.05	0.40
44:2m:49:THR:O	44:2m:53:VAL:HG23	2.22	0.40
1:1A:182:A:H2	1:1A:433:C:O2	2.04	0.40
1:1A:330:A:H2	1:1A:1210:A:C2'	2.34	0.40
1:1A:395:U:O2'	1:1A:396:G:N7	2.46	0.40
1:1A:927:G:H2'	1:1A:928:G:O4'	2.21	0.40
1:1A:1096:A:H2'	1:1A:1097:U:H5"	2.03	0.40
1:1A:1175:U:HO2'	1:1A:1176:G:P	2.44	0.40
1:1A:1458:C:H4'	1:1A:1459:G:O5'	2.21	0.40
1:1A:1631(A):A:OP1	62:1A:4196:HOH:O	2.22	0.40
1:1A:1923:U:H2'	1:1A:1924:C:H6	1.86	0.40
1:1A:2180:U:H2'	1:1A:2181:G:C8	2.56	0.40
1:1A:2203:U:O2'	1:1A:2205:C:H5'	2.22	0.40
1:1A:2287:A:C8	1:1A:2289:G:C8	3.09	0.40
3:1D:148:GLU:OE1	3:1D:151:LYS:NZ	2.37	0.40
6:1G:20:ILE:HG13	6:1G:20:ILE:H	1.72	0.40
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.56	0.40
19:1X:88:LYS:HG2	19:1X:93:GLU:HG3	2.03	0.40
21:1Z:14:LYS:HZ3	21:1Z:16:SER:H	1.68	0.40
21:1Z:65:GLN:NE2	21:1Z:67:LEU:HD21	2.37	0.40
27:15:45:VAL:HG11	27:15:58:LEU:HD21	2.04	0.40
28:16:11:LEU:HB3	28:16:49:HIS:HB3	2.03	0.40
32:1a:116:A:H61	32:1a:313:A:H1'	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:279:A:C8	48:1q:98:LEU:HD23	2.56	0.40
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.68	0.40
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.37	0.40
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.50	0.40
34:1c:50:ALA:O	34:1c:70:VAL:HG22	2.22	0.40
35:1d:88:VAL:HG13	36:1e:97:GLY:HA2	2.04	0.40
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.21	0.40
36:1e:48:ALA:HB3	36:1e:54:ALA:HB2	2.04	0.40
41:1j:18:ALA:O	41:1j:22:LYS:HG3	2.21	0.40
43:1l:27:LEU:HD23	43:1l:27:LEU:HA	1.95	0.40
51:1t:76:ALA:HA	51:1t:79:ARG:NH1	2.37	0.40
1:2A:570:G:H2'	1:2A:2030:A:N7	2.36	0.40
1:2A:684:G:OP1	29:27:16:HIS:ND1	2.54	0.40
1:2A:828:U:H4'	1:2A:831:G:N1	2.37	0.40
12:2Q:108:GLY:HA3	21:2Z:116:VAL:HG13	2.02	0.40
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	2.02	0.40
20:2Y:5:MET:HE2	20:2Y:32:PRO:HA	2.04	0.40
32:2a:941:G:H2'	32:2a:942:G:O4'	2.22	0.40
32:2a:1089:G:C6	32:2a:1090:U:C4	3.10	0.40
35:2d:36:ARG:HB3	35:2d:38:TYR:CE2	2.56	0.40
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.75	0.40
51:2t:72:LEU:HD23	51:2t:72:LEU:HA	1.86	0.40
7:1H:105:LEU:HD23	7:1H:105:LEU:HA	1.92	0.40
21:1Z:5:LEU:HD11	21:1Z:44:PHE:HA	2.03	0.40
21:1Z:35:ARG:HA	21:1Z:35:ARG:HD2	1.97	0.40
21:1Z:96:VAL:O	21:1Z:127:LYS:HA	2.21	0.40
21:1Z:120:ILE:HG22	21:1Z:121:HIS:HD1	1.87	0.40
32:1a:22:G:OP2	62:1a:4618:HOH:O	2.22	0.40
32:1a:269:C:H2'	32:1a:270:A:C8	2.56	0.40
32:1a:418:C:H1'	32:1a:540:G:O2'	2.21	0.40
32:1a:431:A:H2'	32:1a:432:A:O4'	2.20	0.40
32:1a:1064:G:H1'	32:1a:1190:G:N2	2.37	0.40
32:1a:1240:U:H1'	38:1g:38:LEU:HD21	2.04	0.40
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.21	0.40
1:2A:69:C:O2	1:2A:73:A:O2'	2.36	0.40
1:2A:243:U:OP1	30:28:6:THR:OG1	2.31	0.40
1:2A:271(V):G:O6	62:2A:3884:HOH:O	2.21	0.40
1:2A:921:G:C5	1:2A:922:U:C4	3.10	0.40
1:2A:1005:C:H4'	1:2A:1012:U:C6	2.57	0.40
1:2A:1668:A:H4'	1:2A:1669:A:O5'	2.21	0.40
1:2A:2118:U:OP1	1:2A:2148:G:O2'	2.31	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2697:G:H2'	1:2A:2698:U:O4'	2.21	0.40
3:2D:72:LYS:HE3	3:2D:72:LYS:HB3	1.89	0.40
3:2D:111:LEU:HD23	3:2D:111:LEU:HA	1.90	0.40
5:2F:34:TRP:CZ3	11:2P:8:PRO:HB3	2.56	0.40
6:2G:28:VAL:O	6:2G:31:VAL:HG13	2.21	0.40
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.55	0.40
14:2S:26:LEU:HD22	14:2S:87:PHE:HD1	1.87	0.40
22:20:21:LEU:HD23	22:20:21:LEU:HA	1.93	0.40
32:2a:1047:G:H5"	45:2n:4:LYS:HD2	2.04	0.40
32:2a:1187:G:H5'	40:2i:113:LYS:HE2	2.04	0.40
33:2b:8:LYS:HA	33:2b:217:ARG:HH12	1.86	0.40
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.36	0.40
35:2d:173:TRP:CD2	35:2d:189:PRO:HB3	2.57	0.40
36:2e:64:ARG:HE	36:2e:64:ARG:HB3	1.67	0.40
40:2i:23:ASN:HB2	40:2i:25:LYS:HD3	2.04	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%)	258 (94%)	15 (6%)	0	100	100
3	2D	273/276 (99%)	257 (94%)	16 (6%)	0	100	100
4	1E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	24	46
4	2E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	24	46
5	1F	201/210 (96%)	193 (96%)	7 (4%)	1 (0%)	24	46
5	2F	201/210 (96%)	185 (92%)	15 (8%)	1 (0%)	24	46
6	1G	179/182 (98%)	159 (89%)	15 (8%)	5 (3%)	4	6
6	2G	179/182 (98%)	146 (82%)	28 (16%)	5 (3%)	4	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	1H	172/180 (96%)	162 (94%)	9 (5%)	1 (1%)	21 42
7	2H	171/180 (95%)	146 (85%)	22 (13%)	3 (2%)	6 14
8	1I	145/148 (98%)	122 (84%)	22 (15%)	1 (1%)	18 38
8	2I	144/148 (97%)	124 (86%)	18 (12%)	2 (1%)	9 19
9	1N	138/140 (99%)	128 (93%)	10 (7%)	0	100 100
9	2N	138/140 (99%)	129 (94%)	9 (6%)	0	100 100
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100 100
10	2O	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16 34
11	1P	147/150 (98%)	136 (92%)	10 (7%)	1 (1%)	18 38
11	2P	147/150 (98%)	136 (92%)	10 (7%)	1 (1%)	18 38
12	1Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
12	2Q	139/141 (99%)	133 (96%)	5 (4%)	1 (1%)	18 38
13	1R	116/118 (98%)	112 (97%)	4 (3%)	0	100 100
13	2R	116/118 (98%)	108 (93%)	7 (6%)	1 (1%)	14 30
14	1S	108/112 (96%)	103 (95%)	4 (4%)	1 (1%)	14 30
14	2S	108/112 (96%)	100 (93%)	8 (7%)	0	100 100
15	1T	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	16 34
15	2T	129/146 (88%)	121 (94%)	8 (6%)	0	100 100
16	1U	114/118 (97%)	114 (100%)	0	0	100 100
16	2U	114/118 (97%)	112 (98%)	2 (2%)	0	100 100
17	1V	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12 28
17	2V	99/101 (98%)	91 (92%)	6 (6%)	2 (2%)	6 12
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100 100
18	2W	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
19	1X	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	11 25
19	2X	93/96 (97%)	86 (92%)	6 (6%)	1 (1%)	11 25
20	1Y	105/110 (96%)	96 (91%)	9 (9%)	0	100 100
20	2Y	105/110 (96%)	93 (89%)	12 (11%)	0	100 100
21	1Z	201/206 (98%)	184 (92%)	17 (8%)	0	100 100
21	2Z	199/206 (97%)	172 (86%)	24 (12%)	3 (2%)	8 18
22	10	81/85 (95%)	77 (95%)	4 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
22	20	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	10 23
23	11	95/98 (97%)	91 (96%)	3 (3%)	1 (1%)	11 25
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11 25
24	12	68/72 (94%)	68 (100%)	0	0	100 100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100 100
25	13	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
25	23	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
26	14	67/71 (94%)	50 (75%)	16 (24%)	1 (2%)	8 18
26	24	67/71 (94%)	48 (72%)	16 (24%)	3 (4%)	2 2
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
27	25	57/60 (95%)	53 (93%)	4 (7%)	0	100 100
28	16	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
28	26	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
29	17	46/49 (94%)	46 (100%)	0	0	100 100
29	27	46/49 (94%)	46 (100%)	0	0	100 100
30	18	62/65 (95%)	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%)	34 (97%)	1 (3%)	0	100 100
33	1b	229/256 (90%)	199 (87%)	24 (10%)	6 (3%)	4 7
33	2b	229/256 (90%)	191 (83%)	32 (14%)	6 (3%)	4 7
34	1c	204/239 (85%)	182 (89%)	21 (10%)	1 (0%)	24 46
34	2c	204/239 (85%)	163 (80%)	38 (19%)	3 (2%)	8 18
35	1d	206/209 (99%)	188 (91%)	17 (8%)	1 (0%)	24 46
35	2d	206/209 (99%)	187 (91%)	18 (9%)	1 (0%)	24 46
36	1e	146/162 (90%)	135 (92%)	9 (6%)	2 (1%)	9 19
36	2e	146/162 (90%)	133 (91%)	13 (9%)	0	100 100
37	1f	98/101 (97%)	91 (93%)	7 (7%)	0	100 100
37	2f	98/101 (97%)	93 (95%)	5 (5%)	0	100 100
38	1g	153/156 (98%)	142 (93%)	10 (6%)	1 (1%)	18 38
38	2g	153/156 (98%)	139 (91%)	12 (8%)	2 (1%)	9 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
39	1h	135/138 (98%)	125 (93%)	10 (7%)	0	100 100
39	2h	135/138 (98%)	124 (92%)	10 (7%)	1 (1%)	18 38
40	1i	125/128 (98%)	107 (86%)	18 (14%)	0	100 100
40	2i	124/128 (97%)	111 (90%)	13 (10%)	0	100 100
41	1j	95/105 (90%)	81 (85%)	9 (10%)	5 (5%)	1 1
41	2j	94/105 (90%)	79 (84%)	13 (14%)	2 (2%)	5 11
42	1k	112/129 (87%)	97 (87%)	14 (12%)	1 (1%)	14 30
42	2k	112/129 (87%)	101 (90%)	10 (9%)	1 (1%)	14 30
43	1l	119/132 (90%)	110 (92%)	9 (8%)	0	100 100
43	2l	119/132 (90%)	113 (95%)	6 (5%)	0	100 100
44	1m	114/126 (90%)	99 (87%)	12 (10%)	3 (3%)	4 7
44	2m	112/126 (89%)	91 (81%)	19 (17%)	2 (2%)	6 14
45	1n	58/61 (95%)	55 (95%)	3 (5%)	0	100 100
45	2n	58/61 (95%)	56 (97%)	2 (3%)	0	100 100
46	1o	86/89 (97%)	80 (93%)	4 (5%)	2 (2%)	5 9
46	2o	86/89 (97%)	79 (92%)	7 (8%)	0	100 100
47	1p	80/88 (91%)	74 (92%)	6 (8%)	0	100 100
47	2p	80/88 (91%)	72 (90%)	8 (10%)	0	100 100
48	1q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	12 28
48	2q	97/105 (92%)	92 (95%)	5 (5%)	0	100 100
49	1r	66/88 (75%)	63 (96%)	3 (4%)	0	100 100
49	2r	66/88 (75%)	65 (98%)	1 (2%)	0	100 100
50	1s	81/93 (87%)	73 (90%)	7 (9%)	1 (1%)	10 23
50	2s	81/93 (87%)	66 (82%)	14 (17%)	1 (1%)	10 23
51	1t	94/106 (89%)	85 (90%)	8 (8%)	1 (1%)	11 25
51	2t	96/106 (91%)	88 (92%)	6 (6%)	2 (2%)	5 11
52	1u	21/27 (78%)	20 (95%)	1 (5%)	0	100 100
52	2u	21/27 (78%)	16 (76%)	5 (24%)	0	100 100
53	1y	95/113 (84%)	93 (98%)	2 (2%)	0	100 100
53	2y	94/113 (83%)	86 (92%)	7 (7%)	1 (1%)	11 25
56	1v	1/3 (33%)	1 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
56	2v	1/3 (33%)	1 (100%)	0	0	100 100
All	All	11643/12360 (94%)	10671 (92%)	882 (8%)	90 (1%)	16 34

All (90) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1G	44	GLY
7	1H	126	PRO
19	1X	94	GLY
33	1b	17	PHE
33	1b	127	ILE
41	1j	55	LYS
44	1m	67	GLU
8	2I	10	GLU
8	2I	117	GLU
26	24	62	ARG
33	2b	16	HIS
33	2b	125	PRO
5	1F	130	ALA
6	1G	47	LYS
6	1G	50	ALA
33	1b	21	ARG
35	1d	179	GLU
36	1e	96	PRO
36	1e	97	GLY
38	1g	55	GLY
41	1j	79	ARG
42	1k	105	VAL
44	1m	3	ARG
51	1t	47	GLY
5	2F	130	ALA
6	2G	48	GLU
6	2G	96	ARG
6	2G	117	PHE
17	2V	79	VAL
19	2X	94	GLY
21	2Z	168	GLU
33	2b	17	PHE
34	2c	98	ASN
35	2d	151	LYS
38	2g	55	GLY
42	2k	89	ALA

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Mol	Chain	Res	Type
17	1V	79	VAL
23	11	3	LYS
33	1b	20	GLU
41	1j	77	PRO
48	1q	68	ARG
7	2H	48	GLY
11	2P	29	LYS
21	2Z	52	SER
23	21	3	LYS
26	24	55	ARG
26	24	56	VAL
33	2b	124	SER
33	2b	190	THR
34	2c	18	TRP
41	2j	79	ARG
41	2j	92	THR
50	2s	26	GLY
51	2t	100	ILE
4	1E	52	LEU
6	1G	49	ASP
14	1S	94	TYR
15	1T	127	ALA
50	1s	24	ALA
4	2E	52	LEU
6	2G	124	SER
7	2H	126	PRO
33	2b	20	GLU
11	1P	4	SER
26	14	47	GLN
33	1b	190	THR
34	1c	49	SER
44	1m	12	ASN
10	2O	5	GLN
12	2Q	59	ARG
13	2R	107	ASP
17	2V	100	ARG
21	2Z	167	PRO
22	20	4	LYS
38	2g	109	ASN
44	2m	8	GLU
8	1I	86	THR
53	2y	45	PRO

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Mol	Chain	Res	Type
7	2H	92	ILE
39	2h	83	ILE
33	1b	232	PRO
6	2G	87	PRO
34	2c	68	VAL
6	1G	52	ILE
46	1o	86	GLY
51	2t	102	GLY
41	1j	31	GLY
46	1o	19	PRO
44	2m	24	GLY
41	1j	91	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	214/218 (98%)	195 (91%)	19 (9%)	9 20
3	2D	215/218 (99%)	198 (92%)	17 (8%)	11 26
4	1E	164/166 (99%)	154 (94%)	10 (6%)	17 37
4	2E	164/166 (99%)	152 (93%)	12 (7%)	13 29
5	1F	160/166 (96%)	143 (89%)	17 (11%)	6 14
5	2F	159/166 (96%)	139 (87%)	20 (13%)	4 9
6	1G	144/156 (92%)	136 (94%)	8 (6%)	19 40
6	2G	142/156 (91%)	128 (90%)	14 (10%)	7 16
7	1H	144/148 (97%)	129 (90%)	15 (10%)	7 14
7	2H	143/148 (97%)	126 (88%)	17 (12%)	5 10
8	1I	111/124 (90%)	96 (86%)	15 (14%)	4 7
8	2I	108/124 (87%)	88 (82%)	20 (18%)	1 3
9	1N	119/119 (100%)	110 (92%)	9 (8%)	12 27
9	2N	118/119 (99%)	109 (92%)	9 (8%)	12 27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
10	1O	100/100 (100%)	95 (95%)	5 (5%)	22 46
10	2O	100/100 (100%)	95 (95%)	5 (5%)	22 46
11	1P	115/116 (99%)	108 (94%)	7 (6%)	17 37
11	2P	115/116 (99%)	109 (95%)	6 (5%)	21 44
12	1Q	111/111 (100%)	107 (96%)	4 (4%)	31 58
12	2Q	111/111 (100%)	100 (90%)	11 (10%)	7 16
13	1R	101/101 (100%)	93 (92%)	8 (8%)	11 26
13	2R	101/101 (100%)	95 (94%)	6 (6%)	18 38
14	1S	87/88 (99%)	84 (97%)	3 (3%)	32 60
14	2S	85/88 (97%)	72 (85%)	13 (15%)	3 5
15	1T	115/127 (91%)	108 (94%)	7 (6%)	17 37
15	2T	113/127 (89%)	108 (96%)	5 (4%)	25 50
16	1U	93/94 (99%)	87 (94%)	6 (6%)	15 35
16	2U	93/94 (99%)	88 (95%)	5 (5%)	20 42
17	1V	81/82 (99%)	75 (93%)	6 (7%)	13 29
17	2V	80/82 (98%)	70 (88%)	10 (12%)	4 9
18	1W	90/92 (98%)	83 (92%)	7 (8%)	11 26
18	2W	90/92 (98%)	83 (92%)	7 (8%)	11 26
19	1X	77/78 (99%)	75 (97%)	2 (3%)	40 68
19	2X	77/78 (99%)	70 (91%)	7 (9%)	9 19
20	1Y	86/91 (94%)	76 (88%)	10 (12%)	5 11
20	2Y	86/91 (94%)	77 (90%)	9 (10%)	6 14
21	1Z	169/179 (94%)	152 (90%)	17 (10%)	7 15
21	2Z	165/179 (92%)	150 (91%)	15 (9%)	9 19
22	10	65/67 (97%)	59 (91%)	6 (9%)	8 19
22	20	64/67 (96%)	62 (97%)	2 (3%)	35 63
23	11	79/83 (95%)	78 (99%)	1 (1%)	61 82
23	21	81/83 (98%)	75 (93%)	6 (7%)	13 29
24	12	65/67 (97%)	63 (97%)	2 (3%)	35 63
24	22	66/67 (98%)	56 (85%)	10 (15%)	3 5
25	13	51/52 (98%)	46 (90%)	5 (10%)	7 17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
25	23	50/52 (96%)	42 (84%)	8 (16%)	2 4
26	14	58/63 (92%)	53 (91%)	5 (9%)	10 22
26	24	54/63 (86%)	45 (83%)	9 (17%)	2 4
27	15	51/52 (98%)	48 (94%)	3 (6%)	18 38
27	25	50/52 (96%)	46 (92%)	4 (8%)	11 25
28	16	51/52 (98%)	48 (94%)	3 (6%)	18 38
28	26	50/52 (96%)	45 (90%)	5 (10%)	7 16
29	17	41/42 (98%)	40 (98%)	1 (2%)	43 70
29	27	41/42 (98%)	39 (95%)	2 (5%)	22 47
30	18	54/55 (98%)	53 (98%)	1 (2%)	50 75
30	28	54/55 (98%)	50 (93%)	4 (7%)	13 29
31	19	34/34 (100%)	32 (94%)	2 (6%)	18 38
31	29	34/34 (100%)	31 (91%)	3 (9%)	9 21
33	1b	191/220 (87%)	168 (88%)	23 (12%)	5 10
33	2b	187/220 (85%)	160 (86%)	27 (14%)	3 6
34	1c	144/188 (77%)	132 (92%)	12 (8%)	10 23
34	2c	140/188 (74%)	124 (89%)	16 (11%)	5 11
35	1d	171/181 (94%)	154 (90%)	17 (10%)	7 16
35	2d	172/181 (95%)	150 (87%)	22 (13%)	4 8
36	1e	114/123 (93%)	100 (88%)	14 (12%)	4 9
36	2e	114/123 (93%)	104 (91%)	10 (9%)	9 21
37	1f	85/90 (94%)	76 (89%)	9 (11%)	6 14
37	2f	85/90 (94%)	78 (92%)	7 (8%)	10 24
38	1g	120/127 (94%)	107 (89%)	13 (11%)	6 13
38	2g	119/127 (94%)	106 (89%)	13 (11%)	6 13
39	1h	116/119 (98%)	105 (90%)	11 (10%)	8 18
39	2h	114/119 (96%)	106 (93%)	8 (7%)	14 31
40	1i	91/99 (92%)	80 (88%)	11 (12%)	5 10
40	2i	88/99 (89%)	75 (85%)	13 (15%)	3 6
41	1j	68/92 (74%)	62 (91%)	6 (9%)	9 21
41	2j	68/92 (74%)	57 (84%)	11 (16%)	2 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
42	1k	83/99 (84%)	78 (94%)	5 (6%)	17 37
42	2k	83/99 (84%)	79 (95%)	4 (5%)	23 47
43	1l	96/108 (89%)	93 (97%)	3 (3%)	35 63
43	2l	96/108 (89%)	92 (96%)	4 (4%)	26 52
44	1m	90/101 (89%)	82 (91%)	8 (9%)	9 20
44	2m	87/101 (86%)	81 (93%)	6 (7%)	14 32
45	1n	49/50 (98%)	45 (92%)	4 (8%)	10 24
45	2n	49/50 (98%)	47 (96%)	2 (4%)	27 54
46	1o	78/80 (98%)	73 (94%)	5 (6%)	16 35
46	2o	78/80 (98%)	69 (88%)	9 (12%)	5 11
47	1p	69/74 (93%)	61 (88%)	8 (12%)	5 11
47	2p	68/74 (92%)	59 (87%)	9 (13%)	4 8
48	1q	94/97 (97%)	85 (90%)	9 (10%)	8 17
48	2q	94/97 (97%)	87 (93%)	7 (7%)	13 29
49	1r	59/77 (77%)	53 (90%)	6 (10%)	7 15
49	2r	59/77 (77%)	54 (92%)	5 (8%)	10 22
50	1s	68/80 (85%)	62 (91%)	6 (9%)	9 21
50	2s	67/80 (84%)	60 (90%)	7 (10%)	7 14
51	1t	71/82 (87%)	62 (87%)	9 (13%)	4 9
51	2t	70/82 (85%)	67 (96%)	3 (4%)	26 51
52	1u	18/22 (82%)	17 (94%)	1 (6%)	19 40
52	2u	18/22 (82%)	18 (100%)	0	100 100
53	1y	82/98 (84%)	74 (90%)	8 (10%)	7 17
53	2y	79/98 (81%)	71 (90%)	8 (10%)	7 15
56	1v	2/2 (100%)	2 (100%)	0	100 100
56	2v	2/2 (100%)	2 (100%)	0	100 100
All	All	9535/10264 (93%)	8691 (91%)	844 (9%)	9 20

All (844) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	37	LEU
3	1D	39	LYS

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Mol	Chain	Res	Type
3	1D	69	ARG
3	1D	88	ARG
3	1D	94	LEU
3	1D	99	ASP
3	1D	103	ARG
3	1D	111	LEU
3	1D	113	VAL
3	1D	140	THR
3	1D	141	VAL
3	1D	142	VAL
3	1D	183	ARG
3	1D	193	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
3	1D	270	ILE
3	1D	275	LYS
4	1E	69	LYS
4	1E	75	VAL
4	1E	116	VAL
4	1E	170	LEU
4	1E	178	GLU
4	1E	181	LEU
4	1E	182	LEU
4	1E	188	VAL
4	1E	195	LEU
4	1E	202	LYS
5	1F	12	LEU
5	1F	24	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	108	LYS
5	1F	132	VAL
5	1F	140	LEU
5	1F	148	LEU
5	1F	157	VAL
5	1F	158	THR
5	1F	162	LEU
5	1F	183	VAL
5	1F	189	THR

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Mol	Chain	Res	Type
5	1F	192	LEU
5	1F	197	ASP
6	1G	7	LEU
6	1G	26	GLN
6	1G	43	LEU
6	1G	52	ILE
6	1G	79	ASN
6	1G	126	ASP
6	1G	159	VAL
6	1G	175	LEU
7	1H	15	VAL
7	1H	23	ARG
7	1H	43	VAL
7	1H	49	VAL
7	1H	52	VAL
7	1H	71	LEU
7	1H	81	GLU
7	1H	88	LEU
7	1H	95	ARG
7	1H	107	VAL
7	1H	119	GLU
7	1H	122	THR
7	1H	125	VAL
7	1H	129	THR
7	1H	134	SER
8	1I	7	GLU
8	1I	9	LEU
8	1I	38	LEU
8	1I	41	GLU
8	1I	60	GLU
8	1I	68	LEU
8	1I	78	THR
8	1I	82	ARG
8	1I	85	GLU
8	1I	92	VAL
8	1I	108	THR
8	1I	109	ILE
8	1I	127	VAL
8	1I	129	THR
8	1I	140	LEU
9	1N	1	MET
9	1N	9	VAL

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Mol	Chain	Res	Type
9	1N	14	VAL
9	1N	33	LEU
9	1N	61	ARG
9	1N	62	VAL
9	1N	73	THR
9	1N	99	LEU
9	1N	133	GLN
10	1O	39	ILE
10	1O	69	ILE
10	1O	94	ARG
10	1O	108	GLU
10	1O	113	LYS
11	1P	57	THR
11	1P	59	LEU
11	1P	83	VAL
11	1P	95	VAL
11	1P	121	LYS
11	1P	135	LEU
11	1P	149	GLU
12	1Q	55	VAL
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	109	VAL
13	1R	36	THR
13	1R	54	LEU
13	1R	67	LEU
13	1R	75	LEU
13	1R	100	LEU
13	1R	102	GLU
13	1R	113	LEU
13	1R	114	VAL
14	1S	46	VAL
14	1S	50	SER
14	1S	59	LYS
15	1T	28	VAL
15	1T	34	VAL
15	1T	36	GLU
15	1T	53	ARG
15	1T	67	SER
15	1T	96	ARG
15	1T	118	ARG
16	1U	8	VAL

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Mol	Chain	Res	Type
16	1U	31	SER
16	1U	59	ARG
16	1U	74	LEU
16	1U	84	LYS
16	1U	117	GLN
17	1V	28	GLU
17	1V	35	LEU
17	1V	44	LYS
17	1V	46	VAL
17	1V	52	VAL
17	1V	79	VAL
18	1W	4	LYS
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	65	LEU
18	1W	78	GLU
18	1W	96	ILE
19	1X	45	THR
19	1X	88	LYS
20	1Y	7	VAL
20	1Y	23	ARG
20	1Y	34	LYS
20	1Y	38	ILE
20	1Y	43	ASN
20	1Y	64	GLU
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	99	CYS
20	1Y	106	LEU
21	1Z	18	LEU
21	1Z	27	VAL
21	1Z	31	ARG
21	1Z	50	GLN
21	1Z	66	SER
21	1Z	81	ARG
21	1Z	86	VAL
21	1Z	93	ASP
21	1Z	94	GLU
21	1Z	98	MET
21	1Z	120	ILE
21	1Z	126	VAL

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Mol	Chain	Res	Type
21	1Z	132	ASN
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	162	GLU
21	1Z	165	VAL
22	10	5	LYS
22	10	44	ARG
22	10	49	LYS
22	10	55	ARG
22	10	59	LEU
22	10	74	ARG
23	11	80	LEU
24	12	45	SER
24	12	53	LEU
25	13	3	ARG
25	13	17	LYS
25	13	38	GLU
25	13	54	VAL
25	13	56	VAL
26	14	22	ILE
26	14	33	VAL
26	14	49	PHE
26	14	50	VAL
26	14	52	THR
27	15	6	VAL
27	15	40	LYS
27	15	58	LEU
28	16	9	LEU
28	16	13	CYS
28	16	52	VAL
29	17	32	LYS
30	18	14	VAL
31	19	13	LYS
31	19	26	ILE
33	1b	8	LYS
33	1b	42	ILE
33	1b	43	ASP
33	1b	61	LEU
33	1b	78	GLN
33	1b	103	THR
33	1b	107	THR
33	1b	111	ARG

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Mol	Chain	Res	Type
33	1b	112	VAL
33	1b	128	GLU
33	1b	139	LYS
33	1b	160	ASP
33	1b	168	THR
33	1b	179	LYS
33	1b	185	ILE
33	1b	200	ILE
33	1b	209	ARG
33	1b	212	GLN
33	1b	214	ILE
33	1b	223	ILE
33	1b	229	VAL
33	1b	230	VAL
33	1b	231	GLU
34	1c	3	ASN
34	1c	26	LYS
34	1c	49	SER
34	1c	58	GLU
34	1c	64	VAL
34	1c	70	VAL
34	1c	89	GLU
34	1c	105	GLU
34	1c	112	SER
34	1c	118	GLN
34	1c	123	GLN
34	1c	161	GLU
35	1d	8	VAL
35	1d	11	LEU
35	1d	25	ARG
35	1d	28	SER
35	1d	59	ARG
35	1d	70	ILE
35	1d	77	ASN
35	1d	83	SER
35	1d	127	THR
35	1d	132	ARG
35	1d	137	SER
35	1d	177	ASP
35	1d	187	ARG
35	1d	191	ARG
35	1d	200	GLU

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Mol	Chain	Res	Type
35	1d	204	ILE
35	1d	209	ARG
36	1e	5	ASP
36	1e	11	ILE
36	1e	18	ARG
36	1e	31	LEU
36	1e	41	VAL
36	1e	64	ARG
36	1e	67	VAL
36	1e	69	VAL
36	1e	72	GLN
36	1e	75	THR
36	1e	79	GLU
36	1e	92	LYS
36	1e	126	ARG
36	1e	131	ILE
37	1f	10	LEU
37	1f	17	SER
37	1f	21	LEU
37	1f	40	VAL
37	1f	45	LEU
37	1f	63	TYR
37	1f	69	GLU
37	1f	73	ASN
37	1f	98	LEU
38	1g	6	ARG
38	1g	9	VAL
38	1g	12	LEU
38	1g	27	ILE
38	1g	41	ARG
38	1g	57	GLU
38	1g	63	LYS
38	1g	66	VAL
38	1g	98	SER
38	1g	104	LEU
38	1g	114	ARG
38	1g	125	MET
38	1g	143	ARG
39	1h	25	ASP
39	1h	26	VAL
39	1h	49	GLU
39	1h	52	ASP

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Mol	Chain	Res	Type
39	1h	54	ASP
39	1h	63	LEU
39	1h	88	LYS
39	1h	95	VAL
39	1h	127	LEU
39	1h	133	LEU
39	1h	137	VAL
40	1i	29	ASN
40	1i	41	VAL
40	1i	42	ARG
40	1i	47	LEU
40	1i	50	LEU
40	1i	56	LEU
40	1i	66	ARG
40	1i	81	ILE
40	1i	104	ARG
40	1i	108	VAL
40	1i	112	LYS
41	1j	42	THR
41	1j	55	LYS
41	1j	65	LEU
41	1j	84	GLN
41	1j	94	VAL
41	1j	96	ILE
42	1k	16	SER
42	1k	24	SER
42	1k	87	THR
42	1k	109	VAL
42	1k	114	VAL
43	1l	33	ARG
43	1l	70	ILE
43	1l	118	SER
44	1m	4	ILE
44	1m	11	ARG
44	1m	14	ARG
44	1m	60	VAL
44	1m	70	LEU
44	1m	88	ARG
44	1m	114	ARG
44	1m	117	VAL
45	1n	18	VAL
45	1n	42	ILE

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Mol	Chain	Res	Type
45	1n	50	LYS
45	1n	57	ARG
46	1o	5	LYS
46	1o	9	GLN
46	1o	26	GLU
46	1o	39	LEU
46	1o	71	GLN
47	1p	11	SER
47	1p	19	ILE
47	1p	29	ASP
47	1p	34	GLU
47	1p	50	LYS
47	1p	62	VAL
47	1p	67	THR
47	1p	79	VAL
48	1q	19	VAL
48	1q	24	GLU
48	1q	53	LEU
48	1q	63	ARG
48	1q	70	ARG
48	1q	74	LEU
48	1q	78	GLU
48	1q	97	SER
48	1q	100	LYS
49	1r	25	THR
49	1r	28	GLU
49	1r	46	GLU
49	1r	47	THR
49	1r	65	ILE
49	1r	76	LEU
50	1s	28	LYS
50	1s	35	SER
50	1s	37	ARG
50	1s	40	ILE
50	1s	48	THR
50	1s	79	THR
51	1t	9	ASN
51	1t	15	ARG
51	1t	29	LYS
51	1t	30	LYS
51	1t	34	LYS
51	1t	37	SER

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Mol	Chain	Res	Type
51	1t	41	ILE
51	1t	70	SER
51	1t	80	ARG
52	1u	20	LYS
53	1y	9	GLN
53	1y	13	THR
53	1y	23	ARG
53	1y	24	LEU
53	1y	42	SER
53	1y	46	GLN
53	1y	62	VAL
53	1y	88	LEU
3	2D	3	VAL
3	2D	4	LYS
3	2D	18	VAL
3	2D	32	SER
3	2D	83	GLU
3	2D	99	ASP
3	2D	106	ILE
3	2D	111	LEU
3	2D	113	VAL
3	2D	116	GLN
3	2D	142	VAL
3	2D	150	LYS
3	2D	183	ARG
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
4	2E	38	THR
4	2E	69	LYS
4	2E	75	VAL
4	2E	116	VAL
4	2E	119	ARG
4	2E	134	ILE
4	2E	152	LYS
4	2E	163	GLU
4	2E	170	LEU
4	2E	181	LEU
4	2E	184	VAL
4	2E	195	LEU
5	2F	20	LEU

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Mol	Chain	Res	Type
5	2F	23	ASP
5	2F	33	LEU
5	2F	43	LYS
5	2F	60	SER
5	2F	74	ARG
5	2F	88	VAL
5	2F	108	LYS
5	2F	112	MET
5	2F	132	VAL
5	2F	136	THR
5	2F	158	THR
5	2F	161	GLU
5	2F	168	ARG
5	2F	170	LEU
5	2F	183	VAL
5	2F	192	LEU
5	2F	197	ASP
5	2F	200	GLU
5	2F	201	VAL
6	2G	7	LEU
6	2G	37	VAL
6	2G	41	GLN
6	2G	53	LEU
6	2G	58	GLN
6	2G	88	ILE
6	2G	91	ARG
6	2G	103	LEU
6	2G	109	VAL
6	2G	126	ASP
6	2G	140	ILE
6	2G	148	MET
6	2G	149	VAL
6	2G	159	VAL
7	2H	11	VAL
7	2H	17	VAL
7	2H	32	GLU
7	2H	33	LEU
7	2H	41	MET
7	2H	43	VAL
7	2H	52	VAL
7	2H	67	LEU
7	2H	68	THR

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Mol	Chain	Res	Type
7	2H	76	VAL
7	2H	97	ARG
7	2H	122	THR
7	2H	133	VAL
7	2H	139	GLN
7	2H	143	GLN
7	2H	148	ILE
7	2H	171	LEU
8	2I	5	LEU
8	2I	9	LEU
8	2I	12	LEU
8	2I	38	LEU
8	2I	40	THR
8	2I	43	ASN
8	2I	47	LEU
8	2I	51	ILE
8	2I	58	LEU
8	2I	64	GLU
8	2I	68	LEU
8	2I	69	LYS
8	2I	76	THR
8	2I	87	LYS
8	2I	116	LEU
8	2I	117	GLU
8	2I	121	LYS
8	2I	127	VAL
8	2I	140	LEU
8	2I	142	VAL
9	2N	9	VAL
9	2N	12	ARG
9	2N	15	LEU
9	2N	43	THR
9	2N	48	MET
9	2N	54	VAL
9	2N	60	ILE
9	2N	62	VAL
9	2N	138	LEU
10	2O	8	LEU
10	2O	35	VAL
10	2O	38	VAL
10	2O	58	VAL
10	2O	78	ARG

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Mol	Chain	Res	Type
11	2P	65	ARG
11	2P	83	VAL
11	2P	95	VAL
11	2P	96	THR
11	2P	99	LEU
11	2P	133	SER
12	2Q	7	MET
12	2Q	21	THR
12	2Q	31	ASP
12	2Q	55	VAL
12	2Q	60	ARG
12	2Q	75	THR
12	2Q	79	LEU
12	2Q	81	VAL
12	2Q	109	VAL
12	2Q	112	GLU
12	2Q	115	MET
13	2R	36	THR
13	2R	54	LEU
13	2R	73	VAL
13	2R	75	LEU
13	2R	96	ARG
13	2R	100	LEU
14	2S	21	THR
14	2S	25	ARG
14	2S	32	LEU
14	2S	38	GLN
14	2S	43	GLU
14	2S	48	LEU
14	2S	52	SER
14	2S	64	GLU
14	2S	69	VAL
14	2S	78	LEU
14	2S	84	GLN
14	2S	85	VAL
14	2S	110	LEU
15	2T	17	THR
15	2T	51	ARG
15	2T	53	ARG
15	2T	89	VAL
15	2T	109	GLU
16	2U	31	SER

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Mol	Chain	Res	Type
16	2U	63	VAL
16	2U	74	LEU
16	2U	111	GLU
16	2U	117	GLN
17	2V	7	THR
17	2V	13	ARG
17	2V	32	THR
17	2V	39	LEU
17	2V	40	LEU
17	2V	46	VAL
17	2V	51	VAL
17	2V	72	VAL
17	2V	79	VAL
17	2V	93	GLU
18	2W	6	ILE
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	28	SER
18	2W	65	LEU
18	2W	100	THR
19	2X	2	LYS
19	2X	5	TYR
19	2X	15	GLU
19	2X	63	LYS
19	2X	66	LEU
19	2X	81	VAL
19	2X	88	LYS
20	2Y	3	VAL
20	2Y	19	LYS
20	2Y	39	VAL
20	2Y	55	TYR
20	2Y	63	LYS
20	2Y	67	LEU
20	2Y	72	VAL
20	2Y	98	VAL
20	2Y	99	CYS
21	2Z	18	LEU
21	2Z	27	VAL
21	2Z	33	LEU
21	2Z	35	ARG
21	2Z	70	LEU

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Mol	Chain	Res	Type
21	2Z	71	VAL
21	2Z	86	VAL
21	2Z	90	VAL
21	2Z	91	LEU
21	2Z	94	GLU
21	2Z	97	GLU
21	2Z	128	VAL
21	2Z	171	ILE
21	2Z	175	VAL
21	2Z	185	GLU
22	20	36	ILE
22	20	68	GLU
23	21	4	VAL
23	21	11	ARG
23	21	40	ARG
23	21	46	LEU
23	21	52	ARG
23	21	85	LEU
24	22	17	SER
24	22	27	GLU
24	22	31	GLU
24	22	32	LEU
24	22	40	SER
24	22	49	LYS
24	22	53	LEU
24	22	60	LEU
24	22	62	THR
24	22	70	GLN
25	23	23	LEU
25	23	26	LEU
25	23	29	ARG
25	23	31	LEU
25	23	37	LEU
25	23	54	VAL
25	23	56	VAL
25	23	59	VAL
26	24	15	ILE
26	24	33	VAL
26	24	44	THR
26	24	50	VAL
26	24	52	THR
26	24	53	GLU

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Mol	Chain	Res	Type
26	24	61	ARG
26	24	67	TYR
26	24	69	LYS
27	25	6	VAL
27	25	25	LEU
27	25	40	LYS
27	25	58	LEU
28	26	9	LEU
28	26	29	ASN
28	26	32	ASN
28	26	34	LEU
28	26	48	VAL
29	27	42	LEU
29	27	48	LYS
30	28	14	VAL
30	28	41	ILE
30	28	49	VAL
30	28	50	LEU
31	29	4	ARG
31	29	13	LYS
31	29	26	ILE
33	2b	7	VAL
33	2b	8	LYS
33	2b	15	VAL
33	2b	58	ILE
33	2b	67	THR
33	2b	71	VAL
33	2b	80	ILE
33	2b	93	VAL
33	2b	96	ARG
33	2b	97	TRP
33	2b	121	LEU
33	2b	127	ILE
33	2b	154	LEU
33	2b	160	ASP
33	2b	172	ILE
33	2b	185	ILE
33	2b	189	ASP
33	2b	191	ASP
33	2b	200	ILE
33	2b	212	GLN
33	2b	215	LEU

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Mol	Chain	Res	Type
33	2b	219	VAL
33	2b	221	LEU
33	2b	223	ILE
33	2b	224	GLN
33	2b	229	VAL
33	2b	230	VAL
34	2c	5	ILE
34	2c	33	LEU
34	2c	34	LEU
34	2c	52	LEU
34	2c	89	GLU
34	2c	101	LEU
34	2c	103	VAL
34	2c	105	GLU
34	2c	111	LEU
34	2c	131	ARG
34	2c	139	GLN
34	2c	143	GLU
34	2c	152	ILE
34	2c	192	THR
34	2c	206	GLU
34	2c	207	VAL
35	2d	5	ILE
35	2d	8	VAL
35	2d	21	LEU
35	2d	28	SER
35	2d	34	GLU
35	2d	52	SER
35	2d	60	GLU
35	2d	67	ILE
35	2d	83	SER
35	2d	104	VAL
35	2d	106	TYR
35	2d	126	ILE
35	2d	127	THR
35	2d	135	LEU
35	2d	141	ARG
35	2d	166	LYS
35	2d	169	LYS
35	2d	175	SER
35	2d	186	LEU
35	2d	203	VAL

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Mol	Chain	Res	Type
35	2d	204	ILE
35	2d	209	ARG
36	2e	11	ILE
36	2e	33	VAL
36	2e	41	VAL
36	2e	47	LYS
36	2e	64	ARG
36	2e	72	GLN
36	2e	75	THR
36	2e	79	GLU
36	2e	82	VAL
36	2e	120	THR
37	2f	22	GLU
37	2f	31	GLU
37	2f	45	LEU
37	2f	61	LEU
37	2f	63	TYR
37	2f	72	VAL
37	2f	73	ASN
38	2g	9	VAL
38	2g	22	LEU
38	2g	32	ARG
38	2g	33	ASP
38	2g	45	ASP
38	2g	50	ILE
38	2g	61	VAL
38	2g	67	GLU
38	2g	97	GLN
38	2g	104	LEU
38	2g	135	VAL
38	2g	138	LYS
38	2g	144	MET
39	2h	4	ASP
39	2h	85	ARG
39	2h	91	ARG
39	2h	114	THR
39	2h	119	LEU
39	2h	122	ARG
39	2h	129	VAL
39	2h	133	LEU
40	2i	3	GLN
40	2i	23	ASN

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Mol	Chain	Res	Type
40	2i	28	VAL
40	2i	40	LEU
40	2i	53	VAL
40	2i	56	LEU
40	2i	65	VAL
40	2i	71	SER
40	2i	78	LYS
40	2i	86	VAL
40	2i	108	VAL
40	2i	111	ARG
40	2i	125	TYR
41	2j	13	HIS
41	2j	16	LEU
41	2j	17	ASP
41	2j	29	ARG
41	2j	34	VAL
41	2j	38	ILE
41	2j	47	PHE
41	2j	58	ASP
41	2j	72	VAL
41	2j	95	GLU
41	2j	98	ILE
42	2k	30	VAL
42	2k	105	VAL
42	2k	109	VAL
42	2k	117	ASN
43	2l	6	THR
43	2l	18	VAL
43	2l	97	ARG
43	2l	100	ILE
44	2m	3	ARG
44	2m	8	GLU
44	2m	15	VAL
44	2m	90	LEU
44	2m	98	VAL
44	2m	116	THR
45	2n	42	ILE
45	2n	57	ARG
46	2o	5	LYS
46	2o	10	LYS
46	2o	14	GLU
46	2o	24	SER

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Mol	Chain	Res	Type
46	2o	39	LEU
46	2o	48	LYS
46	2o	68	ARG
46	2o	71	GLN
46	2o	87	ILE
47	2p	1	MET
47	2p	2	VAL
47	2p	20	VAL
47	2p	28	ARG
47	2p	45	THR
47	2p	53	VAL
47	2p	57	ARG
47	2p	62	VAL
47	2p	67	THR
48	2q	9	VAL
48	2q	48	GLU
48	2q	59	ILE
48	2q	70	ARG
48	2q	78	GLU
48	2q	96	GLU
48	2q	98	LEU
49	2r	25	THR
49	2r	28	GLU
49	2r	69	THR
49	2r	82	THR
49	2r	85	LEU
50	2s	5	LEU
50	2s	13	ASP
50	2s	38	SER
50	2s	41	VAL
50	2s	48	THR
50	2s	62	ILE
50	2s	77	THR
51	2t	36	LEU
51	2t	62	LEU
51	2t	100	ILE
53	2y	6	THR
53	2y	13	THR
53	2y	24	LEU
53	2y	42	SER
53	2y	54	ILE
53	2y	62	VAL

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Mol	Chain	Res	Type
53	2y	70	MET
53	2y	71	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (164) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	253	GLN
4	1E	55	ASN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	108	ASN
8	1I	74	ASN
8	1I	104	GLN
8	1I	105	HIS
9	1N	94	HIS
9	1N	133	GLN
10	1O	3	GLN
11	1P	84	ASN
12	1Q	12	GLN
12	1Q	57	HIS
13	1R	13	HIS
13	1R	24	GLN
13	1R	50	HIS
15	1T	58	ASN
15	1T	123	GLN
16	1U	94	ASN
16	1U	117	GLN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	92	ASN
21	1Z	32	HIS
21	1Z	65	GLN
21	1Z	73	GLN
21	1Z	151	HIS
24	12	46	GLN
25	13	32	GLN
26	14	60	GLN
33	1b	224	GLN
34	1c	6	HIS

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Mol	Chain	Res	Type
34	1c	63	ASN
34	1c	69	HIS
34	1c	102	ASN
34	1c	108	ASN
34	1c	110	ASN
34	1c	123	GLN
35	1d	45	GLN
35	1d	123	HIS
35	1d	125	HIS
35	1d	129	ASN
35	1d	201	GLN
36	1e	20	GLN
36	1e	65	ASN
36	1e	141	GLN
37	1f	64	GLN
37	1f	73	ASN
38	1g	28	ASN
38	1g	56	GLN
38	1g	96	GLN
38	1g	110	GLN
39	1h	70	GLN
40	1i	3	GLN
40	1i	73	GLN
40	1i	87	GLN
40	1i	117	HIS
41	1j	56	HIS
42	1k	93	GLN
43	1l	80	HIS
43	1l	99	HIS
44	1m	40	ASN
44	1m	92	HIS
45	1n	49	HIS
46	1o	9	GLN
46	1o	13	GLN
46	1o	28	GLN
46	1o	71	GLN
47	1p	13	HIS
48	1q	93	GLN
50	1s	47	HIS
50	1s	69	HIS
50	1s	83	HIS
51	1t	16	HIS

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Mol	Chain	Res	Type
51	1t	18	GLN
51	1t	45	GLN
53	1y	4	ASN
53	1y	19	HIS
53	1y	38	HIS
3	2D	126	GLN
3	2D	166	GLN
3	2D	253	GLN
4	2E	48	GLN
4	2E	55	ASN
5	2F	69	HIS
5	2F	75	HIS
6	2G	138	GLN
7	2H	143	GLN
8	2I	11	ASN
8	2I	74	ASN
8	2I	104	GLN
12	2Q	12	GLN
12	2Q	89	ASN
12	2Q	123	HIS
13	2R	13	HIS
13	2R	50	HIS
15	2T	58	ASN
16	2U	94	ASN
17	2V	64	HIS
19	2X	82	GLN
20	2Y	92	ASN
22	20	17	GLN
24	22	56	GLN
25	23	32	GLN
26	24	60	GLN
28	26	20	ASN
28	26	32	ASN
30	28	35	GLN
33	2b	19	HIS
33	2b	76	GLN
33	2b	95	GLN
33	2b	135	GLN
34	2c	3	ASN
34	2c	37	GLN
34	2c	104	GLN
34	2c	108	ASN

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Mol	Chain	Res	Type
34	2c	139	GLN
35	2d	42	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	123	HIS
35	2d	125	HIS
35	2d	160	GLN
36	2e	20	GLN
36	2e	78	HIS
36	2e	130	ASN
37	2f	32	ASN
37	2f	64	GLN
37	2f	73	ASN
38	2g	13	GLN
38	2g	64	GLN
38	2g	86	GLN
38	2g	109	ASN
39	2h	81	HIS
40	2i	3	GLN
40	2i	29	ASN
40	2i	38	GLN
40	2i	73	GLN
40	2i	87	GLN
41	2j	69	ASN
41	2j	84	GLN
42	2k	26	ASN
43	2l	78	GLN
43	2l	80	HIS
43	2l	99	HIS
44	2m	77	ASN
46	2o	13	GLN
46	2o	28	GLN
46	2o	71	GLN
47	2p	76	GLN
48	2q	45	HIS
48	2q	93	GLN
50	2s	23	ASN
50	2s	57	HIS
50	2s	83	HIS
51	2t	16	HIS
53	2y	38	HIS
53	2y	46	GLN

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Mol	Chain	Res	Type
53	2y	55	ASN
53	2y	84	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	419 (14%)	28 (0%)
1	2A	2858/2915 (98%)	476 (16%)	30 (1%)
2	1B	119/121 (98%)	11 (9%)	0
2	2B	119/121 (98%)	19 (15%)	0
32	1a	1497/1521 (98%)	255 (17%)	0
32	2a	1501/1521 (98%)	272 (18%)	0
54	1w	1/4 (25%)	0	0
54	2w	1/4 (25%)	0	0
55	1x	1/4 (25%)	0	0
55	2x	1/4 (25%)	0	0
All	All	8963/9130 (98%)	1452 (16%)	58 (0%)

All (1452) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	34	C
1	1A	36	G
1	1A	45	C
1	1A	61	G
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	94	C
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	149	A
1	1A	181	A
1	1A	182	A
1	1A	196	A
1	1A	199	A
1	1A	205	G
1	1A	216	A
1	1A	221	A

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Mol	Chain	Res	Type
1	1A	222	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	265	A
1	1A	266	G
1	1A	271(I)	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(O)	C
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	311	A
1	1A	330	A
1	1A	352	G
1	1A	363	G
1	1A	363(B)	G
1	1A	372	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	421	U
1	1A	422	A
1	1A	428	A
1	1A	448	U
1	1A	454	A
1	1A	456	C
1	1A	457	A
1	1A	479	A
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	508	G
1	1A	509	C
1	1A	512	G
1	1A	530	G
1	1A	531	C
1	1A	532	A

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Mol	Chain	Res	Type
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	586	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	615	G
1	1A	616	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(E)	G
1	1A	652(F)	G
1	1A	652(T)	C
1	1A	669	G
1	1A	686	G
1	1A	730	C
1	1A	740	U
1	1A	774	A
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	783	A
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G
1	1A	866	A
1	1A	882	G
1	1A	884	C
1	1A	886	C
1	1A	887	A
1	1A	888	C

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Mol	Chain	Res	Type
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	899	A
1	1A	907	U
1	1A	910	A
1	1A	915	C
1	1A	932	G
1	1A	938	G
1	1A	945	A
1	1A	946	G
1	1A	949	C
1	1A	958	U
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1005	C
1	1A	1008	C
1	1A	1012	U
1	1A	1013	C
1	1A	1026	U
1	1A	1033	U
1	1A	1039	G
1	1A	1042	G
1	1A	1043	C
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1055	G
1	1A	1058	G
1	1A	1060	U
1	1A	1061	U
1	1A	1062	G
1	1A	1065	U
1	1A	1066	U
1	1A	1067	A
1	1A	1068	G

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Mol	Chain	Res	Type
1	1A	1069	A
1	1A	1070	A
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U
1	1A	1079	C
1	1A	1080	C
1	1A	1082	U
1	1A	1083	U
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1093	G
1	1A	1096	A
1	1A	1097	U
1	1A	1098	A
1	1A	1100	C
1	1A	1101	U
1	1A	1104	C
1	1A	1109	C
1	1A	1110	G
1	1A	1112	G
1	1A	1116	C
1	1A	1135	C
1	1A	1136	G
1	1A	1170	G
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1210	A
1	1A	1211	U
1	1A	1220	A
1	1A	1236	G
1	1A	1241	A
1	1A	1253	A

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Mol	Chain	Res	Type
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1281	G
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1321	A
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1449	A
1	1A	1450	G
1	1A	1455	G
1	1A	1460	A
1	1A	1467	C
1	1A	1471	A
1	1A	1478	G
1	1A	1482	G
1	1A	1493	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1514	U
1	1A	1531	C
1	1A	1542	A
1	1A	1543	C
1	1A	1547	C
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A

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Mol	Chain	Res	Type
1	1A	1578	U
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1610	A
1	1A	1616	A
1	1A	1639	U
1	1A	1647	G
1	1A	1648	C
1	1A	1654	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1747	G
1	1A	1762	A
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C
1	1A	1786	A
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1812	A
1	1A	1816	G
1	1A	1829	A
1	1A	1847	A
1	1A	1877	A
1	1A	1878	G
1	1A	1889	A
1	1A	1896	G
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1929	G
1	1A	1930	G

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Mol	Chain	Res	Type
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1960	A
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2033	A
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2080	G
1	1A	2093	G
1	1A	2103	C
1	1A	2107	C
1	1A	2108	C
1	1A	2116	G
1	1A	2117	A
1	1A	2118	U
1	1A	2119	A
1	1A	2123	G
1	1A	2125	G
1	1A	2126	A
1	1A	2127	G
1	1A	2132	U
1	1A	2133	G
1	1A	2135	A
1	1A	2137	C
1	1A	2146	C
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G

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Mol	Chain	Res	Type
1	1A	2161	C
1	1A	2164	C
1	1A	2165	G
1	1A	2170	A
1	1A	2173	A
1	1A	2183	C
1	1A	2185	C
1	1A	2186	G
1	1A	2187	G
1	1A	2189	U
1	1A	2190	G
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2279	G
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2308	G
1	1A	2318	G
1	1A	2320	A
1	1A	2322	A
1	1A	2324	C
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2383	G
1	1A	2385	C
1	1A	2406	U
1	1A	2407	G
1	1A	2422	A

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Mol	Chain	Res	Type
1	1A	2423	U
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2432	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2476	A
1	1A	2491	U
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2520	C
1	1A	2525	G
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2662	A
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2751	G

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Mol	Chain	Res	Type
1	1A	2757	A
1	1A	2758	A
1	1A	2761	G
1	1A	2764	A
1	1A	2765	A
1	1A	2766	G
1	1A	2769	C
1	1A	2778	A
1	1A	2791	C
1	1A	2802	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2850	A
1	1A	2872	G
1	1A	2873	A
1	1A	2880	C
1	1A	2892	A
1	1A	2894	G
1	1A	2895	U
2	1B	7	G
2	1B	13	A
2	1B	32	C
2	1B	45	A
2	1B	53	A
2	1B	56	G
2	1B	73	A
2	1B	84	C
2	1B	106	G
2	1B	110	G
2	1B	116	G
32	1a	7	G
32	1a	9	G
32	1a	22	G
32	1a	32	A
32	1a	39	G
32	1a	44	G
32	1a	47	C
32	1a	48	C
32	1a	50	A
32	1a	51	A

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Mol	Chain	Res	Type
32	1a	55	A
32	1a	61	G
32	1a	66	G
32	1a	69	G
32	1a	78	G
32	1a	79	G
32	1a	91	C
32	1a	93	G
32	1a	97	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	141	A
32	1a	144	G
32	1a	154	C
32	1a	163	C
32	1a	169	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	183	G
32	1a	189(D)	C
32	1a	189(G)	G
32	1a	190	U
32	1a	195	A
32	1a	197	A
32	1a	201	C
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	220	G
32	1a	231	G
32	1a	247	G
32	1a	250	A
32	1a	251	G
32	1a	254	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G

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Mol	Chain	Res	Type
32	1a	301	G
32	1a	305	G
32	1a	306	G
32	1a	318	G
32	1a	321	A
32	1a	328	C
32	1a	329	A
32	1a	332	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	414	A
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	430	A
32	1a	439	A
32	1a	442	C
32	1a	443	C
32	1a	452	A
32	1a	470	C
32	1a	475	G
32	1a	477	A
32	1a	479	C
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	532	A

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Mol	Chain	Res	Type
32	1a	547	A
32	1a	550	G
32	1a	559	A
32	1a	560	U
32	1a	561	U
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	607	A
32	1a	619	U
32	1a	630	G
32	1a	632	A
32	1a	642	A
32	1a	653	A
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	724	G
32	1a	731	G
32	1a	734	G
32	1a	753	A
32	1a	755	G
32	1a	760	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	816	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	829	G
32	1a	839	U
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	851	G
32	1a	870	U
32	1a	902	G
32	1a	914	A

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Mol	Chain	Res	Type
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	942	G
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	983	A
32	1a	992	U
32	1a	993	G
32	1a	998	G
32	1a	999	C
32	1a	1004	A
32	1a	1005	A
32	1a	1006	C
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1030(D)	A
32	1a	1032	G
32	1a	1034	G
32	1a	1035	A
32	1a	1036	G
32	1a	1037	C
32	1a	1042	G
32	1a	1044	A
32	1a	1046	A
32	1a	1053	G

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Mol	Chain	Res	Type
32	1a	1065	U
32	1a	1066	C
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1121	U
32	1a	1124	G
32	1a	1130	A
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1150	U
32	1a	1152	A
32	1a	1155	G
32	1a	1159	U
32	1a	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1204	A
32	1a	1208	C
32	1a	1212	U
32	1a	1213	A
32	1a	1214	C
32	1a	1225	A
32	1a	1227	A
32	1a	1238	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1270	C
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1297	C
32	1a	1298	C

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Mol	Chain	Res	Type
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1319	A
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	1364	U
32	1a	1370	G
32	1a	1394	A
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1469	G
32	1a	1487	G
32	1a	1492	A
32	1a	1493	A
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	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	10	G
1	2A	15	G
1	2A	16	G
1	2A	34	C
1	2A	45	C
1	2A	61	G
1	2A	63	U

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Mol	Chain	Res	Type
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	98	G
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	139(A)	G
1	2A	141	A
1	2A	149	A
1	2A	157	U
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	265	A
1	2A	266	G
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(A)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	304	G
1	2A	311	A
1	2A	327	G
1	2A	329	G
1	2A	330	A

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Mol	Chain	Res	Type
1	2A	333	G
1	2A	352	G
1	2A	363	G
1	2A	372	G
1	2A	386	G
1	2A	389	G
1	2A	396	G
1	2A	411	G
1	2A	412	A
1	2A	418	G
1	2A	428	A
1	2A	441	U
1	2A	444	C
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	467	G
1	2A	470	A
1	2A	481	G
1	2A	492	A
1	2A	496	G
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	567	A
1	2A	573	G
1	2A	575	A
1	2A	595	C
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	627	A
1	2A	634	C

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Mol	Chain	Res	Type
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	653	A
1	2A	669	G
1	2A	686	G
1	2A	730	C
1	2A	740	U
1	2A	751	A
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	765	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	793	A
1	2A	794	G
1	2A	805	G
1	2A	812	C
1	2A	827	U
1	2A	828	U
1	2A	857	C
1	2A	859	G
1	2A	869	G
1	2A	877	U
1	2A	880	G
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	896	A
1	2A	897	C
1	2A	900	A
1	2A	901	A
1	2A	910	A

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Mol	Chain	Res	Type
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	959	A
1	2A	961	C
1	2A	965	C
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1033	U
1	2A	1041	C
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1048	A
1	2A	1049	C
1	2A	1051	G
1	2A	1052	C
1	2A	1053	C
1	2A	1054	A
1	2A	1057	A
1	2A	1060	U
1	2A	1063	G
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1070	A
1	2A	1071	G

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Mol	Chain	Res	Type
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1081	U
1	2A	1082	U
1	2A	1083	U
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
1	2A	1088	A
1	2A	1089	G
1	2A	1090	U
1	2A	1091	G
1	2A	1092	C
1	2A	1093	G
1	2A	1095	A
1	2A	1097	U
1	2A	1098	A
1	2A	1109	C
1	2A	1111	A
1	2A	1112	G
1	2A	1114	G
1	2A	1116	C
1	2A	1117	G
1	2A	1128	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1171	G
1	2A	1220	A
1	2A	1229	G
1	2A	1241	A
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1287	A
1	2A	1296	G

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Mol	Chain	Res	Type
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1319	G
1	2A	1342	A
1	2A	1349	A
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1455	G
1	2A	1459	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
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	1539	G
1	2A	1542	A
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1559	G
1	2A	1566	A

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Mol	Chain	Res	Type
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	1629	U
1	2A	1640	C
1	2A	1647	G
1	2A	1648	C
1	2A	1664	A
1	2A	1674	G
1	2A	1700	A
1	2A	1701	A
1	2A	1721	G
1	2A	1722	A
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	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	1816	G
1	2A	1828	G
1	2A	1829	A
1	2A	1835	G
1	2A	1839	G
1	2A	1847	A
1	2A	1861	G
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1929	G

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Mol	Chain	Res	Type
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1960	A
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2032	G
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2093	G
1	2A	2096	U
1	2A	2100	G
1	2A	2101	G
1	2A	2103	C
1	2A	2104	G
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2110	G
1	2A	2111	C
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2120	G
1	2A	2121	G
1	2A	2123	G

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Mol	Chain	Res	Type
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2139	C
1	2A	2140	C
1	2A	2142	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2150	U
1	2A	2151	G
1	2A	2152	G
1	2A	2153	G
1	2A	2158	A
1	2A	2159	G
1	2A	2162	G
1	2A	2166	G
1	2A	2172	U
1	2A	2173	A
1	2A	2184	G
1	2A	2187	G
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	2219	G
1	2A	2225	A
1	2A	2232	U
1	2A	2238	G
1	2A	2268	A
1	2A	2269	A
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A

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Mol	Chain	Res	Type
1	2A	2289	G
1	2A	2305	A
1	2A	2308	G
1	2A	2311	A
1	2A	2312	U
1	2A	2314	C
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2327	A
1	2A	2334	G
1	2A	2335	A
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2388	A
1	2A	2391	G
1	2A	2402	C
1	2A	2406	U
1	2A	2410	G
1	2A	2422	A
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2440	C
1	2A	2441	C
1	2A	2448	A
1	2A	2465	C
1	2A	2468	G
1	2A	2470	G
1	2A	2474	C
1	2A	2476	A
1	2A	2480	C
1	2A	2491	U

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Mol	Chain	Res	Type
1	2A	2494	G
1	2A	2502	G
1	2A	2505	G
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2543	G
1	2A	2549	G
1	2A	2554	U
1	2A	2556	C
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2582	G
1	2A	2602	A
1	2A	2611	U
1	2A	2612	C
1	2A	2615	U
1	2A	2630	G
1	2A	2654	A
1	2A	2660	A
1	2A	2689	U
1	2A	2690	C
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2726	U
1	2A	2733	A
1	2A	2744	G
1	2A	2752	C
1	2A	2757	A
1	2A	2758	A
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2802	G
1	2A	2820	A
1	2A	2821	A
1	2A	2836	U

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Mol	Chain	Res	Type
1	2A	2872	G
1	2A	2873	A
1	2A	2879	C
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	7	G
2	2B	9	G
2	2B	12	C
2	2B	13	A
2	2B	19	G
2	2B	32	C
2	2B	33	G
2	2B	35	U
2	2B	41	U
2	2B	42	C
2	2B	51	G
2	2B	54	G
2	2B	56	G
2	2B	73	A
2	2B	75	G
2	2B	84	C
2	2B	110	G
2	2B	115	G
32	2a	5	U
32	2a	7	G
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	61	G
32	2a	65	U
32	2a	66	G
32	2a	88	A
32	2a	89	C
32	2a	96	U
32	2a	97	G

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Mol	Chain	Res	Type
32	2a	101	A
32	2a	116	A
32	2a	120	A
32	2a	121	C
32	2a	131	C
32	2a	142	G
32	2a	156	G
32	2a	163	C
32	2a	165	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(E)	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	231	G
32	2a	240	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	298	A
32	2a	301	G
32	2a	306	G
32	2a	316	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A

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Mol	Chain	Res	Type
32	2a	378	G
32	2a	382	A
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	411	A
32	2a	412	A
32	2a	421	U
32	2a	429	U
32	2a	430	A
32	2a	431	A
32	2a	439	A
32	2a	442	C
32	2a	443	C
32	2a	452	A
32	2a	453	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	476	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	506	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G
32	2a	527	G7M
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G

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Mol	Chain	Res	Type
32	2a	596	C
32	2a	630	G
32	2a	632	A
32	2a	633	G
32	2a	652	U
32	2a	653	A
32	2a	661	G
32	2a	665	A
32	2a	666	G
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	734	G
32	2a	748	C
32	2a	749	C
32	2a	753	A
32	2a	755	G
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	798	G
32	2a	815	A
32	2a	816	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G
32	2a	840	C
32	2a	841	U
32	2a	848	C
32	2a	851	G
32	2a	854	G
32	2a	859	A
32	2a	872	A
32	2a	873	A
32	2a	889	A
32	2a	902	G

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Mol	Chain	Res	Type
32	2a	914	A
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	933	G
32	2a	934	C
32	2a	935	A
32	2a	939	G
32	2a	942	G
32	2a	954	G
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	985	C
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	997	U
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1017	G
32	2a	1020	U
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1031	G
32	2a	1034	G

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Mol	Chain	Res	Type
32	2a	1041	A
32	2a	1043	C
32	2a	1053	G
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1071	C
32	2a	1081	G
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1118	C
32	2a	1122	U
32	2a	1124	G
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1147	C
32	2a	1148	U
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1160	G
32	2a	1161	C
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1212	U
32	2a	1213	A
32	2a	1214	C
32	2a	1227	A
32	2a	1228	C
32	2a	1236	A
32	2a	1238	A
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U

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Mol	Chain	Res	Type
32	2a	1258	G
32	2a	1260	C
32	2a	1270	C
32	2a	1277	C
32	2a	1278	U
32	2a	1279	A
32	2a	1281	U
32	2a	1282	C
32	2a	1285	A
32	2a	1287	A
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1306	A
32	2a	1316	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1358	U
32	2a	1363	C
32	2a	1370	G
32	2a	1397	C
32	2a	1398	A
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1456	G
32	2a	1460	A
32	2a	1462	G
32	2a	1487	G
32	2a	1492	A
32	2a	1497	G
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1519	MA6
32	2a	1520	G

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Mol	Chain	Res	Type
32	2a	1525	G
32	2a	1528	U
32	2a	1529	G
32	2a	1530	G

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	249	C
1	1A	266	G
1	1A	271(K)	U
1	1A	278	A
1	1A	573	G
1	1A	746	A
1	1A	774	A
1	1A	840	C
1	1A	895	U
1	1A	974	G
1	1A	1047	G
1	1A	1065	U
1	1A	1089	G
1	1A	1175	U
1	1A	1176	G
1	1A	1210	A
1	1A	1301	A
1	1A	1442	G
1	1A	1608	A
1	1A	1653	G
1	1A	2126	A
1	1A	2238	G
1	1A	2422	A
1	1A	2430	A
1	1A	2439	A
1	1A	2689	U
1	1A	2756	U
1	2A	196	A
1	2A	271(M)	G
1	2A	277	C
1	2A	752	A
1	2A	764	A
1	2A	827	U

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Mol	Chain	Res	Type
1	2A	840	C
1	2A	856	C
1	2A	960	A
1	2A	1047	G
1	2A	1053	C
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1076	C
1	2A	1108	U
1	2A	1240	U
1	2A	1379	A
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2321	G
1	2A	2406	U
1	2A	2439	A
1	2A	2689	U
1	2A	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	PSU	1A	1911	1	18,21,22	1.37	2 (11%)	21,30,33	2.04	4 (19%)
32	5MC	1a	967	32	19,22,23	1.66	3 (15%)	26,32,35	1.18	2 (7%)
55	8AN	2x	76	57,56,55	21,24,25	1.38	3 (14%)	26,35,38	2.34	11 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MU	1A	1915	57,1	19,22,23	1.45	4 (21%)	27,32,35	2.38	10 (37%)
32	5MC	1a	1400	32	19,22,23	1.69	3 (15%)	26,32,35	1.19	2 (7%)
32	UR3	1a	1498	32	19,22,23	0.94	1 (5%)	26,32,35	1.70	2 (7%)
1	PSU	1A	1917	1	18,21,22	1.36	2 (11%)	21,30,33	2.03	3 (14%)
1	2MU	1A	2552	57,1	19,22,24	1.30	4 (21%)	25,31,36	2.11	6 (24%)
1	2MA	2A	2503	57,1	22,25,26	1.43	4 (18%)	32,37,40	2.41	9 (28%)
32	PSU	1a	516	32,57	18,21,22	1.39	3 (16%)	21,30,33	2.11	4 (19%)
32	5MC	2a	1400	32	19,22,23	1.64	3 (15%)	26,32,35	1.16	3 (11%)
56	FME	1v	1	56	8,9,10	1.02	0	8,9,11	0.62	0
32	MA6	1a	1518	32	23,26,27	0.41	0	33,38,41	1.96	10 (30%)
1	OMC	1A	1920	1	19,22,23	0.81	0	25,31,34	1.14	3 (12%)
32	5MC	2a	967	32	19,22,23	1.83	3 (15%)	26,32,35	1.11	2 (7%)
32	5MC	1a	1407	32	19,22,23	1.57	2 (10%)	26,32,35	1.17	3 (11%)
43	0TD	1l	92	43	8,9,10	4.77	1 (12%)	6,11,13	5.36	3 (50%)
32	5MC	2a	1407	32	19,22,23	1.70	2 (10%)	26,32,35	1.13	3 (11%)
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	0.97	1 (4%)
32	G7M	1a	527	32,57	23,26,27	1.58	3 (13%)	34,39,42	1.69	4 (11%)
32	PSU	2a	516	32,57	18,21,22	1.38	3 (16%)	21,30,33	2.04	5 (23%)
43	0TD	2l	92	43	8,9,10	4.49	1 (12%)	6,11,13	1.75	2 (33%)
1	5MC	1A	1942	1	19,22,23	1.56	3 (15%)	26,32,35	1.22	3 (11%)
32	4OC	1a	1402	32	20,23,24	0.76	0	25,32,35	0.90	1 (4%)
56	FME	2v	1	56	8,9,10	0.94	0	8,9,11	0.77	0
32	M2G	1a	966	32	24,27,28	1.32	3 (12%)	33,40,43	1.89	5 (15%)
1	PSU	2A	1917	1	18,21,22	1.39	2 (11%)	21,30,33	2.02	3 (14%)
32	M2G	2a	966	32	24,27,28	1.36	3 (12%)	33,40,43	1.85	5 (15%)
54	PPU	1w	76	1,54	37,40,41	2.88	22 (59%)	47,57,60	2.15	14 (29%)
32	MA6	2a	1518	32	23,26,27	0.38	0	33,38,41	2.01	9 (27%)
32	5MC	2a	1404	32	19,22,23	1.84	2 (10%)	26,32,35	1.19	3 (11%)
32	MA6	2a	1519	32	23,26,27	0.41	0	33,38,41	2.11	9 (27%)
32	G7M	2a	527	32	23,26,27	1.52	3 (13%)	34,39,42	1.69	4 (11%)
1	PSU	2A	2605	1	18,21,22	1.35	3 (16%)	21,30,33	1.97	4 (19%)
1	5MC	1A	1962	57,1	19,22,23	1.71	3 (15%)	26,32,35	1.13	3 (11%)
1	OMG	1A	2251	57,1,55	23,26,27	1.31	3 (13%)	32,38,41	1.99	5 (15%)
54	PPU	2w	76	1,54	37,40,41	2.43	17 (45%)	47,57,60	2.21	14 (29%)
1	5MU	2A	1939	57,1	19,22,23	1.46	5 (26%)	27,32,35	2.15	8 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	OMC	2A	1920	1	19,22,23	0.81	0	25,31,34	1.03	1 (4%)
1	2MA	1A	2503	57,1	22,25,26	1.46	5 (22%)	32,37,40	2.26	8 (25%)
1	5MC	2A	1942	1	19,22,23	1.74	3 (15%)	26,32,35	1.27	2 (7%)
1	5MC	2A	1962	1	19,22,23	1.61	3 (15%)	26,32,35	1.10	2 (7%)
1	2MU	2A	2552	57,1	19,22,24	1.28	3 (15%)	25,31,36	1.83	5 (20%)
32	2MG	1a	1207	32,57	23,26,27	1.23	4 (17%)	33,38,41	2.33	10 (30%)
32	UR3	2a	1498	32	19,22,23	0.96	1 (5%)	26,32,35	1.66	3 (11%)
1	PSU	1A	2605	1	18,21,22	1.35	2 (11%)	21,30,33	2.15	4 (19%)
32	2MG	2a	1207	32	23,26,27	1.24	4 (17%)	33,38,41	2.11	8 (24%)
1	5MU	1A	1939	57,1	19,22,23	1.39	4 (21%)	27,32,35	2.10	6 (22%)
32	5MC	1a	1404	32	19,22,23	1.51	3 (15%)	26,32,35	1.13	3 (11%)
1	5MU	2A	1915	1	19,22,23	1.47	4 (21%)	27,32,35	2.11	8 (29%)
55	8AN	1x	76	57,56,55	21,24,25	1.32	3 (14%)	26,35,38	2.38	10 (38%)
1	PSU	2A	1911	1	18,21,22	1.40	3 (16%)	21,30,33	2.04	3 (14%)
32	MA6	1a	1519	32	23,26,27	0.43	0	33,38,41	1.99	8 (24%)
1	OMG	2A	2251	57,1,55	23,26,27	1.28	3 (13%)	32,38,41	1.96	6 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
55	8AN	2x	76	57,56,55	-	3/7/25/26	0/3/3/3
1	5MU	1A	1915	57,1	-	2/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
1	2MU	1A	2552	57,1	-	0/9/27/28	0/2/2/2
1	2MA	2A	2503	57,1	-	1/7/25/26	0/3/3/3
32	PSU	1a	516	32,57	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	4/7/25/26	0/2/2/2
56	FME	1v	1	56	-	5/7/9/11	-
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
1	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	2/7/12/14	-
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	1/9/29/30	0/2/2/2
32	G7M	1a	527	32,57	-	0/7/25/26	0/3/3/3
32	PSU	2a	516	32,57	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	1/9/29/30	0/2/2/2
56	FME	2v	1	56	-	1/7/9/11	-
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
54	PPU	1w	76	1,54	-	2/25/43/44	0/4/4/4
32	MA6	2a	1518	32	-	1/11/29/30	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
32	G7M	2a	527	32	-	3/7/25/26	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1962	57,1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	57,1,55	-	0/9/27/28	0/3/3/3
54	PPU	2w	76	1,54	-	2/25/43/44	0/4/4/4
1	5MU	2A	1939	57,1	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
1	2MA	1A	2503	57,1	-	1/7/25/26	0/3/3/3
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1	-	2/7/25/26	0/2/2/2
1	2MU	2A	2552	57,1	-	0/9/27/28	0/2/2/2
32	2MG	1a	1207	32,57	-	0/9/27/28	0/3/3/3
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	1	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
1	5MU	1A	1939	57,1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
55	8AN	1x	76	57,56,55	-	1/7/25/26	0/3/3/3
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
1	OMG	2A	2251	57,1,55	-	0/9/27/28	0/3/3/3

All (161) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-13.04	1.69	1.82
43	2l	92	0TD	CB-SB	-12.36	1.69	1.82
32	2a	1404	5MC	C5-C4	6.93	1.49	1.44
32	2a	967	5MC	C5-C4	6.77	1.49	1.44
1	2A	1942	5MC	C5-C4	6.28	1.48	1.44
1	1A	1962	5MC	C5-C4	6.18	1.48	1.44
32	2a	1407	5MC	C5-C4	6.12	1.48	1.44
32	1a	1400	5MC	C5-C4	6.07	1.48	1.44
54	1w	76	PPU	C8-N9	-5.99	1.27	1.37
32	1a	967	5MC	C5-C4	5.98	1.48	1.44
54	1w	76	PPU	C5-N7	-5.96	1.28	1.39
54	2w	76	PPU	C5-N7	-5.90	1.28	1.39
32	2a	1400	5MC	C5-C4	5.84	1.48	1.44
1	2A	1962	5MC	C5-C4	5.58	1.48	1.44
54	1w	76	PPU	O-C	-5.46	1.12	1.23
32	1a	1407	5MC	C5-C4	5.45	1.48	1.44
54	1w	76	PPU	C4-N9	-5.32	1.26	1.37
32	1a	1404	5MC	C5-C4	5.29	1.48	1.44
1	1A	1942	5MC	C5-C4	5.28	1.48	1.44
32	1a	527	G7M	C5-N7	-4.93	1.33	1.39
54	2w	76	PPU	C8-N9	-4.75	1.29	1.37
32	2a	527	G7M	C5-N7	-4.74	1.33	1.39
54	2w	76	PPU	C2'-C3'	-4.64	1.45	1.53
54	1w	76	PPU	C2-N1	-4.23	1.26	1.33
1	1A	2503	2MA	C5-C4	4.22	1.46	1.39
54	2w	76	PPU	C4-N9	-4.19	1.29	1.37
1	2A	2503	2MA	C5-C4	4.14	1.46	1.39
54	2w	76	PPU	O4'-C4'	-3.88	1.36	1.45
55	2x	76	8AN	C5-N7	-3.81	1.32	1.39
1	1A	1911	PSU	C6-C5	3.64	1.39	1.35
54	1w	76	PPU	O4'-C4'	-3.61	1.37	1.45
54	1w	76	PPU	C2'-C3'	-3.58	1.47	1.53
55	1x	76	8AN	C5-N7	-3.54	1.32	1.39
32	2a	516	PSU	C6-C5	3.52	1.39	1.35
54	1w	76	PPU	C2-N3	-3.48	1.27	1.33
54	2w	76	PPU	O-C	-3.47	1.16	1.23
1	2A	1917	PSU	C6-C5	3.46	1.39	1.35
1	1A	1917	PSU	C6-C5	3.46	1.39	1.35
54	1w	76	PPU	O5'-C5'	-3.45	1.34	1.44
54	1w	76	PPU	C-N3'	-3.39	1.26	1.34
32	1a	527	G7M	C5-C4	3.38	1.46	1.38
54	2w	76	PPU	C4'-C3'	-3.32	1.46	1.52
32	1a	516	PSU	C6-C5	3.32	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	966	M2G	C5-C4	3.27	1.47	1.38
32	1a	966	M2G	C5-C4	3.26	1.47	1.38
1	2A	1911	PSU	C6-C5	3.25	1.38	1.35
1	1A	1915	5MU	C2-N1	3.23	1.43	1.38
1	1A	2251	OMG	C5-C4	3.22	1.47	1.38
32	2a	966	M2G	C2-N2	3.22	1.41	1.35
32	2a	1207	2MG	C5-C4	3.21	1.47	1.38
32	2a	527	G7M	C5-C4	3.20	1.46	1.38
1	2A	2251	OMG	C5-C4	3.17	1.47	1.38
1	1A	2605	PSU	C4-N3	-3.16	1.32	1.38
1	2A	1962	5MC	C6-C5	3.15	1.39	1.34
32	1a	1207	2MG	C5-C4	3.11	1.47	1.38
32	1a	1407	5MC	C6-C5	3.07	1.39	1.34
1	2A	1915	5MU	C6-C5	3.06	1.39	1.34
55	2x	76	8AN	C5-C4	-3.05	1.33	1.39
1	1A	2251	OMG	C6-N1	-3.03	1.33	1.38
32	2a	1407	5MC	C6-C5	3.03	1.39	1.34
32	2a	967	5MC	C6-C5	3.02	1.39	1.34
32	2a	1404	5MC	C6-C5	3.02	1.39	1.34
1	1A	1942	5MC	C6-C5	3.01	1.39	1.34
1	1A	1939	5MU	C6-C5	3.00	1.39	1.34
1	2A	2251	OMG	C5-N7	-2.99	1.33	1.39
32	2a	1400	5MC	C6-C5	2.97	1.39	1.34
1	1A	2552	2MU	C4-N3	-2.97	1.33	1.38
1	2A	2605	PSU	C4-N3	-2.92	1.33	1.38
54	1w	76	PPU	CE2-CD2	-2.91	1.34	1.38
1	2A	1911	PSU	C4-N3	-2.87	1.33	1.38
32	1a	966	M2G	C2-N2	2.86	1.40	1.35
1	2A	1942	5MC	C6-C5	2.86	1.39	1.34
1	1A	2605	PSU	C6-C5	2.84	1.38	1.35
1	2A	1915	5MU	C2-N1	2.81	1.42	1.38
1	2A	1939	5MU	C6-C5	2.78	1.39	1.34
32	1a	1400	5MC	C6-C5	2.76	1.39	1.34
1	2A	1939	5MU	C4-C5	2.76	1.49	1.44
54	1w	76	PPU	C4-N3	-2.75	1.29	1.34
54	1w	76	PPU	CE1-CD1	-2.74	1.34	1.38
32	1a	1404	5MC	C6-C5	2.72	1.39	1.34
55	1x	76	8AN	C5-C4	-2.72	1.34	1.39
1	2A	2605	PSU	C6-C5	2.70	1.38	1.35
32	1a	966	M2G	C6-N1	-2.69	1.33	1.38
54	1w	76	PPU	CD2-CG	-2.68	1.33	1.38
1	2A	1915	5MU	C4-N3	-2.66	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	967	5MC	C6-C5	2.66	1.38	1.34
1	2A	1939	5MU	C4-N3	-2.65	1.33	1.38
32	2a	966	M2G	C6-N1	-2.64	1.33	1.38
1	1A	1962	5MC	C6-C5	2.63	1.38	1.34
54	2w	76	PPU	O2'-C2'	-2.63	1.36	1.43
54	1w	76	PPU	CE1-CZ	-2.62	1.33	1.38
55	1x	76	8AN	C5-C6	-2.62	1.33	1.41
1	2A	2503	2MA	C5-C6	2.61	1.48	1.41
1	2A	2552	2MU	C4-N3	-2.60	1.34	1.38
54	1w	76	PPU	O4'-C1'	-2.59	1.36	1.42
1	1A	1962	5MC	C6-N1	-2.58	1.33	1.38
32	1a	516	PSU	C4-N3	-2.56	1.34	1.38
55	2x	76	8AN	C5-C6	-2.56	1.33	1.41
1	1A	1939	5MU	C4-C5	2.55	1.49	1.44
1	1A	1939	5MU	C4-N3	-2.55	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.54	1.34	1.38
1	1A	1911	PSU	C4-N3	-2.53	1.34	1.38
1	1A	1915	5MU	C4-C5	2.52	1.48	1.44
1	1A	1917	PSU	C4-N3	-2.51	1.34	1.38
1	1A	1915	5MU	C6-C5	2.51	1.38	1.34
1	2A	1915	5MU	C4-C5	2.48	1.48	1.44
1	2A	1939	5MU	C6-N1	-2.47	1.33	1.38
1	2A	2503	2MA	C5-N7	-2.45	1.34	1.39
32	2a	516	PSU	C4-N3	-2.45	1.34	1.38
32	1a	1400	5MC	C6-N1	-2.45	1.33	1.38
1	2A	2251	OMG	C6-N1	-2.45	1.34	1.38
1	2A	1942	5MC	C6-N1	-2.43	1.33	1.38
1	2A	2552	2MU	C2-N1	2.42	1.42	1.38
1	1A	2503	2MA	C4-N9	-2.41	1.32	1.37
54	2w	76	PPU	C2-N3	-2.41	1.29	1.33
1	1A	2503	2MA	C5-N7	-2.40	1.34	1.39
32	1a	527	G7M	C6-N1	-2.39	1.34	1.38
1	1A	2503	2MA	C5-C6	2.39	1.47	1.41
54	2w	76	PPU	CE1-CZ	-2.38	1.34	1.38
54	1w	76	PPU	C2'-C1'	-2.38	1.46	1.53
54	1w	76	PPU	C6-N1	-2.37	1.30	1.34
32	1a	967	5MC	C6-N1	-2.37	1.34	1.38
1	2A	2552	2MU	C5-C4	2.36	1.48	1.43
54	2w	76	PPU	C4-N3	-2.36	1.30	1.34
1	1A	1915	5MU	C4-N3	-2.36	1.34	1.38
54	1w	76	PPU	C3'-N3'	-2.35	1.42	1.45
32	1a	1207	2MG	C6-N1	-2.35	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	527	G7M	C6-N1	-2.33	1.34	1.38
1	1A	2251	OMG	C5-N7	-2.29	1.34	1.39
1	2A	2605	PSU	C2-N3	-2.29	1.33	1.37
1	2A	1911	PSU	C2-N3	-2.27	1.33	1.37
1	1A	1939	5MU	C2-N3	-2.26	1.34	1.38
54	1w	76	PPU	O2'-C2'	-2.24	1.37	1.43
1	1A	1942	5MC	C6-N1	-2.24	1.34	1.38
54	2w	76	PPU	CE1-CD1	-2.23	1.35	1.38
32	2a	1400	5MC	C6-N1	-2.22	1.34	1.38
1	1A	2552	2MU	C2-N3	-2.21	1.34	1.38
54	2w	76	PPU	OC-CZ	-2.20	1.33	1.37
1	2A	2503	2MA	C8-N7	2.20	1.35	1.31
32	2a	516	PSU	O4'-C1'	-2.20	1.40	1.43
32	2a	1207	2MG	C6-N1	-2.18	1.34	1.38
54	2w	76	PPU	C2'-C1'	-2.17	1.46	1.53
54	1w	76	PPU	CD1-CG	-2.15	1.34	1.38
32	2a	1498	UR3	C6-C5	2.15	1.40	1.35
1	2A	1939	5MU	C2-N3	-2.14	1.34	1.38
54	2w	76	PPU	O4'-C1'	-2.13	1.37	1.42
32	2a	1207	2MG	C2-N3	2.13	1.36	1.32
32	1a	516	PSU	C2-N3	-2.12	1.34	1.37
32	1a	1404	5MC	C6-N1	-2.10	1.34	1.38
32	2a	1207	2MG	C5-N7	-2.09	1.34	1.39
32	1a	1207	2MG	C2-N3	2.09	1.35	1.32
1	1A	2552	2MU	C5-C4	2.07	1.48	1.43
1	1A	2503	2MA	C8-N7	2.07	1.35	1.31
54	2w	76	PPU	O5'-C5'	-2.06	1.38	1.44
54	2w	76	PPU	C2-N1	-2.06	1.30	1.33
32	2a	967	5MC	C6-N1	-2.05	1.34	1.38
54	1w	76	PPU	CE2-CZ	-2.03	1.34	1.38
32	1a	1498	UR3	C6-C5	2.03	1.39	1.35
1	1A	2552	2MU	C2-N1	2.03	1.41	1.38
1	2A	1962	5MC	C6-N1	-2.02	1.34	1.38
32	1a	1207	2MG	C5-N7	-2.00	1.35	1.39

All (269) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	1l	92	0TD	CSB-SB-CB	-12.44	80.00	102.36
1	2A	2503	2MA	C5-C4-N3	-8.60	118.12	127.18
1	1A	2503	2MA	C5-C4-N3	-7.85	118.91	127.18
32	1a	1207	2MG	C2-N3-C4	7.25	121.06	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1498	UR3	C4-N3-C2	-6.89	119.04	124.58
32	2a	1207	2MG	C2-N3-C4	6.76	120.45	112.00
32	2a	1498	UR3	C4-N3-C2	-6.72	119.17	124.58
1	2A	2503	2MA	N3-C4-N9	6.66	135.45	126.99
1	1A	2605	PSU	N1-C2-N3	6.59	122.12	115.17
1	2A	2251	OMG	C5-C4-N3	-6.48	118.08	128.39
32	1a	516	PSU	N1-C2-N3	6.41	121.92	115.17
54	1w	76	PPU	C5-C4-N3	-6.40	117.90	126.72
32	1a	966	M2G	C5-C4-N3	-6.40	118.20	128.39
1	1A	2251	OMG	C5-C4-N3	-6.38	118.24	128.39
1	1A	1911	PSU	N1-C2-N3	6.36	121.88	115.17
1	2A	1911	PSU	N1-C2-N3	6.36	121.88	115.17
1	2A	1917	PSU	N1-C2-N3	6.35	121.87	115.17
54	2w	76	PPU	C5-C4-N3	-6.34	117.98	126.72
1	1A	2503	2MA	N3-C4-N9	6.32	135.01	126.99
32	2a	966	M2G	C5-C4-N3	-6.26	118.42	128.39
32	2a	516	PSU	N1-C2-N3	6.23	121.74	115.17
1	1A	1917	PSU	N1-C2-N3	6.18	121.69	115.17
1	2A	2605	PSU	N1-C2-N3	5.98	121.47	115.17
55	2x	76	8AN	N1-C2-N3	-5.96	119.56	128.58
55	1x	76	8AN	N1-C2-N3	-5.89	119.66	128.58
32	1a	1207	2MG	C5-C4-N3	-5.89	119.01	128.39
32	2a	1207	2MG	C5-C4-N3	-5.78	119.19	128.39
55	1x	76	8AN	C5-C4-N3	-5.64	118.94	126.72
1	2A	1939	5MU	N3-C2-N1	5.47	122.01	114.89
32	2a	527	G7M	N9-C4-N3	5.46	136.87	125.95
32	1a	527	G7M	N9-C4-N3	5.39	136.73	125.95
1	1A	2552	2MU	N3-C2-N1	5.38	121.89	114.89
32	1a	1519	MA6	N1-C2-N3	-5.33	120.52	128.58
32	1a	527	G7M	C5-C4-N3	-5.32	118.09	128.15
1	2A	1939	5MU	C4-N3-C2	-5.29	120.40	127.34
1	2A	2552	2MU	N3-C2-N1	5.29	121.78	114.89
32	2a	527	G7M	C5-C4-N3	-5.29	118.15	128.15
1	2A	1915	5MU	N3-C2-N1	5.22	121.68	114.89
55	2x	76	8AN	C5-C4-N3	-5.16	119.61	126.72
1	2A	2251	OMG	N9-C4-N3	5.00	135.95	125.95
1	1A	1939	5MU	C4-N3-C2	-4.98	120.81	127.34
1	1A	2251	OMG	C2-N3-C4	4.92	120.78	112.30
1	1A	1939	5MU	N3-C2-N1	4.86	121.22	114.89
1	1A	1915	5MU	C1'-N1-C2	4.85	126.30	117.59
32	2a	1519	MA6	N1-C2-N3	-4.84	121.25	128.58
1	1A	2552	2MU	C4-N3-C2	-4.79	120.67	126.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2251	OMG	C2-N3-C4	4.78	120.54	112.30
1	1A	1939	5MU	C5-C4-N3	4.66	119.38	115.32
1	1A	2552	2MU	C2'-C1'-N1	-4.66	105.40	114.24
32	1a	966	M2G	C2-N3-C4	4.66	121.12	112.51
54	2w	76	PPU	O2'-C2'-C3'	-4.66	99.76	111.16
1	1A	2605	PSU	C4-N3-C2	-4.65	119.97	126.37
54	2w	76	PPU	N3-C4-N9	4.64	135.07	127.17
1	1A	1915	5MU	C4-N3-C2	-4.63	121.27	127.34
32	2a	966	M2G	C2-N3-C4	4.61	121.03	112.51
1	2A	1915	5MU	C4-N3-C2	-4.60	121.31	127.34
32	2a	966	M2G	N9-C4-N3	4.57	135.08	125.95
32	1a	527	G7M	C2-N3-C4	4.56	120.15	112.30
1	1A	1915	5MU	N3-C2-N1	4.54	120.80	114.89
32	2a	1518	MA6	N1-C2-N3	-4.53	121.72	128.58
32	2a	1519	MA6	C5-C4-N3	-4.53	120.48	126.72
32	2a	527	G7M	C2-N3-C4	4.52	120.08	112.30
54	2w	76	PPU	N1-C6-N6	4.50	122.34	116.86
1	2A	2552	2MU	C4-N3-C2	-4.48	121.05	126.61
1	1A	1915	5MU	C1'-N1-C6	-4.48	113.77	121.15
54	1w	76	PPU	N3-C4-N9	4.48	134.79	127.17
54	1w	76	PPU	C2-N3-C4	4.40	122.57	111.83
32	2a	1518	MA6	C5-C4-N3	-4.36	120.71	126.72
32	1a	966	M2G	N9-C4-N3	4.35	134.65	125.95
32	1a	1518	MA6	N1-C2-N3	-4.34	122.01	128.58
32	1a	1519	MA6	C2-N1-C6	4.32	122.38	111.83
32	1a	516	PSU	C4-N3-C2	-4.31	120.43	126.37
1	1A	1915	5MU	C5-C4-N3	4.29	119.06	115.32
1	1A	1917	PSU	O2-C2-N1	-4.28	118.37	122.79
54	1w	76	PPU	N1-C6-N6	4.27	122.06	116.86
1	1A	2251	OMG	N9-C4-N3	4.26	134.47	125.95
32	2a	1207	2MG	N9-C4-N3	4.25	134.44	125.95
1	1A	1915	5MU	O4-C4-C5	-4.20	120.11	124.92
54	1w	76	PPU	C4-C5-N7	-4.18	105.81	110.58
1	2A	2605	PSU	C4-N3-C2	-4.15	120.66	126.37
32	2a	516	PSU	C4-N3-C2	-4.14	120.67	126.37
32	2a	1519	MA6	C4-C5-N7	-4.11	105.88	110.58
1	2A	1942	5MC	C5-C6-N1	-4.10	118.86	123.31
1	1A	1911	PSU	C4-N3-C2	-4.09	120.74	126.37
32	2a	1519	MA6	C2-N1-C6	4.03	121.66	111.83
32	2a	1518	MA6	C2-N1-C6	4.02	121.65	111.83
32	1a	1518	MA6	C5-C4-N3	-4.02	121.18	126.72
32	2a	1519	MA6	C5-N7-C8	4.01	109.76	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1207	2MG	N9-C4-N3	4.01	133.98	125.95
1	1A	1939	5MU	O4-C4-C5	-4.01	120.33	124.92
1	2A	1911	PSU	C4-N3-C2	-4.01	120.85	126.37
54	2w	76	PPU	CA-C-N3'	3.99	121.62	116.21
1	2A	1939	5MU	C5-C4-N3	3.97	118.77	115.32
32	1a	1519	MA6	C5-C4-N3	-3.95	121.28	126.72
32	1a	1518	MA6	C2-N1-C6	3.94	121.46	111.83
54	2w	76	PPU	C2-N3-C4	3.93	121.42	111.83
32	2a	1400	5MC	C5-C6-N1	-3.92	119.06	123.31
1	2A	1917	PSU	O2-C2-N1	-3.88	118.79	122.79
32	1a	1518	MA6	C5-N7-C8	3.87	109.53	103.45
32	2a	1404	5MC	C5-C6-N1	-3.87	119.11	123.31
1	1A	1917	PSU	C4-N3-C2	-3.84	121.09	126.37
32	2a	1518	MA6	C5-N7-C8	3.81	109.44	103.45
1	2A	1915	5MU	C5-C4-N3	3.80	118.62	115.32
1	2A	1917	PSU	C4-N3-C2	-3.79	121.14	126.37
1	1A	1942	5MC	C5-C6-N1	-3.79	119.20	123.31
1	2A	2503	2MA	C4-C5-N7	-3.77	106.27	110.58
54	1w	76	PPU	C2-N1-C6	3.77	121.03	111.83
32	1a	516	PSU	O2-C2-N1	-3.74	118.93	122.79
32	2a	1518	MA6	C4-C5-N7	-3.72	106.33	110.58
32	1a	1400	5MC	C5-C6-N1	-3.72	119.27	123.31
1	1A	1939	5MU	C5-C6-N1	-3.70	119.30	123.31
1	2A	1939	5MU	C5-C6-N1	-3.69	119.30	123.31
55	1x	76	8AN	C2-N3-C4	3.64	120.73	111.83
32	1a	1518	MA6	C4-C5-N7	-3.64	106.42	110.58
32	2a	967	5MC	C5-C6-N1	-3.63	119.37	123.31
54	1w	76	PPU	C5-C6-N6	-3.62	119.61	125.33
32	1a	1518	MA6	N9-C8-N7	-3.61	108.82	113.94
1	1A	2251	OMG	C6-C5-N7	3.59	136.82	130.29
55	1x	76	8AN	N9-C8-N7	-3.56	108.88	113.94
32	1a	1207	2MG	C6-C5-N7	3.56	136.76	130.29
55	2x	76	8AN	C2-N3-C4	3.53	120.45	111.83
32	2a	1519	MA6	N9-C8-N7	-3.51	108.96	113.94
1	1A	1911	PSU	O2-C2-N1	-3.50	119.17	122.79
55	2x	76	8AN	N9-C8-N7	-3.48	109.00	113.94
1	2A	1915	5MU	C1'-N1-C2	3.47	123.83	117.59
1	2A	1911	PSU	O2-C2-N1	-3.43	119.25	122.79
54	2w	76	PPU	C5-C6-N6	-3.43	119.91	125.33
32	2a	1519	MA6	C2-N3-C4	3.43	120.20	111.83
32	1a	1519	MA6	C5-N7-C8	3.42	108.83	103.45
1	2A	1915	5MU	O4-C4-C5	-3.41	121.02	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	1518	MA6	N9-C8-N7	-3.40	109.11	113.94
32	1a	1519	MA6	C2-N3-C4	3.39	120.12	111.83
32	1a	967	5MC	C5-C6-N1	-3.37	119.65	123.31
1	1A	2605	PSU	O2-C2-N1	-3.35	119.33	122.79
54	2w	76	PPU	C2-N1-C6	3.34	120.00	111.83
32	1a	966	M2G	C6-C5-N7	3.34	136.37	130.29
32	2a	1498	UR3	C5-C4-N3	3.29	119.38	115.04
32	1a	1498	UR3	C5-C4-N3	3.29	119.38	115.04
32	1a	1519	MA6	C4-C5-N7	-3.29	106.83	110.58
1	1A	2503	2MA	C4-C5-N7	-3.27	106.85	110.58
54	2w	76	PPU	C4-C5-N7	-3.25	106.87	110.58
1	2A	1962	5MC	C5-C6-N1	-3.25	119.79	123.31
1	1A	2503	2MA	C4-N9-C8	3.24	109.14	105.74
1	2A	1939	5MU	O4-C4-C5	-3.20	121.26	124.92
32	2a	1518	MA6	C2-N3-C4	3.19	119.62	111.83
32	2a	1207	2MG	C6-C5-N7	3.17	136.05	130.29
55	1x	76	8AN	C5-N7-C8	3.16	108.42	103.45
43	1l	92	0TD	OD2-CG-CB	3.14	119.93	113.15
32	2a	1407	5MC	C5-C4-N3	-3.13	118.55	121.75
32	1a	1207	2MG	N1-C2-N2	3.13	119.75	116.56
43	2l	92	0TD	OD2-CG-CB	3.11	119.86	113.15
32	1a	1519	MA6	N9-C8-N7	-3.10	109.54	113.94
32	2a	516	PSU	O2-C2-N1	-3.09	119.60	122.79
32	2a	966	M2G	C6-C5-N7	3.07	135.88	130.29
1	2A	1939	5MU	O2-C2-N1	-3.06	118.82	122.80
54	1w	76	PPU	N3-C2-N1	-3.04	123.98	128.58
32	1a	1404	5MC	C5-C4-N3	-3.02	118.66	121.75
54	2w	76	PPU	CB-CA-N	-3.00	99.91	111.40
1	2A	2503	2MA	C5-N7-C8	2.99	108.15	103.45
32	1a	1518	MA6	C2-N3-C4	2.98	119.12	111.83
55	2x	76	8AN	C4'-O4'-C1'	-2.98	102.88	109.47
1	1A	2251	OMG	C4-C5-N7	-2.97	105.96	110.67
55	1x	76	8AN	C5-C4-N9	2.95	109.03	105.81
1	2A	2503	2MA	N6-C6-N1	2.95	121.00	117.03
55	2x	76	8AN	C5-N7-C8	2.93	108.06	103.45
1	1A	1915	5MU	C5M-C5-C4	2.90	121.87	118.78
1	1A	1920	OMC	C1'-N1-C2	2.89	124.82	118.44
55	1x	76	8AN	N3-C4-N9	2.86	132.03	127.17
32	1a	1407	5MC	C5-C6-N1	-2.85	120.22	123.31
32	1a	1400	5MC	C5-C4-N3	-2.85	118.83	121.75
1	1A	2503	2MA	N6-C6-N1	2.83	120.85	117.03
1	1A	2552	2MU	C5-C4-N3	2.83	118.76	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	966	M2G	C4-C5-N7	-2.80	106.24	110.67
1	2A	2552	2MU	C5-C4-N3	2.78	118.70	114.80
32	1a	1407	5MC	C5-C4-N3	-2.78	118.90	121.75
55	2x	76	8AN	N3-C4-N9	2.77	131.87	127.17
32	2a	967	5MC	C5-C4-N3	-2.76	118.93	121.75
54	1w	76	PPU	C6-C5-N7	2.75	137.82	133.43
32	2a	1518	MA6	C4-C5-C6	2.73	118.73	115.91
32	2a	1518	MA6	N3-C4-N9	2.73	131.81	127.17
1	1A	1939	5MU	O2-C2-N1	-2.73	119.25	122.80
1	1A	2552	2MU	O4-C4-C5	-2.71	120.49	125.16
1	2A	2503	2MA	C4-N9-C8	2.70	108.57	105.74
55	1x	76	8AN	C4-C5-N7	-2.70	107.50	110.58
1	1A	1962	5MC	C5-C6-N1	-2.68	120.40	123.31
1	1A	1962	5MC	C5-C4-N3	-2.68	119.01	121.75
1	2A	2251	OMG	O6-C6-C5	-2.67	119.47	126.53
32	1a	1207	2MG	C4-C5-N7	-2.67	106.44	110.67
1	2A	2605	PSU	O2-C2-N1	-2.67	120.04	122.79
32	1a	967	5MC	C5-C4-N3	-2.65	119.03	121.75
1	2A	1942	5MC	C5-C4-N3	-2.65	119.04	121.75
1	2A	1915	5MU	C1'-N1-C6	-2.65	116.79	121.15
1	1A	2605	PSU	C5-C6-N1	-2.64	118.48	122.14
1	2A	1915	5MU	C5-C6-N1	-2.63	120.46	123.31
1	2A	2552	2MU	O2-C2-N1	-2.62	119.39	122.80
55	1x	76	8AN	C6-C5-C4	2.61	120.75	117.18
54	1w	76	PPU	CA-C-N3'	2.61	119.74	116.21
32	2a	1519	MA6	N3-C4-N9	2.60	131.59	127.17
1	2A	1920	OMC	O2-C2-N3	-2.59	118.25	122.33
1	1A	1942	5MC	O2-C2-N3	-2.57	118.28	122.33
32	1a	1518	MA6	N3-C4-N9	2.57	131.53	127.17
32	1a	1407	5MC	O2-C2-N3	-2.55	118.30	122.33
54	2w	76	PPU	CM-OC-CZ	2.55	122.97	117.50
1	2A	2552	2MU	O4-C4-C5	-2.54	120.78	125.16
32	1a	1404	5MC	C5-C6-N1	-2.54	120.56	123.31
55	2x	76	8AN	O4'-C1'-N9	2.53	112.95	108.09
1	1A	1920	OMC	O2-C2-N3	-2.53	118.34	122.33
1	1A	2503	2MA	C5-N7-C8	2.53	107.43	103.45
32	2a	966	M2G	C4-C5-N7	-2.52	106.67	110.67
1	1A	1942	5MC	C5-C4-N3	-2.52	119.17	121.75
54	1w	76	PPU	O2'-C2'-C3'	-2.51	105.01	111.16
32	1a	1518	MA6	C4-C5-C6	2.51	118.50	115.91
54	2w	76	PPU	N3-C2-N1	-2.50	124.79	128.58
32	2a	1519	MA6	C4-C5-C6	2.50	118.50	115.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	1404	5MC	C5-C4-N3	-2.49	119.20	121.75
32	2a	1207	2MG	C4-C5-N7	-2.49	106.72	110.67
32	1a	1519	MA6	N3-C4-N9	2.49	131.40	127.17
43	2l	92	0TD	OD1-CG-CB	-2.48	117.24	122.44
55	2x	76	8AN	C5-C4-N9	2.48	108.51	105.81
1	1A	2503	2MA	N9-C8-N7	-2.41	110.51	113.94
1	2A	1962	5MC	C5-C4-N3	-2.41	119.29	121.75
32	1a	1404	5MC	O2-C2-N3	-2.39	118.56	122.33
32	2a	1407	5MC	C5-C6-N1	-2.39	120.72	123.31
32	2a	1407	5MC	O2-C2-N3	-2.38	118.57	122.33
32	2a	516	PSU	O4'-C1'-C2'	2.37	108.43	105.15
1	2A	2503	2MA	N9-C8-N7	-2.37	110.57	113.94
1	2A	1915	5MU	O2-C2-N3	-2.37	117.12	121.49
54	1w	76	PPU	C5-N7-C8	2.36	107.16	103.45
1	1A	1915	5MU	C5-C6-N1	-2.34	120.77	123.31
32	2a	1207	2MG	N1-C2-N2	2.34	118.95	116.56
1	1A	2503	2MA	C2-N1-C6	2.34	121.69	118.10
1	2A	1939	5MU	C5M-C5-C4	2.33	121.27	118.78
55	2x	76	8AN	C6-C5-C4	2.31	120.33	117.18
32	2a	527	G7M	O6-C6-C5	-2.30	122.89	128.01
32	2a	516	PSU	C5-C6-N1	-2.29	118.96	122.14
1	1A	2552	2MU	O2-C2-N1	-2.29	119.82	122.80
54	1w	76	PPU	CM-OC-CZ	2.28	122.40	117.50
43	1l	92	0TD	OD1-CG-CB	-2.27	117.68	122.44
32	1a	1402	4OC	C6-C5-C4	2.26	119.72	117.00
32	2a	1400	5MC	C5-C4-N3	-2.26	119.44	121.75
54	2w	76	PPU	C5-N7-C8	2.25	106.99	103.45
32	1a	1207	2MG	N2-C2-N3	-2.25	117.64	120.51
54	2w	76	PPU	C4-C5-C6	2.25	118.24	115.91
32	1a	1207	2MG	CM2-N2-C2	-2.24	118.83	123.65
1	1A	1915	5MU	O2-C2-N3	-2.23	117.37	121.49
1	2A	2503	2MA	C6-C5-N7	2.23	136.39	132.09
1	2A	2503	2MA	C2-N1-C6	2.23	121.52	118.10
1	2A	2251	OMG	C6-C5-N7	2.22	134.32	130.29
55	1x	76	8AN	C4'-O4'-C1'	-2.21	104.58	109.47
32	1a	1207	2MG	O3'-C3'-C2'	2.16	118.75	111.82
1	2A	1939	5MU	C5M-C5-C6	-2.16	119.92	122.85
32	2a	1402	4OC	C6-C5-C4	2.16	119.60	117.00
32	2a	1404	5MC	O2-C2-N3	-2.16	118.93	122.33
32	1a	516	PSU	O4'-C1'-C2'	2.15	108.12	105.15
1	1A	1915	5MU	C5M-C5-C6	-2.14	119.95	122.85
32	1a	527	G7M	O6-C6-C5	-2.11	123.29	128.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2605	PSU	C5-C6-N1	-2.11	119.21	122.14
54	1w	76	PPU	O4'-C1'-N9	-2.11	104.04	108.09
1	2A	2251	OMG	C4-C5-N7	-2.11	107.33	110.67
32	2a	1207	2MG	O6-C6-C5	-2.11	120.98	126.53
55	2x	76	8AN	C4-C5-N7	-2.10	108.18	110.58
32	1a	1518	MA6	C4-N9-C8	2.10	107.94	105.74
32	1a	1207	2MG	O6-C6-C5	-2.08	121.03	126.53
1	1A	1962	5MC	CM5-C5-C6	-2.04	120.09	122.85
1	1A	1920	OMC	C1'-N1-C6	-2.03	116.44	120.78
1	1A	1911	PSU	O4'-C1'-C2'	2.03	107.95	105.15
32	2a	1207	2MG	N2-C2-N3	-2.01	117.95	120.51
32	2a	1498	UR3	C3U-N3-C4	2.01	120.65	117.87
32	2a	1400	5MC	O2-C2-N3	-2.00	119.17	122.33

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1915	5MU	O4'-C1'-N1-C2
1	1A	1915	5MU	O4'-C1'-N1-C6
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
32	2a	1519	MA6	O4'-C4'-C5'-O5'
43	2l	92	0TD	O-C-CA-CB
55	1x	76	8AN	C4'-C5'-O5'-P
55	2x	76	8AN	O4'-C4'-C5'-O5'
55	2x	76	8AN	C3'-C4'-C5'-O5'
56	1v	1	FME	O1-CN-N-CA
56	1v	1	FME	O-C-CA-CB
56	2v	1	FME	O1-CN-N-CA
56	1v	1	FME	CA-CB-CG-SD
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C2'-C1'-N1-C6
54	2w	76	PPU	N-CA-CB-CG
54	1w	76	PPU	O-C-N3'-C3'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
56	1v	1	FME	CB-CG-SD-CE
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB

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Mol	Chain	Res	Type	Atoms
32	2a	1400	5MC	O4'-C1'-N1-C6
55	2x	76	8AN	C4'-C5'-O5'-P
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
1	1A	2503	2MA	C4'-C5'-O5'-P
54	2w	76	PPU	C4'-C5'-O5'-P
43	1l	92	0TD	CA-CB-SB-CSB
32	2a	1400	5MC	O4'-C1'-N1-C2
32	2a	1518	MA6	O4'-C4'-C5'-O5'
1	1A	1920	OMC	C2'-C1'-N1-C6
32	2a	1400	5MC	C2'-C1'-N1-C2
56	1v	1	FME	CB-CA-N-CN
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	2a	527	G7M	C4'-C5'-O5'-P
54	1w	76	PPU	CA-C-N3'-C3'
32	1a	1519	MA6	C4'-C5'-O5'-P
32	2a	1519	MA6	C4'-C5'-O5'-P
1	2A	1962	5MC	O4'-C1'-N1-C6
1	2A	1962	5MC	C2'-C1'-N1-C6

There are no ring outliers.

29 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	967	5MC	1	0
55	2x	76	8AN	2	0
32	1a	1400	5MC	2	0
1	2A	2503	2MA	1	0
32	2a	1400	5MC	2	0
56	1v	1	FME	1	0
32	1a	1518	MA6	4	0
1	1A	1920	OMC	1	0
32	2a	967	5MC	1	0
32	2a	1402	4OC	1	0
43	2l	92	0TD	4	0
1	1A	1942	5MC	1	0
32	1a	1402	4OC	1	0
56	2v	1	FME	2	0
1	2A	1917	PSU	1	0
54	1w	76	PPU	1	0
32	2a	1518	MA6	2	0
32	2a	1404	5MC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1519	MA6	3	0
1	1A	2251	OMG	1	0
54	2w	76	PPU	4	0
1	2A	1939	5MU	1	0
1	2A	1920	OMC	1	0
1	2A	1962	5MC	1	0
1	2A	2552	2MU	2	0
32	2a	1207	2MG	1	0
1	1A	1939	5MU	1	0
32	1a	1519	MA6	2	0
1	2A	2251	OMG	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2513 ligands modelled in this entry, 2502 are monoatomic - leaving 11 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
61	SF4	2d	501	35	0,12,12	-	-	-		
59	MPD	2A	3737	-	7,7,7	0.34	0	9,10,10	0.24	0
59	MPD	1a	1874	-	7,7,7	0.41	0	9,10,10	0.38	0
61	SF4	1d	306	35	0,12,12	-	-	-		
59	MPD	2A	3736	-	7,7,7	0.34	0	9,10,10	0.27	0
58	ARG	1A	4030	-	10,11,11	0.70	0	9,13,13	0.98	1 (11%)
59	MPD	1a	1873	-	7,7,7	0.30	0	9,10,10	0.36	0
59	MPD	18	103	-	7,7,7	0.36	0	9,10,10	0.76	0
59	MPD	1A	4031	-	7,7,7	0.36	0	9,10,10	0.18	0
59	MPD	2A	3735	-	7,7,7	0.33	0	9,10,10	0.33	0
58	ARG	1B	230	57	10,11,11	0.81	1 (10%)	9,13,13	1.20	1 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	SF4	2d	501	35	-	-	0/6/5/5
59	MPD	2A	3737	-	-	2/5/5/5	-
59	MPD	1a	1874	-	-	1/5/5/5	-
61	SF4	1d	306	35	-	-	0/6/5/5
59	MPD	2A	3736	-	-	0/5/5/5	-
58	ARG	1A	4030	-	-	1/11/11/11	-
59	MPD	1a	1873	-	-	1/5/5/5	-
59	MPD	18	103	-	-	3/5/5/5	-
59	MPD	1A	4031	-	-	2/5/5/5	-
59	MPD	2A	3735	-	-	1/5/5/5	-
58	ARG	1B	230	57	-	3/11/11/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	1B	230	ARG	OXT-C	-2.38	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
58	1B	230	ARG	OXT-C-O	-3.48	116.18	124.08
58	1A	4030	ARG	OXT-C-O	-2.80	117.72	124.08

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	18	103	MPD	C2-C3-C4-C5
58	1B	230	ARG	NE-CD-CG-CB
58	1A	4030	ARG	C-CA-CB-CG
59	18	103	MPD	CM-C2-C3-C4
59	2A	3737	MPD	C1-C2-C3-C4
59	1a	1874	MPD	C2-C3-C4-C5
58	1B	230	ARG	CA-CB-CG-CD
59	1A	4031	MPD	O2-C2-C3-C4
59	1a	1873	MPD	C2-C3-C4-O4
58	1B	230	ARG	OXT-C-CA-N

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Mol	Chain	Res	Type	Atoms
59	1A	4031	MPD	C1-C2-C3-C4
59	18	103	MPD	C1-C2-C3-C4
59	2A	3735	MPD	C1-C2-C3-C4
59	2A	3737	MPD	CM-C2-C3-C4

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	2d	501	SF4	2	0
59	1a	1874	MPD	2	0
58	1A	4030	ARG	4	0
59	1a	1873	MPD	2	0
59	1A	4031	MPD	1	0
59	2A	3735	MPD	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	2861/2915 (98%)	-0.49	125 (4%) 39 33	17, 35, 88, 103	0
1	2A	2856/2915 (97%)	0.05	152 (5%) 32 26	31, 56, 91, 102	0
2	1B	120/121 (99%)	-0.29	1 (0%) 82 80	28, 49, 63, 77	0
2	2B	120/121 (99%)	1.18	19 (15%) 5 4	58, 78, 87, 92	0
3	1D	275/276 (99%)	-0.24	2 (0%) 84 82	21, 35, 49, 69	0
3	2D	275/276 (99%)	0.20	3 (1%) 78 74	32, 49, 61, 78	0
4	1E	204/206 (99%)	-0.16	0 100 100	20, 41, 58, 75	0
4	2E	204/206 (99%)	0.24	3 (1%) 72 68	32, 56, 68, 77	0
5	1F	203/210 (96%)	-0.16	1 (0%) 87 85	19, 41, 66, 77	0
5	2F	203/210 (96%)	0.53	5 (2%) 58 52	35, 63, 75, 82	0
6	1G	181/182 (99%)	0.57	6 (3%) 49 43	45, 61, 73, 85	0
6	2G	181/182 (99%)	1.54	42 (23%) 2 1	68, 78, 83, 89	0
7	1H	174/180 (96%)	0.10	3 (1%) 69 64	38, 52, 63, 71	0
7	2H	173/180 (96%)	1.12	21 (12%) 8 6	65, 76, 81, 86	0
8	1I	147/148 (99%)	0.66	5 (3%) 48 42	41, 68, 78, 84	0
8	2I	146/148 (98%)	1.06	10 (6%) 23 19	51, 71, 79, 84	0
9	1N	140/140 (100%)	-0.30	0 100 100	25, 38, 57, 70	0
9	2N	140/140 (100%)	0.47	2 (1%) 73 69	44, 62, 73, 76	0
10	1O	122/122 (100%)	-0.14	0 100 100	29, 41, 60, 65	0
10	2O	122/122 (100%)	0.17	1 (0%) 82 80	40, 53, 65, 77	0
11	1P	149/150 (99%)	0.03	0 100 100	20, 45, 66, 77	0
11	2P	149/150 (99%)	0.52	1 (0%) 84 82	38, 62, 77, 86	0
12	1Q	141/141 (100%)	-0.22	0 100 100	25, 38, 51, 60	0
12	2Q	141/141 (100%)	0.84	7 (4%) 34 28	42, 62, 70, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.28	0 100 100	26, 35, 48, 56	0
13	2R	118/118 (100%)	0.13	0 100 100	39, 51, 60, 68	0
14	1S	110/112 (98%)	0.26	0 100 100	38, 49, 61, 64	0
14	2S	110/112 (98%)	1.34	20 (18%) 3 3	63, 72, 77, 78	0
15	1T	131/146 (89%)	-0.01	4 (3%) 51 45	33, 44, 64, 78	0
15	2T	131/146 (89%)	0.32	0 100 100	48, 56, 74, 77	0
16	1U	116/118 (98%)	-0.41	0 100 100	21, 30, 46, 58	0
16	2U	116/118 (98%)	0.36	0 100 100	38, 58, 70, 79	0
17	1V	101/101 (100%)	-0.21	0 100 100	21, 40, 54, 65	0
17	2V	101/101 (100%)	0.63	2 (1%) 65 60	44, 67, 74, 78	0
18	1W	112/113 (99%)	-0.30	0 100 100	23, 31, 50, 78	0
18	2W	112/113 (99%)	0.14	2 (1%) 67 63	38, 49, 65, 81	0
19	1X	95/96 (98%)	-0.14	2 (2%) 63 58	27, 36, 60, 74	0
19	2X	95/96 (98%)	0.74	3 (3%) 50 44	51, 60, 72, 79	0
20	1Y	107/110 (97%)	0.16	1 (0%) 81 78	32, 48, 67, 75	0
20	2Y	107/110 (97%)	0.94	2 (1%) 66 61	56, 68, 76, 81	0
21	1Z	203/206 (98%)	0.29	2 (0%) 79 76	39, 55, 69, 77	0
21	2Z	201/206 (97%)	1.13	12 (5%) 27 22	64, 73, 80, 84	0
22	10	83/85 (97%)	-0.17	0 100 100	23, 37, 50, 56	0
22	20	83/85 (97%)	0.74	3 (3%) 46 40	48, 62, 70, 75	0
23	11	97/98 (98%)	0.08	2 (2%) 63 58	28, 41, 65, 70	0
23	21	97/98 (98%)	0.22	1 (1%) 79 76	36, 54, 70, 76	0
24	12	70/72 (97%)	0.14	2 (2%) 53 48	35, 50, 60, 70	0
24	22	70/72 (97%)	0.81	3 (4%) 40 34	57, 68, 74, 79	0
25	13	59/60 (98%)	-0.23	0 100 100	27, 36, 60, 66	0
25	23	59/60 (98%)	0.59	3 (5%) 33 28	51, 60, 73, 81	0
26	14	69/71 (97%)	0.96	10 (14%) 6 4	51, 75, 84, 87	0
26	24	69/71 (97%)	1.59	18 (26%) 1 1	75, 83, 90, 92	0
27	15	59/60 (98%)	-0.34	1 (1%) 69 64	20, 31, 47, 61	0
27	25	59/60 (98%)	0.05	0 100 100	37, 49, 63, 70	0
28	16	53/54 (98%)	-0.30	0 100 100	34, 42, 54, 60	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.23	0 100 100	52, 59, 65, 71	0
29	17	48/49 (97%)	-0.33	0 100 100	20, 28, 54, 64	0
29	27	48/49 (97%)	0.06	3 (6%) 26 20	33, 43, 58, 70	0
30	18	64/65 (98%)	-0.34	0 100 100	25, 34, 41, 55	0
30	28	64/65 (98%)	0.45	0 100 100	42, 54, 59, 67	0
31	19	37/37 (100%)	-0.07	0 100 100	28, 39, 54, 57	0
31	29	37/37 (100%)	0.93	1 (2%) 56 50	54, 63, 73, 75	0
32	1a	1488/1521 (97%)	0.38	36 (2%) 59 54	35, 67, 88, 100	0
32	2a	1492/1521 (98%)	0.62	101 (6%) 23 19	42, 72, 90, 102	0
33	1b	231/256 (90%)	1.16	36 (15%) 5 4	65, 74, 83, 88	0
33	2b	231/256 (90%)	1.40	48 (20%) 2 2	68, 78, 85, 92	0
34	1c	206/239 (86%)	1.00	14 (6%) 23 19	60, 72, 80, 83	0
34	2c	206/239 (86%)	1.38	39 (18%) 3 2	69, 79, 84, 87	0
35	1d	208/209 (99%)	0.76	12 (5%) 29 23	56, 69, 78, 82	0
35	2d	208/209 (99%)	0.78	4 (1%) 66 61	57, 67, 75, 83	0
36	1e	148/162 (91%)	0.58	3 (2%) 65 60	46, 63, 73, 85	0
36	2e	148/162 (91%)	0.79	4 (2%) 56 50	59, 68, 76, 85	0
37	1f	100/101 (99%)	0.57	3 (3%) 52 47	49, 63, 72, 76	0
37	2f	100/101 (99%)	0.45	1 (1%) 79 76	55, 65, 75, 79	0
38	1g	155/156 (99%)	0.71	10 (6%) 25 19	59, 68, 76, 82	0
38	2g	155/156 (99%)	1.12	21 (13%) 7 5	67, 76, 82, 87	0
39	1h	137/138 (99%)	0.74	5 (3%) 46 40	55, 65, 72, 77	0
39	2h	137/138 (99%)	1.00	10 (7%) 21 17	60, 69, 75, 77	0
40	1i	127/128 (99%)	1.29	24 (18%) 3 2	57, 75, 81, 83	0
40	2i	126/128 (98%)	1.99	53 (42%) 0 0	69, 81, 86, 91	0
41	1j	97/105 (92%)	1.32	13 (13%) 7 5	61, 75, 83, 87	0
41	2j	96/105 (91%)	2.05	43 (44%) 0 0	73, 81, 86, 89	0
42	1k	114/129 (88%)	0.56	3 (2%) 57 51	40, 61, 72, 75	0
42	2k	114/129 (88%)	0.72	6 (5%) 32 26	57, 69, 77, 79	0
43	1l	121/132 (91%)	0.40	2 (1%) 69 64	48, 59, 67, 73	0
43	2l	121/132 (91%)	0.59	3 (2%) 58 52	54, 63, 69, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	116/126 (92%)	0.96	8 (6%) 23 18	60, 70, 76, 79	0
44	2m	114/126 (90%)	1.55	27 (23%) 2 1	73, 79, 83, 86	0
45	1n	60/61 (98%)	1.07	5 (8%) 17 13	61, 69, 75, 76	0
45	2n	60/61 (98%)	2.12	33 (55%) 0 0	70, 79, 83, 85	0
46	1o	88/89 (98%)	0.77	6 (6%) 23 19	45, 63, 75, 82	0
46	2o	88/89 (98%)	0.84	5 (5%) 29 24	54, 67, 75, 81	0
47	1p	82/88 (93%)	1.24	11 (13%) 7 5	60, 70, 78, 83	0
47	2p	82/88 (93%)	0.93	6 (7%) 21 17	59, 66, 76, 81	0
48	1q	99/105 (94%)	0.94	5 (5%) 33 28	53, 65, 73, 77	0
48	2q	99/105 (94%)	0.67	3 (3%) 52 47	55, 66, 74, 75	0
49	1r	68/88 (77%)	0.59	1 (1%) 72 68	52, 61, 73, 81	0
49	2r	68/88 (77%)	0.71	1 (1%) 72 68	58, 68, 75, 80	0
50	1s	83/93 (89%)	0.95	4 (4%) 35 30	60, 72, 80, 84	0
50	2s	83/93 (89%)	1.65	24 (28%) 1 1	71, 81, 85, 88	0
51	1t	96/106 (90%)	1.05	11 (11%) 9 7	62, 70, 78, 81	0
51	2t	98/106 (92%)	0.78	8 (8%) 17 14	54, 66, 75, 79	0
52	1u	23/27 (85%)	1.18	5 (21%) 2 2	66, 70, 74, 77	0
52	2u	23/27 (85%)	2.00	10 (43%) 0 0	73, 78, 82, 86	0
53	1y	97/113 (85%)	0.69	7 (7%) 21 17	49, 60, 71, 75	0
53	2y	96/113 (84%)	1.61	26 (27%) 1 1	66, 75, 80, 86	0
54	1w	3/4 (75%)	-0.40	0 100 100	30, 30, 35, 47	0
54	2w	3/4 (75%)	-0.75	0 100 100	44, 44, 45, 52	0
55	1x	3/4 (75%)	-0.50	0 100 100	23, 23, 25, 35	0
55	2x	3/4 (75%)	0.22	1 (33%) 1 1	35, 35, 43, 47	0
56	1v	2/3 (66%)	-0.03	0 100 100	27, 27, 27, 30	0
56	2v	2/3 (66%)	0.02	0 100 100	44, 44, 44, 47	0
All	All	20794/21490 (96%)	0.36	1207 (5%) 29 23	17, 61, 84, 103	0

All (1207) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1A	1087	G	8.4
53	1y	98	ALA	6.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1076	C	6.4
45	2n	2	ALA	6.4
1	1A	1071	G	5.7
7	1H	2	SER	5.6
1	1A	1077	A	5.5
1	2A	1076	C	5.4
41	2j	34	VAL	5.4
44	1m	2	ALA	5.3
1	1A	1086	A	5.2
1	1A	1057	A	5.2
41	2j	37	PRO	5.1
1	1A	1064	C	5.1
1	1A	1092	C	5.1
1	2A	2803	C	5.0
23	11	2	SER	5.0
1	1A	1094	U	5.0
1	1A	1089	G	5.0
40	2i	11	LYS	4.9
1	2A	2159	G	4.9
32	2a	1036	G	4.9
21	2Z	1	MET	4.8
53	2y	98	ALA	4.8
1	1A	1080	C	4.7
1	1A	1090	U	4.7
40	1i	106	ALA	4.7
1	2A	2805	G	4.6
40	1i	66	ARG	4.6
52	2u	14	TRP	4.6
1	2A	2804	C	4.5
39	2h	2	LEU	4.5
1	2A	2153	G	4.5
44	2m	102	ARG	4.4
1	1A	1072	C	4.4
1	1A	1067	A	4.3
40	2i	108	VAL	4.3
1	1A	1068	G	4.3
1	1A	1074	G	4.3
1	1A	1081	U	4.3
1	1A	1102	C	4.3
34	1c	90	GLU	4.3
40	2i	6	GLY	4.3
1	2A	1091	G	4.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2138	C	4.3
1	1A	1093	G	4.2
32	1a	1036	G	4.2
32	2a	1030(A)	G	4.2
40	1i	126	SER	4.2
41	2j	26	ALA	4.2
1	1A	1065	U	4.1
40	2i	109	VAL	4.1
45	2n	13	THR	4.1
1	1A	1104	C	4.1
32	2a	1030(B)	C	4.1
1	2A	2124	G	4.1
12	2Q	104	PHE	4.1
20	2Y	1	MET	4.1
45	2n	29	ARG	4.1
26	24	56	VAL	4.1
52	2u	2	GLY	4.0
1	1A	1099	G	4.0
45	1n	2	ALA	4.0
1	2A	1046	A	4.0
1	1A	1062	G	4.0
40	2i	106	ALA	4.0
50	1s	68	GLY	4.0
51	1t	103	GLY	4.0
53	2y	8	LYS	4.0
1	1A	1060	U	4.0
1	2A	2150	U	4.0
53	2y	7	SER	3.9
1	1A	1091	G	3.9
1	1A	1085	A	3.9
1	1A	1082	U	3.9
19	2X	68	ARG	3.9
25	23	60	GLU	3.9
6	2G	39	ILE	3.9
1	1A	1088	A	3.9
1	1A	1098	A	3.9
47	2p	82	GLN	3.9
8	2I	146	ALA	3.9
1	1A	1103	A	3.9
40	2i	68	GLY	3.9
8	1I	147	GLN	3.8
1	2A	2136	C	3.8

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Mol	Chain	Res	Type	RSRZ
1	2A	2137	C	3.8
1	2A	2174	C	3.8
2	2B	118	G	3.8
1	1A	1026	U	3.8
1	1A	1075	C	3.8
40	2i	13	ALA	3.8
32	2a	1033	G	3.8
1	2A	2143	C	3.8
41	2j	54	PHE	3.8
33	2b	165	VAL	3.8
1	1A	2117	A	3.7
40	2i	76	ALA	3.7
1	1A	1079	C	3.7
32	1a	1035	A	3.7
1	2A	1089	G	3.7
1	2A	2125	G	3.7
1	2A	2894	G	3.7
1	2A	1064	C	3.7
1	2A	1072	C	3.7
1	2A	1536	C	3.7
40	2i	49	PRO	3.7
1	1A	1095	A	3.7
1	1A	1066	U	3.7
40	2i	56	LEU	3.7
36	1e	85	GLY	3.7
1	1A	1070	A	3.6
1	1A	1061	U	3.6
1	1A	1056	G	3.6
40	1i	128	ARG	3.6
21	1Z	1	MET	3.6
33	1b	229	VAL	3.6
45	2n	25	VAL	3.6
1	1A	1097	U	3.6
1	2A	2173	A	3.6
6	2G	2	PRO	3.6
51	2t	6	PRO	3.6
47	1p	42	ARG	3.6
41	2j	19	SER	3.6
41	2j	40	LEU	3.6
1	1A	2803	C	3.5
1	2A	1079	C	3.5
32	2a	1003	G	3.5

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Mol	Chain	Res	Type	RSRZ
49	2r	20	ALA	3.5
52	2u	11	GLY	3.5
26	14	59	PHE	3.5
53	2y	38	HIS	3.5
1	1A	1100	C	3.5
1	2A	1070	A	3.5
6	2G	71	THR	3.5
41	2j	36	GLY	3.5
6	2G	160	VAL	3.5
39	1h	112	LEU	3.5
40	2i	102	LEU	3.5
14	2S	53	SER	3.5
1	2A	2133	G	3.5
1	2A	2152	G	3.5
1	2A	2109	U	3.5
1	2A	2134	A	3.5
34	1c	2	GLY	3.5
40	2i	67	GLY	3.5
33	1b	12	GLU	3.5
6	2G	90	LEU	3.5
6	2G	149	VAL	3.5
50	2s	9	VAL	3.5
40	2i	36	TYR	3.4
26	24	52	THR	3.4
32	1a	1001(A)	G	3.4
34	2c	2	GLY	3.4
39	1h	2	LEU	3.4
41	2j	65	LEU	3.4
50	2s	71	LEU	3.4
1	2A	2107	C	3.4
32	2a	1028	C	3.4
8	2I	55	ALA	3.4
26	14	51	ASP	3.4
1	1A	1083	U	3.4
40	2i	9	ARG	3.4
32	1a	1024	G	3.4
34	2c	77	ILE	3.4
1	1A	1073	A	3.4
1	2A	1067	A	3.4
41	1j	76	ASN	3.4
1	1A	888	C	3.4
1	2A	2139	C	3.4

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Mol	Chain	Res	Type	RSRZ
38	2g	16	LEU	3.4
52	2u	6	ARG	3.4
44	2m	65	LYS	3.3
1	1A	1101	U	3.3
2	2B	1	U	3.3
32	2a	1037	C	3.3
1	2A	2892	A	3.3
2	2B	26	A	3.3
41	2j	27	ALA	3.3
40	1i	127	LYS	3.3
1	1A	1078	U	3.3
45	2n	34	TYR	3.3
51	1t	69	GLY	3.3
51	2t	103	GLY	3.3
1	2A	2151	G	3.3
6	2G	145	THR	3.3
7	2H	71	LEU	3.3
25	23	2	PRO	3.3
45	2n	55	GLY	3.3
32	2a	1116	C	3.3
46	1o	88	ARG	3.3
32	2a	1202	G	3.3
50	2s	2	PRO	3.3
21	2Z	191	VAL	3.3
26	24	49	PHE	3.3
1	1A	2794	C	3.2
40	2i	7	THR	3.2
41	2j	67	THR	3.2
1	2A	2127	G	3.2
32	2a	1034	G	3.2
26	14	56	VAL	3.2
33	1b	17	PHE	3.2
1	1A	2150	U	3.2
22	20	74	ARG	3.2
38	2g	5	ARG	3.2
1	2A	34	C	3.2
19	2X	92	LEU	3.2
45	2n	5	ALA	3.2
45	2n	7	ILE	3.2
41	2j	76	ASN	3.2
1	2A	1062	G	3.2
1	2A	2802	G	3.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1124	G	3.2
44	2m	54	VAL	3.2
40	1i	56	LEU	3.2
37	1f	90	VAL	3.2
1	2A	2896	C	3.1
38	2g	33	ASP	3.1
32	2a	1257	U	3.1
38	2g	27	ILE	3.1
41	2j	6	ILE	3.1
40	2i	59	PHE	3.1
21	2Z	99	TYR	3.1
32	1a	1026	G	3.1
32	2a	1002	G	3.1
29	27	48	LYS	3.1
1	1A	1069	A	3.1
1	2A	1085	A	3.1
1	2A	2135	A	3.1
32	2a	1030(D)	A	3.1
6	2G	20	ILE	3.1
21	2Z	192	ALA	3.1
41	1j	75	ILE	3.1
44	2m	72	ALA	3.1
1	1A	2113	U	3.1
32	1a	1257	U	3.1
6	2G	146	TYR	3.1
50	1s	13	ASP	3.1
1	1A	1063	G	3.1
1	2A	2162	G	3.1
1	1A	2161	C	3.1
1	2A	2140	C	3.1
34	2c	8	ILE	3.1
7	2H	45	VAL	3.1
1	2A	2144	U	3.1
48	1q	26	GLN	3.1
1	1A	1059	G	3.1
1	2A	2106	G	3.1
1	2A	2149	G	3.1
44	2m	6	GLY	3.1
50	2s	33	THR	3.1
53	2y	92	GLY	3.1
15	1T	131	ALA	3.1
34	2c	168	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
40	1i	15	ALA	3.1
40	1i	43	ALA	3.1
41	2j	38	ILE	3.1
41	2j	79	ARG	3.1
50	2s	4	SER	3.1
50	2s	35	SER	3.1
15	1T	37	GLY	3.0
26	24	45	GLY	3.0
33	1b	228	GLY	3.0
33	2b	237	ALA	3.0
53	1y	95	ARG	3.0
1	1A	1055	G	3.0
1	1A	1058	G	3.0
1	2A	2141	G	3.0
1	2A	2155	G	3.0
32	2a	1117	G	3.0
40	2i	96	LEU	3.0
44	2m	19	LEU	3.0
1	1A	1053	C	3.0
32	1a	1030	C	3.0
41	2j	69	ASN	3.0
41	2j	77	PRO	3.0
44	2m	88	ARG	3.0
45	2n	3	ARG	3.0
50	2s	34	TRP	3.0
1	1A	2147	G	3.0
1	1A	2156	G	3.0
1	2A	2115	G	3.0
1	2A	2168	G	3.0
32	1a	630	G	3.0
1	2A	645	C	3.0
1	1A	2158	A	3.0
1	2A	1073	A	3.0
1	2A	2126	A	3.0
32	1a	1005	A	3.0
40	2i	66	ARG	3.0
34	2c	159	GLY	3.0
40	2i	39	GLY	3.0
40	2i	64	THR	3.0
1	2A	1083	U	3.0
35	1d	179	GLU	3.0
3	1D	276	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
6	2G	93	THR	3.0
1	2A	1058	G	3.0
1	2A	2165	G	3.0
36	1e	21	ALA	3.0
26	14	49	PHE	3.0
32	1a	1001	A	3.0
40	2i	18	PHE	3.0
14	2S	50	SER	2.9
33	2b	132	LYS	2.9
14	2S	7	TYR	2.9
44	1m	4	ILE	2.9
50	2s	31	ILE	2.9
53	2y	52	ALA	2.9
6	2G	133	LEU	2.9
1	1A	34	C	2.9
1	1A	2157	G	2.9
1	2A	1084	A	2.9
1	2A	2123	G	2.9
1	2A	2176	A	2.9
14	2S	33	LYS	2.9
21	2Z	197	ILE	2.9
33	1b	214	ILE	2.9
44	2m	78	ILE	2.9
41	2j	42	THR	2.9
53	1y	2	THR	2.9
41	2j	63	PHE	2.9
53	2y	41	LEU	2.9
1	1A	2136	C	2.9
1	1A	2145	C	2.9
1	2A	1096	A	2.9
1	2A	2108	C	2.9
32	1a	1286	A	2.9
1	1A	1176	G	2.9
1	2A	1060	U	2.9
1	2A	1087	G	2.9
1	2A	2116	G	2.9
32	1a	1030(A)	G	2.9
14	2S	35	ILE	2.9
41	1j	4	ILE	2.9
33	2b	38	GLY	2.9
36	2e	94	ALA	2.9
41	1j	32	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
45	2n	59	ALA	2.9
33	2b	69	LEU	2.9
34	2c	207	VAL	2.9
50	1s	9	VAL	2.9
53	2y	3	MET	2.9
53	2y	4	ASN	2.9
1	2A	1092	C	2.9
1	2A	2119	A	2.9
32	2a	1150	U	2.9
34	2c	184	TYR	2.9
34	2c	185	GLY	2.9
46	1o	89	GLY	2.9
1	2A	1099	G	2.9
1	2A	2110	G	2.9
1	2A	2157	G	2.9
1	2A	2793	G	2.9
1	2A	2807	G	2.9
6	2G	139	LEU	2.9
32	2a	1026	G	2.9
32	2a	1156	G	2.9
33	2b	22	LYS	2.9
40	1i	12	GLU	2.8
34	2c	3	ASN	2.8
40	2i	115	GLY	2.8
44	2m	105	THR	2.8
14	2S	46	VAL	2.8
32	1a	1493	A	2.8
32	2a	1035	A	2.8
1	2A	886	C	2.8
1	2A	1509	C	2.8
1	2A	2129	C	2.8
32	2a	1030(C)	G	2.8
33	2b	21	ARG	2.8
40	2i	10	ARG	2.8
46	2o	68	ARG	2.8
51	2t	25	ARG	2.8
40	2i	126	SER	2.8
45	2n	17	LYS	2.8
40	2i	69	GLY	2.8
50	2s	26	GLY	2.8
6	2G	3	LEU	2.8
38	2g	154	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
41	2j	16	LEU	2.8
45	2n	44	LEU	2.8
6	2G	70	VAL	2.8
43	2l	18	VAL	2.8
50	2s	41	VAL	2.8
1	1A	2130	U	2.8
24	22	55	ARG	2.8
52	2u	15	ARG	2.8
1	1A	2170	A	2.8
1	1A	2173	A	2.8
47	1p	33	ILE	2.8
1	2A	2160	G	2.8
32	2a	1031	G	2.8
44	2m	106	ASN	2.8
33	2b	40	HIS	2.8
34	2c	92	ALA	2.8
34	2c	149	ALA	2.8
34	2c	187	ALA	2.8
26	24	57	GLU	2.8
34	1c	107	GLN	2.8
1	2A	1094	U	2.8
1	2A	2130	U	2.8
1	2A	887	A	2.8
53	2y	40	ILE	2.8
1	1A	2111	C	2.8
1	2A	2179	C	2.8
33	2b	121	LEU	2.8
50	2s	82	GLY	2.8
6	2G	15	VAL	2.8
1	1A	2159	G	2.8
1	2A	2120	G	2.8
6	1G	146	TYR	2.8
26	24	63	TYR	2.8
40	1i	125	TYR	2.8
40	2i	88	TYR	2.8
44	2m	104	ARG	2.8
42	2k	13	GLN	2.7
32	1a	1532	U	2.7
1	1A	2174	C	2.7
1	2A	2111	C	2.7
2	2B	12	C	2.7
6	1G	48	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
32	2a	1223	C	2.7
39	1h	84	ARG	2.7
40	2i	14	VAL	2.7
53	2y	6	THR	2.7
53	2y	11	GLU	2.7
40	2i	4	TYR	2.7
40	2i	127	LYS	2.7
2	2B	23	G	2.7
32	2a	971	G	2.7
32	2a	1001(A)	G	2.7
32	2a	1032	G	2.7
32	2a	1373	G	2.7
44	2m	4	ILE	2.7
23	21	2	SER	2.7
1	1A	2167	U	2.7
1	2A	1065	U	2.7
1	2A	1090	U	2.7
6	2G	158	ALA	2.7
26	24	50	VAL	2.7
33	1b	225	ALA	2.7
34	2c	75	VAL	2.7
44	2m	75	ALA	2.7
53	1y	97	ALA	2.7
1	1A	2169	A	2.7
1	2A	1445	A	2.7
38	1g	154	TYR	2.7
45	2n	21	TYR	2.7
47	1p	82	GLN	2.7
33	1b	41	ILE	2.7
33	2b	200	ILE	2.7
33	2b	10	LEU	2.7
1	1A	2115	G	2.7
1	2A	1171	G	2.7
1	2A	2166	G	2.7
32	1a	1023	G	2.7
32	2a	1017	G	2.7
33	2b	113	HIS	2.7
41	1j	10	GLY	2.7
12	2Q	59	ARG	2.7
33	2b	231	GLU	2.7
8	2I	3	VAL	2.7
40	2i	101	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
41	2j	72	VAL	2.7
43	1l	91	LYS	2.7
44	2m	23	TYR	2.7
1	2A	2117	A	2.7
1	2A	2158	A	2.7
1	1A	886	C	2.7
1	2A	2142	C	2.7
32	1a	63	C	2.7
32	2a	970	C	2.7
32	2a	1029	C	2.7
32	2a	1030	C	2.7
38	2g	81	GLY	2.7
44	2m	3	ARG	2.7
47	1p	11	SER	2.7
7	2H	44	VAL	2.7
33	2b	57	PHE	2.7
40	2i	15	ALA	2.7
45	2n	15	LYS	2.7
50	2s	67	VAL	2.7
32	2a	976	G	2.6
1	1A	2144	U	2.6
1	2A	2132	U	2.6
40	2i	125	TYR	2.6
44	2m	9	ILE	2.6
50	2s	66	MET	2.6
1	1A	1096	A	2.6
32	2a	1004	A	2.6
33	2b	118	LEU	2.6
38	1g	12	LEU	2.6
50	2s	15	LEU	2.6
44	2m	71	ARG	2.6
1	2A	2105	C	2.6
43	2l	17	LYS	2.6
8	1I	107	VAL	2.6
44	2m	7	VAL	2.6
50	2s	10	PHE	2.6
40	2i	5	TYR	2.6
41	2j	50	ILE	2.6
1	2A	271(K)	U	2.6
32	2a	1219	U	2.6
9	2N	26	LEU	2.6
33	2b	44	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
8	2I	90	GLY	2.6
1	2A	1095	A	2.6
33	1b	131	PRO	2.6
41	1j	20	ALA	2.6
44	2m	113	PRO	2.6
53	2y	53	THR	2.6
2	2B	6	C	2.6
32	1a	1030(B)	C	2.6
38	1g	42	ILE	2.6
14	2S	3	ARG	2.6
40	2i	12	GLU	2.6
7	2H	174	GLY	2.6
34	1c	9	GLY	2.6
1	1A	275	G	2.6
1	1A	2112	G	2.6
1	2A	2100	G	2.6
1	2A	2154	G	2.6
32	2a	1224	G	2.6
33	1b	165	VAL	2.6
12	2Q	65	PHE	2.6
45	2n	30	ALA	2.6
1	1A	1084	A	2.6
1	2A	652(B)	A	2.6
40	2i	91	ASP	2.6
26	24	5	ILE	2.6
1	1A	889	C	2.6
1	1A	2164	C	2.6
26	24	9	LEU	2.6
32	2a	1018	C	2.6
32	2a	1066	C	2.6
32	2a	1128	C	2.6
32	2a	1354	C	2.6
7	2H	175	LYS	2.6
6	2G	35	GLU	2.6
1	2A	2172	U	2.6
7	2H	102	ALA	2.6
33	1b	34	ALA	2.6
34	2c	76	VAL	2.6
44	2m	18	ALA	2.6
52	2u	23	PRO	2.6
34	1c	10	PHE	2.6
45	2n	61	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
1	1A	2149	G	2.5
1	2A	2318	G	2.5
32	1a	1033	G	2.5
41	2j	82	ILE	2.5
1	1A	548	A	2.5
1	2A	2114	A	2.5
6	2G	53	LEU	2.5
32	2a	1123	A	2.5
33	1b	22	LYS	2.5
35	1d	209	ARG	2.5
1	1A	2107	C	2.5
1	1A	2804	C	2.5
1	2A	2161	C	2.5
32	2a	1027	C	2.5
32	2a	1038	C	2.5
6	2G	92	VAL	2.5
33	2b	15	VAL	2.5
33	2b	164	VAL	2.5
53	2y	60	VAL	2.5
34	2c	129	ALA	2.5
40	1i	64	THR	2.5
1	2A	2118	U	2.5
1	2A	2122	U	2.5
32	2a	950	U	2.5
32	2a	1235	U	2.5
6	2G	147	ASP	2.5
14	2S	34	HIS	2.5
1	1A	2116	G	2.5
1	1A	2152	G	2.5
1	1A	2153	G	2.5
1	1A	2154	G	2.5
1	2A	1071	G	2.5
32	2a	963	G	2.5
1	1A	887	A	2.5
1	2A	2169	A	2.5
26	14	63	TYR	2.5
32	2a	1001	A	2.5
32	2a	1447	A	2.5
34	1c	193	TYR	2.5
10	2O	62	VAL	2.5
33	2b	136	VAL	2.5
34	2c	99	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	151	VAL	2.5
21	2Z	164	ALA	2.5
34	2c	169	ALA	2.5
38	2g	128	ALA	2.5
1	2A	2146	C	2.5
1	2A	2183	C	2.5
2	2B	88	C	2.5
6	2G	29	TRP	2.5
38	2g	36	LYS	2.5
1	1A	2132	U	2.5
1	2A	1097	U	2.5
1	2A	2167	U	2.5
32	2a	1000	U	2.5
44	2m	81	LEU	2.5
45	1n	3	ARG	2.5
51	1t	10	LEU	2.5
23	11	75	GLU	2.5
6	2G	87	PRO	2.5
1	2A	529	A	2.5
1	2A	2319	G	2.5
1	2A	2893	G	2.5
5	1F	6	VAL	2.5
33	1b	37	ASN	2.5
41	2j	81	THR	2.5
51	2t	9	ASN	2.5
6	2G	88	ILE	2.5
21	2Z	166	SER	2.5
44	2m	90	LEU	2.5
53	2y	61	LEU	2.5
1	2A	1075	C	2.5
1	2A	2145	C	2.5
32	2a	1149	C	2.5
40	2i	105	ASP	2.5
1	1A	2172	U	2.5
1	2A	2113	U	2.5
8	1I	10	GLU	2.5
32	2a	1025	U	2.5
32	2a	1205	U	2.5
32	2a	1532	U	2.5
7	2H	22	GLY	2.5
33	2b	131	PRO	2.5
35	2d	20	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
41	2j	91	PRO	2.5
38	1g	17	VAL	2.5
38	2g	9	VAL	2.5
6	2G	57	ALA	2.5
6	2G	110	ALA	2.5
45	1n	20	ALA	2.5
45	2n	20	ALA	2.5
3	1D	275	LYS	2.4
53	2y	91	LYS	2.4
32	2a	1531	A	2.4
46	2o	88	ARG	2.4
7	2H	88	LEU	2.4
14	2S	80	LEU	2.4
33	1b	11	LEU	2.4
40	2i	99	LEU	2.4
41	2j	71	LEU	2.4
1	1A	2155	G	2.4
32	2a	1370	G	2.4
40	2i	2	GLU	2.4
41	2j	83	GLU	2.4
1	1A	2143	C	2.4
2	2B	109	C	2.4
32	1a	1029	C	2.4
2	2B	41	U	2.4
32	1a	1040	U	2.4
32	2a	1020	U	2.4
32	2a	1148	U	2.4
40	2i	21	PRO	2.4
33	2b	236	TYR	2.4
14	2S	49	VAL	2.4
19	2X	83	VAL	2.4
38	2g	83	ALA	2.4
45	2n	16	PHE	2.4
6	2G	161	THR	2.4
14	2S	17	ARG	2.4
52	2u	24	ARG	2.4
33	1b	10	LEU	2.4
33	2b	11	LEU	2.4
33	1b	19	HIS	2.4
51	1t	11	SER	2.4
53	2y	64	SER	2.4
1	1A	1177	A	2.4

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Mol	Chain	Res	Type	RSRZ
1	2A	1088	A	2.4
32	2a	1005	A	2.4
32	2a	1357	A	2.4
1	1A	2125	G	2.4
1	1A	2127	G	2.4
1	2A	2182	G	2.4
32	2a	1353	G	2.4
1	1A	645	C	2.4
1	2A	2128	C	2.4
1	2A	2175	C	2.4
7	2H	19	VAL	2.4
38	2g	61	VAL	2.4
40	2i	41	VAL	2.4
50	2s	11	VAL	2.4
1	2A	12	U	2.4
1	2A	362	U	2.4
6	2G	50	ALA	2.4
40	1i	94	ALA	2.4
52	2u	9	ARG	2.4
6	2G	52	ILE	2.4
33	1b	168	THR	2.4
44	2m	116	THR	2.4
48	1q	90	ILE	2.4
50	2s	63	THR	2.4
53	2y	35	ILE	2.4
51	1t	75	ASN	2.4
5	2F	153	SER	2.4
47	1p	48	TRP	2.4
1	2A	6	A	2.4
6	1G	42	GLY	2.4
18	2W	112	GLY	2.4
34	2c	171	GLY	2.4
24	22	70	GLN	2.4
12	2Q	102	VAL	2.4
34	2c	195	VAL	2.4
40	2i	65	VAL	2.4
41	2j	24	VAL	2.4
1	2A	1093	G	2.4
1	2A	2121	G	2.4
26	24	67	TYR	2.4
32	2a	973	G	2.4
33	1b	236	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
35	1d	3	ARG	2.4
45	2n	26	ARG	2.4
6	1G	53	LEU	2.4
38	1g	16	LEU	2.4
1	2A	1066	U	2.4
2	2B	22	U	2.4
32	1a	1000	U	2.4
32	1a	1020	U	2.4
32	2a	1281	U	2.4
41	2j	74	ILE	2.4
45	2n	22	THR	2.4
46	2o	3	ILE	2.4
41	2j	78	ASN	2.4
33	1b	129	GLU	2.4
51	2t	11	SER	2.4
35	1d	173	TRP	2.4
26	14	69	LYS	2.4
39	2h	135	CYS	2.4
26	24	41	PRO	2.4
26	14	54	GLY	2.4
45	2n	38	GLY	2.4
46	1o	20	GLY	2.4
50	2s	8	GLY	2.4
24	12	70	GLN	2.4
33	2b	174	VAL	2.4
34	1c	76	VAL	2.4
38	2g	80	VAL	2.4
52	1u	9	ARG	2.4
1	1A	1045	A	2.4
1	2A	2171	A	2.4
32	1a	1041	A	2.4
32	1a	1447	A	2.4
32	2a	1157	A	2.4
15	1T	130	ALA	2.4
22	20	75	LEU	2.3
34	1c	94	LEU	2.3
51	2t	10	LEU	2.3
53	1y	71	TYR	2.3
33	2b	108	ILE	2.3
38	2g	50	ILE	2.3
44	1m	49	THR	2.3
1	1A	2109	U	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	2138	C	2.3
1	2A	1104	C	2.3
32	2a	1218	C	2.3
39	2h	98	LYS	2.3
48	1q	100	LYS	2.3
52	2u	5	ASP	2.3
33	1b	97	TRP	2.3
52	1u	23	PRO	2.3
53	2y	37	PRO	2.3
7	1H	174	GLY	2.3
17	2V	63	GLY	2.3
33	2b	100	GLY	2.3
8	2I	67	ARG	2.3
33	2b	225	ALA	2.3
47	2p	9	PHE	2.3
14	2S	54	LEU	2.3
51	1t	99	LEU	2.3
33	1b	127	ILE	2.3
1	2A	229	A	2.3
26	14	52	THR	2.3
32	2a	949	A	2.3
32	2a	983	A	2.3
33	1b	40	HIS	2.3
33	2b	190	THR	2.3
38	2g	24	THR	2.3
40	2i	29	ASN	2.3
42	1k	117	ASN	2.3
26	14	57	GLU	2.3
26	24	28	LYS	2.3
45	2n	58	LYS	2.3
1	2A	1082	U	2.3
1	1A	2110	G	2.3
1	1A	2131	G	2.3
1	1A	2133	G	2.3
1	2A	11	G	2.3
6	2G	17	PRO	2.3
1	1A	1532	C	2.3
1	2A	2103	C	2.3
32	1a	1028	C	2.3
32	2a	1270	C	2.3
41	1j	31	GLY	2.3
50	2s	3	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
34	2c	173	VAL	2.3
40	2i	53	VAL	2.3
33	2b	221	LEU	2.3
40	2i	19	LEU	2.3
41	2j	47	PHE	2.3
20	2Y	78	ALA	2.3
34	2c	152	ILE	2.3
38	2g	120	ILE	2.3
26	24	43	TYR	2.3
33	2b	199	TYR	2.3
52	1u	18	TYR	2.3
6	2G	182	LYS	2.3
20	1Y	1	MET	2.3
39	1h	136	GLU	2.3
1	1A	229	A	2.3
1	2A	1077	A	2.3
1	2A	2801(A)	A	2.3
34	1c	62	ASP	2.3
41	2j	41	PRO	2.3
1	1A	271(K)	U	2.3
1	2A	2897	U	2.3
41	2j	85	LEU	2.3
53	2y	48	PHE	2.3
1	1A	1106	G	2.3
1	2A	1533	G	2.3
8	2I	120	ILE	2.3
21	2Z	187	ALA	2.3
33	2b	32	ILE	2.3
34	2c	65	ALA	2.3
36	2e	17	ALA	2.3
32	2a	1310	G	2.3
45	2n	42	ILE	2.3
1	2A	2314	C	2.3
32	1a	1008	C	2.3
32	2a	1039	C	2.3
34	2c	177	THR	2.3
6	2G	12	TYR	2.3
46	1o	6	GLU	2.3
33	2b	26	PRO	2.3
34	2c	172	ARG	2.3
35	1d	102	ASP	2.3
40	1i	9	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
41	2j	30	SER	2.3
46	1o	19	PRO	2.3
1	2A	1103	A	2.3
32	1a	383	A	2.3
32	2a	975	A	2.3
41	1j	33	GLN	2.3
33	1b	38	GLY	2.3
36	2e	22	GLY	2.3
6	2G	38	VAL	2.3
33	2b	230	VAL	2.3
41	1j	85	LEU	2.3
45	2n	18	VAL	2.3
33	2b	163	PHE	2.3
33	2b	214	ILE	2.2
40	2i	122	ALA	2.2
41	2j	18	ALA	2.2
49	1r	24	ALA	2.2
53	2y	94	ALA	2.2
40	2i	117	HIS	2.2
22	20	43	THR	2.2
1	1A	2137	C	2.2
1	1A	2793	G	2.2
1	1A	2805	G	2.2
1	2A	1059	G	2.2
2	2B	117	G	2.2
32	2a	1190	G	2.2
32	2a	1216	G	2.2
35	1d	122	ARG	2.2
38	1g	4	ARG	2.2
44	1m	114	ARG	2.2
48	2q	68	ARG	2.2
50	2s	29	ARG	2.2
52	1u	24	ARG	2.2
46	1o	21	ASP	2.2
46	2o	9	GLN	2.2
14	2S	45	GLY	2.2
38	1g	34	GLY	2.2
40	1i	68	GLY	2.2
46	2o	86	GLY	2.2
38	1g	156	TRP	2.2
7	2H	43	VAL	2.2
45	1n	53	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	1A	2135	A	2.2
32	2a	532	A	2.2
34	2c	203	PHE	2.2
38	1g	26	PHE	2.2
33	1b	29	ALA	2.2
35	1d	195	ALA	2.2
41	2j	14	LYS	2.2
41	2j	75	ILE	2.2
45	2n	49	HIS	2.2
50	2s	57	HIS	2.2
53	2y	12	ILE	2.2
55	2x	73	A	2.2
33	1b	128	GLU	2.2
41	1j	87	THR	2.2
41	2j	100	THR	2.2
50	2s	79	THR	2.2
33	1b	33	TYR	2.2
39	2h	58	TYR	2.2
33	2b	144	ARG	2.2
40	1i	42	ARG	2.2
45	2n	57	ARG	2.2
7	2H	21	PRO	2.2
32	2a	972	C	2.2
32	2a	1158	C	2.2
32	2a	1321	C	2.2
1	2A	271(M)	G	2.2
1	2A	2131	G	2.2
8	1I	38	LEU	2.2
32	1a	1042	G	2.2
35	1d	194	LEU	2.2
37	1f	45	LEU	2.2
45	2n	6	LEU	2.2
45	2n	47	LEU	2.2
6	2G	100	TRP	2.2
21	2Z	96	VAL	2.2
33	2b	184	VAL	2.2
40	2i	17	VAL	2.2
7	2H	123	PHE	2.2
21	2Z	136	PHE	2.2
24	22	1	MET	2.2
29	27	1	MET	2.2
33	2b	172	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
34	2c	176	HIS	2.2
35	1d	149	ALA	2.2
44	2m	69	GLU	2.2
32	2a	968	A	2.2
32	2a	1280	A	2.2
1	2A	271(N)	U	2.2
15	1T	129	ARG	2.2
14	2S	92	TYR	2.2
32	2a	1125	U	2.2
32	2a	1358	U	2.2
48	1q	63	ARG	2.2
51	2t	22	ARG	2.2
33	1b	94	ASN	2.2
39	2h	94	TYR	2.2
39	2h	5	PRO	2.2
6	2G	41	GLN	2.2
19	1X	95	LEU	2.2
31	29	37	GLY	2.2
33	1b	61	LEU	2.2
34	2c	4	LYS	2.2
39	2h	54	ASP	2.2
40	1i	75	ASP	2.2
47	1p	49	LEU	2.2
48	2q	98	LEU	2.2
53	1y	41	LEU	2.2
7	2H	52	VAL	2.2
45	2n	33	VAL	2.2
7	2H	89	ILE	2.2
8	2I	71	ILE	2.2
9	2N	51	PHE	2.2
32	2a	999	C	2.2
32	2a	1006	C	2.2
33	1b	39	ILE	2.2
53	2y	39	ILE	2.2
5	2F	21	ALA	2.2
12	2Q	44	ALA	2.2
2	2B	54	G	2.2
2	2B	56	G	2.2
32	1a	1030(C)	G	2.2
32	1a	1031	G	2.2
32	1a	1034	G	2.2
26	24	55	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
33	1b	36	ARG	2.2
2	2B	120	A	2.2
18	2W	60	ASN	2.2
33	1b	125	PRO	2.2
34	2c	48	TYR	2.2
42	2k	75	TYR	2.2
1	1A	272(A)	U	2.2
1	1A	2189	U	2.2
2	1B	1	U	2.2
32	2a	1126	U	2.2
43	2l	47	LYS	2.2
5	2F	180	GLY	2.2
33	2b	66	GLY	2.2
34	2c	80	GLY	2.2
34	2c	175	LEU	2.2
51	1t	101	GLY	2.2
6	2G	49	ASP	2.2
6	1G	76	SER	2.2
6	1G	52	ILE	2.2
38	2g	141	VAL	2.2
33	2b	17	PHE	2.2
33	2b	152	PHE	2.2
33	1b	218	ALA	2.1
33	2b	29	ALA	2.1
33	2b	186	ALA	2.1
38	2g	116	ALA	2.1
40	1i	52	ALA	2.1
41	1j	18	ALA	2.1
1	1A	1509	C	2.1
32	2a	1277	C	2.1
40	1i	104	ARG	2.1
45	2n	12	ARG	2.1
1	1A	2166	G	2.1
32	2a	630	G	2.1
19	1X	69	TYR	2.1
26	24	46	GLN	2.1
35	1d	138	TYR	2.1
47	2p	38	TYR	2.1
48	1q	87	LYS	2.1
34	2c	87	LEU	2.1
1	1A	1174	A	2.1
1	1A	2119	A	2.1

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Mol	Chain	Res	Type	RSRZ
2	2B	58	A	2.1
4	2E	10	GLY	2.1
32	2a	1286	A	2.1
40	1i	39	GLY	2.1
1	2A	2180	U	2.1
7	2H	113	VAL	2.1
7	2H	115	VAL	2.1
32	1a	992	U	2.1
32	1a	1212	U	2.1
32	2a	1372	U	2.1
33	1b	7	VAL	2.1
40	1i	41	VAL	2.1
40	2i	28	VAL	2.1
47	1p	19	ILE	2.1
47	1p	20	VAL	2.1
48	2q	99	SER	2.1
51	1t	55	ILE	2.1
51	1t	70	SER	2.1
34	2c	71	ALA	2.1
33	2b	86	GLU	2.1
41	2j	70	ARG	2.1
47	2p	26	ARG	2.1
14	2S	57	LYS	2.1
32	2a	1114	C	2.1
32	2a	1118	C	2.1
3	2D	37	LEU	2.1
26	14	67	TYR	2.1
44	1m	56	LEU	2.1
40	2i	72	GLY	2.1
41	2j	93	GLY	2.1
42	2k	46	GLY	2.1
1	1A	2151	G	2.1
6	2G	157	ILE	2.1
7	2H	72	ILE	2.1
7	2H	136	ILE	2.1
32	2a	1347	G	2.1
33	1b	222	ILE	2.1
33	2b	39	ILE	2.1
33	2b	189	ASP	2.1
34	1c	207	VAL	2.1
34	2c	5	ILE	2.1
50	2s	69	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
17	2V	5	VAL	2.1
21	1Z	96	VAL	2.1
32	2a	1011	G	2.1
32	2a	1013	G	2.1
35	1d	170	VAL	2.1
36	1e	69	VAL	2.1
47	1p	62	VAL	2.1
41	2j	35	SER	2.1
1	1A	2171	A	2.1
1	2A	2320	A	2.1
6	2G	151	ALA	2.1
14	2S	79	ALA	2.1
6	2G	54	GLU	2.1
32	1a	182	U	2.1
34	2c	50	ALA	2.1
34	2c	60	ALA	2.1
45	2n	11	LYS	2.1
51	1t	29	LYS	2.1
51	2t	14	LYS	2.1
5	2F	14	PRO	2.1
33	2b	187	LEU	2.1
51	1t	13	LEU	2.1
26	24	39	CYS	2.1
38	2g	28	ASN	2.1
7	2H	66	GLY	2.1
26	24	54	GLY	2.1
34	1c	201	TYR	2.1
35	1d	4	TYR	2.1
42	1k	25	TYR	2.1
43	1l	63	GLY	2.1
44	2m	95	GLY	2.1
1	2A	2178	C	2.1
8	2I	18	VAL	2.1
8	2I	79	ILE	2.1
32	2a	1045	C	2.1
32	2a	1320	C	2.1
34	1c	39	ILE	2.1
37	1f	88	VAL	2.1
40	1i	109	VAL	2.1
52	2u	13	ILE	2.1
3	2D	135	PHE	2.1
4	2E	204	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
39	2h	29	SER	2.1
40	1i	10	ARG	2.1
40	1i	13	ALA	2.1
44	1m	5	ALA	2.1
45	1n	5	ALA	2.1
1	2A	10	G	2.1
1	2A	2104	G	2.1
1	2A	2147	G	2.1
2	2B	24	G	2.1
7	1H	175	LYS	2.1
8	2I	121	LYS	2.1
32	2a	951	G	2.1
32	2a	1127	G	2.1
38	2g	156	TRP	2.1
8	1I	108	THR	2.1
32	2a	969	A	2.1
32	2a	1016	A	2.1
32	2a	1040	U	2.1
7	2H	173	PRO	2.1
45	2n	14	PRO	2.1
53	2y	45	PRO	2.1
41	2j	33	GLN	2.1
35	2d	120	LEU	2.1
6	2G	24	GLY	2.1
11	2P	82	GLY	2.1
12	2Q	30	GLY	2.1
34	1c	96	GLY	2.1
42	1k	102	GLY	2.1
44	1m	112	GLY	2.1
52	1u	16	GLY	2.1
40	2i	62	TYR	2.1
14	2S	28	VAL	2.1
14	2S	69	VAL	2.1
35	2d	112	VAL	2.1
41	2j	44	VAL	2.1
21	2Z	88	PHE	2.1
41	1j	54	PHE	2.1
45	2n	37	PHE	2.1
53	1y	48	PHE	2.1
40	2i	42	ARG	2.0
34	1c	71	ALA	2.0
41	2j	59	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	652(T)	C	2.0
3	2D	276	LYS	2.0
47	2p	48	TRP	2.0
40	1i	7	THR	2.0
42	2k	31	THR	2.0
6	2G	155	MET	2.0
34	2c	91	LEU	2.0
34	2c	94	LEU	2.0
53	2y	9	GLN	2.0
53	2y	27	LEU	2.0
1	2A	1056	G	2.0
1	2A	2101	G	2.0
1	2A	2170	A	2.0
32	2a	1022	G	2.0
32	2a	1024	G	2.0
12	2Q	62	GLY	2.0
34	2c	155	GLY	2.0
42	2k	40	ILE	2.0
4	2E	59	VAL	2.0
21	2Z	71	VAL	2.0
25	23	59	VAL	2.0
26	24	35	VAL	2.0
27	15	60	VAL	2.0
33	1b	15	VAL	2.0
36	2e	90	VAL	2.0
40	2i	114	TYR	2.0
44	2m	45	VAL	2.0
6	2G	95	ARG	2.0
6	2G	102	PHE	2.0
29	27	47	ARG	2.0
37	2f	77	ARG	2.0
39	1h	41	ARG	2.0
44	2m	11	ARG	2.0
50	1s	27	GLU	2.0
5	2F	137	LYS	2.0
14	2S	93	LYS	2.0
38	2g	40	ALA	2.0
38	2g	65	ALA	2.0
39	2h	56	LYS	2.0
35	2d	33	MET	2.0
33	1b	234	PRO	2.0
1	1A	2146	C	2.0

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Mol	Chain	Res	Type	RSRZ
2	2B	4	C	2.0
2	2B	27	C	2.0
14	2S	38	GLN	2.0
32	1a	1027	C	2.0
32	2a	1254	C	2.0
32	2a	1322	C	2.0
39	2h	59	LEU	2.0
47	1p	6	LEU	2.0
47	2p	16	HIS	2.0
1	1A	1175	U	2.0
1	2A	2189	U	2.0
7	2H	166	GLY	2.0
33	2b	41	ILE	2.0
41	1j	50	ILE	2.0
42	2k	90	GLY	2.0
44	1m	78	ILE	2.0
50	2s	68	GLY	2.0
1	1A	890	A	2.0
1	1A	2134	A	2.0
1	2A	1057	A	2.0
1	2A	1098	A	2.0
2	2B	25	A	2.0
24	12	69	ARG	2.0
32	1a	532	A	2.0
33	1b	112	VAL	2.0
33	2b	197	VAL	2.0
38	1g	5	ARG	2.0
40	2i	16	ARG	2.0
47	1p	17	TYR	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
1	5MU	2A	1915	21/22	0.83	0.11	77,82,87,96	0
32	M2G	2a	966	25/26	0.86	0.16	61,70,84,98	0
1	PSU	2A	1917	20/21	0.88	0.09	73,79,99,100	0
1	5MU	1A	1915	21/22	0.88	0.12	67,73,81,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	5MC	2a	967	21/22	0.88	0.15	55,73,79,83	0
32	2MG	2a	1207	24/25	0.89	0.11	77,84,88,94	0
1	PSU	2A	1911	20/21	0.90	0.10	64,73,77,77	0
1	PSU	1A	1917	20/21	0.90	0.10	56,68,75,79	0
32	2MG	1a	1207	24/25	0.90	0.12	67,75,79,80	0
32	PSU	2a	516	20/21	0.91	0.11	68,75,81,84	0
43	0TD	2l	92	10/11	0.91	0.13	62,64,67,72	0
32	G7M	2a	527	24/25	0.92	0.11	57,68,73,78	0
32	4OC	2a	1402	22/23	0.93	0.12	61,65,72,75	0
32	5MC	2a	1404	21/22	0.93	0.11	55,61,63,67	0
1	OMC	2A	1920	21/22	0.93	0.11	59,67,72,73	0
43	0TD	1l	92	10/11	0.94	0.10	44,56,60,71	0
1	5MC	2A	1942	21/22	0.94	0.12	43,56,62,69	0
32	PSU	1a	516	20/21	0.94	0.10	61,66,71,75	0
32	5MC	1a	967	21/22	0.94	0.11	60,63,71,76	0
1	PSU	1A	1911	20/21	0.94	0.09	53,66,68,68	0
56	FME	1v	1	10/11	0.94	0.15	22,37,47,68	0
32	5MC	2a	1400	21/22	0.95	0.11	62,69,72,75	0
32	MA6	1a	1519	24/25	0.95	0.10	38,47,52,53	0
32	M2G	1a	966	25/26	0.95	0.10	52,59,70,78	0
32	UR3	2a	1498	21/22	0.95	0.10	58,62,69,71	0
32	MA6	2a	1518	24/25	0.95	0.12	57,63,70,70	0
32	5MC	1a	1407	21/22	0.95	0.09	47,53,57,62	0
32	UR3	1a	1498	21/22	0.95	0.11	47,51,57,63	0
56	FME	2v	1	10/11	0.95	0.13	47,57,60,77	0
32	5MC	2a	1407	21/22	0.96	0.09	50,62,68,72	0
32	G7M	1a	527	24/25	0.96	0.09	45,55,58,65	0
1	2MA	2A	2503	23/24	0.96	0.08	31,36,39,39	0
32	MA6	2a	1519	24/25	0.96	0.12	59,63,70,74	0
1	OMC	1A	1920	21/22	0.96	0.09	47,55,59,60	0
55	8AN	2x	76	22/23	0.96	0.08	34,39,42,45	0
32	5MC	1a	1400	21/22	0.96	0.10	53,58,64,65	0
32	5MC	1a	1404	21/22	0.96	0.08	44,49,52,56	0
32	4OC	1a	1402	22/23	0.97	0.08	48,53,55,60	0
1	OMG	2A	2251	24/25	0.97	0.09	30,37,44,45	0
1	5MC	1A	1942	21/22	0.97	0.07	28,34,41,42	0
1	2MU	2A	2552	21/23	0.97	0.07	32,38,42,47	0
54	PPU	1w	76	37/38	0.97	0.07	18,23,27,31	0
54	PPU	2w	76	37/38	0.97	0.09	29,38,42,49	0
1	PSU	2A	2605	20/21	0.97	0.09	30,39,44,50	0
32	MA6	1a	1518	24/25	0.97	0.09	41,46,48,53	0
1	5MU	2A	1939	21/22	0.97	0.09	36,41,47,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	OMG	1A	2251	24/25	0.98	0.06	19,21,24,25	0
1	2MA	1A	2503	23/24	0.98	0.07	18,22,26,28	0
1	2MU	1A	2552	21/23	0.98	0.07	21,31,34,35	0
1	PSU	1A	2605	20/21	0.98	0.08	21,29,32,35	0
1	5MU	1A	1939	21/22	0.98	0.06	22,27,29,30	0
1	5MC	2A	1962	21/22	0.98	0.08	37,44,49,56	0
1	5MC	1A	1962	21/22	0.98	0.07	30,34,39,44	0
55	8AN	1x	76	22/23	0.99	0.05	18,21,26,27	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3703	1/1	0.37	0.22	67,67,67,67	0
57	MG	2A	3483	1/1	0.57	0.30	76,76,76,76	0
57	MG	1A	3468	1/1	0.59	0.29	70,70,70,70	0
57	MG	2a	3048	1/1	0.60	0.28	89,89,89,89	0
57	MG	1A	4004	1/1	0.61	0.27	66,66,66,66	0
57	MG	2n	101	1/1	0.62	0.34	76,76,76,76	0
57	MG	2A	3533	1/1	0.65	0.21	65,65,65,65	0
57	MG	1A	3729	1/1	0.66	0.14	64,64,64,64	0
57	MG	1a	1753	1/1	0.66	0.34	71,71,71,71	0
57	MG	1A	3995	1/1	0.66	0.17	76,76,76,76	0
57	MG	1a	1863	1/1	0.67	0.31	71,71,71,71	0
57	MG	2A	3719	1/1	0.67	0.19	71,71,71,71	0
57	MG	2A	3449	1/1	0.69	0.20	89,89,89,89	0
57	MG	1A	3650	1/1	0.69	0.24	57,57,57,57	0
57	MG	1a	1794	1/1	0.70	0.32	77,77,77,77	0
57	MG	2A	3536	1/1	0.70	0.19	71,71,71,71	0
57	MG	1A	3765	1/1	0.70	0.26	55,55,55,55	0
57	MG	2A	3724	1/1	0.70	0.19	77,77,77,77	0
57	MG	2a	3022	1/1	0.70	0.35	71,71,71,71	0
57	MG	2A	3504	1/1	0.70	0.15	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3114	1/1	0.70	0.26	64,64,64,64	0
57	MG	2A	3516	1/1	0.70	0.22	74,74,74,74	0
57	MG	1A	3710	1/1	0.71	0.17	75,75,75,75	0
57	MG	1a	1696	1/1	0.71	0.20	79,79,79,79	0
57	MG	2A	3297	1/1	0.71	0.14	78,78,78,78	0
57	MG	1A	3736	1/1	0.71	0.18	42,42,42,42	0
57	MG	1a	1785	1/1	0.71	0.14	84,84,84,84	0
57	MG	1a	1866	1/1	0.72	0.15	69,69,69,69	0
57	MG	1A	4024	1/1	0.72	0.25	69,69,69,69	0
57	MG	2A	3532	1/1	0.72	0.16	61,61,61,61	0
57	MG	1A	3806	1/1	0.72	0.12	78,78,78,78	0
57	MG	1A	3853	1/1	0.72	0.16	72,72,72,72	0
57	MG	2A	3661	1/1	0.72	0.27	73,73,73,73	0
57	MG	1a	1827	1/1	0.73	0.15	75,75,75,75	0
57	MG	2B	207	1/1	0.73	0.27	83,83,83,83	0
57	MG	1a	1871	1/1	0.73	0.43	88,88,88,88	0
57	MG	2A	3491	1/1	0.73	0.21	72,72,72,72	0
57	MG	1A	3816	1/1	0.73	0.19	72,72,72,72	0
57	MG	2a	3121	1/1	0.73	0.26	72,72,72,72	0
57	MG	2A	3389	1/1	0.73	0.16	74,74,74,74	0
57	MG	1a	1666	1/1	0.74	0.18	75,75,75,75	0
57	MG	1a	1782	1/1	0.74	0.22	74,74,74,74	0
57	MG	2A	3085	1/1	0.74	0.24	77,77,77,77	0
57	MG	2A	3291	1/1	0.74	0.55	74,74,74,74	0
57	MG	2A	3484	1/1	0.74	0.26	71,71,71,71	0
57	MG	2p	101	1/1	0.74	0.36	70,70,70,70	0
57	MG	2A	3470	1/1	0.75	0.20	64,64,64,64	0
57	MG	2a	3057	1/1	0.75	0.29	74,74,74,74	0
57	MG	1A	3339	1/1	0.75	0.16	69,69,69,69	0
57	MG	2A	3279	1/1	0.75	0.33	73,73,73,73	0
57	MG	2A	3538	1/1	0.75	0.17	82,82,82,82	0
57	MG	2A	3575	1/1	0.75	0.28	70,70,70,70	0
57	MG	1a	1868	1/1	0.76	0.30	80,80,80,80	0
57	MG	1A	4008	1/1	0.76	0.13	45,45,45,45	0
57	MG	1d	301	1/1	0.76	0.18	79,79,79,79	0
57	MG	2A	3355	1/1	0.76	0.16	76,76,76,76	0
57	MG	2a	3066	1/1	0.76	0.25	72,72,72,72	0
57	MG	1a	1836	1/1	0.76	0.17	78,78,78,78	0
57	MG	2A	3238	1/1	0.76	0.21	68,68,68,68	0
57	MG	2A	3468	1/1	0.76	0.20	72,72,72,72	0
57	MG	2A	3728	1/1	0.76	0.19	78,78,78,78	0
57	MG	1a	1754	1/1	0.77	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
57	MG	1a	1736	1/1	0.77	0.15	81,81,81,81	0
57	MG	2a	3076	1/1	0.77	0.15	74,74,74,74	0
57	MG	1A	3460	1/1	0.77	0.28	65,65,65,65	0
57	MG	2A	3157	1/1	0.77	0.19	66,66,66,66	0
57	MG	2A	3621	1/1	0.77	0.12	80,80,80,80	0
57	MG	2A	3229	1/1	0.77	0.27	61,61,61,61	0
57	MG	2A	3269	1/1	0.78	0.19	63,63,63,63	0
57	MG	2A	3275	1/1	0.78	0.17	59,59,59,59	0
57	MG	1a	1813	1/1	0.78	0.32	76,76,76,76	0
57	MG	2B	214	1/1	0.78	0.15	79,79,79,79	0
57	MG	1A	3606	1/1	0.78	0.13	36,36,36,36	0
57	MG	1d	302	1/1	0.78	0.18	76,76,76,76	0
57	MG	2A	3325	1/1	0.78	0.26	60,60,60,60	0
57	MG	1A	3929	1/1	0.78	0.15	53,53,53,53	0
57	MG	2A	3106	1/1	0.78	0.17	65,65,65,65	0
57	MG	2A	3118	1/1	0.78	0.36	66,66,66,66	0
57	MG	1B	206	1/1	0.78	0.33	63,63,63,63	0
57	MG	1a	1787	1/1	0.78	0.20	83,83,83,83	0
57	MG	1V	205	1/1	0.78	0.14	63,63,63,63	0
57	MG	1a	1810	1/1	0.79	0.17	79,79,79,79	0
57	MG	2A	3509	1/1	0.79	0.17	64,64,64,64	0
57	MG	1A	3992	1/1	0.79	0.18	59,59,59,59	0
57	MG	2P	201	1/1	0.79	0.25	61,61,61,61	0
57	MG	2a	3002	1/1	0.79	0.31	65,65,65,65	0
57	MG	1A	3342	1/1	0.79	0.12	58,58,58,58	0
57	MG	1a	1763	1/1	0.79	0.20	80,80,80,80	0
57	MG	2A	3391	1/1	0.79	0.19	60,60,60,60	0
57	MG	1a	1772	1/1	0.79	0.14	65,65,65,65	0
57	MG	1A	3322	1/1	0.79	0.21	64,64,64,64	0
57	MG	2a	3086	1/1	0.79	0.29	72,72,72,72	0
57	MG	2a	3094	1/1	0.79	0.39	64,64,64,64	0
57	MG	1a	1698	1/1	0.79	0.27	74,74,74,74	0
57	MG	1a	1702	1/1	0.79	0.14	68,68,68,68	0
57	MG	2a	3144	1/1	0.79	0.16	66,66,66,66	0
57	MG	1B	211	1/1	0.79	0.23	63,63,63,63	0
57	MG	1a	1809	1/1	0.79	0.23	69,69,69,69	0
57	MG	1a	1662	1/1	0.80	0.15	74,74,74,74	0
57	MG	2A	3090	1/1	0.80	0.42	79,79,79,79	0
57	MG	1A	3528	1/1	0.80	0.21	75,75,75,75	0
57	MG	2A	3288	1/1	0.80	0.33	67,67,67,67	0
57	MG	1A	3399	1/1	0.80	0.19	66,66,66,66	0
57	MG	2A	3146	1/1	0.80	0.34	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1B	220	1/1	0.80	0.12	30,30,30,30	0
57	MG	2A	3328	1/1	0.80	0.28	71,71,71,71	0
57	MG	2A	3731	1/1	0.80	0.19	65,65,65,65	0
57	MG	2A	3214	1/1	0.80	0.24	60,60,60,60	0
57	MG	1A	3803	1/1	0.80	0.21	63,63,63,63	0
57	MG	2a	3166	1/1	0.80	0.23	72,72,72,72	0
57	MG	2I	201	1/1	0.80	0.15	76,76,76,76	0
57	MG	2A	3070	1/1	0.80	0.34	76,76,76,76	0
57	MG	1a	1803	1/1	0.81	0.29	74,74,74,74	0
57	MG	2A	3040	1/1	0.81	0.24	68,68,68,68	0
57	MG	2B	212	1/1	0.81	0.14	81,81,81,81	0
57	MG	1a	1673	1/1	0.81	0.22	68,68,68,68	0
57	MG	2A	3512	1/1	0.81	0.18	70,70,70,70	0
57	MG	1A	3720	1/1	0.81	0.21	52,52,52,52	0
57	MG	2T	203	1/1	0.81	0.17	71,71,71,71	0
57	MG	2A	3526	1/1	0.81	0.18	48,48,48,48	0
57	MG	1A	3689	1/1	0.81	0.17	61,61,61,61	0
57	MG	1a	1824	1/1	0.81	0.26	72,72,72,72	0
57	MG	1A	3435	1/1	0.81	0.19	60,60,60,60	0
57	MG	2a	3059	1/1	0.81	0.34	81,81,81,81	0
57	MG	2a	3062	1/1	0.81	0.24	65,65,65,65	0
57	MG	1a	1828	1/1	0.81	0.26	74,74,74,74	0
57	MG	1a	1703	1/1	0.81	0.28	70,70,70,70	0
57	MG	1a	1784	1/1	0.81	0.17	69,69,69,69	0
57	MG	2A	3659	1/1	0.81	0.11	54,54,54,54	0
57	MG	1a	1718	1/1	0.81	0.14	74,74,74,74	0
57	MG	2A	3689	1/1	0.81	0.15	71,71,71,71	0
57	MG	2A	3712	1/1	0.81	0.28	75,75,75,75	0
57	MG	1A	3200	1/1	0.81	0.12	64,64,64,64	0
57	MG	1a	1793	1/1	0.81	0.15	83,83,83,83	0
57	MG	1a	1748	1/1	0.81	0.15	79,79,79,79	0
57	MG	2A	3366	1/1	0.82	0.12	48,48,48,48	0
57	MG	2A	3694	1/1	0.82	0.17	61,61,61,61	0
57	MG	2A	3709	1/1	0.82	0.23	63,63,63,63	0
57	MG	1A	3698	1/1	0.82	0.16	59,59,59,59	0
57	MG	2A	3716	1/1	0.82	0.17	74,74,74,74	0
57	MG	1a	1636	1/1	0.82	0.24	68,68,68,68	0
57	MG	1a	1849	1/1	0.82	0.13	66,66,66,66	0
57	MG	2A	3464	1/1	0.82	0.22	63,63,63,63	0
57	MG	1a	1722	1/1	0.82	0.20	68,68,68,68	0
57	MG	1A	3389	1/1	0.82	0.13	50,50,50,50	0
57	MG	1A	3757	1/1	0.82	0.13	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3223	1/1	0.82	0.27	60,60,60,60	0
57	MG	1A	3863	1/1	0.82	0.13	27,27,27,27	0
57	MG	2A	3230	1/1	0.82	0.23	65,65,65,65	0
57	MG	1a	1676	1/1	0.82	0.26	66,66,66,66	0
57	MG	1A	3892	1/1	0.82	0.28	62,62,62,62	0
57	MG	1n	103	1/1	0.82	0.25	70,70,70,70	0
57	MG	2A	3021	1/1	0.82	0.17	71,71,71,71	0
57	MG	1A	3192	1/1	0.82	0.24	56,56,56,56	0
57	MG	2A	3041	1/1	0.82	0.17	55,55,55,55	0
57	MG	2A	3055	1/1	0.82	0.25	58,58,58,58	0
57	MG	1a	1777	1/1	0.82	0.17	76,76,76,76	0
57	MG	2a	3071	1/1	0.82	0.37	78,78,78,78	0
57	MG	2A	3557	1/1	0.82	0.19	65,65,65,65	0
57	MG	2A	3559	1/1	0.82	0.11	74,74,74,74	0
57	MG	2A	3075	1/1	0.82	0.22	67,67,67,67	0
57	MG	2A	3613	1/1	0.82	0.19	60,60,60,60	0
57	MG	2A	3617	1/1	0.82	0.20	71,71,71,71	0
57	MG	2A	3329	1/1	0.82	0.23	75,75,75,75	0
57	MG	2A	3351	1/1	0.82	0.18	67,67,67,67	0
57	MG	2a	3180	1/1	0.82	0.25	70,70,70,70	0
57	MG	1A	3574	1/1	0.82	0.23	55,55,55,55	0
57	MG	2A	3688	1/1	0.82	0.12	66,66,66,66	0
57	MG	2A	3564	1/1	0.83	0.12	70,70,70,70	0
57	MG	1A	3454	1/1	0.83	0.13	25,25,25,25	0
57	MG	2A	3583	1/1	0.83	0.13	54,54,54,54	0
57	MG	2A	3607	1/1	0.83	0.11	52,52,52,52	0
57	MG	1B	227	1/1	0.83	0.13	58,58,58,58	0
57	MG	1A	3224	1/1	0.83	0.14	66,66,66,66	0
57	MG	2a	3006	1/1	0.83	0.15	55,55,55,55	0
57	MG	1a	1631	1/1	0.83	0.22	66,66,66,66	0
57	MG	2a	3024	1/1	0.83	0.35	65,65,65,65	0
57	MG	1A	3696	1/1	0.83	0.14	65,65,65,65	0
57	MG	2a	3049	1/1	0.83	0.19	68,68,68,68	0
57	MG	2a	3056	1/1	0.83	0.19	71,71,71,71	0
57	MG	1a	1650	1/1	0.83	0.20	66,66,66,66	0
57	MG	2A	3684	1/1	0.83	0.11	65,65,65,65	0
57	MG	2A	3125	1/1	0.83	0.22	62,62,62,62	0
57	MG	1A	3193	1/1	0.83	0.32	71,71,71,71	0
57	MG	1A	3515	1/1	0.83	0.12	35,35,35,35	0
57	MG	1A	3395	1/1	0.83	0.13	55,55,55,55	0
57	MG	2A	3710	1/1	0.83	0.11	75,75,75,75	0
57	MG	1a	1823	1/1	0.83	0.13	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3226	1/1	0.83	0.16	49,49,49,49	0
57	MG	2A	3376	1/1	0.83	0.14	54,54,54,54	0
57	MG	1A	3338	1/1	0.83	0.13	60,60,60,60	0
57	MG	2a	3154	1/1	0.83	0.12	73,73,73,73	0
57	MG	1A	3188	1/1	0.83	0.26	52,52,52,52	0
57	MG	2A	3404	1/1	0.83	0.14	53,53,53,53	0
57	MG	2A	3732	1/1	0.83	0.22	69,69,69,69	0
57	MG	1A	3889	1/1	0.83	0.15	45,45,45,45	0
59	MPD	2A	3736	8/8	0.83	0.28	67,72,77,77	0
57	MG	1A	3537	1/1	0.84	0.12	47,47,47,47	0
57	MG	1a	1786	1/1	0.84	0.18	71,71,71,71	0
57	MG	2A	3730	1/1	0.84	0.19	76,76,76,76	0
57	MG	15	3108	1/1	0.84	0.12	57,57,57,57	0
57	MG	1a	1605	1/1	0.84	0.23	67,67,67,67	0
57	MG	2A	3733	1/1	0.84	0.26	68,68,68,68	0
57	MG	1a	1607	1/1	0.84	0.17	61,61,61,61	0
57	MG	1a	1801	1/1	0.84	0.15	69,69,69,69	0
57	MG	1A	3521	1/1	0.84	0.13	52,52,52,52	0
57	MG	1a	1726	1/1	0.84	0.15	54,54,54,54	0
57	MG	1a	1634	1/1	0.84	0.25	71,71,71,71	0
57	MG	2A	3321	1/1	0.84	0.24	67,67,67,67	0
57	MG	28	101	1/1	0.84	0.18	62,62,62,62	0
57	MG	1A	4022	1/1	0.84	0.21	66,66,66,66	0
57	MG	2A	3083	1/1	0.84	0.21	77,77,77,77	0
57	MG	2a	3014	1/1	0.84	0.23	71,71,71,71	0
57	MG	1a	1822	1/1	0.84	0.18	67,67,67,67	0
57	MG	2A	3338	1/1	0.84	0.24	71,71,71,71	0
57	MG	1A	3576	1/1	0.84	0.14	46,46,46,46	0
57	MG	2A	3610	1/1	0.84	0.18	51,51,51,51	0
57	MG	1A	3946	1/1	0.84	0.08	79,79,79,79	0
57	MG	2A	3615	1/1	0.84	0.12	67,67,67,67	0
57	MG	1a	1758	1/1	0.84	0.16	66,66,66,66	0
57	MG	1A	3300	1/1	0.84	0.15	56,56,56,56	0
57	MG	2a	3064	1/1	0.84	0.16	75,75,75,75	0
57	MG	2A	3636	1/1	0.84	0.10	59,59,59,59	0
57	MG	2A	3135	1/1	0.84	0.20	54,54,54,54	0
57	MG	2A	3136	1/1	0.84	0.17	66,66,66,66	0
57	MG	2A	3670	1/1	0.84	0.25	61,61,61,61	0
57	MG	1A	3534	1/1	0.84	0.17	32,32,32,32	0
57	MG	2A	3426	1/1	0.84	0.27	75,75,75,75	0
57	MG	2A	3150	1/1	0.84	0.17	52,52,52,52	0
57	MG	2a	3128	1/1	0.84	0.12	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3691	1/1	0.84	0.26	76,76,76,76	0
57	MG	1a	1775	1/1	0.84	0.20	61,61,61,61	0
57	MG	2A	3159	1/1	0.84	0.24	84,84,84,84	0
57	MG	2a	3175	1/1	0.84	0.16	55,55,55,55	0
57	MG	2A	3191	1/1	0.84	0.23	72,72,72,72	0
57	MG	1A	3997	1/1	0.84	0.18	67,67,67,67	0
57	MG	1a	1692	1/1	0.84	0.22	63,63,63,63	0
57	MG	1F	314	1/1	0.84	0.12	48,48,48,48	0
57	MG	1A	3776	1/1	0.85	0.13	48,48,48,48	0
57	MG	1a	1682	1/1	0.85	0.24	68,68,68,68	0
57	MG	2E	305	1/1	0.85	0.13	32,32,32,32	0
57	MG	1A	3778	1/1	0.85	0.15	65,65,65,65	0
57	MG	1A	3292	1/1	0.85	0.10	75,75,75,75	0
57	MG	1A	3294	1/1	0.85	0.11	72,72,72,72	0
57	MG	21	102	1/1	0.85	0.11	49,49,49,49	0
57	MG	1A	3593	1/1	0.85	0.14	63,63,63,63	0
57	MG	2A	3086	1/1	0.85	0.13	76,76,76,76	0
57	MG	2a	3004	1/1	0.85	0.16	60,60,60,60	0
57	MG	1A	3844	1/1	0.85	0.10	47,47,47,47	0
57	MG	1a	1705	1/1	0.85	0.18	73,73,73,73	0
57	MG	1A	3596	1/1	0.85	0.18	54,54,54,54	0
57	MG	2A	3357	1/1	0.85	0.23	67,67,67,67	0
57	MG	1A	3010	1/1	0.85	0.15	51,51,51,51	0
57	MG	2A	3622	1/1	0.85	0.26	54,54,54,54	0
57	MG	1A	3872	1/1	0.85	0.10	37,37,37,37	0
57	MG	1a	1734	1/1	0.85	0.14	60,60,60,60	0
57	MG	1A	3876	1/1	0.85	0.12	61,61,61,61	0
57	MG	2A	3148	1/1	0.85	0.12	66,66,66,66	0
57	MG	15	3106	1/1	0.85	0.27	36,36,36,36	0
57	MG	1A	3721	1/1	0.85	0.11	60,60,60,60	0
57	MG	1A	3724	1/1	0.85	0.16	53,53,53,53	0
57	MG	2A	3465	1/1	0.85	0.13	72,72,72,72	0
57	MG	2A	3167	1/1	0.85	0.30	66,66,66,66	0
57	MG	1a	1862	1/1	0.85	0.24	71,71,71,71	0
57	MG	2a	3097	1/1	0.85	0.30	72,72,72,72	0
57	MG	1A	3900	1/1	0.85	0.15	58,58,58,58	0
57	MG	1a	1760	1/1	0.85	0.17	75,75,75,75	0
57	MG	1A	3308	1/1	0.85	0.12	40,40,40,40	0
57	MG	1A	3938	1/1	0.85	0.11	63,63,63,63	0
57	MG	1A	3559	1/1	0.85	0.18	47,47,47,47	0
57	MG	2a	3165	1/1	0.85	0.22	67,67,67,67	0
57	MG	1A	3975	1/1	0.85	0.13	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3168	1/1	0.85	0.21	69,69,69,69	0
57	MG	2A	3243	1/1	0.85	0.11	53,53,53,53	0
57	MG	2A	3268	1/1	0.85	0.22	71,71,71,71	0
57	MG	1A	3692	1/1	0.85	0.10	51,51,51,51	0
57	MG	1A	3694	1/1	0.85	0.12	58,58,58,58	0
59	MPD	2A	3735	8/8	0.85	0.27	38,48,56,61	0
57	MG	1A	3775	1/1	0.85	0.12	54,54,54,54	0
59	MPD	2A	3737	8/8	0.85	0.20	56,68,70,73	0
57	MG	2A	3723	1/1	0.86	0.25	69,69,69,69	0
57	MG	2A	3395	1/1	0.86	0.20	75,75,75,75	0
57	MG	1A	3786	1/1	0.86	0.13	24,24,24,24	0
57	MG	1A	3983	1/1	0.86	0.10	68,68,68,68	0
57	MG	2A	3119	1/1	0.86	0.22	66,66,66,66	0
57	MG	1A	3988	1/1	0.86	0.22	42,42,42,42	0
57	MG	1A	3990	1/1	0.86	0.18	38,38,38,38	0
57	MG	1A	3789	1/1	0.86	0.09	29,29,29,29	0
57	MG	1A	3600	1/1	0.86	0.38	48,48,48,48	0
57	MG	1A	3601	1/1	0.86	0.23	53,53,53,53	0
57	MG	1A	3539	1/1	0.86	0.14	47,47,47,47	0
57	MG	1A	3622	1/1	0.86	0.12	31,31,31,31	0
57	MG	2A	3495	1/1	0.86	0.21	66,66,66,66	0
57	MG	1A	4021	1/1	0.86	0.20	51,51,51,51	0
57	MG	1A	3002	1/1	0.86	0.17	58,58,58,58	0
57	MG	2A	3173	1/1	0.86	0.10	68,68,68,68	0
57	MG	2A	3187	1/1	0.86	0.26	65,65,65,65	0
57	MG	1A	3678	1/1	0.86	0.17	55,55,55,55	0
57	MG	1A	4027	1/1	0.86	0.16	62,62,62,62	0
57	MG	1A	3569	1/1	0.86	0.13	67,67,67,67	0
57	MG	2a	3017	1/1	0.86	0.12	67,67,67,67	0
57	MG	2A	3224	1/1	0.86	0.12	59,59,59,59	0
57	MG	1a	1706	1/1	0.86	0.17	60,60,60,60	0
57	MG	2a	3031	1/1	0.86	0.28	65,65,65,65	0
57	MG	1a	1707	1/1	0.86	0.25	69,69,69,69	0
57	MG	1a	1711	1/1	0.86	0.26	72,72,72,72	0
57	MG	1a	1716	1/1	0.86	0.15	64,64,64,64	0
57	MG	1B	209	1/1	0.86	0.12	55,55,55,55	0
57	MG	2A	3582	1/1	0.86	0.10	51,51,51,51	0
57	MG	1a	1864	1/1	0.86	0.10	68,68,68,68	0
57	MG	1A	3350	1/1	0.86	0.13	50,50,50,50	0
57	MG	2A	3270	1/1	0.86	0.11	77,77,77,77	0
57	MG	2A	3612	1/1	0.86	0.12	47,47,47,47	0
57	MG	1A	3761	1/1	0.86	0.09	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1B	226	1/1	0.86	0.17	69,69,69,69	0
57	MG	1A	3764	1/1	0.86	0.19	52,52,52,52	0
57	MG	1E	305	1/1	0.86	0.11	49,49,49,49	0
57	MG	2a	3105	1/1	0.86	0.20	48,48,48,48	0
57	MG	1d	305	1/1	0.86	0.08	85,85,85,85	0
57	MG	2A	3313	1/1	0.86	0.26	76,76,76,76	0
57	MG	1A	3383	1/1	0.86	0.10	43,43,43,43	0
57	MG	1G	202	1/1	0.86	0.10	50,50,50,50	0
57	MG	1A	3261	1/1	0.86	0.25	60,60,60,60	0
57	MG	1A	3937	1/1	0.86	0.13	46,46,46,46	0
57	MG	2A	3044	1/1	0.86	0.22	68,68,68,68	0
57	MG	2A	3343	1/1	0.86	0.21	62,62,62,62	0
57	MG	1A	3176	1/1	0.86	0.22	45,45,45,45	0
57	MG	15	3109	1/1	0.86	0.18	72,72,72,72	0
57	MG	2j	201	1/1	0.86	0.13	68,68,68,68	0
57	MG	1A	3943	1/1	0.86	0.18	73,73,73,73	0
57	MG	1a	1776	1/1	0.86	0.11	83,83,83,83	0
58	ARG	1A	4030	12/12	0.86	0.17	45,63,76,76	0
57	MG	1A	3699	1/1	0.86	0.13	68,68,68,68	0
57	MG	1a	1609	1/1	0.86	0.16	48,48,48,48	0
57	MG	1A	3954	1/1	0.86	0.12	52,52,52,52	0
57	MG	10	104	1/1	0.87	0.09	45,45,45,45	0
57	MG	2G	202	1/1	0.87	0.19	76,76,76,76	0
57	MG	2A	3153	1/1	0.87	0.17	60,60,60,60	0
57	MG	2N	201	1/1	0.87	0.11	72,72,72,72	0
57	MG	1A	3926	1/1	0.87	0.13	46,46,46,46	0
57	MG	2A	3568	1/1	0.87	0.14	37,37,37,37	0
57	MG	2A	3569	1/1	0.87	0.11	43,43,43,43	0
57	MG	1A	3640	1/1	0.87	0.15	44,44,44,44	0
57	MG	2A	3579	1/1	0.87	0.12	51,51,51,51	0
57	MG	2A	3350	1/1	0.87	0.09	59,59,59,59	0
57	MG	1A	3428	1/1	0.87	0.23	54,54,54,54	0
57	MG	1A	3817	1/1	0.87	0.17	26,26,26,26	0
57	MG	2a	3016	1/1	0.87	0.22	64,64,64,64	0
57	MG	1a	1791	1/1	0.87	0.22	75,75,75,75	0
57	MG	2A	3190	1/1	0.87	0.25	67,67,67,67	0
57	MG	1A	4025	1/1	0.87	0.14	63,63,63,63	0
57	MG	2A	3209	1/1	0.87	0.23	65,65,65,65	0
57	MG	1A	3827	1/1	0.87	0.14	34,34,34,34	0
57	MG	1B	203	1/1	0.87	0.14	62,62,62,62	0
57	MG	2a	3052	1/1	0.87	0.22	61,61,61,61	0
57	MG	1A	3676	1/1	0.87	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
57	MG	2A	3409	1/1	0.87	0.15	62,62,62,62	0
57	MG	2A	3644	1/1	0.87	0.14	66,66,66,66	0
57	MG	2a	3060	1/1	0.87	0.15	74,74,74,74	0
57	MG	2A	3414	1/1	0.87	0.13	39,39,39,39	0
57	MG	2A	3417	1/1	0.87	0.13	58,58,58,58	0
57	MG	2A	3418	1/1	0.87	0.11	50,50,50,50	0
57	MG	2A	3678	1/1	0.87	0.13	57,57,57,57	0
57	MG	1a	1733	1/1	0.87	0.16	60,60,60,60	0
57	MG	2a	3080	1/1	0.87	0.18	76,76,76,76	0
57	MG	2a	3085	1/1	0.87	0.14	59,59,59,59	0
57	MG	1A	3386	1/1	0.87	0.15	34,34,34,34	0
57	MG	2A	3460	1/1	0.87	0.14	43,43,43,43	0
57	MG	1A	3481	1/1	0.87	0.16	32,32,32,32	0
57	MG	2A	3078	1/1	0.87	0.22	57,57,57,57	0
57	MG	1B	215	1/1	0.87	0.12	53,53,53,53	0
57	MG	2a	3116	1/1	0.87	0.14	72,72,72,72	0
57	MG	1a	1663	1/1	0.87	0.16	66,66,66,66	0
57	MG	1A	3489	1/1	0.87	0.12	55,55,55,55	0
57	MG	2a	3131	1/1	0.87	0.09	72,72,72,72	0
57	MG	2a	3134	1/1	0.87	0.12	82,82,82,82	0
57	MG	1A	3610	1/1	0.87	0.19	51,51,51,51	0
57	MG	2a	3149	1/1	0.87	0.18	68,68,68,68	0
57	MG	1A	3881	1/1	0.87	0.08	50,50,50,50	0
57	MG	2A	3278	1/1	0.87	0.24	65,65,65,65	0
57	MG	1a	1835	1/1	0.87	0.18	78,78,78,78	0
57	MG	2A	3285	1/1	0.87	0.27	64,64,64,64	0
57	MG	1A	3360	1/1	0.87	0.12	57,57,57,57	0
57	MG	1a	1767	1/1	0.87	0.24	60,60,60,60	0
57	MG	2A	3294	1/1	0.87	0.17	54,54,54,54	0
57	MG	1E	309	1/1	0.87	0.15	63,63,63,63	0
57	MG	2B	203	1/1	0.87	0.19	74,74,74,74	0
57	MG	1A	3891	1/1	0.87	0.18	54,54,54,54	0
57	MG	2B	211	1/1	0.87	0.15	54,54,54,54	0
57	MG	1A	3798	1/1	0.87	0.23	63,63,63,63	0
57	MG	1A	3637	1/1	0.87	0.13	24,24,24,24	0
57	MG	2F	303	1/1	0.88	0.17	50,50,50,50	0
57	MG	2A	3544	1/1	0.88	0.13	53,53,53,53	0
57	MG	2A	3554	1/1	0.88	0.16	71,71,71,71	0
57	MG	2A	3092	1/1	0.88	0.16	60,60,60,60	0
57	MG	1a	1816	1/1	0.88	0.16	68,68,68,68	0
57	MG	1a	1821	1/1	0.88	0.12	66,66,66,66	0
57	MG	1A	3715	1/1	0.88	0.20	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	23	101	1/1	0.88	0.16	63,63,63,63	0
57	MG	1a	1610	1/1	0.88	0.14	58,58,58,58	0
57	MG	2A	3129	1/1	0.88	0.24	63,63,63,63	0
57	MG	2A	3131	1/1	0.88	0.23	62,62,62,62	0
57	MG	2A	3581	1/1	0.88	0.12	67,67,67,67	0
57	MG	2a	3012	1/1	0.88	0.17	71,71,71,71	0
57	MG	1A	3580	1/1	0.88	0.16	63,63,63,63	0
57	MG	1A	3662	1/1	0.88	0.17	67,67,67,67	0
57	MG	1a	1739	1/1	0.88	0.21	79,79,79,79	0
57	MG	1A	3674	1/1	0.88	0.09	37,37,37,37	0
57	MG	1a	1644	1/1	0.88	0.16	63,63,63,63	0
57	MG	1A	3535	1/1	0.88	0.10	36,36,36,36	0
57	MG	1a	1851	1/1	0.88	0.10	52,52,52,52	0
57	MG	2A	3381	1/1	0.88	0.22	59,59,59,59	0
57	MG	2A	3618	1/1	0.88	0.10	56,56,56,56	0
57	MG	2a	3054	1/1	0.88	0.26	62,62,62,62	0
57	MG	1a	1859	1/1	0.88	0.15	84,84,84,84	0
57	MG	1A	3041	1/1	0.88	0.13	52,52,52,52	0
57	MG	1A	3832	1/1	0.88	0.09	15,15,15,15	0
57	MG	2A	3184	1/1	0.88	0.29	54,54,54,54	0
57	MG	1A	3972	1/1	0.88	0.14	48,48,48,48	0
57	MG	1A	3756	1/1	0.88	0.16	59,59,59,59	0
57	MG	1A	3688	1/1	0.88	0.12	55,55,55,55	0
57	MG	2A	3672	1/1	0.88	0.14	55,55,55,55	0
57	MG	1B	228	1/1	0.88	0.14	65,65,65,65	0
57	MG	1a	1684	1/1	0.88	0.14	51,51,51,51	0
57	MG	1A	3860	1/1	0.88	0.10	64,64,64,64	0
57	MG	1A	3213	1/1	0.88	0.06	47,47,47,47	0
57	MG	2a	3091	1/1	0.88	0.29	63,63,63,63	0
57	MG	1A	3552	1/1	0.88	0.19	58,58,58,58	0
57	MG	1A	3993	1/1	0.88	0.36	54,54,54,54	0
57	MG	2a	3098	1/1	0.88	0.32	63,63,63,63	0
57	MG	2A	3703	1/1	0.88	0.11	63,63,63,63	0
57	MG	2A	3029	1/1	0.88	0.17	60,60,60,60	0
57	MG	1A	3874	1/1	0.88	0.11	38,38,38,38	0
57	MG	1A	3553	1/1	0.88	0.09	28,28,28,28	0
57	MG	13	103	1/1	0.88	0.18	64,64,64,64	0
57	MG	1A	3088	1/1	0.88	0.16	61,61,61,61	0
57	MG	1a	1709	1/1	0.88	0.16	61,61,61,61	0
57	MG	2A	3271	1/1	0.88	0.11	61,61,61,61	0
57	MG	2a	3146	1/1	0.88	0.19	70,70,70,70	0
57	MG	2A	3273	1/1	0.88	0.20	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1800	1/1	0.88	0.19	70,70,70,70	0
57	MG	1A	3462	1/1	0.88	0.20	62,62,62,62	0
57	MG	2A	3082	1/1	0.88	0.16	44,44,44,44	0
57	MG	2A	3530	1/1	0.88	0.35	48,48,48,48	0
57	MG	1A	3464	1/1	0.88	0.10	35,35,35,35	0
57	MG	2B	205	1/1	0.88	0.20	58,58,58,58	0
57	MG	2a	3184	1/1	0.88	0.21	63,63,63,63	0
57	MG	1A	3032	1/1	0.88	0.25	55,55,55,55	0
57	MG	1a	1720	1/1	0.88	0.12	63,63,63,63	0
57	MG	2A	3537	1/1	0.88	0.14	55,55,55,55	0
57	MG	1A	3645	1/1	0.88	0.15	54,54,54,54	0
57	MG	2B	216	1/1	0.88	0.12	70,70,70,70	0
57	MG	2A	3543	1/1	0.88	0.15	64,64,64,64	0
57	MG	2F	302	1/1	0.88	0.10	47,47,47,47	0
57	MG	1A	3869	1/1	0.89	0.11	43,43,43,43	0
57	MG	1A	3289	1/1	0.89	0.30	46,46,46,46	0
57	MG	1A	3744	1/1	0.89	0.09	43,43,43,43	0
57	MG	2A	3361	1/1	0.89	0.23	59,59,59,59	0
57	MG	1A	3752	1/1	0.89	0.14	54,54,54,54	0
57	MG	2A	3370	1/1	0.89	0.09	38,38,38,38	0
57	MG	1A	3560	1/1	0.89	0.09	25,25,25,25	0
57	MG	2A	3091	1/1	0.89	0.14	66,66,66,66	0
57	MG	1a	1788	1/1	0.89	0.22	62,62,62,62	0
57	MG	2A	3093	1/1	0.89	0.16	60,60,60,60	0
57	MG	1a	1789	1/1	0.89	0.16	64,64,64,64	0
57	MG	1B	202	1/1	0.89	0.12	54,54,54,54	0
57	MG	1a	1677	1/1	0.89	0.13	70,70,70,70	0
57	MG	1a	1678	1/1	0.89	0.14	65,65,65,65	0
57	MG	2A	3126	1/1	0.89	0.14	60,60,60,60	0
57	MG	1a	1796	1/1	0.89	0.17	67,67,67,67	0
57	MG	1a	1797	1/1	0.89	0.13	71,71,71,71	0
57	MG	2A	3440	1/1	0.89	0.12	44,44,44,44	0
57	MG	2A	3133	1/1	0.89	0.18	63,63,63,63	0
57	MG	2E	304	1/1	0.89	0.17	54,54,54,54	0
57	MG	2A	3450	1/1	0.89	0.13	61,61,61,61	0
57	MG	1a	1799	1/1	0.89	0.12	66,66,66,66	0
57	MG	1A	3110	1/1	0.89	0.12	67,67,67,67	0
57	MG	1A	3405	1/1	0.89	0.11	52,52,52,52	0
57	MG	1a	1691	1/1	0.89	0.11	60,60,60,60	0
57	MG	1B	207	1/1	0.89	0.29	63,63,63,63	0
57	MG	2A	3472	1/1	0.89	0.15	68,68,68,68	0
57	MG	1A	3425	1/1	0.89	0.09	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3682	1/1	0.89	0.12	27,27,27,27	0
57	MG	1a	1701	1/1	0.89	0.16	63,63,63,63	0
57	MG	1A	3922	1/1	0.89	0.13	28,28,28,28	0
57	MG	2A	3496	1/1	0.89	0.18	66,66,66,66	0
57	MG	1A	3683	1/1	0.89	0.09	48,48,48,48	0
57	MG	1A	3501	1/1	0.89	0.11	34,34,34,34	0
57	MG	1A	3931	1/1	0.89	0.10	53,53,53,53	0
57	MG	1A	3325	1/1	0.89	0.13	69,69,69,69	0
57	MG	2A	3521	1/1	0.89	0.20	70,70,70,70	0
57	MG	2A	3522	1/1	0.89	0.11	63,63,63,63	0
57	MG	1a	1708	1/1	0.89	0.17	62,62,62,62	0
57	MG	2A	3193	1/1	0.89	0.17	57,57,57,57	0
57	MG	2a	3030	1/1	0.89	0.20	64,64,64,64	0
57	MG	2A	3201	1/1	0.89	0.30	69,69,69,69	0
57	MG	2a	3039	1/1	0.89	0.21	63,63,63,63	0
57	MG	2a	3044	1/1	0.89	0.17	72,72,72,72	0
57	MG	2a	3046	1/1	0.89	0.10	61,61,61,61	0
57	MG	2A	3206	1/1	0.89	0.14	58,58,58,58	0
57	MG	1A	3378	1/1	0.89	0.08	17,17,17,17	0
57	MG	1A	3523	1/1	0.89	0.12	48,48,48,48	0
57	MG	2a	3053	1/1	0.89	0.13	56,56,56,56	0
57	MG	1a	1843	1/1	0.89	0.11	48,48,48,48	0
57	MG	2A	3539	1/1	0.89	0.12	59,59,59,59	0
57	MG	1a	1715	1/1	0.89	0.15	61,61,61,61	0
57	MG	1A	3441	1/1	0.89	0.14	71,71,71,71	0
57	MG	2A	3552	1/1	0.89	0.11	63,63,63,63	0
57	MG	1A	3447	1/1	0.89	0.12	33,33,33,33	0
57	MG	1A	3958	1/1	0.89	0.10	70,70,70,70	0
57	MG	1A	3971	1/1	0.89	0.16	48,48,48,48	0
57	MG	2a	3069	1/1	0.89	0.09	71,71,71,71	0
57	MG	2A	3242	1/1	0.89	0.10	51,51,51,51	0
57	MG	1A	3449	1/1	0.89	0.08	28,28,28,28	0
57	MG	2A	3245	1/1	0.89	0.14	59,59,59,59	0
57	MG	1a	1727	1/1	0.89	0.13	65,65,65,65	0
57	MG	1A	3814	1/1	0.89	0.10	52,52,52,52	0
57	MG	1A	3980	1/1	0.89	0.10	54,54,54,54	0
57	MG	1A	3335	1/1	0.89	0.16	58,58,58,58	0
57	MG	1A	3625	1/1	0.89	0.11	46,46,46,46	0
57	MG	2A	3585	1/1	0.89	0.19	53,53,53,53	0
57	MG	2A	3588	1/1	0.89	0.11	45,45,45,45	0
57	MG	2a	3111	1/1	0.89	0.23	59,59,59,59	0
57	MG	1d	303	1/1	0.89	0.14	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1d	304	1/1	0.89	0.14	55,55,55,55	0
57	MG	1a	1606	1/1	0.89	0.11	64,64,64,64	0
57	MG	2a	3123	1/1	0.89	0.10	67,67,67,67	0
57	MG	1g	201	1/1	0.89	0.30	68,68,68,68	0
57	MG	2A	3286	1/1	0.89	0.19	56,56,56,56	0
57	MG	2A	3287	1/1	0.89	0.16	52,52,52,52	0
57	MG	1A	3632	1/1	0.89	0.10	43,43,43,43	0
57	MG	1A	3718	1/1	0.89	0.15	33,33,33,33	0
57	MG	2A	3292	1/1	0.89	0.22	62,62,62,62	0
57	MG	1A	3457	1/1	0.89	0.15	58,58,58,58	0
57	MG	1a	1617	1/1	0.89	0.11	69,69,69,69	0
57	MG	2A	3655	1/1	0.89	0.12	71,71,71,71	0
57	MG	2a	3167	1/1	0.89	0.07	89,89,89,89	0
57	MG	2A	3300	1/1	0.89	0.10	63,63,63,63	0
57	MG	2a	3169	1/1	0.89	0.13	84,84,84,84	0
57	MG	2a	3171	1/1	0.89	0.13	59,59,59,59	0
57	MG	1a	1629	1/1	0.89	0.10	52,52,52,52	0
57	MG	2A	3320	1/1	0.89	0.23	60,60,60,60	0
57	MG	1A	3080	1/1	0.89	0.14	43,43,43,43	0
57	MG	2A	3050	1/1	0.89	0.17	66,66,66,66	0
57	MG	1A	3858	1/1	0.89	0.10	37,37,37,37	0
57	MG	2A	3062	1/1	0.89	0.13	60,60,60,60	0
57	MG	2A	3330	1/1	0.89	0.17	30,30,30,30	0
59	MPD	1a	1873	8/8	0.89	0.15	53,68,74,75	0
57	MG	1a	1635	1/1	0.89	0.09	50,50,50,50	0
57	MG	1A	3643	1/1	0.89	0.12	20,20,20,20	0
57	MG	1A	3203	1/1	0.89	0.19	40,40,40,40	0
57	MG	2A	3385	1/1	0.90	0.12	38,38,38,38	0
57	MG	2A	3722	1/1	0.90	0.12	52,52,52,52	0
57	MG	1A	3911	1/1	0.90	0.07	22,22,22,22	0
57	MG	1A	3484	1/1	0.90	0.17	62,62,62,62	0
57	MG	2A	3726	1/1	0.90	0.07	76,76,76,76	0
57	MG	1A	3779	1/1	0.90	0.11	55,55,55,55	0
57	MG	1a	1680	1/1	0.90	0.26	76,76,76,76	0
57	MG	2A	3405	1/1	0.90	0.13	68,68,68,68	0
57	MG	1A	3337	1/1	0.90	0.16	54,54,54,54	0
57	MG	1B	217	1/1	0.90	0.10	60,60,60,60	0
57	MG	2A	3734	1/1	0.90	0.14	58,58,58,58	0
57	MG	2A	3415	1/1	0.90	0.16	49,49,49,49	0
57	MG	2A	3416	1/1	0.90	0.11	63,63,63,63	0
57	MG	1a	1687	1/1	0.90	0.16	60,60,60,60	0
57	MG	1a	1688	1/1	0.90	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
57	MG	2A	3422	1/1	0.90	0.13	58,58,58,58	0
57	MG	1A	3557	1/1	0.90	0.19	49,49,49,49	0
57	MG	2A	3434	1/1	0.90	0.19	63,63,63,63	0
57	MG	2A	3435	1/1	0.90	0.09	38,38,38,38	0
57	MG	1a	1811	1/1	0.90	0.08	55,55,55,55	0
57	MG	2E	306	1/1	0.90	0.09	60,60,60,60	0
57	MG	1B	224	1/1	0.90	0.13	45,45,45,45	0
57	MG	1A	3936	1/1	0.90	0.09	50,50,50,50	0
57	MG	2A	3160	1/1	0.90	0.11	52,52,52,52	0
57	MG	1A	3791	1/1	0.90	0.20	56,56,56,56	0
57	MG	1A	3795	1/1	0.90	0.14	59,59,59,59	0
57	MG	2A	3176	1/1	0.90	0.14	68,68,68,68	0
57	MG	2A	3180	1/1	0.90	0.11	56,56,56,56	0
57	MG	1B	229	1/1	0.90	0.11	50,50,50,50	0
57	MG	2A	3480	1/1	0.90	0.11	54,54,54,54	0
57	MG	1D	314	1/1	0.90	0.12	59,59,59,59	0
57	MG	1a	1704	1/1	0.90	0.15	67,67,67,67	0
57	MG	1A	3272	1/1	0.90	0.09	48,48,48,48	0
57	MG	1A	3277	1/1	0.90	0.12	48,48,48,48	0
57	MG	2a	3007	1/1	0.90	0.29	67,67,67,67	0
57	MG	1A	3950	1/1	0.90	0.11	31,31,31,31	0
57	MG	2A	3205	1/1	0.90	0.14	67,67,67,67	0
57	MG	1A	3711	1/1	0.90	0.12	57,57,57,57	0
57	MG	2A	3208	1/1	0.90	0.12	64,64,64,64	0
57	MG	1N	203	1/1	0.90	0.08	62,62,62,62	0
57	MG	1R	203	1/1	0.90	0.26	59,59,59,59	0
57	MG	2a	3027	1/1	0.90	0.20	64,64,64,64	0
57	MG	2A	3217	1/1	0.90	0.12	63,63,63,63	0
57	MG	1a	1713	1/1	0.90	0.22	57,57,57,57	0
57	MG	2a	3038	1/1	0.90	0.09	76,76,76,76	0
57	MG	1T	203	1/1	0.90	0.17	63,63,63,63	0
57	MG	2a	3040	1/1	0.90	0.25	64,64,64,64	0
57	MG	2a	3043	1/1	0.90	0.14	72,72,72,72	0
57	MG	1A	3564	1/1	0.90	0.07	33,33,33,33	0
57	MG	1W	204	1/1	0.90	0.13	48,48,48,48	0
57	MG	1a	1719	1/1	0.90	0.14	58,58,58,58	0
57	MG	2A	3234	1/1	0.90	0.24	44,44,44,44	0
57	MG	2a	3050	1/1	0.90	0.25	63,63,63,63	0
57	MG	2A	3235	1/1	0.90	0.20	66,66,66,66	0
57	MG	1a	1867	1/1	0.90	0.12	65,65,65,65	0
57	MG	1A	3311	1/1	0.90	0.12	41,41,41,41	0
57	MG	10	110	1/1	0.90	0.17	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3244	1/1	0.90	0.28	63,63,63,63	0
57	MG	13	102	1/1	0.90	0.09	36,36,36,36	0
57	MG	1A	3572	1/1	0.90	0.08	30,30,30,30	0
57	MG	2a	3061	1/1	0.90	0.30	63,63,63,63	0
57	MG	1A	3658	1/1	0.90	0.13	58,58,58,58	0
57	MG	1A	3345	1/1	0.90	0.09	37,37,37,37	0
57	MG	1A	3837	1/1	0.90	0.15	48,48,48,48	0
57	MG	1A	3838	1/1	0.90	0.11	47,47,47,47	0
57	MG	2A	3572	1/1	0.90	0.09	47,47,47,47	0
57	MG	2a	3075	1/1	0.90	0.21	63,63,63,63	0
57	MG	1n	102	1/1	0.90	0.14	66,66,66,66	0
57	MG	2A	3576	1/1	0.90	0.15	54,54,54,54	0
57	MG	1a	1745	1/1	0.90	0.10	59,59,59,59	0
57	MG	1w	101	1/1	0.90	0.13	63,63,63,63	0
57	MG	1A	3668	1/1	0.90	0.10	47,47,47,47	0
57	MG	1a	1750	1/1	0.90	0.32	61,61,61,61	0
57	MG	1A	3526	1/1	0.90	0.09	43,43,43,43	0
57	MG	1A	3401	1/1	0.90	0.19	53,53,53,53	0
57	MG	2a	3100	1/1	0.90	0.16	68,68,68,68	0
57	MG	2A	3597	1/1	0.90	0.13	70,70,70,70	0
57	MG	2a	3110	1/1	0.90	0.18	65,65,65,65	0
57	MG	1A	3747	1/1	0.90	0.14	52,52,52,52	0
57	MG	2a	3112	1/1	0.90	0.26	65,65,65,65	0
57	MG	1A	3677	1/1	0.90	0.10	31,31,31,31	0
57	MG	2A	3051	1/1	0.90	0.27	70,70,70,70	0
57	MG	1A	3753	1/1	0.90	0.13	41,41,41,41	0
57	MG	2A	3059	1/1	0.90	0.20	61,61,61,61	0
57	MG	2a	3126	1/1	0.90	0.14	75,75,75,75	0
57	MG	2a	3127	1/1	0.90	0.12	65,65,65,65	0
57	MG	2A	3310	1/1	0.90	0.22	53,53,53,53	0
57	MG	2a	3129	1/1	0.90	0.12	72,72,72,72	0
57	MG	1a	1765	1/1	0.90	0.14	67,67,67,67	0
57	MG	2A	3315	1/1	0.90	0.15	47,47,47,47	0
57	MG	2a	3136	1/1	0.90	0.12	73,73,73,73	0
57	MG	2A	3064	1/1	0.90	0.27	55,55,55,55	0
57	MG	2A	3624	1/1	0.90	0.28	67,67,67,67	0
57	MG	1a	1630	1/1	0.90	0.23	66,66,66,66	0
57	MG	2a	3150	1/1	0.90	0.10	69,69,69,69	0
57	MG	2a	3151	1/1	0.90	0.23	64,64,64,64	0
57	MG	1A	4006	1/1	0.90	0.12	44,44,44,44	0
57	MG	2a	3155	1/1	0.90	0.15	68,68,68,68	0
57	MG	1A	3531	1/1	0.90	0.07	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3594	1/1	0.90	0.10	62,62,62,62	0
57	MG	1A	3079	1/1	0.90	0.20	49,49,49,49	0
57	MG	1a	1780	1/1	0.90	0.15	65,65,65,65	0
57	MG	2A	3339	1/1	0.90	0.12	64,64,64,64	0
57	MG	1A	3090	1/1	0.90	0.08	53,53,53,53	0
57	MG	2A	3679	1/1	0.90	0.11	67,67,67,67	0
57	MG	1A	3374	1/1	0.90	0.19	48,48,48,48	0
57	MG	2a	3181	1/1	0.90	0.23	60,60,60,60	0
57	MG	1a	1658	1/1	0.90	0.12	65,65,65,65	0
57	MG	2a	3187	1/1	0.90	0.15	74,74,74,74	0
57	MG	1a	1661	1/1	0.90	0.18	65,65,65,65	0
57	MG	1A	3768	1/1	0.90	0.14	53,53,53,53	0
57	MG	2A	3099	1/1	0.90	0.23	64,64,64,64	0
57	MG	2x	101	1/1	0.90	0.19	47,47,47,47	0
57	MG	2A	3363	1/1	0.90	0.13	57,57,57,57	0
57	MG	1A	3072	1/1	0.90	0.11	45,45,45,45	0
59	MPD	1a	1874	8/8	0.90	0.16	57,66,70,71	0
57	MG	1A	3893	1/1	0.90	0.11	54,54,54,54	0
57	MG	1a	1667	1/1	0.90	0.14	65,65,65,65	0
57	MG	1A	3548	1/1	0.90	0.14	61,61,61,61	0
57	MG	1a	1814	1/1	0.91	0.26	64,64,64,64	0
57	MG	2A	3729	1/1	0.91	0.18	59,59,59,59	0
57	MG	2A	3151	1/1	0.91	0.09	55,55,55,55	0
57	MG	1A	3398	1/1	0.91	0.09	63,63,63,63	0
57	MG	1A	3098	1/1	0.91	0.14	54,54,54,54	0
57	MG	1T	201	1/1	0.91	0.06	32,32,32,32	0
57	MG	1A	3282	1/1	0.91	0.14	55,55,55,55	0
57	MG	2A	3423	1/1	0.91	0.12	47,47,47,47	0
57	MG	1A	3669	1/1	0.91	0.29	48,48,48,48	0
57	MG	2A	3430	1/1	0.91	0.09	40,40,40,40	0
57	MG	2B	210	1/1	0.91	0.25	69,69,69,69	0
57	MG	1A	3985	1/1	0.91	0.17	54,54,54,54	0
57	MG	2A	3174	1/1	0.91	0.17	58,58,58,58	0
57	MG	1Y	201	1/1	0.91	0.15	61,61,61,61	0
57	MG	1a	1830	1/1	0.91	0.09	62,62,62,62	0
57	MG	2D	309	1/1	0.91	0.09	33,33,33,33	0
57	MG	2E	301	1/1	0.91	0.17	68,68,68,68	0
57	MG	1A	3847	1/1	0.91	0.12	43,43,43,43	0
57	MG	1A	3181	1/1	0.91	0.16	52,52,52,52	0
57	MG	2A	3461	1/1	0.91	0.14	59,59,59,59	0
57	MG	1a	1840	1/1	0.91	0.19	68,68,68,68	0
57	MG	11	102	1/1	0.91	0.11	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2G	201	1/1	0.91	0.10	70,70,70,70	0
57	MG	1a	1712	1/1	0.91	0.12	57,57,57,57	0
57	MG	1a	1850	1/1	0.91	0.16	50,50,50,50	0
57	MG	1A	3504	1/1	0.91	0.11	31,31,31,31	0
57	MG	2A	3473	1/1	0.91	0.13	64,64,64,64	0
57	MG	2A	3475	1/1	0.91	0.10	59,59,59,59	0
57	MG	2V	202	1/1	0.91	0.26	57,57,57,57	0
57	MG	2W	202	1/1	0.91	0.22	57,57,57,57	0
57	MG	1a	1857	1/1	0.91	0.10	60,60,60,60	0
57	MG	1A	3340	1/1	0.91	0.29	53,53,53,53	0
57	MG	1A	3204	1/1	0.91	0.11	50,50,50,50	0
57	MG	29	101	1/1	0.91	0.23	67,67,67,67	0
57	MG	2A	3487	1/1	0.91	0.09	55,55,55,55	0
57	MG	15	3107	1/1	0.91	0.12	44,44,44,44	0
57	MG	1A	3038	1/1	0.91	0.19	48,48,48,48	0
57	MG	2A	3219	1/1	0.91	0.23	72,72,72,72	0
57	MG	2a	3008	1/1	0.91	0.09	61,61,61,61	0
57	MG	2a	3009	1/1	0.91	0.11	50,50,50,50	0
57	MG	1A	4000	1/1	0.91	0.16	50,50,50,50	0
57	MG	2A	3505	1/1	0.91	0.12	49,49,49,49	0
57	MG	1a	1604	1/1	0.91	0.13	61,61,61,61	0
57	MG	1A	3762	1/1	0.91	0.18	56,56,56,56	0
57	MG	2a	3020	1/1	0.91	0.10	80,80,80,80	0
57	MG	1A	3216	1/1	0.91	0.18	35,35,35,35	0
57	MG	1A	3443	1/1	0.91	0.14	62,62,62,62	0
57	MG	1A	4019	1/1	0.91	0.08	36,36,36,36	0
57	MG	1A	3128	1/1	0.91	0.17	57,57,57,57	0
57	MG	1A	3886	1/1	0.91	0.12	27,27,27,27	0
57	MG	2a	3033	1/1	0.91	0.25	65,65,65,65	0
57	MG	2a	3034	1/1	0.91	0.15	61,61,61,61	0
57	MG	2a	3037	1/1	0.91	0.09	69,69,69,69	0
57	MG	1a	1741	1/1	0.91	0.08	61,61,61,61	0
57	MG	1e	203	1/1	0.91	0.36	68,68,68,68	0
57	MG	2A	3535	1/1	0.91	0.12	52,52,52,52	0
57	MG	2a	3041	1/1	0.91	0.27	64,64,64,64	0
57	MG	1A	3772	1/1	0.91	0.14	50,50,50,50	0
57	MG	1A	3774	1/1	0.91	0.07	34,34,34,34	0
57	MG	2a	3045	1/1	0.91	0.22	58,58,58,58	0
57	MG	2A	3266	1/1	0.91	0.23	57,57,57,57	0
57	MG	1A	3533	1/1	0.91	0.10	23,23,23,23	0
57	MG	2A	3541	1/1	0.91	0.10	60,60,60,60	0
57	MG	1u	101	1/1	0.91	0.22	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1y	202	1/1	0.91	0.09	60,60,60,60	0
57	MG	1a	1751	1/1	0.91	0.11	63,63,63,63	0
57	MG	1a	1633	1/1	0.91	0.09	45,45,45,45	0
57	MG	2A	3024	1/1	0.91	0.13	52,52,52,52	0
57	MG	1A	3448	1/1	0.91	0.10	27,27,27,27	0
57	MG	2A	3561	1/1	0.91	0.11	61,61,61,61	0
57	MG	2A	3031	1/1	0.91	0.17	60,60,60,60	0
57	MG	2A	3566	1/1	0.91	0.10	60,60,60,60	0
57	MG	2A	3281	1/1	0.91	0.09	53,53,53,53	0
57	MG	1A	3225	1/1	0.91	0.11	52,52,52,52	0
57	MG	2A	3571	1/1	0.91	0.11	39,39,39,39	0
57	MG	1B	205	1/1	0.91	0.08	52,52,52,52	0
57	MG	2a	3070	1/1	0.91	0.10	61,61,61,61	0
57	MG	2A	3042	1/1	0.91	0.20	61,61,61,61	0
57	MG	1A	3619	1/1	0.91	0.12	34,34,34,34	0
57	MG	1A	3781	1/1	0.91	0.10	39,39,39,39	0
57	MG	1a	1656	1/1	0.91	0.30	66,66,66,66	0
57	MG	1a	1769	1/1	0.91	0.12	53,53,53,53	0
57	MG	1a	1771	1/1	0.91	0.11	63,63,63,63	0
57	MG	1A	3784	1/1	0.91	0.10	41,41,41,41	0
57	MG	2A	3306	1/1	0.91	0.15	44,44,44,44	0
57	MG	2A	3309	1/1	0.91	0.32	59,59,59,59	0
57	MG	2A	3605	1/1	0.91	0.16	52,52,52,52	0
57	MG	1a	1659	1/1	0.91	0.16	57,57,57,57	0
57	MG	1A	3321	1/1	0.91	0.14	59,59,59,59	0
57	MG	2a	3109	1/1	0.91	0.32	62,62,62,62	0
57	MG	1B	212	1/1	0.91	0.09	56,56,56,56	0
57	MG	2A	3076	1/1	0.91	0.18	67,67,67,67	0
57	MG	1A	3246	1/1	0.91	0.09	58,58,58,58	0
57	MG	2A	3616	1/1	0.91	0.14	39,39,39,39	0
57	MG	2A	3323	1/1	0.91	0.23	69,69,69,69	0
57	MG	1A	3541	1/1	0.91	0.21	57,57,57,57	0
57	MG	1A	3133	1/1	0.91	0.24	32,32,32,32	0
57	MG	1a	1669	1/1	0.91	0.25	62,62,62,62	0
57	MG	1A	3712	1/1	0.91	0.17	39,39,39,39	0
57	MG	2A	3333	1/1	0.91	0.12	55,55,55,55	0
57	MG	2A	3639	1/1	0.91	0.10	54,54,54,54	0
57	MG	1A	3713	1/1	0.91	0.18	36,36,36,36	0
57	MG	2A	3650	1/1	0.91	0.10	75,75,75,75	0
57	MG	2A	3652	1/1	0.91	0.08	50,50,50,50	0
57	MG	1A	3326	1/1	0.91	0.26	56,56,56,56	0
57	MG	1A	3393	1/1	0.91	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3953	1/1	0.91	0.12	50,50,50,50	0
57	MG	2A	3098	1/1	0.91	0.25	60,60,60,60	0
57	MG	1D	311	1/1	0.91	0.10	47,47,47,47	0
57	MG	2A	3675	1/1	0.91	0.18	55,55,55,55	0
57	MG	2A	3676	1/1	0.91	0.11	60,60,60,60	0
57	MG	1A	3198	1/1	0.91	0.09	47,47,47,47	0
57	MG	1a	1686	1/1	0.91	0.14	47,47,47,47	0
57	MG	1A	3955	1/1	0.91	0.09	54,54,54,54	0
57	MG	2A	3686	1/1	0.91	0.28	47,47,47,47	0
57	MG	2A	3122	1/1	0.91	0.22	73,73,73,73	0
57	MG	2a	3170	1/1	0.91	0.09	57,57,57,57	0
57	MG	1A	3648	1/1	0.91	0.09	23,23,23,23	0
57	MG	2a	3172	1/1	0.91	0.12	78,78,78,78	0
57	MG	2a	3174	1/1	0.91	0.10	78,78,78,78	0
57	MG	1A	3968	1/1	0.91	0.10	37,37,37,37	0
57	MG	2a	3179	1/1	0.91	0.07	76,76,76,76	0
57	MG	2A	3380	1/1	0.91	0.16	61,61,61,61	0
57	MG	2A	3697	1/1	0.91	0.09	66,66,66,66	0
57	MG	2a	3183	1/1	0.91	0.25	56,56,56,56	0
57	MG	1F	315	1/1	0.91	0.11	55,55,55,55	0
57	MG	2a	3186	1/1	0.91	0.15	77,77,77,77	0
57	MG	1a	1694	1/1	0.91	0.10	53,53,53,53	0
57	MG	2f	201	1/1	0.91	0.10	53,53,53,53	0
57	MG	1a	1805	1/1	0.91	0.17	55,55,55,55	0
57	MG	2A	3711	1/1	0.91	0.23	46,46,46,46	0
57	MG	2A	3134	1/1	0.91	0.09	59,59,59,59	0
57	MG	2A	3392	1/1	0.91	0.09	38,38,38,38	0
57	MG	2A	3718	1/1	0.91	0.23	64,64,64,64	0
57	MG	1a	1695	1/1	0.91	0.27	61,61,61,61	0
57	MG	1A	3478	1/1	0.91	0.11	60,60,60,60	0
57	MG	1G	203	1/1	0.91	0.08	49,49,49,49	0
57	MG	2A	3408	1/1	0.91	0.11	59,59,59,59	0
57	MG	1a	1700	1/1	0.91	0.13	68,68,68,68	0
57	MG	1a	1613	1/1	0.92	0.10	71,71,71,71	0
57	MG	1A	3586	1/1	0.92	0.15	45,45,45,45	0
57	MG	2A	3365	1/1	0.92	0.09	29,29,29,29	0
57	MG	1a	1625	1/1	0.92	0.08	51,51,51,51	0
57	MG	1a	1768	1/1	0.92	0.15	53,53,53,53	0
57	MG	1a	1628	1/1	0.92	0.18	53,53,53,53	0
57	MG	2A	3087	1/1	0.92	0.17	47,47,47,47	0
57	MG	2A	3725	1/1	0.92	0.23	66,66,66,66	0
57	MG	2A	3089	1/1	0.92	0.27	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3727	1/1	0.92	0.11	76,76,76,76	0
57	MG	1A	3998	1/1	0.92	0.10	68,68,68,68	0
57	MG	2A	3388	1/1	0.92	0.08	40,40,40,40	0
57	MG	1A	3397	1/1	0.92	0.13	42,42,42,42	0
57	MG	1A	3841	1/1	0.92	0.09	44,44,44,44	0
57	MG	1A	3843	1/1	0.92	0.08	33,33,33,33	0
57	MG	2A	3394	1/1	0.92	0.14	46,46,46,46	0
57	MG	1A	3169	1/1	0.92	0.15	43,43,43,43	0
57	MG	2A	3396	1/1	0.92	0.15	52,52,52,52	0
57	MG	2B	204	1/1	0.92	0.26	61,61,61,61	0
57	MG	1A	3498	1/1	0.92	0.07	18,18,18,18	0
57	MG	1A	4020	1/1	0.92	0.17	69,69,69,69	0
57	MG	2A	3407	1/1	0.92	0.06	36,36,36,36	0
57	MG	2A	3107	1/1	0.92	0.17	60,60,60,60	0
57	MG	2A	3109	1/1	0.92	0.27	57,57,57,57	0
57	MG	2A	3110	1/1	0.92	0.12	51,51,51,51	0
57	MG	1A	3599	1/1	0.92	0.17	43,43,43,43	0
57	MG	1a	1645	1/1	0.92	0.20	55,55,55,55	0
57	MG	1A	3855	1/1	0.92	0.09	41,41,41,41	0
57	MG	2A	3123	1/1	0.92	0.25	58,58,58,58	0
57	MG	2A	3124	1/1	0.92	0.24	65,65,65,65	0
57	MG	1a	1654	1/1	0.92	0.16	71,71,71,71	0
57	MG	1A	4023	1/1	0.92	0.12	61,61,61,61	0
57	MG	1a	1657	1/1	0.92	0.11	62,62,62,62	0
57	MG	1A	3103	1/1	0.92	0.11	53,53,53,53	0
57	MG	1a	1792	1/1	0.92	0.16	61,61,61,61	0
57	MG	1A	3075	1/1	0.92	0.12	41,41,41,41	0
57	MG	2A	3445	1/1	0.92	0.17	59,59,59,59	0
57	MG	1a	1660	1/1	0.92	0.17	69,69,69,69	0
57	MG	2R	202	1/1	0.92	0.15	60,60,60,60	0
57	MG	1A	3507	1/1	0.92	0.07	22,22,22,22	0
57	MG	2A	3453	1/1	0.92	0.08	40,40,40,40	0
57	MG	2A	3456	1/1	0.92	0.18	56,56,56,56	0
57	MG	1B	201	1/1	0.92	0.17	46,46,46,46	0
57	MG	1A	3866	1/1	0.92	0.08	46,46,46,46	0
57	MG	25	102	1/1	0.92	0.24	43,43,43,43	0
57	MG	25	103	1/1	0.92	0.08	56,56,56,56	0
57	MG	1A	3513	1/1	0.92	0.08	28,28,28,28	0
57	MG	1A	3618	1/1	0.92	0.07	31,31,31,31	0
57	MG	1A	3242	1/1	0.92	0.14	34,34,34,34	0
57	MG	2A	3154	1/1	0.92	0.16	48,48,48,48	0
57	MG	1a	1671	1/1	0.92	0.11	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1807	1/1	0.92	0.20	60,60,60,60	0
57	MG	1A	3621	1/1	0.92	0.13	52,52,52,52	0
57	MG	2A	3476	1/1	0.92	0.22	39,39,39,39	0
57	MG	2A	3477	1/1	0.92	0.07	57,57,57,57	0
57	MG	1a	1674	1/1	0.92	0.14	48,48,48,48	0
57	MG	2A	3170	1/1	0.92	0.22	35,35,35,35	0
57	MG	1A	3743	1/1	0.92	0.08	46,46,46,46	0
57	MG	2a	3018	1/1	0.92	0.11	47,47,47,47	0
57	MG	1B	210	1/1	0.92	0.16	60,60,60,60	0
57	MG	1A	3406	1/1	0.92	0.11	35,35,35,35	0
57	MG	2A	3493	1/1	0.92	0.11	58,58,58,58	0
57	MG	2a	3026	1/1	0.92	0.24	59,59,59,59	0
57	MG	1A	3887	1/1	0.92	0.13	57,57,57,57	0
57	MG	2A	3183	1/1	0.92	0.20	71,71,71,71	0
57	MG	1a	1818	1/1	0.92	0.19	55,55,55,55	0
57	MG	2A	3186	1/1	0.92	0.23	55,55,55,55	0
57	MG	1A	3423	1/1	0.92	0.10	19,19,19,19	0
57	MG	1A	3151	1/1	0.92	0.11	45,45,45,45	0
57	MG	1A	3307	1/1	0.92	0.18	71,71,71,71	0
57	MG	2A	3520	1/1	0.92	0.08	75,75,75,75	0
57	MG	1A	3258	1/1	0.92	0.18	43,43,43,43	0
57	MG	2A	3198	1/1	0.92	0.21	43,43,43,43	0
57	MG	2A	3524	1/1	0.92	0.17	63,63,63,63	0
57	MG	1A	3439	1/1	0.92	0.11	22,22,22,22	0
57	MG	1A	3907	1/1	0.92	0.07	43,43,43,43	0
57	MG	2A	3531	1/1	0.92	0.13	61,61,61,61	0
57	MG	1A	3644	1/1	0.92	0.10	50,50,50,50	0
57	MG	1a	1833	1/1	0.92	0.12	53,53,53,53	0
57	MG	1A	3920	1/1	0.92	0.09	48,48,48,48	0
57	MG	2a	3051	1/1	0.92	0.22	66,66,66,66	0
57	MG	2A	3213	1/1	0.92	0.07	50,50,50,50	0
57	MG	1D	307	1/1	0.92	0.09	47,47,47,47	0
57	MG	1A	3351	1/1	0.92	0.12	15,15,15,15	0
57	MG	1a	1697	1/1	0.92	0.19	53,53,53,53	0
57	MG	1A	3357	1/1	0.92	0.09	15,15,15,15	0
57	MG	1A	3445	1/1	0.92	0.09	35,35,35,35	0
57	MG	1A	3654	1/1	0.92	0.21	29,29,29,29	0
57	MG	1A	3538	1/1	0.92	0.07	59,59,59,59	0
57	MG	1A	3359	1/1	0.92	0.11	37,37,37,37	0
57	MG	2A	3555	1/1	0.92	0.25	59,59,59,59	0
57	MG	1a	1861	1/1	0.92	0.11	79,79,79,79	0
57	MG	1A	3667	1/1	0.92	0.23	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3191	1/1	0.92	0.09	44,44,44,44	0
57	MG	2A	3240	1/1	0.92	0.10	65,65,65,65	0
57	MG	2A	3565	1/1	0.92	0.13	59,59,59,59	0
57	MG	2A	3241	1/1	0.92	0.10	53,53,53,53	0
57	MG	1A	3367	1/1	0.92	0.19	61,61,61,61	0
57	MG	1N	204	1/1	0.92	0.16	57,57,57,57	0
57	MG	1Q	202	1/1	0.92	0.14	53,53,53,53	0
57	MG	1A	3948	1/1	0.92	0.08	27,27,27,27	0
57	MG	2A	3259	1/1	0.92	0.20	67,67,67,67	0
57	MG	2a	3095	1/1	0.92	0.28	54,54,54,54	0
57	MG	2A	3263	1/1	0.92	0.11	39,39,39,39	0
57	MG	1A	3551	1/1	0.92	0.08	47,47,47,47	0
57	MG	1A	3675	1/1	0.92	0.10	25,25,25,25	0
57	MG	2a	3102	1/1	0.92	0.33	53,53,53,53	0
57	MG	1A	3783	1/1	0.92	0.09	32,32,32,32	0
57	MG	2a	3108	1/1	0.92	0.18	46,46,46,46	0
57	MG	1W	201	1/1	0.92	0.26	51,51,51,51	0
57	MG	1A	3319	1/1	0.92	0.06	30,30,30,30	0
57	MG	1A	3957	1/1	0.92	0.10	44,44,44,44	0
57	MG	1A	3456	1/1	0.92	0.10	37,37,37,37	0
57	MG	10	107	1/1	0.92	0.09	48,48,48,48	0
57	MG	2a	3115	1/1	0.92	0.14	54,54,54,54	0
57	MG	2A	3606	1/1	0.92	0.13	68,68,68,68	0
57	MG	1i	201	1/1	0.92	0.17	67,67,67,67	0
57	MG	1l	201	1/1	0.92	0.22	57,57,57,57	0
57	MG	2a	3124	1/1	0.92	0.15	60,60,60,60	0
57	MG	1l	202	1/1	0.92	0.07	64,64,64,64	0
57	MG	10	108	1/1	0.92	0.12	57,57,57,57	0
57	MG	1a	1724	1/1	0.92	0.16	65,65,65,65	0
57	MG	1A	3320	1/1	0.92	0.30	47,47,47,47	0
57	MG	1A	3271	1/1	0.92	0.15	29,29,29,29	0
57	MG	1a	1728	1/1	0.92	0.10	52,52,52,52	0
57	MG	2A	3619	1/1	0.92	0.09	73,73,73,73	0
57	MG	2a	3137	1/1	0.92	0.09	57,57,57,57	0
57	MG	2a	3142	1/1	0.92	0.15	48,48,48,48	0
57	MG	2A	3620	1/1	0.92	0.07	63,63,63,63	0
57	MG	2A	3001	1/1	0.92	0.32	65,65,65,65	0
57	MG	2A	3002	1/1	0.92	0.11	52,52,52,52	0
57	MG	2A	3298	1/1	0.92	0.27	61,61,61,61	0
57	MG	2A	3626	1/1	0.92	0.13	75,75,75,75	0
57	MG	2a	3152	1/1	0.92	0.15	66,66,66,66	0
57	MG	2A	3014	1/1	0.92	0.21	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3019	1/1	0.92	0.07	45,45,45,45	0
57	MG	2a	3161	1/1	0.92	0.12	62,62,62,62	0
57	MG	2A	3307	1/1	0.92	0.17	62,62,62,62	0
57	MG	2A	3646	1/1	0.92	0.11	41,41,41,41	0
57	MG	2A	3308	1/1	0.92	0.30	61,61,61,61	0
57	MG	1a	1731	1/1	0.92	0.09	66,66,66,66	0
57	MG	1A	3461	1/1	0.92	0.06	15,15,15,15	0
57	MG	1A	3209	1/1	0.92	0.15	39,39,39,39	0
57	MG	2A	3660	1/1	0.92	0.10	45,45,45,45	0
57	MG	1A	3976	1/1	0.92	0.13	53,53,53,53	0
57	MG	2a	3173	1/1	0.92	0.11	60,60,60,60	0
57	MG	2A	3319	1/1	0.92	0.28	52,52,52,52	0
57	MG	1A	3273	1/1	0.92	0.17	53,53,53,53	0
57	MG	1A	3390	1/1	0.92	0.07	32,32,32,32	0
57	MG	1a	1742	1/1	0.92	0.13	71,71,71,71	0
57	MG	1A	3477	1/1	0.92	0.10	49,49,49,49	0
57	MG	1a	1746	1/1	0.92	0.15	69,69,69,69	0
57	MG	18	102	1/1	0.92	0.26	40,40,40,40	0
57	MG	2A	3685	1/1	0.92	0.14	59,59,59,59	0
57	MG	2A	3054	1/1	0.92	0.16	58,58,58,58	0
57	MG	2e	202	1/1	0.92	0.08	70,70,70,70	0
57	MG	2A	3687	1/1	0.92	0.07	65,65,65,65	0
57	MG	1A	3695	1/1	0.92	0.08	52,52,52,52	0
57	MG	1A	3157	1/1	0.92	0.16	55,55,55,55	0
57	MG	1a	1752	1/1	0.92	0.17	68,68,68,68	0
57	MG	1A	3819	1/1	0.92	0.10	27,27,27,27	0
57	MG	2A	3067	1/1	0.92	0.10	49,49,49,49	0
57	MG	2A	3701	1/1	0.92	0.16	69,69,69,69	0
57	MG	1A	3578	1/1	0.92	0.10	50,50,50,50	0
57	MG	2A	3353	1/1	0.92	0.09	50,50,50,50	0
57	MG	1A	3994	1/1	0.92	0.18	31,31,31,31	0
57	MG	1A	3278	1/1	0.92	0.19	52,52,52,52	0
57	MG	1A	3767	1/1	0.93	0.07	34,34,34,34	0
57	MG	2A	3382	1/1	0.93	0.07	29,29,29,29	0
57	MG	1a	1672	1/1	0.93	0.23	68,68,68,68	0
57	MG	1B	223	1/1	0.93	0.12	58,58,58,58	0
57	MG	1A	3913	1/1	0.93	0.08	18,18,18,18	0
57	MG	1a	1675	1/1	0.93	0.19	49,49,49,49	0
57	MG	1A	3440	1/1	0.93	0.12	24,24,24,24	0
57	MG	1A	3502	1/1	0.93	0.12	25,25,25,25	0
57	MG	1A	3670	1/1	0.93	0.09	59,59,59,59	0
57	MG	1A	3060	1/1	0.93	0.13	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3341	1/1	0.93	0.11	52,52,52,52	0
57	MG	1A	3159	1/1	0.93	0.33	40,40,40,40	0
57	MG	1a	1685	1/1	0.93	0.25	71,71,71,71	0
57	MG	1D	313	1/1	0.93	0.15	57,57,57,57	0
57	MG	1A	3579	1/1	0.93	0.07	41,41,41,41	0
57	MG	2A	3410	1/1	0.93	0.21	61,61,61,61	0
57	MG	1A	3780	1/1	0.93	0.09	22,22,22,22	0
57	MG	1E	307	1/1	0.93	0.07	49,49,49,49	0
57	MG	1A	3940	1/1	0.93	0.17	60,60,60,60	0
57	MG	1a	1826	1/1	0.93	0.28	67,67,67,67	0
57	MG	2B	201	1/1	0.93	0.09	67,67,67,67	0
57	MG	1A	3190	1/1	0.93	0.25	31,31,31,31	0
57	MG	1A	3584	1/1	0.93	0.11	42,42,42,42	0
57	MG	1A	3519	1/1	0.93	0.09	64,64,64,64	0
57	MG	1A	3949	1/1	0.93	0.11	22,22,22,22	0
57	MG	1a	1834	1/1	0.93	0.12	45,45,45,45	0
57	MG	1A	3785	1/1	0.93	0.08	34,34,34,34	0
57	MG	1A	3349	1/1	0.93	0.12	25,25,25,25	0
57	MG	2B	213	1/1	0.93	0.13	71,71,71,71	0
57	MG	2A	3439	1/1	0.93	0.15	67,67,67,67	0
57	MG	1A	3522	1/1	0.93	0.08	52,52,52,52	0
57	MG	2D	306	1/1	0.93	0.18	51,51,51,51	0
57	MG	2A	3443	1/1	0.93	0.08	50,50,50,50	0
57	MG	2D	310	1/1	0.93	0.08	54,54,54,54	0
57	MG	2D	311	1/1	0.93	0.30	59,59,59,59	0
57	MG	1a	1841	1/1	0.93	0.18	59,59,59,59	0
57	MG	1A	3790	1/1	0.93	0.14	47,47,47,47	0
57	MG	1a	1846	1/1	0.93	0.11	61,61,61,61	0
57	MG	2A	3179	1/1	0.93	0.21	67,67,67,67	0
57	MG	1A	3027	1/1	0.93	0.06	58,58,58,58	0
57	MG	2A	3181	1/1	0.93	0.13	58,58,58,58	0
57	MG	1T	202	1/1	0.93	0.09	67,67,67,67	0
57	MG	1A	3693	1/1	0.93	0.10	47,47,47,47	0
57	MG	2A	3185	1/1	0.93	0.17	63,63,63,63	0
57	MG	2A	3467	1/1	0.93	0.08	45,45,45,45	0
57	MG	1V	203	1/1	0.93	0.10	43,43,43,43	0
57	MG	2Q	201	1/1	0.93	0.29	65,65,65,65	0
57	MG	2A	3469	1/1	0.93	0.09	56,56,56,56	0
57	MG	1A	3960	1/1	0.93	0.08	49,49,49,49	0
57	MG	2V	201	1/1	0.93	0.07	63,63,63,63	0
57	MG	2A	3471	1/1	0.93	0.10	49,49,49,49	0
57	MG	1a	1860	1/1	0.93	0.13	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	20	101	1/1	0.93	0.18	53,53,53,53	0
57	MG	21	101	1/1	0.93	0.07	53,53,53,53	0
57	MG	1A	3961	1/1	0.93	0.10	53,53,53,53	0
57	MG	2A	3192	1/1	0.93	0.11	51,51,51,51	0
57	MG	25	101	1/1	0.93	0.41	46,46,46,46	0
57	MG	1A	3524	1/1	0.93	0.09	44,44,44,44	0
57	MG	2A	3196	1/1	0.93	0.15	62,62,62,62	0
57	MG	1A	3175	1/1	0.93	0.08	43,43,43,43	0
57	MG	1A	3323	1/1	0.93	0.12	30,30,30,30	0
57	MG	1a	1865	1/1	0.93	0.10	60,60,60,60	0
57	MG	1A	3529	1/1	0.93	0.11	53,53,53,53	0
57	MG	1A	3530	1/1	0.93	0.08	38,38,38,38	0
57	MG	1A	3979	1/1	0.93	0.10	56,56,56,56	0
57	MG	2A	3210	1/1	0.93	0.09	59,59,59,59	0
57	MG	1a	1870	1/1	0.93	0.19	76,76,76,76	0
57	MG	2A	3500	1/1	0.93	0.09	36,36,36,36	0
57	MG	1a	1717	1/1	0.93	0.13	71,71,71,71	0
57	MG	2A	3215	1/1	0.93	0.10	61,61,61,61	0
57	MG	2A	3506	1/1	0.93	0.17	47,47,47,47	0
57	MG	2A	3508	1/1	0.93	0.13	63,63,63,63	0
57	MG	2a	3019	1/1	0.93	0.16	49,49,49,49	0
57	MG	11	101	1/1	0.93	0.10	59,59,59,59	0
57	MG	1A	3701	1/1	0.93	0.09	38,38,38,38	0
57	MG	2A	3514	1/1	0.93	0.11	57,57,57,57	0
57	MG	2a	3025	1/1	0.93	0.18	65,65,65,65	0
57	MG	2A	3515	1/1	0.93	0.15	56,56,56,56	0
57	MG	2A	3220	1/1	0.93	0.18	40,40,40,40	0
57	MG	1A	3612	1/1	0.93	0.10	44,44,44,44	0
57	MG	1A	3614	1/1	0.93	0.07	31,31,31,31	0
57	MG	2a	3032	1/1	0.93	0.17	67,67,67,67	0
57	MG	2A	3225	1/1	0.93	0.26	54,54,54,54	0
57	MG	1A	3617	1/1	0.93	0.07	47,47,47,47	0
57	MG	2a	3036	1/1	0.93	0.15	63,63,63,63	0
57	MG	1e	201	1/1	0.93	0.19	52,52,52,52	0
57	MG	1e	202	1/1	0.93	0.12	50,50,50,50	0
57	MG	1A	3291	1/1	0.93	0.09	42,42,42,42	0
57	MG	1A	3991	1/1	0.93	0.14	53,53,53,53	0
57	MG	2A	3236	1/1	0.93	0.15	54,54,54,54	0
57	MG	1h	202	1/1	0.93	0.11	67,67,67,67	0
57	MG	1A	3402	1/1	0.93	0.09	42,42,42,42	0
57	MG	1A	3259	1/1	0.93	0.09	44,44,44,44	0
57	MG	19	102	1/1	0.93	0.12	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1601	1/1	0.93	0.15	58,58,58,58	0
57	MG	2A	3540	1/1	0.93	0.15	54,54,54,54	0
57	MG	1a	1603	1/1	0.93	0.22	57,57,57,57	0
57	MG	2A	3542	1/1	0.93	0.12	52,52,52,52	0
57	MG	1o	3101	1/1	0.93	0.19	51,51,51,51	0
57	MG	2A	3251	1/1	0.93	0.22	44,44,44,44	0
57	MG	2A	3547	1/1	0.93	0.14	38,38,38,38	0
57	MG	2A	3550	1/1	0.93	0.11	50,50,50,50	0
57	MG	2A	3254	1/1	0.93	0.25	43,43,43,43	0
57	MG	2A	3256	1/1	0.93	0.10	62,62,62,62	0
57	MG	1A	3125	1/1	0.93	0.17	47,47,47,47	0
57	MG	1A	3623	1/1	0.93	0.22	28,28,28,28	0
57	MG	1A	3419	1/1	0.93	0.05	40,40,40,40	0
57	MG	2A	3267	1/1	0.93	0.20	54,54,54,54	0
57	MG	1x	101	1/1	0.93	0.07	39,39,39,39	0
57	MG	1x	102	1/1	0.93	0.11	34,34,34,34	0
57	MG	1A	3467	1/1	0.93	0.12	52,52,52,52	0
57	MG	1A	3728	1/1	0.93	0.34	34,34,34,34	0
57	MG	2A	3006	1/1	0.93	0.10	40,40,40,40	0
57	MG	2A	3570	1/1	0.93	0.09	77,77,77,77	0
57	MG	1A	4001	1/1	0.93	0.13	72,72,72,72	0
57	MG	2A	3277	1/1	0.93	0.27	61,61,61,61	0
57	MG	2A	3015	1/1	0.93	0.15	60,60,60,60	0
57	MG	2a	3090	1/1	0.93	0.12	56,56,56,56	0
57	MG	2A	3018	1/1	0.93	0.14	39,39,39,39	0
57	MG	1A	4003	1/1	0.93	0.14	24,24,24,24	0
57	MG	2A	3284	1/1	0.93	0.15	44,44,44,44	0
57	MG	2a	3096	1/1	0.93	0.28	58,58,58,58	0
57	MG	1A	3422	1/1	0.93	0.07	20,20,20,20	0
57	MG	2A	3022	1/1	0.93	0.12	60,60,60,60	0
57	MG	2a	3099	1/1	0.93	0.33	59,59,59,59	0
57	MG	1a	1618	1/1	0.93	0.09	52,52,52,52	0
57	MG	2a	3101	1/1	0.93	0.23	60,60,60,60	0
57	MG	2A	3586	1/1	0.93	0.09	47,47,47,47	0
57	MG	2A	3026	1/1	0.93	0.13	58,58,58,58	0
57	MG	2A	3589	1/1	0.93	0.16	44,44,44,44	0
57	MG	2A	3591	1/1	0.93	0.12	59,59,59,59	0
57	MG	2A	3596	1/1	0.93	0.09	37,37,37,37	0
57	MG	1a	1619	1/1	0.93	0.14	66,66,66,66	0
57	MG	2A	3601	1/1	0.93	0.10	58,58,58,58	0
57	MG	1A	3732	1/1	0.93	0.09	30,30,30,30	0
57	MG	1A	3734	1/1	0.93	0.08	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3469	1/1	0.93	0.15	62,62,62,62	0
57	MG	2a	3119	1/1	0.93	0.10	64,64,64,64	0
57	MG	2A	3608	1/1	0.93	0.14	62,62,62,62	0
57	MG	1A	3868	1/1	0.93	0.07	41,41,41,41	0
57	MG	1A	3738	1/1	0.93	0.07	49,49,49,49	0
57	MG	2A	3303	1/1	0.93	0.17	61,61,61,61	0
57	MG	2A	3045	1/1	0.93	0.10	54,54,54,54	0
57	MG	2A	3046	1/1	0.93	0.25	63,63,63,63	0
57	MG	2A	3049	1/1	0.93	0.11	50,50,50,50	0
57	MG	2a	3130	1/1	0.93	0.24	72,72,72,72	0
57	MG	1A	3370	1/1	0.93	0.10	50,50,50,50	0
57	MG	1A	3373	1/1	0.93	0.10	40,40,40,40	0
57	MG	1A	3875	1/1	0.93	0.07	39,39,39,39	0
57	MG	1A	3267	1/1	0.93	0.13	49,49,49,49	0
57	MG	2a	3138	1/1	0.93	0.20	56,56,56,56	0
57	MG	2A	3316	1/1	0.93	0.37	45,45,45,45	0
57	MG	1A	3482	1/1	0.93	0.07	14,14,14,14	0
57	MG	1a	1773	1/1	0.93	0.19	70,70,70,70	0
57	MG	2A	3627	1/1	0.93	0.10	52,52,52,52	0
57	MG	2A	3634	1/1	0.93	0.08	65,65,65,65	0
57	MG	1a	1774	1/1	0.93	0.16	58,58,58,58	0
57	MG	1A	3554	1/1	0.93	0.09	40,40,40,40	0
57	MG	1a	1649	1/1	0.93	0.18	63,63,63,63	0
57	MG	2A	3327	1/1	0.93	0.08	53,53,53,53	0
57	MG	2a	3159	1/1	0.93	0.16	61,61,61,61	0
57	MG	2A	3648	1/1	0.93	0.07	27,27,27,27	0
57	MG	2a	3162	1/1	0.93	0.13	63,63,63,63	0
57	MG	2a	3163	1/1	0.93	0.10	58,58,58,58	0
57	MG	1A	3755	1/1	0.93	0.09	55,55,55,55	0
57	MG	2A	3651	1/1	0.93	0.09	76,76,76,76	0
57	MG	1A	3651	1/1	0.93	0.13	44,44,44,44	0
57	MG	2A	3077	1/1	0.93	0.10	52,52,52,52	0
57	MG	1B	204	1/1	0.93	0.09	52,52,52,52	0
57	MG	1A	3890	1/1	0.93	0.07	47,47,47,47	0
57	MG	1A	3432	1/1	0.93	0.08	37,37,37,37	0
57	MG	2A	3667	1/1	0.93	0.13	37,37,37,37	0
57	MG	1A	3486	1/1	0.93	0.08	44,44,44,44	0
57	MG	2A	3346	1/1	0.93	0.08	40,40,40,40	0
57	MG	2A	3674	1/1	0.93	0.10	45,45,45,45	0
57	MG	2a	3176	1/1	0.93	0.07	63,63,63,63	0
57	MG	1A	3661	1/1	0.93	0.17	30,30,30,30	0
57	MG	1A	3894	1/1	0.93	0.17	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3352	1/1	0.93	0.22	60,60,60,60	0
57	MG	1A	3197	1/1	0.93	0.10	55,55,55,55	0
57	MG	1a	1790	1/1	0.93	0.13	74,74,74,74	0
57	MG	2A	3356	1/1	0.93	0.14	61,61,61,61	0
57	MG	1A	3905	1/1	0.93	0.07	58,58,58,58	0
57	MG	2e	201	1/1	0.93	0.11	65,65,65,65	0
57	MG	1A	3219	1/1	0.93	0.18	55,55,55,55	0
57	MG	1A	3909	1/1	0.93	0.10	21,21,21,21	0
57	MG	1a	1668	1/1	0.93	0.27	64,64,64,64	0
57	MG	2A	3690	1/1	0.93	0.08	59,59,59,59	0
57	MG	1B	218	1/1	0.93	0.07	48,48,48,48	0
57	MG	2A	3105	1/1	0.93	0.11	53,53,53,53	0
57	MG	1a	1670	1/1	0.93	0.15	59,59,59,59	0
59	MPD	1A	4031	8/8	0.93	0.18	50,54,58,60	0
57	MG	2A	3377	1/1	0.93	0.12	45,45,45,45	0
57	MG	2A	3702	1/1	0.93	0.14	60,60,60,60	0
57	MG	1a	1798	1/1	0.93	0.09	49,49,49,49	0
57	MG	2A	3707	1/1	0.93	0.12	66,66,66,66	0
57	MG	2A	3708	1/1	0.93	0.12	63,63,63,63	0
57	MG	1A	3251	1/1	0.94	0.12	55,55,55,55	0
57	MG	2A	3047	1/1	0.94	0.14	48,48,48,48	0
57	MG	2A	3048	1/1	0.94	0.17	43,43,43,43	0
57	MG	2A	3336	1/1	0.94	0.14	40,40,40,40	0
57	MG	1A	3011	1/1	0.94	0.09	44,44,44,44	0
57	MG	1A	3076	1/1	0.94	0.14	34,34,34,34	0
57	MG	2A	3342	1/1	0.94	0.15	59,59,59,59	0
57	MG	10	109	1/1	0.94	0.08	50,50,50,50	0
57	MG	1A	3540	1/1	0.94	0.06	24,24,24,24	0
57	MG	2A	3347	1/1	0.94	0.07	42,42,42,42	0
57	MG	2A	3348	1/1	0.94	0.07	40,40,40,40	0
57	MG	1a	1749	1/1	0.94	0.16	41,41,41,41	0
57	MG	2A	3057	1/1	0.94	0.21	69,69,69,69	0
57	MG	1A	3777	1/1	0.94	0.06	20,20,20,20	0
57	MG	2A	3060	1/1	0.94	0.06	47,47,47,47	0
57	MG	2A	3061	1/1	0.94	0.06	45,45,45,45	0
57	MG	1A	3166	1/1	0.94	0.25	58,58,58,58	0
57	MG	1A	3262	1/1	0.94	0.13	48,48,48,48	0
57	MG	1A	3659	1/1	0.94	0.17	50,50,50,50	0
57	MG	2A	3715	1/1	0.94	0.10	58,58,58,58	0
57	MG	15	3102	1/1	0.94	0.07	34,34,34,34	0
57	MG	1a	1756	1/1	0.94	0.17	58,58,58,58	0
57	MG	15	3104	1/1	0.94	0.12	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3720	1/1	0.94	0.20	61,61,61,61	0
57	MG	2A	3721	1/1	0.94	0.11	56,56,56,56	0
57	MG	1A	3959	1/1	0.94	0.09	59,59,59,59	0
57	MG	1a	1761	1/1	0.94	0.12	54,54,54,54	0
57	MG	2A	3081	1/1	0.94	0.17	45,45,45,45	0
57	MG	1A	3388	1/1	0.94	0.14	61,61,61,61	0
57	MG	1A	3782	1/1	0.94	0.06	38,38,38,38	0
57	MG	1a	1766	1/1	0.94	0.09	61,61,61,61	0
57	MG	1A	3966	1/1	0.94	0.13	42,42,42,42	0
57	MG	2A	3386	1/1	0.94	0.12	63,63,63,63	0
57	MG	18	101	1/1	0.94	0.08	39,39,39,39	0
57	MG	1A	3324	1/1	0.94	0.15	53,53,53,53	0
57	MG	1a	1770	1/1	0.94	0.11	55,55,55,55	0
57	MG	1A	3664	1/1	0.94	0.08	41,41,41,41	0
57	MG	1A	3665	1/1	0.94	0.08	56,56,56,56	0
57	MG	1A	3264	1/1	0.94	0.07	39,39,39,39	0
57	MG	2A	3094	1/1	0.94	0.09	63,63,63,63	0
57	MG	2A	3402	1/1	0.94	0.09	41,41,41,41	0
57	MG	1A	3167	1/1	0.94	0.08	47,47,47,47	0
57	MG	2B	206	1/1	0.94	0.14	61,61,61,61	0
57	MG	1A	3470	1/1	0.94	0.13	52,52,52,52	0
57	MG	1A	3558	1/1	0.94	0.14	22,22,22,22	0
57	MG	1A	3792	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3476	1/1	0.94	0.08	62,62,62,62	0
57	MG	2A	3108	1/1	0.94	0.10	56,56,56,56	0
57	MG	1A	3329	1/1	0.94	0.24	56,56,56,56	0
57	MG	1A	3989	1/1	0.94	0.10	37,37,37,37	0
57	MG	2A	3111	1/1	0.94	0.15	63,63,63,63	0
57	MG	1a	1614	1/1	0.94	0.11	63,63,63,63	0
57	MG	1a	1616	1/1	0.94	0.10	63,63,63,63	0
57	MG	2A	3419	1/1	0.94	0.09	50,50,50,50	0
57	MG	2A	3421	1/1	0.94	0.10	34,34,34,34	0
57	MG	2E	303	1/1	0.94	0.10	47,47,47,47	0
57	MG	1A	3065	1/1	0.94	0.08	50,50,50,50	0
57	MG	1A	3804	1/1	0.94	0.14	49,49,49,49	0
57	MG	1A	3567	1/1	0.94	0.10	39,39,39,39	0
57	MG	2F	301	1/1	0.94	0.11	49,49,49,49	0
57	MG	1a	1624	1/1	0.94	0.10	68,68,68,68	0
57	MG	2A	3432	1/1	0.94	0.09	35,35,35,35	0
57	MG	1A	3807	1/1	0.94	0.08	29,29,29,29	0
57	MG	2A	3127	1/1	0.94	0.29	60,60,60,60	0
57	MG	2A	3436	1/1	0.94	0.14	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3437	1/1	0.94	0.10	39,39,39,39	0
57	MG	1a	1626	1/1	0.94	0.23	65,65,65,65	0
57	MG	1A	3810	1/1	0.94	0.10	38,38,38,38	0
57	MG	2A	3442	1/1	0.94	0.17	59,59,59,59	0
57	MG	2T	202	1/1	0.94	0.12	52,52,52,52	0
57	MG	1A	3171	1/1	0.94	0.11	32,32,32,32	0
57	MG	1A	3815	1/1	0.94	0.29	52,52,52,52	0
57	MG	1A	3679	1/1	0.94	0.09	18,18,18,18	0
57	MG	1A	3999	1/1	0.94	0.12	47,47,47,47	0
57	MG	2Y	201	1/1	0.94	0.14	52,52,52,52	0
57	MG	2A	3451	1/1	0.94	0.07	56,56,56,56	0
57	MG	2A	3138	1/1	0.94	0.16	50,50,50,50	0
57	MG	2A	3454	1/1	0.94	0.26	61,61,61,61	0
57	MG	21	103	1/1	0.94	0.11	55,55,55,55	0
57	MG	2A	3140	1/1	0.94	0.17	58,58,58,58	0
57	MG	1A	3570	1/1	0.94	0.22	61,61,61,61	0
57	MG	1A	3571	1/1	0.94	0.13	25,25,25,25	0
57	MG	1A	4002	1/1	0.94	0.13	33,33,33,33	0
57	MG	27	101	1/1	0.94	0.13	46,46,46,46	0
57	MG	1a	1637	1/1	0.94	0.27	63,63,63,63	0
57	MG	1a	1638	1/1	0.94	0.10	69,69,69,69	0
57	MG	1a	1640	1/1	0.94	0.15	63,63,63,63	0
57	MG	2a	3003	1/1	0.94	0.27	53,53,53,53	0
57	MG	2A	3156	1/1	0.94	0.20	46,46,46,46	0
57	MG	1a	1808	1/1	0.94	0.13	66,66,66,66	0
57	MG	1a	1641	1/1	0.94	0.16	52,52,52,52	0
57	MG	1a	1643	1/1	0.94	0.20	49,49,49,49	0
57	MG	2A	3162	1/1	0.94	0.10	61,61,61,61	0
57	MG	2A	3166	1/1	0.94	0.12	55,55,55,55	0
57	MG	1A	3687	1/1	0.94	0.10	44,44,44,44	0
57	MG	2a	3015	1/1	0.94	0.13	54,54,54,54	0
57	MG	2A	3168	1/1	0.94	0.06	63,63,63,63	0
57	MG	1A	3069	1/1	0.94	0.17	43,43,43,43	0
57	MG	2A	3482	1/1	0.94	0.20	59,59,59,59	0
57	MG	1a	1648	1/1	0.94	0.12	50,50,50,50	0
57	MG	1A	3120	1/1	0.94	0.13	29,29,29,29	0
57	MG	2A	3175	1/1	0.94	0.11	59,59,59,59	0
57	MG	2A	3489	1/1	0.94	0.08	61,61,61,61	0
57	MG	1A	3178	1/1	0.94	0.16	36,36,36,36	0
57	MG	2A	3492	1/1	0.94	0.08	65,65,65,65	0
57	MG	1a	1653	1/1	0.94	0.16	50,50,50,50	0
57	MG	2a	3028	1/1	0.94	0.14	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3029	1/1	0.94	0.08	56,56,56,56	0
57	MG	1A	3839	1/1	0.94	0.10	46,46,46,46	0
57	MG	1A	3403	1/1	0.94	0.13	47,47,47,47	0
57	MG	2A	3182	1/1	0.94	0.12	53,53,53,53	0
57	MG	2A	3503	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	3842	1/1	0.94	0.08	36,36,36,36	0
57	MG	1A	3492	1/1	0.94	0.05	25,25,25,25	0
57	MG	1A	3493	1/1	0.94	0.12	48,48,48,48	0
57	MG	1A	3582	1/1	0.94	0.12	54,54,54,54	0
57	MG	1A	3496	1/1	0.94	0.12	22,22,22,22	0
57	MG	2A	3188	1/1	0.94	0.23	54,54,54,54	0
57	MG	1a	1831	1/1	0.94	0.11	54,54,54,54	0
57	MG	1A	3083	1/1	0.94	0.19	51,51,51,51	0
57	MG	1A	3590	1/1	0.94	0.11	41,41,41,41	0
57	MG	1A	3859	1/1	0.94	0.10	45,45,45,45	0
57	MG	1A	3499	1/1	0.94	0.07	29,29,29,29	0
57	MG	2A	3197	1/1	0.94	0.09	48,48,48,48	0
57	MG	1a	1837	1/1	0.94	0.18	70,70,70,70	0
57	MG	2A	3199	1/1	0.94	0.07	56,56,56,56	0
57	MG	2A	3529	1/1	0.94	0.16	54,54,54,54	0
57	MG	1A	3706	1/1	0.94	0.10	41,41,41,41	0
57	MG	1A	3865	1/1	0.94	0.09	48,48,48,48	0
57	MG	1A	3707	1/1	0.94	0.07	47,47,47,47	0
57	MG	2a	3055	1/1	0.94	0.17	64,64,64,64	0
57	MG	1A	3085	1/1	0.94	0.09	46,46,46,46	0
57	MG	2A	3534	1/1	0.94	0.17	63,63,63,63	0
57	MG	2a	3058	1/1	0.94	0.20	64,64,64,64	0
57	MG	1a	1848	1/1	0.94	0.14	52,52,52,52	0
57	MG	1A	3595	1/1	0.94	0.11	25,25,25,25	0
57	MG	2A	3211	1/1	0.94	0.11	56,56,56,56	0
57	MG	1A	3418	1/1	0.94	0.07	37,37,37,37	0
57	MG	1A	3343	1/1	0.94	0.14	45,45,45,45	0
57	MG	2a	3065	1/1	0.94	0.10	64,64,64,64	0
57	MG	1a	1852	1/1	0.94	0.15	60,60,60,60	0
57	MG	2a	3068	1/1	0.94	0.14	61,61,61,61	0
57	MG	2A	3216	1/1	0.94	0.09	52,52,52,52	0
57	MG	1A	3022	1/1	0.94	0.11	43,43,43,43	0
57	MG	2A	3218	1/1	0.94	0.23	55,55,55,55	0
57	MG	2a	3073	1/1	0.94	0.15	62,62,62,62	0
57	MG	1A	3716	1/1	0.94	0.16	34,34,34,34	0
57	MG	2A	3545	1/1	0.94	0.10	37,37,37,37	0
57	MG	1A	3346	1/1	0.94	0.13	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3082	1/1	0.94	0.28	64,64,64,64	0
57	MG	2A	3222	1/1	0.94	0.26	49,49,49,49	0
57	MG	1A	3347	1/1	0.94	0.09	46,46,46,46	0
57	MG	2A	3553	1/1	0.94	0.07	52,52,52,52	0
57	MG	1A	3609	1/1	0.94	0.15	58,58,58,58	0
57	MG	1A	3517	1/1	0.94	0.11	52,52,52,52	0
57	MG	1A	3230	1/1	0.94	0.12	38,38,38,38	0
57	MG	2A	3558	1/1	0.94	0.07	36,36,36,36	0
57	MG	2A	3227	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3293	1/1	0.94	0.09	43,43,43,43	0
57	MG	1A	3731	1/1	0.94	0.15	33,33,33,33	0
57	MG	2A	3232	1/1	0.94	0.18	60,60,60,60	0
57	MG	1A	3615	1/1	0.94	0.08	48,48,48,48	0
57	MG	1A	3616	1/1	0.94	0.07	36,36,36,36	0
57	MG	1A	3895	1/1	0.94	0.11	28,28,28,28	0
57	MG	1D	309	1/1	0.94	0.22	38,38,38,38	0
57	MG	1A	3896	1/1	0.94	0.10	56,56,56,56	0
57	MG	1A	3433	1/1	0.94	0.17	53,53,53,53	0
57	MG	1A	3904	1/1	0.94	0.10	59,59,59,59	0
57	MG	1D	315	1/1	0.94	0.10	55,55,55,55	0
57	MG	2a	3113	1/1	0.94	0.07	47,47,47,47	0
57	MG	2A	3577	1/1	0.94	0.08	60,60,60,60	0
57	MG	1A	3737	1/1	0.94	0.09	42,42,42,42	0
57	MG	1a	1699	1/1	0.94	0.22	68,68,68,68	0
57	MG	2a	3118	1/1	0.94	0.17	53,53,53,53	0
57	MG	1A	3232	1/1	0.94	0.44	44,44,44,44	0
57	MG	1A	3352	1/1	0.94	0.09	20,20,20,20	0
57	MG	2a	3122	1/1	0.94	0.13	53,53,53,53	0
57	MG	2A	3255	1/1	0.94	0.18	51,51,51,51	0
57	MG	1f	201	1/1	0.94	0.14	63,63,63,63	0
57	MG	2A	3587	1/1	0.94	0.15	53,53,53,53	0
57	MG	1f	202	1/1	0.94	0.09	46,46,46,46	0
57	MG	2A	3261	1/1	0.94	0.08	50,50,50,50	0
57	MG	1A	3620	1/1	0.94	0.10	51,51,51,51	0
57	MG	1h	201	1/1	0.94	0.17	56,56,56,56	0
57	MG	1A	3353	1/1	0.94	0.21	49,49,49,49	0
57	MG	2a	3133	1/1	0.94	0.07	33,33,33,33	0
57	MG	2A	3599	1/1	0.94	0.11	45,45,45,45	0
57	MG	2a	3135	1/1	0.94	0.19	53,53,53,53	0
57	MG	1G	201	1/1	0.94	0.06	67,67,67,67	0
57	MG	2A	3602	1/1	0.94	0.08	55,55,55,55	0
57	MG	2A	3604	1/1	0.94	0.07	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3141	1/1	0.94	0.15	68,68,68,68	0
57	MG	1A	3915	1/1	0.94	0.15	26,26,26,26	0
57	MG	1A	3919	1/1	0.94	0.17	39,39,39,39	0
57	MG	1G	204	1/1	0.94	0.11	46,46,46,46	0
57	MG	1A	3527	1/1	0.94	0.07	24,24,24,24	0
57	MG	1A	3237	1/1	0.94	0.14	29,29,29,29	0
57	MG	2A	3611	1/1	0.94	0.07	63,63,63,63	0
57	MG	1a	1710	1/1	0.94	0.20	51,51,51,51	0
57	MG	2a	3153	1/1	0.94	0.07	57,57,57,57	0
57	MG	1y	201	1/1	0.94	0.08	58,58,58,58	0
57	MG	2A	3614	1/1	0.94	0.11	74,74,74,74	0
57	MG	1O	202	1/1	0.94	0.08	56,56,56,56	0
57	MG	1A	3143	1/1	0.94	0.17	42,42,42,42	0
57	MG	1Q	204	1/1	0.94	0.08	31,31,31,31	0
57	MG	1A	3927	1/1	0.94	0.09	47,47,47,47	0
57	MG	1R	205	1/1	0.94	0.14	50,50,50,50	0
57	MG	1A	3629	1/1	0.94	0.15	35,35,35,35	0
57	MG	2A	3004	1/1	0.94	0.12	57,57,57,57	0
57	MG	1A	3089	1/1	0.94	0.14	44,44,44,44	0
57	MG	2A	3007	1/1	0.94	0.15	40,40,40,40	0
57	MG	2A	3293	1/1	0.94	0.19	52,52,52,52	0
57	MG	2A	3009	1/1	0.94	0.13	66,66,66,66	0
57	MG	2A	3631	1/1	0.94	0.13	51,51,51,51	0
57	MG	2A	3011	1/1	0.94	0.12	55,55,55,55	0
57	MG	1A	3633	1/1	0.94	0.10	46,46,46,46	0
57	MG	1T	204	1/1	0.94	0.08	61,61,61,61	0
57	MG	1a	1721	1/1	0.94	0.16	63,63,63,63	0
57	MG	2A	3304	1/1	0.94	0.22	66,66,66,66	0
57	MG	2A	3305	1/1	0.94	0.08	49,49,49,49	0
57	MG	1U	206	1/1	0.94	0.10	37,37,37,37	0
57	MG	1A	3635	1/1	0.94	0.13	57,57,57,57	0
57	MG	1a	1725	1/1	0.94	0.15	51,51,51,51	0
57	MG	2A	3654	1/1	0.94	0.10	55,55,55,55	0
57	MG	1A	3362	1/1	0.94	0.05	40,40,40,40	0
57	MG	1A	3366	1/1	0.94	0.07	37,37,37,37	0
57	MG	1W	202	1/1	0.94	0.14	45,45,45,45	0
57	MG	1A	3248	1/1	0.94	0.11	50,50,50,50	0
57	MG	2A	3663	1/1	0.94	0.14	58,58,58,58	0
57	MG	2A	3664	1/1	0.94	0.10	41,41,41,41	0
57	MG	2A	3032	1/1	0.94	0.12	54,54,54,54	0
57	MG	2A	3033	1/1	0.94	0.10	49,49,49,49	0
57	MG	2A	3038	1/1	0.94	0.14	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3314	1/1	0.94	0.10	35,35,35,35	0
57	MG	1Z	301	1/1	0.94	0.14	44,44,44,44	0
57	MG	10	101	1/1	0.94	0.28	40,40,40,40	0
57	MG	1a	1737	1/1	0.94	0.11	68,68,68,68	0
57	MG	10	103	1/1	0.94	0.09	50,50,50,50	0
57	MG	2A	3682	1/1	0.94	0.11	60,60,60,60	0
57	MG	2A	3359	1/1	0.95	0.09	59,59,59,59	0
57	MG	2A	3100	1/1	0.95	0.19	60,60,60,60	0
57	MG	2A	3362	1/1	0.95	0.09	51,51,51,51	0
57	MG	1a	1621	1/1	0.95	0.07	66,66,66,66	0
57	MG	1A	3544	1/1	0.95	0.06	49,49,49,49	0
57	MG	1A	3331	1/1	0.95	0.12	40,40,40,40	0
57	MG	2A	3368	1/1	0.95	0.09	47,47,47,47	0
57	MG	2A	3692	1/1	0.95	0.17	53,53,53,53	0
57	MG	2A	3693	1/1	0.95	0.08	34,34,34,34	0
57	MG	1A	3549	1/1	0.95	0.11	56,56,56,56	0
57	MG	2A	3695	1/1	0.95	0.08	41,41,41,41	0
57	MG	2A	3372	1/1	0.95	0.11	38,38,38,38	0
57	MG	2A	3698	1/1	0.95	0.23	61,61,61,61	0
57	MG	1a	1627	1/1	0.95	0.15	57,57,57,57	0
57	MG	1a	1795	1/1	0.95	0.10	48,48,48,48	0
57	MG	2A	3378	1/1	0.95	0.08	30,30,30,30	0
57	MG	2A	3706	1/1	0.95	0.09	50,50,50,50	0
57	MG	1A	3671	1/1	0.95	0.11	48,48,48,48	0
57	MG	2A	3114	1/1	0.95	0.18	44,44,44,44	0
57	MG	2A	3116	1/1	0.95	0.22	41,41,41,41	0
57	MG	1A	3813	1/1	0.95	0.07	46,46,46,46	0
57	MG	1A	3236	1/1	0.95	0.20	57,57,57,57	0
57	MG	2A	3387	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3008	1/1	0.95	0.12	39,39,39,39	0
57	MG	1A	3239	1/1	0.95	0.14	35,35,35,35	0
57	MG	2A	3390	1/1	0.95	0.06	33,33,33,33	0
57	MG	1A	3241	1/1	0.95	0.18	38,38,38,38	0
57	MG	1A	3818	1/1	0.95	0.09	43,43,43,43	0
57	MG	1a	1804	1/1	0.95	0.29	59,59,59,59	0
57	MG	1A	3555	1/1	0.95	0.08	48,48,48,48	0
57	MG	1A	3820	1/1	0.95	0.10	52,52,52,52	0
57	MG	2A	3401	1/1	0.95	0.09	59,59,59,59	0
57	MG	1A	3821	1/1	0.95	0.06	42,42,42,42	0
57	MG	1A	3823	1/1	0.95	0.07	40,40,40,40	0
57	MG	1A	3825	1/1	0.95	0.07	58,58,58,58	0
57	MG	1A	4016	1/1	0.95	0.06	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3095	1/1	0.95	0.10	39,39,39,39	0
57	MG	2A	3137	1/1	0.95	0.15	38,38,38,38	0
57	MG	1A	3831	1/1	0.95	0.09	48,48,48,48	0
57	MG	2A	3411	1/1	0.95	0.06	59,59,59,59	0
57	MG	2A	3412	1/1	0.95	0.07	63,63,63,63	0
57	MG	2A	3413	1/1	0.95	0.07	33,33,33,33	0
57	MG	2A	3139	1/1	0.95	0.21	61,61,61,61	0
57	MG	1A	3096	1/1	0.95	0.08	15,15,15,15	0
57	MG	2A	3142	1/1	0.95	0.13	55,55,55,55	0
57	MG	2A	3145	1/1	0.95	0.13	63,63,63,63	0
57	MG	1A	3833	1/1	0.95	0.22	38,38,38,38	0
57	MG	2A	3147	1/1	0.95	0.10	45,45,45,45	0
57	MG	2B	209	1/1	0.95	0.16	55,55,55,55	0
57	MG	1a	1820	1/1	0.95	0.06	69,69,69,69	0
57	MG	1A	3835	1/1	0.95	0.06	23,23,23,23	0
57	MG	1a	1651	1/1	0.95	0.08	49,49,49,49	0
57	MG	2A	3424	1/1	0.95	0.09	44,44,44,44	0
57	MG	2A	3425	1/1	0.95	0.14	61,61,61,61	0
57	MG	1A	3836	1/1	0.95	0.06	41,41,41,41	0
57	MG	2D	303	1/1	0.95	0.14	53,53,53,53	0
57	MG	2D	304	1/1	0.95	0.37	43,43,43,43	0
57	MG	2A	3429	1/1	0.95	0.11	50,50,50,50	0
57	MG	2D	308	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3247	1/1	0.95	0.20	51,51,51,51	0
57	MG	2A	3155	1/1	0.95	0.09	50,50,50,50	0
57	MG	1A	3097	1/1	0.95	0.07	43,43,43,43	0
57	MG	1A	3562	1/1	0.95	0.10	42,42,42,42	0
57	MG	2A	3158	1/1	0.95	0.24	63,63,63,63	0
57	MG	1A	3451	1/1	0.95	0.07	17,17,17,17	0
57	MG	1A	3691	1/1	0.95	0.08	66,66,66,66	0
57	MG	1A	3565	1/1	0.95	0.23	50,50,50,50	0
57	MG	2E	308	1/1	0.95	0.15	59,59,59,59	0
57	MG	2A	3441	1/1	0.95	0.10	63,63,63,63	0
57	MG	2A	3165	1/1	0.95	0.10	43,43,43,43	0
57	MG	1A	3173	1/1	0.95	0.10	35,35,35,35	0
57	MG	2A	3444	1/1	0.95	0.22	59,59,59,59	0
57	MG	1A	3253	1/1	0.95	0.09	35,35,35,35	0
57	MG	2A	3448	1/1	0.95	0.27	57,57,57,57	0
57	MG	1A	3174	1/1	0.95	0.06	44,44,44,44	0
57	MG	2A	3169	1/1	0.95	0.09	46,46,46,46	0
57	MG	1A	3348	1/1	0.95	0.09	46,46,46,46	0
57	MG	1A	3004	1/1	0.95	0.07	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1839	1/1	0.95	0.14	70,70,70,70	0
57	MG	1A	3260	1/1	0.95	0.06	46,46,46,46	0
57	MG	2T	204	1/1	0.95	0.11	50,50,50,50	0
57	MG	2A	3457	1/1	0.95	0.06	38,38,38,38	0
57	MG	2A	3459	1/1	0.95	0.11	55,55,55,55	0
57	MG	1A	3575	1/1	0.95	0.07	41,41,41,41	0
57	MG	1A	3702	1/1	0.95	0.15	40,40,40,40	0
57	MG	2A	3463	1/1	0.95	0.10	65,65,65,65	0
57	MG	1A	3100	1/1	0.95	0.09	43,43,43,43	0
57	MG	1a	1847	1/1	0.95	0.15	67,67,67,67	0
57	MG	2A	3466	1/1	0.95	0.06	70,70,70,70	0
57	MG	1A	3042	1/1	0.95	0.06	30,30,30,30	0
57	MG	1A	3107	1/1	0.95	0.14	28,28,28,28	0
57	MG	1A	3355	1/1	0.95	0.06	21,21,21,21	0
57	MG	1A	3266	1/1	0.95	0.07	67,67,67,67	0
57	MG	1A	3471	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3475	1/1	0.95	0.12	57,57,57,57	0
57	MG	1A	3589	1/1	0.95	0.05	55,55,55,55	0
57	MG	2A	3474	1/1	0.95	0.10	56,56,56,56	0
57	MG	1a	1679	1/1	0.95	0.21	60,60,60,60	0
57	MG	1A	3877	1/1	0.95	0.08	29,29,29,29	0
57	MG	2a	3005	1/1	0.95	0.07	52,52,52,52	0
57	MG	1a	1681	1/1	0.95	0.11	66,66,66,66	0
57	MG	1D	305	1/1	0.95	0.12	34,34,34,34	0
57	MG	2A	3194	1/1	0.95	0.08	41,41,41,41	0
57	MG	1a	1683	1/1	0.95	0.08	55,55,55,55	0
57	MG	1A	3186	1/1	0.95	0.09	32,32,32,32	0
57	MG	2A	3485	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3591	1/1	0.95	0.07	40,40,40,40	0
57	MG	1A	3108	1/1	0.95	0.07	34,34,34,34	0
57	MG	2A	3490	1/1	0.95	0.09	32,32,32,32	0
57	MG	1D	312	1/1	0.95	0.14	36,36,36,36	0
57	MG	2A	3202	1/1	0.95	0.13	60,60,60,60	0
57	MG	2A	3203	1/1	0.95	0.08	50,50,50,50	0
57	MG	2A	3204	1/1	0.95	0.06	46,46,46,46	0
57	MG	1a	1869	1/1	0.95	0.17	55,55,55,55	0
57	MG	2A	3497	1/1	0.95	0.07	42,42,42,42	0
57	MG	1A	3047	1/1	0.95	0.19	48,48,48,48	0
57	MG	2A	3501	1/1	0.95	0.14	56,56,56,56	0
57	MG	2A	3207	1/1	0.95	0.25	61,61,61,61	0
57	MG	1a	1690	1/1	0.95	0.18	67,67,67,67	0
57	MG	1a	1872	1/1	0.95	0.07	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3723	1/1	0.95	0.06	55,55,55,55	0
57	MG	2A	3507	1/1	0.95	0.06	44,44,44,44	0
57	MG	1A	3479	1/1	0.95	0.07	58,58,58,58	0
57	MG	1E	304	1/1	0.95	0.07	21,21,21,21	0
57	MG	2a	3035	1/1	0.95	0.06	46,46,46,46	0
57	MG	2A	3510	1/1	0.95	0.11	49,49,49,49	0
57	MG	2A	3511	1/1	0.95	0.10	55,55,55,55	0
57	MG	1A	3725	1/1	0.95	0.14	41,41,41,41	0
57	MG	2A	3513	1/1	0.95	0.09	60,60,60,60	0
57	MG	1A	3052	1/1	0.95	0.07	32,32,32,32	0
57	MG	1A	3056	1/1	0.95	0.10	42,42,42,42	0
57	MG	1F	307	1/1	0.95	0.28	27,27,27,27	0
57	MG	2A	3517	1/1	0.95	0.07	44,44,44,44	0
57	MG	2A	3519	1/1	0.95	0.13	58,58,58,58	0
57	MG	1F	313	1/1	0.95	0.10	42,42,42,42	0
57	MG	2a	3047	1/1	0.95	0.26	63,63,63,63	0
57	MG	1A	3730	1/1	0.95	0.26	39,39,39,39	0
57	MG	1A	3483	1/1	0.95	0.07	25,25,25,25	0
57	MG	2A	3523	1/1	0.95	0.09	61,61,61,61	0
57	MG	1A	3126	1/1	0.95	0.18	52,52,52,52	0
57	MG	1A	3903	1/1	0.95	0.06	33,33,33,33	0
57	MG	1A	3485	1/1	0.95	0.08	46,46,46,46	0
57	MG	1A	3608	1/1	0.95	0.10	57,57,57,57	0
57	MG	1A	3281	1/1	0.95	0.14	58,58,58,58	0
57	MG	1A	3908	1/1	0.95	0.06	15,15,15,15	0
57	MG	2A	3228	1/1	0.95	0.21	60,60,60,60	0
57	MG	1m	201	1/1	0.95	0.06	72,72,72,72	0
57	MG	1O	201	1/1	0.95	0.06	48,48,48,48	0
57	MG	2A	3231	1/1	0.95	0.15	48,48,48,48	0
57	MG	1A	3082	1/1	0.95	0.08	33,33,33,33	0
57	MG	1P	202	1/1	0.95	0.14	25,25,25,25	0
57	MG	1t	201	1/1	0.95	0.12	60,60,60,60	0
57	MG	1A	3739	1/1	0.95	0.06	31,31,31,31	0
57	MG	2A	3237	1/1	0.95	0.22	47,47,47,47	0
57	MG	1A	3129	1/1	0.95	0.18	68,68,68,68	0
57	MG	1R	202	1/1	0.95	0.17	33,33,33,33	0
57	MG	1A	3379	1/1	0.95	0.11	34,34,34,34	0
57	MG	1A	3290	1/1	0.95	0.12	56,56,56,56	0
57	MG	2A	3546	1/1	0.95	0.14	55,55,55,55	0
57	MG	2a	3074	1/1	0.95	0.09	59,59,59,59	0
57	MG	1A	3199	1/1	0.95	0.16	56,56,56,56	0
57	MG	2A	3548	1/1	0.95	0.12	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3131	1/1	0.95	0.06	35,35,35,35	0
57	MG	2a	3081	1/1	0.95	0.06	69,69,69,69	0
57	MG	1A	3923	1/1	0.95	0.05	23,23,23,23	0
57	MG	2a	3083	1/1	0.95	0.22	66,66,66,66	0
57	MG	2a	3084	1/1	0.95	0.07	65,65,65,65	0
57	MG	1A	3201	1/1	0.95	0.21	50,50,50,50	0
57	MG	2A	3253	1/1	0.95	0.10	32,32,32,32	0
57	MG	2a	3087	1/1	0.95	0.10	61,61,61,61	0
57	MG	1T	205	1/1	0.95	0.06	49,49,49,49	0
57	MG	2A	3556	1/1	0.95	0.08	63,63,63,63	0
57	MG	2a	3092	1/1	0.95	0.33	58,58,58,58	0
57	MG	1U	201	1/1	0.95	0.18	29,29,29,29	0
57	MG	2A	3008	1/1	0.95	0.08	43,43,43,43	0
57	MG	2A	3258	1/1	0.95	0.45	61,61,61,61	0
57	MG	1a	1723	1/1	0.95	0.16	56,56,56,56	0
57	MG	1A	3202	1/1	0.95	0.07	31,31,31,31	0
57	MG	1U	207	1/1	0.95	0.16	49,49,49,49	0
57	MG	2A	3265	1/1	0.95	0.12	30,30,30,30	0
57	MG	1A	3928	1/1	0.95	0.11	48,48,48,48	0
57	MG	1A	3035	1/1	0.95	0.12	44,44,44,44	0
57	MG	2a	3103	1/1	0.95	0.15	50,50,50,50	0
57	MG	1A	3394	1/1	0.95	0.07	47,47,47,47	0
57	MG	2A	3020	1/1	0.95	0.21	45,45,45,45	0
57	MG	1A	3933	1/1	0.95	0.11	38,38,38,38	0
57	MG	1A	3512	1/1	0.95	0.09	60,60,60,60	0
57	MG	2A	3023	1/1	0.95	0.13	42,42,42,42	0
57	MG	2A	3274	1/1	0.95	0.12	61,61,61,61	0
57	MG	1A	3302	1/1	0.95	0.12	34,34,34,34	0
57	MG	2A	3025	1/1	0.95	0.06	34,34,34,34	0
57	MG	1A	3396	1/1	0.95	0.10	34,34,34,34	0
57	MG	1A	3134	1/1	0.95	0.21	35,35,35,35	0
57	MG	2A	3030	1/1	0.95	0.17	52,52,52,52	0
57	MG	2A	3283	1/1	0.95	0.07	53,53,53,53	0
57	MG	2a	3120	1/1	0.95	0.10	57,57,57,57	0
57	MG	1A	3941	1/1	0.95	0.05	27,27,27,27	0
57	MG	1A	3141	1/1	0.95	0.07	41,41,41,41	0
57	MG	1A	3944	1/1	0.95	0.07	35,35,35,35	0
57	MG	2A	3036	1/1	0.95	0.20	56,56,56,56	0
57	MG	2a	3125	1/1	0.95	0.10	61,61,61,61	0
57	MG	2A	3593	1/1	0.95	0.13	58,58,58,58	0
57	MG	1A	3945	1/1	0.95	0.06	47,47,47,47	0
57	MG	1A	3771	1/1	0.95	0.07	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3598	1/1	0.95	0.06	33,33,33,33	0
57	MG	1a	1747	1/1	0.95	0.09	65,65,65,65	0
57	MG	1A	3309	1/1	0.95	0.09	48,48,48,48	0
57	MG	1A	3773	1/1	0.95	0.12	47,47,47,47	0
57	MG	2A	3603	1/1	0.95	0.10	44,44,44,44	0
57	MG	2A	3295	1/1	0.95	0.21	54,54,54,54	0
57	MG	1A	3212	1/1	0.95	0.15	46,46,46,46	0
57	MG	1A	3312	1/1	0.95	0.05	16,16,16,16	0
57	MG	1A	3638	1/1	0.95	0.06	22,22,22,22	0
57	MG	2a	3140	1/1	0.95	0.12	58,58,58,58	0
57	MG	2A	3302	1/1	0.95	0.20	53,53,53,53	0
57	MG	1A	3063	1/1	0.95	0.14	52,52,52,52	0
57	MG	1A	3956	1/1	0.95	0.07	54,54,54,54	0
57	MG	15	3105	1/1	0.95	0.06	38,38,38,38	0
57	MG	2a	3148	1/1	0.95	0.09	68,68,68,68	0
57	MG	1A	3641	1/1	0.95	0.07	49,49,49,49	0
57	MG	1A	3148	1/1	0.95	0.21	59,59,59,59	0
57	MG	1A	3217	1/1	0.95	0.09	31,31,31,31	0
57	MG	1a	1762	1/1	0.95	0.11	55,55,55,55	0
57	MG	1A	3410	1/1	0.95	0.05	32,32,32,32	0
57	MG	2A	3311	1/1	0.95	0.14	52,52,52,52	0
57	MG	17	101	1/1	0.95	0.06	33,33,33,33	0
57	MG	2a	3156	1/1	0.95	0.11	69,69,69,69	0
57	MG	2A	3314	1/1	0.95	0.24	50,50,50,50	0
57	MG	1A	3413	1/1	0.95	0.08	27,27,27,27	0
57	MG	1A	3963	1/1	0.95	0.07	54,54,54,54	0
57	MG	19	101	1/1	0.95	0.14	51,51,51,51	0
57	MG	2A	3065	1/1	0.95	0.07	51,51,51,51	0
57	MG	1A	3965	1/1	0.95	0.07	41,41,41,41	0
57	MG	2A	3322	1/1	0.95	0.18	57,57,57,57	0
57	MG	1A	3414	1/1	0.95	0.09	21,21,21,21	0
57	MG	2A	3072	1/1	0.95	0.12	63,63,63,63	0
57	MG	2A	3638	1/1	0.95	0.12	58,58,58,58	0
57	MG	1a	1602	1/1	0.95	0.10	63,63,63,63	0
57	MG	1A	3086	1/1	0.95	0.16	39,39,39,39	0
57	MG	2A	3645	1/1	0.95	0.13	39,39,39,39	0
57	MG	1A	3222	1/1	0.95	0.07	26,26,26,26	0
57	MG	1A	3153	1/1	0.95	0.06	59,59,59,59	0
57	MG	1A	3037	1/1	0.95	0.09	42,42,42,42	0
57	MG	2a	3177	1/1	0.95	0.10	64,64,64,64	0
57	MG	2a	3178	1/1	0.95	0.10	74,74,74,74	0
57	MG	2A	3334	1/1	0.95	0.08	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3228	1/1	0.95	0.13	34,34,34,34	0
57	MG	1A	3427	1/1	0.95	0.18	61,61,61,61	0
57	MG	2A	3084	1/1	0.95	0.07	40,40,40,40	0
57	MG	1a	1778	1/1	0.95	0.13	46,46,46,46	0
57	MG	1A	3066	1/1	0.95	0.09	39,39,39,39	0
57	MG	2A	3344	1/1	0.95	0.10	58,58,58,58	0
57	MG	2a	3188	1/1	0.95	0.18	47,47,47,47	0
57	MG	1a	1781	1/1	0.95	0.23	67,67,67,67	0
57	MG	1a	1611	1/1	0.95	0.10	58,58,58,58	0
57	MG	1a	1783	1/1	0.95	0.07	62,62,62,62	0
57	MG	2A	3669	1/1	0.95	0.07	56,56,56,56	0
57	MG	1A	3982	1/1	0.95	0.21	46,46,46,46	0
57	MG	2A	3671	1/1	0.95	0.11	47,47,47,47	0
57	MG	2t	201	1/1	0.95	0.10	43,43,43,43	0
57	MG	1A	3793	1/1	0.95	0.15	33,33,33,33	0
57	MG	1A	3327	1/1	0.95	0.10	55,55,55,55	0
58	ARG	1B	230	12/12	0.95	0.09	28,43,53,54	0
57	MG	1A	3666	1/1	0.95	0.07	54,54,54,54	0
59	MPD	18	103	8/8	0.95	0.13	28,35,38,40	0
57	MG	2A	3354	1/1	0.95	0.06	31,31,31,31	0
57	MG	2A	3095	1/1	0.95	0.12	56,56,56,56	0
57	MG	1A	3800	1/1	0.95	0.09	47,47,47,47	0
57	MG	1A	3164	1/1	0.95	0.19	36,36,36,36	0
57	MG	2A	3358	1/1	0.95	0.09	34,34,34,34	0
60	ZN	24	501	1/1	0.95	0.14	136,136,136,136	0
57	MG	1A	3935	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3714	1/1	0.96	0.07	53,53,53,53	0
57	MG	1A	3751	1/1	0.96	0.10	39,39,39,39	0
57	MG	1A	3487	1/1	0.96	0.06	58,58,58,58	0
57	MG	2A	3717	1/1	0.96	0.11	52,52,52,52	0
57	MG	1A	3611	1/1	0.96	0.06	24,24,24,24	0
57	MG	1A	3939	1/1	0.96	0.07	49,49,49,49	0
57	MG	1A	3754	1/1	0.96	0.09	45,45,45,45	0
57	MG	1A	3091	1/1	0.96	0.11	37,37,37,37	0
57	MG	17	102	1/1	0.96	0.14	35,35,35,35	0
57	MG	2A	3141	1/1	0.96	0.10	46,46,46,46	0
57	MG	17	104	1/1	0.96	0.13	51,51,51,51	0
57	MG	2A	3143	1/1	0.96	0.20	48,48,48,48	0
57	MG	1A	3942	1/1	0.96	0.11	48,48,48,48	0
57	MG	1A	3303	1/1	0.96	0.06	48,48,48,48	0
57	MG	1A	3391	1/1	0.96	0.08	22,22,22,22	0
57	MG	1A	3758	1/1	0.96	0.13	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3420	1/1	0.96	0.10	48,48,48,48	0
57	MG	2A	3149	1/1	0.96	0.16	66,66,66,66	0
57	MG	19	103	1/1	0.96	0.06	68,68,68,68	0
57	MG	1A	3759	1/1	0.96	0.06	24,24,24,24	0
57	MG	1A	3494	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3392	1/1	0.96	0.08	48,48,48,48	0
57	MG	2B	202	1/1	0.96	0.25	69,69,69,69	0
57	MG	1a	1806	1/1	0.96	0.14	64,64,64,64	0
57	MG	1A	3763	1/1	0.96	0.15	54,54,54,54	0
57	MG	1A	3951	1/1	0.96	0.07	50,50,50,50	0
57	MG	2A	3431	1/1	0.96	0.16	51,51,51,51	0
57	MG	1A	3304	1/1	0.96	0.10	32,32,32,32	0
57	MG	2B	208	1/1	0.96	0.11	52,52,52,52	0
57	MG	1A	3306	1/1	0.96	0.18	43,43,43,43	0
57	MG	1a	1608	1/1	0.96	0.08	56,56,56,56	0
57	MG	2A	3161	1/1	0.96	0.19	62,62,62,62	0
57	MG	1A	3766	1/1	0.96	0.05	32,32,32,32	0
57	MG	2A	3164	1/1	0.96	0.11	43,43,43,43	0
57	MG	1A	3221	1/1	0.96	0.15	54,54,54,54	0
57	MG	2B	215	1/1	0.96	0.14	64,64,64,64	0
57	MG	1A	3092	1/1	0.96	0.10	47,47,47,47	0
57	MG	2B	217	1/1	0.96	0.06	69,69,69,69	0
57	MG	1a	1817	1/1	0.96	0.19	66,66,66,66	0
57	MG	1A	3769	1/1	0.96	0.08	40,40,40,40	0
57	MG	2D	305	1/1	0.96	0.13	37,37,37,37	0
57	MG	1A	3503	1/1	0.96	0.06	43,43,43,43	0
57	MG	2D	307	1/1	0.96	0.18	41,41,41,41	0
57	MG	1A	3007	1/1	0.96	0.10	37,37,37,37	0
57	MG	2A	3446	1/1	0.96	0.14	45,45,45,45	0
57	MG	2A	3171	1/1	0.96	0.12	53,53,53,53	0
57	MG	1A	3506	1/1	0.96	0.09	27,27,27,27	0
57	MG	1A	3626	1/1	0.96	0.15	28,28,28,28	0
57	MG	1A	3964	1/1	0.96	0.14	34,34,34,34	0
57	MG	1a	1825	1/1	0.96	0.08	51,51,51,51	0
57	MG	2A	3178	1/1	0.96	0.12	51,51,51,51	0
57	MG	1A	3310	1/1	0.96	0.11	35,35,35,35	0
57	MG	1A	3509	1/1	0.96	0.14	18,18,18,18	0
57	MG	1A	3062	1/1	0.96	0.07	36,36,36,36	0
57	MG	1A	3634	1/1	0.96	0.08	35,35,35,35	0
57	MG	1A	3400	1/1	0.96	0.07	26,26,26,26	0
57	MG	1A	3227	1/1	0.96	0.05	40,40,40,40	0
57	MG	1A	3313	1/1	0.96	0.15	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3977	1/1	0.96	0.08	55,55,55,55	0
57	MG	1A	3978	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3132	1/1	0.96	0.12	46,46,46,46	0
57	MG	1A	3520	1/1	0.96	0.08	48,48,48,48	0
57	MG	1A	3981	1/1	0.96	0.07	24,24,24,24	0
57	MG	1A	3642	1/1	0.96	0.13	45,45,45,45	0
57	MG	1a	1842	1/1	0.96	0.06	58,58,58,58	0
57	MG	1A	3229	1/1	0.96	0.08	39,39,39,39	0
57	MG	1a	1845	1/1	0.96	0.06	64,64,64,64	0
57	MG	1A	3045	1/1	0.96	0.09	23,23,23,23	0
57	MG	2W	201	1/1	0.96	0.23	45,45,45,45	0
57	MG	1A	3986	1/1	0.96	0.06	45,45,45,45	0
57	MG	1A	3407	1/1	0.96	0.06	40,40,40,40	0
57	MG	2A	3200	1/1	0.96	0.11	51,51,51,51	0
57	MG	2A	3479	1/1	0.96	0.07	57,57,57,57	0
57	MG	1a	1642	1/1	0.96	0.17	58,58,58,58	0
57	MG	1A	3647	1/1	0.96	0.06	31,31,31,31	0
57	MG	1A	3409	1/1	0.96	0.05	25,25,25,25	0
57	MG	1A	3525	1/1	0.96	0.07	39,39,39,39	0
57	MG	1a	1853	1/1	0.96	0.16	50,50,50,50	0
57	MG	1a	1855	1/1	0.96	0.10	60,60,60,60	0
57	MG	1a	1647	1/1	0.96	0.13	50,50,50,50	0
57	MG	1A	3034	1/1	0.96	0.05	40,40,40,40	0
57	MG	1A	3794	1/1	0.96	0.12	24,24,24,24	0
57	MG	1A	3652	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3796	1/1	0.96	0.06	41,41,41,41	0
57	MG	2A	3212	1/1	0.96	0.05	43,43,43,43	0
57	MG	1A	3653	1/1	0.96	0.14	41,41,41,41	0
57	MG	1A	3799	1/1	0.96	0.12	54,54,54,54	0
57	MG	1a	1655	1/1	0.96	0.12	50,50,50,50	0
57	MG	1A	3411	1/1	0.96	0.06	29,29,29,29	0
57	MG	1A	3801	1/1	0.96	0.09	31,31,31,31	0
57	MG	2a	3010	1/1	0.96	0.09	52,52,52,52	0
57	MG	2a	3011	1/1	0.96	0.08	62,62,62,62	0
57	MG	1A	3802	1/1	0.96	0.07	43,43,43,43	0
57	MG	1A	3655	1/1	0.96	0.06	23,23,23,23	0
57	MG	1A	3234	1/1	0.96	0.14	34,34,34,34	0
57	MG	2A	3221	1/1	0.96	0.12	50,50,50,50	0
57	MG	1A	3136	1/1	0.96	0.10	43,43,43,43	0
57	MG	1A	4005	1/1	0.96	0.06	30,30,30,30	0
57	MG	1A	3417	1/1	0.96	0.09	25,25,25,25	0
57	MG	1a	1665	1/1	0.96	0.07	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3021	1/1	0.96	0.09	50,50,50,50	0
57	MG	1A	3180	1/1	0.96	0.17	21,21,21,21	0
57	MG	1A	4010	1/1	0.96	0.09	57,57,57,57	0
57	MG	1A	4014	1/1	0.96	0.06	40,40,40,40	0
57	MG	1A	3811	1/1	0.96	0.09	34,34,34,34	0
57	MG	1A	4017	1/1	0.96	0.20	29,29,29,29	0
57	MG	1A	3663	1/1	0.96	0.10	29,29,29,29	0
57	MG	2A	3518	1/1	0.96	0.06	65,65,65,65	0
57	MG	1A	3137	1/1	0.96	0.07	39,39,39,39	0
57	MG	1A	3420	1/1	0.96	0.09	14,14,14,14	0
57	MG	1A	3182	1/1	0.96	0.10	28,28,28,28	0
57	MG	1A	3183	1/1	0.96	0.10	55,55,55,55	0
57	MG	1A	3328	1/1	0.96	0.13	48,48,48,48	0
57	MG	1A	3426	1/1	0.96	0.09	28,28,28,28	0
57	MG	2A	3239	1/1	0.96	0.12	54,54,54,54	0
57	MG	2A	3528	1/1	0.96	0.06	39,39,39,39	0
57	MG	1A	3184	1/1	0.96	0.31	40,40,40,40	0
57	MG	1A	4029	1/1	0.96	0.06	52,52,52,52	0
57	MG	1A	3140	1/1	0.96	0.07	44,44,44,44	0
57	MG	1n	101	1/1	0.96	0.13	55,55,55,55	0
57	MG	2a	3042	1/1	0.96	0.20	48,48,48,48	0
57	MG	1A	3822	1/1	0.96	0.07	38,38,38,38	0
57	MG	1A	3672	1/1	0.96	0.12	51,51,51,51	0
57	MG	2A	3247	1/1	0.96	0.08	47,47,47,47	0
57	MG	2A	3248	1/1	0.96	0.07	43,43,43,43	0
57	MG	1A	3430	1/1	0.96	0.06	54,54,54,54	0
57	MG	1A	3545	1/1	0.96	0.07	37,37,37,37	0
57	MG	1A	3334	1/1	0.96	0.19	40,40,40,40	0
57	MG	1A	3049	1/1	0.96	0.09	38,38,38,38	0
57	MG	1A	3189	1/1	0.96	0.15	35,35,35,35	0
57	MG	1y	203	1/1	0.96	0.08	68,68,68,68	0
57	MG	1A	3142	1/1	0.96	0.08	51,51,51,51	0
57	MG	2A	3260	1/1	0.96	0.25	55,55,55,55	0
57	MG	1a	1689	1/1	0.96	0.15	45,45,45,45	0
57	MG	1A	3680	1/1	0.96	0.06	38,38,38,38	0
57	MG	1A	3254	1/1	0.96	0.29	34,34,34,34	0
57	MG	1A	3256	1/1	0.96	0.22	45,45,45,45	0
57	MG	1a	1693	1/1	0.96	0.17	58,58,58,58	0
57	MG	1B	216	1/1	0.96	0.11	44,44,44,44	0
57	MG	1A	3684	1/1	0.96	0.06	51,51,51,51	0
57	MG	1A	3840	1/1	0.96	0.09	36,36,36,36	0
57	MG	2a	3063	1/1	0.96	0.29	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3257	1/1	0.96	0.22	44,44,44,44	0
57	MG	1A	3556	1/1	0.96	0.09	54,54,54,54	0
57	MG	1A	3444	1/1	0.96	0.10	24,24,24,24	0
57	MG	2a	3067	1/1	0.96	0.18	54,54,54,54	0
57	MG	1B	225	1/1	0.96	0.06	57,57,57,57	0
57	MG	2A	3016	1/1	0.96	0.29	42,42,42,42	0
57	MG	1A	3690	1/1	0.96	0.11	30,30,30,30	0
57	MG	2A	3563	1/1	0.96	0.07	74,74,74,74	0
57	MG	2a	3072	1/1	0.96	0.25	40,40,40,40	0
57	MG	1A	3084	1/1	0.96	0.28	40,40,40,40	0
57	MG	2A	3280	1/1	0.96	0.18	48,48,48,48	0
57	MG	1A	3852	1/1	0.96	0.11	49,49,49,49	0
57	MG	2A	3282	1/1	0.96	0.07	42,42,42,42	0
57	MG	2a	3077	1/1	0.96	0.14	49,49,49,49	0
57	MG	2a	3078	1/1	0.96	0.13	62,62,62,62	0
57	MG	2a	3079	1/1	0.96	0.39	59,59,59,59	0
57	MG	1A	3446	1/1	0.96	0.16	36,36,36,36	0
57	MG	1D	304	1/1	0.96	0.06	36,36,36,36	0
57	MG	1A	3145	1/1	0.96	0.06	38,38,38,38	0
57	MG	1A	3856	1/1	0.96	0.06	29,29,29,29	0
57	MG	1A	3067	1/1	0.96	0.09	42,42,42,42	0
57	MG	1A	3195	1/1	0.96	0.13	30,30,30,30	0
57	MG	2A	3289	1/1	0.96	0.14	38,38,38,38	0
57	MG	2A	3290	1/1	0.96	0.21	43,43,43,43	0
57	MG	2a	3089	1/1	0.96	0.19	53,53,53,53	0
57	MG	1A	3196	1/1	0.96	0.22	44,44,44,44	0
57	MG	1A	3453	1/1	0.96	0.10	44,44,44,44	0
57	MG	1A	3568	1/1	0.96	0.13	38,38,38,38	0
57	MG	1A	3039	1/1	0.96	0.11	39,39,39,39	0
57	MG	1a	1714	1/1	0.96	0.14	56,56,56,56	0
57	MG	2A	3296	1/1	0.96	0.25	58,58,58,58	0
57	MG	1A	3455	1/1	0.96	0.07	28,28,28,28	0
57	MG	1A	3152	1/1	0.96	0.10	39,39,39,39	0
57	MG	1A	3871	1/1	0.96	0.06	36,36,36,36	0
57	MG	2A	3592	1/1	0.96	0.08	60,60,60,60	0
57	MG	2A	3301	1/1	0.96	0.06	56,56,56,56	0
57	MG	2A	3594	1/1	0.96	0.07	61,61,61,61	0
57	MG	1A	3704	1/1	0.96	0.07	52,52,52,52	0
57	MG	2a	3104	1/1	0.96	0.14	56,56,56,56	0
57	MG	1F	305	1/1	0.96	0.12	37,37,37,37	0
57	MG	2a	3106	1/1	0.96	0.36	60,60,60,60	0
57	MG	1A	3873	1/1	0.96	0.06	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1F	309	1/1	0.96	0.19	47,47,47,47	0
57	MG	1A	3705	1/1	0.96	0.10	57,57,57,57	0
57	MG	1A	3020	1/1	0.96	0.29	35,35,35,35	0
57	MG	1A	3573	1/1	0.96	0.07	43,43,43,43	0
57	MG	1A	3708	1/1	0.96	0.05	34,34,34,34	0
57	MG	1A	3878	1/1	0.96	0.06	46,46,46,46	0
57	MG	1A	3880	1/1	0.96	0.05	27,27,27,27	0
57	MG	2A	3052	1/1	0.96	0.24	60,60,60,60	0
57	MG	2a	3117	1/1	0.96	0.06	77,77,77,77	0
57	MG	1A	3268	1/1	0.96	0.07	40,40,40,40	0
57	MG	1H	201	1/1	0.96	0.06	51,51,51,51	0
57	MG	2A	3056	1/1	0.96	0.08	38,38,38,38	0
57	MG	2A	3317	1/1	0.96	0.21	59,59,59,59	0
57	MG	2A	3318	1/1	0.96	0.09	51,51,51,51	0
57	MG	1H	202	1/1	0.96	0.10	61,61,61,61	0
57	MG	1N	201	1/1	0.96	0.10	44,44,44,44	0
57	MG	1a	1735	1/1	0.96	0.07	55,55,55,55	0
57	MG	1A	3882	1/1	0.96	0.11	34,34,34,34	0
57	MG	1A	3883	1/1	0.96	0.06	24,24,24,24	0
57	MG	2A	3324	1/1	0.96	0.23	73,73,73,73	0
57	MG	1a	1738	1/1	0.96	0.09	33,33,33,33	0
57	MG	1A	3154	1/1	0.96	0.10	45,45,45,45	0
57	MG	1A	3156	1/1	0.96	0.07	35,35,35,35	0
57	MG	2A	3623	1/1	0.96	0.07	50,50,50,50	0
57	MG	2A	3069	1/1	0.96	0.08	51,51,51,51	0
57	MG	1A	3114	1/1	0.96	0.12	36,36,36,36	0
57	MG	2A	3331	1/1	0.96	0.17	60,60,60,60	0
57	MG	2A	3071	1/1	0.96	0.06	45,45,45,45	0
57	MG	1a	1744	1/1	0.96	0.17	60,60,60,60	0
57	MG	2a	3139	1/1	0.96	0.15	67,67,67,67	0
57	MG	2A	3073	1/1	0.96	0.09	48,48,48,48	0
57	MG	2A	3074	1/1	0.96	0.07	52,52,52,52	0
57	MG	1P	203	1/1	0.96	0.12	37,37,37,37	0
57	MG	2a	3143	1/1	0.96	0.07	68,68,68,68	0
57	MG	2A	3642	1/1	0.96	0.05	50,50,50,50	0
57	MG	1Q	201	1/1	0.96	0.05	28,28,28,28	0
57	MG	2a	3147	1/1	0.96	0.15	51,51,51,51	0
57	MG	1A	3714	1/1	0.96	0.10	45,45,45,45	0
57	MG	1A	3158	1/1	0.96	0.21	40,40,40,40	0
57	MG	2A	3079	1/1	0.96	0.13	48,48,48,48	0
57	MG	1A	3073	1/1	0.96	0.06	27,27,27,27	0
57	MG	1A	3581	1/1	0.96	0.06	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3349	1/1	0.96	0.05	41,41,41,41	0
57	MG	1A	3206	1/1	0.96	0.08	46,46,46,46	0
57	MG	1A	3160	1/1	0.96	0.09	33,33,33,33	0
57	MG	2A	3656	1/1	0.96	0.09	58,58,58,58	0
57	MG	2a	3157	1/1	0.96	0.07	66,66,66,66	0
57	MG	1A	3283	1/1	0.96	0.05	40,40,40,40	0
57	MG	1A	3898	1/1	0.96	0.12	40,40,40,40	0
57	MG	1a	1755	1/1	0.96	0.11	54,54,54,54	0
57	MG	2A	3088	1/1	0.96	0.07	49,49,49,49	0
57	MG	2a	3164	1/1	0.96	0.12	61,61,61,61	0
57	MG	1A	3472	1/1	0.96	0.07	44,44,44,44	0
57	MG	2A	3666	1/1	0.96	0.07	62,62,62,62	0
57	MG	1A	3901	1/1	0.96	0.06	37,37,37,37	0
57	MG	2A	3668	1/1	0.96	0.08	42,42,42,42	0
57	MG	1A	3902	1/1	0.96	0.06	21,21,21,21	0
57	MG	1U	203	1/1	0.96	0.23	35,35,35,35	0
57	MG	2A	3360	1/1	0.96	0.08	51,51,51,51	0
57	MG	1U	205	1/1	0.96	0.19	37,37,37,37	0
57	MG	2A	3673	1/1	0.96	0.06	43,43,43,43	0
57	MG	1A	3286	1/1	0.96	0.08	45,45,45,45	0
57	MG	1A	3726	1/1	0.96	0.05	30,30,30,30	0
57	MG	2A	3097	1/1	0.96	0.12	56,56,56,56	0
57	MG	1A	3727	1/1	0.96	0.09	31,31,31,31	0
57	MG	2A	3367	1/1	0.96	0.14	55,55,55,55	0
57	MG	1A	3210	1/1	0.96	0.24	55,55,55,55	0
57	MG	2A	3683	1/1	0.96	0.06	56,56,56,56	0
57	MG	2A	3369	1/1	0.96	0.09	58,58,58,58	0
57	MG	1A	3371	1/1	0.96	0.11	67,67,67,67	0
57	MG	1A	3161	1/1	0.96	0.13	34,34,34,34	0
57	MG	1A	3163	1/1	0.96	0.23	28,28,28,28	0
57	MG	1A	3480	1/1	0.96	0.06	61,61,61,61	0
57	MG	1A	3597	1/1	0.96	0.09	23,23,23,23	0
57	MG	1A	3918	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3214	1/1	0.96	0.21	49,49,49,49	0
57	MG	1A	3123	1/1	0.96	0.10	35,35,35,35	0
57	MG	10	105	1/1	0.96	0.07	46,46,46,46	0
57	MG	1A	3057	1/1	0.96	0.16	47,47,47,47	0
57	MG	2A	3117	1/1	0.96	0.08	40,40,40,40	0
57	MG	1A	3605	1/1	0.96	0.07	44,44,44,44	0
57	MG	1a	1779	1/1	0.96	0.16	63,63,63,63	0
57	MG	2A	3700	1/1	0.96	0.06	49,49,49,49	0
57	MG	1A	3924	1/1	0.96	0.09	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3741	1/1	0.96	0.07	35,35,35,35	0
57	MG	1A	3742	1/1	0.96	0.10	36,36,36,36	0
57	MG	1A	3385	1/1	0.96	0.07	45,45,45,45	0
57	MG	13	101	1/1	0.96	0.10	27,27,27,27	0
57	MG	1A	3218	1/1	0.96	0.35	38,38,38,38	0
57	MG	2A	3398	1/1	0.96	0.14	46,46,46,46	0
57	MG	1A	3301	1/1	0.96	0.07	29,29,29,29	0
57	MG	1A	3749	1/1	0.96	0.10	48,48,48,48	0
57	MG	2A	3276	1/1	0.97	0.07	39,39,39,39	0
57	MG	1A	3879	1/1	0.97	0.15	26,26,26,26	0
57	MG	1A	3518	1/1	0.97	0.10	20,20,20,20	0
57	MG	2E	302	1/1	0.97	0.08	41,41,41,41	0
57	MG	1a	1639	1/1	0.97	0.10	53,53,53,53	0
57	MG	1A	3421	1/1	0.97	0.05	18,18,18,18	0
57	MG	2A	3080	1/1	0.97	0.07	35,35,35,35	0
57	MG	1B	208	1/1	0.97	0.07	46,46,46,46	0
57	MG	1A	3624	1/1	0.97	0.08	55,55,55,55	0
57	MG	1A	3269	1/1	0.97	0.14	30,30,30,30	0
57	MG	1a	1802	1/1	0.97	0.12	49,49,49,49	0
57	MG	1A	3033	1/1	0.97	0.05	39,39,39,39	0
57	MG	1A	3748	1/1	0.97	0.06	28,28,28,28	0
57	MG	1a	1646	1/1	0.97	0.09	51,51,51,51	0
57	MG	1A	3888	1/1	0.97	0.07	33,33,33,33	0
57	MG	1A	3628	1/1	0.97	0.21	30,30,30,30	0
57	MG	1A	3059	1/1	0.97	0.10	50,50,50,50	0
57	MG	2P	202	1/1	0.97	0.06	55,55,55,55	0
57	MG	1A	3631	1/1	0.97	0.14	30,30,30,30	0
57	MG	2Q	202	1/1	0.97	0.31	57,57,57,57	0
57	MG	1B	219	1/1	0.97	0.05	27,27,27,27	0
57	MG	2A	3525	1/1	0.97	0.07	64,64,64,64	0
57	MG	1A	3130	1/1	0.97	0.03	26,26,26,26	0
57	MG	2A	3527	1/1	0.97	0.06	60,60,60,60	0
57	MG	1a	1812	1/1	0.97	0.10	62,62,62,62	0
57	MG	1B	221	1/1	0.97	0.05	48,48,48,48	0
57	MG	2A	3096	1/1	0.97	0.12	42,42,42,42	0
57	MG	1B	222	1/1	0.97	0.05	38,38,38,38	0
57	MG	2W	203	1/1	0.97	0.10	60,60,60,60	0
57	MG	1A	3274	1/1	0.97	0.10	36,36,36,36	0
57	MG	1A	3276	1/1	0.97	0.12	26,26,26,26	0
57	MG	1A	3087	1/1	0.97	0.40	40,40,40,40	0
57	MG	2A	3101	1/1	0.97	0.05	37,37,37,37	0
57	MG	2A	3103	1/1	0.97	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	21	104	1/1	0.97	0.13	51,51,51,51	0
57	MG	1A	3431	1/1	0.97	0.07	21,21,21,21	0
57	MG	1A	3017	1/1	0.97	0.23	29,29,29,29	0
57	MG	1A	3279	1/1	0.97	0.06	47,47,47,47	0
57	MG	1A	3434	1/1	0.97	0.04	25,25,25,25	0
57	MG	1A	3061	1/1	0.97	0.10	36,36,36,36	0
57	MG	1A	3436	1/1	0.97	0.04	35,35,35,35	0
57	MG	1A	3437	1/1	0.97	0.06	35,35,35,35	0
57	MG	2a	3001	1/1	0.97	0.09	42,42,42,42	0
57	MG	2A	3312	1/1	0.97	0.07	38,38,38,38	0
57	MG	2A	3112	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3113	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3177	1/1	0.97	0.09	29,29,29,29	0
57	MG	1D	310	1/1	0.97	0.12	23,23,23,23	0
57	MG	1A	3906	1/1	0.97	0.07	49,49,49,49	0
57	MG	2A	3551	1/1	0.97	0.06	67,67,67,67	0
57	MG	1A	3018	1/1	0.97	0.14	26,26,26,26	0
57	MG	1a	1832	1/1	0.97	0.14	54,54,54,54	0
57	MG	2A	3120	1/1	0.97	0.09	54,54,54,54	0
57	MG	2A	3121	1/1	0.97	0.11	39,39,39,39	0
57	MG	2a	3013	1/1	0.97	0.05	48,48,48,48	0
57	MG	1A	3285	1/1	0.97	0.05	37,37,37,37	0
57	MG	1A	3649	1/1	0.97	0.07	56,56,56,56	0
57	MG	1A	3442	1/1	0.97	0.04	28,28,28,28	0
57	MG	1E	301	1/1	0.97	0.12	35,35,35,35	0
57	MG	2A	3326	1/1	0.97	0.10	54,54,54,54	0
57	MG	2A	3562	1/1	0.97	0.06	52,52,52,52	0
57	MG	1A	3135	1/1	0.97	0.19	33,33,33,33	0
57	MG	1A	3288	1/1	0.97	0.07	22,22,22,22	0
57	MG	1A	3916	1/1	0.97	0.06	40,40,40,40	0
57	MG	2a	3023	1/1	0.97	0.06	39,39,39,39	0
57	MG	2A	3130	1/1	0.97	0.18	46,46,46,46	0
57	MG	1A	3542	1/1	0.97	0.09	57,57,57,57	0
57	MG	2A	3332	1/1	0.97	0.05	28,28,28,28	0
57	MG	1A	3226	1/1	0.97	0.15	32,32,32,32	0
57	MG	1A	3019	1/1	0.97	0.18	25,25,25,25	0
57	MG	1A	3921	1/1	0.97	0.09	53,53,53,53	0
57	MG	2A	3573	1/1	0.97	0.06	56,56,56,56	0
57	MG	1F	311	1/1	0.97	0.09	49,49,49,49	0
57	MG	1A	3657	1/1	0.97	0.12	33,33,33,33	0
57	MG	2A	3340	1/1	0.97	0.18	39,39,39,39	0
57	MG	2A	3578	1/1	0.97	0.08	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3341	1/1	0.97	0.10	49,49,49,49	0
57	MG	1A	3547	1/1	0.97	0.25	21,21,21,21	0
57	MG	1A	3064	1/1	0.97	0.07	28,28,28,28	0
57	MG	1A	3925	1/1	0.97	0.07	58,58,58,58	0
57	MG	1A	3361	1/1	0.97	0.08	28,28,28,28	0
57	MG	1A	3138	1/1	0.97	0.13	26,26,26,26	0
57	MG	1A	3363	1/1	0.97	0.09	35,35,35,35	0
57	MG	2A	3144	1/1	0.97	0.06	41,41,41,41	0
57	MG	1a	1854	1/1	0.97	0.06	56,56,56,56	0
57	MG	1A	3139	1/1	0.97	0.22	28,28,28,28	0
57	MG	1A	3231	1/1	0.97	0.07	35,35,35,35	0
57	MG	1A	3295	1/1	0.97	0.07	53,53,53,53	0
57	MG	1A	3298	1/1	0.97	0.11	45,45,45,45	0
57	MG	2A	3595	1/1	0.97	0.09	48,48,48,48	0
57	MG	1A	3372	1/1	0.97	0.10	26,26,26,26	0
57	MG	1A	3458	1/1	0.97	0.07	40,40,40,40	0
57	MG	1A	3459	1/1	0.97	0.05	58,58,58,58	0
57	MG	1A	3299	1/1	0.97	0.07	28,28,28,28	0
57	MG	2A	3600	1/1	0.97	0.05	38,38,38,38	0
57	MG	1A	3093	1/1	0.97	0.18	32,32,32,32	0
57	MG	1A	3375	1/1	0.97	0.08	28,28,28,28	0
57	MG	1A	3463	1/1	0.97	0.06	40,40,40,40	0
57	MG	1A	3566	1/1	0.97	0.05	30,30,30,30	0
57	MG	1Q	205	1/1	0.97	0.08	51,51,51,51	0
57	MG	1A	3377	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3797	1/1	0.97	0.05	34,34,34,34	0
57	MG	1A	3465	1/1	0.97	0.07	50,50,50,50	0
57	MG	2A	3609	1/1	0.97	0.05	29,29,29,29	0
57	MG	2A	3163	1/1	0.97	0.15	50,50,50,50	0
57	MG	1b	301	1/1	0.97	0.12	60,60,60,60	0
57	MG	1A	3947	1/1	0.97	0.06	24,24,24,24	0
57	MG	1A	3187	1/1	0.97	0.21	37,37,37,37	0
57	MG	2A	3373	1/1	0.97	0.07	28,28,28,28	0
57	MG	2A	3375	1/1	0.97	0.08	44,44,44,44	0
57	MG	1A	3235	1/1	0.97	0.15	28,28,28,28	0
57	MG	1A	3681	1/1	0.97	0.11	56,56,56,56	0
57	MG	1A	3380	1/1	0.97	0.06	25,25,25,25	0
57	MG	1A	3381	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3382	1/1	0.97	0.07	51,51,51,51	0
57	MG	1A	3805	1/1	0.97	0.11	55,55,55,55	0
57	MG	1A	3685	1/1	0.97	0.06	44,44,44,44	0
57	MG	1A	3006	1/1	0.97	0.05	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3013	1/1	0.97	0.04	20,20,20,20	0
57	MG	2A	3625	1/1	0.97	0.05	58,58,58,58	0
57	MG	2A	3177	1/1	0.97	0.07	61,61,61,61	0
57	MG	1g	202	1/1	0.97	0.06	55,55,55,55	0
57	MG	2A	3629	1/1	0.97	0.12	54,54,54,54	0
57	MG	1A	3238	1/1	0.97	0.15	32,32,32,32	0
57	MG	2A	3632	1/1	0.97	0.07	38,38,38,38	0
57	MG	1A	3812	1/1	0.97	0.10	51,51,51,51	0
57	MG	1A	3577	1/1	0.97	0.12	41,41,41,41	0
57	MG	2A	3393	1/1	0.97	0.13	39,39,39,39	0
57	MG	1A	3040	1/1	0.97	0.10	38,38,38,38	0
57	MG	2A	3640	1/1	0.97	0.08	56,56,56,56	0
57	MG	1A	3240	1/1	0.97	0.14	22,22,22,22	0
57	MG	1A	3023	1/1	0.97	0.07	28,28,28,28	0
57	MG	1A	3024	1/1	0.97	0.10	27,27,27,27	0
57	MG	10	102	1/1	0.97	0.09	29,29,29,29	0
57	MG	1A	3243	1/1	0.97	0.19	35,35,35,35	0
57	MG	2A	3649	1/1	0.97	0.05	49,49,49,49	0
57	MG	2A	3403	1/1	0.97	0.18	54,54,54,54	0
57	MG	1A	3970	1/1	0.97	0.08	37,37,37,37	0
57	MG	2A	3189	1/1	0.97	0.13	53,53,53,53	0
57	MG	1A	3583	1/1	0.97	0.14	49,49,49,49	0
57	MG	1A	3697	1/1	0.97	0.14	52,52,52,52	0
57	MG	1a	1729	1/1	0.97	0.08	42,42,42,42	0
57	MG	2A	3658	1/1	0.97	0.05	41,41,41,41	0
57	MG	1a	1730	1/1	0.97	0.10	39,39,39,39	0
57	MG	1A	3244	1/1	0.97	0.13	33,33,33,33	0
57	MG	2A	3195	1/1	0.97	0.08	54,54,54,54	0
57	MG	2a	3107	1/1	0.97	0.29	64,64,64,64	0
57	MG	1A	3585	1/1	0.97	0.07	47,47,47,47	0
57	MG	1A	3150	1/1	0.97	0.10	24,24,24,24	0
57	MG	1A	3587	1/1	0.97	0.07	13,13,13,13	0
57	MG	1A	3826	1/1	0.97	0.10	21,21,21,21	0
57	MG	1A	3588	1/1	0.97	0.05	29,29,29,29	0
57	MG	1A	3828	1/1	0.97	0.07	36,36,36,36	0
57	MG	2A	3005	1/1	0.97	0.15	38,38,38,38	0
57	MG	1A	3194	1/1	0.97	0.12	27,27,27,27	0
57	MG	1a	1740	1/1	0.97	0.11	37,37,37,37	0
57	MG	1A	3315	1/1	0.97	0.18	34,34,34,34	0
57	MG	15	3103	1/1	0.97	0.15	30,30,30,30	0
57	MG	2A	3010	1/1	0.97	0.12	48,48,48,48	0
57	MG	1A	3984	1/1	0.97	0.07	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3677	1/1	0.97	0.06	54,54,54,54	0
57	MG	2A	3013	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3317	1/1	0.97	0.19	35,35,35,35	0
57	MG	2A	3680	1/1	0.97	0.11	47,47,47,47	0
57	MG	1A	3592	1/1	0.97	0.06	35,35,35,35	0
57	MG	1A	3044	1/1	0.97	0.07	31,31,31,31	0
57	MG	2A	3017	1/1	0.97	0.13	54,54,54,54	0
57	MG	2A	3433	1/1	0.97	0.08	63,63,63,63	0
57	MG	1A	3709	1/1	0.97	0.14	48,48,48,48	0
57	MG	1A	3106	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3025	1/1	0.97	0.16	38,38,38,38	0
57	MG	1A	3014	1/1	0.97	0.08	43,43,43,43	0
57	MG	2A	3438	1/1	0.97	0.07	34,34,34,34	0
57	MG	17	103	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3255	1/1	0.97	0.12	28,28,28,28	0
57	MG	17	105	1/1	0.97	0.06	40,40,40,40	0
57	MG	1A	3109	1/1	0.97	0.13	32,32,32,32	0
57	MG	1A	3028	1/1	0.97	0.18	25,25,25,25	0
57	MG	2A	3696	1/1	0.97	0.08	46,46,46,46	0
57	MG	2A	3028	1/1	0.97	0.08	31,31,31,31	0
57	MG	1a	1757	1/1	0.97	0.07	61,61,61,61	0
57	MG	2A	3699	1/1	0.97	0.04	37,37,37,37	0
57	MG	1A	3030	1/1	0.97	0.07	25,25,25,25	0
57	MG	2A	3447	1/1	0.97	0.06	51,51,51,51	0
57	MG	1a	1759	1/1	0.97	0.11	58,58,58,58	0
57	MG	1A	3717	1/1	0.97	0.07	54,54,54,54	0
57	MG	1A	3848	1/1	0.97	0.06	29,29,29,29	0
57	MG	2A	3034	1/1	0.97	0.13	64,64,64,64	0
57	MG	2A	3452	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3035	1/1	0.97	0.10	45,45,45,45	0
57	MG	1A	3849	1/1	0.97	0.18	43,43,43,43	0
57	MG	2A	3455	1/1	0.97	0.07	53,53,53,53	0
57	MG	2A	3037	1/1	0.97	0.18	52,52,52,52	0
57	MG	1A	3850	1/1	0.97	0.06	53,53,53,53	0
57	MG	2A	3458	1/1	0.97	0.09	56,56,56,56	0
57	MG	2A	3039	1/1	0.97	0.06	27,27,27,27	0
57	MG	1A	3602	1/1	0.97	0.08	48,48,48,48	0
57	MG	1A	3603	1/1	0.97	0.07	36,36,36,36	0
57	MG	2A	3462	1/1	0.97	0.05	46,46,46,46	0
57	MG	1A	3854	1/1	0.97	0.04	42,42,42,42	0
57	MG	1A	3604	1/1	0.97	0.14	42,42,42,42	0
57	MG	1A	3722	1/1	0.97	0.08	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	4007	1/1	0.97	0.31	43,43,43,43	0
57	MG	1A	3857	1/1	0.97	0.14	38,38,38,38	0
57	MG	1A	4009	1/1	0.97	0.05	50,50,50,50	0
57	MG	1A	3500	1/1	0.97	0.05	21,21,21,21	0
57	MG	1a	1612	1/1	0.97	0.07	27,27,27,27	0
57	MG	2A	3246	1/1	0.97	0.18	38,38,38,38	0
57	MG	1A	4011	1/1	0.97	0.07	38,38,38,38	0
57	MG	1A	3081	1/1	0.97	0.05	34,34,34,34	0
57	MG	2A	3249	1/1	0.97	0.15	52,52,52,52	0
57	MG	2A	3250	1/1	0.97	0.09	29,29,29,29	0
57	MG	1A	3408	1/1	0.97	0.08	28,28,28,28	0
57	MG	2A	3252	1/1	0.97	0.07	46,46,46,46	0
57	MG	2A	3478	1/1	0.97	0.09	33,33,33,33	0
57	MG	1A	3121	1/1	0.97	0.10	18,18,18,18	0
57	MG	1A	3053	1/1	0.97	0.10	29,29,29,29	0
57	MG	2a	3182	1/1	0.97	0.07	57,57,57,57	0
57	MG	1A	3124	1/1	0.97	0.05	35,35,35,35	0
57	MG	2A	3058	1/1	0.97	0.10	38,38,38,38	0
57	MG	2a	3185	1/1	0.97	0.08	57,57,57,57	0
57	MG	1a	1620	1/1	0.97	0.04	47,47,47,47	0
57	MG	1A	3867	1/1	0.97	0.09	41,41,41,41	0
57	MG	2A	3486	1/1	0.97	0.07	47,47,47,47	0
57	MG	1A	3332	1/1	0.97	0.07	52,52,52,52	0
57	MG	2A	3488	1/1	0.97	0.05	45,45,45,45	0
57	MG	1A	3508	1/1	0.97	0.06	46,46,46,46	0
57	MG	2A	3262	1/1	0.97	0.16	45,45,45,45	0
57	MG	2A	3063	1/1	0.97	0.08	46,46,46,46	0
57	MG	2A	3264	1/1	0.97	0.30	36,36,36,36	0
57	MG	1A	3054	1/1	0.97	0.19	24,24,24,24	0
57	MG	1A	3510	1/1	0.97	0.08	25,25,25,25	0
57	MG	1A	4026	1/1	0.97	0.10	49,49,49,49	0
57	MG	2D	301	1/1	0.97	0.14	42,42,42,42	0
57	MG	2D	302	1/1	0.97	0.26	33,33,33,33	0
57	MG	1A	3016	1/1	0.97	0.12	35,35,35,35	0
57	MG	1A	4028	1/1	0.97	0.08	44,44,44,44	0
57	MG	1A	3336	1/1	0.97	0.06	23,23,23,23	0
57	MG	1A	3514	1/1	0.97	0.05	24,24,24,24	0
57	MG	1A	3127	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3168	1/1	0.97	0.10	28,28,28,28	0
57	MG	1A	3740	1/1	0.97	0.05	50,50,50,50	0
57	MG	1F	312	1/1	0.98	0.08	34,34,34,34	0
57	MG	1A	3368	1/1	0.98	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
57	MG	1a	1664	1/1	0.98	0.08	52,52,52,52	0
57	MG	1A	3750	1/1	0.98	0.04	16,16,16,16	0
57	MG	1a	1815	1/1	0.98	0.16	65,65,65,65	0
57	MG	1A	3036	1/1	0.98	0.03	28,28,28,28	0
57	MG	1A	3851	1/1	0.98	0.03	20,20,20,20	0
57	MG	1A	3223	1/1	0.98	0.04	29,29,29,29	0
57	MG	1A	3099	1/1	0.98	0.09	28,28,28,28	0
57	MG	2A	3427	1/1	0.98	0.04	32,32,32,32	0
57	MG	2A	3428	1/1	0.98	0.08	42,42,42,42	0
57	MG	1A	3967	1/1	0.98	0.05	27,27,27,27	0
57	MG	1A	3155	1/1	0.98	0.19	33,33,33,33	0
57	MG	1A	3969	1/1	0.98	0.06	51,51,51,51	0
57	MG	1A	3316	1/1	0.98	0.06	16,16,16,16	0
57	MG	1N	202	1/1	0.98	0.12	37,37,37,37	0
57	MG	1A	3438	1/1	0.98	0.05	25,25,25,25	0
57	MG	1A	3012	1/1	0.98	0.26	41,41,41,41	0
57	MG	1A	3973	1/1	0.98	0.09	18,18,18,18	0
57	MG	1a	1829	1/1	0.98	0.08	55,55,55,55	0
57	MG	1A	3376	1/1	0.98	0.04	20,20,20,20	0
57	MG	2A	3257	1/1	0.98	0.07	22,22,22,22	0
57	MG	1A	3318	1/1	0.98	0.11	15,15,15,15	0
57	MG	1A	3516	1/1	0.98	0.06	42,42,42,42	0
57	MG	2A	3628	1/1	0.98	0.05	62,62,62,62	0
57	MG	1A	3861	1/1	0.98	0.04	43,43,43,43	0
57	MG	2A	3630	1/1	0.98	0.05	40,40,40,40	0
57	MG	1A	3270	1/1	0.98	0.16	28,28,28,28	0
57	MG	1Q	203	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3864	1/1	0.98	0.06	31,31,31,31	0
57	MG	2A	3635	1/1	0.98	0.06	54,54,54,54	0
57	MG	1A	3673	1/1	0.98	0.07	32,32,32,32	0
57	MG	2A	3637	1/1	0.98	0.11	56,56,56,56	0
57	MG	1a	1838	1/1	0.98	0.10	57,57,57,57	0
57	MG	1A	3101	1/1	0.98	0.16	35,35,35,35	0
57	MG	1A	3102	1/1	0.98	0.25	27,27,27,27	0
57	MG	1R	204	1/1	0.98	0.06	40,40,40,40	0
57	MG	2A	3643	1/1	0.98	0.06	40,40,40,40	0
57	MG	1A	3046	1/1	0.98	0.09	10,10,10,10	0
57	MG	1A	3105	1/1	0.98	0.21	25,25,25,25	0
57	MG	2A	3104	1/1	0.98	0.06	52,52,52,52	0
57	MG	2A	3647	1/1	0.98	0.05	37,37,37,37	0
57	MG	1a	1844	1/1	0.98	0.04	53,53,53,53	0
57	MG	1A	3870	1/1	0.98	0.05	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3987	1/1	0.98	0.04	21,21,21,21	0
57	MG	1A	3275	1/1	0.98	0.17	30,30,30,30	0
57	MG	1A	3384	1/1	0.98	0.04	15,15,15,15	0
57	MG	1A	3005	1/1	0.98	0.09	17,17,17,17	0
57	MG	1U	202	1/1	0.98	0.11	41,41,41,41	0
57	MG	1A	3598	1/1	0.98	0.11	33,33,33,33	0
57	MG	2A	3657	1/1	0.98	0.05	43,43,43,43	0
57	MG	1U	204	1/1	0.98	0.18	27,27,27,27	0
57	MG	1A	3450	1/1	0.98	0.10	21,21,21,21	0
57	MG	2A	3115	1/1	0.98	0.10	45,45,45,45	0
57	MG	1A	3003	1/1	0.98	0.04	26,26,26,26	0
57	MG	2A	3662	1/1	0.98	0.03	38,38,38,38	0
57	MG	1A	3387	1/1	0.98	0.10	16,16,16,16	0
57	MG	1V	201	1/1	0.98	0.08	21,21,21,21	0
57	MG	2A	3665	1/1	0.98	0.05	58,58,58,58	0
57	MG	1a	1858	1/1	0.98	0.06	60,60,60,60	0
57	MG	1A	3233	1/1	0.98	0.13	37,37,37,37	0
57	MG	1V	204	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3996	1/1	0.98	0.04	44,44,44,44	0
57	MG	1V	206	1/1	0.98	0.05	56,56,56,56	0
57	MG	1A	3686	1/1	0.98	0.07	40,40,40,40	0
57	MG	1A	3078	1/1	0.98	0.09	33,33,33,33	0
57	MG	1A	3280	1/1	0.98	0.15	43,43,43,43	0
57	MG	1A	3330	1/1	0.98	0.05	38,38,38,38	0
57	MG	1A	3532	1/1	0.98	0.04	24,24,24,24	0
57	MG	1A	3885	1/1	0.98	0.04	40,40,40,40	0
57	MG	1A	3607	1/1	0.98	0.05	29,29,29,29	0
57	MG	2A	3299	1/1	0.98	0.03	49,49,49,49	0
57	MG	2A	3481	1/1	0.98	0.08	45,45,45,45	0
57	MG	1A	3050	1/1	0.98	0.10	34,34,34,34	0
57	MG	2A	3681	1/1	0.98	0.04	53,53,53,53	0
57	MG	1A	3051	1/1	0.98	0.33	46,46,46,46	0
57	MG	1A	3112	1/1	0.98	0.23	28,28,28,28	0
57	MG	10	106	1/1	0.98	0.03	47,47,47,47	0
57	MG	1A	3536	1/1	0.98	0.07	15,15,15,15	0
57	MG	1A	3787	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3788	1/1	0.98	0.07	39,39,39,39	0
57	MG	1A	3284	1/1	0.98	0.14	32,32,32,32	0
57	MG	1A	3613	1/1	0.98	0.13	39,39,39,39	0
57	MG	1A	4012	1/1	0.98	0.03	32,32,32,32	0
57	MG	11	103	1/1	0.98	0.10	33,33,33,33	0
57	MG	1A	4013	1/1	0.98	0.04	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3494	1/1	0.98	0.10	49,49,49,49	0
57	MG	2a	3088	1/1	0.98	0.17	45,45,45,45	0
57	MG	1A	3113	1/1	0.98	0.11	40,40,40,40	0
57	MG	1A	4015	1/1	0.98	0.07	37,37,37,37	0
57	MG	13	104	1/1	0.98	0.06	37,37,37,37	0
57	MG	2A	3499	1/1	0.98	0.06	56,56,56,56	0
57	MG	2a	3093	1/1	0.98	0.15	45,45,45,45	0
57	MG	1A	3001	1/1	0.98	0.04	31,31,31,31	0
57	MG	1A	3287	1/1	0.98	0.07	27,27,27,27	0
57	MG	2A	3502	1/1	0.98	0.06	49,49,49,49	0
57	MG	1A	4018	1/1	0.98	0.13	47,47,47,47	0
57	MG	1a	1732	1/1	0.98	0.07	40,40,40,40	0
57	MG	2A	3152	1/1	0.98	0.05	38,38,38,38	0
57	MG	2A	3704	1/1	0.98	0.04	22,22,22,22	0
57	MG	2A	3705	1/1	0.98	0.08	42,42,42,42	0
57	MG	1A	3172	1/1	0.98	0.23	31,31,31,31	0
57	MG	1A	3116	1/1	0.98	0.07	39,39,39,39	0
57	MG	1A	3205	1/1	0.98	0.06	46,46,46,46	0
57	MG	1A	3117	1/1	0.98	0.09	31,31,31,31	0
57	MG	1A	3546	1/1	0.98	0.04	23,23,23,23	0
57	MG	1A	3207	1/1	0.98	0.18	45,45,45,45	0
57	MG	1A	3344	1/1	0.98	0.10	25,25,25,25	0
57	MG	2A	3713	1/1	0.98	0.17	46,46,46,46	0
57	MG	1A	3208	1/1	0.98	0.17	42,42,42,42	0
57	MG	1A	3550	1/1	0.98	0.04	23,23,23,23	0
57	MG	1A	3118	1/1	0.98	0.07	36,36,36,36	0
57	MG	1a	1743	1/1	0.98	0.06	58,58,58,58	0
57	MG	1A	3910	1/1	0.98	0.05	29,29,29,29	0
57	MG	1A	3627	1/1	0.98	0.16	30,30,30,30	0
57	MG	1A	3912	1/1	0.98	0.04	26,26,26,26	0
57	MG	1A	3119	1/1	0.98	0.17	31,31,31,31	0
57	MG	2A	3335	1/1	0.98	0.07	60,60,60,60	0
57	MG	1A	3297	1/1	0.98	0.11	17,17,17,17	0
57	MG	1A	3630	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3917	1/1	0.98	0.04	15,15,15,15	0
57	MG	1A	3809	1/1	0.98	0.08	42,42,42,42	0
57	MG	2A	3172	1/1	0.98	0.07	60,60,60,60	0
57	MG	1A	3249	1/1	0.98	0.23	27,27,27,27	0
57	MG	1A	3211	1/1	0.98	0.13	40,40,40,40	0
57	MG	1A	3412	1/1	0.98	0.09	35,35,35,35	0
57	MG	2A	3345	1/1	0.98	0.07	39,39,39,39	0
57	MG	1A	3719	1/1	0.98	0.05	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3144	1/1	0.98	0.18	22,22,22,22	0
57	MG	1B	213	1/1	0.98	0.08	49,49,49,49	0
57	MG	2A	3012	1/1	0.98	0.05	27,27,27,27	0
57	MG	2a	3132	1/1	0.98	0.04	57,57,57,57	0
57	MG	1B	214	1/1	0.98	0.04	33,33,33,33	0
57	MG	1A	3094	1/1	0.98	0.13	26,26,26,26	0
57	MG	1A	3636	1/1	0.98	0.04	42,42,42,42	0
57	MG	1A	3415	1/1	0.98	0.06	20,20,20,20	0
57	MG	1A	3416	1/1	0.98	0.06	23,23,23,23	0
57	MG	1a	1615	1/1	0.98	0.09	56,56,56,56	0
57	MG	1a	1764	1/1	0.98	0.06	60,60,60,60	0
57	MG	1A	3561	1/1	0.98	0.06	33,33,33,33	0
57	MG	1A	3146	1/1	0.98	0.07	32,32,32,32	0
57	MG	1A	3563	1/1	0.98	0.05	24,24,24,24	0
57	MG	1A	3932	1/1	0.98	0.05	53,53,53,53	0
57	MG	1A	3354	1/1	0.98	0.04	22,22,22,22	0
57	MG	2a	3145	1/1	0.98	0.08	68,68,68,68	0
57	MG	1A	3215	1/1	0.98	0.06	34,34,34,34	0
57	MG	1a	1622	1/1	0.98	0.14	49,49,49,49	0
57	MG	2A	3549	1/1	0.98	0.05	54,54,54,54	0
57	MG	2A	3364	1/1	0.98	0.10	55,55,55,55	0
57	MG	2A	3027	1/1	0.98	0.05	41,41,41,41	0
57	MG	1a	1623	1/1	0.98	0.14	54,54,54,54	0
57	MG	1A	3824	1/1	0.98	0.06	49,49,49,49	0
57	MG	1A	3356	1/1	0.98	0.03	30,30,30,30	0
57	MG	1A	3026	1/1	0.98	0.13	26,26,26,26	0
57	MG	1A	3305	1/1	0.98	0.05	31,31,31,31	0
57	MG	1A	3733	1/1	0.98	0.05	25,25,25,25	0
57	MG	1D	301	1/1	0.98	0.12	41,41,41,41	0
57	MG	2a	3158	1/1	0.98	0.08	40,40,40,40	0
57	MG	1D	302	1/1	0.98	0.08	39,39,39,39	0
57	MG	2a	3160	1/1	0.98	0.09	51,51,51,51	0
57	MG	1D	303	1/1	0.98	0.04	33,33,33,33	0
57	MG	1a	1632	1/1	0.98	0.08	35,35,35,35	0
57	MG	1A	3829	1/1	0.98	0.18	30,30,30,30	0
57	MG	1A	3830	1/1	0.98	0.19	34,34,34,34	0
57	MG	1A	3149	1/1	0.98	0.05	26,26,26,26	0
57	MG	1A	3495	1/1	0.98	0.07	50,50,50,50	0
57	MG	2A	3567	1/1	0.98	0.08	58,58,58,58	0
57	MG	2A	3383	1/1	0.98	0.05	37,37,37,37	0
57	MG	2A	3384	1/1	0.98	0.05	36,36,36,36	0
57	MG	1A	3424	1/1	0.98	0.06	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3043	1/1	0.98	0.24	56,56,56,56	0
57	MG	1A	3834	1/1	0.98	0.06	31,31,31,31	0
57	MG	1A	3497	1/1	0.98	0.07	37,37,37,37	0
57	MG	2A	3574	1/1	0.98	0.08	30,30,30,30	0
57	MG	1A	3122	1/1	0.98	0.06	26,26,26,26	0
57	MG	1A	3021	1/1	0.98	0.08	35,35,35,35	0
57	MG	1A	3220	1/1	0.98	0.16	26,26,26,26	0
57	MG	1A	3656	1/1	0.98	0.08	33,33,33,33	0
57	MG	1E	302	1/1	0.98	0.26	38,38,38,38	0
57	MG	2A	3580	1/1	0.98	0.05	53,53,53,53	0
57	MG	2R	201	1/1	0.98	0.06	53,53,53,53	0
57	MG	1E	303	1/1	0.98	0.04	26,26,26,26	0
57	MG	2T	201	1/1	0.98	0.14	59,59,59,59	0
57	MG	1A	3952	1/1	0.98	0.07	38,38,38,38	0
57	MG	2A	3053	1/1	0.98	0.10	44,44,44,44	0
57	MG	2A	3584	1/1	0.98	0.06	52,52,52,52	0
57	MG	1A	3364	1/1	0.98	0.07	27,27,27,27	0
57	MG	1E	306	1/1	0.98	0.07	29,29,29,29	0
57	MG	1A	3055	1/1	0.98	0.10	33,33,33,33	0
57	MG	1E	308	1/1	0.98	0.04	35,35,35,35	0
57	MG	1A	3745	1/1	0.98	0.09	27,27,27,27	0
57	MG	2X	101	1/1	0.98	0.11	54,54,54,54	0
57	MG	1a	1652	1/1	0.98	0.10	58,58,58,58	0
57	MG	2A	3406	1/1	0.98	0.07	44,44,44,44	0
57	MG	1F	301	1/1	0.98	0.09	23,23,23,23	0
57	MG	1F	302	1/1	0.98	0.16	28,28,28,28	0
57	MG	1F	304	1/1	0.98	0.18	30,30,30,30	0
57	MG	1A	3746	1/1	0.98	0.06	44,44,44,44	0
57	MG	1F	306	1/1	0.98	0.04	31,31,31,31	0
57	MG	1A	3263	1/1	0.98	0.12	27,27,27,27	0
57	MG	2A	3233	1/1	0.98	0.27	44,44,44,44	0
57	MG	2A	3066	1/1	0.98	0.17	38,38,38,38	0
57	MG	25	104	1/1	0.98	0.09	57,57,57,57	0
57	MG	1A	3845	1/1	0.98	0.09	52,52,52,52	0
57	MG	1F	310	1/1	0.98	0.06	31,31,31,31	0
60	ZN	14	501	1/1	0.98	0.10	112,112,112,112	0
60	ZN	2Y	202	1/1	0.98	0.05	82,82,82,82	0
57	MG	1A	3660	1/1	0.98	0.12	49,49,49,49	0
60	ZN	29	102	1/1	0.98	0.04	63,63,63,63	0
60	ZN	2n	102	1/1	0.98	0.04	88,88,88,88	0
61	SF4	1d	306	8/8	0.98	0.04	55,64,73,75	0
61	SF4	2d	501	8/8	0.98	0.05	58,70,76,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3250	1/1	0.99	0.15	32,32,32,32	0
57	MG	1A	3165	1/1	0.99	0.04	33,33,33,33	0
57	MG	1F	308	1/1	0.99	0.06	26,26,26,26	0
57	MG	1A	3252	1/1	0.99	0.18	28,28,28,28	0
57	MG	1A	3646	1/1	0.99	0.08	22,22,22,22	0
57	MG	2A	3068	1/1	0.99	0.09	22,22,22,22	0
57	MG	2E	307	1/1	0.99	0.07	33,33,33,33	0
57	MG	1A	3029	1/1	0.99	0.04	27,27,27,27	0
57	MG	1A	3358	1/1	0.99	0.07	34,34,34,34	0
57	MG	1A	3488	1/1	0.99	0.04	40,40,40,40	0
57	MG	2A	3003	1/1	0.99	0.03	40,40,40,40	0
57	MG	2F	304	1/1	0.99	0.08	47,47,47,47	0
57	MG	1A	3735	1/1	0.99	0.05	43,43,43,43	0
57	MG	1A	3452	1/1	0.99	0.05	29,29,29,29	0
57	MG	1A	3490	1/1	0.99	0.04	36,36,36,36	0
57	MG	1A	3491	1/1	0.99	0.07	22,22,22,22	0
57	MG	15	3101	1/1	0.99	0.07	26,26,26,26	0
57	MG	1A	3930	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3015	1/1	0.99	0.05	35,35,35,35	0
57	MG	2A	3371	1/1	0.99	0.05	41,41,41,41	0
57	MG	1A	3104	1/1	0.99	0.06	20,20,20,20	0
57	MG	1A	3333	1/1	0.99	0.07	33,33,33,33	0
57	MG	2A	3374	1/1	0.99	0.08	31,31,31,31	0
57	MG	1A	3934	1/1	0.99	0.07	32,32,32,32	0
57	MG	1A	3068	1/1	0.99	0.07	32,32,32,32	0
57	MG	1A	3170	1/1	0.99	0.05	29,29,29,29	0
57	MG	1A	3048	1/1	0.99	0.08	22,22,22,22	0
57	MG	2A	3379	1/1	0.99	0.08	37,37,37,37	0
57	MG	1A	3884	1/1	0.99	0.03	48,48,48,48	0
57	MG	1A	3365	1/1	0.99	0.06	39,39,39,39	0
57	MG	1P	201	1/1	0.99	0.09	26,26,26,26	0
57	MG	1A	3070	1/1	0.99	0.19	26,26,26,26	0
57	MG	1a	1856	1/1	0.99	0.10	35,35,35,35	0
57	MG	1A	3071	1/1	0.99	0.16	31,31,31,31	0
57	MG	1A	3429	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3043	1/1	0.99	0.07	19,19,19,19	0
57	MG	1A	3369	1/1	0.99	0.08	23,23,23,23	0
57	MG	1A	3543	1/1	0.99	0.06	18,18,18,18	0
57	MG	1A	3031	1/1	0.99	0.09	15,15,15,15	0
57	MG	1R	201	1/1	0.99	0.09	32,32,32,32	0
57	MG	2A	3633	1/1	0.99	0.09	43,43,43,43	0
57	MG	1A	3505	1/1	0.99	0.11	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3111	1/1	0.99	0.16	24,24,24,24	0
57	MG	1A	3846	1/1	0.99	0.04	30,30,30,30	0
57	MG	1A	3074	1/1	0.99	0.05	29,29,29,29	0
57	MG	2A	3102	1/1	0.99	0.05	54,54,54,54	0
57	MG	2A	3397	1/1	0.99	0.04	38,38,38,38	0
57	MG	1A	3897	1/1	0.99	0.04	30,30,30,30	0
57	MG	2A	3641	1/1	0.99	0.08	48,48,48,48	0
57	MG	2A	3400	1/1	0.99	0.03	42,42,42,42	0
57	MG	2A	3560	1/1	0.99	0.04	22,22,22,22	0
57	MG	1A	3265	1/1	0.99	0.12	30,30,30,30	0
57	MG	1D	306	1/1	0.99	0.05	16,16,16,16	0
57	MG	1A	3899	1/1	0.99	0.06	39,39,39,39	0
57	MG	1D	308	1/1	0.99	0.10	30,30,30,30	0
57	MG	1A	3404	1/1	0.99	0.04	40,40,40,40	0
57	MG	1A	3009	1/1	0.99	0.08	24,24,24,24	0
57	MG	1A	3511	1/1	0.99	0.06	35,35,35,35	0
57	MG	1A	3760	1/1	0.99	0.08	31,31,31,31	0
57	MG	1A	3179	1/1	0.99	0.08	29,29,29,29	0
57	MG	2A	3653	1/1	0.99	0.02	34,34,34,34	0
57	MG	1A	3473	1/1	0.99	0.04	20,20,20,20	0
57	MG	1A	3808	1/1	0.99	0.09	26,26,26,26	0
57	MG	1D	316	1/1	0.99	0.05	38,38,38,38	0
57	MG	1V	202	1/1	0.99	0.18	29,29,29,29	0
57	MG	1A	3058	1/1	0.99	0.04	22,22,22,22	0
57	MG	1A	3962	1/1	0.99	0.04	41,41,41,41	0
57	MG	1A	3115	1/1	0.99	0.14	28,28,28,28	0
57	MG	2A	3337	1/1	0.99	0.08	44,44,44,44	0
57	MG	1A	3245	1/1	0.99	0.13	23,23,23,23	0
57	MG	1a	1819	1/1	0.99	0.07	48,48,48,48	0
57	MG	1A	3296	1/1	0.99	0.13	21,21,21,21	0
57	MG	1A	3162	1/1	0.99	0.10	30,30,30,30	0
57	MG	1W	203	1/1	0.99	0.15	25,25,25,25	0
57	MG	1A	3639	1/1	0.99	0.09	28,28,28,28	0
57	MG	1A	3862	1/1	0.99	0.04	33,33,33,33	0
57	MG	1A	3914	1/1	0.99	0.06	33,33,33,33	0
57	MG	2A	3272	1/1	0.99	0.05	38,38,38,38	0
57	MG	2A	3128	1/1	0.99	0.07	29,29,29,29	0
60	ZN	1Y	202	1/1	0.99	0.03	59,59,59,59	0
57	MG	1A	3077	1/1	0.99	0.15	31,31,31,31	0
60	ZN	19	104	1/1	0.99	0.06	42,42,42,42	0
57	MG	1A	3770	1/1	0.99	0.17	32,32,32,32	0
57	MG	2A	3590	1/1	0.99	0.04	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
60	ZN	26	501	1/1	0.99	0.02	56,56,56,56	0
57	MG	1F	303	1/1	0.99	0.15	30,30,30,30	0
57	MG	2A	3132	1/1	0.99	0.10	50,50,50,50	0
57	MG	1A	3147	1/1	0.99	0.03	31,31,31,31	0
57	MG	1A	3185	1/1	0.99	0.05	26,26,26,26	0
57	MG	2A	3399	1/1	1.00	0.03	30,30,30,30	0
60	ZN	1n	104	1/1	1.00	0.02	66,66,66,66	0
57	MG	1A	3700	1/1	1.00	0.05	32,32,32,32	0
57	MG	1A	3974	1/1	1.00	0.02	25,25,25,25	0
60	ZN	25	105	1/1	1.00	0.04	53,53,53,53	0
57	MG	1A	3474	1/1	1.00	0.06	17,17,17,17	0
57	MG	2A	3498	1/1	1.00	0.04	35,35,35,35	0
57	MG	1A	3466	1/1	1.00	0.02	19,19,19,19	0
60	ZN	15	3110	1/1	1.00	0.04	40,40,40,40	0
60	ZN	16	501	1/1	1.00	0.05	41,41,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.