Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:55 AM UTC

PDB ID	:	7RQD / pdb_00007rqd
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with protein Y, A-site deacylated tRNA analog CACCA, P-site MTI-tripeptidyl-tRNA analog ACCA-ITM, and chloramphenicol at 2.50A resolution
Authors	:	Syroegin, E.A.; Flemmich, L.; Klepacki, D.; Vazquez-Laslop, N.; Micura, R.; Polikanov, Y.S.
Deposited on	:	2021-08-06
Resolution	:	2.50 Å(reported)

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

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

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

The following versions of software and data (see references (1)) were used in the production of this report:

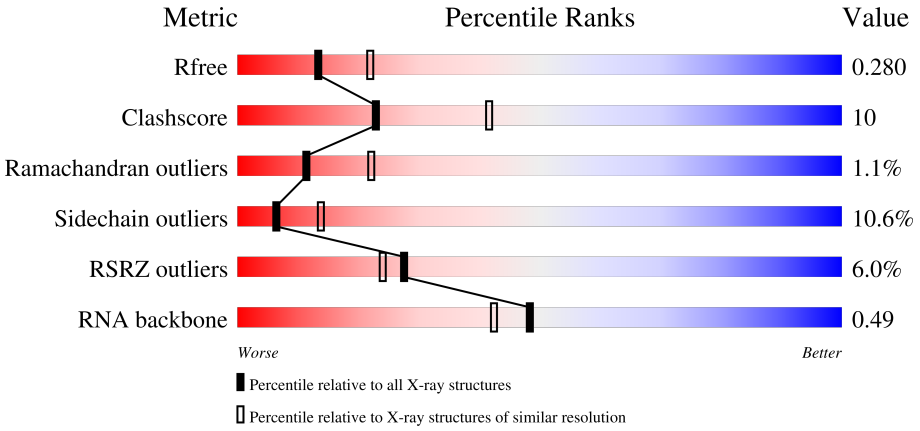
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)
RNA backbone	3983	1003 (2.78-2.22)

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% 61% 31% 7%
1	2A	2915	5% 55% 35% 8%
2	1B	121	% 67% 27% 5%
2	2B	121	% 60% 37%

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Mol	Chain	Length	Quality of chain
3	1D	276	73% 25%
3	2D	276	70% 24% 5%
4	1E	206	75% 20%
4	2E	206	76% 19%
5	1F	210	68% 27%
5	2F	210	60% 31%
6	1G	182	6% 62% 28% 9%
6	2G	182	26% 48% 45% 5%
7	1H	180	64% 31%
7	2H	180	14% 51% 42%
8	1I	148	4% 61% 32% 5%
8	2I	148	14% 53% 39% 5%
9	1N	140	76% 19% 5%
9	2N	140	4% 72% 25%
10	1O	122	73% 25%
10	2O	122	76% 22%
11	1P	150	75% 23%
11	2P	150	3% 70% 27%
12	1Q	141	79% 19%
12	2Q	141	65% 31%
13	1R	118	67% 28% 5%
13	2R	118	75% 20%
14	1S	112	68% 27%
14	2S	112	12% 50% 44%
15	1T	146	62% 25% 10%

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Mol	Chain	Length	Quality of chain
15	2T	146	2% 62% 26% 10%
16	1U	118	81% 18%
16	2U	118	3% 64% 32%
17	1V	101	79% 20%
17	2V	101	4% 59% 37%
18	1W	113	% 79% 19%
18	2W	113	2% 73% 24%
19	1X	96	% 57% 38%
19	2X	96	8% 69% 28%
20	1Y	110	2% 64% 31%
20	2Y	110	7% 57% 34% 6%
21	1Z	206	2% 70% 24%
21	2Z	206	6% 67% 26% 5%
22	10	85	7% 74% 22%
22	20	85	7% 65% 32%
23	11	98	68% 30%
23	21	98	% 56% 39%
24	12	72	3% 65% 28%
24	22	72	60% 35%
25	13	60	63% 32%
25	23	60	5% 77% 22%
26	14	71	15% 52% 39% 6%
26	24	71	35% 35% 45% 15%
27	15	60	2% 77% 20%
27	25	60	75% 20%

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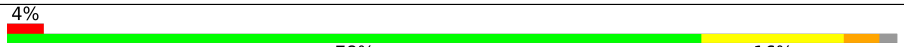
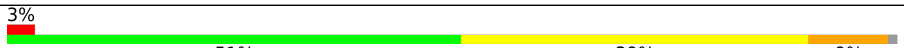
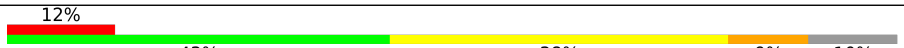
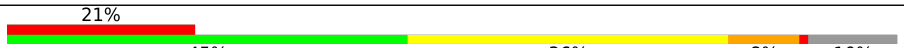
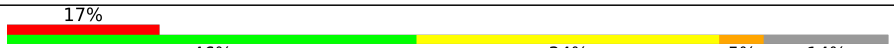
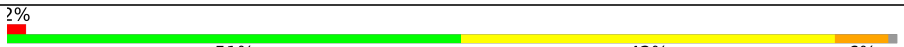
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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Mol	Chain	Length	Quality of chain
40	2i	128	50% 42% 49% 7%
41	1j	105	12% 53% 33% 6% 8%
41	2j	105	42% 64% 23% 5% 9%
42	1k	129	3% 67% 19% 12%
42	2k	129	5% 53% 33% 12%
43	1l	132	3% 64% 25% 8%
43	2l	132	3% 60% 30% 8%
44	1m	126	13% 50% 37% 5% 8%
44	2m	126	16% 42% 42% 6% 10%
45	1n	61	8% 52% 44%
45	2n	61	31% 56% 33% 10%
46	1o	89	7% 65% 33%
46	2o	89	6% 65% 27% 7%
47	1p	88	11% 57% 32% 5% 7%
47	2p	88	10% 56% 33% 5% 7%
48	1q	105	7% 59% 32% 6%
48	2q	105	3% 63% 29% 6%
49	1r	88	% 55% 16% 7% 23%
49	2r	88	7% 55% 19% 23%
50	1s	93	6% 46% 40% 11%
50	2s	93	17% 47% 39% 11%
51	1t	106	15% 58% 28% 5% 9%
51	2t	106	8% 67% 22% 8%
52	1u	27	19% 48% 33% 15%
52	2u	27	52% 48% 33% 15%

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Mol	Chain	Length	Quality of chain
53	1y	113	4% 60% 22% 14%
53	2y	113	64% 50% 30% 15%
54	1w	5	80% 20%
54	2w	5	20% 80% 20%
55	1x	4	50% 50% 50%
55	2x	4	25% 50% 50%
56	1v	3	67% 67% 33%
56	2v	3	100% 67% 33%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
62	SF4	1d	306	-	-	X	-

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 297633 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	C	N	O	S	0	0	0
			933	588	171	170	4			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total	C	N	O	0	0	0
			877	553	175	149			
14	2S	110	Total	C	N	O	0	0	0
			870	549	173	148			

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

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

- 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 Deacylated tRNA Analog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	4	Total	C	N	O	P	0	0	1
			63	28	11	21	3			
54	2w	4	Total	C	N	O	P	0	0	1
			63	28	11	21	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
			23	15	3	4	1			
56	2v	3	Total	C	N	O	S	0	0	0
			23	15	3	4	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1021	Total	Mg	0	0
			1021	1021		
57	1B	31	Total	Mg	0	0
			31	31		
57	1D	18	Total	Mg	0	0
			18	18		
57	1E	9	Total	Mg	0	0
			9	9		
57	1F	18	Total	Mg	0	0
			18	18		

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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	5	Total Mg 5 5	0	0
57	1O	1	Total Mg 1 1	0	0
57	1P	4	Total Mg 4 4	0	0
57	1Q	4	Total Mg 4 4	0	0
57	1R	3	Total Mg 3 3	0	0
57	1T	6	Total Mg 6 6	0	0
57	1U	7	Total Mg 7 7	0	0
57	1V	6	Total Mg 6 6	0	0
57	1W	5	Total Mg 5 5	0	0
57	1X	1	Total Mg 1 1	0	0
57	1Y	1	Total Mg 1 1	0	0
57	1Z	1	Total Mg 1 1	0	0
57	10	8	Total Mg 8 8	0	0
57	11	5	Total Mg 5 5	0	0
57	13	3	Total Mg 3 3	0	0
57	15	10	Total Mg 10 10	0	0
57	17	5	Total Mg 5 5	0	0
57	18	2	Total Mg 2 2	0	0
57	19	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1a	270	Total Mg 270 270	0	0
57	1b	1	Total Mg 1 1	0	0
57	1d	5	Total Mg 5 5	0	0
57	1e	1	Total Mg 1 1	0	0
57	1f	2	Total Mg 2 2	0	0
57	1g	3	Total Mg 3 3	0	0
57	1h	2	Total Mg 2 2	0	0
57	1i	2	Total Mg 2 2	0	0
57	1l	2	Total Mg 2 2	0	0
57	1m	2	Total Mg 2 2	0	0
57	1n	3	Total Mg 3 3	0	0
57	1o	2	Total Mg 2 2	0	0
57	1t	2	Total Mg 2 2	0	0
57	1y	3	Total Mg 3 3	0	0
57	2A	726	Total Mg 726 726	0	0
57	2B	17	Total Mg 17 17	0	0
57	2D	9	Total Mg 9 9	0	0
57	2E	8	Total Mg 8 8	0	0
57	2F	4	Total Mg 4 4	0	0
57	2G	3	Total Mg 3 3	0	0
57	2I	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2N	1	Total Mg 1 1	0	0
57	2O	2	Total Mg 2 2	0	0
57	2P	2	Total Mg 2 2	0	0
57	2Q	3	Total Mg 3 3	0	0
57	2R	2	Total Mg 2 2	0	0
57	2T	4	Total Mg 4 4	0	0
57	2U	1	Total Mg 1 1	0	0
57	2V	3	Total Mg 3 3	0	0
57	2W	2	Total Mg 2 2	0	0
57	2Y	1	Total Mg 1 1	0	0
57	20	2	Total Mg 2 2	0	0
57	21	3	Total Mg 3 3	0	0
57	23	1	Total Mg 1 1	0	0
57	25	4	Total Mg 4 4	0	0
57	27	3	Total Mg 3 3	0	0
57	28	3	Total Mg 3 3	0	0
57	29	1	Total Mg 1 1	0	0
57	2a	189	Total Mg 189 189	0	0
57	2e	1	Total Mg 1 1	0	0
57	2f	1	Total Mg 1 1	0	0
57	2j	1	Total Mg 1 1	0	0

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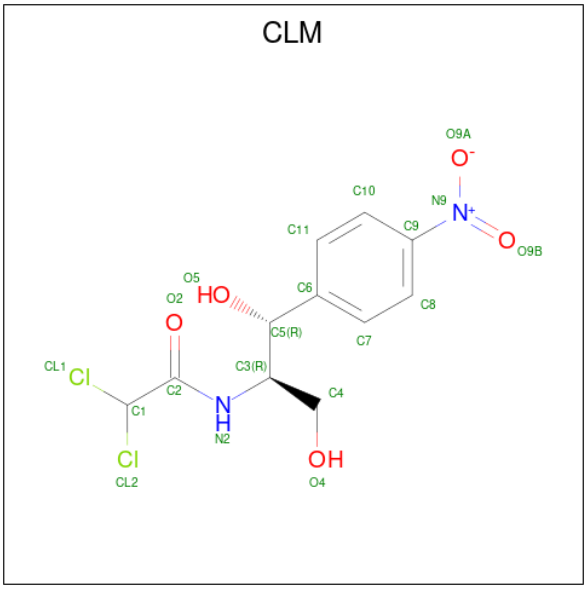
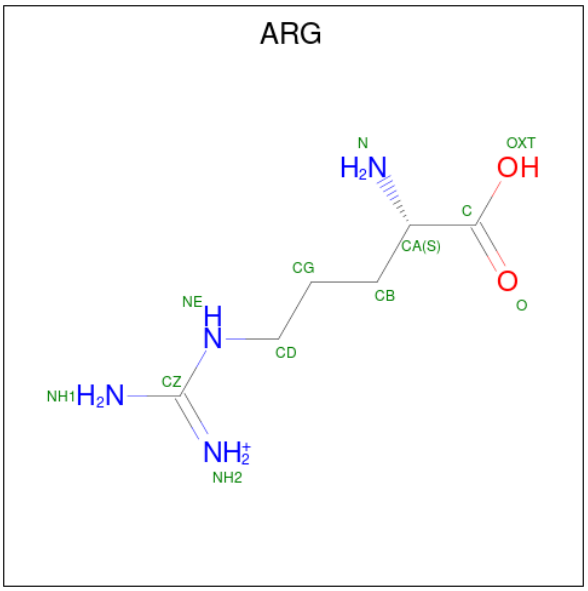
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2l	2	Total Mg 2 2	0	0
57	2n	1	Total Mg 1 1	0	0
57	2p	1	Total Mg 1 1	0	0
57	2t	1	Total Mg 1 1	0	0
57	2x	1	Total Mg 1 1	0	0

- Molecule 58 is CHLORAMPHENICOL (CCD ID: CLM) (formula: $C_{11}H_{12}Cl_2N_2O_5$).



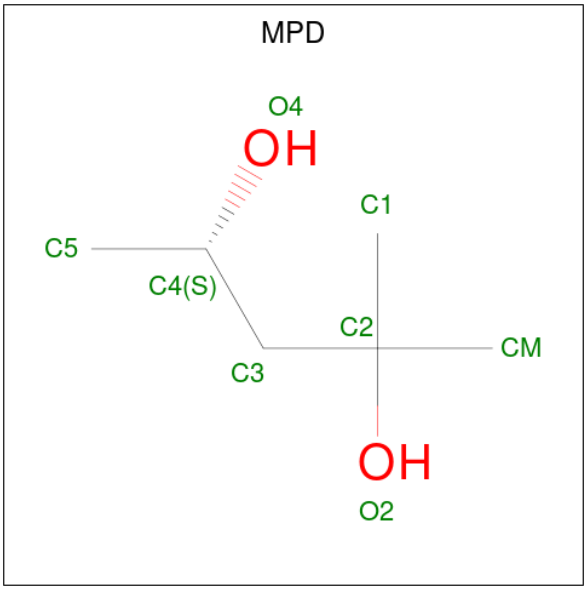
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1A	1	Total C Cl N O 20 11 2 2 5	0	0
58	2A	1	Total C Cl N O 20 11 2 2 5	0	0

- Molecule 59 is ARGININE (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	1	Total C N O 12 6 4 2	0	0
59	1B	1	Total C N O 12 6 4 2	0	0

- Molecule 60 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	1	Total C O 8 6 2	0	0
60	1T	1	Total C O 8 6 2	0	0

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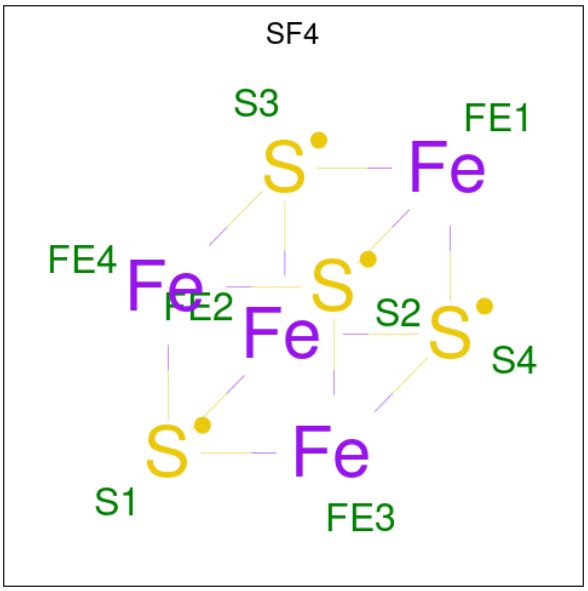
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	18	1	Total C O 8 6 2	0	0
60	1a	1	Total C O 8 6 2	0	0
60	2A	1	Total C O 8 6 2	0	0
60	2B	1	Total C O 8 6 2	0	0

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	1Y	1	Total Zn 1 1	0	0
61	14	1	Total Zn 1 1	0	0
61	15	1	Total Zn 1 1	0	0
61	16	1	Total Zn 1 1	0	0
61	19	1	Total Zn 1 1	0	0
61	1n	1	Total Zn 1 1	0	0
61	2Y	1	Total Zn 1 1	0	0
61	24	1	Total Zn 1 1	0	0
61	25	1	Total Zn 1 1	0	0
61	26	1	Total Zn 1 1	0	0
61	29	1	Total Zn 1 1	0	0
61	2n	1	Total Zn 1 1	0	0

- Molecule 62 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	1d	1	Total Fe S 8 4 4	0	0
62	2d	1	Total Fe S 8 4 4	0	0

- Molecule 63 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1A	3946	Total O 3946 3946	0	0
63	1B	90	Total O 90 90	0	0
63	1D	121	Total O 121 121	0	0
63	1E	80	Total O 80 80	0	0
63	1F	59	Total O 59 59	0	0
63	1G	19	Total O 19 19	0	0
63	1H	13	Total O 13 13	0	0
63	1I	5	Total O 5 5	0	0
63	1N	50	Total O 50 50	0	0
63	1O	33	Total O 33 33	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1P	65	Total O 65 65	0	0
63	1Q	35	Total O 35 35	0	0
63	1R	32	Total O 32 32	0	0
63	1S	15	Total O 15 15	0	0
63	1T	28	Total O 28 28	0	0
63	1U	46	Total O 46 46	0	0
63	1V	41	Total O 41 41	0	0
63	1W	30	Total O 30 30	0	0
63	1X	28	Total O 28 28	0	0
63	1Y	21	Total O 21 21	0	0
63	1Z	13	Total O 13 13	0	0
63	10	25	Total O 25 25	0	0
63	11	26	Total O 26 26	0	0
63	12	15	Total O 15 15	0	0
63	13	24	Total O 24 24	0	0
63	14	2	Total O 2 2	0	0
63	15	24	Total O 24 24	0	0
63	16	18	Total O 18 18	0	0
63	17	17	Total O 17 17	0	0
63	18	26	Total O 26 26	0	0
63	19	7	Total O 7 7	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	1a	412	Total O 412 412	0	0
63	1b	1	Total O 1 1	0	0
63	1c	1	Total O 1 1	0	0
63	1d	7	Total O 7 7	0	0
63	1e	2	Total O 2 2	0	0
63	1f	3	Total O 3 3	0	0
63	1h	1	Total O 1 1	0	0
63	1j	1	Total O 1 1	0	0
63	1l	5	Total O 5 5	0	0
63	1o	2	Total O 2 2	0	0
63	1p	3	Total O 3 3	0	0
63	1t	1	Total O 1 1	0	0
63	1y	5	Total O 5 5	0	0
63	1w	5	Total O 5 5	0	0
63	1x	5	Total O 5 5	0	0
63	2A	2126	Total O 2126 2126	0	0
63	2B	46	Total O 46 46	0	0
63	2D	54	Total O 54 54	0	0
63	2E	26	Total O 26 26	0	0
63	2F	24	Total O 24 24	0	0
63	2G	7	Total O 7 7	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	2H	3	Total O 3 3	0	0
63	2I	6	Total O 6 6	0	0
63	2N	3	Total O 3 3	0	0
63	2O	22	Total O 22 22	0	0
63	2P	28	Total O 28 28	0	0
63	2Q	19	Total O 19 19	0	0
63	2R	17	Total O 17 17	0	0
63	2S	4	Total O 4 4	0	0
63	2T	11	Total O 11 11	0	0
63	2U	13	Total O 13 13	0	0
63	2V	7	Total O 7 7	0	0
63	2W	19	Total O 19 19	0	0
63	2X	9	Total O 9 9	0	0
63	2Y	4	Total O 4 4	0	0
63	2Z	10	Total O 10 10	0	0
63	20	12	Total O 12 12	0	0
63	21	20	Total O 20 20	0	0
63	22	2	Total O 2 2	0	0
63	23	3	Total O 3 3	0	0
63	24	1	Total O 1 1	0	0
63	25	10	Total O 10 10	0	0

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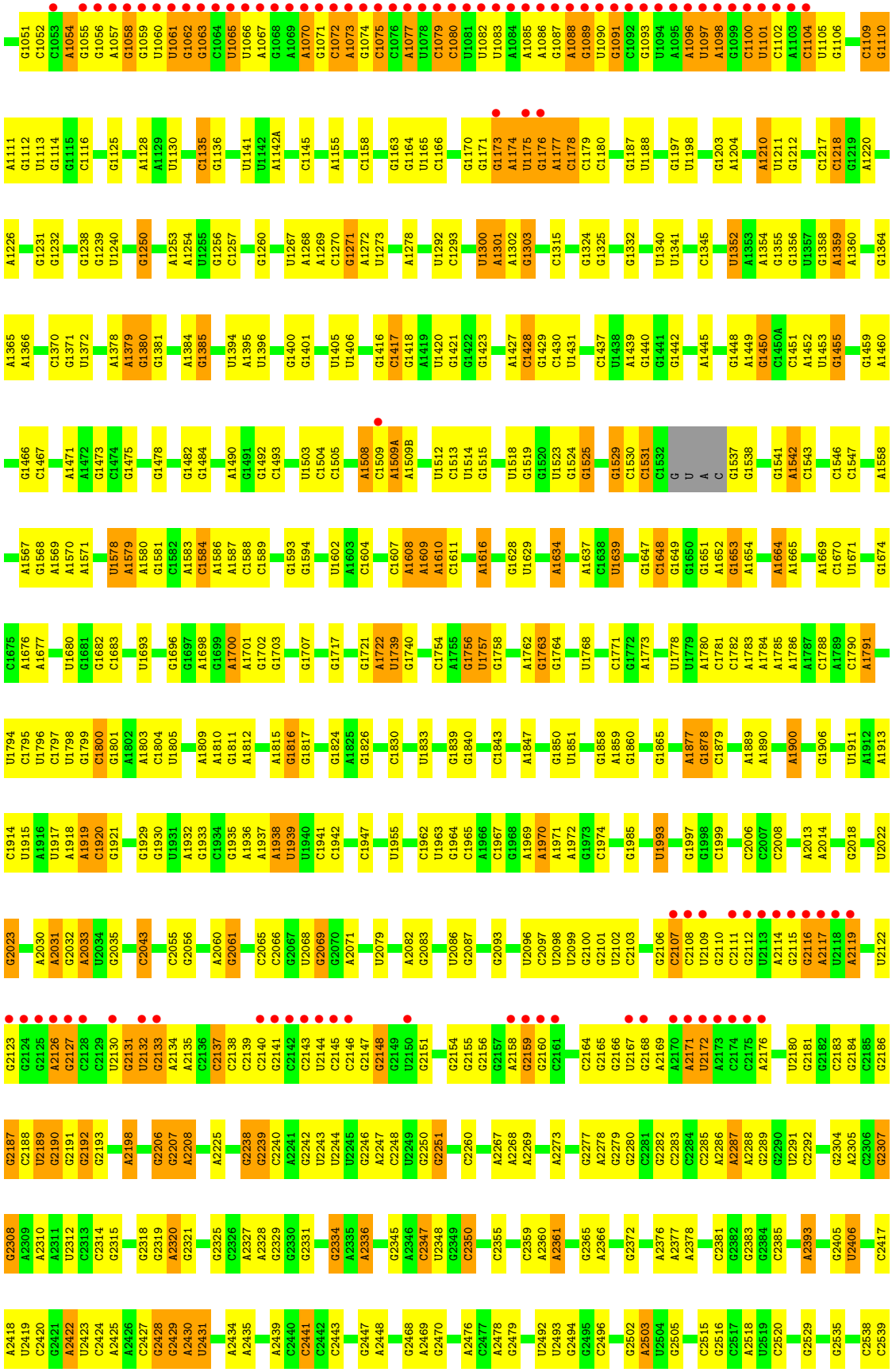
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
63	26	5	Total O 5 5	0	0
63	27	8	Total O 8 8	0	0
63	28	13	Total O 13 13	0	0
63	29	1	Total O 1 1	0	0
63	2a	294	Total O 294 294	0	0
63	2d	2	Total O 2 2	0	0
63	2e	2	Total O 2 2	0	0
63	2f	2	Total O 2 2	0	0
63	2j	2	Total O 2 2	0	0
63	2l	2	Total O 2 2	0	0
63	2n	1	Total O 1 1	0	0
63	2o	3	Total O 3 3	0	0
63	2p	1	Total O 1 1	0	0
63	2r	3	Total O 3 3	0	0
63	2t	2	Total O 2 2	0	0
63	2y	2	Total O 2 2	0	0
63	2w	2	Total O 2 2	0	0
63	2x	2	Total O 2 2	0	0

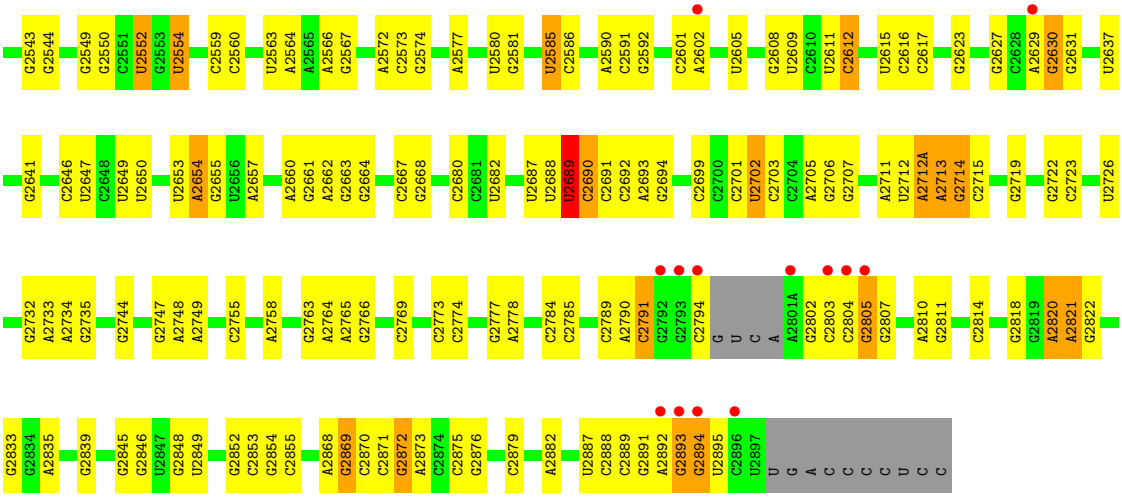
3 Residue-property plots (i)

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

- Molecule 1: 23S Ribosomal RNA

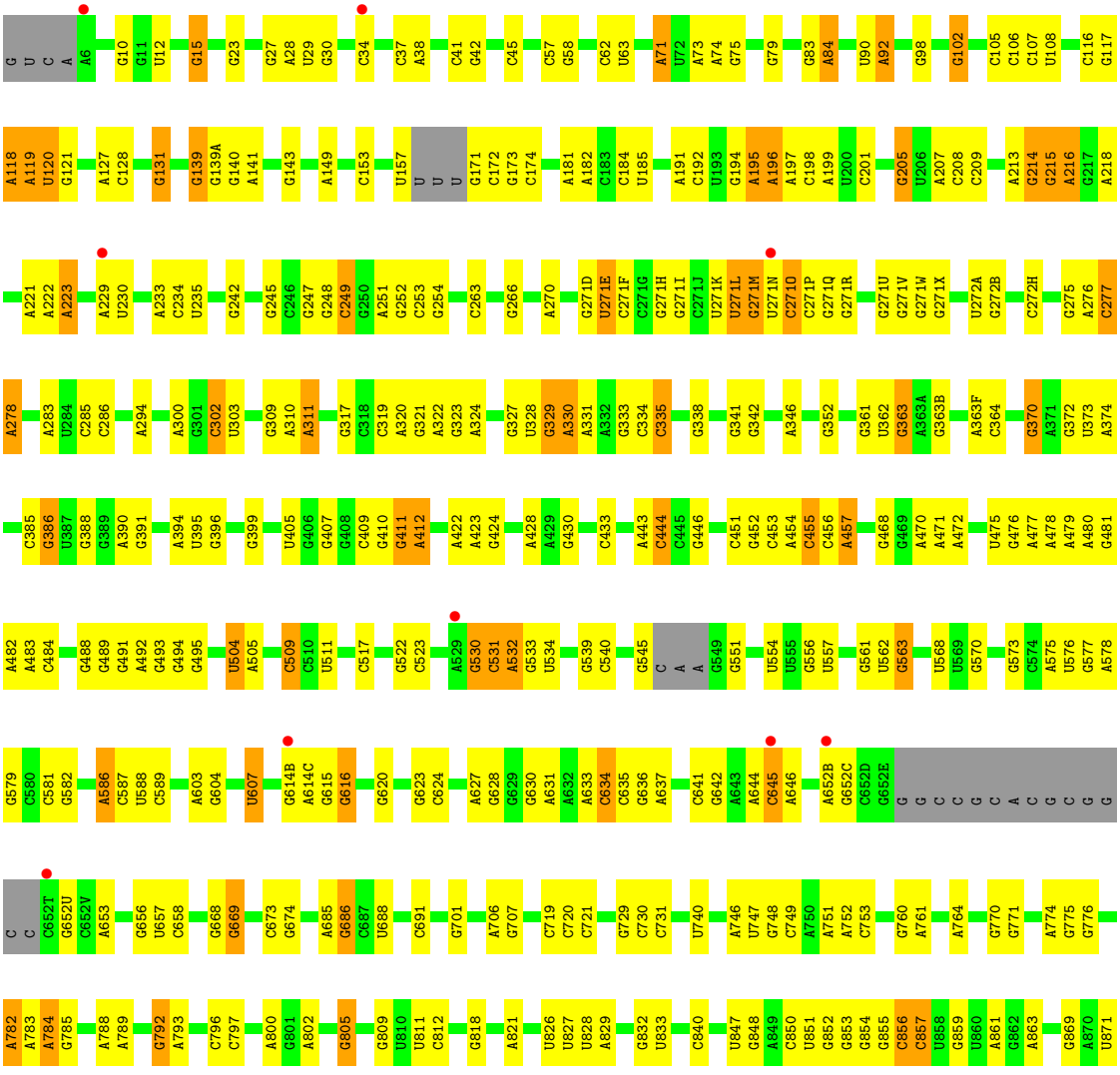
Chain 1A:

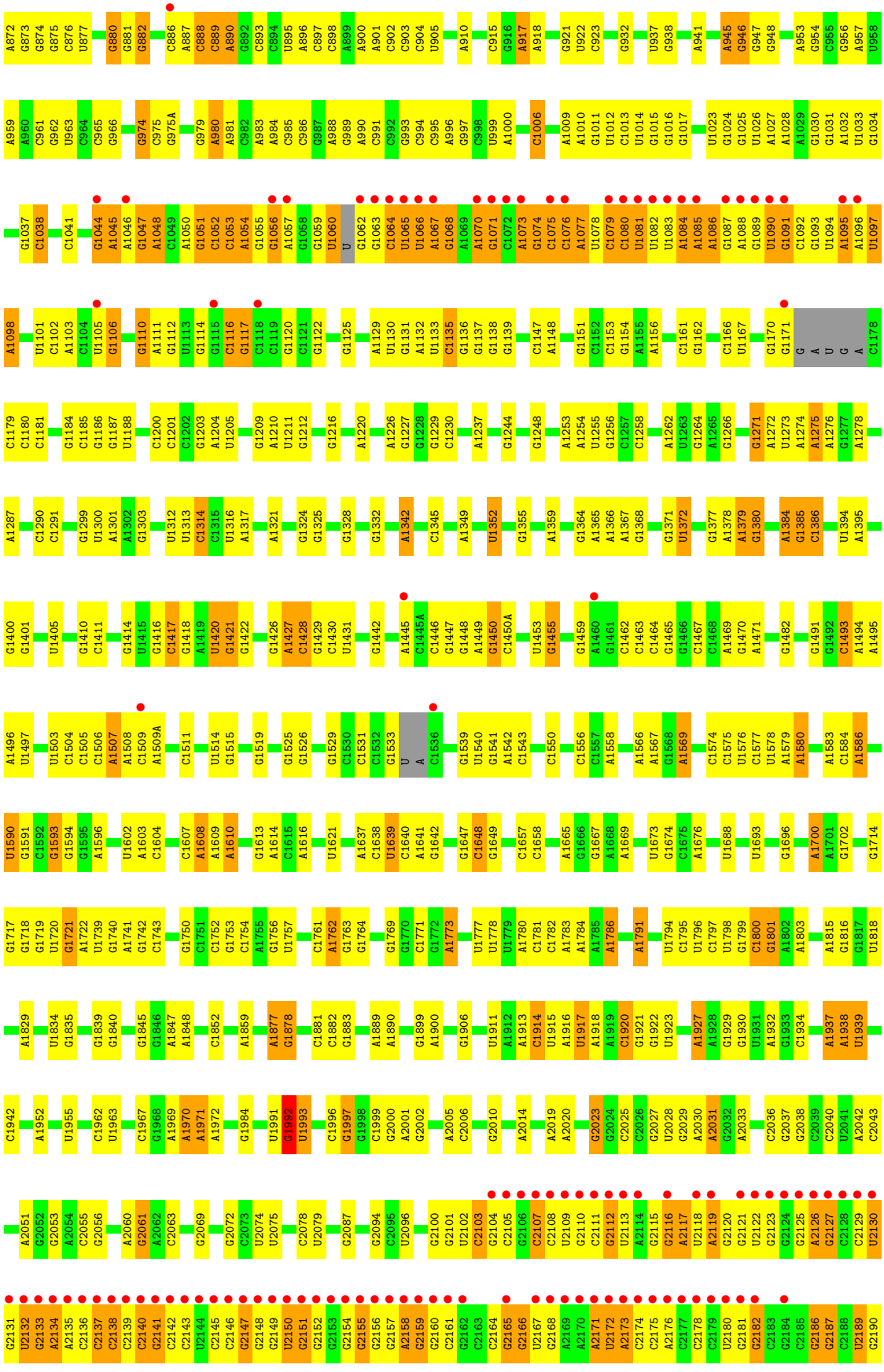


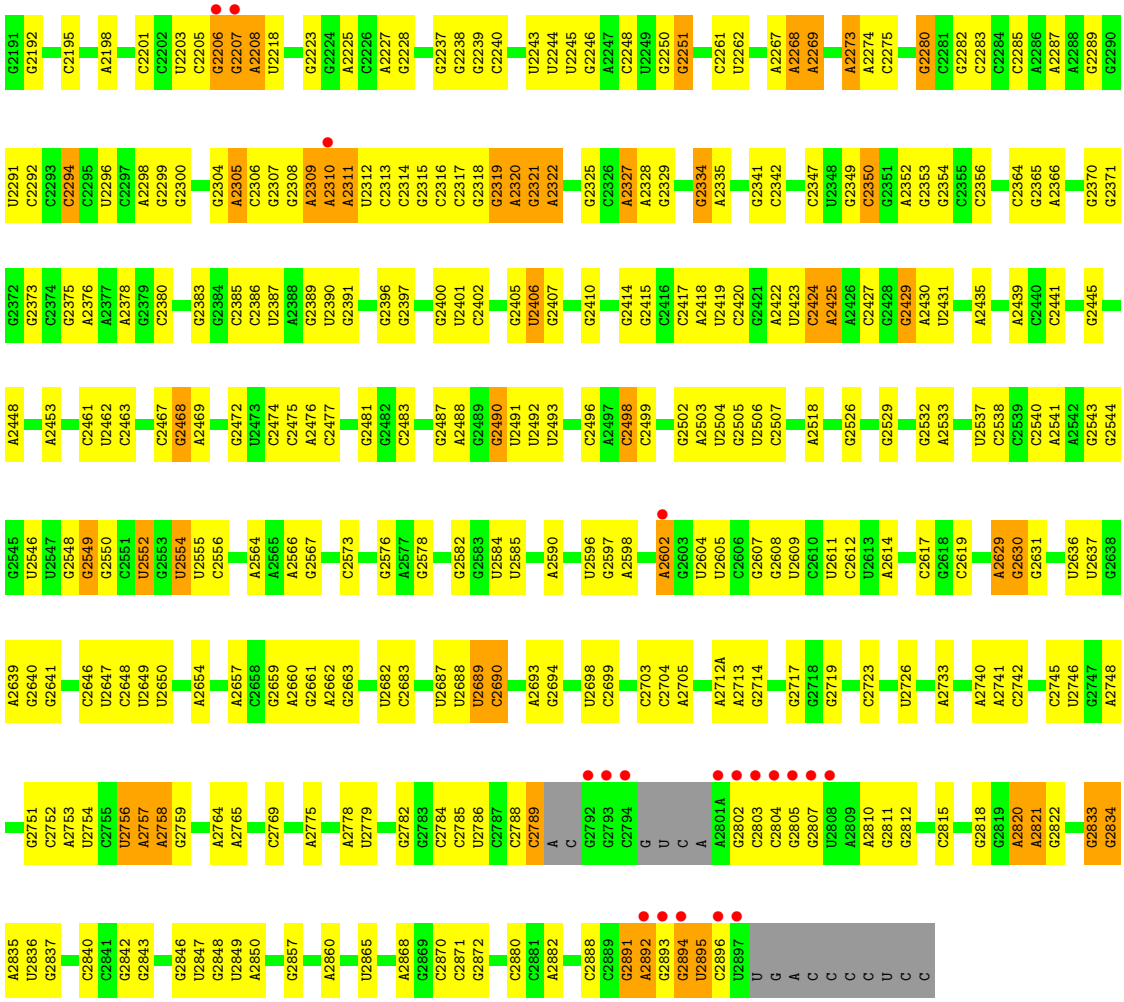


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

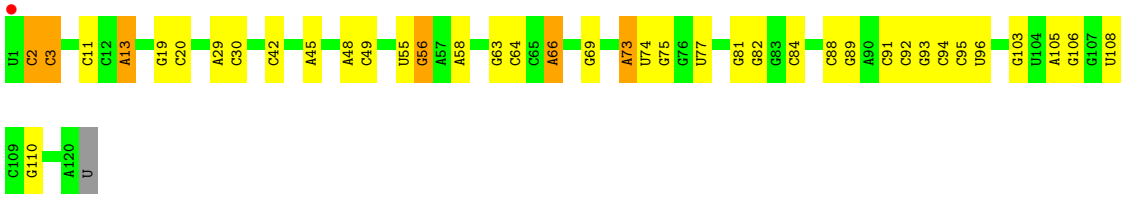






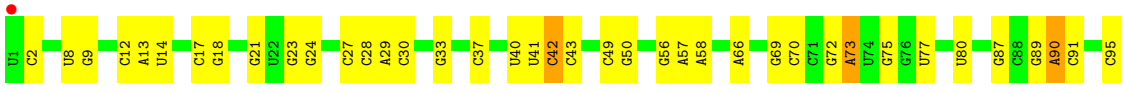
• Molecule 2: 5S Ribosomal RNA

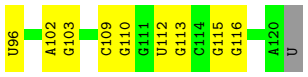
Chain 1B:



• Molecule 2: 5S Ribosomal RNA

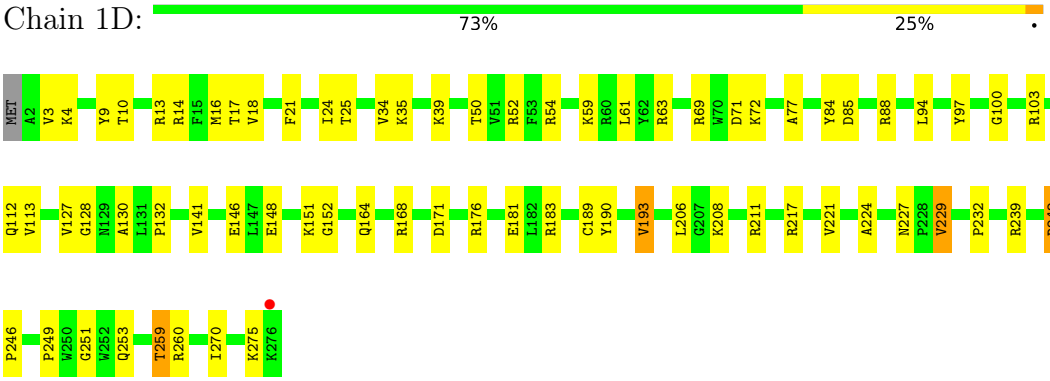
Chain 2B:





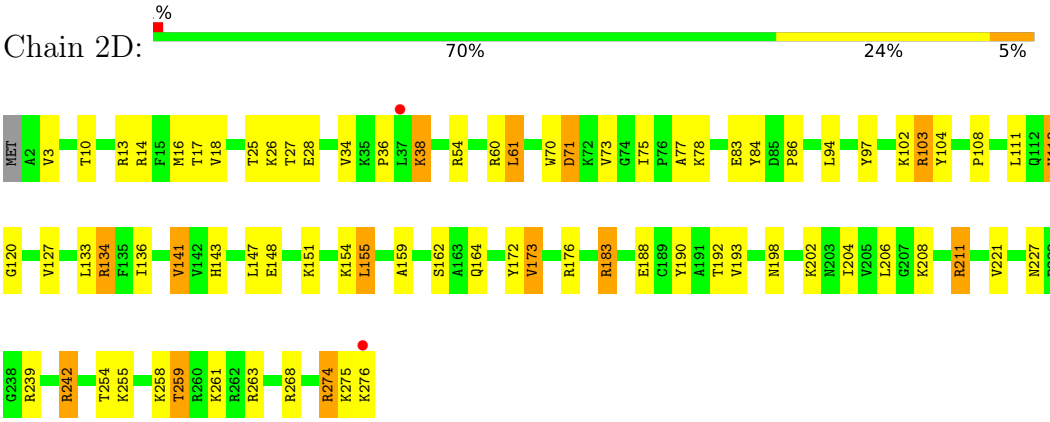
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



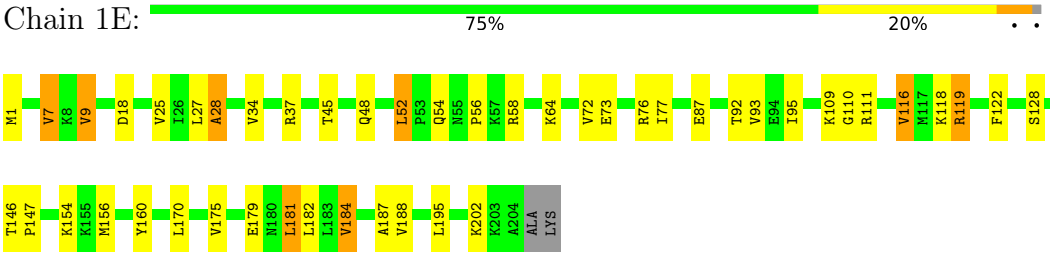
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



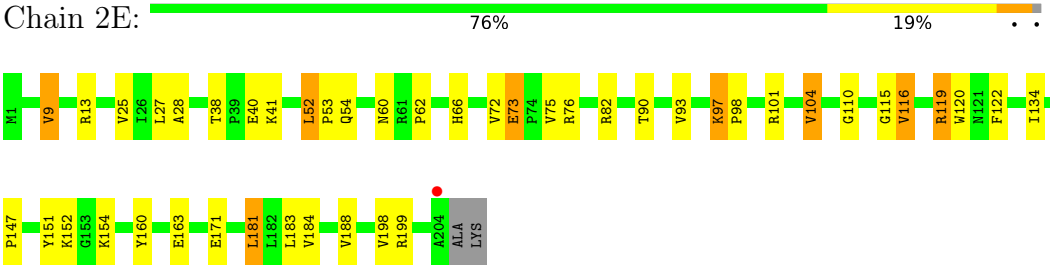
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



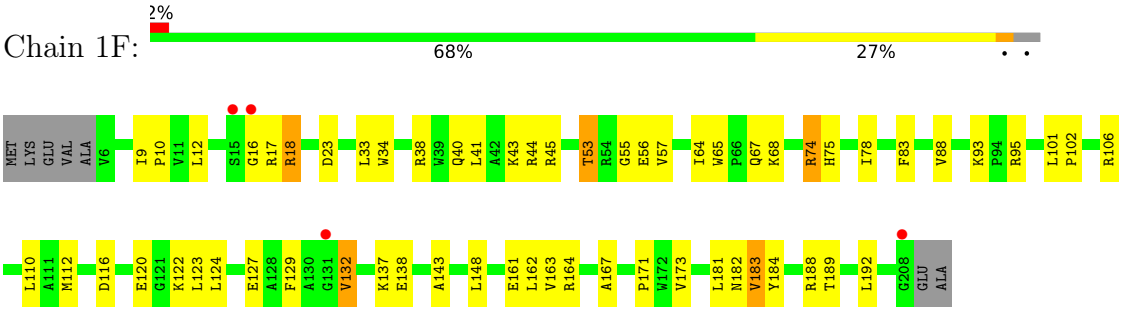
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



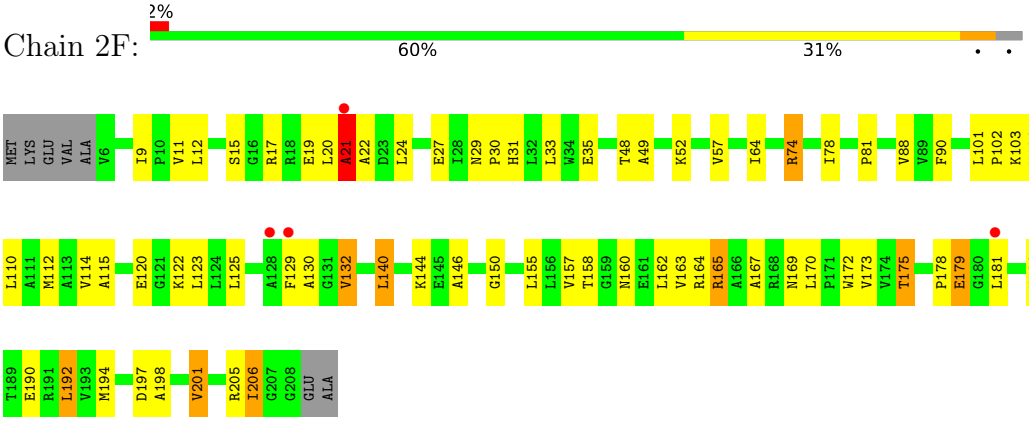
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



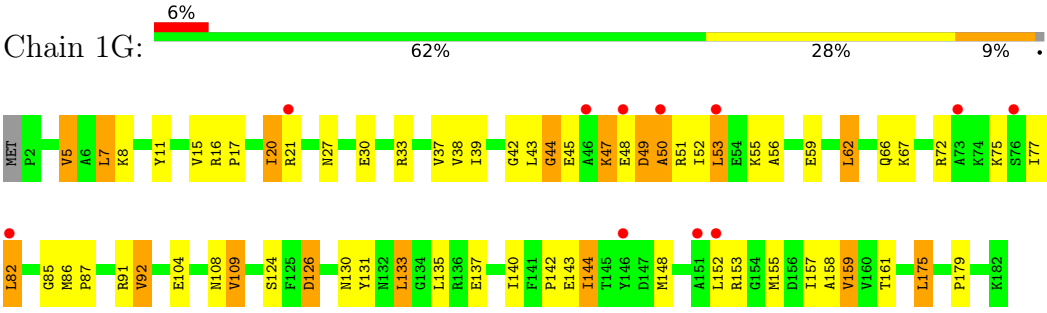
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



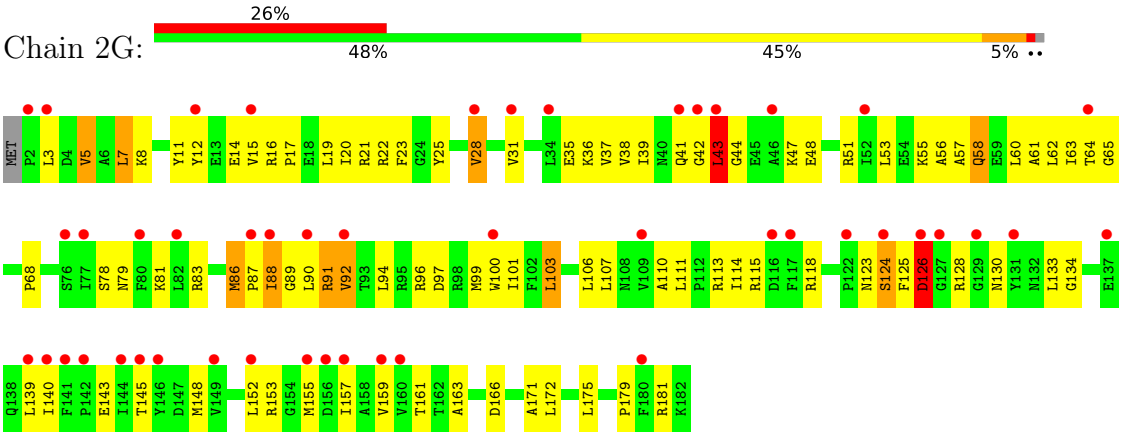
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



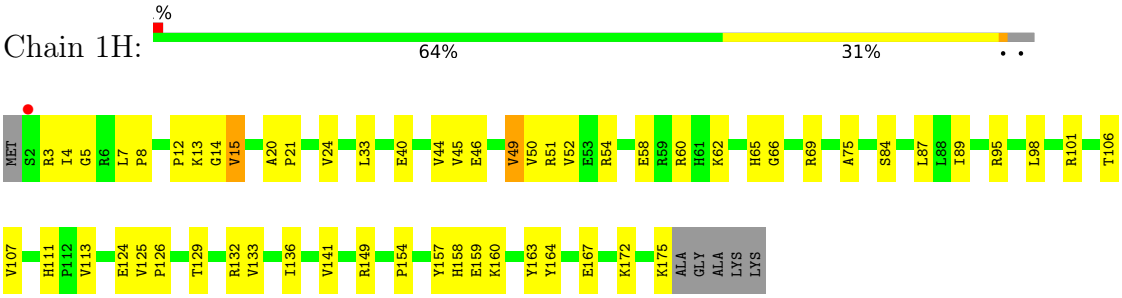
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



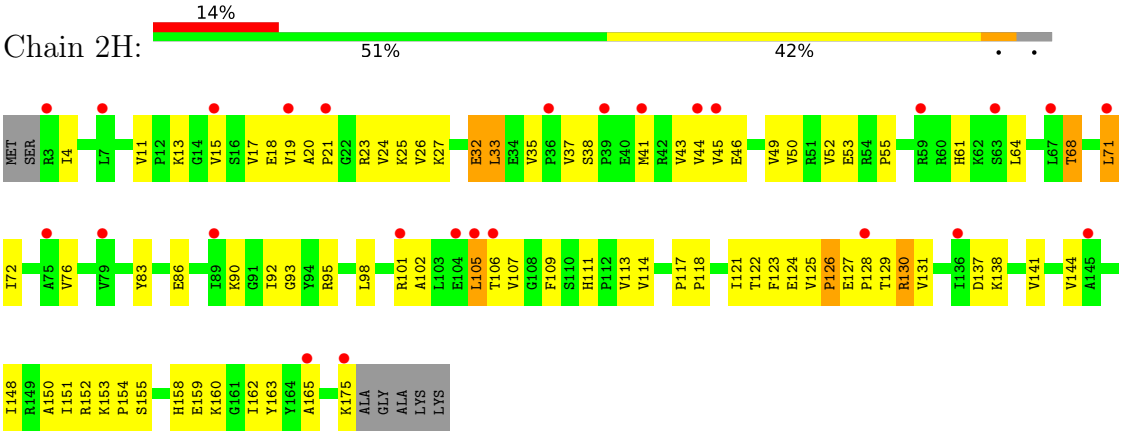
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



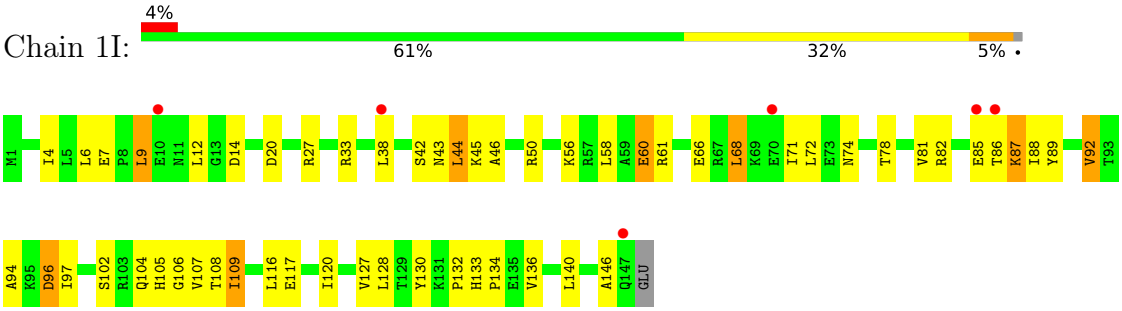
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



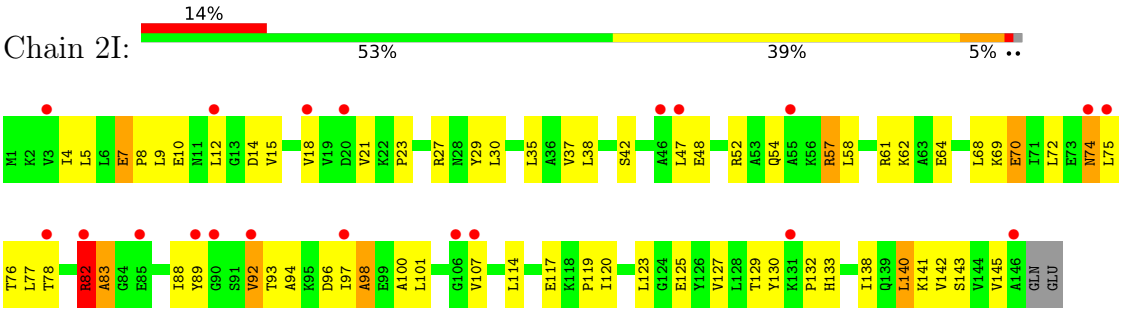
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



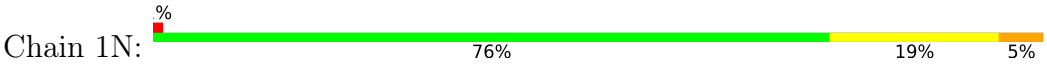
• Molecule 8: 50S ribosomal protein L9

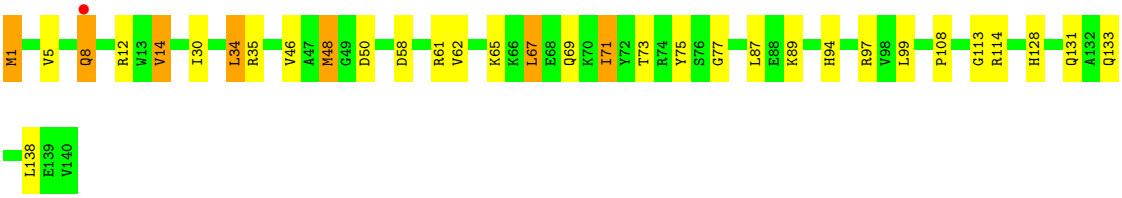
Chain 2I:



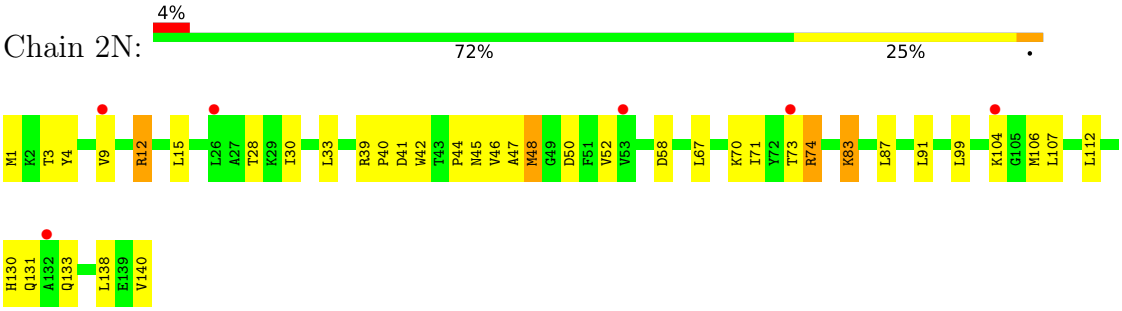
• Molecule 9: 50S ribosomal protein L13

Chain 1N:

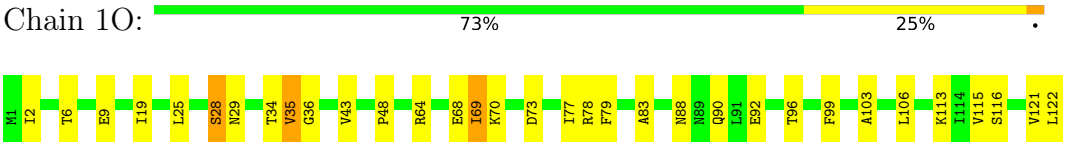




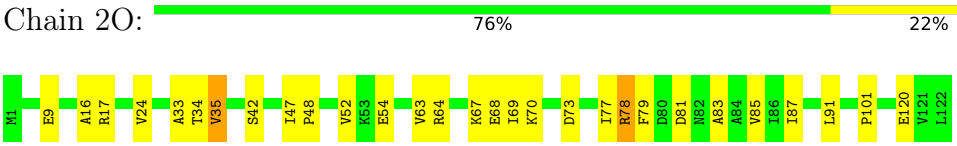
• Molecule 9: 50S ribosomal protein L13



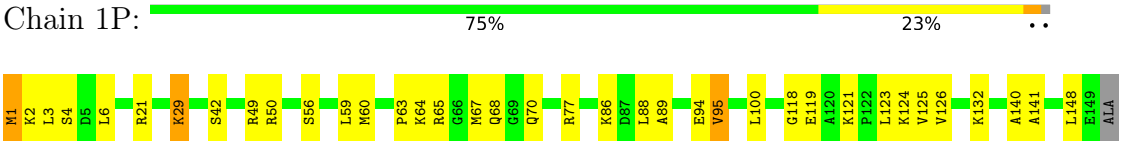
• Molecule 10: 50S ribosomal protein L14



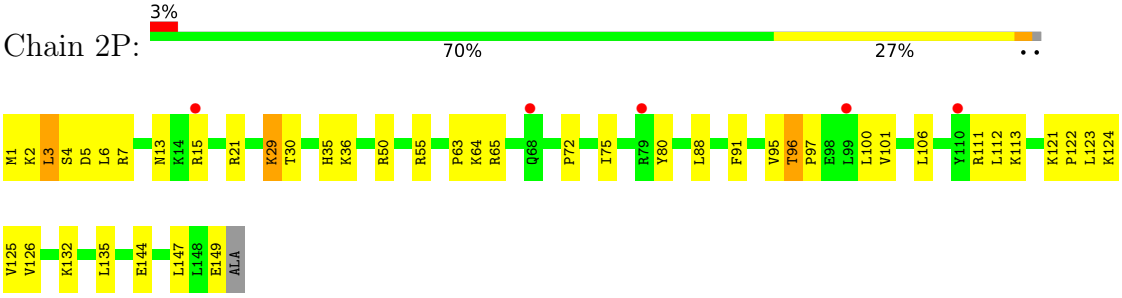
• Molecule 10: 50S ribosomal protein L14



• Molecule 11: 50S ribosomal protein L15

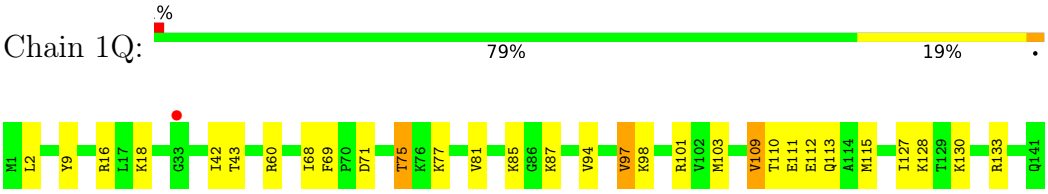


• Molecule 11: 50S ribosomal protein L15



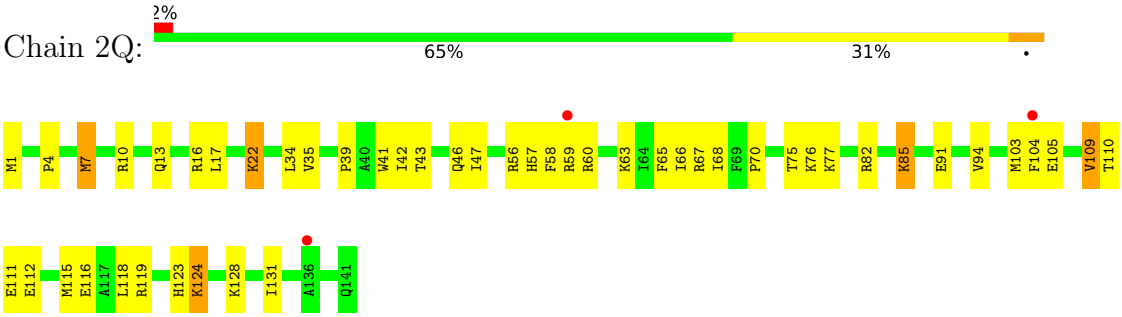
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



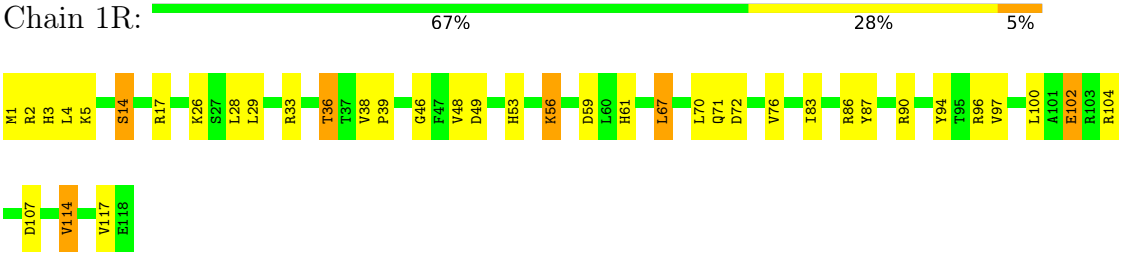
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



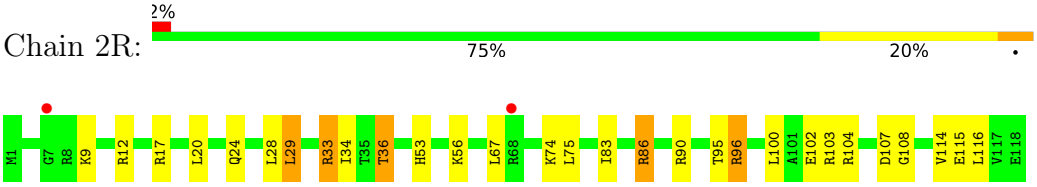
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



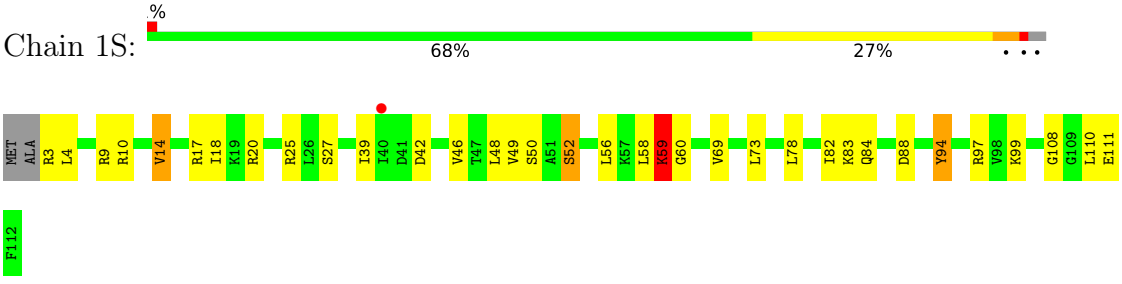
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



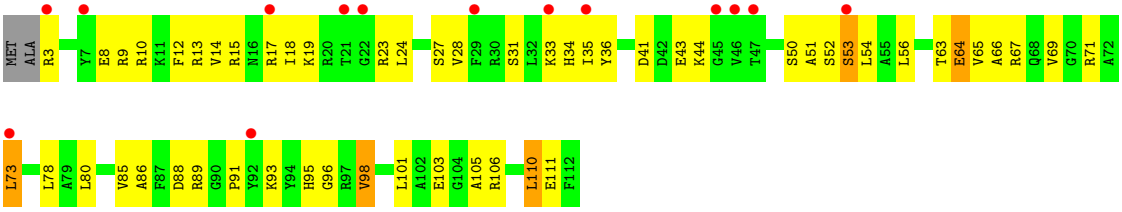
• Molecule 14: 50S ribosomal protein L18

Chain 1S:

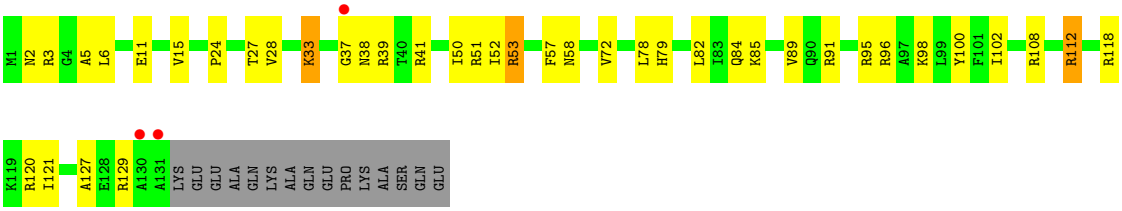


• Molecule 14: 50S ribosomal protein L18

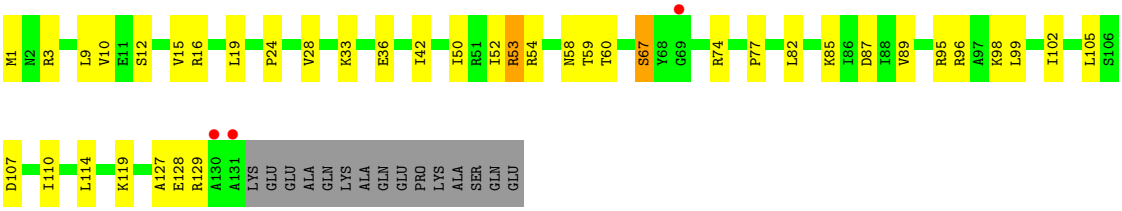
Chain 2S:



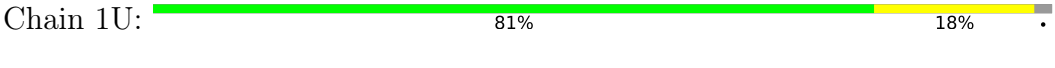
• Molecule 15: 50S ribosomal protein L19

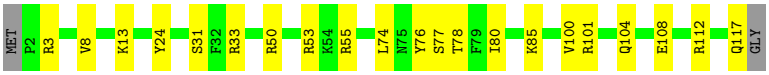


• Molecule 15: 50S ribosomal protein L19

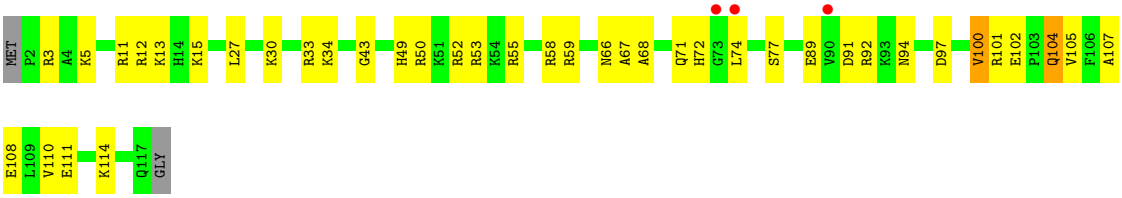


• Molecule 16: 50S ribosomal protein L20

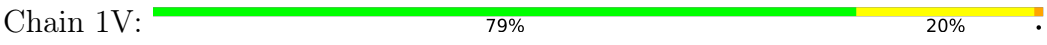




• Molecule 16: 50S ribosomal protein L20

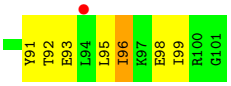


• Molecule 17: 50S ribosomal protein L21



• Molecule 17: 50S ribosomal protein L21

Chain 2V:

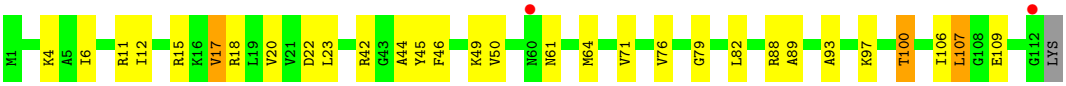


• Molecule 18: 50S ribosomal protein L22

Chain 1W:

• Molecule 18: 50S ribosomal protein L22

Chain 2W:

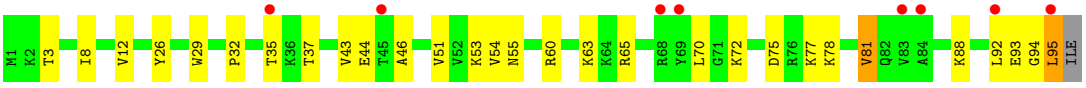


• Molecule 19: 50S ribosomal protein L23

Chain 1X:

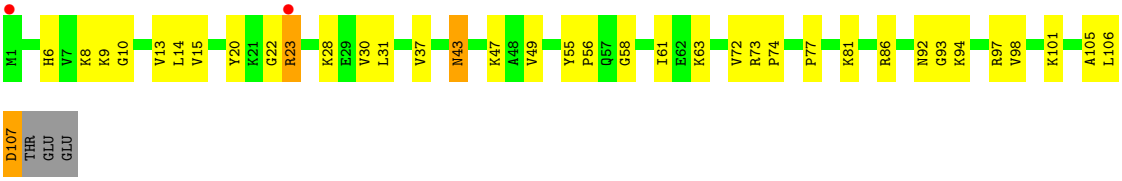
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



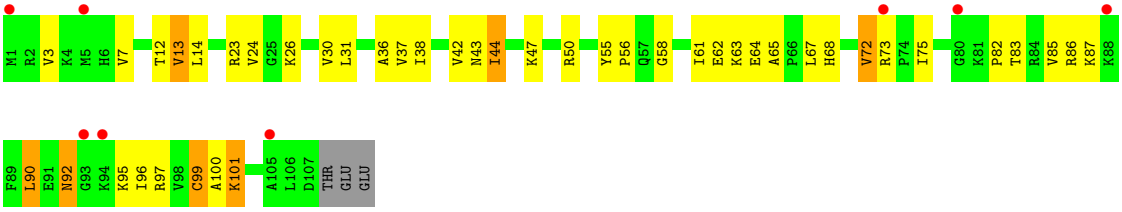
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



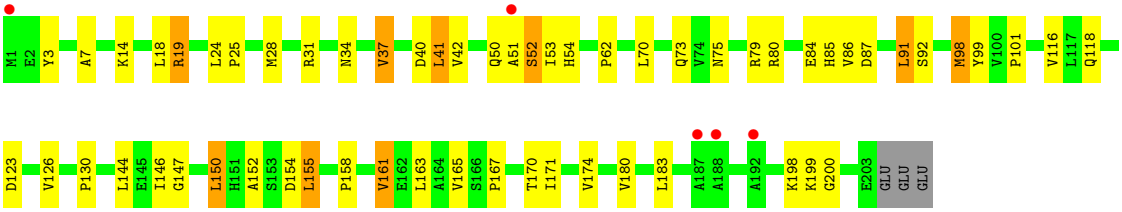
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



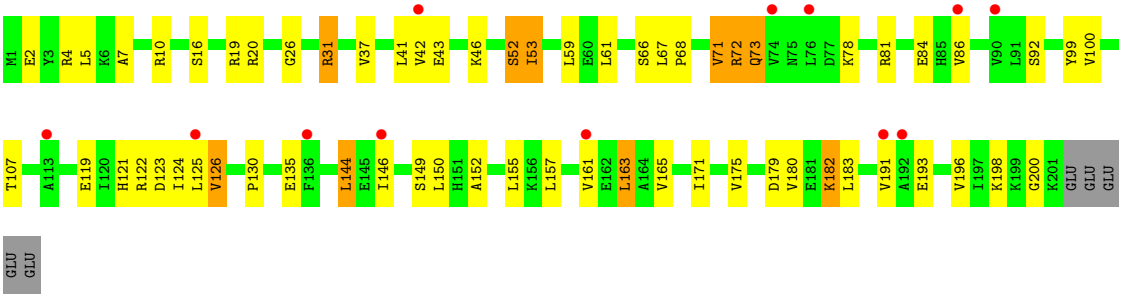
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



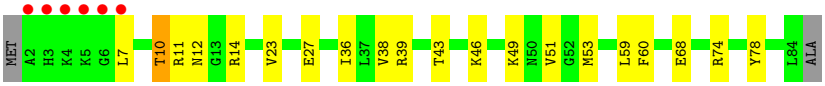
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



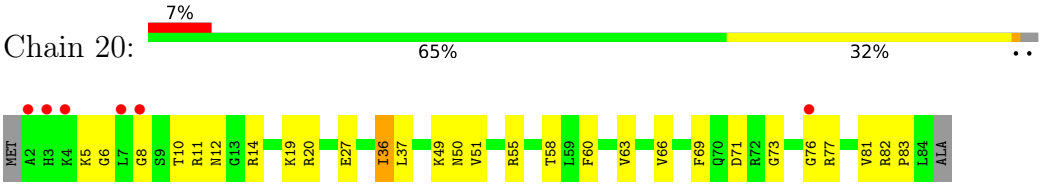
• Molecule 22: 50S ribosomal protein L27

Chain 10:



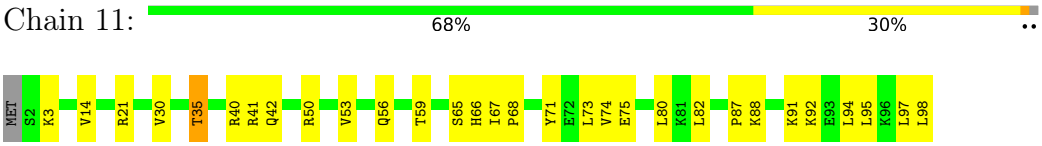
• Molecule 22: 50S ribosomal protein L27

Chain 20:



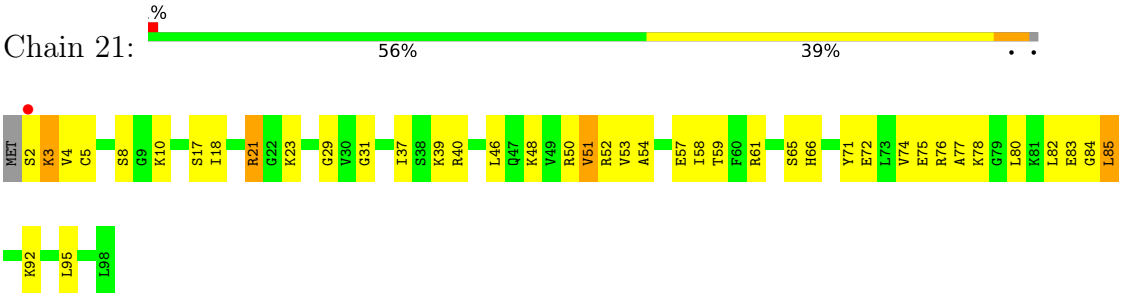
• Molecule 23: 50S ribosomal protein L28

Chain 11:



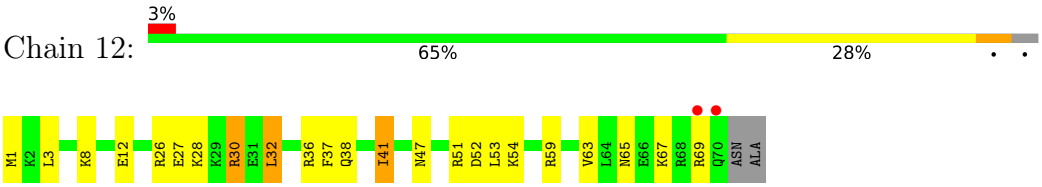
• Molecule 23: 50S ribosomal protein L28

Chain 21:



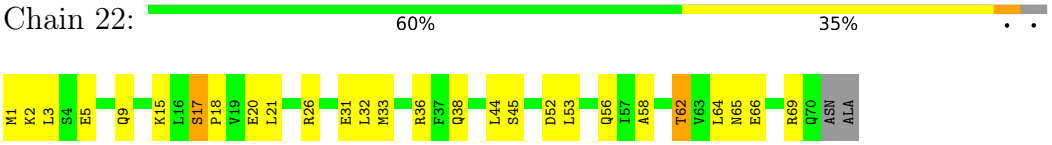
• Molecule 24: 50S ribosomal protein L29

Chain 12:



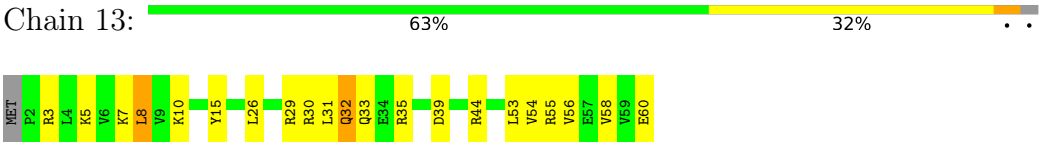
• Molecule 24: 50S ribosomal protein L29

Chain 22:



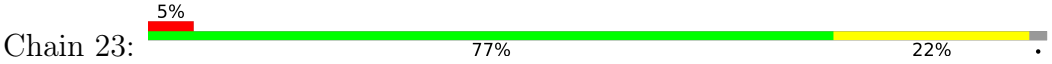
• Molecule 25: 50S ribosomal protein L30

Chain 13:



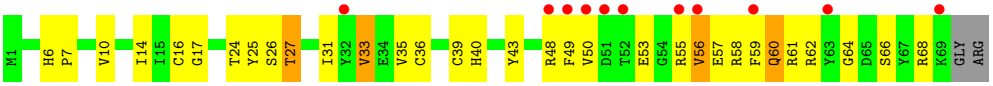
• Molecule 25: 50S ribosomal protein L30

Chain 23:



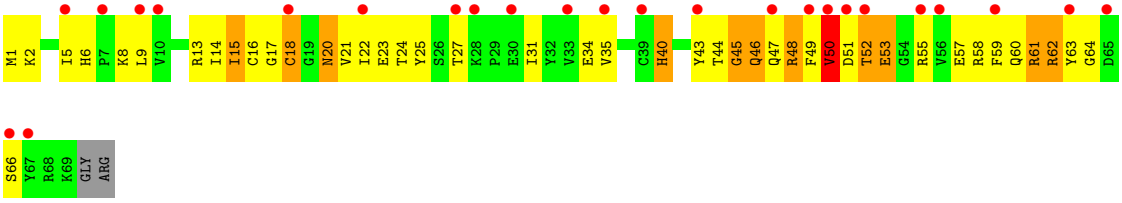
• Molecule 26: 50S ribosomal protein L31

Chain 14:



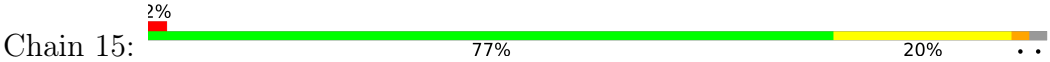
• Molecule 26: 50S ribosomal protein L31

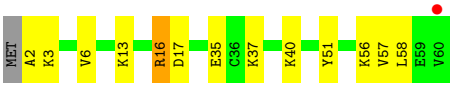
Chain 24:



• Molecule 27: 50S ribosomal protein L32

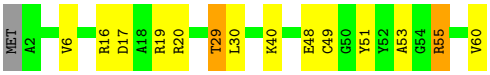
Chain 15:





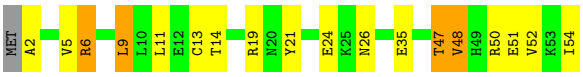
• Molecule 27: 50S ribosomal protein L32

Chain 25:



• Molecule 28: 50S ribosomal protein L33

Chain 16:

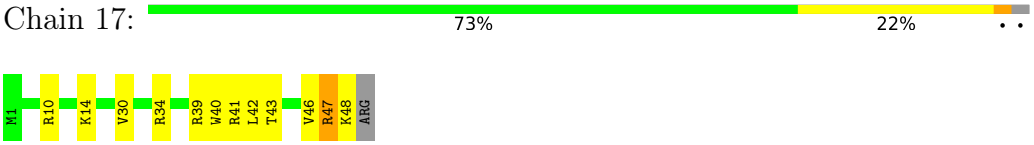


• Molecule 28: 50S ribosomal protein L33

Chain 26:

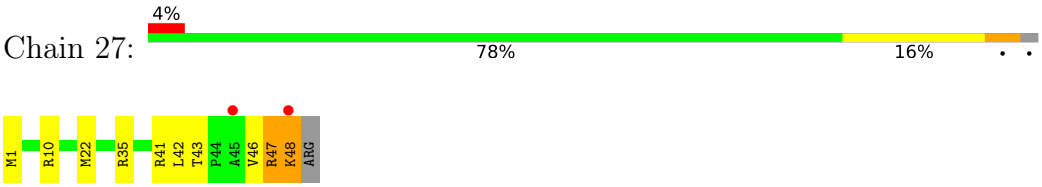
• Molecule 29: 50S ribosomal protein L34

Chain 17:



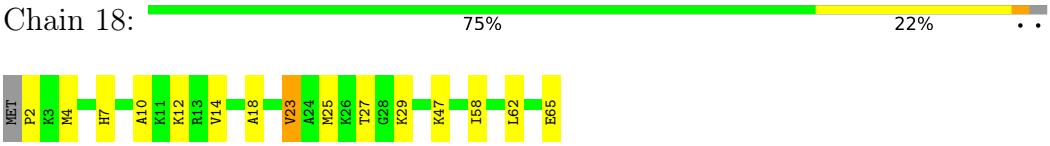
• Molecule 29: 50S ribosomal protein L34

Chain 27:



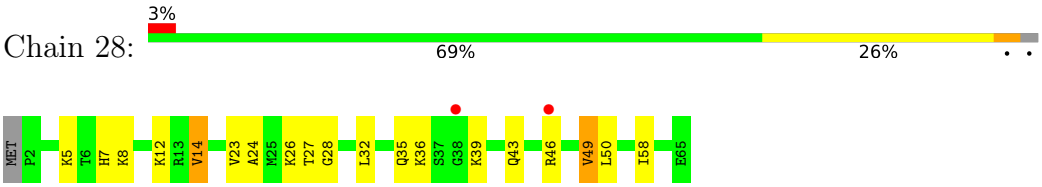
• Molecule 30: 50S ribosomal protein L35

Chain 18:



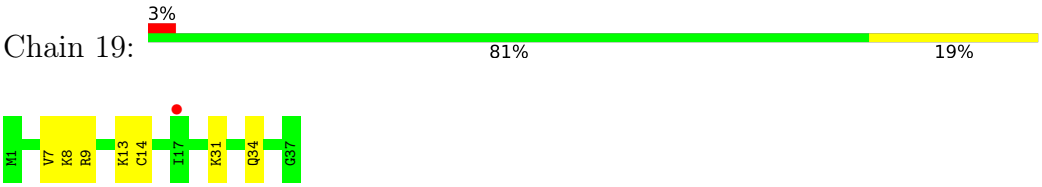
• Molecule 30: 50S ribosomal protein L35

Chain 28:



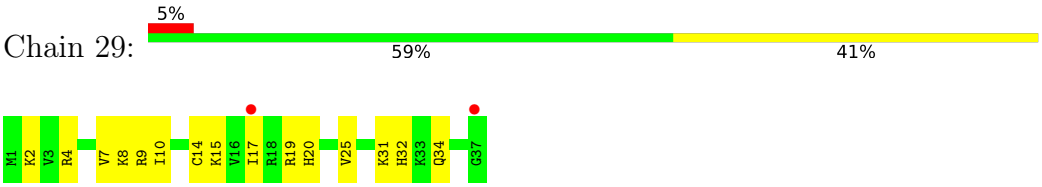
• Molecule 31: 50S ribosomal protein L36

Chain 19:



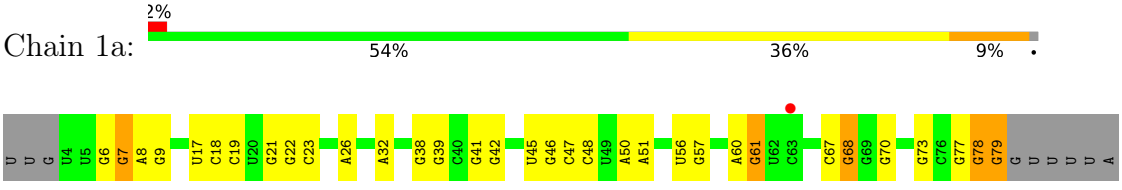
• Molecule 31: 50S ribosomal protein L36

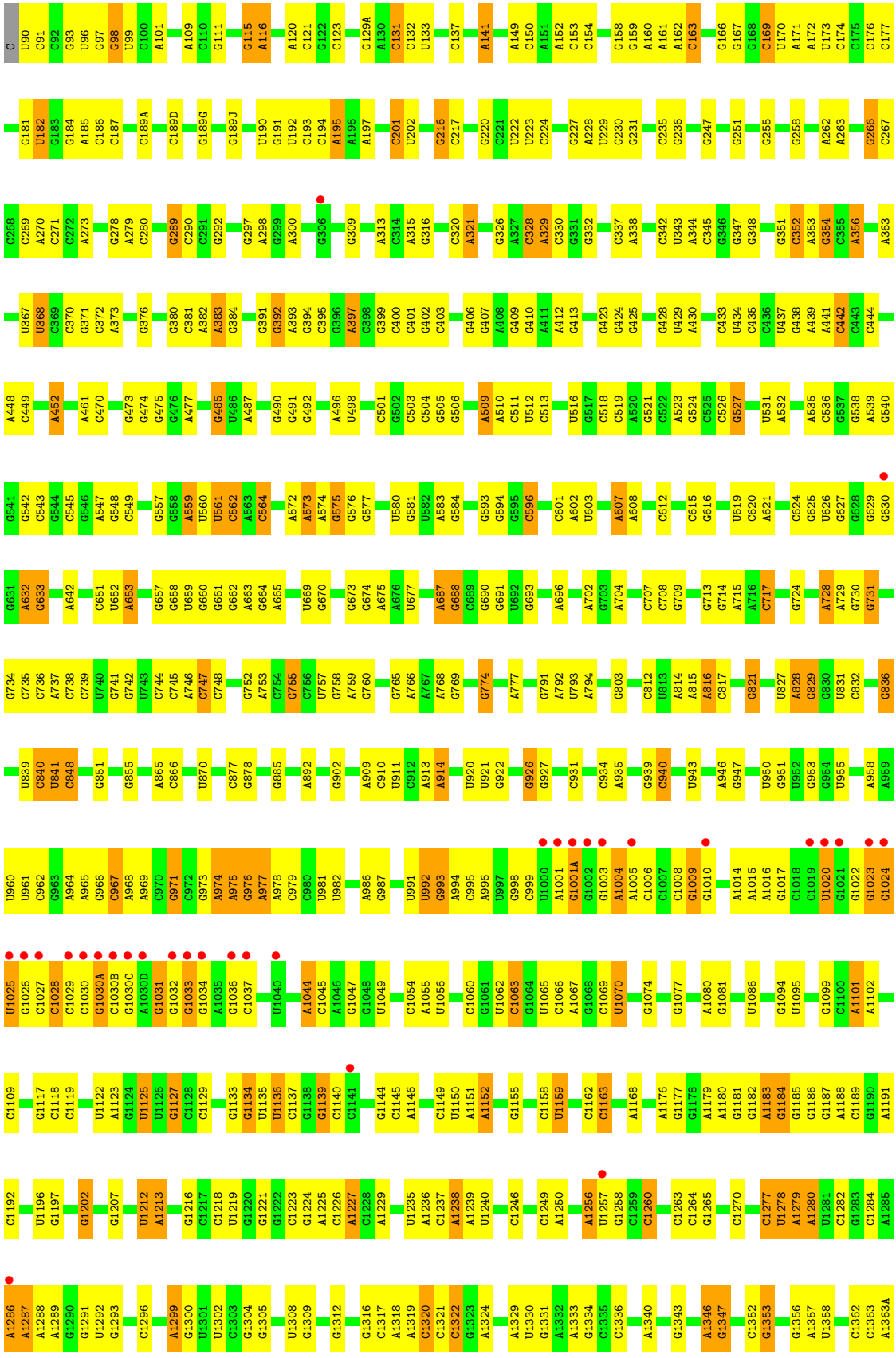
Chain 29:



• Molecule 32: 16S Ribosomal RNA

Chain 1a:




C U90 C91 C92 G93 U96 G97 G98 U99 C100 A101 A109 C110 G111 G115 A116 A120 C121 G122 C123 G129A A130 C131 C132 U133 C137 A141 A149 C150 A151 A152 C153 C154 G158 G159 A160 A161 A162 C163 G166 G167 G168 C169 U170 A171 A172 U173 C174 C175 C176 C177
G181 U182 G183 G184 A185 C186 C187 C189A C189D G189G G189J U190 G191 U192 C193 C194 A195 A196 A197 C201 U202 G216 C217 G220 C221 U222 U223 C224 G227 A228 U229 G230 G231 C235 G236 G247 G251 G255 G258 A262 A263 G266 C267
C268 C269 A270 C271 C272 A273 G278 A279 C280 G289 C290 C291 G292 G297 A298 G299 A300 G306 G309 A313 C314 A315 G316 C320 A321 G326 A327 C328 A329 G331 G332 C337 A338 C342 U343 A344 C345 G346 G347 G348 G351 C352 A353 G354 C355 A356 A363
U367 U368 C369 C370 G371 C372 A373 G376 G380 C381 A382 A383 G384 G391 G392 A393 G394 C395 G396 A397 C398 G399 C400 C401 G402 C403 G406 G407 A408 G409 G410 A411 A412 G413 G423 G424 G425 G428 U429 A430 C433 U434 C435 C436 U437 G438 A439 A441 C442 C443 C444
A448 C449 A452 A461 C470 G473 G474 G475 G476 A477 G485 U486 A487 G490 G491 G492 A496 U498 C501 G502 C503 C504 G505 G506 A509 A510 C511 U512 C513 U516 G517 C518 C519 A520 G521 C522 A523 G524 C525 C526 G527 U531 A532 A535 C536 G537 G538 A539 G540
G541 G542 C543 G544 C545 G546 A547 G548 C549 G557 G558 A559 U560 U561 C562 A563 C564 A572 A573 A574 G575 G576 G577 U580 G581 U582 A583 G584 G593 G594 G595 C596 C601 A602 U603 A607 A608 C612 C615 G616 U619 C620 A621 C624 G625 U626 G627 G628 G629 G630
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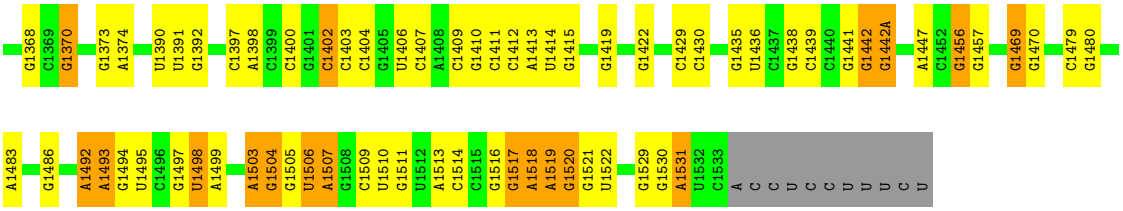
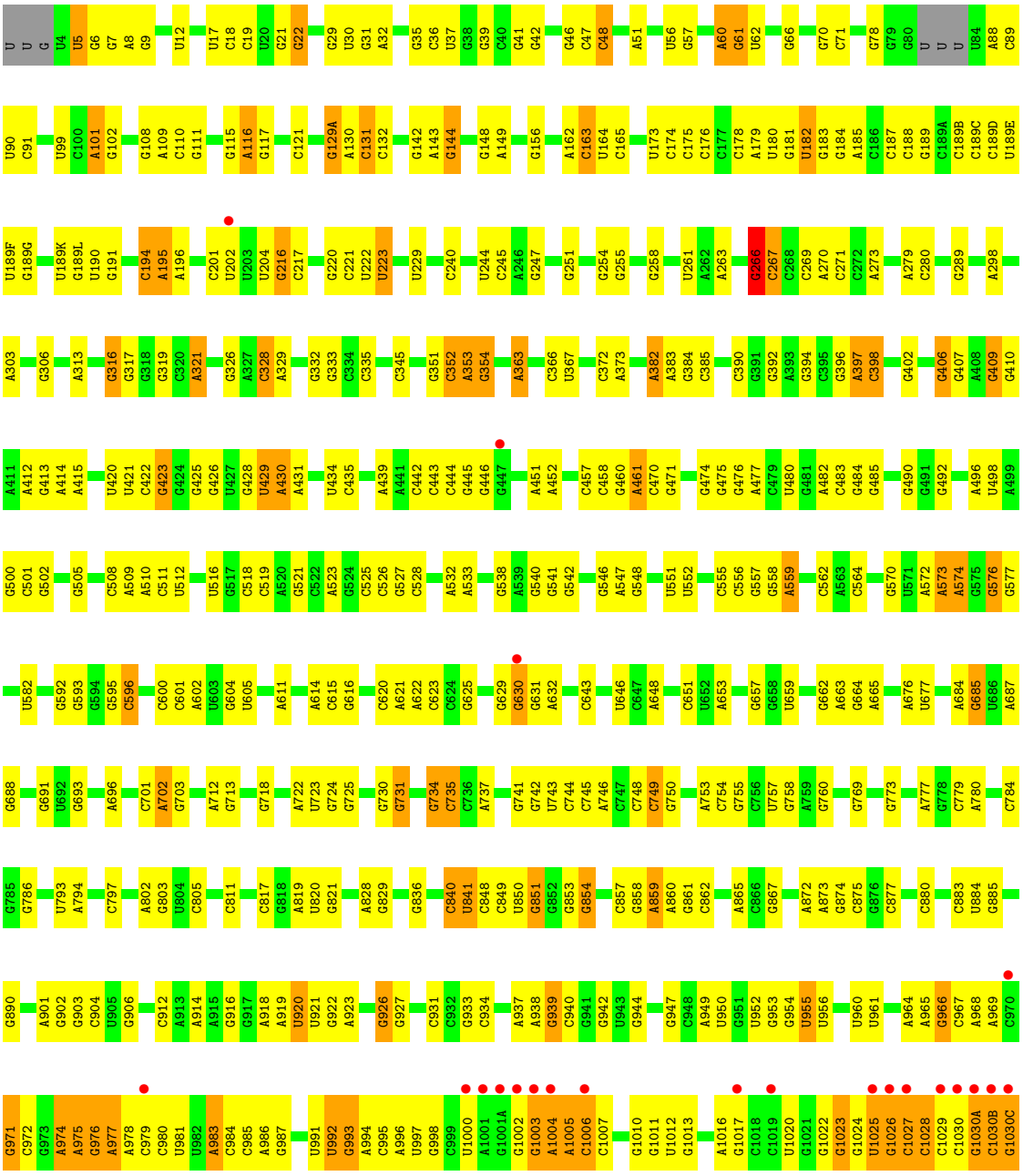
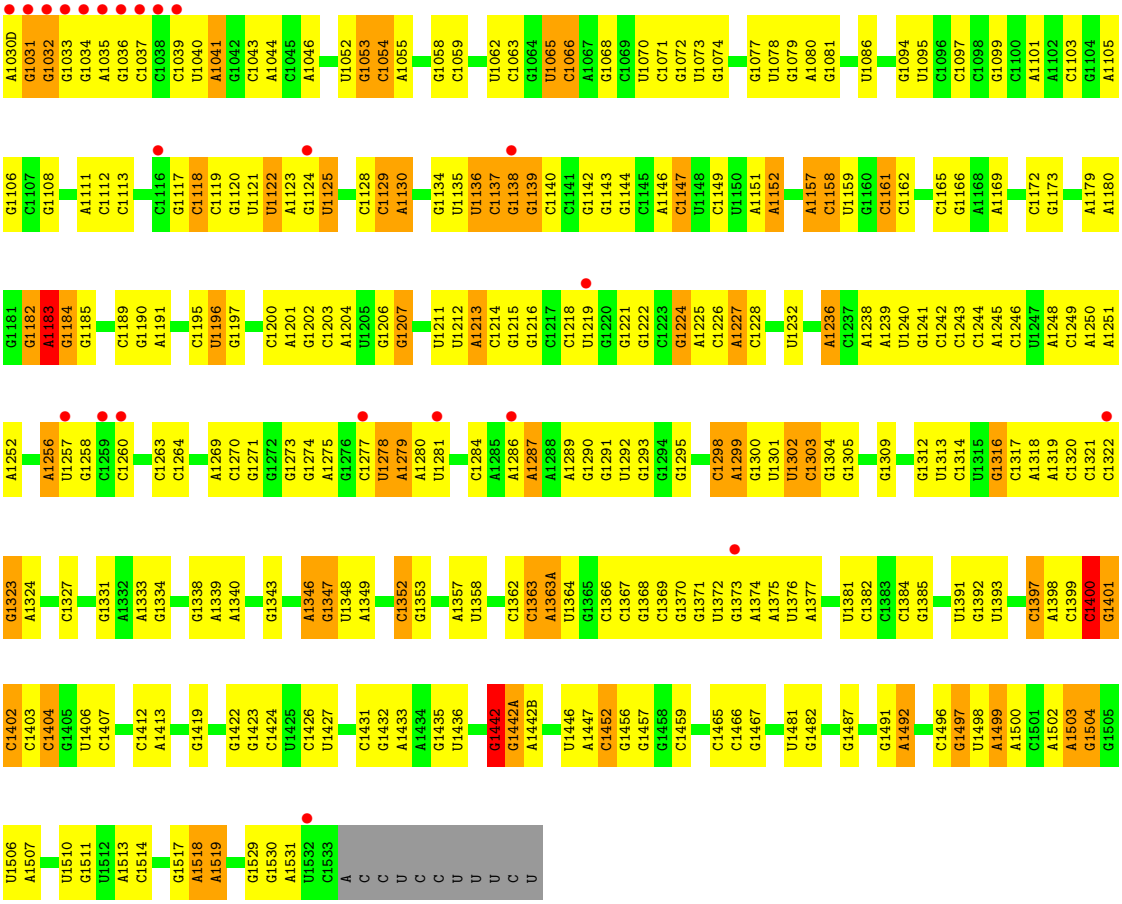
G734 C735 C736 A737 C738 C739 U740 G741 G742 U743 C744 C745 A746 C747 C748 G752 A753 C754 G755 G756 U757 G758 A759 G760 G765 A766 A767 A768 G769 G774 A777 G791 A792 U793 A794 G803 C812 U813 A814 A815 A816 C817 G821 U827 A828 G829 G830 U831 C832 G836
U839 C840 U841 C848 G851 G855 A865 C866 U870 C877 G878 G885 A892 G902 A909 C910 U911 C912 A913 A914 U920 U921 G922 G926 G927 C931 C934 A935 G939 G940 U943 A946 G947 U960 G961 U952 G953 G954 U955 A958 A959
U960 U961 C962 G963 A964 A965 G966 C967 A968 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978 C979 C980 U981 U982 A986 G987 U991 U992 G993 A994 C995 A996 U997 G998 C999 U1000 A1001 G1001A G1002 G1003 A1004 A1005 C1006 C1007 C1008 G1009 G1010 A1014 A1015 A1016 G1017 C1018 C1019 U1020 G1021 G1022 G1023 G1024
U1025 G1026 C1027 C1028 C1029 C1030 G1030A C1030B G1030C A1030D G1031 G1032 G1033 G1034 A1035 G1036 C1037 U1040 A1044 C1045 A1046 G1047 G1048 U1049 C1054 A1055 U1056 C1060 G1061 U1062 C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 G1074 G1077 A1080 G1081 U1086 G1094 U1095 G1099 C1100 A1101 A1102
C1109 G1117 C1118 C1119 U1122 A1123 G1124 U1125 U1126 G1127 C1128 C1129 G1133 G1134 U1135 U1136 C1137 C1138 G1139 C1140 C1141 G1144 C1145 A1146 C1149 U1150 A1151 A1152 G1155 C1158 U1159 C1162 C1163 A1168 A1176 G1177 G1178 A1179 A1180 G1181 G1182 A1183 G1184 G1185 G1186 G1187 A1188 C1189 G1190 A1191
C1192 U1196 G1197 G1202 G1207 U1212 A1213 G1216 C1217 C1218 U1219 G1220 G1221 G1222 C1223 G1224 A1225 C1226 A1227 C1228 A1229 U1235 A1236 C1237 A1238 A1239 U1240 C1246 C1249 A1250 A1256 U1257 G1258 C1259 C1260 C1263 C1264 G1265 C1270 C1277 U1278 A1279 A1280 U1281 C1282 G1283 C1284 A1285
A1286 A1287 A1288 A1289 G1290 G1291 U1292 G1293 C1296 A1299 G1300 U1301 U1302 C1303 G1304 G1305 U1308 G1309 G1312 C1316 C1317 A1318 A1319 C1320 C1321 C1322 G1323 A1324 A1329 U1330 G1331 A1332 A1333 G1334 C1335 C1336 A1340 G1343 A1346 G1347 C1352 G1353 G1356 A1357 U1358 C1362 C1363 A1363A



• Molecule 32: 16S Ribosomal RNA

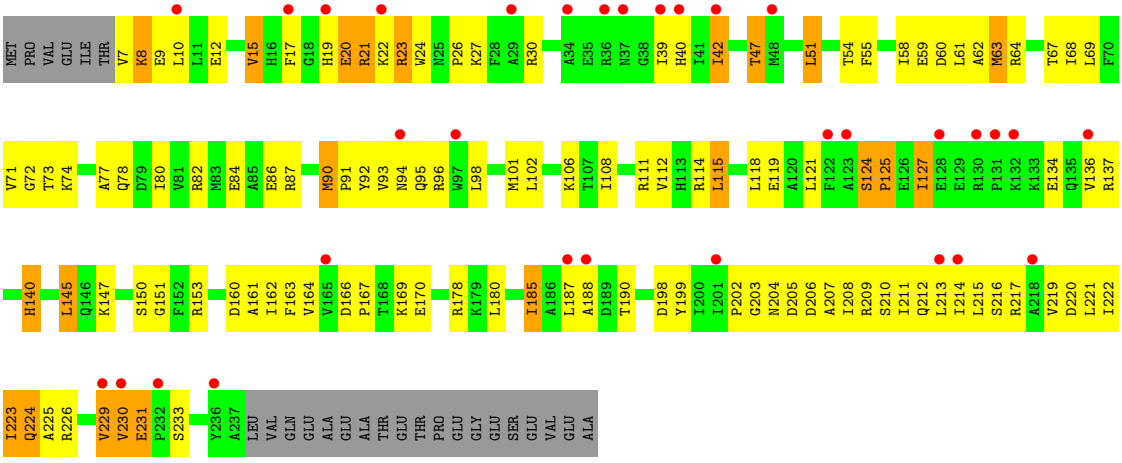
Chain 2a:





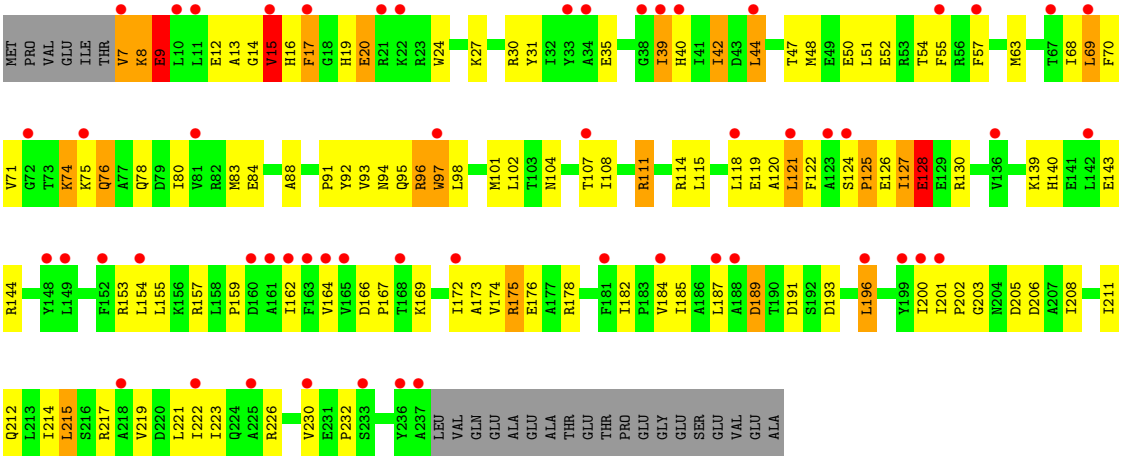
• Molecule 33: 30S ribosomal protein S2

Chain 1b:



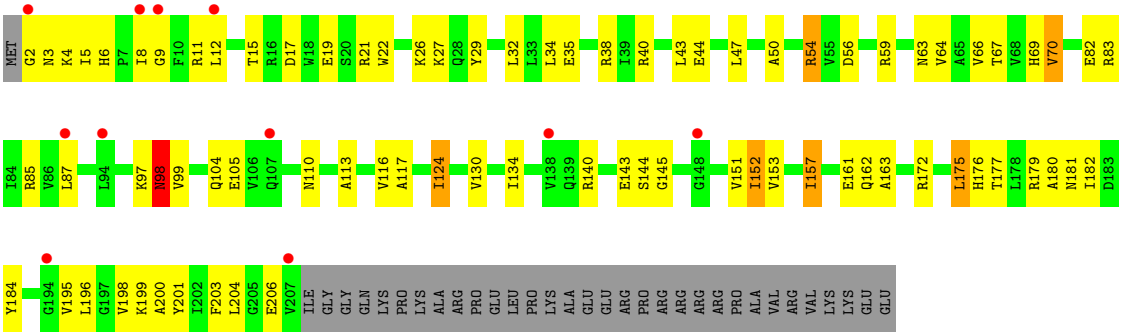
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



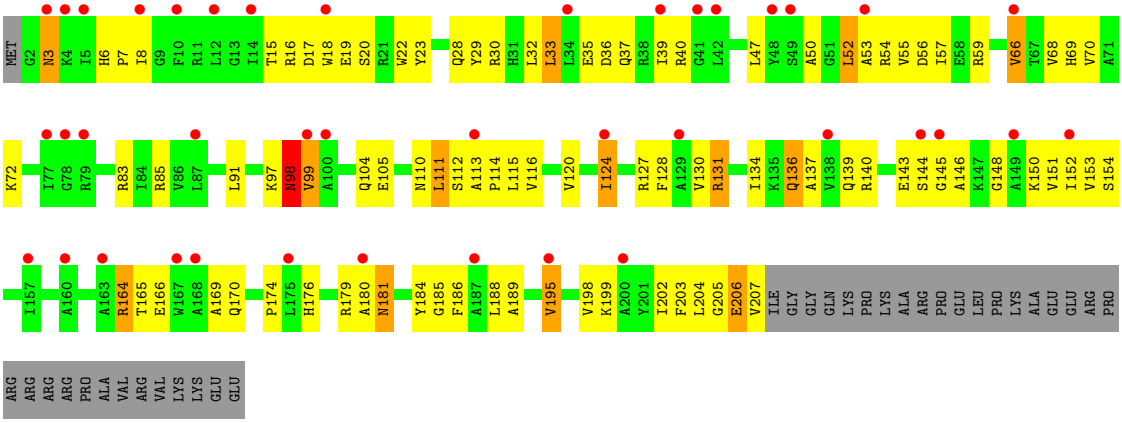
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



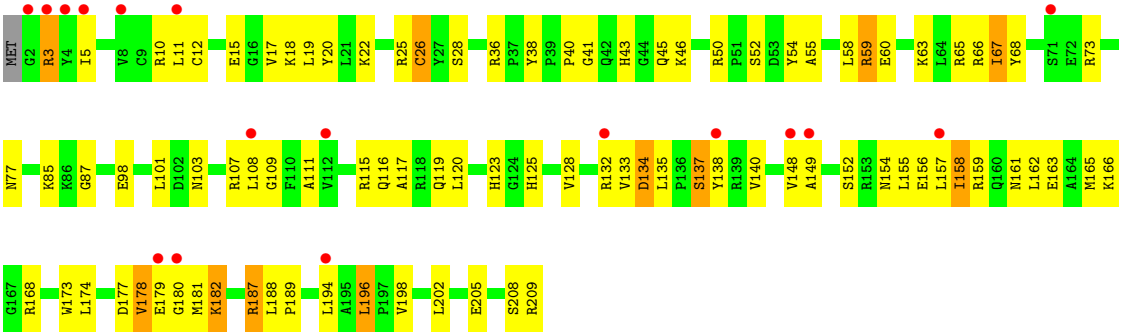
• Molecule 34: 30S ribosomal protein S3

Chain 2c:

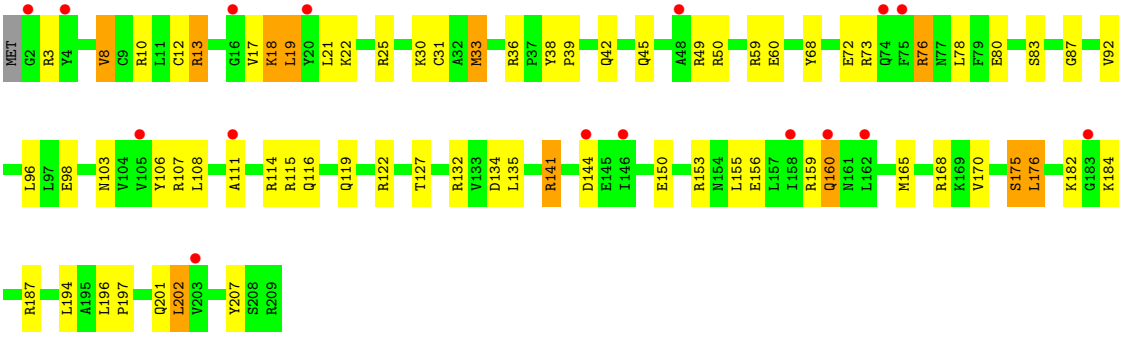


• Molecule 35: 30S ribosomal protein S4

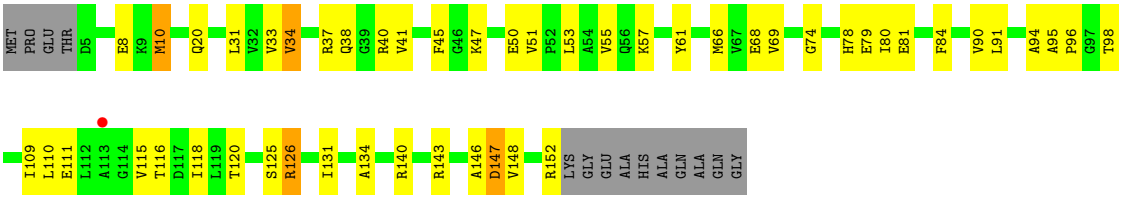
Chain 1d:



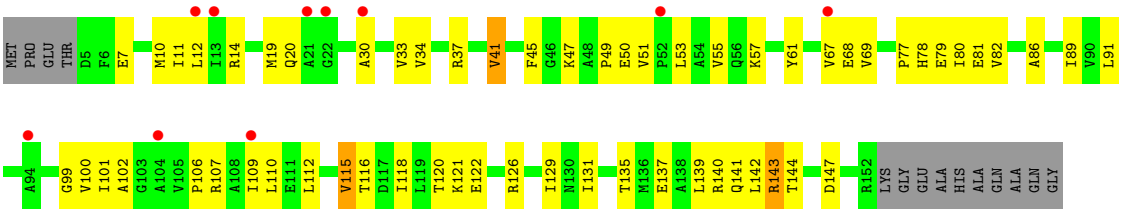
• Molecule 35: 30S ribosomal protein S4



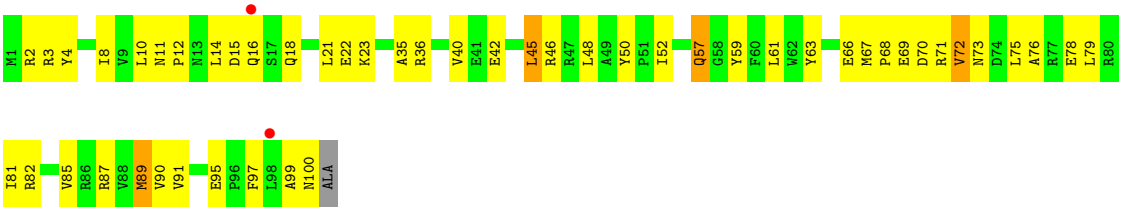
• Molecule 36: 30S ribosomal protein S5



• Molecule 36: 30S ribosomal protein S5

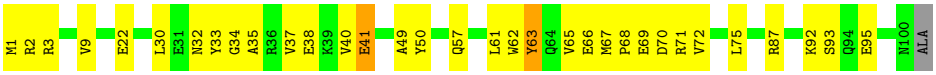


• Molecule 37: 30S ribosomal protein S6



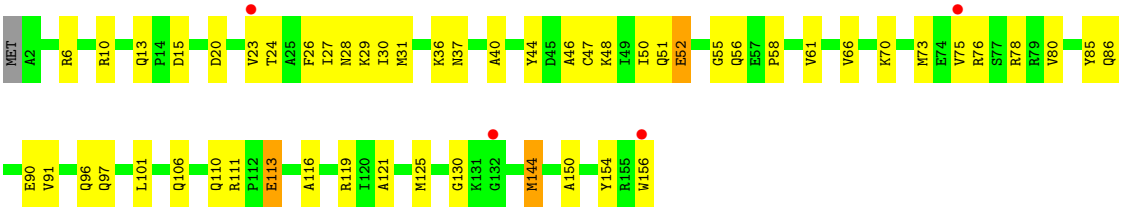
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



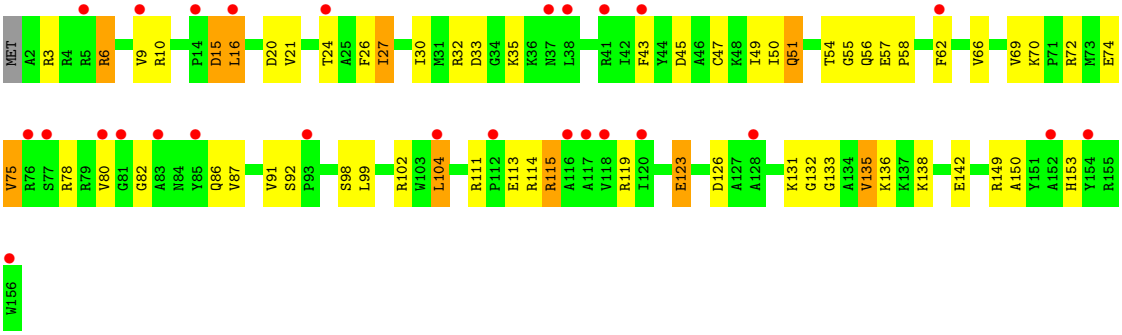
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



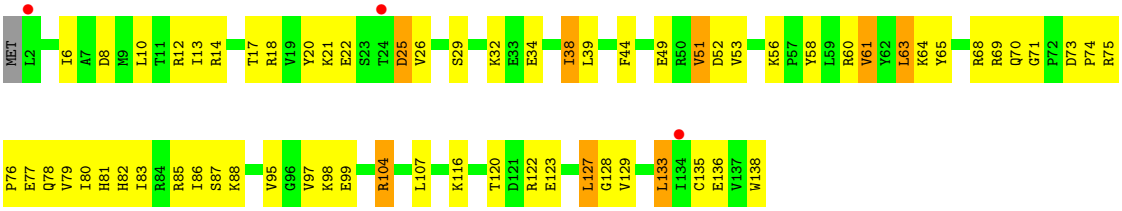
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



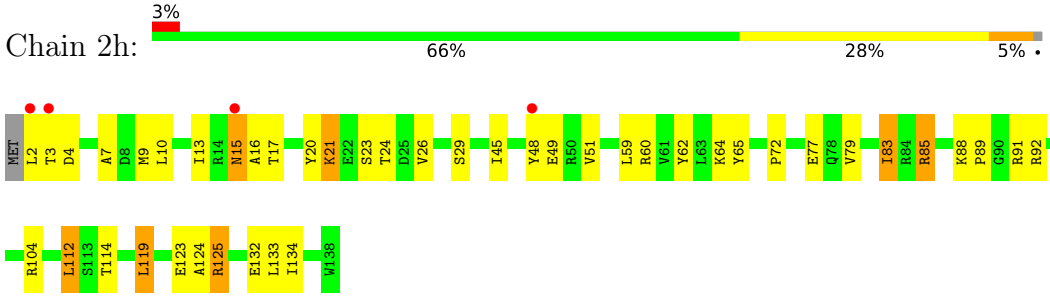
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



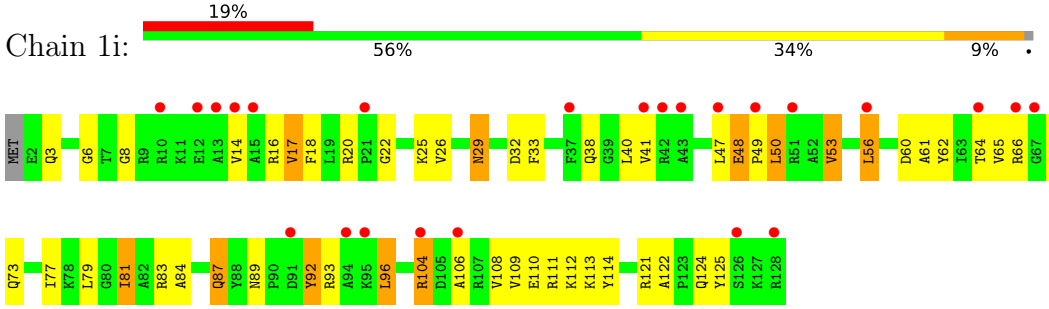
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



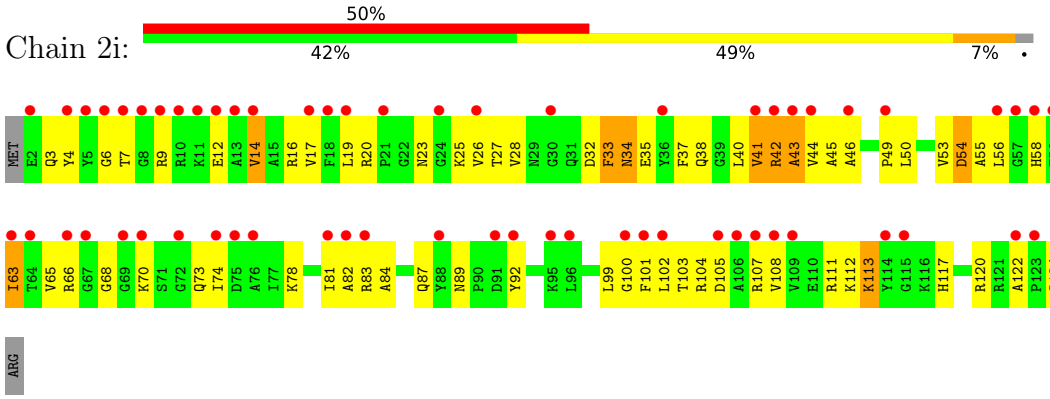
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



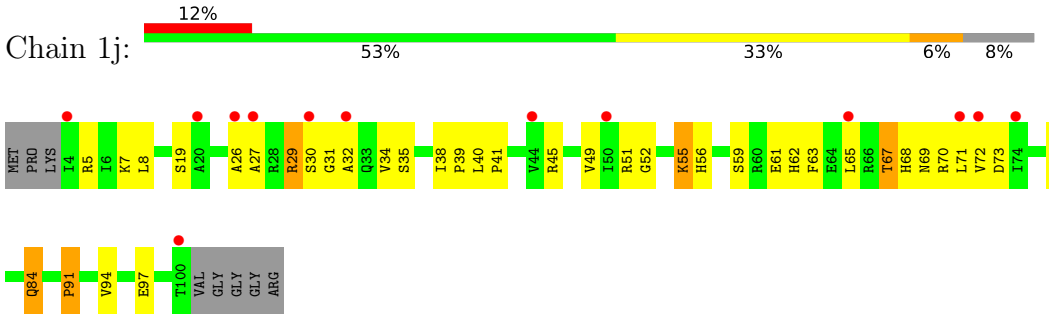
• Molecule 40: 30S ribosomal protein S9

Chain 2i:



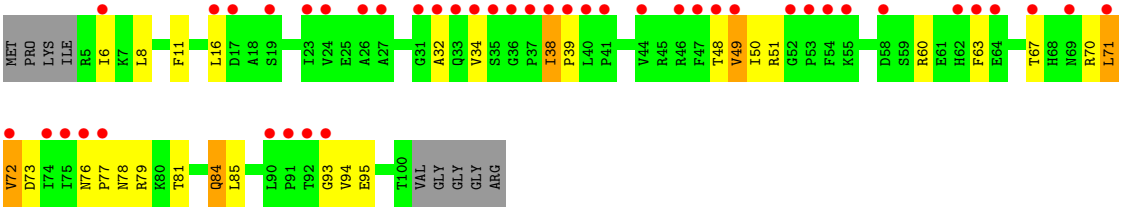
• Molecule 41: 30S ribosomal protein S10

Chain 1j:



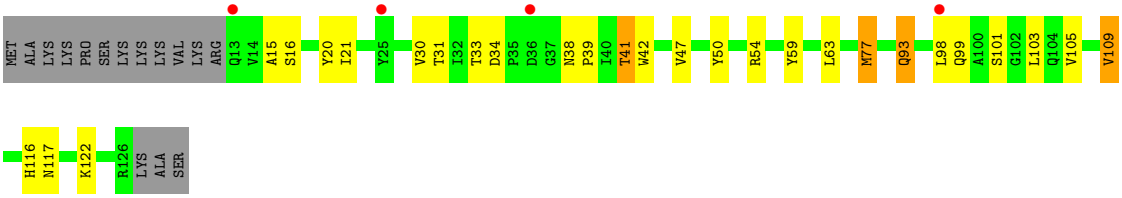
• Molecule 41: 30S ribosomal protein S10

Chain 2j:



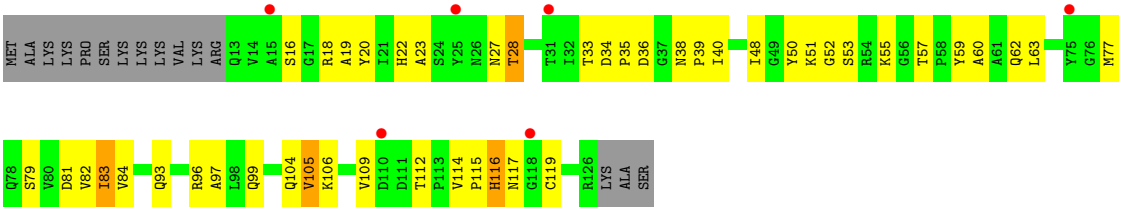
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



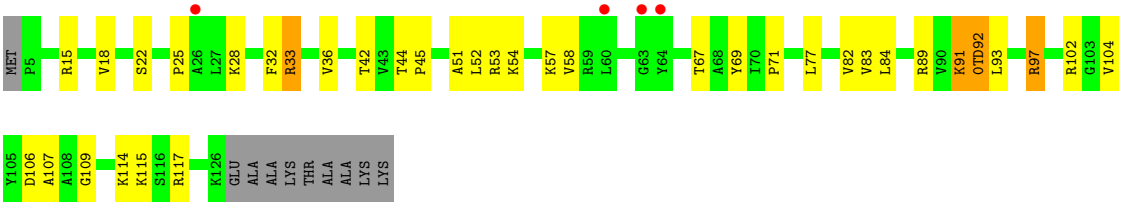
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



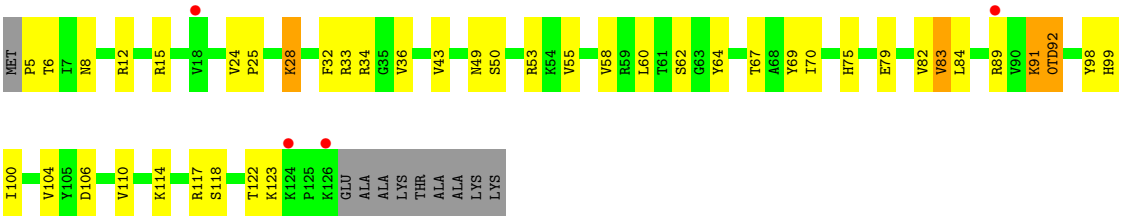
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



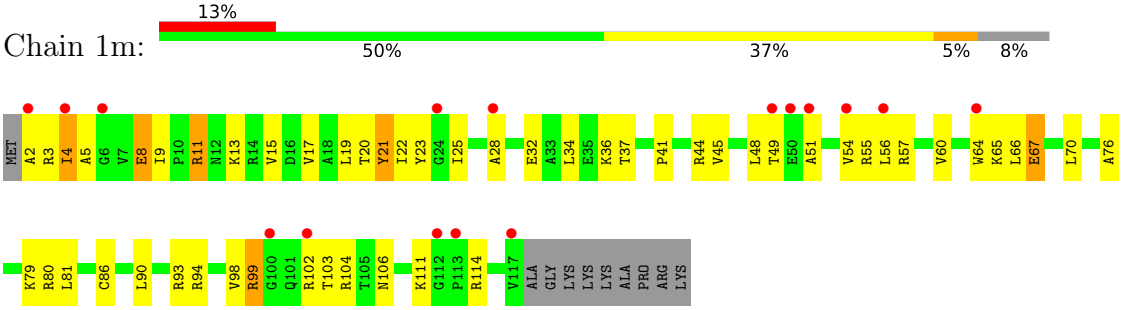
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



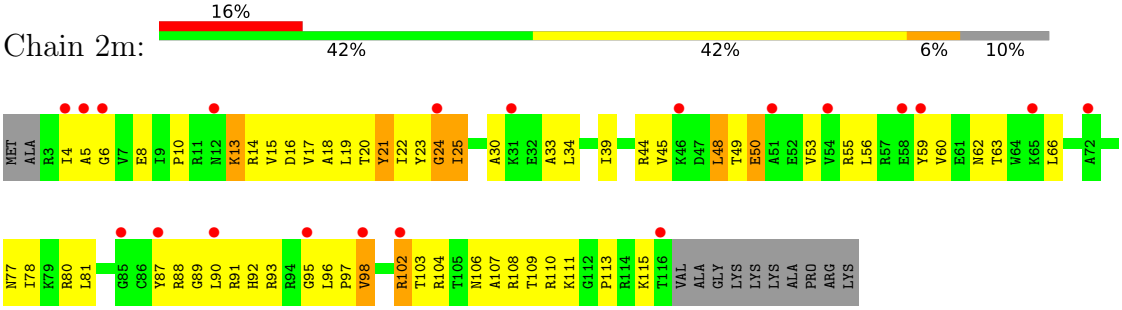
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



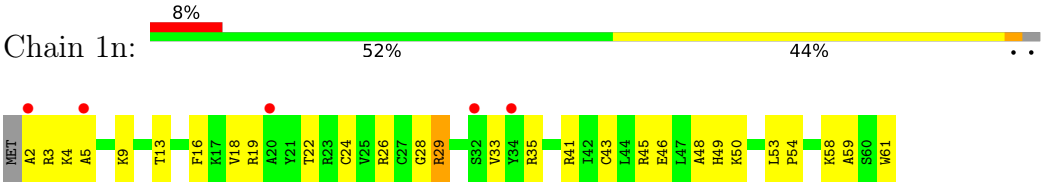
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



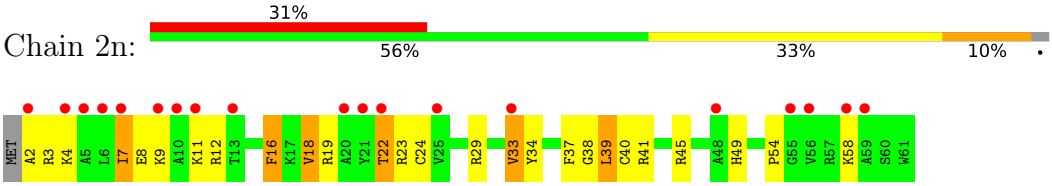
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



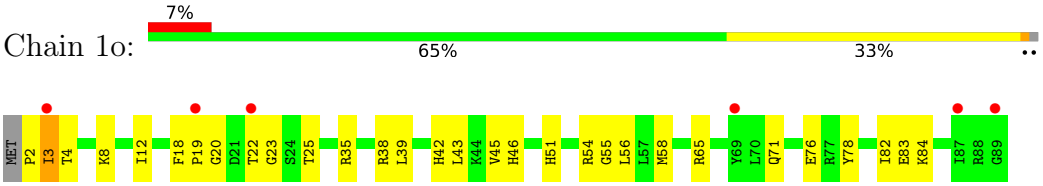
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:



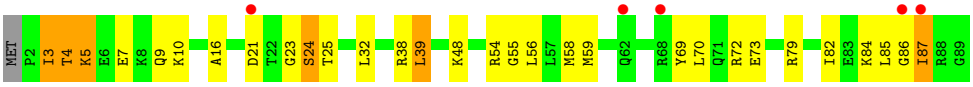
• Molecule 46: 30S ribosomal protein S15

Chain 1o:

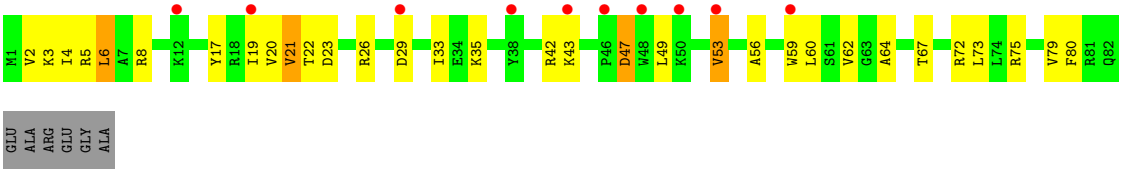


• Molecule 46: 30S ribosomal protein S15

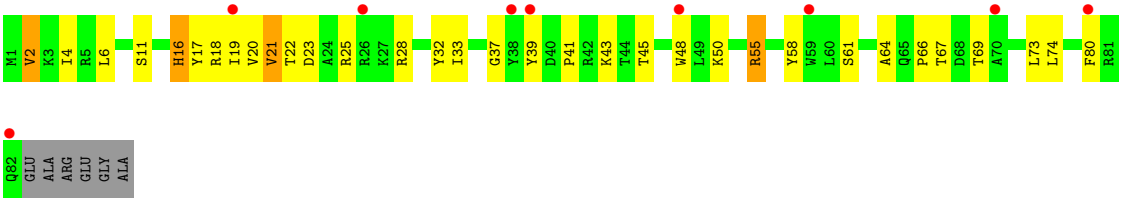
Chain 2o:



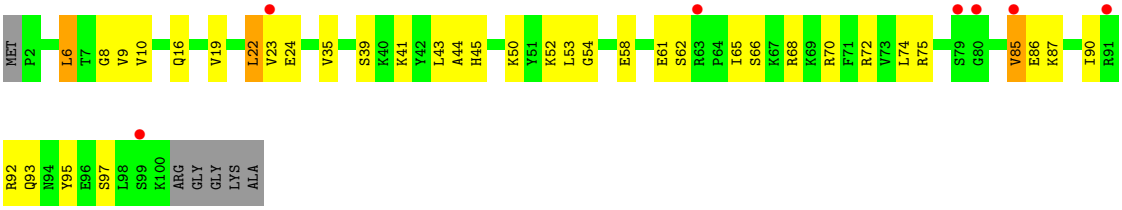
• Molecule 47: 30S ribosomal protein S16



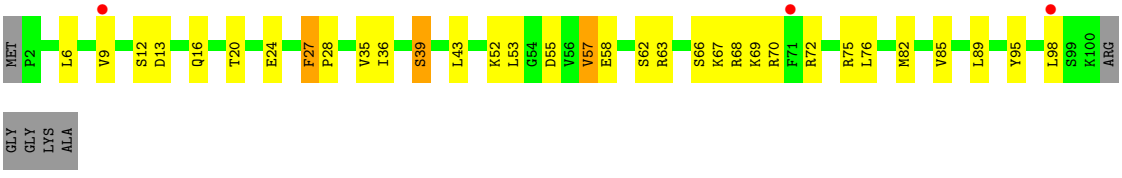
• Molecule 47: 30S ribosomal protein S16



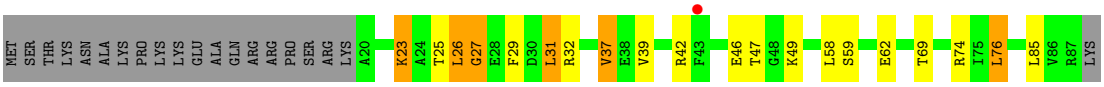
• Molecule 48: 30S ribosomal protein S17



• Molecule 48: 30S ribosomal protein S17

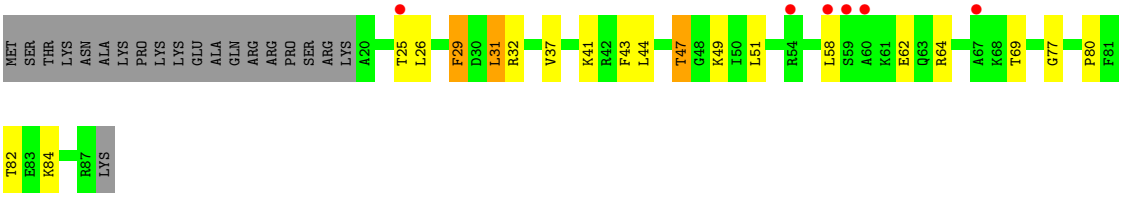


• Molecule 49: 30S ribosomal protein S18



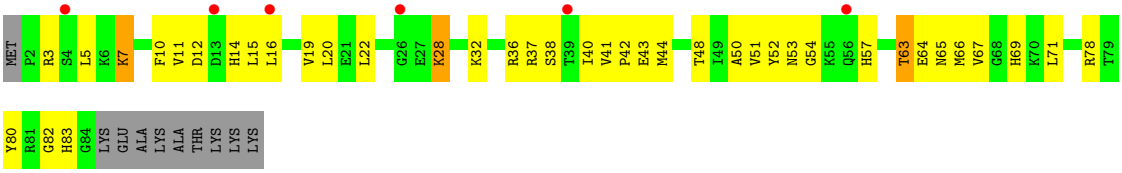
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



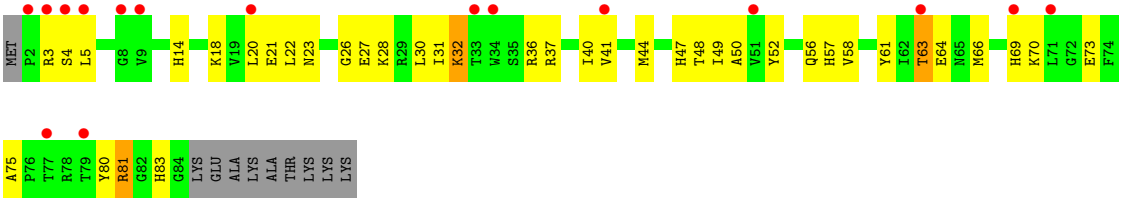
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



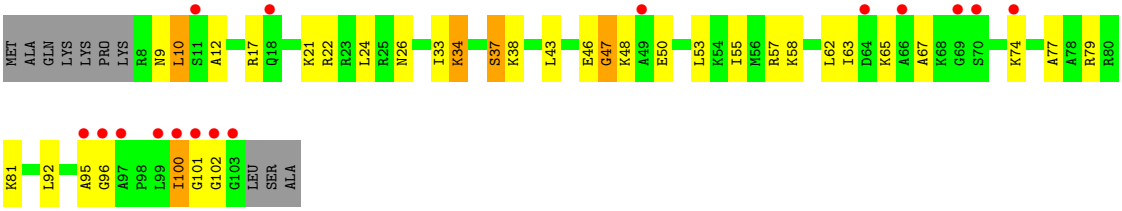
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



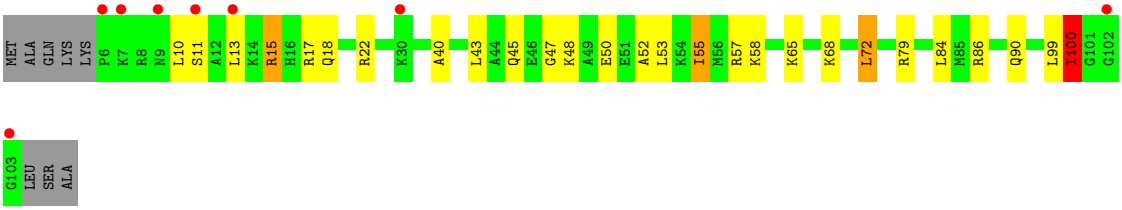
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



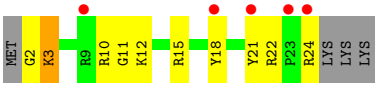
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



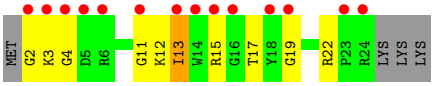
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



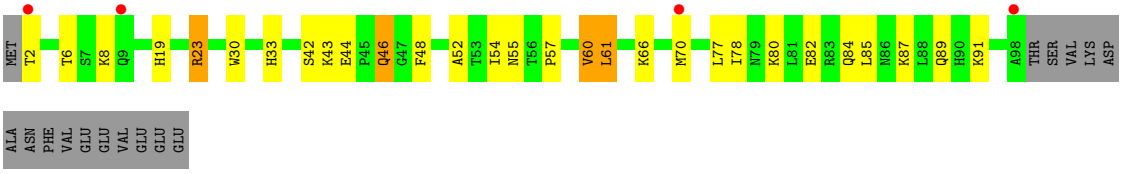
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



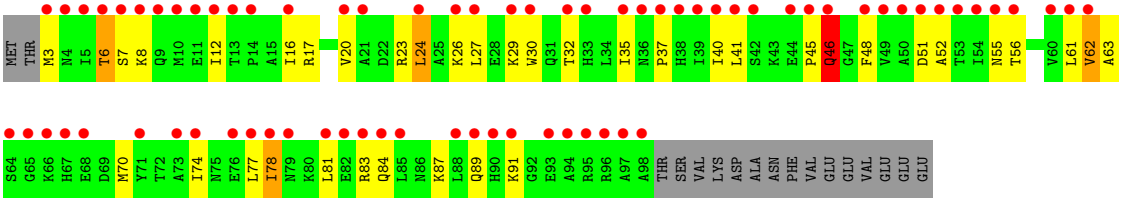
• Molecule 53: Ribosome-associated inhibitor A

Chain 1y:



• Molecule 53: Ribosome-associated inhibitor A

Chain 2y:



• Molecule 54: A-site Deacylated tRNA Analog

Chain 1w:

• Molecule 54: A-site Deacylated 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	209.71Å 449.95Å 621.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	224.98 – 2.50 224.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.5 (224.98-2.50) 98.5 (224.98-2.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.16 (at 2.52Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.229 , 0.280 0.230 , 0.280	Depositor DCC
R_{free} test set	98581 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	46.2	Xtriage
Anisotropy	0.157	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 65.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.35$, $< L^2 > = 0.18$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	297633	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.63% 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: MPD, 5MC, 2MA, 0TD, UR3, OMC, 4OC, 2MU, OMG, CLM, 5MU, 8AN, ZN, MA6, PSU, MG, G7M, M2G, SF4, 2MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1A	0.29	0/69030	0.49	4/107750 (0.0%)
1	2A	0.23	0/68902	0.43	1/107548 (0.0%)
2	1B	0.25	0/2876	0.44	0/4486
2	2B	0.19	0/2878	0.37	0/4490
3	1D	0.28	0/2181	0.52	0/2940
3	2D	0.24	0/2186	0.51	0/2944
4	1E	0.26	0/1592	0.51	0/2149
4	2E	0.22	0/1592	0.45	0/2149
5	1F	0.27	0/1619	0.50	0/2193
5	2F	0.23	0/1615	0.51	2/2188 (0.1%)
6	1G	0.21	0/1451	0.45	0/1961
6	2G	0.21	0/1449	0.46	0/1957
7	1H	0.23	0/1356	0.45	0/1834
7	2H	0.21	0/1350	0.45	0/1826
8	1I	0.20	0/1109	0.45	0/1512
8	2I	1.30	3/1091 (0.3%)	0.82	3/1490 (0.2%)
9	1N	0.26	0/1148	0.49	0/1547
9	2N	0.22	0/1144	0.42	0/1543
10	1O	0.26	0/943	0.48	0/1269
10	2O	0.23	0/943	0.42	0/1269
11	1P	0.28	0/1152	0.53	0/1533
11	2P	0.21	0/1152	0.49	0/1533
12	1Q	0.26	0/1143	0.50	0/1527
12	2Q	0.24	0/1143	0.49	0/1527
13	1R	0.28	0/982	0.51	0/1312
13	2R	0.24	0/982	0.48	0/1312
14	1S	0.23	0/887	0.49	0/1180
14	2S	0.21	0/880	0.44	0/1172
15	1T	0.26	0/1105	0.52	0/1477
15	2T	0.22	0/1097	0.42	0/1468
16	1U	0.29	0/977	0.51	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
16	2U	0.21	0/977	0.43	0/1301
17	1V	0.28	0/786	0.52	0/1053
17	2V	0.20	0/782	0.45	0/1049
18	1W	0.29	0/897	0.48	0/1205
18	2W	0.23	0/897	0.43	0/1205
19	1X	0.27	0/764	0.52	0/1025
19	2X	0.22	0/764	0.46	0/1025
20	1Y	0.25	0/823	0.51	0/1099
20	2Y	0.21	0/823	0.45	0/1100
21	1Z	0.23	0/1620	0.44	0/2200
21	2Z	0.20	0/1590	0.47	0/2162
22	10	0.27	0/662	0.53	0/881
22	20	0.23	0/659	0.55	0/877
23	11	0.24	0/761	0.43	0/1013
23	21	0.22	0/766	0.43	0/1018
24	12	0.23	0/590	0.48	0/781
24	22	0.20	0/594	0.40	0/785
25	13	0.26	0/474	0.50	0/635
25	23	0.22	0/469	0.50	0/630
26	14	0.25	0/559	0.57	0/754
26	24	0.32	0/549	0.70	0/741
27	15	0.34	0/473	0.57	0/639
27	25	0.21	0/469	0.48	0/635
28	16	0.24	0/460	0.46	0/613
28	26	0.21	0/456	0.46	0/608
29	17	0.31	0/426	0.56	0/561
29	27	0.24	0/426	0.49	0/561
30	18	0.28	0/525	0.55	0/691
30	28	0.22	0/525	0.40	0/691
31	19	0.27	0/310	0.50	0/407
31	29	0.24	0/310	0.46	0/407
32	1a	0.34	6/35795 (0.0%)	0.39	0/55864
32	2a	0.20	0/35890	0.39	4/56012 (0.0%)
33	1b	0.22	0/1876	0.47	0/2533
33	2b	0.23	0/1860	0.54	1/2518 (0.0%)
34	1c	0.19	0/1582	0.45	0/2137
34	2c	0.20	0/1566	0.45	0/2119
35	1d	0.21	0/1695	0.48	0/2274
35	2d	0.21	0/1698	0.45	0/2277
36	1e	0.21	0/1149	0.46	0/1548
36	2e	0.20	0/1149	0.43	0/1548
37	1f	0.19	0/827	0.43	0/1120
37	2f	0.20	0/829	0.44	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.19	0/1254	0.39	0/1683
38	2g	0.19	0/1248	0.39	0/1676
39	1h	0.19	0/1118	0.45	0/1506
39	2h	0.20	0/1108	0.44	0/1494
40	1i	0.21	0/1005	0.47	0/1351
40	2i	0.23	0/985	0.54	0/1329
41	1j	0.19	0/732	0.40	0/993
41	2j	0.23	0/723	0.45	0/984
42	1k	0.20	0/849	0.42	0/1150
42	2k	0.18	0/848	0.42	0/1149
43	1l	0.21	0/937	0.45	0/1260
43	2l	0.20	0/937	0.43	0/1260
44	1m	0.21	0/924	0.46	0/1242
44	2m	0.23	0/905	0.47	0/1217
45	1n	0.21	0/501	0.47	0/664
45	2n	0.22	0/501	0.48	0/664
46	1o	0.21	0/739	0.40	0/985
46	2o	0.18	0/739	0.38	0/985
47	1p	0.21	0/697	0.50	0/939
47	2p	0.20	0/693	0.48	0/935
48	1q	0.20	0/836	0.40	0/1117
48	2q	0.20	0/836	0.45	0/1117
49	1r	0.20	0/560	0.46	0/746
49	2r	0.19	0/560	0.42	0/746
50	1s	0.19	0/663	0.42	0/895
50	2s	0.20	0/660	0.45	0/893
51	1t	0.21	0/734	0.47	0/969
51	2t	0.20	0/736	0.42	0/976
52	1u	0.19	0/203	0.45	0/266
52	2u	0.18	0/203	0.48	0/266
53	1y	0.20	0/776	0.42	0/1048
53	2y	0.22	0/761	0.39	0/1030
54	1w	0.26	0/69	0.45	0/106
54	2w	0.21	0/69	0.34	0/106
55	1x	0.32	0/44	0.50	0/67
55	2x	0.41	0/44	0.48	0/67
56	1v	0.33	0/22	0.38	0/28
56	2v	0.26	0/22	0.62	0/28
All	All	0.27	9/310298 (0.0%)	0.45	15/463749 (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
26	24	0	1
33	1b	0	1
All	All	0	2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	2I	82	ARG	CD-NE	39.05	2.00	1.46
32	1a	368	U	N3-C4	24.40	1.87	1.38
32	1a	368	U	C2-N3	23.32	1.84	1.37
32	1a	368	U	N1-C2	20.62	1.79	1.38
32	1a	368	U	C4-C5	19.52	1.82	1.43
32	1a	368	U	N1-C6	19.29	1.76	1.38
32	1a	368	U	C5-C6	17.41	1.69	1.34
8	2I	82	ARG	NE-CZ	15.55	1.50	1.33
8	2I	82	ARG	CG-CD	6.09	1.70	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	2I	82	ARG	CD-NE-CZ	21.88	155.03	124.40
8	2I	82	ARG	CG-CD-NE	10.58	135.28	112.00
1	1A	1042	G	OP1-P-O3'	-9.20	80.39	108.00
1	1A	1042	G	OP2-P-O3'	-7.56	85.32	108.00
8	2I	82	ARG	NE-CZ-NH1	7.49	128.99	121.50
33	2b	13	ALA	N-CA-C	-7.08	104.76	113.19
1	2A	1992	G	C2'-C3'-O3'	6.17	118.75	109.50
5	2F	21	ALA	CA-C-N	5.64	131.86	121.70
5	2F	21	ALA	C-N-CA	5.64	131.86	121.70
32	2a	266	G	C2'-C3'-O3'	5.38	117.58	109.50
32	2a	1442	G	OP1-P-O3'	5.37	117.02	105.20
1	1A	2689	U	C4'-C3'-O3'	5.33	117.40	109.40
32	2a	266	G	P-O3'-C3'	5.30	128.15	120.20
1	1A	784	A	P-O3'-C3'	5.26	128.09	120.20
32	2a	1183	A	P-O3'-C3'	5.01	127.72	120.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	1b	231	GLU	Peptide

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Mol	Chain	Res	Type	Group
26	24	18	CYS	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	31202	761	0
1	2A	61758	0	31151	860	0
2	1B	2572	0	1305	31	0
2	2B	2573	0	1306	33	0
3	1D	2131	0	2207	54	0
3	2D	2136	0	2218	67	0
4	1E	1559	0	1618	35	0
4	2E	1559	0	1618	28	0
5	1F	1584	0	1625	42	0
5	2F	1580	0	1619	54	0
6	1G	1426	0	1445	44	0
6	2G	1424	0	1441	69	0
7	1H	1330	0	1407	40	0
7	2H	1324	0	1402	49	0
8	1I	1094	0	1127	26	0
8	2I	1076	0	1094	37	7
9	1N	1121	0	1195	18	0
9	2N	1117	0	1184	25	0
10	1O	933	0	996	23	0
10	2O	933	0	996	18	0
11	1P	1135	0	1212	37	0
11	2P	1135	0	1212	33	0
12	1Q	1122	0	1179	25	0
12	2Q	1122	0	1177	35	0
13	1R	968	0	1033	29	0
13	2R	968	0	1033	20	0
14	1S	877	0	938	23	0
14	2S	870	0	923	35	0
15	1T	1091	0	1151	28	0
15	2T	1083	0	1136	27	0
16	1U	959	0	1019	13	0
16	2U	959	0	1019	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	1V	775	0	841	19	0
17	2V	771	0	830	25	0
18	1W	886	0	940	10	0
18	2W	886	0	940	23	0
19	1X	750	0	814	28	0
19	2X	750	0	814	21	0
20	1Y	810	0	892	28	0
20	2Y	810	0	887	27	0
21	1Z	1587	0	1598	35	0
21	2Z	1557	0	1564	40	0
22	10	653	0	674	18	0
22	20	650	0	665	22	0
23	11	754	0	823	25	0
23	21	759	0	837	32	0
24	12	588	0	643	17	0
24	22	592	0	654	14	0
25	13	469	0	518	13	0
25	23	464	0	514	8	0
26	14	546	0	522	26	0
26	24	536	0	514	32	0
27	15	459	0	476	9	0
27	25	455	0	465	9	0
28	16	453	0	473	12	0
28	26	449	0	469	9	0
29	17	418	0	467	9	0
29	27	418	0	467	7	0
30	18	517	0	582	16	0
30	28	517	0	582	14	0
31	19	307	0	335	4	0
31	29	307	0	335	9	0
32	1a	32246	0	16294	478	7
32	2a	32331	0	16338	506	0
33	1b	1842	0	1862	81	0
33	2b	1825	0	1828	73	0
34	1c	1558	0	1557	54	0
34	2c	1542	0	1517	63	0
35	1d	1665	0	1687	68	0
35	2d	1668	0	1703	55	0
36	1e	1133	0	1191	29	0
36	2e	1133	0	1191	40	0
37	1f	814	0	808	33	0
37	2f	816	0	808	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	1g	1235	0	1249	33	0
38	2g	1229	0	1238	42	0
39	1h	1098	0	1143	49	0
39	2h	1088	0	1126	27	0
40	1i	986	0	990	44	0
40	2i	966	0	953	64	0
41	1j	719	0	672	29	0
41	2j	710	0	661	21	0
42	1k	834	0	838	18	0
42	2k	833	0	836	32	0
43	1l	932	0	981	24	0
43	2l	932	0	981	26	0
44	1m	914	0	954	38	0
44	2m	895	0	920	40	0
45	1n	492	0	529	29	0
45	2n	492	0	529	25	0
46	1o	728	0	760	18	0
46	2o	728	0	760	20	0
47	1p	681	0	697	17	0
47	2p	677	0	686	17	0
48	1q	823	0	891	21	0
48	2q	823	0	891	22	0
49	1r	555	0	618	18	0
49	2r	555	0	618	12	0
50	1s	648	0	658	29	0
50	2s	645	0	635	33	0
51	1t	732	0	809	21	0
51	2t	733	0	795	17	0
52	1u	199	0	208	9	0
52	2u	199	0	208	9	0
53	1y	764	0	785	16	0
53	2y	749	0	757	27	0
54	1w	63	0	34	0	0
54	2w	63	0	34	0	0
55	1x	63	0	33	1	0
55	2x	63	0	33	1	0
56	1v	23	0	29	3	0
56	2v	23	0	29	4	0
57	10	8	0	0	0	0
57	11	5	0	0	0	0
57	13	3	0	0	0	0
57	15	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	17	5	0	0	0	0
57	18	2	0	0	0	0
57	19	2	0	0	0	0
57	1A	1021	0	0	0	0
57	1B	31	0	0	0	0
57	1D	18	0	0	0	0
57	1E	9	0	0	0	0
57	1F	18	0	0	0	0
57	1G	4	0	0	0	0
57	1H	2	0	0	0	0
57	1N	5	0	0	0	0
57	1O	1	0	0	0	0
57	1P	4	0	0	0	0
57	1Q	4	0	0	0	0
57	1R	3	0	0	0	0
57	1T	6	0	0	0	0
57	1U	7	0	0	0	0
57	1V	6	0	0	0	0
57	1W	5	0	0	0	0
57	1X	1	0	0	0	0
57	1Y	1	0	0	0	0
57	1Z	1	0	0	0	0
57	1a	270	0	0	0	0
57	1b	1	0	0	0	0
57	1d	5	0	0	0	0
57	1e	1	0	0	0	0
57	1f	2	0	0	0	0
57	1g	3	0	0	0	0
57	1h	2	0	0	0	0
57	1i	2	0	0	0	0
57	1l	2	0	0	0	0
57	1m	2	0	0	0	0
57	1n	3	0	0	0	0
57	1o	2	0	0	0	0
57	1t	2	0	0	0	0
57	1y	3	0	0	0	0
57	20	2	0	0	0	0
57	21	3	0	0	0	0
57	23	1	0	0	0	0
57	25	4	0	0	0	0
57	27	3	0	0	0	0
57	28	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	29	1	0	0	0	0
57	2A	726	0	0	0	0
57	2B	17	0	0	0	0
57	2D	9	0	0	0	0
57	2E	8	0	0	0	0
57	2F	4	0	0	0	0
57	2G	3	0	0	0	0
57	2I	1	0	0	0	0
57	2N	1	0	0	0	0
57	2O	2	0	0	0	0
57	2P	2	0	0	0	0
57	2Q	3	0	0	0	0
57	2R	2	0	0	0	0
57	2T	4	0	0	0	0
57	2U	1	0	0	0	0
57	2V	3	0	0	0	0
57	2W	2	0	0	0	0
57	2Y	1	0	0	0	0
57	2a	189	0	0	0	0
57	2e	1	0	0	0	0
57	2f	1	0	0	0	0
57	2j	1	0	0	0	0
57	2l	2	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	20	0	11	2	0
58	2A	20	0	11	1	0
59	1A	12	0	12	2	0
59	1B	12	0	12	1	0
60	18	8	0	14	0	0
60	1A	8	0	14	1	0
60	1T	8	0	14	1	0
60	1a	8	0	14	3	0
60	2A	8	0	14	0	0
60	2B	8	0	14	0	0
61	14	1	0	0	0	0
61	15	1	0	0	0	0
61	16	1	0	0	0	0
61	19	1	0	0	0	0
61	1Y	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	1n	1	0	0	0	0
61	24	1	0	0	0	0
61	25	1	0	0	0	0
61	26	1	0	0	0	0
61	29	1	0	0	0	0
61	2Y	1	0	0	0	0
61	2n	1	0	0	0	0
62	1d	8	0	0	2	0
62	2d	8	0	0	0	0
63	10	25	0	0	0	0
63	11	26	0	0	1	0
63	12	15	0	0	2	0
63	13	24	0	0	2	0
63	14	2	0	0	0	0
63	15	24	0	0	0	0
63	16	18	0	0	1	0
63	17	17	0	0	1	0
63	18	26	0	0	0	0
63	19	7	0	0	0	0
63	1A	3946	0	0	162	0
63	1B	90	0	0	6	0
63	1D	121	0	0	3	0
63	1E	80	0	0	5	0
63	1F	59	0	0	3	0
63	1G	19	0	0	0	0
63	1H	13	0	0	1	0
63	1I	5	0	0	0	0
63	1N	50	0	0	3	0
63	1O	33	0	0	1	0
63	1P	65	0	0	3	0
63	1Q	35	0	0	3	0
63	1R	32	0	0	2	0
63	1S	15	0	0	1	0
63	1T	28	0	0	0	0
63	1U	46	0	0	4	0
63	1V	41	0	0	3	0
63	1W	30	0	0	1	0
63	1X	28	0	0	0	0
63	1Y	21	0	0	3	0
63	1Z	13	0	0	0	0
63	1a	412	0	0	25	0
63	1b	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	1c	1	0	0	0	0
63	1d	7	0	0	2	0
63	1e	2	0	0	0	0
63	1f	3	0	0	0	0
63	1h	1	0	0	0	0
63	1j	1	0	0	0	0
63	1l	5	0	0	1	0
63	1o	2	0	0	0	0
63	1p	3	0	0	0	0
63	1t	1	0	0	0	0
63	1w	5	0	0	0	0
63	1x	5	0	0	0	0
63	1y	5	0	0	1	0
63	20	12	0	0	1	0
63	21	20	0	0	3	0
63	22	2	0	0	0	0
63	23	3	0	0	1	0
63	24	1	0	0	0	0
63	25	10	0	0	0	0
63	26	5	0	0	2	0
63	27	8	0	0	0	0
63	28	13	0	0	3	0
63	29	1	0	0	0	0
63	2A	2126	0	0	161	0
63	2B	46	0	0	6	0
63	2D	54	0	0	9	0
63	2E	26	0	0	1	0
63	2F	24	0	0	4	0
63	2G	7	0	0	0	0
63	2H	3	0	0	0	0
63	2I	6	0	0	1	0
63	2N	3	0	0	0	0
63	2O	22	0	0	2	0
63	2P	28	0	0	3	0
63	2Q	19	0	0	2	0
63	2R	17	0	0	2	0
63	2S	4	0	0	0	0
63	2T	11	0	0	0	0
63	2U	13	0	0	1	0
63	2V	7	0	0	1	0
63	2W	19	0	0	3	0
63	2X	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	2Y	4	0	0	0	0
63	2Z	10	0	0	2	0
63	2a	294	0	0	18	0
63	2d	2	0	0	0	0
63	2e	2	0	0	0	0
63	2f	2	0	0	0	0
63	2j	2	0	0	0	0
63	2l	2	0	0	0	0
63	2n	1	0	0	0	0
63	2o	3	0	0	0	0
63	2p	1	0	0	0	0
63	2r	3	0	0	0	0
63	2t	2	0	0	0	0
63	2w	2	0	0	0	0
63	2x	2	0	0	0	0
63	2y	2	0	0	0	0
All	All	297633	0	194805	4850	7

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

All (4850) 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)
32:1a:368:U:C4	32:1a:368:U:C5	1.82	1.66
32:1a:368:U:C6	32:1a:368:U:N1	1.76	1.50
32:1a:368:U:N1	32:1a:368:U:C2	1.79	1.48
32:1a:368:U:C2	32:1a:368:U:N3	1.84	1.46
32:1a:368:U:C4	32:1a:368:U:N3	1.87	1.41
8:2I:82:ARG:NE	8:2I:82:ARG:CD	2.00	1.24
1:1A:1082:U:H3	1:1A:1086:A:N6	1.40	1.16
32:1a:78:G:H1	32:1a:91:C:N4	1.49	1.08
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.23	1.04
1:1A:2137:C:H42	1:1A:2154:G:H1	1.02	1.01
1:1A:2137:C:N4	1:1A:2154:G:H1	1.59	0.99
1:1A:517:C:OP1	27:15:16:ARG:NH2	1.97	0.97
1:2A:962:G:OP1	63:2A:3803:HOH:O	1.83	0.96
1:2A:2139:C:N4	1:2A:2152:G:H1	1.64	0.95
8:2I:82:ARG:HG3	8:2I:89:TYR:HB2	1.48	0.95
1:1A:1054:A:H61	1:1A:1105:U:H3	0.96	0.95
1:2A:2139:C:H42	1:2A:2152:G:H1	0.95	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.30	0.94
1:1A:1082:U:H3	1:1A:1086:A:H61	1.05	0.92
1:1A:1082:U:O4	1:1A:1086:A:N1	2.03	0.91
1:2A:83:G:H1	1:2A:102:G:HO2'	1.18	0.90
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.52	0.90
1:2A:2139:C:N3	1:2A:2152:G:N2	2.18	0.90
1:1A:1054:A:N6	1:1A:1105:U:H3	1.68	0.89
1:2A:1970:A:OP1	63:2A:3804:HOH:O	1.90	0.89
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.53	0.89
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.38	0.87
10:1O:116:SER:HA	60:1a:3271:MPD:HM2	1.56	0.87
32:2a:954:G:H21	32:2a:1227:A:H62	1.21	0.87
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.37	0.87
32:1a:78:G:H1	32:1a:91:C:H42	0.89	0.87
32:1a:78:G:N2	32:1a:91:C:N3	2.22	0.87
1:1A:1082:U:N3	1:1A:1086:A:N6	2.15	0.87
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.08	0.86
34:2c:54:ARG:HB2	34:2c:69:HIS:HB2	1.55	0.86
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.39	0.86
1:1A:1634:A:OP2	63:1A:4104:HOH:O	1.92	0.85
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.59	0.84
1:1A:302:C:OP2	20:1Y:73:ARG:NH2	2.11	0.84
41:2j:81:THR:HA	41:2j:84:GLN:HB3	1.59	0.84
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.59	0.83
1:1A:2822:G:OP2	63:1A:4107:HOH:O	1.96	0.83
1:2A:1065:U:H3	1:2A:1073:A:H61	1.25	0.83
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.61	0.83
1:1A:2875:C:OP1	15:1T:3:ARG:NH1	2.12	0.83
32:2a:1086:U:H3	32:2a:1099:G:H22	1.23	0.83
1:1A:1665:A:OP2	63:1A:4105:HOH:O	1.95	0.83
32:1a:1086:U:H3	32:1a:1099:G:H22	1.24	0.83
1:1A:1173:G:H21	1:1A:1177:A:H2	1.22	0.82
19:2X:88:LYS:HE3	19:2X:93:GLU:HG3	1.60	0.82
1:1A:1669:A:OP2	63:1A:4110:HOH:O	1.98	0.82
36:2e:140:ARG:O	36:2e:143:ARG:NH2	2.12	0.82
11:2P:2:LYS:HE2	11:2P:4:SER:H	1.44	0.82
1:1A:2137:C:N3	1:1A:2154:G:N2	2.27	0.82
32:1a:612:C:O2	32:1a:629:G:N2	2.12	0.82
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.61	0.82
1:1A:826:U:OP1	63:1A:4109:HOH:O	1.98	0.82
32:1a:1025:U:O2	32:1a:1036:G:O6	1.98	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2427:C:OP1	63:2A:3805:HOH:O	1.97	0.82
1:1A:1648:C:OP1	63:1A:4111:HOH:O	1.98	0.81
1:1A:279:C:H42	1:1A:361:G:H1	1.25	0.81
1:1A:1352:U:OP1	63:1A:4108:HOH:O	1.98	0.81
8:1I:85:GLU:O	8:1I:87:LYS:N	2.13	0.81
32:1a:1024:G:H21	32:1a:1025:U:H5"	1.44	0.81
1:2A:2353:G:N7	63:2A:3849:HOH:O	2.12	0.81
1:2A:1359:A:N6	1:2A:1372:U:O4	2.13	0.81
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.61	0.81
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.45	0.81
1:2A:194:G:OP2	63:2A:3806:HOH:O	1.98	0.81
1:2A:1314:C:OP1	63:2A:3807:HOH:O	1.99	0.81
8:1I:9:LEU:HB3	8:1I:12:LEU:HB3	1.63	0.81
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.14	0.80
32:2a:573:A:OP2	63:2a:3201:HOH:O	1.98	0.80
2:1B:81:G:N7	59:1B:232:ARG:NH2	2.29	0.80
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.64	0.80
33:2b:80:ILE:HD11	33:2b:212:GLN:HE21	1.47	0.80
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.14	0.80
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.61	0.80
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.13	0.80
32:2a:1046:A:N6	32:2a:1211:U:O2	2.15	0.80
33:2b:7:VAL:O	33:2b:217:ARG:NH1	2.14	0.79
1:1A:1024:G:OP2	63:1A:4112:HOH:O	2.00	0.79
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.56	0.79
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.63	0.79
22:20:10:THR:HG22	22:20:12:ASN:H	1.48	0.79
32:2a:975:A:H4'	32:2a:976:G:H5"	1.63	0.79
39:2h:95:VAL:HB	39:2h:99:GLU:HG3	1.64	0.79
1:1A:249:C:O2'	11:1P:64:LYS:NZ	2.16	0.79
26:14:57:GLU:HB2	26:14:58:ARG:HG2	1.61	0.79
1:2A:2100:G:H1	1:2A:2189:U:H3	1.28	0.79
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.63	0.78
1:1A:1771:C:OP1	63:1A:4113:HOH:O	2.02	0.78
32:1a:538:G:H5"	43:1l:114:LYS:HB2	1.66	0.78
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.64	0.78
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.48	0.78
1:1A:956:G:H5"	12:1Q:77:LYS:HD2	1.65	0.78
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.47	0.78
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.65	0.78
1:1A:1059:G:H1	1:1A:1079:C:H42	1.30	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:16:CYS:SG	26:14:17:GLY:N	2.57	0.78
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.63	0.78
18:1W:94:ASP:OD1	63:1W:301:HOH:O	2.02	0.77
1:1A:741:G:OP2	63:1A:4114:HOH:O	2.02	0.77
1:2A:826:U:OP1	63:2A:3805:HOH:O	2.02	0.77
63:1A:4107:HOH:O	13:1R:3:HIS:NE2	2.17	0.77
5:1F:12:LEU:HG	5:1F:124:LEU:HD11	1.66	0.77
1:2A:2125:G:H22	1:2A:2172:U:H3'	1.49	0.77
1:1A:2427:C:OP1	63:1A:4109:HOH:O	2.02	0.77
1:1A:1023:U:OP2	63:1A:4112:HOH:O	2.02	0.77
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.49	0.77
11:2P:29:LYS:HD3	11:2P:30:THR:HG23	1.65	0.77
1:1A:1702:G:N7	63:1A:4185:HOH:O	2.18	0.77
32:2a:1129:C:N4	32:2a:1143:G:H1	1.82	0.77
1:1A:886:C:H3'	1:1A:887:A:H5"	1.67	0.77
1:1A:1039:G:O6	1:1A:1116:C:N4	2.16	0.77
1:1A:1664:A:OP1	63:1A:4105:HOH:O	2.02	0.76
1:1A:2879:C:OP2	63:1A:4119:HOH:O	2.04	0.76
1:2A:412:A:OP1	63:2A:3811:HOH:O	2.03	0.76
1:1A:1418:G:OP2	63:1A:4116:HOH:O	2.03	0.76
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.66	0.76
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.67	0.76
1:1A:1267:U:OP1	63:1A:4118:HOH:O	2.03	0.76
1:1A:1332:G:OP1	63:1A:4115:HOH:O	2.02	0.76
32:1a:1318:A:OP1	50:1s:7:LYS:NZ	2.18	0.76
1:2A:2137:C:N3	1:2A:2154:G:O6	2.18	0.76
1:2A:1602:U:O4	63:2A:3809:HOH:O	2.02	0.76
33:2b:12:GLU:HA	33:2b:15:VAL:HG23	1.66	0.76
22:20:11:ARG:O	22:20:14:ARG:NH2	2.19	0.76
1:2A:1364:G:OP1	23:21:2:SER:N	2.18	0.76
1:2A:1647:G:OP1	63:2A:3808:HOH:O	2.02	0.76
6:2G:37:VAL:HG23	6:2G:99:MET:HG3	1.67	0.76
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.19	0.76
1:1A:2099:U:H3	1:1A:2190:G:H1	1.32	0.76
1:1A:2623:G:OP1	63:1A:4117:HOH:O	2.03	0.76
42:1k:15:ALA:HA	42:1k:77:MET:HA	1.67	0.76
1:2A:792:G:O6	63:2A:3816:HOH:O	2.04	0.76
20:2Y:83:THR:HG21	20:2Y:99:CYS:HB2	1.68	0.76
1:1A:947:G:N7	63:1A:4193:HOH:O	2.19	0.76
26:14:56:VAL:O	26:14:60:GLN:NE2	2.17	0.75
1:2A:468:G:OP1	63:2A:3812:HOH:O	2.03	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:188:ARG:HA	11:2P:3:LEU:HD11	1.67	0.75
1:2A:131:G:OP1	63:2A:3815:HOH:O	2.04	0.75
1:2A:691:C:OP1	63:2A:3814:HOH:O	2.04	0.75
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.19	0.75
1:2A:2499:C:OP1	63:2A:3810:HOH:O	2.03	0.75
32:2a:548:G:OP1	63:2a:3202:HOH:O	2.04	0.75
1:2A:1783:A:OP2	63:2A:3813:HOH:O	2.03	0.75
34:2c:57:ILE:HG12	34:2c:66:VAL:HG13	1.69	0.75
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.67	0.75
32:1a:975:A:H4'	32:1a:976:G:H5"	1.69	0.75
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.51	0.75
1:2A:2000:G:OP2	63:2A:3817:HOH:O	2.05	0.75
28:26:14:THR:OG1	28:26:48:VAL:O	2.05	0.75
33:2b:121:LEU:HA	33:2b:125:PRO:HG2	1.69	0.75
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.34	0.75
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.20	0.75
22:10:11:ARG:O	22:10:14:ARG:NH2	2.15	0.74
1:1A:330:A:H2	1:1A:1210:A:HO2'	1.33	0.74
1:1A:2690:C:OP1	13:1R:17:ARG:NH2	2.20	0.74
32:1a:38:G:H22	32:1a:397:A:H5'	1.52	0.74
17:2V:18:LEU:HB3	17:2V:96:ILE:HD11	1.69	0.74
33:2b:122:PHE:HA	33:2b:127:ILE:HG12	1.69	0.74
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD13	1.68	0.74
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.21	0.74
32:2a:1403:C:O2	32:2a:1499:A:N6	2.18	0.74
1:2A:1226:A:OP1	17:2V:84:LYS:NZ	2.17	0.74
1:2A:1676:A:N7	63:2A:3921:HOH:O	2.20	0.74
32:2a:528:C:N4	43:2l:49:ASN:OD1	2.20	0.74
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.69	0.74
1:1A:496:G:N7	63:1A:4194:HOH:O	2.19	0.74
1:2A:2122:U:H3	1:2A:2176:A:H61	1.34	0.74
20:2Y:82:PRO:O	20:2Y:101:LYS:NZ	2.20	0.74
1:2A:2141:G:O6	1:2A:2150:U:O2	2.06	0.74
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.70	0.74
16:1U:101:ARG:NH2	63:1U:301:HOH:O	2.21	0.74
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.21	0.74
50:2s:20:LEU:HA	50:2s:23:ASN:HB2	1.68	0.74
1:2A:881:G:H1	1:2A:895:U:H3	1.33	0.74
32:2a:981:U:O4	63:2a:3203:HOH:O	2.05	0.74
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.68	0.74
28:16:2:ALA:N	63:16:7301:HOH:O	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1604:C:OP1	63:2A:3818:HOH:O	2.05	0.73
1:2A:2115:G:H21	1:2A:2171:A:H61	1.35	0.73
1:2A:963:U:OP2	63:2A:3803:HOH:O	2.06	0.73
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.19	0.73
1:2A:1031:G:H5"	31:29:8:LYS:HE3	1.70	0.73
1:2A:1081:U:H3'	1:2A:1085:A:H61	1.53	0.73
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.21	0.73
4:2E:199:ARG:NH1	63:2E:402:HOH:O	2.21	0.73
1:1A:1026:U:OP1	63:1A:4112:HOH:O	2.07	0.73
1:1A:1260:G:OP1	63:1A:4120:HOH:O	2.06	0.73
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.22	0.73
7:2H:27:LYS:HG2	7:2H:32:GLU:HB3	1.71	0.73
29:17:34:ARG:NH2	63:17:201:HOH:O	2.19	0.73
1:2A:2042:A:OP1	63:2A:3820:HOH:O	2.07	0.73
1:1A:1604:C:N4	63:1A:4207:HOH:O	2.20	0.73
1:1A:1670:C:OP2	63:1A:4110:HOH:O	2.06	0.73
26:14:53:GLU:HB2	26:14:56:VAL:HG12	1.71	0.73
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.20	0.73
1:2A:731:C:OP1	63:2A:3819:HOH:O	2.06	0.73
1:2A:1971:A:OP1	63:2A:3804:HOH:O	2.05	0.73
1:1A:1101:U:H2'	1:1A:1102:C:H6	1.54	0.73
1:1A:2350:C:OP2	63:1A:4124:HOH:O	2.07	0.73
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.71	0.73
1:2A:948:G:OP1	63:2A:3803:HOH:O	2.05	0.72
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.70	0.72
1:1A:256:A:OP2	63:1A:4121:HOH:O	2.06	0.72
38:2g:70:LYS:O	38:2g:138:LYS:NZ	2.22	0.72
1:1A:2660:A:N7	7:1H:175:LYS:NZ	2.37	0.72
14:1S:3:ARG:NH1	14:1S:4:LEU:O	2.20	0.72
1:1A:2355:C:H1'	22:10:39:ARG:HH21	1.54	0.72
1:1A:2763:G:OP2	63:1A:4126:HOH:O	2.07	0.72
32:1a:1373:G:H5"	38:1g:36:LYS:HD2	1.69	0.72
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.71	0.72
32:2a:402:G:N7	63:2a:3219:HOH:O	2.23	0.72
1:1A:1542:A:O2'	63:1A:4127:HOH:O	2.07	0.72
63:1A:4107:HOH:O	4:1E:110:GLY:O	2.07	0.72
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.21	0.72
1:1A:249:C:OP1	63:1A:4122:HOH:O	2.06	0.72
1:1A:2601:C:H4'	55:1x:74:C:H5"	1.69	0.72
15:1T:84:GLN:HG2	15:1T:85:LYS:HG3	1.70	0.72
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:760:G:OP1	63:1A:4123:HOH:O	2.07	0.72
5:1F:10:PRO:HB3	5:1F:17:ARG:HH21	1.54	0.72
32:1a:664:G:H22	32:1a:741:G:H1	1.35	0.72
32:1a:812:C:N3	63:1a:3322:HOH:O	2.22	0.72
1:2A:2036:C:OP2	63:2A:3825:HOH:O	2.07	0.72
1:2A:2717:G:N7	63:2A:3940:HOH:O	2.22	0.72
32:2a:1500:A:OP1	63:2a:3204:HOH:O	2.07	0.72
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.70	0.72
1:2A:1079:C:N4	1:2A:1080:C:O2	2.22	0.72
32:2a:718:G:C8	42:2k:116:HIS:HB3	2.25	0.72
1:1A:557:U:OP1	63:1A:4128:HOH:O	2.08	0.72
14:2S:15:ARG:HB3	14:2S:19:LYS:HE3	1.72	0.72
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.70	0.71
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	1.71	0.71
1:2A:2027:G:N7	63:2A:3934:HOH:O	2.22	0.71
1:1A:2116:G:OP1	1:1A:2166:G:N2	2.23	0.71
15:1T:39:ARG:HH21	32:1a:345:C:H5"	1.55	0.71
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.72	0.71
1:1A:614(B):G:OP1	59:1A:4023:ARG:N	2.23	0.71
1:1A:2821:A:OP2	63:1A:4107:HOH:O	2.09	0.71
1:2A:965:C:OP2	63:2A:3827:HOH:O	2.08	0.71
32:2a:492:G:OP2	63:2a:3205:HOH:O	2.08	0.71
32:1a:964:A:OP1	63:1y:301:HOH:O	2.08	0.71
1:2A:1665:A:N7	63:2A:3946:HOH:O	2.23	0.71
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.24	0.71
7:2H:101:ARG:NH2	7:2H:117:PRO:O	2.24	0.71
18:1W:33:ARG:NH2	18:1W:52:GLU:OE1	2.23	0.71
36:1e:140:ARG:O	36:1e:143:ARG:NH2	2.23	0.71
1:2A:947:G:OP2	63:2A:3822:HOH:O	2.07	0.71
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.72	0.71
32:1a:300:A:O2'	32:1a:564:C:N3	2.20	0.71
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.73	0.71
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.21	0.71
1:2A:1602:U:OP1	63:2A:3826:HOH:O	2.07	0.71
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.23	0.71
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.23	0.71
11:1P:42:SER:O	63:1P:301:HOH:O	2.08	0.71
1:2A:1352:U:OP1	63:2A:3824:HOH:O	2.07	0.71
1:2A:2431:U:OP1	63:2A:3821:HOH:O	2.07	0.71
11:1P:141:ALA:HA	25:23:38:GLU:HG2	1.72	0.71
33:1b:178:ARG:HH21	39:1h:74:PRO:HB3	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:74:ASN:N	8:2I:74:ASN:OD1	2.24	0.71
32:2a:977:A:N6	32:2a:1224:G:OP1	2.22	0.71
1:1A:1016:G:N7	63:1A:4249:HOH:O	2.24	0.71
2:2B:66:A:H61	2:2B:109:C:H5'	1.56	0.71
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.24	0.71
34:2c:120:VAL:HG21	34:2c:137:ALA:HB2	1.73	0.71
32:2a:70:G:H1	32:2a:99:U:H3	1.38	0.70
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.73	0.70
1:2A:2102:U:OP2	63:2A:3829:HOH:O	2.09	0.70
4:2E:110:GLY:O	63:2R:301:HOH:O	2.08	0.70
32:2a:991:U:H2'	32:2a:1212:U:C4	2.26	0.70
40:2i:125:TYR:HE1	40:2i:127:LYS:HD3	1.55	0.70
41:1j:5:ARG:NE	41:1j:73:ASP:OD1	2.23	0.70
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.23	0.70
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.92	0.70
4:2E:54:GLN:HB2	4:2E:76:ARG:HG3	1.72	0.70
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.73	0.70
23:21:31:GLY:O	63:21:201:HOH:O	2.09	0.70
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.72	0.70
32:1a:1056:U:H5'	34:1c:163:ALA:HB2	1.72	0.70
37:1f:35:ALA:HA	37:1f:67:MET:HB3	1.72	0.70
38:1g:75:VAL:HG21	38:1g:144:MET:HG2	1.73	0.70
1:2A:98:G:H5'	24:22:3:LEU:HD23	1.73	0.70
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.23	0.70
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.23	0.70
1:1A:1173:G:N2	1:1A:1176:G:OP2	2.24	0.70
1:2A:1076:C:H1'	1:2A:1077:A:H5'	1.74	0.70
38:2g:113:GLU:HB2	38:2g:119:ARG:HG3	1.72	0.70
1:1A:370:G:OP2	63:1A:4130:HOH:O	2.09	0.70
32:1a:803:G:OP1	63:1a:3302:HOH:O	2.10	0.70
1:2A:2137:C:O2	1:2A:2154:G:N1	2.19	0.70
1:2A:2820:A:OP2	1:2A:2821:A:N6	2.22	0.70
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.55	0.70
34:2c:181:ASN:HD21	34:2c:205:GLY:H	1.40	0.70
1:1A:1381:G:N7	63:1A:4257:HOH:O	2.24	0.70
33:1b:80:ILE:HD11	33:1b:212:GLN:HB2	1.74	0.70
1:2A:674:G:OP2	63:2A:3828:HOH:O	2.09	0.70
1:2A:1055:G:H3'	1:2A:1056:G:H8	1.57	0.70
1:2A:2240:C:OP2	63:2A:3833:HOH:O	2.10	0.70
21:2Z:16:SER:OG	21:2Z:20:ARG:NH2	2.24	0.70
1:1A:1757:U:OP1	63:1A:4134:HOH:O	2.09	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.73	0.70
1:2A:342:G:O6	63:2A:3831:HOH:O	2.09	0.70
1:2A:1090:U:H2'	1:2A:1091:G:H8	1.55	0.70
1:2A:2328:A:OP1	63:2A:3832:HOH:O	2.09	0.70
1:1A:615:G:OP2	5:1F:43:LYS:NZ	2.20	0.69
12:1Q:127:ILE:O	63:1Q:301:HOH:O	2.10	0.69
32:1a:368:U:C2	32:1a:368:U:C1'	2.74	0.69
7:2H:101:ARG:HG2	7:2H:117:PRO:HG2	1.74	0.69
33:2b:111:ARG:HH11	33:2b:111:ARG:HA	1.57	0.69
1:1A:521:G:O6	63:1A:4131:HOH:O	2.09	0.69
1:1A:2707:G:OP2	63:1A:4132:HOH:O	2.09	0.69
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.04	0.69
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.25	0.69
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.74	0.69
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.72	0.69
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.25	0.69
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.25	0.69
33:2b:201:ILE:HG21	33:2b:214:ILE:HG21	1.75	0.69
1:1A:1840:G:N7	63:1A:4254:HOH:O	2.24	0.69
1:1A:2329:G:N7	63:1A:4256:HOH:O	2.24	0.69
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	1.75	0.69
1:2A:989:G:O2'	63:2A:3823:HOH:O	2.07	0.69
1:2A:1519:G:OP2	63:2A:3837:HOH:O	2.10	0.69
42:2k:52:GLY:H	42:2k:55:LYS:HZ3	1.39	0.69
3:1D:16:MET:HG2	3:1D:211:ARG:HH21	1.56	0.69
21:1Z:152:ALA:HB1	21:1Z:163:LEU:HD21	1.74	0.69
32:1a:1152:A:OP1	41:1j:68:HIS:ND1	2.21	0.69
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.74	0.69
1:2A:855:G:O6	63:2A:3835:HOH:O	2.10	0.69
21:2Z:146:ILE:H	21:2Z:146:ILE:HD12	1.56	0.69
25:23:13:ILE:O	63:23:201:HOH:O	2.11	0.69
32:2a:944:G:N1	32:2a:1338:G:OP2	2.26	0.69
34:2c:3:ASN:N	34:2c:3:ASN:OD1	2.26	0.69
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.26	0.69
32:2a:557:G:OP1	63:2a:3206:HOH:O	2.09	0.69
32:2a:937:A:OP2	63:2a:3207:HOH:O	2.10	0.69
1:1A:1031:G:OP1	63:1A:4135:HOH:O	2.10	0.69
6:1G:43:LEU:O	6:1G:45:GLU:N	2.22	0.69
1:1A:2585:U:H1'	56:1v:1:MET:HE2	1.74	0.68
34:1c:35:GLU:OE1	34:1c:59:ARG:NH2	2.24	0.68
39:1h:95:VAL:HB	39:1h:99:GLU:HG3	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:202:LYS:NZ	32:2a:773:G:O2'	2.23	0.68
1:1A:409:C:OP1	63:1A:4137:HOH:O	2.10	0.68
1:1A:982:C:OP2	63:1A:4133:HOH:O	2.09	0.68
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.73	0.68
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.58	0.68
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.26	0.68
1:1A:1085:A:O2'	1:1A:1104:C:O2'	2.10	0.68
1:1A:2130:U:O2'	1:1A:2133:G:O2'	2.11	0.68
23:11:59:THR:O	23:11:91:LYS:NZ	2.27	0.68
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.27	0.68
1:2A:1087:G:H1	1:2A:1102:C:H42	1.38	0.68
1:2A:2640:G:O3'	9:2N:74:ARG:NH2	2.21	0.68
1:1A:1356:G:OP2	63:1A:4139:HOH:O	2.11	0.68
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.06	0.68
18:2W:22:ASP:OD2	63:2W:301:HOH:O	2.11	0.68
1:1A:2166:G:N1	1:1A:2172:U:O4	2.19	0.68
22:20:36:ILE:O	63:20:201:HOH:O	2.12	0.68
1:1A:944:G:OP1	63:1A:4138:HOH:O	2.11	0.68
20:1Y:92:ASN:H	20:1Y:93:GLY:HA2	1.57	0.68
36:1e:8:GLU:HG3	36:1e:34:VAL:HG23	1.74	0.68
11:2P:121:LYS:O	11:2P:123:LEU:N	2.26	0.68
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.58	0.68
48:2q:24:GLU:HG3	48:2q:39:SER:HB3	1.74	0.68
1:2A:848:G:OP1	63:2A:3841:HOH:O	2.11	0.68
1:2A:854:G:H2'	1:2A:855:G:H8	1.58	0.68
1:2A:1045:A:N7	1:2A:1111:A:N6	2.41	0.68
1:2A:1426:G:O2'	63:2A:3836:HOH:O	2.10	0.68
7:2H:98:LEU:HG	7:2H:125:VAL:HG23	1.75	0.68
32:2a:754:C:H5'	46:2o:72:ARG:HH12	1.59	0.68
43:1l:84:LEU:HB3	43:1l:104:VAL:HG21	1.76	0.68
1:2A:491:G:N2	63:2A:3861:HOH:O	2.14	0.68
1:2A:1009:A:OP2	63:2A:3839:HOH:O	2.11	0.68
1:2A:1237:A:OP1	63:2A:3845:HOH:O	2.12	0.68
32:2a:1129:C:OP1	40:2i:16:ARG:NH1	2.27	0.68
32:1a:330:C:OP2	63:1a:3304:HOH:O	2.11	0.68
32:1a:506:G:OP1	63:1a:3305:HOH:O	2.11	0.68
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.58	0.68
1:2A:2139:C:N4	1:2A:2152:G:N1	2.30	0.68
33:2b:71:VAL:HG12	33:2b:93:VAL:HB	1.76	0.68
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.76	0.67
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.08	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.76	0.67
1:1A:60:G:OP1	63:1A:4141:HOH:O	2.12	0.67
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.12	0.67
1:2A:630:G:N2	1:2A:633:A:OP2	2.27	0.67
1:2A:2130:U:O2	1:2A:2159:G:N2	2.26	0.67
32:2a:266:G:H3'	48:2q:67:LYS:HB2	1.77	0.67
33:2b:114:ARG:HD2	33:2b:118:LEU:HG	1.75	0.67
50:2s:63:THR:HG23	50:2s:66:MET:HE3	1.75	0.67
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.74	0.67
1:2A:509:C:OP1	63:2A:3847:HOH:O	2.12	0.67
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.28	0.67
1:2A:1648:C:OP1	63:2A:3808:HOH:O	2.12	0.67
1:2A:981:A:OP1	63:2A:3842:HOH:O	2.12	0.67
39:2h:64:LYS:HB3	39:2h:79:VAL:HG11	1.76	0.67
1:1A:1059:G:H1	1:1A:1079:C:N4	1.92	0.67
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.94	0.67
4:1E:154:LYS:NZ	63:1E:404:HOH:O	2.25	0.67
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.76	0.67
32:1a:792:A:OP2	63:1a:3306:HOH:O	2.13	0.67
32:2a:115:G:OP1	63:2a:3208:HOH:O	2.12	0.67
1:1A:1858:G:O6	63:1A:4136:HOH:O	2.10	0.67
1:1A:1932:A:OP2	63:1A:4146:HOH:O	2.13	0.67
1:1A:2260:C:OP2	63:1A:4145:HOH:O	2.13	0.67
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.77	0.67
20:1Y:23:ARG:NH1	63:1Y:303:HOH:O	2.20	0.67
32:1a:1179:A:OP2	40:1i:93:ARG:NH2	2.28	0.67
1:2A:1970:A:N1	63:2A:3964:HOH:O	2.26	0.67
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.30	0.67
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.27	0.67
33:2b:27:LYS:NZ	33:2b:193:ASP:OD1	2.26	0.67
2:1B:94:C:N4	63:1B:304:HOH:O	2.28	0.67
3:1D:25:THR:HG21	3:1D:113:VAL:HG21	1.76	0.67
35:1d:163:GLU:HA	35:1d:166:LYS:HG2	1.76	0.67
40:1i:26:VAL:HG12	40:1i:61:ALA:HB3	1.77	0.67
23:21:54:ALA:HB1	23:21:83:GLU:HG3	1.77	0.67
32:2a:130:A:OP2	48:2q:63:ARG:NE	2.27	0.67
1:1A:1890:A:OP2	63:1A:4140:HOH:O	2.11	0.67
1:2A:271(P):C:O3'	8:2I:42:SER:OG	2.12	0.67
1:2A:1642:G:OP2	63:2A:3848:HOH:O	2.12	0.67
3:2D:71:ASP:OD2	3:2D:103:ARG:NH2	2.22	0.67
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:16:ARG:HH11	40:1i:64:THR:HG21	1.59	0.66
1:1A:889:C:O2'	1:1A:890:A:O5'	2.12	0.66
1:1A:1070:A:O2'	1:1A:1098:A:OP1	2.12	0.66
1:1A:1610:A:N7	63:1A:4288:HOH:O	2.27	0.66
1:1A:1754:C:OP1	15:1T:96:ARG:NH1	2.28	0.66
1:2A:407:G:OP2	63:2A:3853:HOH:O	2.13	0.66
1:2A:1275:A:OP2	63:2A:3854:HOH:O	2.13	0.66
1:2A:1761:C:O2	63:2A:3844:HOH:O	2.12	0.66
5:2F:9:ILE:HG12	5:2F:123:LEU:HD23	1.76	0.66
1:1A:572:A:OP2	17:1V:78:LYS:NZ	2.28	0.66
2:1B:11:C:OP1	63:1B:301:HOH:O	2.13	0.66
6:1G:126:ASP:N	6:1G:130:ASN:O	2.26	0.66
32:1a:6:G:H4'	32:1a:298:A:H4'	1.77	0.66
32:1a:176:C:H2'	32:1a:177:C:H6	1.60	0.66
1:2A:1603:A:OP1	63:2A:3843:HOH:O	2.12	0.66
1:2A:2504:U:OP2	63:2A:3852:HOH:O	2.13	0.66
1:2A:2775:A:OP2	63:2A:3855:HOH:O	2.13	0.66
1:1A:278:A:O2'	1:1A:279:C:OP1	2.14	0.66
1:1A:491:G:N3	63:1A:4302:HOH:O	2.28	0.66
10:2O:101:PRO:HG3	15:2T:67:SER:HB3	1.77	0.66
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HD13	1.76	0.66
1:2A:2846:G:OP2	63:2A:3850:HOH:O	2.12	0.66
1:1A:2115:G:N3	1:1A:2117:A:N6	2.42	0.66
1:2A:2005:A:N6	63:2A:3980:HOH:O	2.27	0.66
10:2O:73:ASP:O	63:2O:301:HOH:O	2.14	0.66
32:2a:971:G:N2	32:2a:1363(A):A:OP2	2.27	0.66
44:2m:107:ALA:HB3	44:2m:111:LYS:HE3	1.78	0.66
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.29	0.66
1:1A:67:U:O4	63:1A:4129:HOH:O	2.08	0.66
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.28	0.66
1:2A:2206:G:H8	1:2A:2207:G:N7	1.93	0.66
3:2D:239:ARG:NH1	63:2D:406:HOH:O	2.28	0.66
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.28	0.66
50:2s:22:LEU:HD13	50:2s:28:LYS:H	1.60	0.66
35:1d:166:LYS:NZ	35:1d:179:GLU:OE2	2.27	0.66
32:1a:1117:G:H21	32:1a:1180:A:H1'	1.61	0.66
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.77	0.66
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.78	0.66
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.77	0.66
1:1A:802:A:OP1	63:1A:4147:HOH:O	2.13	0.66
2:1B:13:A:N1	2:1B:69:G:O2'	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.29	0.66
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.11	0.66
25:13:29:ARG:HG3	25:13:30:ARG:HG3	1.77	0.66
35:1d:154:ASN:HA	35:1d:159:ARG:HE	1.59	0.66
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.22	0.66
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.25	0.66
39:2h:4:ASP:OD1	39:2h:7:ALA:N	2.20	0.66
1:1A:674:G:OP2	63:1A:4151:HOH:O	2.14	0.65
1:1A:2114:A:H1'	1:1A:2168:G:H5'	1.78	0.65
1:2A:1364:G:OP2	23:21:3:LYS:HG3	1.96	0.65
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.30	0.65
31:29:2:LYS:NZ	31:29:31:LYS:O	2.25	0.65
32:2a:803:G:OP1	63:2a:3210:HOH:O	2.14	0.65
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.78	0.65
1:1A:1007:C:OP2	63:1A:4143:HOH:O	2.12	0.65
19:1X:41:ASN:O	19:1X:45:THR:HG23	1.96	0.65
20:1Y:30:VAL:HG13	20:1Y:37:VAL:HG12	1.77	0.65
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.77	0.65
1:2A:511:U:OP2	63:2A:3856:HOH:O	2.14	0.65
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.28	0.65
1:1A:2240:C:OP2	63:1A:4149:HOH:O	2.14	0.65
6:1G:5:VAL:HG22	6:1G:8:LYS:H	1.61	0.65
34:1c:34:LEU:HG	34:1c:38:ARG:HD2	1.78	0.65
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.45	0.65
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.95	0.65
1:2A:1332:G:OP1	63:2A:3807:HOH:O	2.13	0.65
1:2A:1762:A:N1	63:2A:3984:HOH:O	2.28	0.65
1:2A:2596:U:OP1	63:2A:3859:HOH:O	2.14	0.65
1:1A:988:A:OP1	63:1A:4152:HOH:O	2.14	0.65
1:1A:1366:A:OP1	23:11:3:LYS:NZ	2.30	0.65
1:1A:2165:G:H2'	1:1A:2166:G:C8	2.32	0.65
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.26	0.65
1:2A:588:U:H2'	1:2A:589:C:C6	2.31	0.65
1:2A:991:C:OP2	63:2A:3863:HOH:O	2.14	0.65
1:2A:1769:G:O6	63:2A:3851:HOH:O	2.13	0.65
32:2a:1149:C:H4'	40:2i:66:ARG:HH12	1.61	0.65
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HG3	1.79	0.65
1:2A:1777:U:OP2	63:2A:3862:HOH:O	2.14	0.65
8:2I:7:GLU:OE1	63:2I:301:HOH:O	2.14	0.65
33:2b:178:ARG:HB3	39:2h:72:PRO:HA	1.79	0.65
1:1A:700:G:N7	63:1A:4319:HOH:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:759:G:OP2	63:1A:4156:HOH:O	2.15	0.65
1:1A:1315:C:OP2	63:1A:4115:HOH:O	2.13	0.65
1:2A:821:A:H2'	1:2A:946:G:H5"	1.79	0.65
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.31	0.65
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.29	0.65
1:2A:2407:G:OP1	63:2A:3846:HOH:O	2.12	0.65
1:1A:380:U:OP1	63:1A:4160:HOH:O	2.15	0.65
1:1A:675:A:OP2	63:1A:4148:HOH:O	2.14	0.65
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.77	0.65
11:1P:119:GLU:HG3	25:23:3:ARG:HH22	1.59	0.65
32:1a:632:A:H3'	32:1a:633:G:H8	1.60	0.65
1:2A:2849:U:OP2	15:2T:95:ARG:NH1	2.30	0.65
32:2a:643:C:O2'	39:2h:132:GLU:OE2	2.11	0.65
1:1A:2140:C:N3	1:1A:2151:G:O6	2.30	0.65
32:1a:73:G:H1	32:1a:96:U:H3	1.45	0.65
1:2A:749:C:OP2	63:2A:3870:HOH:O	2.15	0.65
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.43	0.65
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.79	0.65
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.79	0.65
21:2Z:52:SER:O	63:2Z:301:HOH:O	2.15	0.65
21:2Z:119:GLU:OE1	21:2Z:122:ARG:NH1	2.30	0.65
1:1A:1830:C:OP2	63:1A:4154:HOH:O	2.14	0.65
1:1A:2008:C:OP2	63:1A:4162:HOH:O	2.15	0.65
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.79	0.65
1:2A:1971:A:N1	63:2A:4004:HOH:O	2.29	0.65
19:2X:54:VAL:HG22	19:2X:81:VAL:HG12	1.78	0.65
42:2k:51:LYS:HA	42:2k:55:LYS:HG3	1.78	0.65
1:1A:1091:G:H1	1:1A:1100:C:N4	1.95	0.65
1:1A:2116:G:P	1:1A:2166:G:H21	2.20	0.65
6:1G:50:ALA:C	6:1G:52:ILE:H	2.05	0.65
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.32	0.65
33:1b:68:ILE:HG12	33:1b:161:ALA:HB3	1.79	0.65
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.31	0.65
29:27:35:ARG:HG3	29:27:42:LEU:HD11	1.79	0.65
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.77	0.65
32:1a:401:C:OP2	35:1d:73:ARG:NH1	2.29	0.64
33:1b:67:THR:HG22	33:1b:90:MET:HE2	1.79	0.64
41:1j:81:THR:O	41:1j:84:GLN:NE2	2.30	0.64
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.45	0.64
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.62	0.64
45:2n:16:PHE:HB2	45:2n:18:VAL:HG23	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:529:A:N1	63:1A:4328:HOH:O	2.30	0.64
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.32	0.64
32:1a:677:U:H3	32:1a:713:G:H22	1.44	0.64
1:2A:2373:G:OP1	63:2A:3864:HOH:O	2.15	0.64
1:2A:2546:U:OP1	63:2A:3871:HOH:O	2.15	0.64
1:1A:1783:A:OP1	63:1A:4161:HOH:O	2.15	0.64
32:1a:158:G:N2	32:1a:163:C:O2	2.20	0.64
32:1a:803:G:OP1	63:1a:3307:HOH:O	2.14	0.64
32:1a:911:U:OP2	43:1l:97:ARG:NH2	2.29	0.64
35:1d:134:ASP:N	35:1d:134:ASP:OD1	2.30	0.64
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.29	0.64
1:1A:279:C:N4	1:1A:361:G:H1	1.94	0.64
41:1j:63:PHE:HE2	45:1n:45:ARG:HA	1.62	0.64
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.79	0.64
1:2A:452:G:OP2	63:2A:3866:HOH:O	2.15	0.64
1:2A:832:G:OP1	63:2A:3867:HOH:O	2.15	0.64
32:2a:1058:G:OP1	34:2c:199:LYS:NZ	2.31	0.64
34:2c:114:PRO:HA	34:2c:185:GLY:HA3	1.80	0.64
1:1A:847:U:OP2	63:1A:4153:HOH:O	2.14	0.64
1:1A:1226:A:OP1	17:1V:84:LYS:NZ	2.29	0.64
19:1X:95:LEU:H	19:1X:95:LEU:HD22	1.62	0.64
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.63	0.64
1:2A:1017:G:O6	63:2A:3838:HOH:O	2.10	0.64
1:2A:2639:A:OP2	63:2A:3865:HOH:O	2.15	0.64
1:1A:2018:G:OP1	63:1A:4163:HOH:O	2.15	0.64
35:1d:196:LEU:O	35:1d:198:VAL:N	2.30	0.64
1:1A:2539:C:OP2	63:1A:4164:HOH:O	2.15	0.64
2:1B:95:C:N4	63:1B:304:HOH:O	2.20	0.64
1:2A:1771:C:OP1	63:2A:3869:HOH:O	2.15	0.64
3:2D:237:GLU:OE2	63:2D:401:HOH:O	2.14	0.64
1:1A:2849:U:OP2	15:1T:95:ARG:NH1	2.31	0.64
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.30	0.64
44:2m:81:LEU:HD13	44:2m:88:ARG:HG2	1.78	0.64
1:1A:1060:U:H4'	1:1A:1061:U:H5'	1.80	0.64
1:1A:2145:C:O2'	1:1A:2147:G:N2	2.31	0.64
32:1a:111:G:OP2	63:1a:3308:HOH:O	2.14	0.64
34:2c:35:GLU:OE2	34:2c:59:ARG:NH2	2.30	0.64
33:1b:47:THR:OG1	33:1b:202:PRO:O	2.16	0.64
1:2A:1969:A:OP1	63:2A:3868:HOH:O	2.15	0.64
9:2N:12:ARG:NH1	9:2N:50:ASP:OD2	2.31	0.64
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:61:GLU:OE1	45:1n:45:ARG:NE	2.31	0.63
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.16	0.63
32:2a:992:U:H4'	32:2a:993:G:O5'	1.98	0.63
40:2i:49:PRO:HB3	40:2i:82:ALA:HB2	1.80	0.63
1:1A:1651:G:OP2	63:1A:4157:HOH:O	2.15	0.63
1:1A:2115:G:H2'	1:1A:2117:A:N6	2.12	0.63
7:1H:45:VAL:HG12	7:1H:50:VAL:HG22	1.79	0.63
32:1a:194:C:H2'	32:1a:195:A:H5"	1.78	0.63
32:1a:702:A:OP2	63:1a:3309:HOH:O	2.15	0.63
32:1a:992:U:H4'	32:1a:993:G:H5'	1.79	0.63
56:1v:1:MET:HE3	56:1v:3:ILE:HD12	1.80	0.63
1:2A:854:G:H2'	1:2A:855:G:C8	2.33	0.63
2:2B:58:A:OP2	63:2B:301:HOH:O	2.15	0.63
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.29	0.63
38:2g:111:ARG:HB2	38:2g:119:ARG:HG2	1.80	0.63
1:1A:1250:G:H5"	63:1U:329:HOH:O	1.98	0.63
32:1a:1102:A:O3'	33:1b:96:ARG:NH2	2.32	0.63
33:1b:40:HIS:HB2	33:1b:190:THR:HG21	1.80	0.63
1:2A:818:G:OP2	63:2A:3872:HOH:O	2.16	0.63
1:2A:1840:G:OP2	63:2A:3873:HOH:O	2.16	0.63
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.31	0.63
1:1A:1300:U:H4'	1:1A:1301:A:H5"	1.81	0.63
16:1U:78:THR:HG22	16:1U:117:GLN:HE22	1.62	0.63
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.32	0.63
6:2G:145:THR:HG22	6:2G:148:MET:HE3	1.78	0.63
37:2f:2:ARG:HE	37:2f:69:GLU:HG2	1.64	0.63
1:1A:400:G:N7	63:1A:4331:HOH:O	2.30	0.63
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.33	0.63
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.63	0.63
14:1S:59:LYS:HD2	14:1S:60:GLY:H	1.62	0.63
37:1f:78:GLU:HA	37:1f:81:ILE:HG13	1.79	0.63
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.33	0.63
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.64	0.63
1:2A:1371:G:HO2'	1:2A:1372:U:H5	1.46	0.63
1:2A:2490:G:O6	63:2A:3834:HOH:O	2.10	0.63
1:2A:2789:C:N3	1:2A:2894:G:N1	2.47	0.63
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.79	0.63
33:2b:119:GLU:HG3	33:2b:153:ARG:HH22	1.64	0.63
38:2g:16:LEU:HD11	40:2i:41:VAL:HG12	1.79	0.63
1:2A:1053:C:H2'	1:2A:1054:A:C8	2.27	0.63
1:2A:1156:A:OP2	63:2A:3857:HOH:O	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:26:5:VAL:HA	28:26:27:LYS:HE2	1.80	0.63
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.27	0.63
39:2h:51:VAL:HG11	39:2h:60:ARG:HH11	1.63	0.63
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.63	0.63
1:1A:2100:G:H1	1:1A:2189:U:H3	1.46	0.63
1:1A:2372:G:O6	63:1A:4158:HOH:O	2.15	0.63
3:1D:52:ARG:O	63:1D:402:HOH:O	2.15	0.63
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.80	0.63
34:1c:134:ILE:HG23	34:1c:151:VAL:HB	1.81	0.63
51:1t:33:ILE:O	51:1t:37:SER:OG	2.16	0.63
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.34	0.63
26:24:16:CYS:SG	26:24:17:GLY:N	2.72	0.63
32:2a:164:U:H2'	32:2a:165:C:C6	2.33	0.63
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.34	0.63
35:1d:119:GLN:O	35:1d:123:HIS:ND1	2.32	0.63
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.31	0.63
26:24:45:GLY:O	26:24:47:GLN:N	2.32	0.63
1:1A:1359:A:H61	1:1A:1372:U:H3	1.46	0.63
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.64	0.63
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.14	0.63
1:1A:379:G:N2	23:11:42:GLN:OE1	2.20	0.62
1:1A:2292:C:OP1	14:1S:17:ARG:NH2	2.32	0.62
29:17:34:ARG:NH1	29:17:41:ARG:O	2.31	0.62
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.99	0.62
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.81	0.62
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.34	0.62
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.63	0.62
32:1a:116:A:H61	32:1a:313:A:H1'	1.64	0.62
32:1a:490:G:OP2	35:1d:132:ARG:NH2	2.26	0.62
1:2A:889:C:O2'	1:2A:890:A:O5'	2.17	0.62
32:2a:36:C:H5"	43:2l:123:LYS:HD3	1.81	0.62
32:2a:56:U:H2'	32:2a:57:G:C8	2.34	0.62
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.32	0.62
34:2c:131:ARG:NH1	34:2c:166:GLU:OE2	2.32	0.62
1:1A:1340:U:OP1	19:1X:16:LYS:NZ	2.31	0.62
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.17	0.62
35:1d:173:TRP:HB3	35:1d:187:ARG:HE	1.63	0.62
50:1s:22:LEU:HD22	50:1s:28:LYS:HA	1.79	0.62
1:2A:2237:G:OP1	63:2A:3876:HOH:O	2.16	0.62
14:2S:105:ALA:HB1	14:2S:110:LEU:HD23	1.78	0.62
15:2T:50:ILE:HG22	15:2T:102:ILE:HD11	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.27	0.62
42:2k:79:SER:HG	42:2k:106:LYS:HZ3	1.43	0.62
1:1A:2405:G:OP1	11:1P:77:ARG:NH2	2.32	0.62
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.17	0.62
50:1s:41:VAL:HG22	50:1s:44:MET:HE3	1.80	0.62
2:2B:75:G:H22	21:2Z:73:GLN:HE22	1.47	0.62
32:2a:979:C:O2	45:2n:19:ARG:NE	2.31	0.62
32:2a:1079:G:H4'	36:2e:14:ARG:HH22	1.62	0.62
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.31	0.62
50:2s:22:LEU:HB3	50:2s:27:GLU:HA	1.81	0.62
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.63	0.62
1:1A:2814:C:OP2	63:1A:4168:HOH:O	2.16	0.62
6:1G:33:ARG:O	6:1G:161:THR:OG1	2.08	0.62
18:1W:37:ARG:HD3	18:1W:38:TYR:CE2	2.35	0.62
1:2A:245:G:O6	30:28:8:LYS:NZ	2.28	0.62
1:2A:2107:C:H42	1:2A:2182:G:H1	1.45	0.62
33:2b:70:PHE:O	33:2b:93:VAL:N	2.30	0.62
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.80	0.62
7:1H:3:ARG:HE	7:1H:54:ARG:HH12	1.46	0.62
15:1T:39:ARG:HH12	15:1T:41:ARG:HD3	1.63	0.62
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.65	0.62
12:2Q:91:GLU:O	63:2Q:301:HOH:O	2.16	0.62
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.82	0.62
35:2d:18:LYS:HD2	35:2d:33:MET:HE3	1.81	0.62
17:1V:66:ARG:NE	63:1V:301:HOH:O	2.18	0.62
32:1a:1414:U:H3	32:1a:1486:G:H1	1.47	0.62
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.34	0.62
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.81	0.62
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.64	0.62
5:2F:17:ARG:HH12	5:2F:19:GLU:HG3	1.64	0.62
23:21:23:LYS:HG2	23:21:29:GLY:HA3	1.82	0.62
32:2a:1393:U:O4	63:2a:3211:HOH:O	2.15	0.62
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.35	0.62
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.64	0.62
34:1c:110:ASN:HD22	34:1c:140:ARG:HB3	1.64	0.62
1:2A:1090:U:H2'	1:2A:1091:G:C8	2.33	0.62
32:2a:1496:C:OP2	53:2y:26:LYS:NZ	2.27	0.62
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.32	0.62
44:2m:13:LYS:HA	44:2m:44:ARG:HD2	1.81	0.62
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.32	0.62
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.82	0.61
32:2a:662:G:H2'	32:2a:663:A:C8	2.35	0.61
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.81	0.61
32:1a:353:A:OP1	63:1a:3311:HOH:O	2.15	0.61
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.33	0.61
1:2A:1063:G:N2	1:2A:1076:C:O2'	2.32	0.61
1:2A:1170:G:H1	1:2A:1179:C:H42	1.47	0.61
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.35	0.61
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.80	0.61
32:1a:224:C:OP1	51:1t:74:LYS:NZ	2.27	0.61
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.33	0.61
1:2A:1062:G:C5	1:2A:1070:A:H1'	2.35	0.61
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.35	0.61
32:2a:1146:A:H3'	32:2a:1147:C:H5"	1.80	0.61
32:2a:1277:C:O2'	32:2a:1279:A:N7	2.33	0.61
5:1F:67:GLN:NE2	63:1F:403:HOH:O	2.32	0.61
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.35	0.61
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.81	0.61
39:1h:73:ASP:OD1	39:1h:75:ARG:NH1	2.34	0.61
1:2A:1014:U:H2'	1:2A:1015:G:C8	2.36	0.61
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.17	0.61
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.82	0.61
32:1a:328:C:H4'	32:1a:329:A:H5"	1.81	0.61
32:1a:545:C:OP2	35:1d:65:ARG:NH2	2.33	0.61
6:2G:8:LYS:HG2	6:2G:12:TYR:HE2	1.65	0.61
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.34	0.61
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.83	0.61
40:2i:7:THR:O	40:2i:83:ARG:NH2	2.33	0.61
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.33	0.61
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.82	0.61
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.29	0.61
5:1F:18:ARG:NH1	5:1F:127:GLU:OE2	2.34	0.61
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	1.83	0.61
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.32	0.61
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.33	0.61
2:2B:28:C:OP2	14:2S:33:LYS:NZ	2.33	0.61
7:2H:35:VAL:HG13	7:2H:71:LEU:HD23	1.81	0.61
23:21:75:GLU:HA	23:21:78:LYS:HZ3	1.64	0.61
36:2e:78:HIS:CE1	36:2e:142:LEU:HD23	2.36	0.61
42:2k:18:ARG:NH2	42:2k:35:PRO:O	2.34	0.61
28:16:13:CYS:SG	28:16:47:THR:HG21	2.40	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1256:A:OP2	32:1a:1279:A:N6	2.34	0.61
53:1y:55:ASN:HA	53:1y:60:VAL:HA	1.82	0.61
26:24:22:ILE:HG22	26:24:24:THR:HB	1.83	0.61
37:2f:1:MET:HE3	37:2f:66:GLU:HG2	1.82	0.61
19:1X:72:LYS:NZ	19:1X:75:ASP:OD1	2.34	0.61
32:1a:840:C:H4'	32:1a:841:U:OP2	2.00	0.61
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.01	0.61
1:2A:2087:G:O6	63:2A:3858:HOH:O	2.14	0.61
3:2D:204:ILE:O	63:2D:402:HOH:O	2.15	0.61
7:2H:90:LYS:HD3	7:2H:159:GLU:HG2	1.83	0.61
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.83	0.61
16:2U:49:HIS:HA	16:2U:52:ARG:HB3	1.83	0.61
6:1G:77:ILE:H	6:1G:82:LEU:HB3	1.66	0.60
17:1V:8:GLY:O	17:1V:10:LYS:NZ	2.34	0.60
32:1a:1010:G:H22	32:1a:1020:U:H1'	1.66	0.60
1:2A:362:U:O2'	1:2A:363:G:H5'	2.01	0.60
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.34	0.60
34:2c:148:GLY:HA3	34:2c:203:PHE:HB3	1.81	0.60
48:2q:95:TYR:HA	48:2q:98:LEU:HD12	1.83	0.60
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.19	0.60
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.34	0.60
32:2a:1040:U:H3'	32:2a:1041:A:H5"	1.83	0.60
35:2d:13:ARG:HH22	35:2d:36:ARG:NE	1.99	0.60
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.42	0.60
1:1A:2494:G:OP2	63:1A:4171:HOH:O	2.16	0.60
19:1X:5:TYR:CE1	24:12:30:ARG:HG3	2.36	0.60
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.82	0.60
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.00	0.60
1:1A:11:G:H2'	1:1A:12:U:H5'	1.83	0.60
35:1d:15:GLU:O	35:1d:63:LYS:NZ	2.34	0.60
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.82	0.60
1:2A:770:G:OP2	63:2A:3878:HOH:O	2.16	0.60
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.31	0.60
21:2Z:42:VAL:O	21:2Z:46:LYS:NZ	2.34	0.60
4:1E:54:GLN:O	63:1E:402:HOH:O	2.16	0.60
5:1F:101:LEU:HD23	5:1F:106:ARG:HG2	1.81	0.60
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.84	0.60
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.83	0.60
32:1a:56:U:H2'	32:1a:57:G:C8	2.36	0.60
40:1i:8:GLY:HA2	40:1i:79:LEU:HD23	1.83	0.60
63:2A:4010:HOH:O	12:2Q:67:ARG:NH2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:87:G:N2	2:2B:90:A:OP2	2.30	0.60
32:2a:538:G:H5"	43:2l:114:LYS:HB2	1.83	0.60
38:2g:15:ASP:OD1	38:2g:20:ASP:N	2.32	0.60
1:1A:493:G:OP2	63:1A:4170:HOH:O	2.16	0.60
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.37	0.60
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.16	0.60
42:1k:34:ASP:OD1	42:1k:38:ASN:N	2.35	0.60
1:2A:918:A:N3	2:2B:80:U:O2'	2.34	0.60
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.37	0.60
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.02	0.60
32:2a:117:G:OP2	63:2a:3212:HOH:O	2.15	0.60
32:2a:266:G:O2'	32:2a:267:C:OP2	2.15	0.60
32:2a:335:C:O2'	32:2a:1433:A:N3	2.29	0.60
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.84	0.60
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.67	0.60
33:2b:76:GLN:HB2	33:2b:208:ILE:HG12	1.84	0.60
1:1A:1045:A:H5'	1:1A:1046:A:H5'	1.81	0.60
5:1F:120:GLU:HB2	5:1F:122:LYS:HG2	1.84	0.60
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.35	0.60
32:1a:548:G:OP1	63:1a:3310:HOH:O	2.15	0.60
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.17	0.60
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.84	0.60
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.84	0.60
1:2A:1076:C:H4'	1:2A:1077:A:OP1	2.01	0.60
14:2S:35:ILE:H	14:2S:53:SER:HB3	1.67	0.60
20:2Y:12:THR:HG22	20:2Y:26:LYS:HG2	1.84	0.60
32:2a:677:U:H3	32:2a:713:G:H22	1.48	0.60
33:2b:24:TRP:HB3	33:2b:40:HIS:CE1	2.37	0.60
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.83	0.60
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.15	0.60
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.83	0.60
23:11:65:SER:HG	23:11:66:HIS:HD1	1.49	0.60
32:1a:270:A:H2'	32:1a:271:C:C6	2.37	0.60
1:2A:120:U:OP2	63:2A:3875:HOH:O	2.16	0.60
1:2A:1071:G:H1'	1:2A:1089:G:N7	2.16	0.60
1:2A:1428:C:O2'	1:2A:1569:A:OP2	2.09	0.60
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.31	0.60
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.66	0.60
34:1c:35:GLU:HA	34:1c:38:ARG:HB2	1.84	0.60
1:2A:2116:G:O2'	1:2A:2117:A:O4'	2.20	0.60
32:2a:254:G:OP1	48:2q:66:SER:OG	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.37	0.60
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.37	0.60
1:2A:424:G:N3	63:2A:4034:HOH:O	2.32	0.60
1:2A:922:U:H2'	1:2A:923:C:C6	2.37	0.60
1:2A:995:C:O2	9:2N:3:THR:OG1	2.20	0.60
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.35	0.60
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	1.82	0.60
9:1N:65:LYS:HE2	9:1N:69:GLN:HE22	1.66	0.59
32:1a:574:A:OP2	63:1a:3313:HOH:O	2.17	0.59
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.18	0.59
33:1b:74:LYS:NZ	33:1b:205:ASP:O	2.24	0.59
39:1h:81:HIS:N	39:1h:138:TRP:O	2.35	0.59
21:2Z:81:ARG:NH2	63:2Z:302:HOH:O	2.23	0.59
32:2a:1263:C:H2'	32:2a:1264:C:H6	1.66	0.59
1:1A:483:A:O2'	20:1Y:49:VAL:O	2.14	0.59
17:1V:58:VAL:HG12	17:1V:97:LYS:HB2	1.85	0.59
32:1a:315:A:OP1	63:1a:3312:HOH:O	2.16	0.59
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.16	0.59
40:1i:32:ASP:OD1	40:1i:33:PHE:N	2.36	0.59
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.83	0.59
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.83	0.59
1:2A:2788:C:N3	1:2A:2789:C:N4	2.50	0.59
17:2V:59:ALA:HA	17:2V:96:ILE:HA	1.84	0.59
27:25:16:ARG:HG2	27:25:16:ARG:HH11	1.66	0.59
30:28:28:GLY:N	63:28:202:HOH:O	2.35	0.59
32:2a:181:G:N2	32:2a:182:U:O4	2.34	0.59
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.25	0.59
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.35	0.59
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.83	0.59
1:2A:1637:A:OP2	63:2A:3879:HOH:O	2.16	0.59
1:2A:2349:G:OP1	63:2A:3882:HOH:O	2.17	0.59
32:2a:394:G:O6	63:2a:3209:HOH:O	2.13	0.59
32:2a:676:A:H1'	42:2k:115:PRO:HB3	1.84	0.59
32:2a:1103:C:OP1	33:2b:96:ARG:NH2	2.27	0.59
35:2d:78:LEU:HD22	35:2d:96:LEU:HB3	1.84	0.59
39:2h:112:LEU:HA	39:2h:134:ILE:HG12	1.84	0.59
11:2P:88:LEU:HD21	11:2P:100:LEU:HD11	1.84	0.59
40:2i:53:VAL:O	40:2i:55:ALA:N	2.35	0.59
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.38	0.59
41:2j:63:PHE:HE1	45:2n:58:LYS:HG2	1.68	0.59
1:1A:305:U:H2'	1:1A:306:U:C6	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:560:U:O2'	32:1a:561:U:OP2	2.19	0.59
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.35	0.59
1:2A:23:G:OP1	1:2A:504:U:N3	2.32	0.59
1:2A:139:G:H2'	1:2A:140:G:N7	2.18	0.59
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.35	0.59
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.84	0.59
35:2d:175:SER:OG	35:2d:176:LEU:N	2.35	0.59
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.84	0.59
33:1b:62:ALA:HB2	33:1b:222:ILE:HG22	1.85	0.59
11:1P:2:LYS:HE2	11:1P:4:SER:H	1.66	0.59
34:1c:175:LEU:HD21	34:1c:201:TYR:HE1	1.67	0.59
37:1f:11:ASN:HB3	37:1f:14:LEU:HG	1.84	0.59
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.10	0.59
1:2A:876:C:H2'	1:2A:877:U:O4'	2.02	0.59
1:2A:1773:A:OP2	63:2A:3874:HOH:O	2.16	0.59
1:2A:1934:C:O2'	63:2A:3884:HOH:O	2.17	0.59
1:2A:2140:C:N3	1:2A:2151:G:O6	2.36	0.59
6:2G:22:ARG:HH21	6:2G:171:ALA:HB2	1.66	0.59
7:2H:105:LEU:HD21	7:2H:162:ILE:HD11	1.83	0.59
40:2i:37:PHE:CZ	40:2i:74:ILE:HG12	2.38	0.59
13:1R:56:LYS:NZ	13:1R:90:ARG:O	2.35	0.59
21:1Z:70:LEU:HD11	21:1Z:98:MET:HE3	1.84	0.59
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.38	0.59
1:2A:1649:G:O2'	13:2R:107:ASP:OD2	2.19	0.59
2:2B:40:U:O2'	2:2B:43:C:OP2	2.15	0.59
5:2F:30:PRO:HB3	11:2P:1:MET:HE1	1.83	0.59
6:2G:35:GLU:HG3	6:2G:36:LYS:HG2	1.85	0.59
19:2X:26:TYR:HB3	19:2X:92:LEU:HD22	1.83	0.59
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.84	0.59
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.68	0.59
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.68	0.59
40:1i:50:LEU:HD13	40:1i:56:LEU:HG	1.83	0.59
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.38	0.59
3:2D:25:THR:HG21	3:2D:113:VAL:HG11	1.82	0.59
1:2A:628:G:O6	63:2A:3881:HOH:O	2.17	0.59
6:2G:55:LYS:HD2	6:2G:58:GLN:HE22	1.66	0.59
20:2Y:55:TYR:CZ	20:2Y:61:ILE:HG21	2.38	0.59
26:24:44:THR:O	26:24:46:GLN:N	2.35	0.59
33:2b:50:GLU:O	33:2b:54:THR:OG1	2.16	0.59
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.85	0.58
17:1V:66:ARG:NH1	63:1V:306:HOH:O	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:940:C:OP1	38:1g:29:LYS:NZ	2.33	0.58
3:2D:268:ARG:NE	63:2D:411:HOH:O	2.35	0.58
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.85	0.58
32:2a:921:U:O2	36:2e:19:MET:HB2	2.02	0.58
38:2g:149:ARG:NE	42:2k:59:TYR:OH	2.36	0.58
5:1F:116:ASP:OD2	11:1P:1:MET:HB3	2.02	0.58
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.38	0.58
32:2a:407:G:H1'	35:2d:119:GLN:HE22	1.67	0.58
45:2n:37:PHE:HB3	45:2n:39:LEU:HD12	1.84	0.58
1:1A:2285:C:OP2	28:16:6:ARG:NH1	2.37	0.58
22:20:14:ARG:HB2	22:20:14:ARG:HH11	1.68	0.58
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.69	0.58
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.03	0.58
34:2c:110:ASN:HD21	34:2c:140:ARG:HB3	1.68	0.58
32:1a:946:A:H2'	32:1a:947:G:C8	2.38	0.58
43:1l:117:ARG:NH1	63:1l:301:HOH:O	2.34	0.58
1:2A:140:G:N2	1:2A:1596:A:H4'	2.18	0.58
1:2A:1055:G:H3'	1:2A:1056:G:C8	2.36	0.58
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.86	0.58
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.85	0.58
1:1A:184:C:H2'	1:1A:185:U:C6	2.39	0.58
32:1a:189(A):C:H42	32:1a:189(J):G:H1	1.52	0.58
8:2I:5:LEU:HD21	8:2I:12:LEU:HB3	1.85	0.58
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.69	0.58
35:2d:10:ARG:HA	35:2d:13:ARG:HD2	1.84	0.58
42:2k:19:ALA:HB3	42:2k:82:VAL:HG22	1.84	0.58
1:1A:278:A:H2'	1:1A:279:C:C6	2.39	0.58
1:1A:784:A:H5'	1:1A:785:G:OP1	2.03	0.58
1:1A:1671:U:O4	63:1A:4110:HOH:O	2.17	0.58
1:1A:1947:C:O2'	32:1a:1483:A:O2'	2.21	0.58
2:1B:66:A:H61	2:1B:108:U:H2'	1.69	0.58
6:1G:62:LEU:HD12	6:1G:148:MET:HE1	1.85	0.58
44:1m:19:LEU:HD21	44:1m:56:LEU:HD11	1.86	0.58
1:2A:1186:G:OP2	63:2A:3863:HOH:O	2.17	0.58
1:2A:2131:G:OP1	1:2A:2132:U:H5'	2.03	0.58
24:22:17:SER:N	24:22:20:GLU:OE1	2.36	0.58
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.37	0.58
1:1A:2279:G:O6	22:10:14:ARG:HG3	2.03	0.58
1:1A:2308:G:O2'	1:1A:2310:A:N7	2.35	0.58
26:14:59:PHE:HB3	26:14:62:ARG:HH21	1.69	0.58
32:1a:1189:C:OP1	45:1n:58:LYS:NZ	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:101:MET:HA	33:1b:108:ILE:HD12	1.85	0.58
1:2A:1187:G:N2	1:2A:1188:U:O4	2.37	0.58
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.38	0.58
40:2i:40:LEU:HD22	40:2i:42:ARG:HB2	1.84	0.58
1:1A:1947:C:HO2'	32:1a:1483:A:HO2'	1.52	0.58
32:1a:1352:C:OP1	52:1u:3:LYS:NZ	2.29	0.58
39:1h:82:HIS:NE2	39:1h:136:GLU:OE2	2.36	0.58
7:2H:11:VAL:HG12	7:2H:15:VAL:HG23	1.84	0.58
32:2a:5:U:H5	35:2d:87:GLY:H	1.51	0.58
32:2a:255:G:P	48:2q:69:LYS:HZ3	2.27	0.58
32:2a:875:C:H1'	39:2h:15:ASN:HD21	1.69	0.58
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.68	0.58
1:1A:2590:A:O3'	3:1D:239:ARG:NH2	2.37	0.58
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.02	0.58
32:2a:131:C:H2'	32:2a:132:C:H6	1.69	0.58
42:2k:16:SER:OG	42:2k:106:LYS:NZ	2.35	0.58
1:1A:1610:A:O3'	63:1A:4176:HOH:O	2.17	0.58
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.04	0.58
12:1Q:43:THR:HA	12:1Q:94:VAL:HG12	1.86	0.58
27:15:16:ARG:HG3	27:15:17:ASP:N	2.17	0.58
32:1a:70:G:H1	32:1a:99:U:H3	1.52	0.58
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	1.86	0.58
1:2A:15:G:OP2	63:2A:3887:HOH:O	2.17	0.58
1:2A:1063:G:H1	1:2A:1075:C:N4	2.01	0.58
12:2Q:76:LYS:HB3	12:2Q:91:GLU:HG3	1.85	0.58
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.33	0.58
32:2a:1161:C:H2'	32:2a:1162:C:H6	1.69	0.58
1:1A:1611:C:OP1	63:1A:4175:HOH:O	2.17	0.57
33:1b:61:LEU:HD23	33:1b:68:ILE:HD11	1.85	0.57
1:2A:121:G:H4'	1:2A:149:A:H5'	1.84	0.57
1:2A:999:U:OP2	63:2A:3885:HOH:O	2.17	0.57
10:2O:64:ARG:HD2	10:2O:81:ASP:OD1	2.04	0.57
10:2O:77:ILE:HB	15:2T:74:ARG:HD3	1.86	0.57
32:2a:179:A:H2'	32:2a:180:U:H6	1.69	0.57
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.69	0.57
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.39	0.57
41:1j:55:LYS:HE3	41:1j:56:HIS:CE1	2.39	0.57
1:2A:586:A:N1	1:2A:809:G:O2'	2.29	0.57
5:2F:190:GLU:O	63:2F:402:HOH:O	2.17	0.57
16:2U:43:GLY:HA3	17:2V:73:SER:HB3	1.86	0.57
32:2a:56:U:H2'	32:2a:57:G:H8	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.86	0.57
1:1A:2165:G:H2'	1:1A:2166:G:H8	1.68	0.57
7:1H:40:GLU:OE2	7:1H:60:ARG:NH1	2.36	0.57
8:1I:104:GLN:O	8:1I:106:GLY:N	2.37	0.57
32:1a:235:C:H2'	32:1a:236:G:H8	1.68	0.57
32:1a:368:U:C6	32:1a:368:U:C1'	2.85	0.57
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.36	0.57
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.86	0.57
26:24:59:PHE:HA	26:24:61:ARG:N	2.19	0.57
35:2d:98:GLU:OE2	35:2d:107:ARG:NH2	2.38	0.57
1:1A:1378:A:OP1	29:17:10:ARG:NH2	2.37	0.57
15:1T:108:ARG:HH12	15:1T:112:ARG:HD3	1.66	0.57
32:1a:1441:G:H5"	32:1a:1442:G:H5'	1.86	0.57
40:1i:64:THR:HG23	40:1i:66:ARG:HH22	1.67	0.57
47:1p:6:LEU:HB3	47:1p:17:TYR:HB3	1.86	0.57
48:1q:43:LEU:HD12	48:1q:68:ARG:HB2	1.85	0.57
1:2A:249:C:O2	30:28:12:LYS:NZ	2.33	0.57
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	1.85	0.57
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.36	0.57
32:2a:1129:C:H42	32:2a:1143:G:H1	1.51	0.57
25:13:26:LEU:O	25:13:35:ARG:NE	2.33	0.57
32:1a:1069:C:OP2	63:1a:3314:HOH:O	2.17	0.57
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.87	0.57
1:2A:2306:C:H3'	1:2A:2307:G:H2'	1.87	0.57
8:2I:78:THR:HG22	8:2I:143:SER:HB3	1.87	0.57
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.69	0.57
33:2b:174:VAL:O	33:2b:178:ARG:HG2	2.04	0.57
35:2d:141:ARG:N	35:2d:144:ASP:OD2	2.35	0.57
39:2h:23:SER:OG	39:2h:60:ARG:NE	2.35	0.57
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.22	0.57
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.45	0.57
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.86	0.57
39:1h:49:GLU:HG3	39:1h:51:VAL:HG22	1.87	0.57
1:2A:2429:G:OP1	63:2A:3805:HOH:O	2.17	0.57
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.86	0.57
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HB	1.86	0.57
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.39	0.57
40:2i:3:GLN:HG3	40:2i:20:ARG:HE	1.69	0.57
4:1E:18:ASP:HB3	15:1T:82:LEU:HD21	1.87	0.57
13:1R:102:GLU:O	63:1R:301:HOH:O	2.18	0.57
20:1Y:107:ASP:OD2	63:1Y:302:HOH:O	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:152:ALA:HB3	21:1Z:167:PRO:HA	1.86	0.57
32:1a:96:U:H2'	32:1a:97:G:C8	2.40	0.57
32:1a:828:A:H2'	32:1a:829:G:O4'	2.04	0.57
34:1c:179:ARG:NH1	34:1c:206:GLU:OE1	2.35	0.57
41:1j:19:SER:OG	41:1j:91:PRO:HD2	2.05	0.57
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.39	0.57
32:2a:353:A:H5'	32:2a:353:A:H8	1.70	0.57
53:2y:87:LYS:O	53:2y:91:LYS:HB2	2.05	0.57
33:1b:71:VAL:HB	33:1b:164:VAL:HG22	1.86	0.57
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.39	0.57
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.40	0.57
32:2a:875:C:H1'	39:2h:15:ASN:ND2	2.19	0.57
32:2a:1035:A:HO2'	32:2a:1036:G:H8	1.51	0.57
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.36	0.57
1:1A:330:A:H2	1:1A:1210:A:O2'	1.88	0.57
3:1D:21:PHE:HB3	3:1D:24:ILE:HD12	1.85	0.57
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.36	0.57
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.37	0.57
5:2F:187:VAL:HG12	11:2P:3:LEU:HG	1.87	0.57
8:2I:140:LEU:HD22	8:2I:141:LYS:H	1.69	0.57
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.85	0.57
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.27	0.57
49:2r:58:LEU:HD23	49:2r:62:GLU:HB3	1.86	0.57
23:11:80:LEU:HD23	23:11:82:LEU:HD21	1.87	0.57
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.68	0.57
32:1a:1498:UR3:H4'	32:1a:1519:MA6:H2	1.87	0.57
34:1c:82:GLU:HA	34:1c:85:ARG:HH21	1.70	0.57
34:1c:172:ARG:NH2	34:1c:206:GLU:OE2	2.38	0.57
47:1p:49:LEU:HD22	47:1p:73:LEU:HD22	1.86	0.57
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.40	0.57
1:2A:1504:C:H2'	1:2A:1505:C:H6	1.69	0.57
1:2A:1506:C:H2'	1:2A:1507:A:H5'	1.87	0.57
17:2V:91:TYR:HE1	17:2V:93:GLU:HG3	1.69	0.57
32:2a:41:G:H2'	32:2a:42:G:C8	2.39	0.57
32:2a:662:G:H2'	32:2a:663:A:H8	1.70	0.57
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.36	0.56
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	1.86	0.56
24:12:47:ASN:O	63:12:101:HOH:O	2.17	0.56
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.24	0.56
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.40	0.56
34:1c:98:ASN:N	34:1c:98:ASN:OD1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:97:PHE:O	49:1r:31:LEU:N	2.34	0.56
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.87	0.56
24:22:2:LYS:N	24:22:5:GLU:OE1	2.38	0.56
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.39	0.56
40:2i:4:TYR:HD1	40:2i:87:GLN:HE22	1.52	0.56
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	1.86	0.56
50:2s:81:ARG:HB2	50:2s:81:ARG:HH11	1.70	0.56
1:1A:247:G:H4'	1:1A:386:G:C5	2.40	0.56
22:10:10:THR:HG23	22:10:12:ASN:H	1.69	0.56
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.38	0.56
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	1.86	0.56
32:2a:1212:U:H4'	32:2a:1213:A:C8	2.41	0.56
35:2d:68:TYR:OH	35:2d:98:GLU:OE2	2.22	0.56
53:2y:35:ILE:HB	53:2y:55:ASN:HB3	1.85	0.56
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.39	0.56
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.06	0.56
20:1Y:77:PRO:HD2	20:1Y:106:LEU:HD23	1.87	0.56
32:1a:509:A:N3	32:1a:543:C:O2'	2.33	0.56
32:1a:1239:A:H62	32:1a:1299:A:N6	2.03	0.56
35:1d:87:GLY:N	63:1d:404:HOH:O	2.37	0.56
37:1f:76:ALA:HA	37:1f:79:LEU:HB2	1.86	0.56
40:1i:20:ARG:O	40:1i:60:ASP:N	2.37	0.56
1:2A:323:G:O2'	1:2A:1205:U:N3	2.36	0.56
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.37	0.56
1:2A:1262:A:OP2	18:2W:97:LYS:NZ	2.38	0.56
1:2A:2822:G:O6	63:2A:3886:HOH:O	2.17	0.56
15:2T:127:ALA:C	15:2T:129:ARG:H	2.14	0.56
17:2V:35:LEU:HB2	17:2V:57:VAL:HG22	1.87	0.56
28:26:8:LYS:NZ	63:26:601:HOH:O	2.22	0.56
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.39	0.56
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.19	0.56
33:2b:97:TRP:NE1	33:2b:173:ALA:HB2	2.20	0.56
40:2i:23:ASN:HB2	40:2i:25:LYS:HE2	1.86	0.56
50:2s:30:LEU:HD12	50:2s:48:THR:HG22	1.86	0.56
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.87	0.56
7:1H:89:ILE:HD12	7:1H:129:THR:HA	1.86	0.56
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.33	0.56
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.21	0.56
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.88	0.56
40:1i:79:LEU:HD22	40:1i:104:ARG:HB2	1.87	0.56
44:1m:80:ARG:HH22	50:1s:69:HIS:HE1	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:58:GLU:OE2	48:1q:75:ARG:NH2	2.38	0.56
51:1t:92:LEU:O	51:1t:96:GLY:N	2.38	0.56
32:2a:1271:G:O2'	63:2a:3213:HOH:O	2.18	0.56
8:1I:27:ARG:HD2	23:11:71:TYR:CE2	2.41	0.56
1:2A:642:G:N2	1:2A:645:C:OP2	2.33	0.56
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.71	0.56
34:2c:47:LEU:HD13	34:2c:68:VAL:HG11	1.87	0.56
35:2d:98:GLU:CD	35:2d:107:ARG:HH21	2.13	0.56
1:1A:118:A:OP1	63:1A:4180:HOH:O	2.18	0.56
1:1A:2469:A:H5'	1:1A:2470:G:OP2	2.06	0.56
17:1V:88:ARG:NH1	63:1V:306:HOH:O	2.38	0.56
26:14:59:PHE:HE2	50:1s:42:PRO:HB3	1.71	0.56
37:1f:50:TYR:OH	49:1r:74:ARG:O	2.19	0.56
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.69	0.56
1:2A:631:A:N3	1:2A:2415:G:O2'	2.37	0.56
6:2G:57:ALA:HB2	6:2G:90:LEU:HD23	1.87	0.56
32:2a:1027:C:H5"	32:2a:1028:C:C5	2.41	0.56
38:2g:133:GLY:HA2	38:2g:136:LYS:HB2	1.87	0.56
1:1A:90:U:H4'	1:1A:92:A:H5'	1.88	0.56
1:1A:270:A:OP2	1:1A:271(X):G:N2	2.32	0.56
1:1A:1101:U:H2'	1:1A:1102:C:C6	2.38	0.56
1:1A:1475:G:O6	63:1A:4169:HOH:O	2.16	0.56
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.41	0.56
3:1D:34:VAL:HG12	3:1D:63:ARG:HG3	1.88	0.56
32:1a:986:A:N3	50:1s:52:TYR:OH	2.34	0.56
33:1b:95:GLN:HG3	33:1b:147:LYS:O	2.05	0.56
1:2A:568:U:O4	63:2A:3860:HOH:O	2.14	0.56
1:2A:850:C:H5"	25:23:18:ASP:HB2	1.88	0.56
5:2F:155:LEU:HB3	5:2F:192:LEU:HD23	1.87	0.56
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.71	0.56
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.39	0.56
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.41	0.56
40:2i:125:TYR:CE1	40:2i:127:LYS:HD3	2.39	0.56
1:1A:2167:U:H2'	1:1A:2168:G:C8	2.41	0.56
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.87	0.56
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.88	0.56
38:1g:91:VAL:HB	38:1g:96:GLN:HE21	1.70	0.56
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.20	0.56
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.45	0.56
1:2A:1352:U:OP2	63:2A:3894:HOH:O	2.18	0.56
1:2A:1464:C:H2'	1:2A:1465:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2111:C:H42	1:2A:2147:G:H22	1.54	0.56
6:2G:111:LEU:HA	6:2G:114:ILE:HD12	1.86	0.56
7:2H:41:MET:HG3	7:2H:68:THR:HG21	1.86	0.56
8:2I:62:LYS:HG2	8:2I:133:HIS:CE1	2.41	0.56
32:2a:17:U:H2'	32:2a:18:C:C6	2.41	0.56
32:2a:614:A:H2'	32:2a:615:C:C6	2.41	0.56
43:2l:69:TYR:HD2	43:2l:99:HIS:CE1	2.23	0.56
1:1A:1788:C:OP1	63:1A:4184:HOH:O	2.18	0.56
1:1A:2171:A:H1'	1:1A:2172:U:C5	2.40	0.56
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.41	0.56
1:1A:2336:A:H61	22:10:43:THR:HG22	1.71	0.56
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.71	0.56
1:2A:2719:G:OP2	63:2A:3888:HOH:O	2.17	0.56
1:1A:588:U:H2'	1:1A:589:C:C6	2.40	0.56
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.40	0.56
32:1a:1309:G:OP2	44:1m:99:ARG:NH2	2.27	0.56
1:2A:523:C:O2	1:2A:554:U:O2'	2.23	0.56
1:2A:956:G:H5"	12:2Q:77:LYS:HD2	1.88	0.56
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.41	0.56
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.88	0.56
8:2I:9:LEU:HB2	8:2I:12:LEU:HB2	1.88	0.56
36:2e:102:ALA:O	36:2e:107:ARG:NH1	2.39	0.56
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.87	0.56
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.06	0.55
5:1F:161:GLU:HG2	5:1F:164:ARG:NH2	2.21	0.55
13:1R:102:GLU:OE2	18:1W:37:ARG:NH2	2.31	0.55
33:1b:178:ARG:NH2	39:1h:74:PRO:HB3	2.21	0.55
1:2A:2107:C:N4	1:2A:2182:G:H1	2.04	0.55
1:2A:2122:U:H3	1:2A:2176:A:N6	2.02	0.55
11:2P:55:ARG:HA	63:2P:303:HOH:O	2.06	0.55
21:2Z:7:ALA:HB3	21:2Z:61:LEU:HD23	1.88	0.55
24:22:1:MET:N	24:22:52:ASP:OD1	2.39	0.55
24:22:66:GLU:HG2	24:22:69:ARG:HH22	1.70	0.55
32:2a:279:A:N6	48:2q:98:LEU:O	2.39	0.55
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.21	0.55
40:2i:99:LEU:HB3	40:2i:101:PHE:CD2	2.40	0.55
4:1E:109:LYS:O	4:1E:111:ARG:NH1	2.39	0.55
11:1P:49:ARG:NH1	30:18:4:MET:HE1	2.21	0.55
40:1i:3:GLN:NE2	40:1i:20:ARG:HH21	2.04	0.55
1:2A:2115:G:H3'	1:2A:2116:G:C5'	2.36	0.55
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:50:GLU:HA	44:2m:53:VAL:HB	1.87	0.55
1:1A:45:C:OP2	1:1A:215:G:H2'	2.06	0.55
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.06	0.55
32:1a:1028:C:H2'	32:1a:1029:C:H4'	1.88	0.55
44:1m:11:ARG:C	44:1m:13:LYS:H	2.14	0.55
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.39	0.55
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.40	0.55
19:2X:65:ARG:HH11	19:2X:70:LEU:HD21	1.71	0.55
21:2Z:4:ARG:NH2	21:2Z:66:SER:OG	2.40	0.55
34:2c:124:ILE:HG13	34:2c:189:ALA:HB1	1.87	0.55
50:2s:36:ARG:HH12	50:2s:75:ALA:HB3	1.71	0.55
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.40	0.55
1:1A:1843:C:H5'	3:1D:253:GLN:NE2	2.22	0.55
4:1E:1:MET:N	63:1E:410:HOH:O	2.38	0.55
12:1Q:85:LYS:HD3	22:10:7:LEU:HD13	1.89	0.55
32:1a:815:A:N7	32:1a:1509:C:O2'	2.39	0.55
1:2A:945:A:OP2	63:2A:3897:HOH:O	2.18	0.55
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.20	0.55
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.41	0.55
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.71	0.55
1:2A:2657:A:O2'	7:2H:160:LYS:NZ	2.39	0.55
2:2B:14:U:OP2	2:2B:70:C:O2'	2.22	0.55
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.88	0.55
8:2I:7:GLU:HG2	8:2I:8:PRO:HD2	1.88	0.55
32:2a:66:G:OP2	63:2a:3214:HOH:O	2.18	0.55
32:2a:110:C:O2'	47:2p:25:ARG:O	2.22	0.55
42:2k:79:SER:OG	42:2k:106:LYS:NZ	2.27	0.55
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.88	0.55
2:1B:92:C:OP1	21:1Z:79:ARG:NH1	2.39	0.55
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.36	0.55
32:1a:757:U:H2'	32:1a:758:G:O4'	2.06	0.55
33:1b:212:GLN:NE2	33:1b:216:SER:OG	2.39	0.55
1:2A:1702:G:O6	63:2A:3880:HOH:O	2.17	0.55
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.22	0.55
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.71	0.55
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.42	0.55
32:2a:890:G:O2'	32:2a:906:G:O6	2.17	0.55
34:2c:8:ILE:HG23	34:2c:16:ARG:HD3	1.88	0.55
40:2i:43:ALA:O	40:2i:45:ALA:N	2.39	0.55
1:1A:2159:G:H2'	1:1A:2160:G:C8	2.41	0.55
9:1N:128:HIS:O	9:1N:131:GLN:NE2	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:99:PHE:HB2	63:1O:315:HOH:O	2.06	0.55
21:1Z:99:TYR:HB3	21:1Z:123:ASP:HB2	1.88	0.55
34:1c:6:HIS:HD2	34:1c:9:GLY:H	1.54	0.55
1:2A:774:A:H2'	1:2A:774:A:N3	2.20	0.55
1:2A:856:C:H2'	1:2A:857:C:C6	2.42	0.55
6:2G:83:ARG:N	6:2G:86:MET:SD	2.78	0.55
8:2I:70:GLU:O	8:2I:74:ASN:ND2	2.40	0.55
8:2I:96:ASP:O	8:2I:98:ALA:N	2.40	0.55
32:2a:363:A:OP1	43:2l:34:ARG:N	2.30	0.55
32:2a:1202:G:O2'	45:2n:29:ARG:HG3	2.07	0.55
37:2f:68:PRO:HB2	37:2f:71:ARG:HD2	1.87	0.55
1:1A:2147:G:H2'	1:1A:2148:G:H4'	1.88	0.55
32:1a:977:A:H2'	32:1a:978:A:H5"	1.89	0.55
34:1c:175:LEU:HD21	34:1c:201:TYR:CE1	2.41	0.55
37:1f:48:LEU:HD13	37:1f:52:ILE:HG13	1.89	0.55
41:1j:67:THR:O	41:1j:67:THR:OG1	2.25	0.55
1:2A:223:A:N1	1:2A:407:G:O2'	2.39	0.55
1:2A:2103:C:O2	1:2A:2187:G:N1	2.39	0.55
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.07	0.55
5:2F:48:THR:OG1	63:2F:401:HOH:O	2.17	0.55
14:2S:24:LEU:HD22	14:2S:41:ASP:HB2	1.89	0.55
20:2Y:43:ASN:HB3	20:2Y:65:ALA:HB3	1.87	0.55
23:21:51:VAL:N	23:21:58:ILE:O	2.40	0.55
32:2a:1095:U:OP2	32:2a:1108:G:N1	2.37	0.55
34:2c:181:ASN:ND2	34:2c:205:GLY:H	2.03	0.55
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.06	0.55
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	1.89	0.55
37:1f:100:ASN:HD21	49:1r:23:LYS:HD3	1.71	0.55
43:1l:45:PRO:HG3	43:1l:53:ARG:HG3	1.89	0.55
43:1l:53:ARG:HD2	43:1l:93:LEU:HD11	1.89	0.55
14:2S:66:ALA:HB1	14:2S:101:LEU:HB2	1.89	0.55
19:2X:94:GLY:HA3	19:2X:95:LEU:C	2.31	0.55
32:2a:1222:G:O6	63:2a:3203:HOH:O	2.17	0.55
33:2b:48:MET:HA	33:2b:51:LEU:HD12	1.89	0.55
1:1A:226:G:H21	1:1A:228:A:H62	1.53	0.55
2:1B:29:A:O2'	2:1B:58:A:N1	2.34	0.55
5:1F:9:ILE:HG12	5:1F:123:LEU:HD23	1.89	0.55
21:1Z:24:LEU:HB2	21:1Z:41:LEU:HD23	1.88	0.55
32:1a:45:U:H2'	32:1a:46:G:C8	2.41	0.55
1:2A:805:G:OP1	63:2A:3899:HOH:O	2.18	0.55
1:2A:1024:G:OP2	63:2A:3898:HOH:O	2.18	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.88	0.55
6:2G:42:GLY:O	6:2G:44:GLY:N	2.37	0.55
40:2i:4:TYR:O	40:2i:19:LEU:N	2.36	0.55
1:1A:1833:U:O2'	1:1A:1969:A:N1	2.36	0.55
1:1A:2319:G:H4'	1:1A:2320:A:OP1	2.06	0.55
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.88	0.55
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.06	0.55
32:1a:181:G:H4'	32:1a:182:U:H5'	1.89	0.55
37:1f:22:GLU:OE2	37:1f:82:ARG:NH2	2.40	0.55
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.72	0.55
1:2A:1815:A:OP1	63:2A:3900:HOH:O	2.18	0.55
11:2P:5:ASP:HA	11:2P:7:ARG:HH22	1.71	0.55
32:2a:901:A:O2'	32:2a:1513:A:OP1	2.16	0.55
32:2a:919:A:C2'	32:2a:920:U:H5'	2.37	0.55
1:1A:747:U:O2	1:1A:2014:A:H1'	2.07	0.54
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.07	0.54
32:1a:744:C:O2'	32:1a:851:G:N2	2.40	0.54
32:1a:1292:U:H5'	40:1i:38:GLN:OE1	2.07	0.54
34:1c:113:ALA:HA	34:1c:116:VAL:HG22	1.89	0.54
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.25	0.54
1:2A:2453:A:OP1	63:2A:3890:HOH:O	2.18	0.54
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.42	0.54
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.72	0.54
8:2I:48:GLU:HG3	8:2I:52:ARG:NH1	2.21	0.54
30:28:14:VAL:HG23	30:28:24:ALA:HB2	1.88	0.54
32:2a:664:G:H22	32:2a:741:G:H1	1.54	0.54
37:2f:3:ARG:NE	37:2f:38:GLU:OE2	2.40	0.54
42:2k:104:GLN:O	42:2k:106:LYS:N	2.40	0.54
47:2p:18:ARG:NH1	47:2p:32:TYR:OH	2.40	0.54
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.07	0.54
1:1A:2682:U:O2'	15:1T:58:ASN:ND2	2.40	0.54
32:1a:269:C:H2'	32:1a:270:A:C8	2.42	0.54
32:1a:986:A:H2'	32:1a:987:G:O4'	2.07	0.54
32:1a:1029:C:N4	32:1a:1030(A):G:N3	2.54	0.54
36:1e:148:VAL:HG21	39:1h:107:LEU:HD22	1.89	0.54
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.90	0.54
32:2a:7:G:O2'	36:2e:120:THR:O	2.25	0.54
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5"	1.89	0.54
32:2a:1191:A:OP2	34:2c:3:ASN:ND2	2.39	0.54
43:2l:84:LEU:HB3	43:2l:104:VAL:HG21	1.88	0.54
1:1A:666:G:H1'	30:18:4:MET:HE3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2079:U:OP1	23:11:21:ARG:NH2	2.40	0.54
1:2A:277:C:O2'	1:2A:278:A:OP1	2.24	0.54
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.42	0.54
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.06	0.54
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.88	0.54
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.88	0.54
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.88	0.54
15:2T:102:ILE:HG22	15:2T:105:LEU:HD12	1.90	0.54
32:2a:1003:G:H1	32:2a:1035:A:N6	2.05	0.54
32:2a:1129:C:N3	32:2a:1143:G:N2	2.47	0.54
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.17	0.54
41:2j:38:ILE:HD13	41:2j:71:LEU:HD22	1.88	0.54
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.07	0.54
1:1A:2893:G:H4'	1:1A:2894:G:O5'	2.07	0.54
2:1B:63:G:H2'	2:1B:64:C:H6	1.72	0.54
4:1E:170:LEU:HD23	4:1E:184:VAL:HG13	1.90	0.54
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.40	0.54
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.90	0.54
32:1a:674:G:H2'	32:1a:675:A:C8	2.42	0.54
34:1c:124:ILE:HG22	34:1c:130:VAL:HG22	1.89	0.54
39:1h:13:ILE:HD11	39:1h:61:VAL:HG21	1.89	0.54
1:2A:1065:U:H3	1:2A:1073:A:N6	2.01	0.54
1:2A:1258:C:OP2	63:2A:3892:HOH:O	2.18	0.54
1:2A:1384:A:N3	1:2A:1405:U:H1'	2.23	0.54
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.42	0.54
1:2A:2375:G:N2	1:2A:2378:A:OP2	2.40	0.54
35:2d:201:GLN:NE2	36:2e:116:THR:O	2.40	0.54
43:2l:24:VAL:HG12	43:2l:98:TYR:HE1	1.70	0.54
44:2m:5:ALA:HB1	44:2m:66:LEU:HD13	1.88	0.54
1:1A:1634:A:N3	63:1A:4389:HOH:O	2.34	0.54
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.40	0.54
1:2A:875:G:H5"	21:2Z:149:SER:CB	2.38	0.54
1:2A:2305:A:H5"	6:2G:134:GLY:HA3	1.89	0.54
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.22	0.54
6:2G:60:LEU:HA	6:2G:63:ILE:HD12	1.89	0.54
22:20:51:VAL:HG22	22:20:81:VAL:HG23	1.88	0.54
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	1.90	0.54
33:2b:69:LEU:HD13	33:2b:159:PRO:HG3	1.88	0.54
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.35	0.54
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	1.88	0.54
12:1Q:110:THR:HB	12:1Q:113:GLN:H	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:15:ASP:HB3	38:1g:24:THR:HG22	1.89	0.54
1:2A:1345:C:OP2	63:2A:3891:HOH:O	2.18	0.54
1:2A:2267:A:H5"	1:2A:2268:A:H5'	1.88	0.54
2:2B:17:C:H2'	2:2B:18:G:O4'	2.08	0.54
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.33	0.54
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.07	0.54
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.53	0.54
32:2a:555:C:H2'	32:2a:556:C:C6	2.42	0.54
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.23	0.54
44:2m:106:ASN:N	44:2m:106:ASN:HD22	2.06	0.54
45:2n:7:ILE:HA	45:2n:23:ARG:HD2	1.88	0.54
1:1A:2304:G:O2'	6:1G:133:LEU:O	2.22	0.54
33:1b:208:ILE:HA	33:1b:211:ILE:HD12	1.90	0.54
38:1g:28:ASN:HA	38:1g:31:MET:HE2	1.89	0.54
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.43	0.54
1:2A:2115:G:H21	1:2A:2171:A:N6	2.03	0.54
1:2A:2155:G:H2'	1:2A:2156:G:O4'	2.08	0.54
1:2A:2477:C:N3	63:2A:4059:HOH:O	2.33	0.54
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.41	0.54
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.90	0.54
44:2m:20:THR:C	44:2m:22:ILE:H	2.16	0.54
45:2n:8:GLU:HA	45:2n:11:LYS:HD2	1.89	0.54
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.89	0.54
1:1A:171:G:H2'	1:1A:172:C:C6	2.43	0.54
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.41	0.54
1:1A:2096:U:H3	1:1A:2193:G:H1	1.56	0.54
26:14:66:SER:O	26:14:68:ARG:NH1	2.40	0.54
32:1a:620:C:C2	35:1d:135:LEU:HD13	2.42	0.54
32:1a:1226:C:H2'	44:1m:103:THR:HB	1.89	0.54
1:2A:954:G:H5"	12:2Q:13:GLN:HB3	1.89	0.54
1:2A:2223:G:OP1	3:2D:172:TYR:OH	2.20	0.54
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.73	0.54
7:2H:105:LEU:HB3	7:2H:113:VAL:HB	1.89	0.54
32:2a:593:G:H1	32:2a:646:U:H3	1.56	0.54
32:2a:997:U:H3	32:2a:1044:A:H61	1.54	0.54
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.25	0.54
34:2c:70:VAL:HG12	34:2c:72:LYS:H	1.73	0.54
1:1A:1721:G:H5'	1:1A:1722:A:OP2	2.08	0.54
1:1A:2447:G:OP2	63:1A:4187:HOH:O	2.18	0.54
3:1D:10:THR:OG1	3:1D:13:ARG:HG2	2.08	0.54
5:1F:10:PRO:HB3	5:1F:17:ARG:HE	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.88	0.54
32:1a:1187:G:H4'	40:1i:111:ARG:HH11	1.72	0.54
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.26	0.54
49:1r:58:LEU:HD23	49:1r:62:GLU:HB3	1.89	0.54
1:2A:1325:G:OP1	1:2A:1647:G:O2'	2.18	0.54
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.89	0.54
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.40	0.54
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.23	0.54
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.43	0.54
32:2a:1503:A:H5'	32:2a:1531:A:H1'	1.90	0.54
1:1A:2171:A:H1'	1:1A:2172:U:C6	2.43	0.54
1:1A:2876:G:OP1	63:1A:4189:HOH:O	2.18	0.54
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.90	0.54
36:1e:40:ARG:HH21	36:1e:66:MET:HE2	1.72	0.54
47:1p:4:ILE:HG22	47:1p:19:ILE:HD11	1.90	0.54
1:2A:171:G:H2'	1:2A:172:C:C6	2.43	0.54
1:2A:251:A:C5	1:2A:252:G:H1'	2.43	0.54
1:2A:2103:C:H2'	1:2A:2104:G:H8	1.71	0.54
1:2A:2807:G:H22	1:2A:2892:A:H62	1.56	0.54
21:2Z:10:ARG:HD3	21:2Z:37:VAL:O	2.08	0.54
32:2a:551:U:H2'	32:2a:552:U:C6	2.42	0.54
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.41	0.54
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.90	0.54
39:2h:16:ALA:HB1	39:2h:21:LYS:HB2	1.88	0.54
1:1A:1054:A:N1	1:1A:1105:U:O2	2.41	0.53
1:1A:1781:C:N4	63:1A:4337:HOH:O	2.40	0.53
14:1S:84:GLN:HG2	14:1S:111:GLU:HB2	1.90	0.53
32:1a:26:A:O2'	35:1d:209:ARG:NH2	2.41	0.53
32:1a:791:G:N2	32:1a:1497:G:O3'	2.41	0.53
33:1b:198:ASP:OD1	39:1h:68:ARG:NH2	2.39	0.53
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.90	0.53
1:1A:2550:G:O6	63:1A:4182:HOH:O	2.18	0.53
4:1E:77:ILE:HG21	4:1E:195:LEU:HD11	1.91	0.53
8:1I:4:ILE:HD11	8:1I:44:LEU:HD13	1.88	0.53
26:14:40:HIS:HB3	26:14:43:TYR:HD2	1.74	0.53
1:2A:975(A):G:H1'	1:2A:990:A:C2	2.43	0.53
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.43	0.53
1:2A:1621:U:OP1	63:2A:3903:HOH:O	2.19	0.53
1:2A:1818:U:OP1	63:2A:3893:HOH:O	2.18	0.53
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.08	0.53
1:2A:2807:G:N2	1:2A:2892:A:H62	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:66:A:N6	2:2B:109:C:H5'	2.22	0.53
10:2O:64:ARG:HG2	10:2O:83:ALA:HB3	1.90	0.53
32:2a:490:G:P	35:2d:132:ARG:HH22	2.31	0.53
35:2d:76:ARG:HD3	35:2d:207:TYR:CE1	2.43	0.53
36:2e:77:PRO:HD2	36:2e:142:LEU:HD22	1.89	0.53
1:1A:1616:A:OP2	63:1A:4178:HOH:O	2.18	0.53
6:1G:42:GLY:O	6:1G:44:GLY:N	2.39	0.53
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.89	0.53
32:1a:926:G:O6	53:1y:87:LYS:HE2	2.09	0.53
32:1a:943:U:H1'	40:1i:124:GLN:HE22	1.73	0.53
40:1i:110:GLU:OE2	40:1i:113:LYS:NZ	2.42	0.53
48:1q:8:GLY:HA3	48:1q:22:LEU:O	2.08	0.53
1:2A:271(W):G:O6	63:2A:3889:HOH:O	2.18	0.53
1:2A:947:G:OP1	63:2A:3904:HOH:O	2.19	0.53
1:2A:1200:C:OP1	63:2A:3905:HOH:O	2.19	0.53
34:2c:181:ASN:ND2	34:2c:205:GLY:O	2.41	0.53
1:1A:659:C:N4	63:1A:4279:HOH:O	2.26	0.53
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.24	0.53
3:1D:4:LYS:HB3	3:1D:18:VAL:HG23	1.90	0.53
3:1D:183:ARG:HG3	3:1D:270:ILE:HG12	1.91	0.53
32:1a:977:A:O2'	32:1a:979:C:OP2	2.21	0.53
32:1a:1302:U:OP2	44:1m:21:TYR:OH	2.18	0.53
33:1b:150:SER:OG	33:1b:151:GLY:N	2.41	0.53
39:1h:69:ARG:HG3	39:1h:76:PRO:HA	1.89	0.53
53:1y:44:GLU:OE2	53:1y:66:LYS:NZ	2.29	0.53
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.40	0.53
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.90	0.53
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.08	0.53
32:2a:443:C:H2'	32:2a:444:C:H6	1.73	0.53
32:2a:457:C:H2'	32:2a:458:C:H6	1.72	0.53
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.43	0.53
34:2c:112:SER:O	34:2c:116:VAL:HG23	2.09	0.53
53:2y:12:ILE:HG22	53:2y:17:ARG:HG3	1.91	0.53
1:1A:1238:G:OP2	63:1A:4179:HOH:O	2.18	0.53
22:10:23:VAL:HG22	22:10:38:VAL:HG22	1.90	0.53
23:11:53:VAL:HG22	23:11:74:VAL:HG13	1.90	0.53
32:1a:279:A:OP2	48:1q:95:TYR:OH	2.18	0.53
38:1g:80:VAL:HB	38:1g:85:TYR:CD2	2.43	0.53
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.90	0.53
1:2A:1640:C:H5'	1:2A:1641:A:OP2	2.09	0.53
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:55:LYS:HD2	6:2G:58:GLN:NE2	2.22	0.53
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.90	0.53
32:2a:328:C:H4'	32:2a:329:A:H5'	1.91	0.53
32:2a:576:G:O6	32:2a:880:C:O2'	2.21	0.53
32:2a:920:U:H2'	32:2a:921:U:C6	2.44	0.53
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.43	0.53
1:1A:763:G:OP1	63:1A:4188:HOH:O	2.18	0.53
1:1A:820:A:OP2	63:1A:4183:HOH:O	2.18	0.53
1:1A:821:A:H2'	1:1A:946:G:H5"	1.89	0.53
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.43	0.53
11:1P:126:VAL:HG12	11:1P:148:LEU:HG	1.90	0.53
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.91	0.53
32:1a:962:C:O2	63:1a:3303:HOH:O	2.11	0.53
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.90	0.53
41:1j:63:PHE:HE1	45:1n:58:LYS:HG2	1.73	0.53
1:2A:668:G:H5'	1:2A:669:G:OP2	2.08	0.53
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.42	0.53
1:2A:1464:C:H2'	1:2A:1465:G:H8	1.72	0.53
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.44	0.53
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.08	0.53
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.42	0.53
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.22	0.53
35:2d:165:MET:SD	35:2d:168:ARG:NH1	2.67	0.53
38:2g:27:ILE:HD11	38:2g:43:PHE:HB3	1.90	0.53
1:1A:2207:G:O2'	1:1A:2208:A:OP1	2.26	0.53
1:1A:2630:G:H2'	1:1A:2631:G:C8	2.43	0.53
32:1a:356:A:N7	63:1a:3346:HOH:O	2.34	0.53
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.90	0.53
1:2A:2167:U:H2'	1:2A:2168:G:C4	2.44	0.53
3:2D:36:PRO:HA	3:2D:61:LEU:HD12	1.91	0.53
32:2a:143:A:H5"	32:2a:144:G:H5'	1.90	0.53
32:2a:410:G:O5'	35:2d:25:ARG:NH2	2.37	0.53
32:2a:611:A:H2	32:2a:630:G:H22	1.57	0.53
32:2a:1138:G:H2'	32:2a:1140:C:H5"	1.91	0.53
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.25	0.53
43:2l:110:VAL:O	43:2l:122:THR:OG1	2.22	0.53
51:2t:13:LEU:O	51:2t:17:ARG:HG3	2.09	0.53
1:1A:1364:G:OP2	23:11:3:LYS:HD3	2.08	0.53
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.23	0.53
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.43	0.53
17:1V:21:ARG:HD3	17:1V:91:TYR:CE1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:717:C:H4'	42:1k:117:ASN:HD22	1.73	0.53
32:1a:1183:A:H3'	32:1a:1184:G:H5"	1.91	0.53
32:1a:1288:A:N3	32:1a:1352:C:O2'	2.39	0.53
32:1a:1346:A:H61	32:1a:1374:A:H3'	1.73	0.53
39:1h:17:THR:HB	39:1h:78:GLN:OE1	2.08	0.53
1:2A:966:G:OP1	63:2A:3901:HOH:O	2.19	0.53
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.44	0.53
1:2A:2116:G:O2'	1:2A:2117:A:O5'	2.26	0.53
23:21:3:LYS:HB2	23:21:61:ARG:HH12	1.74	0.53
28:26:25:LYS:NZ	28:26:32:ASN:O	2.41	0.53
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.43	0.53
33:2b:12:GLU:C	33:2b:14:GLY:H	2.16	0.53
42:2k:23:ALA:HA	42:2k:28:THR:HG23	1.90	0.53
49:2r:25:THR:HB	49:2r:26:LEU:HD12	1.91	0.53
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.41	0.53
9:1N:69:GLN:O	9:1N:71:ILE:HD12	2.08	0.53
32:1a:158:G:N1	32:1a:163:C:N3	2.44	0.53
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.09	0.53
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.30	0.53
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.91	0.53
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.27	0.53
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.44	0.53
1:2A:2585:U:O4'	56:2v:3:ILE:HB	2.08	0.53
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.73	0.53
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.90	0.53
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.74	0.53
17:2V:33:VAL:HG23	17:2V:59:ALA:HB3	1.90	0.53
32:2a:184:G:H2'	32:2a:185:A:C8	2.44	0.53
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.73	0.53
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.23	0.53
44:2m:10:PRO:HD2	44:2m:18:ALA:HB1	1.90	0.53
1:1A:1086:A:H3'	1:1A:1086:A:N3	2.24	0.53
1:1A:1843:C:H5'	3:1D:253:GLN:HE22	1.74	0.53
1:1A:2143:C:H2'	1:1A:2144:U:H4'	1.90	0.53
1:1A:2282:G:N2	63:1A:4478:HOH:O	2.41	0.53
1:1A:2563:U:H4'	10:1O:28:SER:HA	1.91	0.53
34:1c:117:ALA:HB2	34:1c:200:ALA:HB2	1.91	0.53
49:1r:47:THR:HG23	49:1r:49:LYS:HG3	1.89	0.53
1:2A:2309:A:H61	6:2G:79:ASN:HD22	1.56	0.53
26:24:13:ARG:HH22	26:24:23:GLU:HB3	1.74	0.53
32:2a:570:G:H1'	32:2a:820:U:C4	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1227:A:H5'	44:2m:111:LYS:HD3	1.91	0.53
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.09	0.53
52:2u:11:GLY:O	52:2u:15:ARG:HG3	2.09	0.53
2:1B:63:G:H2'	2:1B:64:C:C6	2.44	0.52
19:1X:1:MET:HE1	24:12:26:ARG:NH2	2.24	0.52
22:10:46:LYS:HB2	22:10:78:TYR:CD1	2.43	0.52
48:1q:19:VAL:HG23	48:1q:44:ALA:HB3	1.91	0.52
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.44	0.52
32:2a:523:A:N1	43:2l:92:0TD:H6	2.24	0.52
42:2k:20:TYR:CE1	42:2k:83:ILE:HD12	2.44	0.52
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.44	0.52
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.92	0.52
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	1.90	0.52
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.08	0.52
9:1N:94:HIS:HB3	9:1N:97:ARG:HD3	1.91	0.52
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.44	0.52
33:1b:167:PRO:HG2	33:1b:188:ALA:HB2	1.91	0.52
48:1q:45:HIS:HB2	48:1q:65:ILE:HD13	1.91	0.52
50:1s:38:SER:HB2	50:1s:71:LEU:HD12	1.90	0.52
1:2A:1993:U:OP2	63:2A:3906:HOH:O	2.19	0.52
1:2A:2112:G:H2'	1:2A:2113:U:C6	2.44	0.52
1:2A:2201:C:OP1	23:21:48:LYS:NZ	2.35	0.52
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.05	0.52
19:2X:60:ARG:NH2	29:27:47:ARG:HH12	2.07	0.52
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.91	0.52
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.24	0.52
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.45	0.52
38:2g:114:ARG:H	38:2g:115:ARG:NH2	2.07	0.52
46:2o:21:ASP:OD1	46:2o:24:SER:HB3	2.09	0.52
1:1A:888:C:H4'	1:1A:889:C:OP1	2.09	0.52
1:1A:2854:G:H2'	1:1A:2855:C:C6	2.44	0.52
26:14:59:PHE:CZ	50:1s:67:VAL:HG21	2.45	0.52
32:1a:509:A:H5'	35:1d:54:TYR:HD2	1.74	0.52
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.09	0.52
32:2a:116:A:H61	32:2a:313:A:H1'	1.74	0.52
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.42	0.52
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.91	0.52
49:2r:26:LEU:HB2	49:2r:29:PHE:HE2	1.74	0.52
1:1A:1790:C:H5"	1:1A:1791:A:OP1	2.10	0.52
1:1A:2690:C:OP2	1:1A:2690:C:H6	1.93	0.52
1:1A:2882:A:OP1	13:1R:96:ARG:HD3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:97:TYR:O	3:1D:100:GLY:N	2.39	0.52
32:1a:1308:U:H2'	32:1a:1309:G:H8	1.74	0.52
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.91	0.52
1:2A:530:G:H4'	1:2A:531:C:OP1	2.09	0.52
1:2A:2425:A:N7	63:2A:4069:HOH:O	2.34	0.52
32:2a:31:G:O2'	32:2a:48:C:N4	2.42	0.52
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	1.90	0.52
15:1T:50:ILE:HG22	15:1T:102:ILE:HD11	1.92	0.52
21:1Z:152:ALA:HA	21:1Z:155:LEU:HD22	1.91	0.52
32:1a:399:G:H2'	32:1a:400:C:C6	2.44	0.52
32:1a:1151:A:O2'	32:1a:1152:A:H8	1.92	0.52
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.91	0.52
43:1l:77:LEU:HD21	43:1l:107:ALA:HA	1.91	0.52
1:2A:800:A:H8	1:2A:800:A:OP1	1.92	0.52
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.09	0.52
8:2I:48:GLU:HG3	8:2I:52:ARG:HH11	1.75	0.52
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.09	0.52
19:2X:35:THR:HG22	19:2X:37:THR:H	1.75	0.52
35:2d:196:LEU:H	35:2d:196:LEU:HD12	1.74	0.52
50:2s:27:GLU:HB3	50:2s:47:HIS:CD2	2.44	0.52
1:1A:61:G:OP1	24:12:51:ARG:NH2	2.42	0.52
1:1A:1062:G:N2	1:1A:1077:A:C2	2.77	0.52
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.45	0.52
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.25	0.52
32:1a:978:A:O2'	32:1a:1322:C:N3	2.33	0.52
47:1p:53:VAL:HG13	47:1p:79:VAL:HG12	1.91	0.52
1:2A:531:C:H4'	1:2A:532:A:H5"	1.89	0.52
1:2A:636:G:N7	11:2P:113:LYS:HE2	2.25	0.52
1:2A:796:C:H2'	1:2A:797:C:C6	2.45	0.52
1:2A:1147:C:H2'	1:2A:1148:A:C8	2.45	0.52
1:2A:1290:C:H2'	1:2A:1291:C:H6	1.75	0.52
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.45	0.52
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.25	0.52
7:2H:18:GLU:HG2	7:2H:19:VAL:H	1.75	0.52
21:2Z:42:VAL:O	21:2Z:46:LYS:HG2	2.08	0.52
34:2c:19:GLU:HB3	34:2c:40:ARG:HH12	1.75	0.52
48:2q:58:GLU:OE1	48:2q:75:ARG:NE	2.42	0.52
1:1A:107:C:H2'	1:1A:108:U:H6	1.72	0.52
1:1A:1158:C:H4'	25:13:32:GLN:HB2	1.90	0.52
6:1G:144:ILE:HA	6:1G:148:MET:HE2	1.91	0.52
32:1a:21:G:OP1	63:1a:3315:HOH:O	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:382:A:H2'	32:1a:383:A:H8	1.74	0.52
1:2A:309:G:N3	1:2A:329:G:O2'	2.43	0.52
3:2D:254:THR:N	63:2D:410:HOH:O	2.43	0.52
32:2a:182:U:C4	32:2a:183:G:H1'	2.44	0.52
32:2a:693:G:O2'	38:2g:82:GLY:N	2.29	0.52
32:2a:923:A:O2'	32:2a:1399:C:OP2	2.26	0.52
36:2e:143:ARG:NH1	39:2h:77:GLU:OE2	2.39	0.52
38:2g:126:ASP:HB3	38:2g:131:LYS:HB2	1.91	0.52
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	2.10	0.52
1:1A:2168:G:C2	1:1A:2171:A:H8	2.27	0.52
5:1F:33:LEU:HD21	5:1F:112:MET:HB2	1.92	0.52
7:1H:87:LEU:HD23	7:1H:164:TYR:HA	1.92	0.52
9:1N:89:LYS:NZ	63:1N:301:HOH:O	2.22	0.52
32:1a:1318:A:H5"	50:1s:3:ARG:NH1	2.25	0.52
33:1b:19:HIS:CE1	33:1b:20:GLU:HG3	2.45	0.52
36:1e:147:ASP:OD1	36:1e:147:ASP:N	2.43	0.52
39:1h:116:LYS:HD3	39:1h:127:LEU:HD23	1.91	0.52
48:1q:24:GLU:HG3	48:1q:39:SER:HB3	1.91	0.52
1:2A:27:G:O2'	1:2A:28:A:OP2	2.28	0.52
1:2A:323:G:OP2	63:2A:3907:HOH:O	2.19	0.52
1:2A:760:G:H2'	1:2A:761:A:O4'	2.08	0.52
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.09	0.52
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.09	0.52
49:2r:41:LYS:HA	49:2r:44:LEU:HD12	1.91	0.52
1:1A:135:G:N7	63:1A:4409:HOH:O	2.34	0.52
1:1A:1784:A:OP2	63:1A:4161:HOH:O	2.19	0.52
1:1A:1918:A:O2'	1:1A:1920:OMC:N4	2.43	0.52
1:1A:2630:G:H2'	1:1A:2631:G:H8	1.75	0.52
6:1G:53:LEU:O	6:1G:56:ALA:N	2.43	0.52
32:1a:60:A:H4'	32:1a:61:G:H5'	1.91	0.52
32:1a:77:G:H2'	32:1a:78:G:H5'	1.91	0.52
32:1a:1456:G:N2	51:1t:43:LEU:HD11	2.25	0.52
35:1d:103:ASN:O	35:1d:107:ARG:HG2	2.10	0.52
35:1d:111:ALA:HB1	35:1d:116:GLN:HB3	1.92	0.52
35:1d:208:SER:O	63:1d:401:HOH:O	2.19	0.52
1:2A:2140:C:H2'	1:2A:2141:G:C8	2.41	0.52
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.44	0.52
1:2A:2756:U:H1'	1:2A:2757:A:H5"	1.92	0.52
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.42	0.52
3:2D:108:PRO:HD2	3:2D:111:LEU:HG	1.92	0.52
32:2a:41:G:H2'	32:2a:42:G:H8	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:120:ALA:C	33:2b:122:PHE:H	2.18	0.52
42:2k:20:TYR:CZ	42:2k:83:ILE:HD12	2.44	0.52
46:2o:39:LEU:HB3	46:2o:56:LEU:HD12	1.91	0.52
1:1A:1058:G:O6	1:1A:1080:C:N3	2.43	0.52
1:1A:1324:G:OP1	63:1A:4195:HOH:O	2.19	0.52
12:1Q:69:PHE:O	63:1Q:302:HOH:O	2.19	0.52
32:1a:320:C:H2'	32:1a:321:A:C8	2.45	0.52
32:1a:1118:C:H2'	32:1a:1119:C:C6	2.45	0.52
33:1b:108:ILE:HA	33:1b:111:ARG:HG2	1.92	0.52
46:1o:3:ILE:HG12	46:1o:38:ARG:HD2	1.92	0.52
1:2A:974:G:OP1	1:2A:1187:G:O2'	2.22	0.52
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.41	0.52
1:2A:1449:A:N3	1:2A:1529:G:H1'	2.25	0.52
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.75	0.52
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.91	0.52
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.90	0.52
33:2b:102:LEU:HD23	33:2b:182:ILE:HD13	1.92	0.52
37:2f:61:LEU:HD13	37:2f:63:TYR:OH	2.09	0.52
1:1A:300:A:OP1	20:1Y:86:ARG:NH2	2.44	0.51
1:1A:1935:G:H1'	1:1A:1964:G:N2	2.25	0.51
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.45	0.51
33:1b:223:ILE:HD12	33:1b:230:VAL:HG12	1.92	0.51
35:1d:20:TYR:HA	35:1d:26:CYS:SG	2.50	0.51
40:1i:40:LEU:HD11	40:1i:70:LYS:HD2	1.90	0.51
43:1l:52:LEU:O	43:1l:54:LYS:NZ	2.39	0.51
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.45	0.51
1:2A:271(R):G:OP1	23:21:76:ARG:NH1	2.43	0.51
1:2A:272(H):C:H42	1:2A:363(B):G:H1	1.56	0.51
1:2A:300:A:H2'	1:2A:334:C:H1'	1.92	0.51
1:2A:2262:U:OP1	1:2A:2387:U:O2'	2.24	0.51
32:2a:222:U:H2'	32:2a:223:U:C6	2.45	0.51
32:2a:1005:A:O2'	32:2a:1036:G:N2	2.43	0.51
35:2d:103:ASN:OD1	35:2d:114:ARG:NE	2.40	0.51
1:1A:240:G:O6	63:1A:4197:HOH:O	2.19	0.51
1:1A:249:C:O2	30:18:12:LYS:NZ	2.33	0.51
1:1A:912:C:OP1	12:1Q:9:TYR:OH	2.20	0.51
1:1A:1062:G:C2	1:1A:1088:A:C8	2.98	0.51
1:1A:1070:A:N7	1:1A:1097:U:O2'	2.42	0.51
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.22	0.51
1:1A:2748:A:H5'	7:1H:4:ILE:HD13	1.92	0.51
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:81:LYS:HE2	20:1Y:101:LYS:HZ3	1.74	0.51
32:1a:159:G:N2	32:1a:162:A:OP2	2.35	0.51
32:1a:337:C:H2'	32:1a:338:A:C8	2.45	0.51
32:1a:425:G:O3'	35:1d:45:GLN:NE2	2.43	0.51
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	1.92	0.51
1:2A:1023:U:OP2	63:2A:3898:HOH:O	2.19	0.51
48:2q:28:PRO:HA	48:2q:35:VAL:HA	1.93	0.51
1:1A:1341:U:O4'	19:1X:57:LEU:HD23	2.09	0.51
1:1A:2314:C:H2'	1:1A:2315:G:C8	2.45	0.51
1:1A:2428:G:OP1	63:1A:4109:HOH:O	2.19	0.51
7:1H:101:ARG:H	7:1H:101:ARG:HD3	1.75	0.51
12:1Q:97:VAL:HG21	12:1Q:103:MET:HE3	1.92	0.51
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.10	0.51
21:1Z:28:MET:HG3	21:1Z:37:VAL:HG11	1.92	0.51
28:16:9:LEU:HD13	28:16:51:GLU:HG3	1.93	0.51
32:1a:41:G:H2'	32:1a:42:G:C8	2.46	0.51
35:1d:154:ASN:HA	35:1d:159:ARG:NE	2.25	0.51
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	1.91	0.51
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.43	0.51
1:2A:1453:U:O2'	1:2A:1455:G:N7	2.36	0.51
1:2A:2115:G:N2	1:2A:2119:A:O5'	2.32	0.51
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.93	0.51
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.45	0.51
32:2a:1161:C:H2'	32:2a:1162:C:C6	2.45	0.51
40:2i:9:ARG:O	40:2i:104:ARG:HG3	2.10	0.51
1:1A:1649:G:O2'	13:1R:107:ASP:OD2	2.20	0.51
1:1A:2713:A:OP1	13:1R:14:SER:HB2	2.11	0.51
10:1O:34:THR:OG1	10:1O:35:VAL:N	2.39	0.51
13:1R:67:LEU:HG	13:1R:76:VAL:HG21	1.91	0.51
14:1S:25:ARG:HD3	14:1S:42:ASP:OD1	2.10	0.51
19:1X:2:LYS:NZ	19:1X:38:GLU:OE1	2.35	0.51
39:1h:51:VAL:HG21	39:1h:60:ARG:HH11	1.75	0.51
48:1q:22:LEU:HD12	48:1q:41:LYS:HG2	1.91	0.51
1:2A:270:A:OP2	1:2A:271(X):G:N1	2.41	0.51
1:2A:686:G:N2	1:2A:788:A:H61	2.08	0.51
1:2A:1139:G:OP2	9:2N:70:LYS:NZ	2.40	0.51
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.44	0.51
1:2A:2751:G:H4'	7:2H:4:ILE:HD11	1.93	0.51
7:2H:17:VAL:HA	7:2H:25:LYS:O	2.11	0.51
7:2H:55:PRO:HG2	7:2H:61:HIS:ND1	2.25	0.51
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.51	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:520:G:N7	63:1A:4406:HOH:O	2.34	0.51
1:1A:1093:G:N2	1:1A:1098:A:OP2	2.40	0.51
1:1A:1174:A:H1'	1:1A:1175:U:H5'	1.91	0.51
32:1a:708:C:H2'	32:1a:709:G:H8	1.76	0.51
32:1a:1256:A:H3'	34:1c:27:LYS:HZ1	1.75	0.51
33:1b:69:LEU:HD13	33:1b:91:PRO:HB2	1.93	0.51
46:1o:3:ILE:HG23	46:1o:38:ARG:HE	1.75	0.51
1:2A:271(W):G:O6	1:2A:271(X):G:N1	2.43	0.51
1:2A:338:G:O6	63:2A:3902:HOH:O	2.19	0.51
1:2A:1063:G:N2	1:2A:1075:C:N3	2.56	0.51
1:2A:1815:A:P	3:2D:54:ARG:HH22	2.32	0.51
1:2A:2130:U:H2'	1:2A:2158:A:N6	2.26	0.51
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.45	0.51
63:2A:3832:HOH:O	21:2Z:200:GLY:N	2.29	0.51
4:2E:13:ARG:HG2	15:2T:58:ASN:HD21	1.76	0.51
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.10	0.51
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.37	0.51
32:2a:926:G:C6	53:2y:87:LYS:HG3	2.45	0.51
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.74	0.51
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.75	0.51
40:2i:70:LYS:O	40:2i:74:ILE:HG13	2.10	0.51
53:2y:20:VAL:O	53:2y:24:LEU:HB2	2.10	0.51
1:1A:795:C:H2'	1:1A:796:C:C6	2.46	0.51
1:1A:811:U:H2'	11:1P:21:ARG:HA	1.92	0.51
1:1A:900:A:H2'	1:1A:901:A:H8	1.76	0.51
1:1A:1096:A:H3'	1:1A:1097:U:H5"	1.92	0.51
32:1a:222:U:H2'	32:1a:223:U:C6	2.45	0.51
47:1p:59:TRP:O	47:1p:64:ALA:N	2.37	0.51
8:2I:77:LEU:HD21	8:2I:100:ALA:HB3	1.92	0.51
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.10	0.51
32:2a:1073:U:H2'	32:2a:1074:G:C8	2.44	0.51
32:2a:1221:G:OP1	32:2a:1320:C:N4	2.39	0.51
32:2a:1248:A:N3	40:2i:70:LYS:NZ	2.57	0.51
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.75	0.51
1:1A:885:C:H2'	1:1A:886:C:O4'	2.09	0.51
11:1P:65:ARG:O	11:1P:68:GLN:NE2	2.44	0.51
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.32	0.51
32:1a:653:A:OP1	39:1h:56:LYS:NZ	2.39	0.51
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.39	0.51
48:1q:86:GLU:O	48:1q:90:ILE:HG12	2.10	0.51
1:2A:2166:G:H2'	1:2A:2167:U:O4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	1.92	0.51
50:2s:61:TYR:CE2	50:2s:63:THR:HG22	2.46	0.51
1:1A:2114:A:H2'	1:1A:2115:G:O4'	2.11	0.51
2:1B:92:C:OP2	63:1B:302:HOH:O	2.20	0.51
26:14:59:PHE:HB3	26:14:62:ARG:NH2	2.26	0.51
32:1a:814:A:N7	32:1a:816:A:C4	2.79	0.51
32:1a:953:G:N7	44:1m:104:ARG:NH2	2.58	0.51
33:1b:63:MET:HE3	33:1b:225:ALA:HB1	1.92	0.51
1:2A:587:C:P	11:2P:21:ARG:HH22	2.33	0.51
21:2Z:125:LEU:HB3	21:2Z:165:VAL:HG13	1.91	0.51
22:20:73:GLY:O	22:20:76:GLY:N	2.37	0.51
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.10	0.51
45:2n:24:CYS:SG	45:2n:40:CYS:N	2.82	0.51
1:1A:62:C:OP1	63:1A:4190:HOH:O	2.19	0.51
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.10	0.51
1:1A:1509(A):A:H2'	1:1A:1509(B):A:C8	2.46	0.51
1:1A:1578:U:C2'	1:1A:1579:A:H5'	2.41	0.51
1:1A:1865:G:OP1	63:1A:4200:HOH:O	2.20	0.51
1:1A:2805:G:H2'	1:1A:2807:G:H8	1.75	0.51
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.26	0.51
32:1a:1191:A:H2'	32:1a:1192:C:C6	2.46	0.51
32:1a:1305:G:OP2	52:1u:2:GLY:N	2.44	0.51
32:1a:1518:MA6:O5'	32:1a:1518:MA6:H8	2.11	0.51
40:1i:22:GLY:HA3	40:1i:60:ASP:OD2	2.11	0.51
53:1y:54:ILE:HB	53:1y:61:LEU:HD12	1.93	0.51
1:2A:310:A:H1'	1:2A:311:A:H2'	1.93	0.51
1:2A:453:C:O2	1:2A:457:A:O2'	2.28	0.51
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.45	0.51
1:2A:1762:A:N6	63:2A:4207:HOH:O	2.44	0.51
1:2A:2641:G:P	9:2N:74:ARG:HH22	2.33	0.51
6:2G:16:ARG:NH1	6:2G:31:VAL:HG21	2.26	0.51
19:2X:72:LYS:NZ	19:2X:75:ASP:OD1	2.44	0.51
21:2Z:180:VAL:HG13	21:2Z:183:LEU:HD12	1.92	0.51
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.46	0.51
32:2a:1232:U:H5"	40:2i:124:GLN:O	2.11	0.51
1:1A:1423:G:H4'	1:1A:1492:G:H21	1.76	0.51
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.10	0.51
32:1a:765:G:C6	32:1a:812:C:C2	2.99	0.51
32:1a:1202:G:N2	45:1n:46:GLU:OE2	2.42	0.51
37:1f:46:ARG:HH22	49:1r:37:VAL:HG11	1.76	0.51
41:1j:62:HIS:O	45:1n:59:ALA:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:1l:82:VAL:O	43:1l:106:ASP:HB2	2.10	0.51
44:1m:49:THR:HG22	44:1m:51:ALA:H	1.76	0.51
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.46	0.51
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.46	0.51
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.44	0.51
32:2a:952:U:H4'	32:2a:964:A:N1	2.26	0.51
32:2a:1244:C:H2'	32:2a:1245:A:H8	1.74	0.51
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.26	0.51
41:2j:77:PRO:O	41:2j:81:THR:OG1	2.24	0.51
1:1A:93:G:H2'	1:1A:94:C:C6	2.46	0.50
1:1A:324:A:H2'	1:1A:325:G:O4'	2.11	0.50
1:1A:1055:G:H2'	1:1A:1056:G:O4'	2.11	0.50
1:1A:1104:C:H2'	1:1A:1105:U:C6	2.46	0.50
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.45	0.50
1:1A:2336:A:H61	22:10:43:THR:CG2	2.24	0.50
1:1A:2549:G:O6	63:1A:4181:HOH:O	2.18	0.50
21:1Z:180:VAL:HG13	21:1Z:183:LEU:HD12	1.93	0.50
32:1a:624:C:H2'	32:1a:625:G:H8	1.75	0.50
32:1a:1308:U:H2'	32:1a:1309:G:C8	2.45	0.50
36:1e:78:HIS:HE1	36:1e:80:ILE:HD13	1.76	0.50
38:1g:50:ILE:HG22	38:1g:125:MET:HG3	1.93	0.50
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.26	0.50
50:1s:36:ARG:NH1	50:1s:52:TYR:O	2.41	0.50
1:2A:422:A:H2'	1:2A:423:A:C8	2.46	0.50
1:2A:1062:G:H2'	1:2A:1063:G:H8	1.75	0.50
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.46	0.50
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.93	0.50
23:21:5:CYS:HB3	23:21:10:LYS:H	1.75	0.50
32:2a:60:A:H4'	32:2a:61:G:O5'	2.11	0.50
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.47	0.50
32:2a:1157:A:C6	32:2a:1180:A:C6	3.00	0.50
63:1A:7366:HOH:O	23:11:65:SER:HA	2.12	0.50
4:1E:92:THR:O	4:1E:95:ILE:HG12	2.11	0.50
16:1U:108:GLU:OE2	16:1U:112:ARG:NE	2.30	0.50
32:1a:974:A:OP2	45:1n:29:ARG:NH2	2.44	0.50
32:1a:1506:U:O2'	63:1a:3316:HOH:O	2.20	0.50
33:1b:124:SER:HA	33:1b:125:PRO:C	2.36	0.50
1:2A:1037:G:H2'	1:2A:1038:C:O4'	2.10	0.50
1:2A:2405:G:OP2	63:2A:3908:HOH:O	2.19	0.50
1:2A:2584:U:O4	63:2A:3895:HOH:O	2.18	0.50
8:2I:9:LEU:HD21	8:2I:35:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:445:G:H2'	32:2a:446:G:O4'	2.10	0.50
33:2b:74:LYS:HG2	33:2b:169:LYS:HG2	1.92	0.50
38:2g:54:THR:O	38:2g:56:GLN:NE2	2.43	0.50
45:2n:4:LYS:HA	45:2n:7:ILE:HG23	1.93	0.50
1:1A:1056:G:H5"	1:1A:1057:A:O4'	2.11	0.50
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.26	0.50
1:1A:2784:C:H2'	1:1A:2785:C:H6	1.76	0.50
2:1B:82:G:OP2	63:1B:303:HOH:O	2.20	0.50
12:1Q:109:VAL:HG22	12:1Q:113:GLN:CD	2.36	0.50
32:1a:7:G:H5'	32:1a:298:A:O4'	2.11	0.50
32:1a:747:C:H3'	32:1a:748:C:C6	2.46	0.50
32:1a:1347:G:N2	32:1a:1374:A:O5'	2.40	0.50
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.11	0.50
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.93	0.50
1:2A:185:U:H4'	1:2A:218:A:H4'	1.93	0.50
1:2A:372:G:H8	23:21:65:SER:O	1.95	0.50
1:2A:657:U:H2'	1:2A:658:C:C6	2.46	0.50
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.26	0.50
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.12	0.50
32:2a:1295:G:H21	32:2a:1302:U:H3	1.59	0.50
33:2b:24:TRP:HB3	33:2b:40:HIS:HE1	1.75	0.50
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.77	0.50
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.47	0.50
1:1A:1057:A:N6	1:1A:1087:G:OP1	2.34	0.50
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.10	0.50
11:1P:59:LEU:HD21	30:18:10:ALA:HB2	1.93	0.50
33:1b:87:ARG:HH21	33:1b:223:ILE:HD11	1.76	0.50
1:2A:1079:C:C4	1:2A:1080:C:H1'	2.46	0.50
1:2A:2397:G:N2	1:2A:2420:C:H1'	2.27	0.50
2:2B:49:C:H2'	2:2B:50:G:C8	2.46	0.50
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.92	0.50
32:2a:965:A:O2'	53:2y:40:ILE:HG21	2.12	0.50
32:2a:1143:G:H2'	32:2a:1144:G:H8	1.75	0.50
32:2a:1376:U:OP1	38:2g:98:SER:OG	2.26	0.50
32:2a:1397:C:H4'	32:2a:1398:A:OP2	2.11	0.50
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.46	0.50
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.46	0.50
1:1A:2820:A:P	13:1R:2:ARG:HH22	2.34	0.50
13:1R:87:TYR:OH	13:1R:117:VAL:O	2.22	0.50
32:1a:658:G:OP1	46:1o:8:LYS:NZ	2.42	0.50
32:1a:738:C:H2'	32:1a:739:C:H6	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.92	0.50
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.12	0.50
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.46	0.50
6:2G:15:VAL:HA	6:2G:175:LEU:HD23	1.93	0.50
13:2R:12:ARG:O	13:2R:17:ARG:NH1	2.44	0.50
26:24:18:CYS:HB2	26:24:20:ASN:H	1.77	0.50
32:2a:859:A:H2'	32:2a:860:A:O4'	2.12	0.50
32:2a:977:A:HO2'	32:2a:981:U:H3	1.58	0.50
32:2a:1151:A:N3	41:2j:39:PRO:HG3	2.26	0.50
38:2g:78:ARG:HH21	38:2g:80:VAL:HG21	1.77	0.50
1:1A:400:G:O6	63:1A:4173:HOH:O	2.17	0.50
1:1A:829:A:N7	1:1A:2248:C:H5'	2.26	0.50
1:1A:879:G:H2'	1:1A:880:G:O4'	2.11	0.50
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.46	0.50
11:1P:89:ALA:O	11:1P:121:LYS:NZ	2.32	0.50
32:1a:946:A:O2'	32:1a:1333:A:N3	2.35	0.50
32:1a:1239:A:H62	32:1a:1299:A:H61	1.59	0.50
34:1c:19:GLU:HB3	34:1c:40:ARG:NH2	2.27	0.50
34:1c:56:ASP:OD2	34:1c:69:HIS:HE1	1.94	0.50
44:1m:60:VAL:HG13	44:1m:64:TRP:HE3	1.77	0.50
1:2A:1151:G:O2'	16:2U:77:SER:O	2.28	0.50
1:2A:1882:C:H2'	1:2A:1883:G:O4'	2.12	0.50
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.47	0.50
1:2A:2262:U:H4'	1:2A:2328:A:H2	1.77	0.50
63:2A:4152:HOH:O	27:25:20:ARG:NH2	2.42	0.50
7:2H:127:GLU:C	7:2H:129:THR:H	2.19	0.50
10:2O:120:GLU:OE1	15:2T:67:SER:OG	2.30	0.50
32:2a:61:G:N7	51:2t:11:SER:OG	2.40	0.50
32:2a:978:A:H61	32:2a:1316:G:H1'	1.76	0.50
32:2a:1318:A:H5"	50:2s:3:ARG:NH2	2.27	0.50
1:1A:569:U:C4	1:1A:570:G:C6	3.00	0.50
1:1A:579:G:H2'	1:1A:580:C:C6	2.47	0.50
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.28	0.50
1:1A:2101:G:H2'	1:1A:2102:U:C6	2.47	0.50
32:1a:160:A:H2'	32:1a:161:A:O4'	2.11	0.50
33:1b:62:ALA:C	33:1b:64:ARG:H	2.19	0.50
39:1h:34:GLU:O	39:1h:38:ILE:HG12	2.12	0.50
40:1i:16:ARG:HG3	40:1i:66:ARG:HH12	1.76	0.50
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.94	0.50
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.26	0.50
1:2A:300:A:H1'	1:2A:319:C:H1'	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1355:G:P	3:2D:38:LYS:HE2	2.52	0.50
1:2A:2400:G:H2'	1:2A:2401:U:H6	1.76	0.50
1:2A:2833:G:H4'	1:2A:2834:G:OP2	2.10	0.50
2:2B:42:C:O2'	63:2B:302:HOH:O	2.20	0.50
11:2P:96:THR:HG22	11:2P:97:PRO:HD2	1.93	0.50
32:2a:677:U:H1'	42:2k:119:CYS:SG	2.51	0.50
48:2q:12:SER:HB3	48:2q:20:THR:HB	1.94	0.50
53:2y:52:ALA:HB1	53:2y:81:LEU:HD11	1.93	0.50
1:1A:1065:U:O2	1:1A:1073:A:N6	2.45	0.50
1:1A:1104:C:H2'	1:1A:1105:U:C5	2.47	0.50
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.26	0.50
1:1A:2443:C:OP1	5:1F:68:LYS:HD3	2.12	0.50
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.94	0.50
10:1O:35:VAL:HG21	10:1O:69:ILE:HD12	1.94	0.50
32:1a:967:5MC:H4'	40:1i:125:TYR:HE1	1.77	0.50
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.47	0.50
33:1b:15:VAL:HG11	33:1b:213:LEU:HD13	1.94	0.50
1:2A:1032:A:H2	1:2A:1122:G:H22	1.58	0.50
1:2A:1105:U:H2'	1:2A:1106:G:C8	2.47	0.50
1:2A:1574:C:H2'	1:2A:1575:C:C6	2.46	0.50
1:2A:2607:G:H2'	1:2A:2608:G:O4'	2.12	0.50
2:2B:115:G:N7	63:2B:309:HOH:O	2.35	0.50
33:2b:71:VAL:HG23	33:2b:164:VAL:HA	1.92	0.50
47:2p:2:VAL:HG22	47:2p:64:ALA:HA	1.93	0.50
1:1A:1919:A:N1	32:1a:1495:U:O2'	2.39	0.50
1:1A:2168:G:C2	1:1A:2171:A:C8	3.00	0.50
1:1A:2657:A:O3'	7:1H:160:LYS:NZ	2.44	0.50
32:1a:235:C:H2'	32:1a:236:G:C8	2.47	0.50
34:1c:6:HIS:CD2	34:1c:9:GLY:H	2.28	0.50
1:2A:534:U:O2'	16:2U:49:HIS:ND1	2.33	0.50
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.27	0.50
1:2A:2115:G:H4'	1:2A:2166:G:O2'	2.12	0.50
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.47	0.50
4:2E:104:VAL:HG13	4:2E:198:VAL:HG22	1.94	0.50
32:2a:601:C:H2'	32:2a:602:A:C8	2.47	0.50
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.94	0.50
1:1A:307:G:H21	1:1A:330:A:H62	1.59	0.49
1:1A:517:C:OP2	27:15:13:LYS:HE3	2.12	0.49
1:1A:2069:G:O6	63:1A:4198:HOH:O	2.19	0.49
1:1A:2319:G:N2	14:1S:3:ARG:HD3	2.17	0.49
32:1a:673:G:H2'	32:1a:674:G:C8	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:728:A:H2'	32:1a:729:A:C8	2.47	0.49
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.46	0.49
1:2A:249:C:HO2'	11:2P:64:LYS:HZ2	1.57	0.49
1:2A:494:G:H4'	18:2W:6:ILE:HB	1.94	0.49
1:2A:1044:G:O2'	1:2A:1048:A:H1'	2.12	0.49
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.45	0.49
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.11	0.49
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.92	0.49
30:28:49:VAL:O	63:28:201:HOH:O	2.20	0.49
32:2a:811:C:O2'	32:2a:901:A:N1	2.43	0.49
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.12	0.49
33:2b:57:PHE:CE2	33:2b:185:ILE:HD11	2.46	0.49
40:2i:89:ASN:HB3	40:2i:92:TYR:CE2	2.47	0.49
1:1A:563:G:O2'	63:1A:4144:HOH:O	2.13	0.49
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.27	0.49
1:1A:1826:G:H4'	3:1D:242:ARG:CZ	2.42	0.49
6:1G:109:VAL:HG22	26:14:33:VAL:HG11	1.94	0.49
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.94	0.49
13:1R:33:ARG:NH2	27:15:57:VAL:O	2.35	0.49
13:1R:53:HIS:ND1	13:1R:94:TYR:OH	2.37	0.49
19:1X:5:TYR:CZ	24:12:30:ARG:HG3	2.46	0.49
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.94	0.49
32:1a:536:C:OP2	63:1a:3317:HOH:O	2.20	0.49
1:2A:577:G:N3	63:2A:4054:HOH:O	2.33	0.49
1:2A:1845:G:OP1	3:2D:258:LYS:NZ	2.42	0.49
1:2A:2261:C:OP1	22:20:19:LYS:NZ	2.44	0.49
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.78	0.49
6:2G:19:LEU:HG	6:2G:175:LEU:HD22	1.93	0.49
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.94	0.49
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.13	0.49
33:2b:76:GLN:NE2	33:2b:206:ASP:O	2.45	0.49
40:2i:99:LEU:HD22	40:2i:101:PHE:HE2	1.75	0.49
1:1A:173:G:H2'	1:1A:174:C:C6	2.48	0.49
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.46	0.49
1:1A:1920:OMC:HM22	1:1A:1921:G:H5'	1.92	0.49
1:1A:2006:C:O5'	1:1A:2006:C:H6	1.94	0.49
1:1A:2068:U:O4	63:1A:4202:HOH:O	2.20	0.49
1:1A:2719:G:OP2	63:1A:4203:HOH:O	2.20	0.49
21:1Z:150:LEU:HB3	21:1Z:171:ILE:HD11	1.94	0.49
32:1a:266:G:H2'	32:1a:266:G:N3	2.27	0.49
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:153:VAL:HG22	34:1c:198:VAL:HG22	1.93	0.49
44:1m:54:VAL:HA	44:1m:57:ARG:HB3	1.93	0.49
1:2A:361:G:O2'	1:2A:362:U:H5'	2.11	0.49
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.48	0.49
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.46	0.49
40:2i:40:LEU:HD13	40:2i:74:ILE:HD11	1.94	0.49
44:2m:87:TYR:HA	44:2m:90:LEU:HG	1.93	0.49
53:2y:30:TRP:HD1	53:2y:89:GLN:HG3	1.77	0.49
1:1A:121:G:H4'	1:1A:149:A:H5'	1.94	0.49
1:1A:414:C:H2'	1:1A:415:A:C8	2.47	0.49
1:1A:512:G:OP2	63:1A:4204:HOH:O	2.20	0.49
1:1A:1179:C:H2'	1:1A:1180:C:C6	2.47	0.49
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.47	0.49
1:1A:2096:U:H2'	1:1A:2097:C:C6	2.47	0.49
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.78	0.49
2:1B:29:A:H2'	2:1B:30:C:O4'	2.12	0.49
32:1a:403:C:OP1	35:1d:137:SER:OG	2.31	0.49
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.46	0.49
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.47	0.49
35:1d:101:LEU:HB2	35:1d:138:TYR:HB3	1.94	0.49
1:2A:2365:G:H4'	22:20:60:PHE:CZ	2.47	0.49
1:2A:2784:C:O3'	4:2E:41:LYS:NZ	2.37	0.49
1:2A:2840:C:O3'	13:2R:53:HIS:NE2	2.46	0.49
24:22:38:GLN:HB3	24:22:44:LEU:HB2	1.94	0.49
32:2a:1030(B):C:H41	32:2a:1030(C):G:H21	1.60	0.49
32:2a:1303:C:H2'	32:2a:1304:G:H5'	1.94	0.49
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.92	0.49
44:2m:107:ALA:O	44:2m:111:LYS:N	2.30	0.49
48:2q:13:ASP:OD1	48:2q:13:ASP:N	2.43	0.49
1:1A:7:G:H2'	1:1A:8:A:O4'	2.11	0.49
1:1A:1448:G:N7	63:1A:4412:HOH:O	2.35	0.49
20:1Y:8:LYS:HA	20:1Y:30:VAL:HG21	1.94	0.49
24:12:63:VAL:O	24:12:67:LYS:HG2	2.12	0.49
32:1a:131:C:H2'	32:1a:132:C:C6	2.47	0.49
32:1a:292:G:O2'	32:1a:608:A:N6	2.46	0.49
32:1a:1028:C:H2'	32:1a:1029:C:C4'	2.43	0.49
32:1a:1278:U:H5'	32:1a:1279:A:H5'	1.95	0.49
40:1i:48:GLU:H	40:1i:49:PRO:CD	2.26	0.49
1:2A:330:A:HO2'	1:2A:331:A:H8	1.61	0.49
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.27	0.49
1:2A:2267:A:OP1	63:2A:3913:HOH:O	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.38	0.49
32:2a:501:C:H2'	32:2a:502:G:C8	2.47	0.49
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.77	0.49
34:2c:6:HIS:HD2	34:2c:7:PRO:HD2	1.77	0.49
40:2i:19:LEU:HD23	40:2i:61:ALA:HB2	1.94	0.49
41:2j:49:VAL:HG22	41:2j:50:ILE:O	2.12	0.49
1:1A:107:C:H2'	1:1A:108:U:C6	2.47	0.49
1:1A:530:G:N1	1:1A:2023:G:OP1	2.31	0.49
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.47	0.49
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.09	0.49
32:1a:950:U:H2'	32:1a:951:G:H8	1.77	0.49
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.13	0.49
1:2A:1287:A:C8	13:2R:104:ARG:HD3	2.47	0.49
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.53	0.49
23:21:65:SER:OG	23:21:66:HIS:ND1	2.40	0.49
28:26:26:ASN:HB3	28:26:29:ASN:HB2	1.94	0.49
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.76	0.49
36:2e:135:THR:O	36:2e:139:LEU:HG	2.12	0.49
39:2h:13:ILE:O	39:2h:17:THR:HG23	2.13	0.49
1:1A:1578:U:H2'	1:1A:1579:A:H5'	1.94	0.49
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.77	0.49
1:1A:1974:C:OP1	63:1A:4186:HOH:O	2.18	0.49
1:1A:2653:U:H5"	1:1A:2654:A:OP2	2.12	0.49
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.78	0.49
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.95	0.49
32:1a:1014:A:H4'	50:1s:14:HIS:CE1	2.46	0.49
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.13	0.49
38:1g:20:ASP:HB3	38:1g:23:VAL:HG23	1.94	0.49
38:1g:48:LYS:O	38:1g:51:GLN:HB3	2.12	0.49
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.95	0.49
1:2A:1166:C:H2'	1:2A:1167:U:H6	1.78	0.49
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.13	0.49
15:2T:24:PRO:HD3	15:2T:52:ILE:HD12	1.95	0.49
23:21:59:THR:HG23	63:21:213:HOH:O	2.12	0.49
32:2a:1005:A:H1'	32:2a:1025:U:C2	2.47	0.49
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.48	0.49
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.13	0.49
1:1A:264:C:O2'	1:1A:265:A:H2'	2.13	0.49
1:1A:848:G:H2'	1:1A:849:A:C8	2.47	0.49
1:1A:1359:A:N6	1:1A:1372:U:H3	2.10	0.49
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2376:A:N6	63:1A:4150:HOH:O	2.14	0.49
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.47	0.49
32:1a:731:G:H5'	32:1a:766:A:H4'	1.93	0.49
32:1a:1249:C:O2'	40:1i:73:GLN:NE2	2.46	0.49
34:1c:5:ILE:HG12	45:1n:58:LYS:HZ2	1.77	0.49
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.78	0.49
1:2A:2309:A:H61	6:2G:79:ASN:ND2	2.10	0.49
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.48	0.49
19:2X:29:TRP:CZ3	19:2X:78:LYS:HG3	2.48	0.49
26:24:34:GLU:HG2	26:24:35:VAL:HG12	1.93	0.49
33:2b:20:GLU:C	33:2b:39:ILE:HG12	2.38	0.49
33:2b:88:ALA:HB1	33:2b:222:ILE:HD11	1.95	0.49
41:2j:6:ILE:HB	41:2j:72:VAL:HG22	1.93	0.49
42:2k:33:THR:HA	42:2k:39:PRO:HA	1.95	0.49
43:2l:82:VAL:O	43:2l:106:ASP:HB2	2.13	0.49
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.93	0.49
1:1A:184:C:H2'	1:1A:185:U:H6	1.77	0.49
1:1A:639:U:H2'	1:1A:640:C:C6	2.48	0.49
1:1A:1042:G:H2'	1:1A:1043:C:C6	2.48	0.49
1:1A:1271:G:H2'	63:1A:4354:HOH:O	2.12	0.49
11:1P:2:LYS:HE3	63:1P:352:HOH:O	2.12	0.49
24:12:28:LYS:HG3	24:12:53:LEU:HD11	1.95	0.49
32:1a:176:C:H2'	32:1a:177:C:C6	2.43	0.49
32:1a:950:U:H5	44:1m:102:ARG:HD3	1.78	0.49
34:1c:130:VAL:HG11	34:1c:157:ILE:HD13	1.94	0.49
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.95	0.49
1:2A:234:C:H2'	1:2A:235:U:C6	2.47	0.49
1:2A:320:A:H4'	1:2A:322:A:N7	2.28	0.49
1:2A:833:U:O2	11:2P:55:ARG:NH1	2.45	0.49
1:2A:2115:G:N2	1:2A:2171:A:H61	2.08	0.49
1:2A:2228:G:OP1	3:2D:261:LYS:NZ	2.33	0.49
2:2B:90:A:C5	2:2B:91:C:H1'	2.48	0.49
2:2B:90:A:N7	2:2B:91:C:H1'	2.28	0.49
17:2V:77:ALA:N	63:2V:302:HOH:O	2.45	0.49
32:2a:615:C:H2'	32:2a:616:G:O4'	2.13	0.49
33:2b:92:TYR:CE1	33:2b:94:ASN:HB2	2.47	0.49
1:1A:1530:C:O2'	1:1A:1531:C:H6	1.96	0.49
1:1A:1693:U:H1'	3:1D:14:ARG:NH1	2.27	0.49
12:1Q:42:ILE:HD13	12:1Q:97:VAL:HB	1.95	0.49
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.47	0.49
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.12	0.49
32:1a:1516:G:N1	32:1a:1519:MA6:OP2	2.45	0.49
35:1d:177:ASP:HB3	35:1d:182:LYS:HG2	1.94	0.49
40:1i:106:ALA:O	40:1i:108:VAL:HG23	2.13	0.49
1:2A:247:G:H4'	1:2A:386:G:C5	2.48	0.49
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.78	0.49
1:2A:1583:A:H5'	1:2A:1586:A:H1'	1.95	0.49
1:2A:2103:C:H2'	1:2A:2104:G:C8	2.47	0.49
32:2a:410:G:P	35:2d:25:ARG:HH21	2.35	0.49
32:2a:848:C:O5'	32:2a:848:C:H6	1.96	0.49
53:2y:30:TRP:CD1	53:2y:89:GLN:HG3	2.47	0.49
1:1A:2018:G:N2	63:1A:4282:HOH:O	2.27	0.48
1:1A:2417:C:OP1	11:1P:65:ARG:NH2	2.46	0.48
1:1A:2543:G:H2'	1:1A:2544:G:C8	2.48	0.48
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.48	0.48
3:1D:69:ARG:HE	3:1D:130:ALA:HB2	1.78	0.48
5:1F:64:ILE:HD12	5:1F:65:TRP:CZ3	2.48	0.48
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.95	0.48
6:1G:77:ILE:HG21	6:1G:80:PHE:CD2	2.48	0.48
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.61	0.48
15:1T:33:LYS:HG2	15:1T:82:LEU:HD23	1.95	0.48
25:13:10:LYS:HB3	25:13:53:LEU:HA	1.95	0.48
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.42	0.48
32:1a:707:C:H2'	32:1a:708:C:H6	1.77	0.48
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.12	0.48
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.48	0.48
37:1f:46:ARG:NH2	49:1r:37:VAL:HG11	2.28	0.48
1:2A:947:G:N7	63:2A:4089:HOH:O	2.35	0.48
1:2A:1342:A:OP2	63:2A:3809:HOH:O	2.19	0.48
1:2A:2811:G:OP1	4:2E:60:ASN:HB2	2.13	0.48
5:2F:11:VAL:HG12	5:2F:12:LEU:H	1.78	0.48
5:2F:179:GLU:CD	5:2F:179:GLU:H	2.19	0.48
7:2H:20:ALA:HB3	7:2H:23:ARG:HB2	1.95	0.48
7:2H:109:PHE:C	7:2H:111:HIS:H	2.21	0.48
14:2S:10:ARG:HG2	14:2S:91:PRO:HA	1.94	0.48
21:2Z:5:LEU:O	21:2Z:59:LEU:HA	2.13	0.48
32:2a:976:G:O4'	32:2a:1363(A):A:N6	2.46	0.48
36:2e:7:GLU:OE1	36:2e:37:ARG:NE	2.43	0.48
36:2e:82:VAL:HG11	36:2e:137:GLU:HB3	1.93	0.48
1:1A:1030:G:OP2	12:1Q:128:LYS:NZ	2.46	0.48
1:1A:2365:G:H4'	22:10:60:PHE:CZ	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2405:G:O2'	1:1A:2406:U:OP1	2.27	0.48
1:1A:2690:C:OP2	13:1R:14:SER:OG	2.31	0.48
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.12	0.48
5:1F:64:ILE:HD11	5:1F:75:HIS:HB2	1.94	0.48
6:1G:143:GLU:OE2	26:14:26:SER:OG	2.19	0.48
11:1P:88:LEU:HD22	11:1P:95:VAL:HG11	1.95	0.48
32:1a:1182:G:C4'	32:1a:1183:A:H5'	2.43	0.48
32:1a:1521:G:H2'	32:1a:1522:U:C6	2.48	0.48
35:1d:25:ARG:HA	35:1d:28:SER:HB3	1.95	0.48
37:1f:89:MET:HE3	49:1r:76:LEU:HD13	1.95	0.48
47:1p:49:LEU:HD13	47:1p:73:LEU:HD13	1.94	0.48
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.95	0.48
1:2A:1450:G:H2'	1:2A:1450(A):C:C6	2.48	0.48
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.25	0.48
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.95	0.48
32:2a:1121:U:H2'	32:2a:1122:U:O4'	2.13	0.48
32:2a:1236:A:OP1	52:2u:2:GLY:HA3	2.13	0.48
34:2c:111:LEU:HD13	34:2c:202:ILE:HG21	1.94	0.48
41:2j:48:THR:O	45:2n:34:TYR:OH	2.30	0.48
1:1A:389:G:O6	11:1P:70:GLN:HB3	2.13	0.48
1:1A:526:A:O2'	1:1A:2043:C:O2	2.23	0.48
1:1A:582:G:H2'	1:1A:583:G:C8	2.48	0.48
1:1A:1187:G:N2	1:1A:1188:U:O4	2.46	0.48
1:1A:1877:A:H5'	1:1A:1878:G:OP2	2.13	0.48
17:1V:40:LEU:HB2	17:1V:46:VAL:HB	1.96	0.48
26:14:62:ARG:C	26:14:64:GLY:HA2	2.37	0.48
32:1a:78:G:N2	32:1a:91:C:C2	2.79	0.48
41:1j:27:ALA:HA	41:1j:30:SER:OG	2.13	0.48
44:1m:20:THR:C	44:1m:22:ILE:H	2.21	0.48
44:1m:32:GLU:OE2	44:1m:36:LYS:NZ	2.46	0.48
1:2A:2001:A:H2'	1:2A:2002:G:H8	1.77	0.48
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.77	0.48
6:2G:106:LEU:HG	6:2G:111:LEU:HG	1.96	0.48
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.47	0.48
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD11	1.94	0.48
26:24:14:ILE:HB	26:24:22:ILE:HB	1.93	0.48
32:2a:1239:A:C4	32:2a:1298:C:N4	2.81	0.48
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.48	0.48
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.16	0.48
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.28	0.48
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:78:LYS:HE2	40:2i:101:PHE:CE1	2.48	0.48
43:2l:8:ASN:O	43:2l:12:ARG:HG3	2.13	0.48
1:1A:2155:G:H2'	1:1A:2156:G:O4'	2.14	0.48
1:1A:2239:G:OP2	63:1A:4208:HOH:O	2.20	0.48
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.47	0.48
1:1A:2637:U:OP2	63:1A:4206:HOH:O	2.20	0.48
6:1G:55:LYS:O	6:1G:59:GLU:HG3	2.13	0.48
7:1H:95:ARG:HG2	7:1H:106:THR:OG1	2.13	0.48
15:1T:15:VAL:HG13	15:1T:79:HIS:CE1	2.48	0.48
26:14:7:PRO:HB2	26:14:27:THR:HG21	1.95	0.48
32:1a:593:G:H2'	32:1a:594:G:O4'	2.13	0.48
32:1a:1001:A:H2'	32:1a:1001(A):G:H8	1.77	0.48
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.28	0.48
52:1u:18:TYR:CE1	52:1u:24:ARG:HG3	2.48	0.48
1:2A:488:G:OP2	63:2A:3910:HOH:O	2.20	0.48
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.42	0.48
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.48	0.48
1:2A:2309:A:H2'	1:2A:2310:A:C8	2.49	0.48
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.49	0.48
3:2D:275:LYS:NZ	63:2D:409:HOH:O	2.30	0.48
7:2H:150:ALA:HA	7:2H:153:LYS:HG3	1.95	0.48
14:2S:65:VAL:O	14:2S:69:VAL:HG23	2.13	0.48
32:2a:954:G:OP1	53:2y:7:SER:HB2	2.13	0.48
32:2a:1053:G:N7	32:2a:1200:C:H5"	2.28	0.48
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.96	0.48
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	1.94	0.48
39:2h:89:PRO:HA	39:2h:92:ARG:HE	1.79	0.48
45:2n:9:LYS:HG3	45:2n:12:ARG:NH2	2.29	0.48
1:1A:220:G:O6	63:1A:4172:HOH:O	2.17	0.48
1:1A:1452:A:OP2	63:1A:4199:HOH:O	2.20	0.48
1:1A:2361:A:OP1	30:18:27:THR:OG1	2.15	0.48
2:1B:88:C:H2'	2:1B:89:G:O4'	2.13	0.48
4:1E:179:GLU:O	63:1E:403:HOH:O	2.20	0.48
14:1S:97:ARG:NH1	63:1S:201:HOH:O	2.30	0.48
16:1U:33:ARG:NH2	63:1U:305:HOH:O	2.46	0.48
28:16:14:THR:HG21	28:16:48:VAL:HG13	1.93	0.48
32:1a:67:C:H2'	32:1a:68:G:C8	2.48	0.48
32:1a:1023:G:H5'	32:1a:1024:G:OP1	2.13	0.48
32:1a:1229:A:H4'	53:1y:2:THR:HG23	1.95	0.48
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.95	0.48
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:150:ALA:HA	42:1k:59:TYR:HB3	1.96	0.48
45:1n:24:CYS:HB3	45:1n:28:GLY:H	1.78	0.48
48:1q:6:LEU:HG	48:1q:23:VAL:HG11	1.96	0.48
1:2A:1056:G:H5"	1:2A:1057:A:O4'	2.14	0.48
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.49	0.48
32:2a:501:C:H2'	32:2a:502:G:H8	1.78	0.48
32:2a:1184:G:H2'	32:2a:1185:G:H8	1.78	0.48
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.14	0.48
35:2d:17:VAL:HG11	35:2d:197:PRO:HB2	1.95	0.48
51:2t:86:ARG:HH21	51:2t:90:GLN:HE22	1.62	0.48
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.22	0.48
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.48	0.48
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.14	0.48
4:1E:154:LYS:HG2	4:1E:156:MET:HE3	1.95	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.55	0.48
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	1.94	0.48
23:11:56:GLN:HE21	23:11:87:PRO:HD3	1.78	0.48
32:1a:201:C:H2'	32:1a:202:U:H2'	1.95	0.48
32:1a:201:C:H42	32:1a:216:G:H22	1.60	0.48
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.48	0.48
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.13	0.48
51:1t:58:LYS:HZ3	51:1t:62:LEU:HD11	1.78	0.48
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.49	0.48
8:2I:93:THR:H	8:2I:96:ASP:HB2	1.78	0.48
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.96	0.48
32:2a:229:U:O2'	47:2p:23:ASP:OD2	2.31	0.48
34:2c:20:SER:HB2	34:2c:40:ARG:HH21	1.78	0.48
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.95	0.48
48:2q:9:VAL:HA	48:2q:55:ASP:O	2.14	0.48
1:1A:271(H):G:O2'	1:1A:271(I):G:OP2	2.23	0.48
1:1A:907:U:HO2'	12:1Q:101:ARG:HH22	1.60	0.48
1:1A:998:C:OP1	63:1A:4209:HOH:O	2.20	0.48
63:1A:4283:HOH:O	28:16:2:ALA:N	2.46	0.48
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.11	0.48
23:11:41:ARG:O	63:11:201:HOH:O	2.20	0.48
28:16:35:GLU:CD	28:16:50:ARG:HH12	2.21	0.48
32:1a:626:U:H2'	32:1a:627:G:C8	2.49	0.48
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.49	0.48
37:1f:8:ILE:HD12	37:1f:63:TYR:HE2	1.79	0.48
1:2A:686:G:H21	1:2A:788:A:H61	1.60	0.48
1:2A:1050:A:H2	1:2A:2751:G:C4	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.14	0.48
30:28:58:ILE:HG13	63:28:204:HOH:O	2.14	0.48
32:2a:743:U:H2'	32:2a:744:C:C6	2.49	0.48
33:2b:19:HIS:CE1	33:2b:206:ASP:HB2	2.48	0.48
40:2i:34:ASN:OD1	40:2i:34:ASN:N	2.47	0.48
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.13	0.48
1:1A:1175:U:H4'	1:1A:1176:G:OP2	2.13	0.48
1:1A:1583:A:H5'	1:1A:1584:C:OP1	2.13	0.48
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.28	0.48
1:1A:2789:C:O2	1:1A:2894:G:N1	2.41	0.48
4:1E:64:LYS:HB3	63:1E:461:HOH:O	2.13	0.48
28:16:6:ARG:HH12	28:16:26:ASN:HB2	1.78	0.48
32:1a:278:G:OP2	48:1q:92:ARG:NH2	2.46	0.48
1:2A:1116:C:H2'	1:2A:1117:G:H8	1.78	0.48
1:2A:2115:G:H1	1:2A:2119:A:P	2.37	0.48
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.39	0.48
14:2S:93:LYS:HG2	14:2S:95:HIS:HB2	1.94	0.48
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.14	0.48
24:22:58:ALA:O	24:22:62:THR:OG1	2.31	0.48
32:2a:457:C:H2'	32:2a:458:C:C6	2.48	0.48
33:2b:75:LYS:HA	33:2b:78:GLN:HB2	1.94	0.48
33:2b:172:ILE:HG22	33:2b:176:GLU:HG3	1.96	0.48
33:2b:178:ARG:NH1	33:2b:196:LEU:O	2.47	0.48
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.49	0.48
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.96	0.48
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.96	0.48
1:1A:2580:U:C5	1:1A:2581:G:C6	3.01	0.48
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.95	0.48
7:1H:111:HIS:CD2	7:1H:111:HIS:H	2.32	0.48
19:1X:29:TRP:CZ3	19:1X:78:LYS:HG3	2.49	0.48
22:10:46:LYS:HB2	22:10:78:TYR:CE1	2.49	0.48
32:1a:193:C:H2'	32:1a:194:C:H6	1.79	0.48
32:1a:690:G:C6	32:1a:691:G:C6	3.02	0.48
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.37	0.48
33:1b:185:ILE:HB	33:1b:199:TYR:HB2	1.96	0.48
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.48	0.48
37:1f:36:ARG:NH2	37:1f:66:GLU:OE1	2.37	0.48
1:2A:1106:G:OP2	1:2A:1106:G:H8	1.96	0.48
1:2A:1204:A:H8	1:2A:1204:A:OP1	1.97	0.48
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.49	0.48
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2316:C:H2'	1:2A:2317:C:H6	1.78	0.48
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.96	0.48
32:2a:190:U:H2'	32:2a:191:G:H8	1.78	0.48
32:2a:954:G:O6	44:2m:104:ARG:NH1	2.47	0.48
32:2a:1302:U:OP2	44:2m:21:TYR:OH	2.19	0.48
36:2e:137:GLU:HG3	36:2e:141:GLN:HE21	1.79	0.48
37:2f:70:ASP:OD1	37:2f:70:ASP:N	2.47	0.48
1:1A:118:A:C8	1:1A:119:A:C8	3.02	0.48
1:1A:272(A):U:H5'	1:1A:272(B):G:OP2	2.14	0.48
1:1A:1088:A:H5'	1:1A:1089:G:H5"	1.95	0.48
1:1A:1231:G:H2'	1:1A:1232:G:C8	2.49	0.48
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.48	0.48
1:1A:2627:G:N2	1:1A:2777:G:OP2	2.45	0.48
4:1E:175:VAL:HG22	4:1E:182:LEU:HD12	1.95	0.48
9:1N:12:ARG:NH1	9:1N:50:ASP:OD2	2.46	0.48
12:1Q:18:LYS:O	12:1Q:98:LYS:NZ	2.30	0.48
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.13	0.48
32:1a:38:G:N2	32:1a:397:A:H5'	2.24	0.48
32:1a:503:C:H2'	32:1a:504:C:H6	1.78	0.48
32:1a:542:G:P	35:1d:10:ARG:HH22	2.36	0.48
32:1a:662:G:H2'	32:1a:663:A:C8	2.49	0.48
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.28	0.48
41:1j:7:LYS:N	41:1j:97:GLU:O	2.47	0.48
1:2A:1400:G:H2'	1:2A:1401:G:C8	2.48	0.48
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.46	0.48
1:2A:2418:A:OP2	63:2A:3917:HOH:O	2.20	0.48
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.78	0.48
32:2a:131:C:H2'	32:2a:132:C:C6	2.49	0.48
33:2b:223:ILE:HA	33:2b:226:ARG:HB2	1.96	0.48
40:2i:43:ALA:C	40:2i:45:ALA:H	2.21	0.48
43:2l:60:LEU:N	43:2l:64:TYR:O	2.44	0.48
1:1A:414:C:H4'	1:1A:1879:C:O2	2.14	0.47
1:1A:987:G:O2'	1:1A:1000:A:N3	2.42	0.47
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.49	0.47
1:1A:2706:G:N2	63:1A:4167:HOH:O	2.16	0.47
5:1F:93:LYS:O	5:1F:95:ARG:HG3	2.14	0.47
7:1H:46:GLU:HB2	7:1H:49:VAL:HG12	1.96	0.47
11:1P:56:SER:N	63:1P:305:HOH:O	2.31	0.47
20:1Y:43:ASN:HA	20:1Y:43:ASN:HD22	1.53	0.47
24:12:32:LEU:HD13	24:12:36:ARG:HH11	1.79	0.47
32:1a:186:C:H2'	32:1a:187:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:741:G:OP1	46:1o:35:ARG:NH2	2.47	0.47
43:1l:25:PRO:O	43:1l:28:LYS:HE3	2.13	0.47
1:2A:84:A:N1	1:2A:98:G:O2'	2.39	0.47
1:2A:253:C:O2'	63:2A:3909:HOH:O	2.20	0.47
1:2A:311:A:C6	1:2A:328:U:C4	3.02	0.47
1:2A:993:G:N2	17:2V:23:GLU:OE2	2.46	0.47
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.22	0.47
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.14	0.47
30:28:32:LEU:O	30:28:36:LYS:HE3	2.14	0.47
32:2a:187:C:H2'	32:2a:188:C:H6	1.78	0.47
32:2a:523:A:H61	43:2l:92:0TD:CG	2.27	0.47
36:2e:51:VAL:O	36:2e:55:VAL:HG23	2.14	0.47
42:2k:50:TYR:HD2	42:2k:60:ALA:HB2	1.79	0.47
44:2m:17:VAL:O	44:2m:20:THR:OG1	2.32	0.47
1:1A:567:A:OP2	11:1P:29:LYS:NZ	2.42	0.47
1:1A:1062:G:N2	1:1A:1088:A:N7	2.61	0.47
15:1T:11:GLU:OE2	15:1T:57:PHE:HB3	2.14	0.47
20:1Y:15:VAL:O	20:1Y:22:GLY:N	2.43	0.47
32:1a:512:U:H2'	32:1a:513:C:C6	2.48	0.47
32:1a:602:A:H2'	32:1a:603:U:O4'	2.14	0.47
32:1a:973:G:H3'	32:1a:974:A:H5"	1.96	0.47
33:1b:21:ARG:HA	33:1b:39:ILE:HG12	1.95	0.47
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.49	0.47
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.31	0.47
42:1k:59:TYR:CZ	42:1k:63:LEU:HD21	2.48	0.47
1:2A:706:A:H2'	1:2A:707:G:O4'	2.14	0.47
1:2A:1791:A:H4'	3:2D:206:LEU:HB2	1.96	0.47
1:2A:2391:G:O6	1:2A:2425:A:H8	1.97	0.47
8:2I:94:ALA:HA	8:2I:114:LEU:HD23	1.96	0.47
12:2Q:67:ARG:NH1	12:2Q:105:GLU:OE2	2.46	0.47
26:24:5:ILE:HG12	26:24:6:HIS:CD2	2.49	0.47
33:2b:51:LEU:HB3	33:2b:55:PHE:CE2	2.48	0.47
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.14	0.47
1:1A:1177:A:H3'	1:1A:1178:C:C6	2.49	0.47
1:1A:1529:G:C5	1:1A:1530:C:C4	3.02	0.47
1:1A:2147:G:H2'	1:1A:2148:G:C4'	2.43	0.47
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.14	0.47
8:1I:104:GLN:C	8:1I:106:GLY:H	2.20	0.47
32:1a:573:A:N1	63:1a:3349:HOH:O	2.35	0.47
32:1a:994:A:H61	32:1a:1047:G:H4'	1.78	0.47
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:12:PRO:HG3	37:1f:57:GLN:O	2.14	0.47
38:1g:40:ALA:HB3	40:1i:41:VAL:HG21	1.95	0.47
39:1h:44:PHE:HB3	39:1h:80:ILE:HD11	1.97	0.47
1:2A:471:A:H8	1:2A:471:A:O5'	1.97	0.47
1:2A:902:C:H2'	1:2A:903:C:C6	2.50	0.47
1:2A:2306:C:OP2	1:2A:2307:G:O2'	2.28	0.47
1:2A:2629:A:H1'	1:2A:2630:G:H5"	1.96	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.14	0.47
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.67	0.47
26:24:53:GLU:CD	26:24:53:GLU:H	2.21	0.47
32:2a:148:G:H2'	32:2a:149:A:C8	2.49	0.47
32:2a:194:C:H2'	32:2a:195:A:H5"	1.96	0.47
34:2c:53:ALA:HB2	34:2c:115:LEU:HD11	1.96	0.47
50:2s:70:LYS:HB2	50:2s:73:GLU:HG2	1.94	0.47
1:1A:392:C:OP1	63:1A:4137:HOH:O	2.20	0.47
1:1A:614(C):A:OP2	59:1A:4023:ARG:HB2	2.14	0.47
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.48	0.47
1:1A:2893:G:H5"	1:1A:2894:G:O4'	2.14	0.47
11:1P:6:LEU:HD23	11:1P:6:LEU:HA	1.70	0.47
11:1P:49:ARG:HH12	30:18:4:MET:HE1	1.79	0.47
19:1X:31:HIS:HB3	19:1X:34:ALA:HB2	1.96	0.47
32:1a:1127:G:H5'	32:1a:1280:A:O2'	2.15	0.47
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.44	0.47
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.14	0.47
34:1c:3:ASN:O	34:1c:4:LYS:HG3	2.14	0.47
40:1i:6:GLY:HA3	40:1i:83:ARG:HB2	1.96	0.47
1:2A:576:U:O4	63:2A:3896:HOH:O	2.18	0.47
1:2A:1102:C:H2'	1:2A:1103:A:C8	2.46	0.47
2:2B:72:G:O2'	2:2B:73:A:O4'	2.29	0.47
12:2Q:59:ARG:O	21:2Z:180:VAL:HG23	2.14	0.47
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.48	0.47
32:2a:429:U:H1'	32:2a:430:A:H5"	1.96	0.47
33:2b:97:TRP:CZ3	33:2b:101:MET:HB2	2.50	0.47
34:2c:188:LEU:HD22	34:2c:195:VAL:HG22	1.96	0.47
35:2d:13:ARG:HG3	35:2d:39:PRO:HA	1.96	0.47
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.32	0.47
36:2e:91:LEU:HD23	36:2e:118:ILE:HD11	1.95	0.47
50:2s:22:LEU:O	50:2s:26:GLY:N	2.47	0.47
53:2y:61:LEU:HB3	53:2y:81:LEU:HD22	1.96	0.47
1:1A:271(P):C:OP1	8:1I:45:LYS:HD3	2.14	0.47
1:1A:1063:G:H5"	1:1A:1065:U:H5	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1203:G:OP2	1:1A:1204:A:O2'	2.21	0.47
1:1A:2109:U:H3	1:1A:2180:U:H3	1.63	0.47
1:1A:2122:U:H3	1:1A:2176:A:H61	1.63	0.47
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.47	0.47
1:1A:2854:G:H2'	1:1A:2855:C:H6	1.78	0.47
11:1P:94:GLU:HA	11:1P:124:LYS:O	2.15	0.47
32:1a:41:G:H2'	32:1a:42:G:H8	1.80	0.47
32:1a:632:A:H3'	32:1a:633:G:C8	2.46	0.47
32:1a:1101:A:OP2	33:1b:96:ARG:NH1	2.46	0.47
35:1d:10:ARG:HB2	35:1d:40:PRO:HG3	1.96	0.47
35:1d:119:GLN:O	35:1d:119:GLN:HG3	2.14	0.47
43:1l:51:ALA:O	43:1l:52:LEU:HD23	2.15	0.47
1:2A:1139:G:H5"	9:2N:70:LYS:NZ	2.29	0.47
1:2A:1287:A:H8	13:2R:104:ARG:HD3	1.78	0.47
1:2A:1313:U:H2'	1:2A:1610:A:C2	2.49	0.47
1:2A:2186:G:H5'	1:2A:2187:G:OP2	2.15	0.47
1:2A:2405:G:H5'	11:2P:75:ILE:HD13	1.97	0.47
1:2A:2892:A:H2'	1:2A:2893:G:H5'	1.96	0.47
10:2O:54:GLU:OE1	63:2O:302:HOH:O	2.19	0.47
14:2S:64:GLU:H	14:2S:64:GLU:CD	2.22	0.47
15:2T:1:MET:HE2	15:2T:3:ARG:HG3	1.96	0.47
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.97	0.47
20:2Y:86:ARG:NH1	20:2Y:100:ALA:O	2.48	0.47
32:2a:745:C:H4'	32:2a:836:G:H21	1.78	0.47
32:2a:1035:A:O2'	32:2a:1036:G:H8	1.97	0.47
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.34	0.47
40:2i:112:LYS:HE2	40:2i:117:HIS:O	2.14	0.47
1:1A:628:G:H5"	30:18:18:ALA:HB2	1.97	0.47
1:1A:732:C:OP1	63:1A:4211:HOH:O	2.20	0.47
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.80	0.47
7:1H:157:TYR:OH	63:1H:301:HOH:O	2.20	0.47
8:1I:96:ASP:OD1	8:1I:96:ASP:N	2.46	0.47
10:1O:115:VAL:O	60:1a:3271:MPD:H11	2.14	0.47
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.48	0.47
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.14	0.47
32:1a:382:A:H2'	32:1a:383:A:C8	2.49	0.47
32:1a:434:U:H2'	32:1a:435:C:C6	2.49	0.47
32:1a:774:G:N7	63:1a:3351:HOH:O	2.36	0.47
32:1a:1008:C:H2'	32:1a:1009:G:O4'	2.15	0.47
32:1a:1246:C:H42	32:1a:1291:G:H1	1.63	0.47
33:1b:114:ARG:O	33:1b:118:LEU:HG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:43:HIS:HB3	35:1d:46:LYS:HD2	1.96	0.47
44:1m:60:VAL:HG13	44:1m:64:TRP:CE3	2.48	0.47
1:2A:1227:G:OP1	16:2U:13:LYS:NZ	2.42	0.47
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.15	0.47
1:2A:1494:A:H2'	1:2A:1495:A:C8	2.48	0.47
2:2B:28:C:OP1	14:2S:31:SER:OG	2.26	0.47
5:2F:74:ARG:HD2	63:2F:413:HOH:O	2.14	0.47
7:2H:45:VAL:HG22	7:2H:50:VAL:HG13	1.96	0.47
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.49	0.47
32:2a:724:G:C2	32:2a:725:G:C8	3.03	0.47
32:2a:861:G:O2'	32:2a:874:G:O2'	2.32	0.47
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.50	0.47
40:2i:105:ASP:HB2	40:2i:107:ARG:HG3	1.96	0.47
41:2j:32:ALA:O	41:2j:76:ASN:N	2.47	0.47
52:2u:12:LYS:HB3	52:2u:17:THR:O	2.15	0.47
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.50	0.47
1:1A:1096:A:H8	1:1A:1096:A:OP2	1.98	0.47
1:1A:1400:G:H2'	1:1A:1401:G:C8	2.49	0.47
1:1A:2206:G:H2'	1:1A:2207:G:N2	2.30	0.47
63:1A:4135:HOH:O	31:19:8:LYS:NZ	2.37	0.47
2:1B:2:C:H2'	2:1B:3:C:C6	2.49	0.47
15:1T:96:ARG:HH11	15:1T:96:ARG:HB2	1.80	0.47
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.23	0.47
23:11:88:LYS:O	23:11:92:LYS:HG3	2.14	0.47
32:1a:227:G:H2'	32:1a:228:A:O4'	2.13	0.47
32:1a:352:C:O2'	32:1a:354:G:OP1	2.21	0.47
32:1a:688:G:O2'	32:1a:704:A:N1	2.38	0.47
32:1a:1227:A:OP2	44:1m:111:LYS:NZ	2.48	0.47
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.79	0.47
36:1e:40:ARG:NH2	36:1e:66:MET:HE2	2.30	0.47
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.96	0.47
1:2A:172:C:H2'	1:2A:173:G:H8	1.78	0.47
1:2A:455:C:N3	1:2A:472:A:H2'	2.30	0.47
1:2A:1203:G:C6	1:2A:1204:A:N6	2.83	0.47
1:2A:1742:G:H2'	1:2A:1743:C:C6	2.50	0.47
1:2A:2138:C:H2'	1:2A:2139:C:O4'	2.14	0.47
1:2A:2142:C:H2'	1:2A:2143:C:H6	1.80	0.47
1:2A:2740:A:H2'	1:2A:2741:A:C8	2.50	0.47
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.97	0.47
23:21:50:ARG:NH1	23:21:57:GLU:OE2	2.47	0.47
32:2a:451:A:N6	32:2a:480:U:H2'	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:975:A:N1	41:2j:48:THR:HB	2.29	0.47
32:2a:980:C:H3'	32:2a:981:U:H6	1.79	0.47
32:2a:1400:5MC:H5'	53:2y:84:GLN:HE21	1.80	0.47
33:2b:12:GLU:C	33:2b:14:GLY:N	2.73	0.47
33:2b:115:LEU:O	33:2b:119:GLU:HG2	2.15	0.47
33:2b:200:ILE:HG22	33:2b:202:PRO:HD3	1.95	0.47
38:2g:86:GLN:HE21	38:2g:86:GLN:HA	1.79	0.47
39:2h:26:VAL:O	39:2h:59:LEU:N	2.40	0.47
40:2i:125:TYR:HD1	40:2i:127:LYS:H	1.63	0.47
42:2k:34:ASP:OD2	42:2k:38:ASN:HB2	2.14	0.47
42:2k:81:ASP:OD1	42:2k:106:LYS:HE2	2.14	0.47
1:1A:1013:C:OP2	63:1A:4212:HOH:O	2.20	0.47
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.30	0.47
1:1A:2478:A:H5'	31:19:31:LYS:HE2	1.95	0.47
1:1A:2503:2MA:H8	58:1A:4022:CLM:O2	2.15	0.47
1:1A:2845:G:H2'	1:1A:2846:G:C8	2.50	0.47
5:1F:40:GLN:NE2	5:1F:182:ASN:HB2	2.30	0.47
5:1F:41:LEU:O	5:1F:44:ARG:HG2	2.15	0.47
6:1G:135:LEU:HD13	6:1G:155:MET:HG2	1.96	0.47
17:1V:27:ALA:CB	17:1V:61:VAL:HG21	2.45	0.47
32:1a:971:G:H22	32:1a:1363(A):A:P	2.38	0.47
32:1a:1237:C:H3'	32:1a:1336:C:H41	1.78	0.47
33:1b:59:GLU:HG3	33:1b:221:LEU:HD23	1.97	0.47
33:1b:84:GLU:O	33:1b:87:ARG:HB2	2.13	0.47
39:1h:120:THR:HG23	39:1h:123:GLU:OE1	2.15	0.47
50:1s:12:ASP:OD1	50:1s:37:ARG:HD2	2.15	0.47
1:2A:644:A:H4'	1:2A:645:C:C5	2.50	0.47
1:2A:1068:G:N1	1:2A:1095:A:N7	2.62	0.47
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.30	0.47
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.50	0.47
6:2G:179:PRO:HG3	26:24:43:TYR:CZ	2.49	0.47
12:2Q:41:TRP:HB3	12:2Q:94:VAL:HB	1.96	0.47
16:2U:102:GLU:HB3	16:2U:104:GLN:HE22	1.80	0.47
17:2V:40:LEU:HB2	17:2V:46:VAL:HG23	1.96	0.47
32:2a:162:A:C5	32:2a:163:C:H1'	2.50	0.47
32:2a:919:A:H2'	32:2a:920:U:H5'	1.95	0.47
32:2a:1256:A:H61	32:2a:1278:U:C1'	2.27	0.47
32:2a:1402:4OC:CM2	32:2a:1403:C:H5'	2.45	0.47
33:2b:140:HIS:HE1	33:2b:144:ARG:HD3	1.79	0.47
34:2c:23:TYR:HB2	41:2j:93:GLY:O	2.15	0.47
35:2d:76:ARG:HD3	35:2d:207:TYR:CZ	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:182:LYS:HB3	35:2d:182:LYS:HE2	1.71	0.47
40:2i:100:GLY:O	40:2i:103:THR:HG22	2.15	0.47
1:1A:185:U:H2'	1:1A:186:G:C8	2.50	0.47
5:1F:38:ARG:NH2	63:1F:411:HOH:O	2.48	0.47
7:1H:40:GLU:CD	7:1H:60:ARG:HH12	2.23	0.47
32:1a:46:G:H1	32:1a:395:C:H42	1.62	0.47
32:1a:189(G):G:H8	32:1a:189(G):G:OP1	1.98	0.47
32:1a:596:C:OP2	63:1a:3318:HOH:O	2.20	0.47
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.49	0.47
33:1b:115:LEU:HB2	33:1b:145:LEU:HD22	1.97	0.47
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.96	0.47
39:1h:29:SER:N	39:1h:32:LYS:HD2	2.30	0.47
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.79	0.47
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.57	0.47
47:1p:22:THR:OG1	47:1p:26:ARG:HG3	2.15	0.47
52:1u:12:LYS:HD2	52:1u:21:TYR:HB2	1.97	0.47
1:2A:576:U:H2'	1:2A:577:G:C8	2.50	0.47
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.15	0.47
1:2A:2597:G:H2'	1:2A:2598:A:C8	2.50	0.47
6:2G:39:ILE:O	6:2G:91:ARG:HA	2.15	0.47
16:2U:110:VAL:O	16:2U:114:LYS:HB2	2.15	0.47
20:2Y:31:LEU:HD11	20:2Y:38:ILE:HD11	1.97	0.47
21:2Z:72:ARG:HA	21:2Z:72:ARG:HD2	1.48	0.47
32:2a:757:U:H2'	32:2a:758:G:O4'	2.15	0.47
32:2a:955:U:H2'	32:2a:956:U:C6	2.50	0.47
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.50	0.47
33:2b:55:PHE:CD1	33:2b:221:LEU:HD22	2.49	0.47
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.15	0.47
35:2d:156:GLU:O	35:2d:159:ARG:N	2.48	0.47
44:2m:16:ASP:HA	44:2m:30:ALA:HB1	1.97	0.47
50:2s:32:LYS:HE2	50:2s:57:HIS:NE2	2.29	0.47
1:1A:228:A:H8	1:1A:229:A:H5'	1.79	0.47
1:1A:272:G:N7	1:1A:421:U:H2'	2.30	0.47
1:1A:515:A:H1'	1:1A:581:C:H1'	1.96	0.47
1:1A:1568:G:H5"	3:1D:61:LEU:HG	1.95	0.47
1:1A:1637:A:OP2	63:1A:4192:HOH:O	2.19	0.47
1:1A:2187:G:H5'	1:1A:2188:C:OP2	2.15	0.47
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.13	0.47
3:1D:72:LYS:HD2	3:1D:103:ARG:NH1	2.30	0.47
16:1U:85:LYS:HE2	16:1U:85:LYS:HB3	1.76	0.47
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:620:C:H2'	32:1a:621:A:O4'	2.16	0.47
32:1a:950:U:H2'	32:1a:951:G:C8	2.50	0.47
44:1m:22:ILE:HB	44:1m:25:ILE:HD13	1.97	0.47
51:1t:34:LYS:O	51:1t:38:LYS:HG2	2.15	0.47
1:2A:1094:U:O2'	1:2A:1096:A:H5"	2.15	0.47
1:2A:1377:G:OP2	63:2A:3919:HOH:O	2.20	0.47
1:2A:1752:C:H2'	1:2A:1753:G:C8	2.50	0.47
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.29	0.47
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.42	0.47
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.25	0.47
32:2a:1240:U:O2'	38:2g:32:ARG:NE	2.45	0.47
32:2a:1304:G:H1'	32:2a:1333:A:H61	1.79	0.47
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.48	0.47
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.48	0.47
39:2h:48:TYR:HA	39:2h:60:ARG:O	2.15	0.47
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.50	0.47
44:2m:24:GLY:HA3	44:2m:66:LEU:HD23	1.97	0.47
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.50	0.46
1:1A:726:G:O2'	1:1A:727:A:OP2	2.33	0.46
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.97	0.46
1:1A:2803:C:H2'	1:1A:2804:C:C6	2.50	0.46
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.50	0.46
32:1a:342:C:H2'	32:1a:343:U:O4'	2.15	0.46
33:1b:73:THR:OG1	33:1b:170:GLU:OE2	2.28	0.46
40:1i:89:ASN:HB3	40:1i:92:TYR:CD2	2.50	0.46
1:2A:285:C:H2'	1:2A:286:C:H6	1.79	0.46
1:2A:302:C:H2'	1:2A:303:U:C6	2.50	0.46
1:2A:578:A:OP1	1:2A:1255:U:O2'	2.28	0.46
1:2A:1718:G:H2'	1:2A:1719:G:H8	1.81	0.46
2:2B:50:G:OP1	14:2S:63:THR:N	2.47	0.46
9:2N:104:LYS:HA	9:2N:107:LEU:HD12	1.97	0.46
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.48	0.46
16:2U:11:ARG:O	16:2U:15:LYS:HG3	2.16	0.46
20:2Y:37:VAL:HG21	20:2Y:72:VAL:HG21	1.97	0.46
32:2a:109:A:C6	32:2a:326:G:C6	3.03	0.46
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.50	0.46
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.50	0.46
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.14	0.46
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.30	0.46
33:2b:42:ILE:HD12	33:2b:203:GLY:HA2	1.97	0.46
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.61	0.46
1:1A:1062:G:H8	1:1A:1062:G:OP2	1.98	0.46
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.45	0.46
9:1N:1:MET:HE3	17:1V:13:ARG:HB3	1.96	0.46
21:1Z:199:LYS:HG2	21:1Z:200:GLY:H	1.81	0.46
31:19:9:ARG:HG2	31:19:14:CYS:HB2	1.97	0.46
32:1a:973:G:N2	63:1a:3303:HOH:O	2.41	0.46
34:1c:97:LYS:O	34:1c:99:VAL:N	2.49	0.46
1:2A:37:C:H2'	1:2A:38:A:C8	2.49	0.46
1:2A:1750:G:O2'	1:2A:2860:A:N1	2.46	0.46
1:2A:2314:C:H5'	6:2G:38:VAL:HG11	1.97	0.46
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.43	0.46
7:2H:95:ARG:HB2	7:2H:128:PRO:HB3	1.97	0.46
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	1.97	0.46
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.16	0.46
32:2a:1002:G:N2	32:2a:1039:C:C2	2.83	0.46
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.47	0.46
34:2c:97:LYS:O	34:2c:99:VAL:N	2.47	0.46
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.97	0.46
50:2s:31:ILE:HD12	50:2s:49:ILE:HD11	1.95	0.46
1:1A:955:C:OP1	12:1Q:87:LYS:NZ	2.43	0.46
1:1A:1063:G:H1	1:1A:1075:C:N4	2.13	0.46
1:1A:1098:A:OP2	1:1A:1098:A:H8	1.97	0.46
1:1A:1179:C:H2'	1:1A:1180:C:H6	1.81	0.46
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.42	0.46
1:1A:2848:G:O6	63:1A:4201:HOH:O	2.20	0.46
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.41	0.46
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.73	0.46
15:1T:91:ARG:HB2	15:1T:121:ILE:HG13	1.97	0.46
19:1X:8:ILE:HD13	19:1X:30:VAL:HG12	1.96	0.46
24:12:1:MET:N	24:12:52:ASP:OD2	2.48	0.46
32:1a:184:G:H2'	32:1a:185:A:H8	1.79	0.46
32:1a:441:A:H8	32:1a:441:A:OP2	1.98	0.46
32:1a:1056:U:OP1	34:1c:163:ALA:N	2.45	0.46
35:1d:108:LEU:HD23	35:1d:174:LEU:HD13	1.96	0.46
36:1e:81:GLU:HG2	36:1e:90:VAL:HG13	1.97	0.46
36:1e:94:ALA:HB1	36:1e:98:THR:HG21	1.98	0.46
1:2A:751:A:C6	1:2A:789:A:C5	3.03	0.46
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.44	0.46
1:2A:2578:G:OP1	1:2A:2614:A:N6	2.42	0.46
29:27:48:LYS:HB2	29:27:48:LYS:HE2	1.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:460:G:H2'	32:2a:461:A:H2'	1.98	0.46
32:2a:1423:G:H2'	32:2a:1424:C:C6	2.50	0.46
40:2i:25:LYS:H	40:2i:60:ASP:HB3	1.80	0.46
1:1A:55:G:O2'	1:1A:127:A:N1	2.46	0.46
1:1A:185:U:H2'	1:1A:186:G:H8	1.80	0.46
1:1A:196:A:O2'	1:1A:805:G:O6	2.24	0.46
1:1A:555:U:O2'	1:1A:556:G:N7	2.45	0.46
1:1A:658:C:H2'	1:1A:659:C:C6	2.50	0.46
1:1A:1047:G:HO2'	1:1A:1048:A:H8	1.64	0.46
2:1B:30:C:OP1	63:1B:305:HOH:O	2.20	0.46
7:1H:149:ARG:NH1	7:1H:167:GLU:OE1	2.49	0.46
14:1S:39:ILE:HD11	14:1S:73:LEU:HD21	1.97	0.46
32:1a:8:A:N6	35:1d:205:GLU:O	2.49	0.46
32:1a:79:G:C2	32:1a:90:U:O2	2.69	0.46
1:2A:851:U:O2'	25:23:42:ALA:O	2.31	0.46
1:2A:1075:C:H2'	1:2A:1076:C:H5'	1.98	0.46
1:2A:2006:C:OP2	63:2A:3916:HOH:O	2.20	0.46
2:2B:13:A:N1	2:2B:69:G:O2'	2.41	0.46
2:2B:91:C:OP2	12:2Q:16:ARG:NH2	2.48	0.46
3:2D:83:GLU:OE1	3:2D:104:TYR:OH	2.19	0.46
6:2G:97:ASP:HA	6:2G:100:TRP:CD1	2.51	0.46
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.51	0.46
17:2V:60:GLU:N	17:2V:95:LEU:O	2.43	0.46
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.31	0.46
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.16	0.46
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.78	0.46
34:2c:47:LEU:HB3	34:2c:52:LEU:HG	1.97	0.46
38:2g:114:ARG:HB2	38:2g:115:ARG:HH21	1.80	0.46
39:2h:60:ARG:HG2	39:2h:62:TYR:CZ	2.51	0.46
50:2s:30:LEU:HD21	50:2s:50:ALA:HB3	1.96	0.46
1:1A:1937:A:H1'	1:1A:1939:5MU:H72	1.96	0.46
6:1G:66:GLN:HE21	6:1G:92:VAL:HG23	1.79	0.46
32:1a:22:G:H4'	32:1a:885:G:C8	2.50	0.46
32:1a:96:U:H2'	32:1a:97:G:H8	1.77	0.46
32:1a:651:C:N4	32:1a:753:A:OP2	2.47	0.46
32:1a:909:A:H2'	32:1a:910:C:O4'	2.15	0.46
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.16	0.46
32:1a:1055:A:O2'	34:1c:161:GLU:O	2.21	0.46
34:1c:8:ILE:HG23	34:1c:184:TYR:HB3	1.98	0.46
1:2A:323:G:H1'	1:2A:1205:U:O2	2.16	0.46
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:747:U:O2	1:2A:2014:A:H1'	2.15	0.46
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.50	0.46
1:2A:2386:C:H2'	1:2A:2387:U:C6	2.50	0.46
1:2A:2400:G:H2'	1:2A:2401:U:C6	2.51	0.46
32:2a:222:U:H2'	32:2a:223:U:H6	1.80	0.46
32:2a:965:A:N7	53:2y:8:LYS:NZ	2.44	0.46
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.48	0.46
32:2a:1366:C:H2'	32:2a:1367:C:H6	1.80	0.46
44:2m:33:ALA:HB1	44:2m:56:LEU:HD11	1.97	0.46
44:2m:34:LEU:HD23	44:2m:39:ILE:HB	1.98	0.46
44:2m:48:LEU:HD13	44:2m:53:VAL:HG23	1.97	0.46
46:2o:85:LEU:HB2	46:2o:87:ILE:HG13	1.98	0.46
50:2s:61:TYR:CD2	50:2s:63:THR:HG22	2.50	0.46
53:2y:6:THR:HG22	53:2y:40:ILE:HG23	1.98	0.46
1:1A:456:C:H4'	63:1A:5005:HOH:O	2.14	0.46
1:1A:2061:G:N2	56:1v:2:THR:HG23	2.31	0.46
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.96	0.46
24:12:1:MET:H1	24:12:52:ASP:CG	2.24	0.46
32:1a:141:A:H1'	32:1a:182:U:O2	2.15	0.46
32:1a:448:A:OP2	32:1a:485:G:N2	2.29	0.46
33:1b:51:LEU:HD21	33:1b:214:ILE:HD12	1.97	0.46
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.15	0.46
34:1c:26:LYS:HE2	34:1c:26:LYS:HB3	1.65	0.46
34:1c:63:ASN:HA	34:1c:98:ASN:HB2	1.97	0.46
41:1j:39:PRO:HB3	41:1j:70:ARG:CZ	2.45	0.46
46:1o:43:LEU:HD12	46:1o:56:LEU:HD12	1.97	0.46
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.49	0.46
1:2A:829:A:N7	1:2A:2248:C:H5'	2.31	0.46
1:2A:988:A:N6	63:2A:4272:HOH:O	2.48	0.46
1:2A:1063:G:N7	1:2A:1070:A:H4'	2.31	0.46
1:2A:1673:U:OP2	63:2A:3922:HOH:O	2.20	0.46
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.51	0.46
6:2G:23:PHE:HB2	6:2G:25:TYR:CE2	2.51	0.46
12:2Q:110:THR:HG22	12:2Q:112:GLU:H	1.81	0.46
32:2a:1240:U:OP2	38:2g:115:ARG:HA	2.15	0.46
37:2f:69:GLU:OE1	37:2f:69:GLU:N	2.49	0.46
47:2p:22:THR:HA	47:2p:33:ILE:HG13	1.97	0.46
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	1.98	0.46
11:1P:121:LYS:HB3	11:1P:123:LEU:HG	1.97	0.46
11:1P:140:ALA:O	25:23:38:GLU:HG2	2.15	0.46
31:19:7:VAL:HG12	31:19:34:GLN:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:262:A:H2'	32:1a:263:A:C8	2.50	0.46
32:1a:263:A:OP1	51:1t:79:ARG:NH1	2.46	0.46
32:1a:979:C:O2	45:1n:19:ARG:NE	2.49	0.46
32:1a:1312:G:H5'	50:1s:5:LEU:HD12	1.98	0.46
32:1a:1330:U:H2'	32:1a:1331:G:H5'	1.97	0.46
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.50	0.46
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.51	0.46
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.47	0.46
1:2A:888:C:H2'	1:2A:889:C:C2	2.50	0.46
3:2D:133:LEU:HB3	3:2D:173:VAL:HG11	1.97	0.46
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.16	0.46
9:2N:39:ARG:NH2	9:2N:41:ASP:OD2	2.49	0.46
9:2N:131:GLN:C	9:2N:133:GLN:H	2.24	0.46
11:2P:124:LYS:HA	11:2P:144:GLU:O	2.16	0.46
13:2R:33:ARG:NH1	13:2R:115:GLU:OE1	2.46	0.46
15:2T:107:ASP:HA	15:2T:110:ILE:HD12	1.96	0.46
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	1.96	0.46
21:2Z:157:LEU:HD22	21:2Z:161:VAL:HG12	1.98	0.46
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.51	0.46
34:2c:17:ASP:OD1	34:2c:18:TRP:N	2.49	0.46
42:2k:96:ARG:NH1	42:2k:99:GLN:HE22	2.14	0.46
50:2s:18:LYS:HZ3	50:2s:31:ILE:HG12	1.80	0.46
1:1A:136:G:N7	63:1A:4445:HOH:O	2.36	0.46
1:1A:746:A:H2'	1:1A:2612:C:H5"	1.98	0.46
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	1.97	0.46
32:1a:19:C:OP1	36:1e:125:SER:OG	2.29	0.46
32:1a:428:G:OP2	35:1d:10:ARG:NH1	2.48	0.46
36:1e:143:ARG:NH1	39:1h:77:GLU:OE2	2.47	0.46
42:1k:33:THR:HG22	42:1k:39:PRO:HA	1.97	0.46
1:2A:320:A:H4'	1:2A:322:A:C8	2.51	0.46
32:2a:434:U:H2'	32:2a:435:C:C6	2.51	0.46
32:2a:1143:G:H2'	32:2a:1144:G:C8	2.51	0.46
32:2a:1298:C:H4'	32:2a:1299:A:O5'	2.16	0.46
32:2a:1442:G:H1'	32:2a:1442(A):G:OP1	2.15	0.46
33:2b:98:LEU:HD23	33:2b:98:LEU:HA	1.85	0.46
33:2b:175:ARG:HB3	33:2b:175:ARG:NH1	2.31	0.46
37:2f:41:GLU:HG3	37:2f:62:TRP:CE3	2.50	0.46
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.97	0.46
1:1A:23:G:OP1	1:1A:504:U:N3	2.39	0.46
1:1A:910:A:N1	1:1A:2277:G:H1'	2.30	0.46
2:1B:19:G:H2'	2:1B:20:C:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.97	0.46
7:1H:133:VAL:HG12	7:1H:141:VAL:HG13	1.98	0.46
9:1N:14:VAL:HG22	9:1N:138:LEU:HG	1.97	0.46
18:1W:12:ILE:HD13	18:1W:17:VAL:HG13	1.98	0.46
27:15:35:GLU:OE1	27:15:35:GLU:N	2.49	0.46
32:1a:391:G:H2'	32:1a:392:G:O4'	2.16	0.46
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.40	0.46
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.51	0.46
34:1c:21:ARG:HE	34:1c:21:ARG:HB2	1.61	0.46
35:1d:155:LEU:HD12	35:1d:156:GLU:H	1.81	0.46
38:1g:52:GLU:H	38:1g:52:GLU:HG2	1.45	0.46
38:1g:78:ARG:HD2	38:1g:156:TRP:CZ3	2.50	0.46
1:2A:1041:C:H42	1:2A:1114:G:H1	1.63	0.46
1:2A:1184:G:C6	1:2A:1185:C:C4	3.04	0.46
1:2A:2207:G:H3'	1:2A:2208:A:H5"	1.97	0.46
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	1.98	0.46
6:2G:41:GLN:O	6:2G:43:LEU:HD22	2.15	0.46
32:2a:261:U:OP2	51:2t:79:ARG:NH2	2.49	0.46
38:2g:72:ARG:NH2	38:2g:142:GLU:OE1	2.49	0.46
1:1A:861:A:H2'	1:1A:862:G:O4'	2.16	0.46
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.51	0.46
1:1A:1639:U:H4'	1:1A:2699:C:H4'	1.97	0.46
21:1Z:28:MET:O	21:1Z:34:ASN:HA	2.16	0.46
32:1a:152:A:N6	32:1a:170:U:C2	2.84	0.46
32:1a:437:U:O2	35:1d:119:GLN:NE2	2.49	0.46
32:1a:473:G:H2'	32:1a:474:G:H8	1.81	0.46
32:1a:687:A:H4'	42:1k:47:VAL:HG22	1.97	0.46
32:1a:707:C:H2'	32:1a:708:C:C6	2.52	0.46
32:1a:1109:C:OP2	34:1c:176:HIS:ND1	2.49	0.46
37:1f:14:LEU:HD22	37:1f:18:GLN:HB3	1.97	0.46
1:2A:208:C:H2'	1:2A:209:C:C6	2.51	0.46
1:2A:391:G:H1'	1:2A:411:G:O4'	2.15	0.46
1:2A:616:G:H5'	5:2F:205:ARG:HD3	1.97	0.46
1:2A:1047:G:O2'	1:2A:1048:A:H8	1.99	0.46
1:2A:1761:C:H2'	1:2A:1762:A:H5"	1.98	0.46
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.98	0.46
7:2H:72:ILE:O	7:2H:76:VAL:HG23	2.16	0.46
15:2T:54:ARG:HA	15:2T:59:THR:HG23	1.98	0.46
15:2T:99:LEU:O	15:2T:102:ILE:HG12	2.16	0.46
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.97	0.46
31:29:10:ILE:HD12	31:29:32:HIS:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:110:C:H2'	32:2a:111:G:O4'	2.15	0.46
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.51	0.46
32:2a:1184:G:H2'	32:2a:1185:G:C8	2.51	0.46
1:1A:196:A:H2'	1:1A:196:A:N3	2.31	0.45
1:1A:226:G:N2	1:1A:228:A:H62	2.14	0.45
1:1A:636:G:OP1	11:1P:132:LYS:HE2	2.16	0.45
1:1A:2538:C:H4'	63:1A:6572:HOH:O	2.15	0.45
1:1A:2690:C:H5"	1:1A:2872:G:N2	2.30	0.45
3:1D:54:ARG:HD3	63:1D:402:HOH:O	2.16	0.45
8:1I:116:LEU:HD22	8:1I:128:LEU:HD11	1.97	0.45
8:1I:133:HIS:ND1	8:1I:134:PRO:O	2.49	0.45
19:1X:84:ALA:HB3	19:1X:87:GLN:HG3	1.97	0.45
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.48	0.45
23:11:95:LEU:O	23:11:98:LEU:HB2	2.15	0.45
32:1a:601:C:H2'	32:1a:602:A:H8	1.81	0.45
32:1a:1347:G:H22	32:1a:1374:A:P	2.39	0.45
33:1b:136:VAL:O	33:1b:140:HIS:HB2	2.17	0.45
44:1m:76:ALA:HA	44:1m:79:LYS:HB3	1.98	0.45
1:2A:557:U:O2'	9:2N:45:ASN:O	2.33	0.45
1:2A:1539:G:H2'	1:2A:1540:U:C6	2.51	0.45
2:2B:27:C:H5"	14:2S:54:LEU:HD11	1.98	0.45
6:2G:15:VAL:O	6:2G:19:LEU:HB2	2.16	0.45
7:2H:55:PRO:HG2	7:2H:61:HIS:CG	2.51	0.45
21:2Z:126:VAL:HG11	21:2Z:161:VAL:HG13	1.98	0.45
22:20:36:ILE:HD13	22:20:58:THR:HG21	1.98	0.45
32:2a:786:G:C2	32:2a:797:C:C2	3.04	0.45
32:2a:865:A:H5'	32:2a:1078:U:O4	2.16	0.45
39:2h:4:ASP:OD2	39:2h:85:ARG:NH1	2.49	0.45
1:1A:862:G:OP1	12:1Q:18:LYS:HE3	2.16	0.45
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.81	0.45
3:1D:71:ASP:OD2	3:1D:103:ARG:NH2	2.48	0.45
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.14	0.45
7:1H:158:HIS:O	7:1H:160:LYS:N	2.49	0.45
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.16	0.45
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.61	0.45
32:1a:132:C:H2'	32:1a:133:U:H6	1.81	0.45
32:1a:441:A:H3'	32:1a:442:C:C6	2.51	0.45
32:1a:575:G:O2'	32:1a:821:G:H5'	2.15	0.45
32:1a:1049:U:OP1	45:1n:3:ARG:HB2	2.16	0.45
32:1a:1187:G:H2'	32:1a:1188:A:C8	2.51	0.45
33:1b:87:ARG:NH1	33:1b:233:SER:OG	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:106:GLN:O	38:1g:110:GLN:HG2	2.16	0.45
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.55	0.45
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.97	0.45
1:2A:1324:G:C4	1:2A:1328:G:O6	2.69	0.45
1:2A:1881:C:H2'	1:2A:1882:C:C6	2.51	0.45
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.77	0.45
5:2F:144:LYS:HB3	5:2F:144:LYS:HE2	1.69	0.45
6:2G:58:GLN:HE21	6:2G:58:GLN:HB3	1.56	0.45
11:2P:135:LEU:HD23	11:2P:135:LEU:HA	1.76	0.45
32:2a:101:A:H5'	51:2t:10:LEU:HD21	1.97	0.45
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.52	0.45
32:2a:175:C:H2'	32:2a:176:C:H6	1.82	0.45
32:2a:420:U:H2'	32:2a:422:C:C5	2.50	0.45
32:2a:592:G:H2'	32:2a:593:G:H8	1.80	0.45
32:2a:659:U:H5"	46:2o:9:GLN:HE22	1.81	0.45
32:2a:853:G:C2'	32:2a:854:G:H5'	2.47	0.45
32:2a:1292:U:H2'	32:2a:1293:G:O4'	2.15	0.45
32:2a:1423:G:H2'	32:2a:1424:C:H6	1.80	0.45
1:1A:271(D):G:H1	1:1A:271(T):C:H42	1.64	0.45
1:1A:793:A:OP2	1:1A:2071:A:O2'	2.33	0.45
1:1A:1379:A:H5"	63:1A:6489:HOH:O	2.17	0.45
1:1A:1568:G:H4'	3:1D:59:LYS:HG2	1.98	0.45
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.51	0.45
4:1E:56:PRO:C	4:1E:58:ARG:H	2.25	0.45
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.51	0.45
8:1I:46:ALA:O	8:1I:50:ARG:HG2	2.16	0.45
10:1O:88:ASN:ND2	10:1O:90:GLN:H	2.14	0.45
15:1T:91:ARG:HD2	15:1T:120:ARG:NH1	2.31	0.45
33:1b:150:SER:O	33:1b:153:ARG:HG2	2.16	0.45
35:1d:3:ARG:HH12	35:1d:115:ARG:HG2	1.81	0.45
1:2A:173:G:H2'	1:2A:174:C:C6	2.50	0.45
1:2A:271(Q):G:H2'	1:2A:271(R):G:C8	2.51	0.45
1:2A:1290:C:H2'	1:2A:1291:C:C6	2.51	0.45
1:2A:1799:G:C2	3:2D:155:LEU:HD12	2.51	0.45
1:2A:2142:C:H2'	1:2A:2143:C:C6	2.51	0.45
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.17	0.45
1:2A:2865:U:OP2	15:2T:119:LYS:NZ	2.50	0.45
3:2D:255:LYS:N	63:2D:410:HOH:O	2.31	0.45
26:24:59:PHE:N	26:24:60:GLN:HB2	2.32	0.45
32:2a:130:A:H1'	32:2a:263:A:O2'	2.17	0.45
32:2a:352:C:H4'	32:2a:354:G:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:938:A:O5'	32:2a:938:A:H8	1.99	0.45
47:2p:58:TYR:O	47:2p:61:SER:OG	2.25	0.45
1:1A:441:U:H2'	1:1A:442:G:C8	2.50	0.45
1:1A:1163:G:OP1	17:1V:24:LYS:NZ	2.46	0.45
1:1A:2140:C:O2	1:1A:2151:G:N1	2.39	0.45
1:1A:2198:A:O5'	8:1I:33:ARG:NH2	2.48	0.45
1:1A:2719:G:OP1	15:1T:100:TYR:OH	2.26	0.45
2:1B:55:U:H2'	2:1B:56:G:O4'	2.16	0.45
4:1E:28:ALA:HB3	4:1E:93:VAL:CG1	2.46	0.45
4:1E:119:ARG:HG2	4:1E:160:TYR:CG	2.52	0.45
8:1I:6:LEU:O	8:1I:7:GLU:HG3	2.15	0.45
10:1O:77:ILE:HD11	10:1O:122:LEU:HB3	1.97	0.45
27:15:35:GLU:HG2	27:15:51:TYR:CD1	2.51	0.45
32:1a:1286:A:H2	52:1u:18:TYR:HH	1.63	0.45
35:1d:155:LEU:HD12	35:1d:156:GLU:N	2.32	0.45
38:1g:26:PHE:HD1	38:1g:101:LEU:HD22	1.81	0.45
38:1g:29:LYS:HD3	38:1g:29:LYS:HA	1.71	0.45
39:1h:104:ARG:HG2	39:1h:138:TRP:CD2	2.52	0.45
40:1i:3:GLN:HE21	40:1i:20:ARG:HH21	1.65	0.45
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.17	0.45
47:1p:21:VAL:HG11	47:1p:59:TRP:NE1	2.31	0.45
1:2A:172:C:H2'	1:2A:173:G:C8	2.51	0.45
1:2A:254:G:OP2	63:2A:3926:HOH:O	2.21	0.45
1:2A:1781:C:H5	29:27:1:MET:HE1	1.80	0.45
7:2H:86:GLU:HB2	7:2H:165:ALA:HB3	1.98	0.45
9:2N:47:ALA:HB2	9:2N:112:LEU:HD11	1.98	0.45
10:2O:64:ARG:HB2	10:2O:79:PHE:CD2	2.51	0.45
12:2Q:58:PHE:O	12:2Q:60:ARG:N	2.45	0.45
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.31	0.45
32:2a:1249:C:O2'	40:2i:68:GLY:O	2.30	0.45
32:2a:1369:C:OP2	40:2i:112:LYS:N	2.39	0.45
32:2a:1372:U:H2'	32:2a:1373:G:O4'	2.17	0.45
51:2t:47:GLY:HA2	51:2t:48:LYS:CB	2.47	0.45
1:1A:271(M):G:O2'	1:1A:271(N):U:H5"	2.16	0.45
1:1A:348:G:N7	63:1A:4453:HOH:O	2.36	0.45
1:1A:534:U:H2'	1:1A:535:C:C6	2.52	0.45
1:1A:2206:G:H2'	1:1A:2207:G:H21	1.82	0.45
1:1A:2655:G:O2'	1:1A:2664:G:O6	2.33	0.45
2:1B:96:U:OP1	21:1Z:14:LYS:NZ	2.50	0.45
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.51	0.45
15:1T:96:ARG:NH1	15:1T:96:ARG:HB2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:35:THR:O	23:11:35:THR:OG1	2.34	0.45
24:12:37:PHE:O	24:12:41:ILE:HG12	2.16	0.45
32:1a:831:U:H2'	32:1a:832:C:C6	2.52	0.45
32:1a:1216:G:H5"	45:1n:5:ALA:HB2	1.98	0.45
44:1m:114:ARG:H	44:1m:114:ARG:HD2	1.82	0.45
1:2A:242:G:C8	30:28:5:LYS:HG2	2.51	0.45
1:2A:873:G:N2	1:2A:905:U:O2	2.50	0.45
1:2A:2094:G:H1	1:2A:2195:C:H42	1.64	0.45
5:2F:104:LYS:O	5:2F:108:LYS:HG3	2.17	0.45
6:2G:61:ALA:O	6:2G:65:GLY:N	2.49	0.45
7:2H:118:PRO:HD2	7:2H:121:ILE:HB	1.99	0.45
8:2I:72:LEU:O	8:2I:75:LEU:HB3	2.17	0.45
12:2Q:10:ARG:HB2	21:2Z:196:VAL:HG21	1.99	0.45
16:2U:67:ALA:O	16:2U:71:GLN:HG3	2.17	0.45
63:26:601:HOH:O	30:28:32:LEU:HA	2.15	0.45
30:28:39:LYS:O	30:28:43:GLN:HG3	2.16	0.45
32:2a:384:G:H2'	32:2a:385:C:C6	2.52	0.45
32:2a:600:C:H2'	32:2a:601:C:C6	2.51	0.45
32:2a:1117:G:H4'	40:2i:104:ARG:NH1	2.31	0.45
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.98	0.45
35:2d:13:ARG:NH2	35:2d:36:ARG:HB2	2.31	0.45
37:2f:33:TYR:HB2	37:2f:75:LEU:HD12	1.99	0.45
43:2l:49:ASN:ND2	43:2l:92:0TD:SB	2.83	0.45
44:2m:5:ALA:CB	44:2m:66:LEU:HD13	2.46	0.45
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.99	0.45
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.51	0.45
1:1A:1268:A:C2	1:1A:2013:A:C4	3.05	0.45
1:1A:2155:G:H3'	1:1A:2156:G:H8	1.80	0.45
1:1A:2712:U:O2'	1:1A:2712(A):A:OP2	2.29	0.45
7:1H:33:LEU:HD12	7:1H:75:ALA:HA	1.99	0.45
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	1.99	0.45
32:1a:1324:A:O4'	32:1a:1362:C:H4'	2.16	0.45
32:1a:1368:G:OP2	40:1i:112:LYS:HD3	2.17	0.45
50:1s:36:ARG:NH1	50:1s:53:ASN:HA	2.32	0.45
1:2A:272(H):C:N4	1:2A:363(B):G:H1	2.14	0.45
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.52	0.45
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.17	0.45
1:2A:2468:G:OP1	12:2Q:119:ARG:NH2	2.26	0.45
63:2A:4222:HOH:O	13:2R:9:LYS:HB3	2.17	0.45
3:2D:127:VAL:HA	3:2D:193:VAL:HG23	1.98	0.45
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.97	0.45
5:2F:184:TYR:CD2	5:2F:188:ARG:HD2	2.52	0.45
8:2I:57:ARG:NH1	8:2I:61:ARG:HH21	2.14	0.45
12:2Q:68:ILE:HD13	12:2Q:103:MET:HG2	1.99	0.45
13:2R:29:LEU:HD12	13:2R:29:LEU:HA	1.76	0.45
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.16	0.45
17:2V:59:ALA:HB2	17:2V:96:ILE:HG22	1.98	0.45
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.81	0.45
26:24:57:GLU:HA	26:24:58:ARG:HA	1.56	0.45
32:2a:730:G:C5	32:2a:731:G:H1'	2.52	0.45
32:2a:1005:A:H5"	32:2a:1006:C:C5	2.52	0.45
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.52	0.45
32:2a:1313:U:OP2	50:2s:5:LEU:HG	2.17	0.45
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.44	0.45
1:1A:1091:G:H1	1:1A:1100:C:H42	1.62	0.45
1:1A:2712:U:H2'	1:1A:2714:G:H5"	1.98	0.45
5:1F:183:VAL:HG13	63:1F:418:HOH:O	2.15	0.45
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.16	0.45
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.60	0.45
21:1Z:150:LEU:O	21:1Z:171:ILE:HG13	2.17	0.45
32:1a:17:U:H1'	32:1a:1080:A:N3	2.31	0.45
32:1a:309:G:O2'	32:1a:607:A:N1	2.49	0.45
32:1a:741:G:H2'	32:1a:742:G:O4'	2.17	0.45
32:1a:971:G:N2	32:1a:1363(A):A:OP2	2.43	0.45
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.41	0.45
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.17	0.45
1:2A:1576:U:H2'	1:2A:1577:C:C6	2.51	0.45
1:2A:1859:A:H62	1:2A:1883:G:H21	1.65	0.45
1:2A:2227:A:O2'	63:2A:3830:HOH:O	2.09	0.45
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.52	0.45
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.50	0.45
1:2A:2639:A:H2'	1:2A:2640:G:O4'	2.16	0.45
3:2D:164:GLN:CD	3:2D:176:ARG:HH22	2.25	0.45
7:2H:90:LYS:HD2	7:2H:163:TYR:CD2	2.52	0.45
12:2Q:66:ILE:HG12	12:2Q:104:PHE:CE1	2.51	0.45
32:2a:557:G:C6	32:2a:558:G:C6	3.05	0.45
32:2a:664:G:N2	32:2a:741:G:H1	2.14	0.45
32:2a:701:C:OP1	32:2a:702:A:O2'	2.24	0.45
32:2a:849:C:H2'	32:2a:850:U:O4'	2.17	0.45
32:2a:977:A:O2'	32:2a:981:U:N3	2.47	0.45
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1348:U:H2'	32:2a:1349:A:H8	1.81	0.45
38:2g:113:GLU:HB2	38:2g:119:ARG:CG	2.44	0.45
39:2h:23:SER:OG	39:2h:24:THR:N	2.50	0.45
1:1A:705:A:H1'	3:1D:9:TYR:CE2	2.52	0.45
1:1A:2328:A:H2'	1:1A:2329:G:H8	1.80	0.45
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.52	0.45
1:1A:2515:C:H2'	1:1A:2516:G:H8	1.82	0.45
3:1D:164:GLN:OE1	3:1D:176:ARG:NH2	2.50	0.45
4:1E:111:ARG:HG2	4:1E:118:LYS:HD3	1.99	0.45
6:1G:72:ARG:HD3	6:1G:85:GLY:O	2.17	0.45
63:1U:315:HOH:O	17:1V:13:ARG:HD2	2.16	0.45
32:1a:166:G:H2'	32:1a:167:G:H8	1.82	0.45
32:1a:601:C:H2'	32:1a:602:A:C8	2.52	0.45
32:1a:1279:A:H5"	32:1a:1280:A:OP1	2.16	0.45
32:1a:1442:G:O2'	32:1a:1442(A):G:O5'	2.32	0.45
33:1b:80:ILE:HD13	33:1b:211:ILE:HB	1.99	0.45
35:1d:133:VAL:HG11	35:1d:138:TYR:CD1	2.51	0.45
44:1m:51:ALA:O	44:1m:55:ARG:HG3	2.17	0.45
1:2A:213:A:H5'	1:2A:214:G:OP2	2.16	0.45
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.46	0.45
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.51	0.45
3:2D:118:VAL:HG22	3:2D:119:ALA:H	1.82	0.45
8:2I:77:LEU:HD13	8:2I:101:LEU:HD23	1.99	0.45
15:2T:110:ILE:O	15:2T:114:LEU:HB2	2.16	0.45
32:2a:955:U:H2'	32:2a:956:U:H6	1.81	0.45
32:2a:1227:A:C4	50:2s:83:HIS:HB3	2.52	0.45
33:2b:30:ARG:HG3	33:2b:31:TYR:CD1	2.52	0.45
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.99	0.45
35:2d:141:ARG:H	35:2d:141:ARG:HG3	1.57	0.45
38:2g:69:VAL:HG22	38:2g:135:VAL:HG12	1.98	0.45
1:1A:446:G:OP1	16:1U:3:ARG:NH1	2.47	0.45
1:1A:796:C:H2'	1:1A:797:C:C6	2.52	0.45
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.17	0.45
1:1A:2428:G:H5"	1:1A:2429:G:OP1	2.17	0.45
1:1A:2612:C:OP2	27:15:2:ALA:N	2.50	0.45
2:1B:73:A:C4	2:1B:105:A:C2	3.05	0.45
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	1.99	0.45
17:1V:27:ALA:HB3	17:1V:61:VAL:HG21	1.98	0.45
32:1a:669:U:H2'	32:1a:670:G:H8	1.82	0.45
32:1a:1029:C:N4	32:1a:1030(A):G:C2	2.85	0.45
32:1a:1519:MA6:H5"	32:1a:1520:G:OP2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:83:ARG:O	34:1c:87:LEU:N	2.42	0.45
1:2A:127:A:H5"	1:2A:128:C:C6	2.52	0.45
1:2A:207:A:N3	63:2A:4101:HOH:O	2.36	0.45
1:2A:451:C:H4'	5:2F:52:LYS:HE2	1.99	0.45
1:2A:1271:G:OP2	63:2A:3808:HOH:O	2.21	0.45
1:2A:2112:G:H2'	1:2A:2113:U:H6	1.81	0.45
1:2A:2245:U:H5"	1:2A:2246:G:H5'	1.99	0.45
8:2I:83:ALA:O	8:2I:88:ILE:HA	2.16	0.45
12:2Q:110:THR:HG22	12:2Q:112:GLU:N	2.32	0.45
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.17	0.45
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	1.98	0.45
28:26:34:LEU:H	28:26:51:GLU:HB3	1.82	0.45
32:2a:280:C:N3	48:2q:39:SER:OG	2.46	0.45
1:1A:30:G:H2'	1:1A:31:C:C6	2.52	0.45
1:1A:592:G:OP2	63:1A:4215:HOH:O	2.21	0.45
1:1A:968:G:O6	63:1A:4159:HOH:O	2.15	0.45
1:1A:1024:G:C6	1:1A:1025:G:C6	3.05	0.45
1:1A:1439:A:H2'	1:1A:1440:G:O4'	2.17	0.45
1:1A:1634:A:O2'	63:1A:4142:HOH:O	2.12	0.45
1:1A:1859:A:H2'	1:1A:1860:G:O4'	2.17	0.45
1:1A:2115:G:H2'	1:1A:2117:A:H61	1.81	0.45
1:1A:2577:A:O4'	27:15:3:LYS:HB2	2.17	0.45
2:1B:91:C:H5'	12:1Q:18:LYS:HA	1.99	0.45
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.34	0.45
25:13:7:LYS:HA	25:13:33:GLN:O	2.17	0.45
32:1a:77:G:C2'	32:1a:78:G:H5'	2.47	0.45
32:1a:123:C:O2'	32:1a:290:C:O2	2.33	0.45
32:1a:344:A:H4'	32:1a:345:C:OP2	2.17	0.45
32:1a:1151:A:H5"	41:1j:41:PRO:HA	1.99	0.45
37:1f:3:ARG:HG3	37:1f:66:GLU:HG3	1.99	0.45
39:1h:12:ARG:NH1	39:1h:25:ASP:O	2.50	0.45
40:1i:16:ARG:HG3	40:1i:66:ARG:NH1	2.32	0.45
51:1t:67:ALA:HB2	51:1t:77:ALA:HB2	1.99	0.45
1:2A:719:C:H2'	1:2A:720:C:C6	2.52	0.45
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.98	0.45
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.99	0.45
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.50	0.45
19:2X:32:PRO:HA	19:2X:77:LYS:HB2	1.99	0.45
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.97	0.45
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.32	0.45
35:2d:155:LEU:HD12	35:2d:156:GLU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:7:GLU:HB3	36:2e:112:LEU:HD22	1.98	0.45
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	2.00	0.45
46:2o:3:ILE:HG23	46:2o:38:ARG:HE	1.82	0.45
1:1A:307:G:H21	1:1A:330:A:N6	2.15	0.44
1:1A:476:G:H4'	1:1A:502:A:N1	2.32	0.44
1:1A:761:A:H5"	63:1A:5574:HOH:O	2.17	0.44
1:1A:1682:G:H2'	1:1A:1683:C:O4'	2.17	0.44
5:1F:34:TRP:HB2	11:1P:6:LEU:HD22	1.98	0.44
5:1F:53:THR:HB	5:1F:56:GLU:OE1	2.17	0.44
22:10:49:LYS:HD2	22:10:49:LYS:HA	1.79	0.44
29:17:10:ARG:O	29:17:14:LYS:HB2	2.17	0.44
35:1d:12:CYS:HB2	62:1d:306:SF4:S2	2.58	0.44
51:1t:101:GLY:HA2	51:1t:102:GLY:HA2	1.66	0.44
1:2A:1057:A:N7	1:2A:1086:A:H2'	2.32	0.44
1:2A:1064:C:H42	1:2A:1074:G:H1	1.65	0.44
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.17	0.44
1:2A:1448:G:H2'	1:2A:1449:A:C8	2.51	0.44
1:2A:2028:U:H2'	1:2A:2029:G:O4'	2.17	0.44
3:2D:133:LEU:HD23	3:2D:136:ILE:HD12	1.98	0.44
6:2G:101:ILE:HG21	26:24:25:TYR:HB2	1.99	0.44
6:2G:126:ASP:HB2	6:2G:130:ASN:HB2	1.99	0.44
6:2G:155:MET:HG3	6:2G:157:ILE:HG13	1.99	0.44
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.98	0.44
16:2U:102:GLU:OE2	17:2V:13:ARG:NH2	2.34	0.44
21:2Z:42:VAL:HG23	21:2Z:43:GLU:HG3	1.99	0.44
32:2a:406:G:O2'	35:2d:3:ARG:NH2	2.50	0.44
32:2a:443:C:H2'	32:2a:444:C:C6	2.52	0.44
32:2a:1002:G:C2	32:2a:1003:G:C8	3.05	0.44
32:2a:1002:G:C2	32:2a:1003:G:N7	2.85	0.44
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	1.99	0.44
38:2g:75:VAL:HA	38:2g:87:VAL:O	2.17	0.44
52:2u:13:ILE:HG13	52:2u:22:ARG:HD2	1.99	0.44
1:1A:241:A:H5"	63:1A:7343:HOH:O	2.15	0.44
1:1A:994:C:O2	17:1V:10:LYS:HE3	2.17	0.44
1:1A:1001:A:H2'	1:1A:1002:G:O4'	2.17	0.44
1:1A:1085:A:H2'	1:1A:1086:A:N9	2.33	0.44
1:1A:1210:A:H5"	1:1A:1212:G:O4'	2.17	0.44
1:1A:2033:A:O2'	1:1A:2035:G:OP2	2.28	0.44
1:1A:2239:G:H5'	3:1D:251:GLY:HA3	2.00	0.44
1:1A:2820:A:C5	13:1R:4:LEU:HD11	2.52	0.44
4:1E:52:LEU:O	4:1E:76:ARG:N	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:41:LEU:HA	5:1F:44:ARG:HD3	1.98	0.44
12:1Q:2:LEU:HB2	63:1Q:311:HOH:O	2.16	0.44
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	1.98	0.44
15:1T:127:ALA:C	15:1T:129:ARG:H	2.23	0.44
32:1a:193:C:H2'	32:1a:194:C:C6	2.52	0.44
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.52	0.44
1:2A:581:C:H2'	1:2A:582:G:C8	2.52	0.44
1:2A:881:G:H2'	1:2A:882:G:C8	2.52	0.44
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.82	0.44
1:2A:2061:G:H22	56:2v:2:THR:HG23	1.83	0.44
1:2A:2660:A:H2'	1:2A:2661:G:O4'	2.17	0.44
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.52	0.44
6:2G:11:TYR:OH	6:2G:16:ARG:HD3	2.17	0.44
6:2G:28:VAL:O	6:2G:31:VAL:HG13	2.17	0.44
6:2G:57:ALA:HB2	6:2G:90:LEU:CD2	2.48	0.44
14:2S:51:ALA:HB3	14:2S:73:LEU:HB2	2.00	0.44
26:24:61:ARG:O	26:24:62:ARG:C	2.59	0.44
32:2a:316:G:H2'	32:2a:317:G:H8	1.82	0.44
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.17	0.44
32:2a:1375:A:H2'	32:2a:1376:U:O4'	2.17	0.44
34:2c:181:ASN:HD21	34:2c:204:LEU:HB2	1.82	0.44
37:2f:69:GLU:C	37:2f:71:ARG:H	2.25	0.44
41:2j:49:VAL:CG2	45:2n:41:ARG:HB2	2.46	0.44
1:1A:1537:G:H2'	1:1A:1538:G:H8	1.82	0.44
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.23	0.44
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.18	0.44
4:1E:111:ARG:HA	13:1R:1:MET:SD	2.57	0.44
6:1G:104:GLU:O	6:1G:108:ASN:ND2	2.45	0.44
8:1I:56:LYS:O	8:1I:60:GLU:HB3	2.16	0.44
11:1P:59:LEU:HD11	30:18:10:ALA:HA	1.99	0.44
32:1a:316:G:OP2	32:1a:351:G:O2'	2.34	0.44
32:1a:438:G:H5'	35:1d:123:HIS:HD2	1.81	0.44
32:1a:674:G:H2'	32:1a:675:A:H8	1.82	0.44
32:1a:1236:A:OP1	52:1u:3:LYS:HD3	2.17	0.44
32:1a:1391:U:H2'	32:1a:1392:G:H8	1.78	0.44
33:1b:92:TYR:OH	33:1b:150:SER:OG	2.32	0.44
36:1e:84:PHE:HB2	36:1e:134:ALA:HB2	1.99	0.44
38:1g:111:ARG:HD2	38:1g:119:ARG:O	2.17	0.44
40:1i:18:PHE:HD2	40:1i:62:TYR:HD2	1.65	0.44
41:1j:51:ARG:HD2	41:1j:59:SER:OG	2.17	0.44
47:1p:56:ALA:O	47:1p:60:LEU:HG	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1r:47:THR:O	49:1r:47:THR:OG1	2.35	0.44
51:1t:43:LEU:HD12	51:1t:55:ILE:HG13	1.99	0.44
53:1y:30:TRP:CH2	53:1y:82:GLU:HG2	2.53	0.44
53:1y:85:LEU:O	53:1y:89:GLN:HG2	2.17	0.44
1:2A:656:G:H2'	1:2A:657:U:O4'	2.18	0.44
1:2A:1032:A:O2'	1:2A:1034:G:OP2	2.26	0.44
1:2A:1920:OMC:O2'	32:2a:1496:C:H4'	2.17	0.44
4:2E:53:PRO:HA	4:2E:75:VAL:HA	1.98	0.44
7:2H:35:VAL:HG11	7:2H:72:ILE:HG13	1.99	0.44
11:2P:36:LYS:HB3	63:2P:313:HOH:O	2.17	0.44
22:20:27:GLU:HB2	22:20:69:PHE:HD1	1.81	0.44
26:24:46:GLN:OE1	26:24:48:ARG:NH2	2.25	0.44
32:2a:691:G:H1'	32:2a:696:A:N6	2.31	0.44
32:2a:922:G:C6	32:2a:923:A:C6	3.05	0.44
32:2a:1135:U:H4'	32:2a:1136:U:H5	1.81	0.44
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	1.98	0.44
1:1A:224:G:H2'	1:1A:225:A:O4'	2.16	0.44
1:1A:1231:G:H2'	1:1A:1232:G:H8	1.82	0.44
1:1A:2784:C:H1'	4:1E:37:ARG:NH1	2.33	0.44
1:1A:2872:G:O2'	1:1A:2873:A:H5'	2.17	0.44
3:1D:3:VAL:HG22	3:1D:17:THR:HB	2.00	0.44
6:1G:50:ALA:C	6:1G:52:ILE:N	2.72	0.44
8:1I:109:ILE:HA	8:1I:109:ILE:HD12	1.64	0.44
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	2.00	0.44
32:1a:186:C:H2'	32:1a:187:C:H6	1.83	0.44
32:1a:376:G:H5"	47:1p:5:ARG:HB2	1.99	0.44
32:1a:986:A:H1'	50:1s:54:GLY:O	2.16	0.44
32:1a:1003:G:H2'	32:1a:1004:A:C4'	2.41	0.44
32:1a:1159:U:C2	32:1a:1182:G:C2	3.05	0.44
35:1d:109:GLY:HA3	35:1d:165:MET:HG3	2.00	0.44
42:1k:98:LEU:O	42:1k:101:SER:OG	2.34	0.44
44:1m:11:ARG:NH1	44:1m:11:ARG:HB2	2.33	0.44
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	1.99	0.44
49:1r:76:LEU:HD12	49:1r:76:LEU:HA	1.80	0.44
51:1t:50:GLU:O	51:1t:100:ILE:HD11	2.18	0.44
1:2A:2019:A:O4'	16:2U:34:LYS:HE2	2.17	0.44
63:2B:307:HOH:O	21:2Z:31:ARG:HG2	2.16	0.44
15:2T:102:ILE:HA	15:2T:105:LEU:HG	1.99	0.44
32:2a:148:G:H2'	32:2a:149:A:H8	1.81	0.44
32:2a:883:C:N4	32:2a:884:U:O4	2.50	0.44
32:2a:1206:G:C6	32:2a:1207:2MG:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1320:C:H1'	50:2s:73:GLU:HB3	2.00	0.44
44:2m:89:GLY:HA2	44:2m:92:HIS:HB2	2.00	0.44
1:1A:557:U:H2'	1:1A:558:G:C8	2.52	0.44
1:1A:1325:G:OP1	1:1A:1647:G:O2'	2.31	0.44
1:1A:2097:C:H2'	1:1A:2098:U:O4'	2.16	0.44
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.39	0.44
5:1F:132:VAL:HG22	5:1F:163:VAL:HG22	1.99	0.44
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.81	0.44
10:1O:88:ASN:ND2	10:1O:90:GLN:OE1	2.51	0.44
21:1Z:54:HIS:HB3	21:1Z:101:PRO:HD3	2.00	0.44
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.18	0.44
23:11:21:ARG:HD2	23:11:35:THR:HG21	2.00	0.44
25:13:55:ARG:NH1	63:13:207:HOH:O	2.51	0.44
32:1a:1304:G:C6	32:1a:1305:G:N1	2.85	0.44
32:1a:1343:G:H4'	40:1i:122:ALA:HB3	2.00	0.44
32:1a:1503:A:OP1	32:1a:1531:A:O2'	2.29	0.44
33:1b:12:GLU:O	33:1b:15:VAL:HG12	2.18	0.44
34:1c:22:TRP:CH2	34:1c:32:LEU:HB2	2.53	0.44
42:1k:21:ILE:HG12	42:1k:30:VAL:HG22	2.00	0.44
1:2A:373:U:H2'	1:2A:374:A:H8	1.82	0.44
1:2A:492:A:H2'	1:2A:493:G:O4'	2.17	0.44
1:2A:782:A:H5'	1:2A:783:A:N7	2.33	0.44
1:2A:2821:A:OP2	63:2R:301:HOH:O	2.21	0.44
6:2G:86:MET:O	6:2G:88:ILE:HG12	2.17	0.44
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.33	0.44
9:2N:40:PRO:HA	16:2U:67:ALA:HB3	2.00	0.44
18:2W:15:ARG:NH1	63:2W:304:HOH:O	2.50	0.44
19:2X:53:LYS:NZ	19:2X:55:ASN:OD1	2.50	0.44
23:21:18:ILE:HG12	23:21:37:ILE:HG12	1.98	0.44
23:21:80:LEU:HB3	23:21:82:LEU:HG	2.00	0.44
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.98	0.44
32:2a:421:U:O2'	32:2a:423:G:N7	2.51	0.44
32:2a:519:C:OP2	43:2l:50:SER:OG	2.33	0.44
32:2a:601:C:H2'	32:2a:602:A:H8	1.82	0.44
32:2a:885:G:H1	32:2a:912:C:H42	1.66	0.44
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.53	0.44
32:2a:1290:G:OP1	38:2g:35:LYS:NZ	2.43	0.44
35:2d:12:CYS:SG	35:2d:19:LEU:HB2	2.57	0.44
49:2r:47:THR:O	49:2r:47:THR:OG1	2.33	0.44
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.57	0.44
51:2t:53:LEU:O	51:2t:57:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:286:C:H2'	1:1A:287:C:C6	2.53	0.44
1:1A:644:A:H4'	1:1A:645:C:C5	2.53	0.44
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.17	0.44
1:1A:2115:G:H4'	1:1A:2167:U:H4'	2.00	0.44
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.99	0.44
9:1N:61:ARG:HA	9:1N:61:ARG:HD3	1.76	0.44
20:1Y:55:TYR:CE1	20:1Y:61:ILE:HG21	2.53	0.44
32:1a:526:C:OP2	43:1l:91:LYS:NZ	2.41	0.44
32:1a:1317:C:N4	45:1n:19:ARG:HH21	2.16	0.44
1:2A:1669:A:H5"	1:2A:2550:G:OP1	2.17	0.44
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.16	0.44
12:2Q:109:VAL:N	63:2Q:305:HOH:O	2.29	0.44
14:2S:67:ARG:NH2	14:2S:103:GLU:OE1	2.50	0.44
31:29:19:ARG:HG2	31:29:20:HIS:ND1	2.33	0.44
32:2a:269:C:H2'	32:2a:270:A:C8	2.52	0.44
32:2a:397:A:H3'	32:2a:397:A:N3	2.32	0.44
32:2a:1004:A:H5"	32:2a:1025:U:C5	2.52	0.44
32:2a:1030(B):C:H41	32:2a:1030(C):G:N2	2.15	0.44
32:2a:1279:A:H2'	32:2a:1279:A:N3	2.33	0.44
33:2b:115:LEU:O	33:2b:119:GLU:N	2.51	0.44
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.18	0.44
50:2s:18:LYS:NZ	50:2s:31:ILE:HG12	2.33	0.44
1:1A:727:A:OP1	1:1A:1431:U:O2'	2.36	0.44
1:1A:740:U:OP2	63:1A:4161:HOH:O	2.21	0.44
1:1A:1604:C:OP2	63:1A:4221:HOH:O	2.21	0.44
1:1A:2314:C:H2'	1:1A:2315:G:H8	1.83	0.44
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.99	0.44
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.18	0.44
8:1I:92:VAL:HG22	8:1I:120:ILE:HD12	2.00	0.44
10:1O:70:LYS:HB3	10:1O:70:LYS:HE2	1.78	0.44
32:1a:501:C:H1'	32:1a:549:C:H1'	2.00	0.44
32:1a:539:A:H2'	32:1a:540:G:C8	2.51	0.44
32:1a:1054:C:H4'	32:1a:1055:A:O5'	2.17	0.44
32:1a:1317:C:O2	50:1s:37:ARG:NH1	2.38	0.44
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	2.00	0.44
35:1d:117:ALA:HA	35:1d:120:LEU:HB2	2.00	0.44
44:1m:2:ALA:HA	44:1m:8:GLU:HB2	1.98	0.44
51:1t:17:ARG:O	51:1t:21:LYS:HG3	2.17	0.44
1:2A:1051:G:O2'	1:2A:1052:C:O5'	2.30	0.44
1:2A:1229:G:H2'	1:2A:1230:C:C6	2.52	0.44
1:2A:1922:G:H2'	1:2A:1923:U:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2282:G:H4'	1:2A:2389:G:O2'	2.17	0.44
1:2A:2789:C:N3	1:2A:2894:G:C6	2.85	0.44
6:2G:89:GLY:C	6:2G:90:LEU:HD12	2.42	0.44
9:2N:40:PRO:HB3	16:2U:68:ALA:HB2	1.99	0.44
14:2S:43:GLU:HG3	14:2S:43:GLU:O	2.17	0.44
32:2a:46:G:H2'	32:2a:366:C:C5	2.52	0.44
32:2a:216:G:O2'	32:2a:217:C:O5'	2.36	0.44
32:2a:396:G:O2'	32:2a:398:C:OP1	2.30	0.44
1:1A:666:G:N2	30:18:2:PRO:O	2.51	0.44
1:1A:800:A:H8	1:1A:800:A:OP1	2.01	0.44
1:1A:1371:G:H2'	1:1A:1372:U:H5	1.82	0.44
1:1A:1593:G:H2'	1:1A:1594:G:H8	1.81	0.44
1:1A:2119:A:N6	1:1A:2171:A:N7	2.65	0.44
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.18	0.44
12:1Q:85:LYS:HG2	22:10:7:LEU:HB3	1.99	0.44
32:1a:192:U:H2'	32:1a:193:C:H6	1.82	0.44
32:1a:401:C:H2'	32:1a:402:G:C8	2.53	0.44
32:1a:814:A:H2'	32:1a:816:A:H5"	1.99	0.44
33:1b:60:ASP:O	33:1b:64:ARG:HD2	2.18	0.44
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.52	0.44
40:1i:92:TYR:O	40:1i:96:LEU:HB2	2.17	0.44
42:1k:20:TYR:O	42:1k:30:VAL:HA	2.17	0.44
43:1l:102:ARG:HB3	43:1l:109:GLY:HA2	1.99	0.44
46:1o:20:GLY:O	46:1o:22:THR:HG23	2.18	0.44
1:2A:729:G:C5	3:2D:208:LYS:HB2	2.53	0.44
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.53	0.44
6:2G:16:ARG:CZ	6:2G:31:VAL:HG21	2.48	0.44
11:2P:6:LEU:HA	11:2P:6:LEU:HD23	1.67	0.44
16:2U:77:SER:H	16:2U:77:SER:HG	1.59	0.44
17:2V:18:LEU:HD22	17:2V:20:LEU:HB2	1.99	0.44
20:2Y:67:LEU:HA	20:2Y:67:LEU:HD23	1.78	0.44
23:21:77:ALA:O	23:21:80:LEU:HB2	2.17	0.44
32:2a:877:C:OP1	39:2h:88:LYS:NZ	2.36	0.44
32:2a:1226:C:H2'	44:2m:103:THR:OG1	2.18	0.44
34:2c:186:PHE:HA	34:2c:198:VAL:O	2.17	0.44
37:2f:1:MET:N	37:2f:69:GLU:OE1	2.43	0.44
40:2i:32:ASP:HB3	40:2i:35:GLU:HB3	2.00	0.44
41:2j:16:LEU:HD13	41:2j:70:ARG:HG2	1.98	0.44
42:2k:50:TYR:CD2	42:2k:60:ALA:HB2	2.53	0.44
49:2r:31:LEU:HD12	49:2r:31:LEU:HA	1.86	0.44
53:2y:52:ALA:O	53:2y:62:VAL:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:776:G:N7	1:1A:793:A:O2'	2.46	0.44
1:1A:2359:C:H2'	1:1A:2360:A:O4'	2.18	0.44
2:1B:93:G:OP1	21:1Z:80:ARG:NH2	2.47	0.44
6:1G:72:ARG:HG2	6:1G:87:PRO:HA	2.00	0.44
14:1S:52:SER:O	14:1S:56:LEU:HD12	2.17	0.44
29:17:47:ARG:HE	29:17:47:ARG:HB3	1.48	0.44
32:1a:509:A:H5"	35:1d:55:ALA:HB2	2.00	0.44
32:1a:892:A:O2'	32:1a:1415:G:H4'	2.18	0.44
33:1b:134:GLU:HG2	33:1b:137:ARG:HH21	1.82	0.44
38:1g:80:VAL:HB	38:1g:85:TYR:HD2	1.81	0.44
43:1l:89:ARG:HA	43:1l:97:ARG:HA	2.00	0.44
1:2A:321:G:N3	5:2F:165:ARG:HD2	2.33	0.44
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.52	0.44
1:2A:2576:G:O2'	63:2A:3920:HOH:O	2.20	0.44
4:2E:119:ARG:HG2	4:2E:160:TYR:HB2	1.99	0.44
16:2U:72:HIS:HB3	16:2U:110:VAL:HG11	2.00	0.44
22:20:50:ASN:HB3	22:20:63:VAL:HG22	2.00	0.44
31:29:7:VAL:HG12	31:29:34:GLN:HB3	2.00	0.44
32:2a:734:G:C2'	32:2a:735:C:H5'	2.48	0.44
32:2a:1124:G:H4'	32:2a:1125:U:OP1	2.18	0.44
32:2a:1269:A:H2	32:2a:1312:G:N3	2.15	0.44
37:2f:2:ARG:HG3	37:2f:69:GLU:HG3	2.00	0.44
44:2m:55:ARG:O	44:2m:59:TYR:HB3	2.17	0.44
46:2o:3:ILE:H	46:2o:3:ILE:HG13	1.59	0.44
53:2y:48:PHE:CD2	53:2y:70:MET:HB2	2.52	0.44
1:1A:878:A:H2'	1:1A:879:G:H5'	2.00	0.43
1:1A:1257:C:H4'	5:1F:83:PHE:CD1	2.52	0.43
1:1A:1541:G:H3'	1:1A:1542:A:H2'	1.99	0.43
1:1A:1680:U:O2'	1:1A:1763:G:N7	2.48	0.43
1:1A:2314:C:H5"	6:1G:38:VAL:HG21	2.00	0.43
1:1A:2701:C:H2'	1:1A:2702:U:H2'	2.00	0.43
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.82	0.43
11:1P:67:MET:HE3	11:1P:67:MET:HB2	1.80	0.43
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.61	0.43
32:1a:491:G:H2'	32:1a:492:G:O4'	2.17	0.43
32:1a:580:U:H2'	32:1a:581:G:C8	2.53	0.43
32:1a:696:A:H8	32:1a:696:A:O5'	2.01	0.43
32:1a:1226:C:H4'	32:1a:1227:A:OP1	2.16	0.43
33:1b:178:ARG:HG3	39:1h:71:GLY:O	2.17	0.43
34:1c:50:ALA:O	34:1c:70:VAL:HG22	2.18	0.43
37:1f:99:ALA:HB3	49:1r:29:PHE:CE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:11:ARG:HB2	44:1m:11:ARG:CZ	2.48	0.43
49:1r:26:LEU:HD22	49:1r:39:VAL:HG13	1.99	0.43
53:1y:19:HIS:O	53:1y:23:ARG:HG2	2.18	0.43
1:2A:271(L):U:H4'	1:2A:271(M):G:H5'	2.00	0.43
1:2A:531:C:OP2	1:2A:561:G:N1	2.51	0.43
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.53	0.43
1:2A:1693:U:H1'	3:2D:14:ARG:NH1	2.33	0.43
1:2A:1714:G:H2'	1:2A:1717:G:H8	1.83	0.43
2:2B:102:A:OP2	63:2B:304:HOH:O	2.21	0.43
3:2D:176:ARG:CZ	3:2D:176:ARG:HB3	2.48	0.43
7:2H:95:ARG:HB2	7:2H:128:PRO:CB	2.48	0.43
9:2N:138:LEU:HD23	9:2N:138:LEU:HA	1.78	0.43
11:2P:106:LEU:HD13	11:2P:112:LEU:HD13	2.00	0.43
26:24:64:GLY:C	26:24:66:SER:H	2.26	0.43
32:2a:429:U:OP2	35:2d:36:ARG:NH2	2.40	0.43
32:2a:779:C:H2'	32:2a:780:A:O4'	2.18	0.43
32:2a:1112:C:O2	34:2c:179:ARG:N	2.44	0.43
32:2a:1503:A:OP1	32:2a:1531:A:O2'	2.33	0.43
34:2c:55:VAL:HG22	34:2c:68:VAL:HG22	2.00	0.43
35:2d:76:ARG:HD2	35:2d:76:ARG:HA	1.59	0.43
35:2d:76:ARG:NH2	35:2d:80:GLU:OE1	2.43	0.43
40:2i:6:GLY:N	40:2i:84:ALA:HB2	2.32	0.43
45:2n:58:LYS:HE2	45:2n:58:LYS:HB3	1.60	0.43
1:1A:249:C:HO2'	11:1P:64:LYS:HZ2	1.57	0.43
1:1A:602:G:O2'	1:1A:655:A:N6	2.49	0.43
1:1A:1301:A:C8	1:1A:1303:G:C8	3.06	0.43
1:1A:1466:G:H2'	1:1A:1547:C:H41	1.82	0.43
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.53	0.43
1:1A:1570:A:OP1	63:1A:4222:HOH:O	2.21	0.43
1:1A:2615:U:H2'	1:1A:2616:C:H6	1.84	0.43
2:1B:75:G:O2'	21:1Z:85:HIS:NE2	2.51	0.43
4:1E:34:VAL:HB	4:1E:48:GLN:HE21	1.83	0.43
32:1a:22:G:H2'	32:1a:23:C:C6	2.53	0.43
32:1a:370:C:H2'	32:1a:371:G:C8	2.53	0.43
32:1a:381:C:H2'	32:1a:382:A:O4'	2.18	0.43
32:1a:1184:G:H2'	32:1a:1185:G:C8	2.53	0.43
36:1e:45:PHE:CD2	36:1e:47:LYS:HD2	2.53	0.43
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.83	0.43
1:2A:322:A:H3'	5:2F:169:ASN:OD1	2.18	0.43
1:2A:483:A:H5"	20:2Y:50:ARG:HD3	2.00	0.43
1:2A:620:G:N3	1:2A:620:G:H5'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1803:A:H4'	3:2D:259:THR:HG23	2.00	0.43
1:2A:1914:C:H5"	63:2A:4134:HOH:O	2.17	0.43
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.17	0.43
17:2V:67:GLY:O	17:2V:88:ARG:HG2	2.18	0.43
19:2X:35:THR:HG22	19:2X:37:THR:N	2.34	0.43
32:2a:574:A:OP2	63:2a:3201:HOH:O	2.20	0.43
32:2a:1111:A:H2'	32:2a:1112:C:C6	2.54	0.43
32:2a:1249:C:O2'	40:2i:73:GLN:NE2	2.50	0.43
33:2b:44:LEU:H	33:2b:44:LEU:HG	1.47	0.43
38:2g:150:ALA:HB1	42:2k:57:THR:HG21	2.00	0.43
39:2h:112:LEU:HD11	39:2h:124:ALA:HB2	2.00	0.43
48:2q:85:VAL:O	48:2q:89:LEU:HG	2.17	0.43
1:1A:861:A:C2	1:1A:917:A:C4	3.07	0.43
1:1A:1082:U:C4	1:1A:1086:A:N1	2.83	0.43
1:1A:2065:C:H2'	1:1A:2066:C:C6	2.53	0.43
1:1A:2169:A:H8	1:1A:2169:A:OP1	2.01	0.43
1:1A:2478:A:H2'	1:1A:2479:G:O4'	2.19	0.43
3:1D:227:ASN:ND2	63:1D:423:HOH:O	2.50	0.43
12:1Q:68:ILE:HD13	12:1Q:103:MET:HB3	2.00	0.43
23:11:73:LEU:HD23	23:11:73:LEU:HA	1.85	0.43
32:1a:97:G:H2'	32:1a:98:G:O4'	2.18	0.43
32:1a:448:A:H2'	32:1a:449:C:C6	2.53	0.43
32:1a:841:U:H3'	32:1a:848:C:O4'	2.18	0.43
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.42	0.43
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.46	0.43
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.52	0.43
1:2A:140:G:H22	1:2A:1596:A:H4'	1.83	0.43
1:2A:871:U:H2'	1:2A:872:A:C8	2.53	0.43
1:2A:1063:G:H1	1:2A:1075:C:H42	1.64	0.43
1:2A:1209:G:OP2	63:2A:3928:HOH:O	2.21	0.43
1:2A:2115:G:H2'	1:2A:2117:A:N6	2.33	0.43
1:2A:2127:G:N2	1:2A:2173:A:N3	2.64	0.43
1:2A:2131:G:C6	1:2A:2158:A:N7	2.86	0.43
2:2B:95:C:H2'	2:2B:96:U:C6	2.52	0.43
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.67	0.43
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.50	0.43
21:2Z:92:SER:O	21:2Z:130:PRO:HG2	2.17	0.43
22:20:5:LYS:HG2	22:20:6:GLY:N	2.32	0.43
26:24:48:ARG:HB3	26:24:52:THR:HB	2.00	0.43
32:2a:1065:U:H1'	32:2a:1066:C:OP2	2.18	0.43
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1135:U:H4'	32:2a:1136:U:C5	2.53	0.43
32:2a:1327:C:OP2	52:2u:12:LYS:NZ	2.48	0.43
35:2d:36:ARG:HD2	35:2d:38:TYR:OH	2.18	0.43
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.19	0.43
43:2l:70:ILE:HG21	43:2l:75:HIS:CD2	2.53	0.43
51:2t:43:LEU:HB3	51:2t:52:ALA:HB2	1.99	0.43
53:2y:27:LEU:HD11	53:2y:81:LEU:HD13	2.00	0.43
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.50	0.43
1:1A:652(F):G:H8	1:1A:652(F):G:O5'	2.01	0.43
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.34	0.43
1:1A:1045:A:H8	1:1A:1111:A:C6	2.37	0.43
1:1A:1063:G:H5"	1:1A:1065:U:C5	2.53	0.43
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.54	0.43
1:1A:1824:G:O3'	3:1D:249:PRO:HD3	2.18	0.43
1:1A:2852:G:H2'	1:1A:2853:C:C6	2.54	0.43
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.17	0.43
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.33	0.43
32:1a:409:G:H2'	32:1a:410:G:O4'	2.18	0.43
33:1b:20:GLU:O	33:1b:39:ILE:HG23	2.19	0.43
33:1b:219:VAL:HG13	33:1b:222:ILE:HD11	2.00	0.43
33:1b:219:VAL:O	33:1b:223:ILE:HG12	2.18	0.43
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	2.00	0.43
42:1k:50:TYR:CD1	42:1k:54:ARG:HD3	2.54	0.43
1:2A:192:C:O2'	1:2A:802:A:N3	2.44	0.43
1:2A:1133:U:O2'	1:2A:1137:G:OP1	2.34	0.43
1:2A:2140:C:O2	1:2A:2151:G:N1	2.42	0.43
8:2I:78:THR:HG22	8:2I:143:SER:CB	2.47	0.43
12:2Q:7:MET:HB2	12:2Q:7:MET:HE3	1.72	0.43
32:2a:1054:C:H41	53:2y:46:GLN:NE2	2.16	0.43
32:2a:1481:U:H2'	32:2a:1482:G:C8	2.54	0.43
34:2c:98:ASN:N	34:2c:98:ASN:OD1	2.50	0.43
36:2e:53:LEU:HD12	36:2e:53:LEU:H	1.83	0.43
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	2.01	0.43
39:2h:125:ARG:H	39:2h:125:ARG:HG2	1.52	0.43
42:2k:77:MET:HE2	42:2k:77:MET:HB2	1.90	0.43
50:2s:52:TYR:HA	50:2s:56:GLN:O	2.19	0.43
1:1A:1359:A:N1	1:1A:1372:U:O4	2.51	0.43
1:1A:1682:G:H2'	1:1A:1683:C:C6	2.53	0.43
1:1A:1803:A:H4'	3:1D:259:THR:HG23	2.00	0.43
1:1A:2714:G:H2'	1:1A:2715:C:H6	1.82	0.43
7:1H:52:VAL:HG12	7:1H:65:HIS:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	2.01	0.43
32:1a:674:G:OP1	37:1f:87:ARG:NH2	2.52	0.43
32:1a:955:U:O2'	50:1s:83:HIS:HD2	2.00	0.43
32:1a:995:C:H1'	45:1n:4:LYS:HE3	2.01	0.43
32:1a:1030(C):G:N7	32:1a:1031:G:N1	2.67	0.43
32:1a:1158:C:H5	32:1a:1181:G:H1	1.63	0.43
32:1a:1187:G:H4'	40:1i:111:ARG:NH1	2.33	0.43
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	2.01	0.43
32:1a:1358:U:OP1	45:1n:35:ARG:HG2	2.18	0.43
33:1b:21:ARG:C	33:1b:23:ARG:H	2.26	0.43
35:1d:36:ARG:HB3	35:1d:38:TYR:CZ	2.54	0.43
37:1f:70:ASP:OD1	37:1f:71:ARG:HG3	2.17	0.43
40:1i:65:VAL:HG21	40:1i:73:GLN:HB3	2.01	0.43
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.82	0.43
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.99	0.43
1:2A:874:G:OP1	12:2Q:63:LYS:NZ	2.51	0.43
1:2A:1053:C:H4'	1:2A:1054:A:OP1	2.19	0.43
1:2A:2304:G:OP1	6:2G:124:SER:OG	2.31	0.43
1:2A:2496:C:OP2	12:2Q:82:ARG:HD3	2.19	0.43
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.36	0.43
7:2H:107:VAL:HB	7:2H:152:ARG:HG2	1.99	0.43
15:2T:33:LYS:HE2	15:2T:82:LEU:HA	2.00	0.43
19:2X:3:THR:HG21	24:22:26:ARG:HG3	1.99	0.43
20:2Y:31:LEU:HD12	20:2Y:36:ALA:HB3	2.01	0.43
20:2Y:90:LEU:HB2	20:2Y:92:ASN:HB2	2.00	0.43
24:22:18:PRO:HA	24:22:21:LEU:HD12	2.00	0.43
26:24:48:ARG:HB3	26:24:52:THR:HA	2.00	0.43
32:2a:984:C:H2'	32:2a:985:C:H6	1.84	0.43
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.54	0.43
35:2d:13:ARG:HH22	35:2d:36:ARG:HE	1.66	0.43
37:2f:49:ALA:HB1	49:2r:80:PRO:HB3	2.00	0.43
1:1A:271(E):U:O4	63:1A:4155:HOH:O	2.15	0.43
1:1A:341:G:H2'	1:1A:342:G:O4'	2.19	0.43
1:1A:2552:2MU:O5'	1:1A:2552:2MU:H6	2.19	0.43
1:1A:2714:G:H2'	1:1A:2715:C:C6	2.53	0.43
4:1E:146:THR:HA	4:1E:147:PRO:HA	1.81	0.43
10:1O:88:ASN:OD1	10:1O:92:GLU:HB2	2.19	0.43
13:1R:49:ASP:OD2	63:1R:302:HOH:O	2.21	0.43
13:1R:83:ILE:O	13:1R:86:ARG:HG2	2.19	0.43
32:1a:920:U:H2'	32:1a:921:U:C6	2.54	0.43
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:124:SER:HA	33:1b:125:PRO:O	2.19	0.43
40:1i:16:ARG:HB2	40:1i:64:THR:CG2	2.49	0.43
1:2A:29:U:H2'	1:2A:30:G:C8	2.53	0.43
1:2A:271(U):G:H2'	1:2A:271(V):G:H8	1.84	0.43
1:2A:634:C:H2'	1:2A:635:C:C6	2.54	0.43
1:2A:673:C:H5"	5:2F:81:PRO:HD2	2.00	0.43
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.17	0.43
1:2A:2107:C:N3	1:2A:2182:G:N2	2.61	0.43
1:2A:2507:C:OP1	63:2A:3925:HOH:O	2.21	0.43
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	2.00	0.43
9:2N:130:HIS:HB3	9:2N:133:GLN:HG3	2.00	0.43
14:2S:23:ARG:HD2	14:2S:86:ALA:HB2	2.00	0.43
17:2V:91:TYR:CE1	17:2V:93:GLU:HG3	2.52	0.43
22:20:37:LEU:HG	22:20:60:PHE:HA	2.00	0.43
22:20:49:LYS:HD2	22:20:49:LYS:HA	1.83	0.43
32:2a:244:U:H4'	32:2a:245:C:H5"	2.01	0.43
32:2a:718:G:N9	42:2k:116:HIS:HB3	2.34	0.43
32:2a:836:G:C6	32:2a:851:G:C6	3.07	0.43
32:2a:984:C:H2'	32:2a:985:C:C6	2.53	0.43
32:2a:1039:C:H2'	32:2a:1040:U:C6	2.53	0.43
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.52	0.43
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	2.01	0.43
43:2l:5:PRO:HD2	43:2l:15:ARG:HH22	1.84	0.43
51:2t:50:GLU:HB2	51:2t:99:LEU:HD13	1.99	0.43
6:1G:21:ARG:HA	6:1G:21:ARG:CZ	2.48	0.43
6:1G:175:LEU:HD12	6:1G:175:LEU:HA	1.88	0.43
8:1I:27:ARG:HD2	23:11:71:TYR:CZ	2.54	0.43
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.36	0.43
26:14:62:ARG:O	26:14:64:GLY:HA2	2.19	0.43
32:1a:714:G:H2'	32:1a:715:A:C8	2.54	0.43
32:1a:738:C:H2'	32:1a:739:C:C6	2.53	0.43
32:1a:1288:A:H2'	32:1a:1289:A:O4'	2.19	0.43
32:1a:1353:G:C2	32:1a:1370:G:C2	3.07	0.43
33:1b:111:ARG:NH1	33:1b:111:ARG:HA	2.34	0.43
40:1i:84:ALA:O	40:1i:87:GLN:HG3	2.18	0.43
52:1u:12:LYS:HD3	52:1u:22:ARG:HB3	2.01	0.43
53:1y:78:ILE:HD13	53:1y:78:ILE:HA	1.84	0.43
1:2A:685:A:H1'	1:2A:688:U:O4	2.18	0.43
1:2A:720:C:H2'	1:2A:721:C:H6	1.84	0.43
1:2A:979:G:H3'	1:2A:980:A:C5'	2.48	0.43
1:2A:1299:G:OP1	63:2A:3931:HOH:O	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1506:C:C2'	1:2A:1507:A:H5'	2.48	0.43
1:2A:2294:C:OP2	14:2S:89:ARG:NH2	2.49	0.43
1:2A:2576:G:H1'	63:2A:4667:HOH:O	2.18	0.43
1:2A:2649:U:H2'	1:2A:2650:U:C6	2.54	0.43
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.19	0.43
7:2H:11:VAL:HG21	7:2H:50:VAL:HG23	2.01	0.43
9:2N:42:TRP:CH2	9:2N:44:PRO:HB3	2.54	0.43
32:2a:482:A:H2'	32:2a:483:C:O4'	2.19	0.43
32:2a:542:G:P	35:2d:10:ARG:HH22	2.42	0.43
1:1A:875:G:H2'	1:1A:876:C:O4'	2.18	0.43
1:1A:1085:A:C4	1:1A:1086:A:C8	3.07	0.43
1:1A:2810:A:H2'	1:1A:2811:G:O4'	2.18	0.43
2:1B:84:C:OP1	25:13:15:TYR:OH	2.28	0.43
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.50	0.43
8:1I:82:ARG:O	8:1I:89:TYR:HD2	2.02	0.43
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.54	0.43
23:11:97:LEU:HD23	23:11:97:LEU:HA	1.84	0.43
32:1a:90:U:H2'	32:1a:91:C:C6	2.53	0.43
32:1a:171:A:H2'	32:1a:172:A:C8	2.53	0.43
32:1a:583:A:H2'	32:1a:584:G:O4'	2.19	0.43
32:1a:659:U:H2'	32:1a:660:G:C8	2.54	0.43
32:1a:914:A:O5'	63:1a:3321:HOH:O	2.22	0.43
32:1a:1122:U:C4	32:1a:1123:A:N7	2.86	0.43
32:1a:1238:A:OP2	63:1a:3319:HOH:O	2.21	0.43
33:1b:224:GLN:HB2	33:1b:229:VAL:HG13	2.00	0.43
35:1d:67:ILE:HG22	35:1d:68:TYR:CD2	2.54	0.43
53:1y:70:MET:HE2	53:1y:70:MET:HB3	1.92	0.43
1:2A:83:G:O2'	1:2A:102:G:N2	2.52	0.43
1:2A:271(O):C:H2'	1:2A:271(P):C:C6	2.54	0.43
1:2A:1073:A:C8	1:2A:1073:A:H3'	2.53	0.43
1:2A:1932:A:OP2	63:2A:3933:HOH:O	2.22	0.43
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.54	0.43
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.53	0.43
1:2A:2788:C:C2	1:2A:2789:C:N4	2.87	0.43
1:2A:2895:U:H2'	1:2A:2896:C:O4'	2.19	0.43
4:2E:97:LYS:HG3	4:2E:98:PRO:HD2	2.00	0.43
10:2O:17:ARG:NH1	10:2O:47:ILE:HD13	2.33	0.43
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.54	0.43
20:2Y:7:VAL:HG11	20:2Y:13:VAL:HG11	2.00	0.43
26:24:59:PHE:HB3	26:24:61:ARG:HG2	2.01	0.43
32:2a:35:G:O2'	43:2l:118:SER:O	2.23	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:4:ILE:O	47:2p:66:PRO:HA	2.19	0.43
1:1A:144:C:H5'	19:1X:2:LYS:HD2	2.01	0.43
1:1A:1071:G:C2	1:1A:1072:C:C2	3.07	0.43
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.19	0.43
1:1A:2082:A:H2'	1:1A:2083:G:O4'	2.19	0.43
1:1A:2287:A:O2'	1:1A:2288:A:H3'	2.19	0.43
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.19	0.43
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.18	0.43
26:14:24:THR:OG1	26:14:25:TYR:N	2.52	0.43
28:16:11:LEU:HB2	28:16:21:TYR:HB2	2.00	0.43
32:1a:760:G:H21	48:1q:97:SER:HB2	1.83	0.43
32:1a:1346:A:H2'	38:1g:10:ARG:HH22	1.84	0.43
32:1a:1409:C:H2'	32:1a:1410:G:C8	2.54	0.43
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.54	0.43
37:1f:45:LEU:HD13	37:1f:59:TYR:HD1	1.83	0.43
37:1f:97:PHE:H	49:1r:32:ARG:HG3	1.84	0.43
38:1g:44:TYR:HA	38:1g:47:CYS:SG	2.59	0.43
46:1o:42:HIS:CE1	46:1o:46:HIS:CD2	3.07	0.43
1:2A:118:A:OP1	29:27:22:MET:HE2	2.18	0.43
1:2A:1006:C:O2'	9:2N:106:MET:O	2.30	0.43
1:2A:2370:G:C6	1:2A:2371:G:C6	3.07	0.43
1:2A:2431:U:OP2	63:2A:3927:HOH:O	2.21	0.43
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.54	0.43
3:2D:97:TYR:OH	63:2D:403:HOH:O	2.21	0.43
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.77	0.43
13:2R:29:LEU:HD12	13:2R:116:LEU:HD11	2.00	0.43
14:2S:67:ARG:HG2	14:2S:71:ARG:NH1	2.34	0.43
23:21:17:SER:O	63:21:202:HOH:O	2.21	0.43
23:21:85:LEU:HD12	23:21:85:LEU:HA	1.87	0.43
32:2a:270:A:C6	32:2a:271:C:C4	3.07	0.43
32:2a:540:G:H2'	32:2a:541:G:O4'	2.19	0.43
32:2a:939:G:H4'	38:2g:102:ARG:HH21	1.84	0.43
32:2a:971:G:H22	32:2a:1363(A):A:H5'	1.82	0.43
32:2a:1226:C:H42	44:2m:104:ARG:HH11	1.66	0.43
32:2a:1291:G:O2'	40:2i:38:GLN:OE1	2.35	0.43
32:2a:1323:G:H4'	32:2a:1363:C:C4	2.54	0.43
34:2c:28:GLN:O	34:2c:30:ARG:N	2.52	0.43
34:2c:153:VAL:HG22	34:2c:198:VAL:HG22	2.00	0.43
40:2i:50:LEU:HB3	40:2i:56:LEU:HA	2.01	0.43
46:2o:69:TYR:CE1	46:2o:73:GLU:HG3	2.54	0.43
1:1A:533:G:H5'	16:1U:24:TYR:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1051:G:H2'	1:1A:1052:C:O4'	2.18	0.43
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.18	0.43
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	2.00	0.43
8:1I:72:LEU:C	8:1I:74:ASN:H	2.26	0.43
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.19	0.43
26:14:7:PRO:HB2	26:14:27:THR:CG2	2.48	0.43
26:14:59:PHE:HE1	50:1s:64:GLU:HG2	1.83	0.43
30:18:62:LEU:HB3	30:18:65:GLU:HG3	2.01	0.43
32:1a:474:G:H2'	32:1a:475:G:C8	2.54	0.43
32:1a:669:U:H2'	32:1a:670:G:C8	2.53	0.43
32:1a:1223:C:OP2	50:1s:78:ARG:NH2	2.49	0.43
32:1a:1304:G:OP2	63:1a:3320:HOH:O	2.21	0.43
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	2.00	0.43
39:1h:86:ILE:HG12	39:1h:135:CYS:HA	2.01	0.43
41:1j:45:ARG:HB3	41:1j:65:LEU:HB3	2.01	0.43
1:2A:539:G:H2'	1:2A:540:C:C6	2.54	0.43
1:2A:1015:G:O2'	1:2A:1016:G:H5'	2.19	0.43
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.54	0.43
1:2A:1170:G:H1	1:2A:1179:C:N4	2.15	0.43
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.53	0.43
3:2D:77:ALA:HB2	3:2D:97:TYR:CD1	2.53	0.43
8:2I:27:ARG:HG2	23:21:71:TYR:CZ	2.53	0.43
21:2Z:19:ARG:NH1	21:2Z:84:GLU:HB2	2.34	0.43
32:2a:144:G:H1	32:2a:178:C:H42	1.67	0.43
32:2a:657:G:C2	32:2a:750:G:C5	3.07	0.43
32:2a:986:A:H2'	32:2a:987:G:O4'	2.19	0.43
32:2a:1040:U:C3'	32:2a:1041:A:H5"	2.49	0.43
32:2a:1189:C:OP1	45:2n:58:LYS:NZ	2.52	0.43
35:2d:13:ARG:HH22	35:2d:36:ARG:CZ	2.30	0.43
37:2f:2:ARG:NE	37:2f:69:GLU:HG2	2.30	0.43
52:2u:12:LYS:HE2	52:2u:19:GLY:HA3	2.00	0.43
1:1A:1197:G:H2'	1:1A:1198:U:C6	2.54	0.42
1:1A:2552:2MU:H6'3	1:1A:2554:U:C6	2.53	0.42
1:1A:2660:A:H2'	1:1A:2661:G:O4'	2.19	0.42
63:1A:4210:HOH:O	22:10:36:ILE:N	2.50	0.42
5:1F:10:PRO:HB3	5:1F:17:ARG:NH2	2.26	0.42
32:1a:660:G:C2	32:1a:746:A:C2	3.07	0.42
34:1c:5:ILE:HD11	45:1n:49:HIS:HE1	1.84	0.42
35:1d:15:GLU:CD	35:1d:59:ARG:HH12	2.27	0.42
47:1p:3:LYS:HB3	47:1p:3:LYS:HE2	1.87	0.42
1:2A:105:C:H2'	1:2A:106:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:363(F):A:O4'	1:2A:364:C:H5	2.02	0.42
1:2A:623:G:H2'	1:2A:624:C:C6	2.54	0.42
1:2A:880:G:N2	1:2A:898:C:C2	2.86	0.42
1:2A:1138:G:N3	9:2N:106:MET:HE2	2.34	0.42
1:2A:1216:G:P	16:2U:12:ARG:HH21	2.42	0.42
1:2A:1446:C:H2'	1:2A:1447:G:C8	2.54	0.42
8:2I:140:LEU:HD22	8:2I:141:LYS:N	2.32	0.42
10:2O:16:ALA:HB2	10:2O:52:VAL:HG21	2.00	0.42
18:2W:88:ARG:HD2	18:2W:88:ARG:HA	1.83	0.42
28:26:39:TYR:HB2	28:26:46:HIS:CE1	2.54	0.42
32:2a:1431:C:H2'	32:2a:1432:G:O4'	2.19	0.42
33:2b:31:TYR:HE2	33:2b:200:ILE:HG21	1.84	0.42
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	2.01	0.42
34:2c:111:LEU:HD11	34:2c:146:ALA:HB2	2.01	0.42
38:2g:45:ASP:O	38:2g:49:ILE:HG13	2.19	0.42
40:2i:26:VAL:HA	40:2i:61:ALA:O	2.19	0.42
46:2o:82:ILE:O	46:2o:86:GLY:N	2.52	0.42
51:2t:58:LYS:HD3	51:2t:58:LYS:HA	1.85	0.42
1:1A:500:G:N1	1:1A:503:A:OP2	2.51	0.42
1:1A:724:U:H2'	1:1A:725:G:O4'	2.19	0.42
1:1A:1784:A:H4'	1:1A:1785:A:O5'	2.20	0.42
1:1A:1803:A:H2'	1:1A:1804:C:O4'	2.19	0.42
1:1A:2114:A:O2'	1:1A:2168:G:OP1	2.37	0.42
1:1A:2137:C:C2	1:1A:2154:G:N2	2.87	0.42
1:1A:2667:C:H2'	1:1A:2668:G:O4'	2.20	0.42
1:1A:2692:C:H2'	1:1A:2693:A:C8	2.54	0.42
5:1F:101:LEU:O	5:1F:106:ARG:NH2	2.51	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.49	0.42
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	2.01	0.42
7:1H:46:GLU:OE2	7:1H:51:ARG:NH2	2.41	0.42
32:1a:401:C:H2'	32:1a:402:G:H8	1.84	0.42
32:1a:407:G:OP1	35:1d:115:ARG:HD3	2.19	0.42
32:1a:1250:A:H4'	40:1i:68:GLY:N	2.35	0.42
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.51	0.42
33:1b:178:ARG:NH1	39:1h:71:GLY:O	2.52	0.42
33:1b:204:ASN:HB3	33:1b:210:SER:CB	2.49	0.42
35:1d:148:VAL:HB	35:1d:181:MET:HB3	2.00	0.42
39:1h:21:LYS:O	39:1h:63:LEU:HD23	2.19	0.42
39:1h:85:ARG:NH2	39:1h:87:SER:O	2.53	0.42
1:2A:71:A:H5"	1:2A:73:A:C8	2.53	0.42
1:2A:1422:G:H4'	1:2A:1493:C:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1720:U:H2'	1:2A:1721:G:O4'	2.19	0.42
1:2A:2111:C:H6	1:2A:2111:C:H2'	1.66	0.42
1:2A:2228:G:P	3:2D:263:ARG:HH22	2.42	0.42
1:2A:2298:A:N6	1:2A:2318:G:C8	2.87	0.42
1:2A:2548:G:H2'	1:2A:2549:G:O4'	2.19	0.42
3:2D:10:THR:OG1	3:2D:13:ARG:HG2	2.18	0.42
3:2D:164:GLN:HB3	3:2D:176:ARG:NH1	2.33	0.42
18:2W:79:GLY:HA3	18:2W:100:THR:HG22	2.01	0.42
23:21:72:GLU:O	23:21:76:ARG:HG3	2.19	0.42
24:22:1:MET:HB3	24:22:5:GLU:CD	2.44	0.42
32:2a:414:A:H2'	32:2a:415:A:H8	1.84	0.42
32:2a:748:C:H4'	32:2a:749:C:O5'	2.19	0.42
32:2a:918:A:H2'	32:2a:919:A:O4'	2.18	0.42
32:2a:1054:C:H4'	32:2a:1055:A:O5'	2.18	0.42
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.34	0.42
33:2b:74:LYS:O	33:2b:78:GLN:N	2.52	0.42
42:2k:59:TYR:O	42:2k:63:LEU:HD12	2.19	0.42
44:2m:88:ARG:HG3	44:2m:98:VAL:HG11	2.01	0.42
1:1A:740:U:H2'	1:1A:741:G:C8	2.54	0.42
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.19	0.42
1:1A:2065:C:H4'	1:1A:2251:OMG:HM22	2.01	0.42
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.54	0.42
25:13:31:LEU:O	63:13:201:HOH:O	2.22	0.42
32:1a:191:G:H2'	32:1a:192:U:C6	2.55	0.42
32:1a:663:A:H5'	32:1a:836:G:OP1	2.19	0.42
32:1a:1212:U:H4'	32:1a:1213:A:C8	2.55	0.42
32:1a:1402:4OC:CM2	32:1a:1403:C:H5'	2.45	0.42
34:1c:124:ILE:H	34:1c:124:ILE:HG12	1.61	0.42
36:1e:31:LEU:HD12	36:1e:31:LEU:HA	1.87	0.42
46:1o:3:ILE:H	46:1o:3:ILE:HG13	1.70	0.42
46:1o:82:ILE:HG13	46:1o:83:GLU:N	2.34	0.42
48:1q:87:LYS:HB3	48:1q:87:LYS:HE3	1.83	0.42
53:1y:52:ALA:HB2	53:1y:77:LEU:HD21	2.02	0.42
1:2A:182:A:N3	1:2A:433:C:O2'	2.39	0.42
1:2A:385:C:O2'	1:2A:388:G:N2	2.53	0.42
1:2A:409:C:OP1	63:2A:3930:HOH:O	2.21	0.42
1:2A:821:A:N1	63:2A:4003:HOH:O	2.37	0.42
1:2A:1130:U:C2	1:2A:2025:C:H5"	2.54	0.42
1:2A:1131:G:C2	1:2A:1132:A:C4	3.06	0.42
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.52	0.42
1:2A:2554:U:H2'	1:2A:2555:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2636:U:H2'	1:2A:2637:U:H6	1.84	0.42
3:2D:60:ARG:HD3	3:2D:86:PRO:HB2	2.00	0.42
5:2F:11:VAL:HG13	5:2F:125:LEU:HB2	2.01	0.42
8:2I:23:PRO:O	8:2I:27:ARG:HB2	2.19	0.42
10:2O:87:ILE:HD12	10:2O:91:LEU:HA	2.01	0.42
22:20:5:LYS:HG2	22:20:6:GLY:H	1.83	0.42
32:2a:17:U:O2'	32:2a:1079:G:H1'	2.19	0.42
32:2a:620:C:H2'	32:2a:621:A:O4'	2.19	0.42
32:2a:1005:A:OP1	32:2a:1006:C:N4	2.52	0.42
32:2a:1144:G:N2	32:2a:1146:A:H62	2.16	0.42
32:2a:1274:G:H2'	32:2a:1275:A:H8	1.84	0.42
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	2.00	0.42
1:1A:244:A:H2'	1:1A:245:G:O4'	2.19	0.42
1:1A:593:G:H2'	1:1A:594:U:C6	2.54	0.42
1:1A:675:A:C8	1:1A:804:A:C6	3.07	0.42
1:1A:1541:G:H5"	1:1A:1542:A:OP2	2.20	0.42
1:1A:1850:G:C6	1:1A:1851:U:C4	3.07	0.42
7:1H:157:TYR:CE1	7:1H:172:LYS:HG3	2.54	0.42
14:1S:58:LEU:HA	14:1S:58:LEU:HD23	1.63	0.42
60:1T:207:MPD:O4	60:1T:207:MPD:O2	2.30	0.42
17:1V:21:ARG:HD3	17:1V:91:TYR:CD1	2.53	0.42
32:1a:153:C:H2'	32:1a:154:C:C6	2.54	0.42
32:1a:1025:U:C2	32:1a:1036:G:O6	2.70	0.42
32:1a:1036:G:H2'	32:1a:1036:G:N3	2.34	0.42
34:1c:162:GLN:HG3	34:1c:163:ALA:O	2.18	0.42
42:1k:109:VAL:HA	49:1r:85:LEU:O	2.19	0.42
50:1s:3:ARG:CZ	50:1s:10:PHE:HB2	2.50	0.42
1:2A:57:C:H2'	1:2A:58:G:O4'	2.20	0.42
1:2A:191:A:H2'	1:2A:192:C:C6	2.54	0.42
1:2A:215:G:O3'	1:2A:216:A:H4'	2.20	0.42
1:2A:321:G:C2	1:2A:341:G:H4'	2.54	0.42
1:2A:444:C:H4'	5:2F:49:ALA:HB2	2.00	0.42
1:2A:579:G:O2'	1:2A:2019:A:OP1	2.30	0.42
1:2A:1074:G:N1	1:2A:1075:C:H1'	2.35	0.42
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.54	0.42
3:2D:147:LEU:HD13	3:2D:155:LEU:HD21	2.00	0.42
3:2D:159:ALA:HB1	3:2D:198:ASN:O	2.19	0.42
26:24:58:ARG:HH21	44:2m:80:ARG:CZ	2.33	0.42
32:2a:939:G:H2'	32:2a:940:C:C6	2.55	0.42
35:2d:201:GLN:NE2	36:2e:99:GLY:HA2	2.34	0.42
48:2q:27:PHE:CE1	48:2q:36:ILE:HD11	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:35:G:H2'	1:1A:36:G:O4'	2.20	0.42
1:1A:298:G:H5"	1:1A:299:A:OP1	2.20	0.42
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.34	0.42
1:1A:1083:U:H1'	1:1A:1086:A:N6	2.34	0.42
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.20	0.42
1:1A:2131:G:OP1	1:1A:2132:U:H3'	2.19	0.42
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.55	0.42
1:1A:2393:A:O2'	11:1P:60:MET:O	2.28	0.42
1:1A:2805:G:H2'	1:1A:2807:G:C8	2.53	0.42
60:1A:4024:MPD:HM2	60:1A:4024:MPD:H4	1.80	0.42
6:1G:39:ILE:O	6:1G:91:ARG:HA	2.19	0.42
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.54	0.42
13:1R:59:ASP:OD2	13:1R:61:HIS:HB3	2.20	0.42
14:1S:59:LYS:H	14:1S:59:LYS:HG3	1.45	0.42
20:1Y:97:ARG:HE	20:1Y:107:ASP:C	2.27	0.42
20:1Y:98:VAL:HG12	20:1Y:105:ALA:HA	2.01	0.42
27:15:56:LYS:HE3	27:15:58:LEU:O	2.20	0.42
32:1a:1260:C:H5'	32:1a:1284:C:H4'	2.01	0.42
35:1d:12:CYS:CB	62:1d:306:SF4:S2	3.07	0.42
35:1d:50:ARG:NH1	36:1e:10:MET:HE2	2.34	0.42
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.67	0.42
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	2.01	0.42
37:1f:2:ARG:NH2	46:1o:2:PRO:HD3	2.35	0.42
1:2A:793:A:OP2	1:2A:2072:G:H5'	2.20	0.42
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.20	0.42
1:2A:1188:U:C4'	17:2V:79:VAL:HG22	2.48	0.42
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.20	0.42
1:2A:1917:PSU:H2'	1:2A:1918:A:O4'	2.19	0.42
1:2A:1999:C:H5"	1:2A:2723:C:O2'	2.20	0.42
1:2A:2134:A:N7	1:2A:2157:G:H5'	2.35	0.42
1:2A:2310:A:H2'	1:2A:2311:A:H5"	2.02	0.42
1:2A:2552:2MU:H2'	1:2A:2554:U:OP2	2.19	0.42
6:2G:8:LYS:HG2	6:2G:12:TYR:CE2	2.49	0.42
6:2G:113:ARG:NH1	6:2G:139:LEU:O	2.52	0.42
7:2H:102:ALA:HA	7:2H:117:PRO:HD3	2.01	0.42
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	2.01	0.42
26:24:59:PHE:CZ	50:2s:64:GLU:HB2	2.53	0.42
32:2a:90:U:H2'	32:2a:91:C:H6	1.85	0.42
32:2a:693:G:N3	38:2g:82:GLY:HA3	2.35	0.42
32:2a:1003:G:N7	32:2a:1004:A:H1'	2.35	0.42
33:2b:97:TRP:HZ3	33:2b:101:MET:H	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	2.01	0.42
40:2i:27:THR:HG22	40:2i:62:TYR:HA	2.01	0.42
40:2i:46:ALA:HB2	40:2i:74:ILE:HG22	2.01	0.42
40:2i:55:ALA:HA	40:2i:58:HIS:CD2	2.54	0.42
42:2k:48:ILE:HG21	42:2k:63:LEU:HD13	2.01	0.42
47:2p:21:VAL:HG22	47:2p:33:ILE:HB	2.01	0.42
47:2p:39:TYR:CZ	47:2p:41:PRO:HB3	2.55	0.42
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.20	0.42
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.20	0.42
1:1A:1682:G:C2	1:1A:1757:U:H1'	2.53	0.42
1:1A:1702:G:H2'	1:1A:1703:G:O4'	2.19	0.42
1:1A:2155:G:H3'	1:1A:2156:G:C8	2.54	0.42
1:1A:2734:A:H2'	1:1A:2735:G:O4'	2.18	0.42
11:1P:88:LEU:HD21	11:1P:100:LEU:HD11	2.01	0.42
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	2.02	0.42
32:1a:1492:A:H2	32:1a:1494:G:N7	2.18	0.42
33:1b:72:GLY:O	33:1b:94:ASN:HA	2.19	0.42
35:1d:36:ARG:HD2	35:1d:38:TYR:OH	2.19	0.42
43:1l:32:PHE:HB3	43:1l:84:LEU:HD11	2.01	0.42
45:1n:53:LEU:HD23	45:1n:53:LEU:HA	1.89	0.42
46:1o:71:GLN:HB2	46:1o:78:TYR:CD1	2.55	0.42
1:2A:478:A:C6	1:2A:480:A:C6	3.08	0.42
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.43	0.42
1:2A:2786:U:O2'	4:2E:62:PRO:O	2.33	0.42
2:2B:57:A:OP2	63:2B:301:HOH:O	2.21	0.42
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	2.02	0.42
7:2H:32:GLU:C	7:2H:33:LEU:HD23	2.44	0.42
10:2O:34:THR:OG1	10:2O:35:VAL:N	2.51	0.42
14:2S:93:LYS:HE2	14:2S:95:HIS:HB2	2.01	0.42
15:2T:9:LEU:O	15:2T:12:SER:OG	2.34	0.42
16:2U:33:ARG:NE	63:2U:302:HOH:O	2.50	0.42
20:2Y:14:LEU:HA	20:2Y:24:VAL:HG22	2.02	0.42
32:2a:184:G:H2'	32:2a:185:A:H8	1.84	0.42
32:2a:316:G:H2'	32:2a:317:G:C8	2.55	0.42
32:2a:622:A:C8	32:2a:623:C:C6	3.08	0.42
32:2a:903:G:H2'	32:2a:904:C:C6	2.54	0.42
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.33	0.42
32:2a:1323:G:H4'	32:2a:1363:C:N3	2.35	0.42
33:2b:47:THR:O	33:2b:51:LEU:HG	2.19	0.42
35:2d:156:GLU:O	35:2d:160:GLN:HG3	2.18	0.42
42:2k:18:ARG:HH21	42:2k:36:ASP:C	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:586:A:H5"	63:1A:6033:HOH:O	2.19	0.42
1:1A:1417:C:H2'	1:1A:1418:G:O4'	2.19	0.42
1:1A:1466:G:H2'	1:1A:1547:C:N4	2.34	0.42
1:1A:2061:G:O6	58:1A:4022:CLM:H3	2.19	0.42
1:1A:2431:U:OP1	63:1A:4218:HOH:O	2.21	0.42
3:1D:132:PRO:HG3	3:1D:190:TYR:CE2	2.55	0.42
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.55	0.42
32:1a:162:A:H3'	32:1a:163:C:H4'	2.01	0.42
32:1a:394:G:H2'	32:1a:395:C:C6	2.54	0.42
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.19	0.42
39:1h:82:HIS:HB3	39:1h:138:TRP:CE2	2.54	0.42
51:1t:63:ILE:HG21	51:1t:81:LYS:HG3	2.00	0.42
1:2A:118:A:H5'	1:2A:119:A:H8	1.85	0.42
1:2A:370:G:OP2	1:2A:370:G:H8	2.03	0.42
1:2A:476:G:N1	1:2A:479:A:OP2	2.49	0.42
1:2A:1786:A:C4	1:2A:1938:A:C6	3.07	0.42
1:2A:2131:G:H21	1:2A:2133:G:N2	2.16	0.42
1:2A:2261:C:C2	1:2A:2280:G:C2	3.07	0.42
1:2A:2812:G:H1	1:2A:2888:C:H42	1.68	0.42
3:2D:26:LYS:HD3	3:2D:83:GLU:OE2	2.20	0.42
6:2G:68:PRO:HA	6:2G:92:VAL:HB	2.00	0.42
21:2Z:16:SER:O	21:2Z:20:ARG:HB2	2.20	0.42
22:20:71:ASP:C	22:20:73:GLY:H	2.28	0.42
32:2a:7:G:H5'	32:2a:298:A:O4'	2.20	0.42
32:2a:37:U:OP2	43:2l:123:LYS:HD2	2.19	0.42
32:2a:500:G:C6	32:2a:546:G:C2	3.08	0.42
32:2a:867:G:O2'	32:2a:873:A:N1	2.41	0.42
32:2a:1304:G:C6	32:2a:1305:G:N1	2.88	0.42
33:2b:74:LYS:H	33:2b:74:LYS:HG3	1.40	0.42
35:2d:132:ARG:HE	35:2d:132:ARG:HB3	1.72	0.42
36:2e:45:PHE:CE2	36:2e:129:ILE:HD13	2.53	0.42
44:2m:108:ARG:HD3	44:2m:108:ARG:HA	1.80	0.42
47:2p:55:ARG:HA	47:2p:55:ARG:HD2	1.79	0.42
1:1A:580:C:H2'	1:1A:581:C:C6	2.54	0.42
1:1A:811:U:OP1	63:1A:4219:HOH:O	2.21	0.42
1:1A:1075:C:H42	1:1A:1077:A:N6	2.17	0.42
1:1A:1269:A:H2'	1:1A:1270:C:C6	2.54	0.42
1:1A:1524:G:H2'	1:1A:1525:G:O4'	2.19	0.42
1:1A:2304:G:H22	1:1A:2312:U:H3	1.67	0.42
3:1D:146:GLU:HB2	3:1D:189:CYS:HB3	2.02	0.42
4:1E:72:VAL:HG12	4:1E:73:GLU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:47:LYS:HD2	20:1Y:63:LYS:HE3	2.00	0.42
21:1Z:3:TYR:CD2	21:1Z:51:ALA:HB2	2.55	0.42
24:12:59:ARG:NH2	63:12:104:HOH:O	2.50	0.42
32:1a:730:G:O6	46:1o:51:HIS:NE2	2.51	0.42
32:1a:1237:C:H3'	32:1a:1336:C:N4	2.34	0.42
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.87	0.42
39:1h:53:VAL:HB	39:1h:58:TYR:CE2	2.55	0.42
39:1h:81:HIS:H	39:1h:138:TRP:C	2.28	0.42
51:1t:53:LEU:HD12	51:1t:100:ILE:HG13	2.01	0.42
1:2A:184:C:H2'	1:2A:185:U:C6	2.54	0.42
1:2A:275:G:H2'	1:2A:276:A:C8	2.55	0.42
1:2A:1427:A:H4'	1:2A:1428:C:O4'	2.20	0.42
1:2A:1515:G:H4'	1:2A:1556:C:O2'	2.19	0.42
1:2A:2010:G:H5"	18:2W:42:ARG:HB2	2.01	0.42
1:2A:2390:U:P	30:28:35:GLN:HE22	2.43	0.42
5:2F:160:ASN:OD1	5:2F:163:VAL:HG23	2.20	0.42
15:2T:16:ARG:HD3	15:2T:19:LEU:HG	2.02	0.42
32:2a:684:A:C6	32:2a:685:G:C6	3.07	0.42
32:2a:1333:A:H3'	32:2a:1334:G:H8	1.84	0.42
32:2a:1343:G:H4'	40:2i:122:ALA:HB3	2.02	0.42
35:2d:153:ARG:O	35:2d:155:LEU:N	2.51	0.42
48:2q:62:SER:OG	48:2q:72:ARG:NH1	2.52	0.42
1:1A:27:G:C2	1:1A:512:G:N3	2.88	0.42
1:1A:458:G:O2'	29:17:39:ARG:HD3	2.20	0.42
1:1A:879:G:H8	1:1A:879:G:O5'	2.03	0.42
1:1A:1002:G:H2'	1:1A:1003:G:O4'	2.20	0.42
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.19	0.42
1:1A:1537:G:H2'	1:1A:1538:G:C8	2.55	0.42
1:1A:2773:C:H2'	1:1A:2774:C:H6	1.84	0.42
63:1A:6914:HOH:O	16:1U:50:ARG:HB3	2.20	0.42
15:1T:27:THR:O	15:1T:89:VAL:HG22	2.20	0.42
22:10:53:MET:HG3	22:10:59:LEU:HD23	2.01	0.42
24:12:54:LYS:HE2	24:12:54:LYS:HB3	1.61	0.42
32:1a:1054:C:H41	53:1y:46:GLN:CG	2.32	0.42
33:1b:84:GLU:HA	33:1b:87:ARG:HD3	2.02	0.42
33:1b:96:ARG:HG2	33:1b:98:LEU:HD23	2.02	0.42
38:1g:27:ILE:HD13	38:1g:27:ILE:HA	1.89	0.42
38:1g:73:MET:SD	38:1g:90:GLU:HA	2.60	0.42
48:1q:54:GLY:HA2	48:1q:85:VAL:HG21	2.01	0.42
1:2A:484:C:H6	1:2A:484:C:O5'	2.03	0.42
1:2A:921:G:H4'	1:2A:2269:A:C5	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1000:A:H62	1:2A:1154:G:H2'	1.84	0.42
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.55	0.42
1:2A:1800:C:P	3:2D:183:ARG:HH12	2.43	0.42
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.55	0.42
4:2E:52:LEU:O	4:2E:76:ARG:N	2.44	0.42
8:2I:29:TYR:HD2	8:2I:30:LEU:HD23	1.85	0.42
16:2U:89:GLU:O	17:2V:11:GLN:NE2	2.53	0.42
18:2W:4:LYS:CB	18:2W:106:ILE:HG12	2.50	0.42
32:2a:12:U:H4'	32:2a:526:C:H4'	2.02	0.42
32:2a:189:G:C2	32:2a:189(L):G:C2	3.08	0.42
32:2a:221:C:H2'	32:2a:222:U:C6	2.55	0.42
32:2a:997:U:H2'	32:2a:998:G:C8	2.54	0.42
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.55	0.42
32:2a:1058:G:H2'	32:2a:1059:C:O4'	2.20	0.42
32:2a:1371:G:OP1	40:2i:12:GLU:HB2	2.19	0.42
40:2i:41:VAL:C	40:2i:43:ALA:H	2.27	0.42
50:2s:18:LYS:HA	50:2s:21:GLU:HB2	2.01	0.42
51:2t:65:LYS:HA	51:2t:68:LYS:HG3	2.02	0.42
1:1A:27:G:N2	1:1A:512:G:H1'	2.35	0.42
1:1A:883:G:C2	1:1A:894:C:C2	3.08	0.42
1:1A:1358:G:O2'	1:1A:1359:A:H5"	2.20	0.42
1:1A:1628:G:H2'	1:1A:1629:U:C6	2.55	0.42
1:1A:1707:G:C5	1:1A:1756:G:C6	3.08	0.42
1:1A:2366:A:OP1	63:1A:4220:HOH:O	2.21	0.42
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.19	0.42
2:1B:48:A:H2'	2:1B:49:C:C6	2.55	0.42
7:1H:69:ARG:C	7:1H:69:ARG:HD3	2.45	0.42
10:1O:36:GLY:HA2	10:1O:106:LEU:HD23	2.01	0.42
12:1Q:71:ASP:OD1	12:1Q:71:ASP:N	2.46	0.42
19:1X:57:LEU:HD11	19:1X:78:LYS:HE3	2.02	0.42
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.35	0.42
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	2.02	0.42
44:1m:19:LEU:HD11	44:1m:56:LEU:HD21	2.02	0.42
44:1m:90:LEU:O	44:1m:94:ARG:HG3	2.19	0.42
1:2A:90:U:H4'	1:2A:92:A:O5'	2.20	0.42
1:2A:107:C:H2'	1:2A:108:U:H6	1.85	0.42
1:2A:271(Q):G:H2'	1:2A:271(R):G:H8	1.85	0.42
1:2A:863:A:P	12:2Q:22:LYS:HD2	2.60	0.42
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.20	0.42
1:2A:1881:C:H2'	1:2A:1882:C:H6	1.84	0.42
1:2A:2637:U:H1'	1:2A:2782:G:N2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:102:LYS:C	3:2D:103:ARG:HG2	2.45	0.42
6:2G:16:ARG:NE	6:2G:31:VAL:HG11	2.34	0.42
16:2U:105:VAL:O	16:2U:108:GLU:HB3	2.20	0.42
18:2W:64:MET:HE3	18:2W:109:GLU:HG3	2.01	0.42
32:2a:363:A:P	43:2l:34:ARG:HB3	2.60	0.42
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.55	0.42
32:2a:1195:C:H5"	32:2a:1196:U:OP2	2.20	0.42
36:2e:41:VAL:HG23	36:2e:67:VAL:HG22	2.02	0.42
40:2i:74:ILE:HG13	40:2i:74:ILE:H	1.64	0.42
53:2y:46:GLN:H	53:2y:46:GLN:HG2	1.49	0.42
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.53	0.41
1:1A:1508:A:H4'	1:1A:1509(A):A:C5	2.55	0.41
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.40	0.41
1:1A:1993:U:H4'	4:1E:128:SER:OG	2.20	0.41
1:1A:2246:G:H2'	1:1A:2247:A:C8	2.54	0.41
4:1E:170:LEU:HD23	4:1E:184:VAL:CG1	2.50	0.41
6:1G:37:VAL:HA	6:1G:158:ALA:O	2.20	0.41
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	2.01	0.41
21:1Z:116:VAL:O	21:1Z:174:VAL:HA	2.20	0.41
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.50	0.41
32:1a:974:A:H8	32:1a:974:A:OP1	2.02	0.41
35:1d:149:ALA:O	35:1d:152:SER:N	2.50	0.41
36:1e:66:MET:HE3	36:1e:66:MET:HB3	1.86	0.41
36:1e:91:LEU:HD23	36:1e:118:ILE:HD11	2.02	0.41
38:1g:66:VAL:O	38:1g:70:LYS:HG3	2.19	0.41
47:1p:2:VAL:HG13	47:1p:64:ALA:HA	2.02	0.41
48:1q:62:SER:OG	48:1q:72:ARG:HG3	2.20	0.41
1:2A:556:G:H2'	1:2A:557:U:C6	2.55	0.41
1:2A:784:A:O4'	3:2D:227:ASN:ND2	2.53	0.41
1:2A:985:C:H2'	1:2A:986:C:H6	1.85	0.41
1:2A:1503:U:H2'	1:2A:1504:C:H6	1.82	0.41
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.21	0.41
1:2A:2111:C:N4	1:2A:2147:G:H22	2.16	0.41
1:2A:2334:G:H5'	14:2S:9:ARG:HG2	2.02	0.41
1:2A:2532:G:C6	1:2A:2533:A:C6	3.08	0.41
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.55	0.41
1:2A:2847:U:OP1	15:2T:98:LYS:NZ	2.44	0.41
4:2E:183:LEU:HD21	15:2T:10:VAL:HG11	2.02	0.41
6:2G:37:VAL:HB	6:2G:94:LEU:HB2	2.02	0.41
7:2H:126:PRO:HG2	7:2H:130:ARG:HH21	1.85	0.41
9:2N:74:ARG:HG3	9:2N:83:LYS:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2U:91:ASP:H	17:2V:11:GLN:CD	2.27	0.41
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.55	0.41
32:2a:190:U:C2	32:2a:191:G:C8	3.08	0.41
32:2a:595:G:H1'	32:2a:596:C:H5	1.85	0.41
32:2a:997:U:H3	32:2a:1044:A:N6	2.17	0.41
32:2a:1025:U:O2'	32:2a:1026:G:N7	2.53	0.41
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.20	0.41
32:2a:1225:A:H2'	32:2a:1226:C:C6	2.55	0.41
33:2b:104:ASN:ND2	33:2b:107:THR:OG1	2.53	0.41
49:2r:43:PHE:HA	49:2r:51:LEU:HD12	2.01	0.41
51:2t:72:LEU:HD23	51:2t:72:LEU:HA	1.88	0.41
1:1A:527:C:H4'	1:1A:528:A:O5'	2.20	0.41
1:1A:1466:G:O2'	1:1A:1546:C:O2'	2.22	0.41
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.82	0.41
1:1A:2106:G:C4	1:1A:2107:C:H1'	2.54	0.41
1:1A:2242:G:OP1	63:1A:4213:HOH:O	2.21	0.41
2:1B:66:A:N6	2:1B:108:U:H2'	2.34	0.41
6:1G:7:LEU:HD23	6:1G:7:LEU:HA	1.86	0.41
6:1G:135:LEU:HD11	6:1G:157:ILE:HD11	2.02	0.41
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.49	0.41
26:14:16:CYS:HA	26:14:33:VAL:HG23	2.02	0.41
29:17:30:VAL:O	29:17:34:ARG:HG3	2.20	0.41
32:1a:345:C:H1'	60:1a:3271:MPD:HM1	2.01	0.41
32:1a:376:G:OP1	47:1p:5:ARG:HB2	2.20	0.41
32:1a:731:G:OP1	32:1a:766:A:H1'	2.20	0.41
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.20	0.41
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	2.01	0.41
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.19	0.41
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	2.03	0.41
42:1k:99:GLN:CG	42:1k:105:VAL:HG21	2.50	0.41
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.85	0.41
1:2A:1059:G:P	1:2A:1060:U:H2'	2.60	0.41
1:2A:1798:U:OP2	3:2D:274:ARG:NH2	2.48	0.41
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.50	0.41
5:2F:31:HIS:CD2	5:2F:35:GLU:HG3	2.55	0.41
6:2G:21:ARG:O	6:2G:23:PHE:N	2.53	0.41
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	2.01	0.41
20:2Y:23:ARG:H	20:2Y:23:ARG:HG2	1.70	0.41
20:2Y:86:ARG:HD2	20:2Y:100:ALA:HA	2.02	0.41
22:20:82:ARG:HA	22:20:83:PRO:HD3	1.96	0.41
26:24:15:ILE:HD12	26:24:31:ILE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:303:A:O2'	32:2a:555:C:H4'	2.19	0.41
32:2a:512:U:H1'	35:2d:42:GLN:HE22	1.85	0.41
32:2a:611:A:H61	32:2a:629:G:H1	1.67	0.41
32:2a:983:A:H5"	32:2a:984:C:OP2	2.19	0.41
34:2c:113:ALA:HB2	34:2c:202:ILE:HG13	2.02	0.41
38:2g:27:ILE:HD13	38:2g:27:ILE:HA	1.96	0.41
44:2m:14:ARG:H	44:2m:14:ARG:HG3	1.65	0.41
1:1A:1217:C:H2'	1:1A:1218:C:H5"	2.01	0.41
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.36	0.41
1:1A:2690:C:H5"	1:1A:2872:G:H21	1.85	0.41
9:1N:67:LEU:HB2	63:1N:342:HOH:O	2.21	0.41
32:1a:93:G:H2'	32:1a:96:U:O4'	2.20	0.41
32:1a:115:G:C2	32:1a:289:G:N7	2.88	0.41
32:1a:149:A:H2'	32:1a:150:C:C6	2.55	0.41
32:1a:230:G:H2'	32:1a:231:G:O4'	2.19	0.41
32:1a:652:U:O4	32:1a:752:G:O2'	2.24	0.41
32:1a:1135:U:H5"	32:1a:1136:U:H5	1.85	0.41
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.54	0.41
35:1d:158:ILE:HA	35:1d:161:ASN:HB2	2.03	0.41
42:1k:77:MET:HE2	42:1k:77:MET:HB2	1.62	0.41
1:2A:196:A:N3	1:2A:196:A:H2'	2.36	0.41
1:2A:271(W):G:C6	1:2A:271(X):G:C2	3.08	0.41
1:2A:477:A:H2'	1:2A:478:A:C8	2.55	0.41
1:2A:2307:G:O6	6:2G:44:GLY:HA3	2.20	0.41
1:2A:2375:G:N1	63:2A:3929:HOH:O	2.21	0.41
1:2A:2619:C:H4'	4:2E:151:TYR:O	2.20	0.41
3:2D:242:ARG:O	63:2D:404:HOH:O	2.21	0.41
6:2G:38:VAL:HG13	6:2G:91:ARG:HD3	2.02	0.41
7:2H:137:ASP:O	7:2H:141:VAL:HG23	2.21	0.41
9:2N:91:LEU:HD23	9:2N:91:LEU:HA	1.91	0.41
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HB3	2.35	0.41
16:2U:104:GLN:H	16:2U:104:GLN:HG3	1.63	0.41
17:2V:57:VAL:HA	17:2V:98:GLU:O	2.20	0.41
20:2Y:36:ALA:HA	20:2Y:67:LEU:O	2.20	0.41
26:24:50:VAL:HG11	44:2m:63:THR:C	2.45	0.41
32:2a:266:G:N3	32:2a:266:G:H5"	2.35	0.41
32:2a:949:A:H2'	32:2a:950:U:O4'	2.20	0.41
32:2a:1243:C:H2'	32:2a:1244:C:C6	2.55	0.41
34:2c:111:LEU:HD21	34:2c:146:ALA:HB2	2.02	0.41
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.53	0.41
38:2g:62:PHE:O	38:2g:66:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:18:LYS:HD3	50:2s:31:ILE:HG23	2.02	0.41
1:1A:350:U:H2'	1:1A:351:G:O4'	2.21	0.41
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.56	0.41
1:1A:1203:G:H5'	11:1P:3:LEU:HD12	2.01	0.41
1:1A:1698:A:C8	1:1A:1700:A:O4'	2.73	0.41
1:1A:2590:A:H2'	1:1A:2591:C:C6	2.55	0.41
1:1A:2687:U:OP2	63:1A:4226:HOH:O	2.22	0.41
1:1A:2711:A:H5"	1:1A:2712:U:H5"	2.03	0.41
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.20	0.41
13:1R:70:LEU:C	13:1R:72:ASP:H	2.29	0.41
15:1T:2:ASN:OD1	15:1T:5:ALA:N	2.50	0.41
20:1Y:43:ASN:ND2	63:1Y:306:HOH:O	2.52	0.41
32:1a:626:U:H2'	32:1a:627:G:H8	1.85	0.41
32:1a:669:U:C2	32:1a:670:G:C8	3.08	0.41
34:1c:40:ARG:HB3	34:1c:44:GLU:OE2	2.20	0.41
42:1k:93:GLN:HA	42:1k:93:GLN:HE21	1.84	0.41
44:1m:81:LEU:HD22	44:1m:86:CYS:SG	2.60	0.41
45:1n:9:LYS:HE2	45:1n:9:LYS:HB3	1.75	0.41
46:1o:2:PRO:HB2	46:1o:3:ILE:H	1.62	0.41
1:2A:106:C:O2'	1:2A:294:A:O2'	2.37	0.41
1:2A:902:C:H2'	1:2A:903:C:H6	1.85	0.41
1:2A:1074:G:C2	1:2A:1075:C:H1'	2.56	0.41
2:2B:37:C:O2'	14:2S:95:HIS:HE1	2.03	0.41
3:2D:143:HIS:CD2	3:2D:192:THR:HB	2.56	0.41
5:2F:20:LEU:HD23	5:2F:21:ALA:N	2.36	0.41
5:2F:107:LYS:HG3	5:2F:206:ILE:HA	2.01	0.41
6:2G:8:LYS:HG3	6:2G:100:TRP:CE2	2.55	0.41
26:24:2:LYS:HB2	26:24:5:ILE:HD13	2.01	0.41
32:2a:108:G:O6	51:2t:15:ARG:HG2	2.21	0.41
32:2a:409:G:H2'	32:2a:410:G:O4'	2.21	0.41
32:2a:745:C:H4'	32:2a:836:G:N2	2.36	0.41
32:2a:903:G:H2'	32:2a:904:C:H6	1.85	0.41
32:2a:1004:A:H5"	32:2a:1025:U:H5	1.85	0.41
33:2b:52:GLU:HG2	33:2b:52:GLU:O	2.20	0.41
34:2c:136:GLN:HG2	34:2c:137:ALA:N	2.31	0.41
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.20	0.41
36:2e:110:LEU:HB3	36:2e:115:VAL:CG1	2.50	0.41
47:2p:73:LEU:H	47:2p:73:LEU:HG	1.63	0.41
1:1A:188:G:H5'	23:11:14:VAL:HG21	2.02	0.41
1:1A:244:A:C2	1:1A:255:A:C4	3.08	0.41
1:1A:592:G:O2'	30:18:4:MET:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1514:U:H2'	1:1A:1515:G:C8	2.56	0.41
1:1A:1567:A:OP2	3:1D:84:TYR:OH	2.23	0.41
1:1A:1721:G:N1	1:1A:1739:U:OP2	2.53	0.41
14:1S:110:LEU:HA	14:1S:110:LEU:HD12	1.78	0.41
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.55	0.41
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD21	2.02	0.41
24:12:8:LYS:O	24:12:12:GLU:HG2	2.20	0.41
32:1a:78:G:C2	32:1a:91:C:N3	2.87	0.41
32:1a:153:C:N4	32:1a:169:C:H42	2.19	0.41
32:1a:297:G:H4'	32:1a:557:G:H4'	2.02	0.41
32:1a:409:G:OP2	35:1d:22:LYS:NZ	2.53	0.41
32:1a:1438:G:H2'	32:1a:1439:C:H6	1.86	0.41
33:1b:213:LEU:O	33:1b:213:LEU:HD23	2.20	0.41
39:1h:65:TYR:HA	39:1h:79:VAL:HG23	2.03	0.41
44:1m:60:VAL:HG22	44:1m:64:TRP:HZ3	1.85	0.41
53:1y:43:LYS:HD3	53:1y:48:PHE:CE1	2.56	0.41
1:2A:904:C:H2'	1:2A:905:U:C6	2.56	0.41
1:2A:957:A:OP2	63:2A:3935:HOH:O	2.22	0.41
1:2A:1590:U:H2'	1:2A:1591:G:C8	2.56	0.41
1:2A:2061:G:C2	1:2A:2063:C:C4	3.09	0.41
1:2A:2078:C:C4	1:2A:2079:U:C4	3.09	0.41
1:2A:2137:C:N3	1:2A:2154:G:C6	2.89	0.41
1:2A:2356:C:O3'	22:20:20:ARG:HD3	2.21	0.41
1:2A:2468:G:C2	1:2A:2481:G:N3	2.88	0.41
3:2D:13:ARG:HD3	3:2D:13:ARG:HA	1.64	0.41
7:2H:64:LEU:HD23	7:2H:64:LEU:HA	1.91	0.41
7:2H:83:TYR:CE2	7:2H:138:LYS:HB2	2.55	0.41
13:2R:104:ARG:HD2	13:2R:107:ASP:OD1	2.21	0.41
21:2Z:66:SER:O	21:2Z:68:PRO:HD3	2.20	0.41
21:2Z:179:ASP:O	21:2Z:182:LYS:HG2	2.20	0.41
32:2a:819:A:H4'	32:2a:820:U:OP2	2.19	0.41
32:2a:840:C:H4'	32:2a:841:U:OP2	2.18	0.41
32:2a:1079:G:H4'	36:2e:14:ARG:NH2	2.34	0.41
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.53	0.41
32:2a:1452:C:H5'	32:2a:1457:G:C4	2.55	0.41
34:2c:110:ASN:ND2	34:2c:140:ARG:HB3	2.32	0.41
43:2l:53:ARG:NH1	43:2l:92:0TD:OD1	2.45	0.41
44:2m:13:LYS:O	44:2m:45:VAL:HG23	2.20	0.41
46:2o:4:THR:HG23	46:2o:7:GLU:HG3	2.03	0.41
1:1A:207:A:H2'	1:1A:208:C:O4'	2.19	0.41
1:1A:308:G:N2	1:1A:477:A:C8	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:459:U:H4'	29:17:40:TRP:CZ3	2.56	0.41
1:1A:729:G:H5'	1:1A:730:C:H5"	2.01	0.41
1:1A:1602:U:H5"	63:1A:5872:HOH:O	2.20	0.41
1:1A:2066:C:H5"	63:1A:6844:HOH:O	2.21	0.41
1:1A:2616:C:O2	63:1A:4224:HOH:O	2.21	0.41
9:1N:35:ARG:NH2	63:1N:308:HOH:O	2.48	0.41
21:1Z:150:LEU:HB3	21:1Z:171:ILE:CD1	2.51	0.41
23:11:71:TYR:O	23:11:75:GLU:HG2	2.20	0.41
29:17:48:LYS:HE2	29:17:48:LYS:HB2	1.67	0.41
32:1a:433:C:H2'	32:1a:434:U:H6	1.86	0.41
32:1a:527:G7M:O2'	32:1a:535:A:N1	2.52	0.41
32:1a:607:A:H2'	32:1a:608:A:O4'	2.21	0.41
32:1a:1499:A:H1'	32:1a:1520:G:H5'	2.02	0.41
33:1b:82:ARG:HD2	33:1b:92:TYR:OH	2.20	0.41
34:1c:181:ASN:ND2	34:1c:204:LEU:HD12	2.35	0.41
38:1g:50:ILE:HD11	38:1g:58:PRO:HB3	2.03	0.41
39:1h:122:ARG:HB3	39:1h:122:ARG:NH1	2.36	0.41
48:1q:10:VAL:HG13	48:1q:19:VAL:HB	2.03	0.41
53:1y:80:LYS:O	53:1y:84:GLN:HG3	2.21	0.41
1:2A:79:G:O2'	1:2A:346:A:N3	2.42	0.41
1:2A:394:A:O2'	1:2A:395:U:H5'	2.20	0.41
1:2A:480:A:OP2	20:2Y:47:LYS:HD3	2.21	0.41
1:2A:588:U:H1'	5:2F:90:PHE:CG	2.56	0.41
1:2A:1540:U:H2'	1:2A:1541:G:O4'	2.20	0.41
1:2A:2023:G:OP2	1:2A:2617:C:H4'	2.21	0.41
1:2A:2596:U:OP2	63:2A:3932:HOH:O	2.21	0.41
1:2A:2850:A:N7	1:2A:2868:A:O2'	2.53	0.41
2:2B:29:A:H2'	2:2B:30:C:O4'	2.21	0.41
3:2D:141:VAL:HG23	3:2D:162:SER:HB2	2.02	0.41
3:2D:143:HIS:CD2	3:2D:143:HIS:C	2.99	0.41
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	2.03	0.41
6:2G:5:VAL:HG23	6:2G:8:LYS:H	1.86	0.41
12:2Q:42:ILE:HG22	12:2Q:47:ILE:HG13	2.03	0.41
13:2R:24:GLN:OE1	13:2R:36:THR:HG21	2.20	0.41
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.56	0.41
26:24:40:HIS:CB	26:24:43:TYR:HB2	2.42	0.41
32:2a:582:U:C2	32:2a:760:G:C6	3.09	0.41
32:2a:953:G:C2	32:2a:954:G:H1'	2.56	0.41
32:2a:1371:G:C6	32:2a:1372:U:C4	3.09	0.41
33:2b:167:PRO:HD3	33:2b:187:LEU:O	2.21	0.41
34:2c:91:LEU:HD22	34:2c:99:VAL:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:99:LEU:HD23	38:2g:102:ARG:HH12	1.86	0.41
38:2g:111:ARG:HE	38:2g:123:GLU:HB2	1.85	0.41
44:2m:102:ARG:HB3	44:2m:102:ARG:NH1	2.36	0.41
48:2q:43:LEU:HD12	48:2q:68:ARG:HB2	2.03	0.41
50:2s:36:ARG:NH1	50:2s:75:ALA:HB3	2.35	0.41
1:1A:251:A:C5	1:1A:252:G:H1'	2.56	0.41
1:1A:774:A:N3	1:1A:774:A:H2'	2.35	0.41
1:1A:1324:G:N7	63:1A:4464:HOH:O	2.37	0.41
1:1A:1364:G:N7	23:11:3:LYS:HE2	2.36	0.41
1:1A:2418:A:H2'	1:1A:2419:U:C6	2.56	0.41
1:1A:2422:A:H5"	63:1A:7294:HOH:O	2.21	0.41
1:1A:2680:C:H1'	4:1E:187:ALA:HB1	2.02	0.41
2:1B:74:U:H2'	2:1B:75:G:O4'	2.20	0.41
5:1F:110:LEU:HD11	5:1F:181:LEU:HG	2.03	0.41
10:1O:25:LEU:HD23	10:1O:25:LEU:HA	1.88	0.41
17:1V:40:LEU:HD23	17:1V:40:LEU:HA	1.88	0.41
32:1a:363:A:OP1	43:1l:33:ARG:HD2	2.21	0.41
32:1a:523:A:N1	43:1l:92:0TD:H6	2.36	0.41
32:1a:539:A:OP2	43:1l:115:LYS:HE3	2.21	0.41
32:1a:981:U:H2'	32:1a:982:U:C5	2.56	0.41
32:1a:1004:A:H5'	32:1a:1024:G:N2	2.36	0.41
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.52	0.41
34:1c:17:ASP:O	34:1c:54:ARG:NH2	2.49	0.41
34:1c:195:VAL:O	34:1c:196:LEU:HD12	2.21	0.41
37:1f:67:MET:HE1	37:1f:75:LEU:HD23	2.02	0.41
39:1h:116:LYS:HD2	39:1h:129:VAL:HG11	2.03	0.41
40:1i:29:ASN:OD1	40:1i:65:VAL:N	2.47	0.41
40:1i:111:ARG:HG3	45:1n:61:TRP:NE1	2.36	0.41
44:1m:23:TYR:CE2	44:1m:70:LEU:HB3	2.56	0.41
50:1s:20:LEU:HD21	50:1s:43:GLU:HG2	2.03	0.41
1:2A:263:C:H1'	1:2A:430:G:H1'	2.03	0.41
1:2A:407:G:H5"	63:2A:3853:HOH:O	2.20	0.41
1:2A:532:A:OP1	1:2A:561:G:N2	2.49	0.41
1:2A:562:U:O2'	1:2A:563:G:OP2	2.33	0.41
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.35	0.41
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.36	0.41
1:2A:2328:A:H2'	1:2A:2329:G:H8	1.83	0.41
1:2A:2419:U:H2'	1:2A:2420:C:C6	2.56	0.41
1:2A:2689:U:H4'	1:2A:2690:C:H5'	2.03	0.41
2:2B:112:U:H2'	2:2B:113:G:H8	1.85	0.41
6:2G:23:PHE:HB2	6:2G:25:TYR:CZ	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:123:LEU:HD11	8:2I:145:VAL:C	2.46	0.41
20:2Y:7:VAL:HG11	20:2Y:13:VAL:CG1	2.50	0.41
32:2a:382:A:H2'	32:2a:383:A:C8	2.56	0.41
32:2a:428:G:C5	32:2a:430:A:C6	3.09	0.41
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.53	0.41
38:2g:69:VAL:HG21	38:2g:104:LEU:HD11	2.03	0.41
43:2l:25:PRO:O	43:2l:28:LYS:HE2	2.20	0.41
47:2p:6:LEU:HD23	47:2p:17:TYR:CG	2.55	0.41
1:1A:557:U:H2'	1:1A:558:G:H8	1.86	0.41
1:1A:963:U:H2'	1:1A:964:C:C6	2.56	0.41
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.21	0.41
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.56	0.41
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.21	0.41
1:1A:1768:U:OP1	63:1A:4225:HOH:O	2.22	0.41
1:1A:2420:C:H5'	28:16:54:ILE:HD11	2.02	0.41
6:1G:137:GLU:HG2	6:1G:152:LEU:HD22	2.03	0.41
10:1O:19:ILE:HG22	10:1O:43:VAL:HG22	2.03	0.41
19:1X:72:LYS:HE3	19:1X:72:LYS:HB3	1.80	0.41
32:1a:17:U:H2'	32:1a:18:C:C6	2.55	0.41
32:1a:153:C:H42	32:1a:169:C:H42	1.69	0.41
32:1a:185:A:H2'	32:1a:186:C:C6	2.55	0.41
32:1a:394:G:H2'	32:1a:395:C:H6	1.86	0.41
32:1a:503:C:H2'	32:1a:504:C:C6	2.55	0.41
32:1a:1015:A:O2'	32:1a:1218:C:O2'	2.35	0.41
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.56	0.41
33:1b:222:ILE:O	33:1b:226:ARG:N	2.54	0.41
34:1c:43:LEU:HD11	34:1c:66:VAL:HG11	2.01	0.41
34:1c:143:GLU:C	34:1c:145:GLY:H	2.29	0.41
37:1f:23:LYS:HG2	37:1f:61:LEU:HD21	2.03	0.41
43:1l:57:LYS:HB2	43:1l:67:THR:HG22	2.02	0.41
44:1m:65:LYS:O	44:1m:66:LEU:HD23	2.21	0.41
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.21	0.41
1:2A:105:C:H2'	1:2A:106:C:H6	1.85	0.41
1:2A:194:G:H2'	1:2A:195:A:O4'	2.20	0.41
1:2A:1077:A:N7	1:2A:1078:U:N3	2.68	0.41
1:2A:2061:G:N2	56:2v:2:THR:HG23	2.36	0.41
1:2A:2102:U:H2'	1:2A:2103:C:O4'	2.21	0.41
1:2A:2298:A:H2'	1:2A:2299:G:O4'	2.20	0.41
1:2A:2506:U:C2	1:2A:2585:U:O4	2.74	0.41
1:2A:2602:A:H5"	55:2x:75:C:OP2	2.21	0.41
5:2F:140:LEU:HD13	5:2F:140:LEU:HA	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:118:LEU:HD13	12:2Q:131:ILE:HG23	2.02	0.41
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.56	0.41
32:2a:21:G:H2'	32:2a:22:G:C8	2.56	0.41
32:2a:421:U:O2	34:2c:127:ARG:NH2	2.52	0.41
32:2a:722:A:N6	32:2a:724:G:C2	2.88	0.41
32:2a:980:C:H3'	32:2a:981:U:C6	2.56	0.41
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.56	0.41
34:2c:22:TRP:CZ2	45:2n:54:PRO:HG2	2.56	0.41
34:2c:33:LEU:O	34:2c:37:GLN:N	2.53	0.41
34:2c:144:SER:O	34:2c:146:ALA:N	2.53	0.41
38:2g:75:VAL:HB	38:2g:86:GLN:HB3	2.03	0.41
42:2k:22:HIS:O	42:2k:28:THR:HA	2.21	0.41
51:2t:40:ALA:HB2	51:2t:55:ILE:HG22	2.01	0.41
53:2y:78:ILE:H	53:2y:78:ILE:HG12	1.53	0.41
1:1A:81:G:HO2'	1:1A:295:G:HO2'	1.68	0.41
1:1A:493:G:H2'	1:1A:494:G:O4'	2.19	0.41
1:1A:668:G:H5'	1:1A:669:G:OP2	2.21	0.41
1:1A:784:A:N6	3:1D:229:VAL:HG11	2.35	0.41
1:1A:1302:A:N6	63:1A:4579:HOH:O	2.43	0.41
1:1A:1332:G:N7	1:1A:1609:A:O2'	2.50	0.41
1:1A:2030:A:H4'	1:1A:2031:A:C8	2.55	0.41
2:1B:42:C:O2'	6:1G:66:GLN:HG2	2.19	0.41
5:1F:64:ILE:CG2	5:1F:78:ILE:HG23	2.51	0.41
6:1G:109:VAL:HG21	26:14:14:ILE:HG21	2.03	0.41
8:1I:81:VAL:HG21	8:1I:88:ILE:HD13	2.01	0.41
12:1Q:75:THR:HG21	12:1Q:87:LYS:HE3	2.03	0.41
19:1X:1:MET:HE3	19:1X:1:MET:HB2	1.98	0.41
21:1Z:19:ARG:HE	21:1Z:19:ARG:HB2	1.69	0.41
23:11:67:ILE:N	23:11:68:PRO:HD2	2.36	0.41
32:1a:109:A:C6	32:1a:326:G:C6	3.09	0.41
32:1a:177:C:OP1	51:1t:65:LYS:NZ	2.35	0.41
32:1a:675:A:H1'	42:1k:116:HIS:CG	2.55	0.41
32:1a:737:A:H5'	37:1f:90:VAL:O	2.21	0.41
32:1a:950:U:OP2	44:1m:102:ARG:HD2	2.21	0.41
32:1a:1044:A:C5	32:1a:1045:C:H1'	2.56	0.41
32:1a:1162:C:H2'	32:1a:1163:C:C6	2.55	0.41
32:1a:1176:A:H2'	32:1a:1177:G:C8	2.55	0.41
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	2.03	0.41
36:1e:90:VAL:O	36:1e:120:THR:HA	2.20	0.41
39:1h:97:VAL:HG21	39:1h:128:GLY:HA2	2.03	0.41
41:1j:52:GLY:O	45:1n:41:ARG:NH1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:41:THR:OG1	42:1k:42:TRP:N	2.53	0.41
47:1p:75:ARG:HB2	47:1p:80:PHE:CE2	2.56	0.41
51:1t:22:ARG:O	51:1t:26:ASN:ND2	2.40	0.41
51:1t:57:ARG:NH1	51:1t:100:ILE:HD12	2.29	0.41
53:1y:33:HIS:HB3	53:1y:57:PRO:HD3	2.03	0.41
1:2A:41:C:H2'	1:2A:42:G:O4'	2.21	0.41
1:2A:62:C:OP1	63:2A:3938:HOH:O	2.22	0.41
1:2A:116:C:H2'	1:2A:117:G:O4'	2.21	0.41
1:2A:153:C:OP2	23:21:92:LYS:NZ	2.48	0.41
1:2A:522:G:H2'	1:2A:523:C:C6	2.56	0.41
1:2A:997:G:OP2	16:2U:58:ARG:NH1	2.54	0.41
1:2A:1047:G:C4	1:2A:1110:G:N1	2.89	0.41
1:2A:1097:U:H2'	1:2A:1098:A:O4'	2.20	0.41
1:2A:1325:G:OP2	1:2A:1616:A:O2'	2.34	0.41
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.02	0.41
1:2A:1604:C:H5'	63:2A:4314:HOH:O	2.19	0.41
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.21	0.41
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.56	0.41
1:2A:2250:G:O2'	1:2A:2496:C:OP1	2.29	0.41
1:2A:2472:G:N1	1:2A:2477:C:OP1	2.40	0.41
1:2A:2882:A:OP1	13:2R:96:ARG:HD3	2.21	0.41
63:2A:4044:HOH:O	5:2F:103:LYS:HD2	2.21	0.41
2:2B:40:U:H2'	26:24:2:LYS:HE3	2.03	0.41
3:2D:70:TRP:HB3	3:2D:190:TYR:CE2	2.56	0.41
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	2.03	0.41
3:2D:77:ALA:HA	3:2D:97:TYR:HA	2.03	0.41
4:2E:115:GLY:O	4:2E:119:ARG:HB2	2.20	0.41
4:2E:119:ARG:HB3	4:2E:120:TRP:CD1	2.56	0.41
6:2G:56:ALA:HB2	6:2G:153:ARG:NE	2.35	0.41
6:2G:103:LEU:O	6:2G:107:LEU:HG	2.21	0.41
7:2H:83:TYR:HB2	7:2H:141:VAL:HG21	2.02	0.41
8:2I:62:LYS:HE2	8:2I:133:HIS:CE1	2.55	0.41
11:2P:63:PRO:HD3	30:28:27:THR:HG22	2.03	0.41
12:2Q:4:PRO:HD3	12:2Q:70:PRO:O	2.20	0.41
13:2R:74:LYS:HB3	13:2R:74:LYS:HE2	1.85	0.41
22:20:14:ARG:HB2	22:20:14:ARG:NH1	2.34	0.41
32:2a:17:U:H1'	32:2a:1080:A:N3	2.35	0.41
32:2a:62:U:OP1	32:2a:385:C:O2'	2.34	0.41
32:2a:321:A:C2	32:2a:333:G:C2	3.09	0.41
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.35	0.41
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1035:A:O2'	32:2a:1036:G:C8	2.70	0.41
32:2a:1122:U:C4	32:2a:1123:A:N7	2.89	0.41
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.20	0.41
32:2a:1496:C:H2'	32:2a:1497:G:O4'	2.21	0.41
36:2e:131:ILE:HD13	36:2e:131:ILE:HA	1.91	0.41
38:2g:51:GLN:HB2	38:2g:58:PRO:HD3	2.03	0.41
38:2g:57:GLU:OE2	38:2g:58:PRO:HD2	2.20	0.41
40:2i:6:GLY:O	40:2i:17:VAL:HG22	2.21	0.41
41:2j:16:LEU:HD23	41:2j:94:VAL:HG22	2.03	0.41
45:2n:22:THR:HB	45:2n:33:VAL:HG11	2.02	0.41
46:2o:48:LYS:HA	46:2o:48:LYS:HD3	1.66	0.41
47:2p:74:LEU:HB3	47:2p:80:PHE:HE2	1.85	0.41
53:2y:23:ARG:HG2	53:2y:74:ILE:HG22	2.03	0.41
1:1A:657:U:H2'	1:1A:658:C:C6	2.56	0.41
1:1A:1999:C:H4'	1:1A:2723:C:O2	2.21	0.41
1:1A:2106:G:C6	1:1A:2107:C:C2	3.08	0.41
1:1A:2122:U:H2'	1:1A:2123:G:O4'	2.20	0.41
1:1A:2250:G:C8	1:1A:2496:C:H5"	2.56	0.41
1:1A:2492:U:H2'	1:1A:2493:U:C6	2.56	0.41
1:1A:2559:C:O2'	1:1A:2560:C:H5'	2.21	0.41
2:1B:91:C:P	12:1Q:16:ARG:HH21	2.44	0.41
7:1H:3:ARG:HE	7:1H:54:ARG:NH1	2.15	0.41
8:1I:94:ALA:HA	8:1I:97:ILE:HB	2.03	0.41
14:1S:94:TYR:CE2	14:1S:99:LYS:HG3	2.56	0.41
15:1T:39:ARG:NH1	15:1T:41:ARG:HB3	2.36	0.41
20:1Y:23:ARG:CZ	20:1Y:23:ARG:HB3	2.51	0.41
26:14:55:ARG:H	26:14:56:VAL:HA	1.86	0.41
32:1a:380:G:C2	32:1a:384:G:C6	3.09	0.41
32:1a:1235:U:H2'	32:1a:1236:A:O4'	2.21	0.41
32:1a:1519:MA6:H8	32:1a:1519:MA6:O5'	2.21	0.41
36:1e:51:VAL:O	36:1e:55:VAL:HG23	2.21	0.41
37:1f:4:TYR:CE2	37:1f:72:VAL:HG11	2.56	0.41
39:1h:8:ASP:O	39:1h:12:ARG:N	2.52	0.41
1:2A:1010:A:H1'	1:2A:1153:C:H1'	2.03	0.41
1:2A:1091:G:N3	1:2A:1091:G:H2'	2.36	0.41
1:2A:1364:G:N7	23:21:3:LYS:HD2	2.36	0.41
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.56	0.41
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.83	0.41
1:2A:2316:C:O2'	6:2G:128:ARG:NH1	2.52	0.41
1:2A:2341:G:H2'	1:2A:2342:C:O4'	2.21	0.41
1:2A:2477:C:N4	31:29:10:ILE:HG23	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:5:VAL:CG2	6:2G:8:LYS:H	2.34	0.41
11:2P:80:TYR:CD1	11:2P:111:ARG:HB2	2.56	0.41
12:2Q:43:THR:OG1	12:2Q:46:GLN:HG3	2.21	0.41
13:2R:28:LEU:HB2	13:2R:34:ILE:HD13	2.03	0.41
18:2W:20:VAL:HG11	18:2W:44:ALA:HA	2.03	0.41
27:25:53:ALA:O	27:25:55:ARG:HG2	2.21	0.41
31:29:9:ARG:HG2	31:29:14:CYS:HB2	2.03	0.41
32:2a:1165:C:H2'	32:2a:1166:G:O4'	2.20	0.41
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.35	0.41
33:2b:35:GLU:HG3	33:2b:39:ILE:O	2.21	0.41
34:2c:35:GLU:O	34:2c:39:ILE:HG13	2.21	0.41
35:2d:92:VAL:O	35:2d:96:LEU:HD13	2.21	0.41
40:2i:23:ASN:OD1	40:2i:23:ASN:N	2.48	0.41
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.86	0.41
44:2m:97:PRO:N	44:2m:110:ARG:HG2	2.36	0.41
52:2u:2:GLY:C	52:2u:4:GLY:H	2.28	0.41
1:1A:608:A:C4	1:1A:621:A:C6	3.09	0.40
1:1A:795:C:H2'	1:1A:796:C:H6	1.86	0.40
1:1A:1805:U:O2	3:1D:50:THR:HB	2.20	0.40
1:1A:1809:A:H2'	1:1A:1810:A:C8	2.56	0.40
1:1A:2238:G:N3	1:1A:2238:G:H2'	2.36	0.40
1:1A:2791:C:H5'	1:1A:2893:G:N2	2.37	0.40
6:1G:153:ARG:NH2	6:1G:153:ARG:HB2	2.36	0.40
9:1N:8:GLN:HE21	9:1N:8:GLN:HB3	1.57	0.40
18:1W:14:PRO:O	18:1W:17:VAL:HG23	2.21	0.40
32:1a:615:C:H2'	32:1a:616:G:O4'	2.21	0.40
32:1a:995:C:O2	45:1n:4:LYS:NZ	2.44	0.40
32:1a:1429:C:H2'	32:1a:1430:C:C6	2.56	0.40
33:1b:7:VAL:O	33:1b:217:ARG:NH2	2.54	0.40
35:1d:165:MET:HA	35:1d:168:ARG:HB2	2.03	0.40
38:1g:46:ALA:HB1	38:1g:121:ALA:HB2	2.03	0.40
39:1h:10:LEU:HD12	39:1h:85:ARG:HD2	2.03	0.40
45:1n:50:LYS:HE2	45:1n:50:LYS:HB3	1.72	0.40
1:2A:285:C:H2'	1:2A:286:C:C6	2.56	0.40
1:2A:373:U:O2'	1:2A:423:A:N3	2.47	0.40
1:2A:570:G:H2'	1:2A:2030:A:N7	2.36	0.40
1:2A:1638:C:H2'	1:2A:1639:U:O4'	2.22	0.40
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.80	0.40
1:2A:1913:A:H2	32:2a:1491:G:N2	2.19	0.40
1:2A:2390:U:O2'	1:2A:2391:G:H5'	2.21	0.40
1:2A:2660:A:N7	7:2H:175:LYS:NZ	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:2A:4065:HOH:O	30:28:32:LEU:HB2	2.21	0.40
3:2D:164:GLN:HB3	3:2D:176:ARG:HH12	1.86	0.40
5:2F:29:ASN:HB3	5:2F:112:MET:HE1	2.03	0.40
11:2P:13:ASN:OD1	63:2P:301:HOH:O	2.22	0.40
15:2T:33:LYS:HE2	15:2T:33:LYS:HB3	1.71	0.40
18:2W:45:TYR:CZ	18:2W:49:LYS:HE3	2.56	0.40
26:24:14:ILE:HG12	26:24:24:THR:HG21	2.03	0.40
32:2a:164:U:H2'	32:2a:165:C:H6	1.83	0.40
32:2a:180:U:H2'	32:2a:181:G:H5'	2.02	0.40
32:2a:474:G:H2'	32:2a:475:G:C8	2.55	0.40
32:2a:737:A:H5"	37:2f:92:LYS:HG3	2.03	0.40
32:2a:918:A:H2'	32:2a:919:A:C8	2.56	0.40
32:2a:1129:C:N4	32:2a:1143:G:N1	2.57	0.40
32:2a:1318:A:H5"	50:2s:3:ARG:HH22	1.86	0.40
32:2a:1357:A:OP2	63:2a:3216:HOH:O	2.21	0.40
32:2a:1426:C:H2'	32:2a:1427:U:H6	1.86	0.40
33:2b:27:LYS:HD3	33:2b:193:ASP:HB2	2.02	0.40
41:2j:38:ILE:HG23	41:2j:71:LEU:O	2.21	0.40
46:2o:10:LYS:HB2	46:2o:10:LYS:HE3	1.75	0.40
1:1A:143:G:H1'	19:1X:37:THR:HG21	2.01	0.40
1:1A:194:G:N3	63:1A:4460:HOH:O	2.37	0.40
1:1A:620:G:N3	1:1A:620:G:H5'	2.36	0.40
1:1A:644:A:H4'	1:1A:645:C:H5	1.86	0.40
1:1A:735:A:H3'	1:1A:736:C:C6	2.56	0.40
1:1A:857:C:N4	1:1A:858:U:O4	2.54	0.40
1:1A:900:A:H2'	1:1A:901:A:C8	2.55	0.40
1:1A:1257:C:H4'	5:1F:83:PHE:CE1	2.57	0.40
1:1A:1394:U:H2'	1:1A:1395:A:O4'	2.21	0.40
1:1A:1449:A:H2'	1:1A:1450:G:O4'	2.21	0.40
1:1A:1669:A:H5"	1:1A:2550:G:OP1	2.22	0.40
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.57	0.40
1:1A:1900:A:N1	1:1A:1970:A:C6	2.89	0.40
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.21	0.40
11:1P:86:LYS:HB3	11:1P:118:GLY:HA3	2.03	0.40
21:1Z:40:ASP:OD2	21:1Z:42:VAL:HG22	2.21	0.40
32:1a:255:G:H1'	48:1q:16:GLN:OE1	2.22	0.40
32:1a:370:C:H2'	32:1a:371:G:H8	1.86	0.40
32:1a:437:U:O3'	35:1d:125:HIS:CE1	2.74	0.40
32:1a:437:U:O3'	35:1d:125:HIS:HE1	2.04	0.40
32:1a:745:C:H2'	32:1a:746:A:C8	2.56	0.40
32:1a:865:A:H2'	32:1a:866:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1015:A:C6	32:1a:1016:A:C6	3.09	0.40
32:1a:1287:A:H2	32:1a:1353:G:N3	2.19	0.40
32:1a:1409:C:H2'	32:1a:1410:G:H8	1.86	0.40
37:1f:89:MET:HE2	37:1f:89:MET:HB2	1.85	0.40
37:1f:100:ASN:HB2	49:1r:27:GLY:O	2.22	0.40
40:1i:114:TYR:CE1	41:1j:59:SER:HA	2.56	0.40
1:2A:195:A:H2'	1:2A:198:C:N4	2.36	0.40
1:2A:205:G:O6	23:21:39:LYS:NZ	2.47	0.40
1:2A:852:G:H2'	1:2A:853:G:C8	2.56	0.40
1:2A:861:A:C2	1:2A:917:A:C4	3.09	0.40
1:2A:1385:G:H1'	1:2A:1386:C:C6	2.56	0.40
1:2A:1394:U:H2'	1:2A:1395:A:O4'	2.21	0.40
1:2A:1462:C:H2'	1:2A:1463:C:C6	2.56	0.40
1:2A:1937:A:N7	1:2A:1939:5MU:O2'	2.42	0.40
1:2A:2053:G:H5'	4:2E:144:ARG:O	2.21	0.40
1:2A:2492:U:H2'	1:2A:2493:U:C6	2.57	0.40
1:2A:2585:U:H1'	56:2v:1:MET:HE2	2.02	0.40
3:2D:26:LYS:HE2	3:2D:28:GLU:O	2.20	0.40
5:2F:155:LEU:HD23	5:2F:192:LEU:HD21	2.02	0.40
5:2F:164:ARG:HD2	5:2F:175:THR:HG23	2.04	0.40
11:2P:2:LYS:HE3	11:2P:2:LYS:HB2	1.92	0.40
27:25:48:GLU:O	27:25:60:VAL:HG11	2.21	0.40
32:2a:857:C:H2'	32:2a:858:G:O4'	2.20	0.40
32:2a:862:C:O4'	32:2a:874:G:H4'	2.22	0.40
32:2a:954:G:H2'	32:2a:955:U:O4'	2.21	0.40
34:2c:83:ARG:C	34:2c:85:ARG:H	2.27	0.40
35:2d:8:VAL:HG13	35:2d:21:LEU:HD12	2.03	0.40
35:2d:73:ARG:HA	35:2d:73:ARG:HD2	1.79	0.40
36:2e:80:ILE:HD12	39:2h:104:ARG:NH2	2.36	0.40
37:2f:32:ASN:C	37:2f:34:GLY:H	2.29	0.40
47:2p:37:GLY:HA3	47:2p:50:LYS:O	2.20	0.40
50:2s:14:HIS:CD2	50:2s:14:HIS:H	2.39	0.40
1:1A:247:G:H4'	1:1A:386:G:C6	2.57	0.40
1:1A:281:G:N2	1:1A:360:G:O6	2.54	0.40
1:1A:1676:A:H2'	1:1A:1677:A:O4'	2.22	0.40
1:1A:2138:C:H2'	1:1A:2139:C:C6	2.56	0.40
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.54	0.40
18:1W:85:VAL:HG13	18:1W:93:ALA:HB1	2.03	0.40
26:14:59:PHE:CE2	50:1s:42:PRO:HB3	2.54	0.40
32:1a:273:A:H1'	48:1q:16:GLN:NE2	2.36	0.40
34:1c:12:LEU:HD23	34:1c:12:LEU:HA	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:178:VAL:C	35:1d:180:GLY:H	2.30	0.40
48:1q:74:LEU:HD23	48:1q:75:ARG:HG2	2.03	0.40
1:2A:275:G:H2'	1:2A:276:A:H8	1.86	0.40
1:2A:784:A:C8	1:2A:792:G:C5	3.09	0.40
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.56	0.40
1:2A:1567:A:OP2	3:2D:84:TYR:OH	2.32	0.40
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	2.03	0.40
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.54	0.40
1:2A:2424:C:O2	1:2A:2429:G:O2'	2.25	0.40
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	2.03	0.40
4:2E:40:GLU:CD	4:2E:40:GLU:H	2.29	0.40
6:2G:47:LYS:CG	6:2G:48:GLU:H	2.34	0.40
6:2G:118:ARG:O	6:2G:181:ARG:HB2	2.20	0.40
6:2G:123:ASN:O	6:2G:125:PHE:N	2.51	0.40
7:2H:35:VAL:O	7:2H:37:VAL:HG23	2.21	0.40
8:2I:69:LYS:HD2	8:2I:138:ILE:HG12	2.03	0.40
14:2S:28:VAL:HG11	14:2S:98:VAL:HG13	2.02	0.40
18:2W:100:THR:N	63:2W:305:HOH:O	2.51	0.40
28:26:10:LEU:HG	28:26:54:ILE:HD12	2.04	0.40
32:2a:1030:C:N4	32:2a:1032:G:O6	2.54	0.40
32:2a:1357:A:N7	32:2a:1358:U:C4	2.89	0.40
32:2a:1381:U:H2'	32:2a:1382:C:H5'	2.02	0.40
32:2a:1466:C:H2'	32:2a:1467:G:O4'	2.21	0.40
38:2g:74:GLU:HG2	38:2g:91:VAL:HG22	2.02	0.40
1:1A:881:G:H2'	1:1A:882:G:O4'	2.21	0.40
1:1A:1826:G:OP1	3:1D:224:ALA:N	2.52	0.40
1:1A:2307:G:O4'	1:1A:2308:G:C5	2.74	0.40
1:1A:2663:G:C6	1:1A:2664:G:C4	3.09	0.40
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.56	0.40
8:1I:68:LEU:HD21	8:1I:109:ILE:HD11	2.03	0.40
19:1X:32:PRO:HA	19:1X:77:LYS:HB2	2.02	0.40
19:1X:89:ILE:O	19:1X:93:GLU:HG2	2.21	0.40
21:1Z:73:GLN:HB3	21:1Z:87:ASP:HB2	2.02	0.40
24:12:65:ASN:O	24:12:69:ARG:HG3	2.22	0.40
32:1a:229:U:O2'	47:1p:23:ASP:OD2	2.37	0.40
32:1a:735:C:H2'	32:1a:736:C:C6	2.57	0.40
32:1a:1069:C:H2'	32:1a:1070:U:O4'	2.21	0.40
32:1a:1390:U:H2'	32:1a:1391:U:C6	2.57	0.40
33:1b:55:PHE:HA	33:1b:58:ILE:HB	2.02	0.40
34:1c:69:HIS:CD2	34:1c:104:GLN:HB3	2.56	0.40
35:1d:173:TRP:CD1	35:1d:189:PRO:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:78:ARG:HD2	38:1g:156:TRP:HZ3	1.87	0.40
39:1h:21:LYS:N	39:1h:65:TYR:OH	2.55	0.40
42:1k:33:THR:HA	42:1k:39:PRO:HA	2.04	0.40
45:1n:26:ARG:HD3	45:1n:43:CYS:HB3	2.02	0.40
1:2A:335:C:H4'	20:2Y:73:ARG:NH1	2.37	0.40
1:2A:391:G:O2'	1:2A:410:G:OP1	2.35	0.40
1:2A:493:G:H2'	1:2A:494:G:O4'	2.21	0.40
1:2A:636:G:OP1	11:2P:132:LYS:HE2	2.21	0.40
1:2A:947:G:H5"	63:2A:3904:HOH:O	2.20	0.40
1:2A:1066:U:O2'	1:2A:1067:A:OP2	2.39	0.40
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.20	0.40
1:2A:2115:G:H22	1:2A:2119:A:P	2.43	0.40
1:2A:2504:U:C4	58:2A:3727:CLM:H42	2.56	0.40
1:2A:2804:C:H2'	1:2A:2805:G:O4'	2.22	0.40
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	2.03	0.40
5:2F:122:LYS:HG3	63:2F:402:HOH:O	2.21	0.40
6:2G:113:ARG:HD2	6:2G:140:ILE:HA	2.03	0.40
11:2P:5:ASP:HA	11:2P:7:ARG:NH2	2.35	0.40
16:2U:30:LYS:HD2	16:2U:30:LYS:N	2.36	0.40
18:2W:18:ARG:CG	18:2W:76:VAL:HB	2.51	0.40
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.30	0.40
32:2a:70:G:H2'	32:2a:71:C:C6	2.56	0.40
32:2a:430:A:H2'	32:2a:431:A:O4'	2.22	0.40
32:2a:474:G:H2'	32:2a:475:G:H8	1.85	0.40
32:2a:525:C:OP1	43:2l:91:LYS:HB2	2.21	0.40
32:2a:604:G:C6	32:2a:605:U:C4	3.10	0.40
32:2a:1054:C:O2	32:2a:1196:U:O2'	2.36	0.40
32:2a:1071:C:H5"	36:2e:49:PRO:HG3	2.02	0.40
32:2a:1362:C:H2'	32:2a:1363:C:H5"	2.03	0.40
33:2b:8:LYS:O	33:2b:9:GLU:HB2	2.22	0.40
33:2b:139:LYS:HZ3	33:2b:143:GLU:HB2	1.86	0.40
35:2d:59:ARG:HA	35:2d:59:ARG:NE	2.36	0.40
40:2i:78:LYS:HE2	40:2i:101:PHE:HE1	1.87	0.40
53:2y:3:MET:HB3	53:2y:37:PRO:HG2	2.04	0.40
1:1A:287:C:H2'	1:1A:288:C:H6	1.86	0.40
1:1A:448:U:C4	1:1A:583:G:H1'	2.56	0.40
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.56	0.40
1:1A:1254:A:N3	63:1A:4461:HOH:O	2.37	0.40
1:1A:1652:A:O2'	1:1A:1653:G:H5'	2.22	0.40
1:1A:1938:A:OP2	63:1A:4229:HOH:O	2.22	0.40
1:1A:2140:C:H2'	1:1A:2141:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2191:G:H5'	1:1A:2192:G:OP2	2.22	0.40
4:1E:37:ARG:O	4:1E:45:THR:HA	2.21	0.40
14:1S:78:LEU:HD11	14:1S:108:GLY:O	2.22	0.40
15:1T:53:ARG:HB3	15:1T:53:ARG:NH1	2.37	0.40
19:1X:11:PRO:HD3	24:12:37:PHE:CD1	2.57	0.40
19:1X:66:LEU:HA	19:1X:66:LEU:HD12	1.65	0.40
24:12:3:LEU:HD23	24:12:3:LEU:HA	1.80	0.40
26:14:35:VAL:HG22	26:14:36:CYS:H	1.87	0.40
32:1a:673:G:H5"	37:1f:87:ARG:NH1	2.36	0.40
33:1b:27:LYS:O	33:1b:30:ARG:NH1	2.55	0.40
35:1d:11:LEU:HD23	35:1d:66:ARG:HB3	2.02	0.40
37:1f:67:MET:HB2	37:1f:68:PRO:HD2	2.02	0.40
41:1j:26:ALA:HA	41:1j:29:ARG:NH1	2.36	0.40
49:1r:26:LEU:HB2	49:1r:29:PHE:CE2	2.57	0.40
52:1u:11:GLY:O	52:1u:15:ARG:HG3	2.22	0.40
1:2A:784:A:C5	3:2D:229:VAL:HG21	2.56	0.40
1:2A:984:A:H5"	1:2A:985:C:C5	2.56	0.40
1:2A:1065:U:H4'	1:2A:1066:U:OP1	2.20	0.40
1:2A:1312:U:OP2	19:2X:63:LYS:NZ	2.40	0.40
1:2A:2173:A:N3	1:2A:2173:A:H2'	2.37	0.40
1:2A:2842:G:H2'	1:2A:2843:G:O4'	2.22	0.40
5:2F:24:LEU:HD21	5:2F:114:VAL:HG12	2.03	0.40
7:2H:155:SER:HB3	7:2H:158:HIS:O	2.22	0.40
12:2Q:85:LYS:HG2	22:20:8:GLY:O	2.20	0.40
13:2R:83:ILE:O	13:2R:86:ARG:HG2	2.21	0.40
14:2S:36:TYR:OH	14:2S:54:LEU:HD22	2.21	0.40
18:2W:82:LEU:HD23	18:2W:82:LEU:HA	1.76	0.40
32:2a:19:C:H5"	36:2e:86:ALA:HB3	2.02	0.40
36:2e:57:LYS:O	36:2e:61:TYR:HD2	2.05	0.40
36:2e:89:ILE:HD12	36:2e:121:LYS:O	2.22	0.40
40:2i:33:PHE:C	40:2i:33:PHE:CD2	3.00	0.40
40:2i:111:ARG:O	40:2i:113:LYS:HD2	2.21	0.40
43:2l:83:VAL:HG21	43:2l:100:ILE:HD13	2.04	0.40
44:2m:20:THR:HA	44:2m:25:ILE:HG22	2.02	0.40
45:2n:16:PHE:C	45:2n:18:VAL:H	2.29	0.40
46:2o:32:LEU:HD22	46:2o:59:MET:HG2	2.04	0.40

All (7) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:368:U:N3	8:2I:82:ARG:NE[2_655]	1.69	0.51
32:1a:368:U:N1	8:2I:82:ARG:NE[2_655]	1.71	0.49
32:1a:368:U:C2	8:2I:82:ARG:NE[2_655]	1.72	0.48
32:1a:368:U:C6	8:2I:82:ARG:NE[2_655]	1.93	0.27
32:1a:368:U:C4	8:2I:82:ARG:NE[2_655]	1.94	0.26
32:1a:368:U:C5	8:2I:82:ARG:NE[2_655]	2.03	0.17
32:1a:368:U:N3	8:2I:82:ARG:CD[2_655]	2.19	0.01

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%)	255 (93%)	18 (7%)	0	100 100
4	1E	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	12 24
4	2E	202/206 (98%)	187 (93%)	14 (7%)	1 (0%)	24 43
5	1F	201/210 (96%)	193 (96%)	7 (4%)	1 (0%)	24 43
5	2F	201/210 (96%)	189 (94%)	9 (4%)	3 (2%)	8 16
6	1G	179/182 (98%)	157 (88%)	17 (10%)	5 (3%)	4 6
6	2G	179/182 (98%)	149 (83%)	24 (13%)	6 (3%)	3 4
7	1H	172/180 (96%)	160 (93%)	10 (6%)	2 (1%)	10 20
7	2H	171/180 (95%)	138 (81%)	31 (18%)	2 (1%)	10 20
8	1I	145/148 (98%)	126 (87%)	16 (11%)	3 (2%)	5 9
8	2I	144/148 (97%)	126 (88%)	13 (9%)	5 (4%)	3 4
9	1N	138/140 (99%)	136 (99%)	2 (1%)	0	100 100
9	2N	138/140 (99%)	126 (91%)	12 (9%)	0	100 100
10	1O	120/122 (98%)	112 (93%)	7 (6%)	1 (1%)	16 31
10	2O	120/122 (98%)	112 (93%)	8 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
11	1P	147/150 (98%)	136 (92%)	10 (7%)	1 (1%)	18 34
11	2P	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	18 34
12	1Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
12	2Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
13	1R	116/118 (98%)	112 (97%)	3 (3%)	1 (1%)	14 27
13	2R	116/118 (98%)	110 (95%)	6 (5%)	0	100 100
14	1S	108/112 (96%)	100 (93%)	6 (6%)	2 (2%)	6 11
14	2S	108/112 (96%)	100 (93%)	7 (6%)	1 (1%)	14 27
15	1T	129/146 (88%)	119 (92%)	10 (8%)	0	100 100
15	2T	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	16 31
16	1U	114/118 (97%)	112 (98%)	2 (2%)	0	100 100
16	2U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
17	1V	99/101 (98%)	93 (94%)	6 (6%)	0	100 100
17	2V	99/101 (98%)	90 (91%)	8 (8%)	1 (1%)	12 24
18	1W	110/113 (97%)	107 (97%)	3 (3%)	0	100 100
18	2W	110/113 (97%)	107 (97%)	3 (3%)	0	100 100
19	1X	93/96 (97%)	89 (96%)	2 (2%)	2 (2%)	5 9
19	2X	93/96 (97%)	91 (98%)	2 (2%)	0	100 100
20	1Y	105/110 (96%)	95 (90%)	10 (10%)	0	100 100
20	2Y	105/110 (96%)	96 (91%)	9 (9%)	0	100 100
21	1Z	201/206 (98%)	182 (90%)	18 (9%)	1 (0%)	24 43
21	2Z	199/206 (97%)	172 (86%)	26 (13%)	1 (0%)	24 43
22	10	81/85 (95%)	78 (96%)	3 (4%)	0	100 100
22	20	81/85 (95%)	73 (90%)	8 (10%)	0	100 100
23	11	95/98 (97%)	89 (94%)	6 (6%)	0	100 100
23	21	95/98 (97%)	89 (94%)	5 (5%)	1 (1%)	11 22
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%)	56 (98%)	1 (2%)	0	100 100
25	23	57/60 (95%)	53 (93%)	4 (7%)	0	100 100
26	14	67/71 (94%)	47 (70%)	17 (25%)	3 (4%)	2 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
26	24	67/71 (94%)	44 (66%)	14 (21%)	9 (13%)	0 0
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
27	25	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
28	26	51/54 (94%)	48 (94%)	3 (6%)	0	100 100
29	17	46/49 (94%)	45 (98%)	1 (2%)	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%)	33 (94%)	2 (6%)	0	100 100
33	1b	229/256 (90%)	189 (82%)	30 (13%)	10 (4%)	2 2
33	2b	229/256 (90%)	182 (80%)	37 (16%)	10 (4%)	2 2
34	1c	204/239 (85%)	180 (88%)	23 (11%)	1 (0%)	24 43
34	2c	204/239 (85%)	160 (78%)	37 (18%)	7 (3%)	3 4
35	1d	206/209 (99%)	185 (90%)	21 (10%)	0	100 100
35	2d	206/209 (99%)	184 (89%)	20 (10%)	2 (1%)	12 24
36	1e	146/162 (90%)	136 (93%)	8 (6%)	2 (1%)	9 17
36	2e	146/162 (90%)	134 (92%)	12 (8%)	0	100 100
37	1f	98/101 (97%)	94 (96%)	4 (4%)	0	100 100
37	2f	98/101 (97%)	90 (92%)	8 (8%)	0	100 100
38	1g	153/156 (98%)	143 (94%)	8 (5%)	2 (1%)	9 18
38	2g	153/156 (98%)	139 (91%)	12 (8%)	2 (1%)	9 18
39	1h	135/138 (98%)	126 (93%)	9 (7%)	0	100 100
39	2h	135/138 (98%)	124 (92%)	11 (8%)	0	100 100
40	1i	125/128 (98%)	111 (89%)	11 (9%)	3 (2%)	4 8
40	2i	124/128 (97%)	108 (87%)	12 (10%)	4 (3%)	3 4
41	1j	95/105 (90%)	80 (84%)	11 (12%)	4 (4%)	2 2
41	2j	94/105 (90%)	77 (82%)	15 (16%)	2 (2%)	5 9
42	1k	112/129 (87%)	102 (91%)	10 (9%)	0	100 100
42	2k	112/129 (87%)	101 (90%)	10 (9%)	1 (1%)	14 27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
43	1l	119/132 (90%)	109 (92%)	9 (8%)	1 (1%)	16 31
43	2l	119/132 (90%)	108 (91%)	10 (8%)	1 (1%)	16 31
44	1m	114/126 (90%)	100 (88%)	11 (10%)	3 (3%)	4 7
44	2m	112/126 (89%)	95 (85%)	12 (11%)	5 (4%)	2 2
45	1n	58/61 (95%)	52 (90%)	6 (10%)	0	100 100
45	2n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	7 13
46	1o	86/89 (97%)	79 (92%)	6 (7%)	1 (1%)	10 20
46	2o	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10 20
47	1p	80/88 (91%)	74 (92%)	6 (8%)	0	100 100
47	2p	80/88 (91%)	69 (86%)	11 (14%)	0	100 100
48	1q	97/105 (92%)	88 (91%)	9 (9%)	0	100 100
48	2q	97/105 (92%)	90 (93%)	6 (6%)	1 (1%)	12 24
49	1r	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	8 16
49	2r	66/88 (75%)	60 (91%)	6 (9%)	0	100 100
50	1s	81/93 (87%)	69 (85%)	12 (15%)	0	100 100
50	2s	81/93 (87%)	68 (84%)	13 (16%)	0	100 100
51	1t	94/106 (89%)	83 (88%)	9 (10%)	2 (2%)	5 9
51	2t	96/106 (91%)	82 (85%)	12 (12%)	2 (2%)	5 9
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%)	87 (93%)	5 (5%)	2 (2%)	5 9
56	1v	1/3 (33%)	1 (100%)	0	0	100 100
56	2v	1/3 (33%)	1 (100%)	0	0	100 100
All	All	11643/12360 (94%)	10591 (91%)	925 (8%)	127 (1%)	11 22

All (127) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1G	47	LYS
8	1I	86	THR
14	1S	59	LYS
19	1X	94	GLY
26	14	61	ARG

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Mol	Chain	Res	Type
33	1b	17	PHE
33	1b	127	ILE
33	1b	231	GLU
43	1l	91	LYS
44	1m	67	GLU
5	2F	130	ALA
26	24	46	GLN
26	24	51	ASP
33	2b	17	PHE
40	2i	43	ALA
40	2i	54	ASP
43	2l	91	LYS
6	1G	44	GLY
7	1H	126	PRO
7	1H	159	GLU
33	1b	125	PRO
34	1c	98	ASN
41	1j	55	LYS
51	1t	47	GLY
6	2G	81	LYS
8	2I	10	GLU
8	2I	97	ILE
8	2I	98	ALA
26	24	45	GLY
26	24	48	ARG
26	24	62	ARG
26	24	63	TYR
33	2b	9	GLU
34	2c	50	ALA
34	2c	145	GLY
35	2d	22	LYS
38	2g	6	ARG
42	2k	105	VAL
53	2y	45	PRO
4	1E	52	LEU
6	1G	51	ARG
8	1I	71	ILE
14	1S	94	TYR
26	14	39	CYS
33	1b	8	LYS
33	1b	21	ARG
33	1b	63	MET

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Mol	Chain	Res	Type
36	1e	38	GLN
38	1g	55	GLY
41	1j	77	PRO
6	2G	124	SER
7	2H	126	PRO
8	2I	83	ALA
26	24	55	ARG
33	2b	20	GLU
33	2b	95	GLN
34	2c	29	TYR
41	2j	78	ASN
41	2j	79	ARG
44	2m	21	TYR
44	2m	23	TYR
6	1G	49	ASP
8	1I	105	HIS
21	1Z	52	SER
26	14	48	ARG
33	1b	20	GLU
33	1b	124	SER
38	1g	130	GLY
40	1i	48	GLU
41	1j	78	ASN
51	1t	95	ALA
5	2F	21	ALA
6	2G	96	ARG
8	2I	117	GLU
14	2S	96	GLY
15	2T	128	GLU
17	2V	79	VAL
23	21	3	LYS
33	2b	121	LEU
33	2b	124	SER
33	2b	128	GLU
34	2c	104	GLN
35	2d	176	LEU
40	2i	33	PHE
40	2i	44	VAL
44	2m	6	GLY
46	2o	79	ARG
53	2y	46	GLN
4	1E	28	ALA

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Mol	Chain	Res	Type
36	1e	146	ALA
40	1i	109	VAL
4	2E	52	LEU
5	2F	146	ALA
6	2G	43	LEU
6	2G	126	ASP
11	2P	122	PRO
21	2Z	52	SER
26	24	49	PHE
34	2c	98	ASN
45	2n	38	GLY
51	2t	45	GLN
6	1G	50	ALA
10	1O	29	ASN
11	1P	29	LYS
13	1R	71	GLN
33	1b	22	LYS
40	1i	53	VAL
41	1j	91	PRO
44	1m	21	TYR
44	1m	106	ASN
34	2c	174	PRO
48	2q	27	PHE
19	1X	67	GLY
46	1o	23	GLY
7	2H	93	GLY
33	2b	125	PRO
38	2g	55	GLY
51	2t	100	ILE
49	1r	27	GLY
5	1F	16	GLY
6	2G	87	PRO
26	24	50	VAL
44	2m	24	GLY
44	2m	113	PRO
33	2b	15	VAL
33	2b	232	PRO
34	2c	99	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	1D	214/218 (98%)	200 (94%)	14 (6%)	15 32
3	2D	215/218 (99%)	191 (89%)	24 (11%)	6 12
4	1E	164/166 (99%)	155 (94%)	9 (6%)	19 40
4	2E	164/166 (99%)	148 (90%)	16 (10%)	7 16
5	1F	160/166 (96%)	148 (92%)	12 (8%)	12 26
5	2F	159/166 (96%)	140 (88%)	19 (12%)	5 11
6	1G	144/156 (92%)	125 (87%)	19 (13%)	4 8
6	2G	142/156 (91%)	119 (84%)	23 (16%)	2 4
7	1H	144/148 (97%)	135 (94%)	9 (6%)	16 34
7	2H	143/148 (97%)	124 (87%)	19 (13%)	4 8
8	1I	111/124 (90%)	88 (79%)	23 (21%)	1 2
8	2I	108/124 (87%)	87 (81%)	21 (19%)	1 2
9	1N	119/119 (100%)	106 (89%)	13 (11%)	6 13
9	2N	118/119 (99%)	104 (88%)	14 (12%)	5 11
10	1O	100/100 (100%)	94 (94%)	6 (6%)	17 36
10	2O	100/100 (100%)	95 (95%)	5 (5%)	22 44
11	1P	115/116 (99%)	112 (97%)	3 (3%)	40 68
11	2P	115/116 (99%)	105 (91%)	10 (9%)	9 21
12	1Q	111/111 (100%)	104 (94%)	7 (6%)	16 34
12	2Q	111/111 (100%)	103 (93%)	8 (7%)	13 28
13	1R	101/101 (100%)	93 (92%)	8 (8%)	11 24
13	2R	101/101 (100%)	90 (89%)	11 (11%)	6 13
14	1S	87/88 (99%)	79 (91%)	8 (9%)	8 19
14	2S	85/88 (97%)	69 (81%)	16 (19%)	1 3
15	1T	115/127 (91%)	108 (94%)	7 (6%)	17 35
15	2T	113/127 (89%)	106 (94%)	7 (6%)	16 34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
16	1U	93/94 (99%)	87 (94%)	6 (6%)	15 32
16	2U	93/94 (99%)	87 (94%)	6 (6%)	15 32
17	1V	81/82 (99%)	77 (95%)	4 (5%)	22 45
17	2V	80/82 (98%)	65 (81%)	15 (19%)	1 3
18	1W	90/92 (98%)	81 (90%)	9 (10%)	7 15
18	2W	90/92 (98%)	85 (94%)	5 (6%)	19 39
19	1X	77/78 (99%)	71 (92%)	6 (8%)	11 24
19	2X	77/78 (99%)	75 (97%)	2 (3%)	40 68
20	1Y	86/91 (94%)	79 (92%)	7 (8%)	11 23
20	2Y	86/91 (94%)	72 (84%)	14 (16%)	2 4
21	1Z	169/179 (94%)	151 (89%)	18 (11%)	6 13
21	2Z	165/179 (92%)	142 (86%)	23 (14%)	3 7
22	10	65/67 (97%)	63 (97%)	2 (3%)	35 62
22	20	64/67 (96%)	62 (97%)	2 (3%)	35 62
23	11	79/83 (95%)	75 (95%)	4 (5%)	21 43
23	21	81/83 (98%)	74 (91%)	7 (9%)	10 21
24	12	65/67 (97%)	60 (92%)	5 (8%)	12 25
24	22	66/67 (98%)	58 (88%)	8 (12%)	5 10
25	13	51/52 (98%)	45 (88%)	6 (12%)	5 11
25	23	50/52 (96%)	45 (90%)	5 (10%)	7 15
26	14	58/63 (92%)	51 (88%)	7 (12%)	5 10
26	24	54/63 (86%)	43 (80%)	11 (20%)	1 2
27	15	51/52 (98%)	47 (92%)	4 (8%)	11 24
27	25	50/52 (96%)	45 (90%)	5 (10%)	7 15
28	16	51/52 (98%)	44 (86%)	7 (14%)	3 7
28	26	50/52 (96%)	43 (86%)	7 (14%)	3 7
29	17	41/42 (98%)	37 (90%)	4 (10%)	7 16
29	27	41/42 (98%)	36 (88%)	5 (12%)	5 10
30	18	54/55 (98%)	50 (93%)	4 (7%)	13 27
30	28	54/55 (98%)	48 (89%)	6 (11%)	6 12
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
31	29	34/34 (100%)	32 (94%)	2 (6%)	18 37
33	1b	191/220 (87%)	164 (86%)	27 (14%)	3 7
33	2b	187/220 (85%)	157 (84%)	30 (16%)	2 5
34	1c	144/188 (77%)	132 (92%)	12 (8%)	10 22
34	2c	140/188 (74%)	117 (84%)	23 (16%)	2 4
35	1d	171/181 (94%)	147 (86%)	24 (14%)	3 7
35	2d	172/181 (95%)	150 (87%)	22 (13%)	4 9
36	1e	114/123 (93%)	104 (91%)	10 (9%)	9 20
36	2e	114/123 (93%)	103 (90%)	11 (10%)	8 17
37	1f	85/90 (94%)	72 (85%)	13 (15%)	3 5
37	2f	85/90 (94%)	77 (91%)	8 (9%)	8 18
38	1g	120/127 (94%)	110 (92%)	10 (8%)	10 22
38	2g	119/127 (94%)	102 (86%)	17 (14%)	3 6
39	1h	116/119 (98%)	102 (88%)	14 (12%)	5 10
39	2h	114/119 (96%)	99 (87%)	15 (13%)	4 8
40	1i	91/99 (92%)	78 (86%)	13 (14%)	3 6
40	2i	88/99 (89%)	77 (88%)	11 (12%)	4 9
41	1j	68/92 (74%)	60 (88%)	8 (12%)	5 11
41	2j	68/92 (74%)	59 (87%)	9 (13%)	4 8
42	1k	83/99 (84%)	75 (90%)	8 (10%)	8 17
42	2k	83/99 (84%)	73 (88%)	10 (12%)	5 10
43	1l	96/108 (89%)	87 (91%)	9 (9%)	8 18
43	2l	96/108 (89%)	84 (88%)	12 (12%)	4 9
44	1m	90/101 (89%)	82 (91%)	8 (9%)	9 20
44	2m	87/101 (86%)	72 (83%)	15 (17%)	2 4
45	1n	49/50 (98%)	43 (88%)	6 (12%)	5 10
45	2n	49/50 (98%)	42 (86%)	7 (14%)	3 6
46	1o	78/80 (98%)	71 (91%)	7 (9%)	9 19
46	2o	78/80 (98%)	71 (91%)	7 (9%)	9 19
47	1p	69/74 (93%)	56 (81%)	13 (19%)	1 3
47	2p	68/74 (92%)	58 (85%)	10 (15%)	3 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
48	1q	94/97 (97%)	84 (89%)	10 (11%)	6 14
48	2q	94/97 (97%)	90 (96%)	4 (4%)	26 51
49	1r	59/77 (77%)	50 (85%)	9 (15%)	3 5
49	2r	59/77 (77%)	53 (90%)	6 (10%)	7 15
50	1s	68/80 (85%)	61 (90%)	7 (10%)	7 14
50	2s	67/80 (84%)	61 (91%)	6 (9%)	9 19
51	1t	71/82 (87%)	64 (90%)	7 (10%)	7 16
51	2t	70/82 (85%)	65 (93%)	5 (7%)	13 29
52	1u	18/22 (82%)	17 (94%)	1 (6%)	19 39
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19 39
53	1y	82/98 (84%)	75 (92%)	7 (8%)	10 22
53	2y	79/98 (81%)	69 (87%)	10 (13%)	4 9
56	1v	3/3 (100%)	2 (67%)	1 (33%)	0 0
56	2v	3/3 (100%)	2 (67%)	1 (33%)	0 0
All	All	9537/10266 (93%)	8525 (89%)	1012 (11%)	6 14

All (1012) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	39	LYS
3	1D	94	LEU
3	1D	111	LEU
3	1D	112	GLN
3	1D	141	VAL
3	1D	168	ARG
3	1D	171	ASP
3	1D	193	VAL
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
3	1D	275	LYS
4	1E	7	VAL
4	1E	9	VAL
4	1E	87	GLU
4	1E	116	VAL

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Mol	Chain	Res	Type
4	1E	119	ARG
4	1E	181	LEU
4	1E	184	VAL
4	1E	188	VAL
4	1E	202	LYS
5	1F	18	ARG
5	1F	23	ASP
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	132	VAL
5	1F	137	LYS
5	1F	162	LEU
5	1F	183	VAL
5	1F	189	THR
5	1F	192	LEU
6	1G	5	VAL
6	1G	7	LEU
6	1G	20	ILE
6	1G	49	ASP
6	1G	53	LEU
6	1G	62	LEU
6	1G	75	LYS
6	1G	78	SER
6	1G	79	ASN
6	1G	82	LEU
6	1G	86	MET
6	1G	92	VAL
6	1G	109	VAL
6	1G	126	ASP
6	1G	133	LEU
6	1G	140	ILE
6	1G	144	ILE
6	1G	159	VAL
6	1G	175	LEU
7	1H	15	VAL
7	1H	24	VAL
7	1H	44	VAL
7	1H	49	VAL
7	1H	58	GLU
7	1H	62	LYS

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Mol	Chain	Res	Type
7	1H	107	VAL
7	1H	113	VAL
7	1H	124	GLU
8	1I	9	LEU
8	1I	14	ASP
8	1I	20	ASP
8	1I	38	LEU
8	1I	42	SER
8	1I	43	ASN
8	1I	44	LEU
8	1I	58	LEU
8	1I	60	GLU
8	1I	61	ARG
8	1I	66	GLU
8	1I	68	LEU
8	1I	78	THR
8	1I	87	LYS
8	1I	92	VAL
8	1I	96	ASP
8	1I	102	SER
8	1I	107	VAL
8	1I	108	THR
8	1I	109	ILE
8	1I	117	GLU
8	1I	127	VAL
8	1I	140	LEU
9	1N	1	MET
9	1N	5	VAL
9	1N	8	GLN
9	1N	14	VAL
9	1N	34	LEU
9	1N	48	MET
9	1N	62	VAL
9	1N	67	LEU
9	1N	71	ILE
9	1N	73	THR
9	1N	87	LEU
9	1N	99	LEU
9	1N	133	GLN
10	1O	9	GLU
10	1O	28	SER
10	1O	35	VAL

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Mol	Chain	Res	Type
10	1O	69	ILE
10	1O	96	THR
10	1O	113	LYS
11	1P	1	MET
11	1P	95	VAL
11	1P	125	VAL
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	81	VAL
12	1Q	97	VAL
12	1Q	109	VAL
12	1Q	112	GLU
12	1Q	130	LYS
13	1R	14	SER
13	1R	29	LEU
13	1R	36	THR
13	1R	56	LYS
13	1R	67	LEU
13	1R	100	LEU
13	1R	102	GLU
13	1R	114	VAL
14	1S	14	VAL
14	1S	46	VAL
14	1S	49	VAL
14	1S	50	SER
14	1S	52	SER
14	1S	59	LYS
14	1S	69	VAL
14	1S	83	LYS
15	1T	6	LEU
15	1T	28	VAL
15	1T	33	LYS
15	1T	53	ARG
15	1T	78	LEU
15	1T	112	ARG
15	1T	118	ARG
16	1U	8	VAL
16	1U	13	LYS
16	1U	31	SER
16	1U	74	LEU
16	1U	100	VAL
16	1U	104	GLN

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Mol	Chain	Res	Type
17	1V	51	VAL
17	1V	58	VAL
17	1V	72	VAL
17	1V	79	VAL
18	1W	6	ILE
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	68	ARG
18	1W	96	ILE
18	1W	100	THR
18	1W	107	LEU
19	1X	33	LYS
19	1X	35	THR
19	1X	38	GLU
19	1X	45	THR
19	1X	88	LYS
19	1X	95	LEU
20	1Y	14	LEU
20	1Y	23	ARG
20	1Y	28	LYS
20	1Y	31	LEU
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	107	ASP
21	1Z	18	LEU
21	1Z	19	ARG
21	1Z	31	ARG
21	1Z	37	VAL
21	1Z	41	LEU
21	1Z	50	GLN
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	98	MET
21	1Z	118	GLN
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	154	ASP
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	165	VAL

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Mol	Chain	Res	Type
21	1Z	170	THR
21	1Z	198	LYS
22	10	10	THR
22	10	74	ARG
23	11	30	VAL
23	11	35	THR
23	11	40	ARG
23	11	94	LEU
24	12	27	GLU
24	12	30	ARG
24	12	32	LEU
24	12	38	GLN
24	12	41	ILE
25	13	5	LYS
25	13	8	LEU
25	13	32	GLN
25	13	54	VAL
25	13	56	VAL
25	13	58	VAL
26	14	10	VAL
26	14	27	THR
26	14	33	VAL
26	14	49	PHE
26	14	50	VAL
26	14	56	VAL
26	14	60	GLN
27	15	6	VAL
27	15	16	ARG
27	15	37	LYS
27	15	40	LYS
28	16	5	VAL
28	16	6	ARG
28	16	9	LEU
28	16	19	ARG
28	16	47	THR
28	16	48	VAL
28	16	52	VAL
29	17	42	LEU
29	17	43	THR
29	17	46	VAL
29	17	47	ARG
30	18	14	VAL

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Mol	Chain	Res	Type
30	18	23	VAL
30	18	29	LYS
30	18	58	ILE
31	19	13	LYS
33	1b	8	LYS
33	1b	9	GLU
33	1b	10	LEU
33	1b	15	VAL
33	1b	23	ARG
33	1b	42	ILE
33	1b	47	THR
33	1b	51	LEU
33	1b	78	GLN
33	1b	90	MET
33	1b	93	VAL
33	1b	106	LYS
33	1b	112	VAL
33	1b	115	LEU
33	1b	119	GLU
33	1b	121	LEU
33	1b	127	ILE
33	1b	140	HIS
33	1b	145	LEU
33	1b	160	ASP
33	1b	162	ILE
33	1b	185	ILE
33	1b	187	LEU
33	1b	223	ILE
33	1b	224	GLN
33	1b	229	VAL
33	1b	230	VAL
34	1c	47	LEU
34	1c	54	ARG
34	1c	64	VAL
34	1c	70	VAL
34	1c	98	ASN
34	1c	105	GLU
34	1c	124	ILE
34	1c	144	SER
34	1c	152	ILE
34	1c	157	ILE
34	1c	175	LEU

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Mol	Chain	Res	Type
34	1c	182	ILE
35	1d	3	ARG
35	1d	5	ILE
35	1d	17	VAL
35	1d	18	LYS
35	1d	19	LEU
35	1d	26	CYS
35	1d	52	SER
35	1d	58	LEU
35	1d	59	ARG
35	1d	67	ILE
35	1d	77	ASN
35	1d	85	LYS
35	1d	128	VAL
35	1d	134	ASP
35	1d	137	SER
35	1d	140	VAL
35	1d	157	LEU
35	1d	158	ILE
35	1d	178	VAL
35	1d	182	LYS
35	1d	187	ARG
35	1d	188	LEU
35	1d	194	LEU
35	1d	196	LEU
36	1e	10	MET
36	1e	34	VAL
36	1e	41	VAL
36	1e	68	GLU
36	1e	69	VAL
36	1e	79	GLU
36	1e	115	VAL
36	1e	126	ARG
36	1e	131	ILE
36	1e	147	ASP
37	1f	10	LEU
37	1f	15	ASP
37	1f	16	GLN
37	1f	21	LEU
37	1f	40	VAL
37	1f	42	GLU
37	1f	45	LEU

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Mol	Chain	Res	Type
37	1f	57	GLN
37	1f	69	GLU
37	1f	72	VAL
37	1f	73	ASN
37	1f	89	MET
37	1f	91	VAL
38	1g	6	ARG
38	1g	13	GLN
38	1g	52	GLU
38	1g	56	GLN
38	1g	61	VAL
38	1g	76	ARG
38	1g	86	GLN
38	1g	97	GLN
38	1g	113	GLU
38	1g	144	MET
39	1h	22	GLU
39	1h	25	ASP
39	1h	26	VAL
39	1h	38	ILE
39	1h	39	LEU
39	1h	51	VAL
39	1h	52	ASP
39	1h	61	VAL
39	1h	63	LEU
39	1h	70	GLN
39	1h	98	LYS
39	1h	104	ARG
39	1h	127	LEU
39	1h	133	LEU
40	1i	14	VAL
40	1i	17	VAL
40	1i	25	LYS
40	1i	29	ASN
40	1i	47	LEU
40	1i	50	LEU
40	1i	53	VAL
40	1i	56	LEU
40	1i	81	ILE
40	1i	87	GLN
40	1i	92	TYR
40	1i	96	LEU

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Mol	Chain	Res	Type
40	1i	104	ARG
41	1j	29	ARG
41	1j	34	VAL
41	1j	38	ILE
41	1j	67	THR
41	1j	72	VAL
41	1j	81	THR
41	1j	84	GLN
41	1j	94	VAL
42	1k	16	SER
42	1k	31	THR
42	1k	41	THR
42	1k	77	MET
42	1k	93	GLN
42	1k	103	LEU
42	1k	109	VAL
42	1k	122	LYS
43	1l	18	VAL
43	1l	22	SER
43	1l	33	ARG
43	1l	36	VAL
43	1l	42	THR
43	1l	44	THR
43	1l	58	VAL
43	1l	83	VAL
43	1l	97	ARG
44	1m	3	ARG
44	1m	4	ILE
44	1m	8	GLU
44	1m	9	ILE
44	1m	11	ARG
44	1m	93	ARG
44	1m	98	VAL
44	1m	99	ARG
45	1n	13	THR
45	1n	16	PHE
45	1n	18	VAL
45	1n	22	THR
45	1n	29	ARG
45	1n	33	VAL
46	1o	3	ILE
46	1o	4	THR

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Mol	Chain	Res	Type
46	1o	25	THR
46	1o	39	LEU
46	1o	45	VAL
46	1o	76	GLU
46	1o	84	LYS
47	1p	6	LEU
47	1p	8	ARG
47	1p	20	VAL
47	1p	21	VAL
47	1p	29	ASP
47	1p	33	ILE
47	1p	35	LYS
47	1p	42	ARG
47	1p	43	LYS
47	1p	47	ASP
47	1p	53	VAL
47	1p	62	VAL
47	1p	67	THR
48	1q	6	LEU
48	1q	9	VAL
48	1q	22	LEU
48	1q	35	VAL
48	1q	50	LYS
48	1q	52	LYS
48	1q	53	LEU
48	1q	61	GLU
48	1q	85	VAL
48	1q	93	GLN
49	1r	23	LYS
49	1r	25	THR
49	1r	26	LEU
49	1r	31	LEU
49	1r	37	VAL
49	1r	42	ARG
49	1r	46	GLU
49	1r	59	SER
49	1r	76	LEU
50	1s	7	LYS
50	1s	28	LYS
50	1s	40	ILE
50	1s	48	THR
50	1s	51	VAL

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Mol	Chain	Res	Type
50	1s	63	THR
50	1s	66	MET
51	1t	9	ASN
51	1t	10	LEU
51	1t	24	LEU
51	1t	34	LYS
51	1t	37	SER
51	1t	46	GLU
51	1t	100	ILE
52	1u	3	LYS
53	1y	6	THR
53	1y	23	ARG
53	1y	42	SER
53	1y	46	GLN
53	1y	60	VAL
53	1y	61	LEU
53	1y	91	LYS
56	1v	2	THR
3	2D	3	VAL
3	2D	18	VAL
3	2D	27	THR
3	2D	34	VAL
3	2D	38	LYS
3	2D	61	LEU
3	2D	71	ASP
3	2D	75	ILE
3	2D	78	LYS
3	2D	94	LEU
3	2D	103	ARG
3	2D	113	VAL
3	2D	134	ARG
3	2D	141	VAL
3	2D	155	LEU
3	2D	173	VAL
3	2D	183	ARG
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	274	ARG
3	2D	276	LYS

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Mol	Chain	Res	Type
4	2E	9	VAL
4	2E	27	LEU
4	2E	38	THR
4	2E	73	GLU
4	2E	90	THR
4	2E	97	LYS
4	2E	104	VAL
4	2E	116	VAL
4	2E	119	ARG
4	2E	134	ILE
4	2E	152	LYS
4	2E	154	LYS
4	2E	163	GLU
4	2E	181	LEU
4	2E	184	VAL
4	2E	188	VAL
5	2F	15	SER
5	2F	27	GLU
5	2F	33	LEU
5	2F	57	VAL
5	2F	74	ARG
5	2F	88	VAL
5	2F	132	VAL
5	2F	140	LEU
5	2F	157	VAL
5	2F	158	THR
5	2F	162	LEU
5	2F	165	ARG
5	2F	170	LEU
5	2F	175	THR
5	2F	179	GLU
5	2F	192	LEU
5	2F	197	ASP
5	2F	201	VAL
5	2F	206	ILE
6	2G	3	LEU
6	2G	5	VAL
6	2G	7	LEU
6	2G	20	ILE
6	2G	28	VAL
6	2G	43	LEU
6	2G	51	ARG

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Mol	Chain	Res	Type
6	2G	53	LEU
6	2G	58	GLN
6	2G	62	LEU
6	2G	78	SER
6	2G	86	MET
6	2G	88	ILE
6	2G	91	ARG
6	2G	92	VAL
6	2G	103	LEU
6	2G	115	ARG
6	2G	126	ASP
6	2G	133	LEU
6	2G	143	GLU
6	2G	152	LEU
6	2G	159	VAL
6	2G	172	LEU
7	2H	13	LYS
7	2H	26	VAL
7	2H	32	GLU
7	2H	33	LEU
7	2H	38	SER
7	2H	43	VAL
7	2H	44	VAL
7	2H	52	VAL
7	2H	53	GLU
7	2H	68	THR
7	2H	71	LEU
7	2H	92	ILE
7	2H	105	LEU
7	2H	106	THR
7	2H	114	VAL
7	2H	122	THR
7	2H	124	GLU
7	2H	130	ARG
7	2H	131	VAL
8	2I	7	GLU
8	2I	21	VAL
8	2I	37	VAL
8	2I	38	LEU
8	2I	47	LEU
8	2I	54	GLN
8	2I	57	ARG

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Mol	Chain	Res	Type
8	2I	58	LEU
8	2I	64	GLU
8	2I	68	LEU
8	2I	70	GLU
8	2I	74	ASN
8	2I	76	THR
8	2I	82	ARG
8	2I	92	VAL
8	2I	107	VAL
8	2I	125	GLU
8	2I	127	VAL
8	2I	129	THR
8	2I	140	LEU
8	2I	142	VAL
9	2N	9	VAL
9	2N	12	ARG
9	2N	15	LEU
9	2N	28	THR
9	2N	33	LEU
9	2N	48	MET
9	2N	67	LEU
9	2N	71	ILE
9	2N	73	THR
9	2N	74	ARG
9	2N	83	LYS
9	2N	87	LEU
9	2N	99	LEU
9	2N	140	VAL
10	2O	9	GLU
10	2O	35	VAL
10	2O	69	ILE
10	2O	70	LYS
10	2O	78	ARG
11	2P	3	LEU
11	2P	15	ARG
11	2P	29	LYS
11	2P	35	HIS
11	2P	95	VAL
11	2P	96	THR
11	2P	101	VAL
11	2P	125	VAL
11	2P	147	LEU

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Mol	Chain	Res	Type
11	2P	149	GLU
12	2Q	1	MET
12	2Q	7	MET
12	2Q	22	LYS
12	2Q	35	VAL
12	2Q	75	THR
12	2Q	85	LYS
12	2Q	109	VAL
12	2Q	124	LYS
13	2R	20	LEU
13	2R	29	LEU
13	2R	33	ARG
13	2R	36	THR
13	2R	67	LEU
13	2R	75	LEU
13	2R	86	ARG
13	2R	96	ARG
13	2R	100	LEU
13	2R	102	GLU
13	2R	114	VAL
14	2S	8	GLU
14	2S	12	PHE
14	2S	13	ARG
14	2S	44	LYS
14	2S	50	SER
14	2S	52	SER
14	2S	53	SER
14	2S	56	LEU
14	2S	64	GLU
14	2S	73	LEU
14	2S	78	LEU
14	2S	80	LEU
14	2S	85	VAL
14	2S	98	VAL
14	2S	110	LEU
14	2S	111	GLU
15	2T	15	VAL
15	2T	28	VAL
15	2T	36	GLU
15	2T	42	ILE
15	2T	53	ARG
15	2T	67	SER

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Mol	Chain	Res	Type
15	2T	89	VAL
16	2U	5	LYS
16	2U	55	ARG
16	2U	59	ARG
16	2U	74	LEU
16	2U	100	VAL
16	2U	104	GLN
17	2V	1	MET
17	2V	5	VAL
17	2V	26	ASP
17	2V	32	THR
17	2V	35	LEU
17	2V	38	LEU
17	2V	39	LEU
17	2V	46	VAL
17	2V	51	VAL
17	2V	53	GLU
17	2V	62	LEU
17	2V	71	LEU
17	2V	79	VAL
17	2V	92	THR
17	2V	96	ILE
18	2W	11	ARG
18	2W	17	VAL
18	2W	23	LEU
18	2W	100	THR
18	2W	107	LEU
19	2X	81	VAL
19	2X	95	LEU
20	2Y	3	VAL
20	2Y	13	VAL
20	2Y	30	VAL
20	2Y	42	VAL
20	2Y	44	ILE
20	2Y	62	GLU
20	2Y	64	GLU
20	2Y	72	VAL
20	2Y	75	ILE
20	2Y	90	LEU
20	2Y	92	ASN
20	2Y	96	ILE
20	2Y	99	CYS

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Mol	Chain	Res	Type
20	2Y	101	LYS
21	2Z	2	GLU
21	2Z	31	ARG
21	2Z	41	LEU
21	2Z	53	ILE
21	2Z	67	LEU
21	2Z	71	VAL
21	2Z	72	ARG
21	2Z	73	GLN
21	2Z	78	LYS
21	2Z	86	VAL
21	2Z	100	VAL
21	2Z	107	THR
21	2Z	121	HIS
21	2Z	126	VAL
21	2Z	135	GLU
21	2Z	144	LEU
21	2Z	163	LEU
21	2Z	171	ILE
21	2Z	175	VAL
21	2Z	182	LYS
21	2Z	191	VAL
21	2Z	193	GLU
21	2Z	198	LYS
22	20	36	ILE
22	20	66	VAL
23	21	4	VAL
23	21	21	ARG
23	21	40	ARG
23	21	46	LEU
23	21	51	VAL
23	21	85	LEU
23	21	95	LEU
24	22	15	LYS
24	22	17	SER
24	22	31	GLU
24	22	32	LEU
24	22	45	SER
24	22	53	LEU
24	22	62	THR
24	22	64	LEU
25	23	31	LEU

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Mol	Chain	Res	Type
25	23	43	ILE
25	23	54	VAL
25	23	57	GLU
25	23	58	VAL
26	24	8	LYS
26	24	9	LEU
26	24	15	ILE
26	24	20	ASN
26	24	21	VAL
26	24	27	THR
26	24	40	HIS
26	24	50	VAL
26	24	52	THR
26	24	53	GLU
26	24	61	ARG
27	25	6	VAL
27	25	29	THR
27	25	30	LEU
27	25	40	LYS
27	25	55	ARG
28	26	14	THR
28	26	20	ASN
28	26	30	THR
28	26	34	LEU
28	26	48	VAL
28	26	50	ARG
28	26	54	ILE
29	27	41	ARG
29	27	43	THR
29	27	46	VAL
29	27	47	ARG
29	27	48	LYS
30	28	14	VAL
30	28	23	VAL
30	28	26	LYS
30	28	46	ARG
30	28	49	VAL
30	28	50	LEU
31	29	4	ARG
31	29	17	ILE
33	2b	7	VAL
33	2b	8	LYS

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Mol	Chain	Res	Type
33	2b	9	GLU
33	2b	15	VAL
33	2b	16	HIS
33	2b	17	PHE
33	2b	39	ILE
33	2b	42	ILE
33	2b	44	LEU
33	2b	63	MET
33	2b	68	ILE
33	2b	69	LEU
33	2b	74	LYS
33	2b	76	GLN
33	2b	83	MET
33	2b	96	ARG
33	2b	97	TRP
33	2b	111	ARG
33	2b	126	GLU
33	2b	127	ILE
33	2b	128	GLU
33	2b	130	ARG
33	2b	154	LEU
33	2b	157	ARG
33	2b	175	ARG
33	2b	189	ASP
33	2b	191	ASP
33	2b	196	LEU
33	2b	215	LEU
33	2b	230	VAL
34	2c	3	ASN
34	2c	15	THR
34	2c	32	LEU
34	2c	33	LEU
34	2c	52	LEU
34	2c	56	ASP
34	2c	66	VAL
34	2c	98	ASN
34	2c	105	GLU
34	2c	111	LEU
34	2c	124	ILE
34	2c	128	PHE
34	2c	130	VAL
34	2c	131	ARG

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Mol	Chain	Res	Type
34	2c	136	GLN
34	2c	152	ILE
34	2c	154	SER
34	2c	164	ARG
34	2c	170	GLN
34	2c	181	ASN
34	2c	195	VAL
34	2c	206	GLU
34	2c	207	VAL
35	2d	8	VAL
35	2d	13	ARG
35	2d	18	LYS
35	2d	19	LEU
35	2d	30	LYS
35	2d	33	MET
35	2d	49	ARG
35	2d	50	ARG
35	2d	76	ARG
35	2d	83	SER
35	2d	106	TYR
35	2d	108	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	141	ARG
35	2d	150	GLU
35	2d	160	GLN
35	2d	170	VAL
35	2d	175	SER
35	2d	187	ARG
35	2d	194	LEU
35	2d	202	LEU
36	2e	10	MET
36	2e	11	ILE
36	2e	34	VAL
36	2e	41	VAL
36	2e	47	LYS
36	2e	68	GLU
36	2e	69	VAL
36	2e	79	GLU
36	2e	81	GLU
36	2e	115	VAL
36	2e	143	ARG

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Mol	Chain	Res	Type
37	2f	22	GLU
37	2f	40	VAL
37	2f	41	GLU
37	2f	57	GLN
37	2f	63	TYR
37	2f	72	VAL
37	2f	93	SER
37	2f	95	GLU
38	2g	6	ARG
38	2g	9	VAL
38	2g	15	ASP
38	2g	16	LEU
38	2g	21	VAL
38	2g	24	THR
38	2g	27	ILE
38	2g	33	ASP
38	2g	47	CYS
38	2g	51	GLN
38	2g	75	VAL
38	2g	92	SER
38	2g	104	LEU
38	2g	115	ARG
38	2g	123	GLU
38	2g	135	VAL
38	2g	153	HIS
39	2h	2	LEU
39	2h	3	THR
39	2h	15	ASN
39	2h	21	LYS
39	2h	29	SER
39	2h	45	ILE
39	2h	49	GLU
39	2h	83	ILE
39	2h	85	ARG
39	2h	91	ARG
39	2h	112	LEU
39	2h	114	THR
39	2h	119	LEU
39	2h	125	ARG
39	2h	133	LEU
40	2i	14	VAL
40	2i	34	ASN

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Mol	Chain	Res	Type
40	2i	41	VAL
40	2i	42	ARG
40	2i	54	ASP
40	2i	63	ILE
40	2i	65	VAL
40	2i	81	ILE
40	2i	102	LEU
40	2i	108	VAL
40	2i	113	LYS
41	2j	34	VAL
41	2j	38	ILE
41	2j	49	VAL
41	2j	71	LEU
41	2j	72	VAL
41	2j	73	ASP
41	2j	84	GLN
41	2j	85	LEU
41	2j	95	GLU
42	2k	28	THR
42	2k	53	SER
42	2k	83	ILE
42	2k	84	VAL
42	2k	93	GLN
42	2k	109	VAL
42	2k	112	THR
42	2k	114	VAL
42	2k	116	HIS
42	2k	117	ASN
43	2l	6	THR
43	2l	28	LYS
43	2l	33	ARG
43	2l	36	VAL
43	2l	43	VAL
43	2l	55	VAL
43	2l	58	VAL
43	2l	62	SER
43	2l	67	THR
43	2l	79	GLU
43	2l	83	VAL
43	2l	89	ARG
44	2m	4	ILE
44	2m	8	GLU

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Mol	Chain	Res	Type
44	2m	13	LYS
44	2m	15	VAL
44	2m	25	ILE
44	2m	48	LEU
44	2m	49	THR
44	2m	50	GLU
44	2m	60	VAL
44	2m	62	ASN
44	2m	93	ARG
44	2m	96	LEU
44	2m	98	VAL
44	2m	102	ARG
44	2m	115	LYS
45	2n	3	ARG
45	2n	7	ILE
45	2n	16	PHE
45	2n	18	VAL
45	2n	22	THR
45	2n	33	VAL
45	2n	39	LEU
46	2o	3	ILE
46	2o	4	THR
46	2o	5	LYS
46	2o	24	SER
46	2o	39	LEU
46	2o	84	LYS
46	2o	87	ILE
47	2p	2	VAL
47	2p	11	SER
47	2p	16	HIS
47	2p	19	ILE
47	2p	20	VAL
47	2p	21	VAL
47	2p	45	THR
47	2p	55	ARG
47	2p	67	THR
47	2p	69	THR
48	2q	6	LEU
48	2q	39	SER
48	2q	52	LYS
48	2q	57	VAL
49	2r	29	PHE

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Mol	Chain	Res	Type
49	2r	31	LEU
49	2r	37	VAL
49	2r	47	THR
49	2r	82	THR
49	2r	84	LYS
50	2s	32	LYS
50	2s	37	ARG
50	2s	41	VAL
50	2s	63	THR
50	2s	69	HIS
50	2s	81	ARG
51	2t	15	ARG
51	2t	55	ILE
51	2t	72	LEU
51	2t	84	LEU
51	2t	100	ILE
52	2u	13	ILE
53	2y	6	THR
53	2y	16	ILE
53	2y	24	LEU
53	2y	29	LYS
53	2y	32	THR
53	2y	41	LEU
53	2y	46	GLN
53	2y	56	THR
53	2y	62	VAL
53	2y	78	ILE
56	2v	2	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (153) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	166	GLN
3	1D	253	GLN
4	1E	48	GLN
5	1F	69	HIS
6	1G	132	ASN
8	1I	43	ASN
9	1N	8	GLN
9	1N	69	GLN
9	1N	94	HIS

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Mol	Chain	Res	Type
9	1N	133	GLN
10	1O	88	ASN
11	1P	84	ASN
13	1R	71	GLN
14	1S	84	GLN
15	1T	58	ASN
15	1T	123	GLN
16	1U	94	ASN
19	1X	31	HIS
20	1Y	6	HIS
20	1Y	43	ASN
21	1Z	32	HIS
21	1Z	50	GLN
21	1Z	151	HIS
22	10	29	GLN
23	11	56	GLN
24	12	65	ASN
25	13	32	GLN
27	15	4	HIS
33	1b	212	GLN
33	1b	224	GLN
34	1c	6	HIS
34	1c	102	ASN
34	1c	104	GLN
34	1c	110	ASN
34	1c	170	GLN
34	1c	181	ASN
35	1d	77	ASN
35	1d	201	GLN
36	1e	65	ASN
36	1e	78	HIS
37	1f	7	ASN
37	1f	57	GLN
37	1f	84	ASN
38	1g	13	GLN
38	1g	28	ASN
38	1g	37	ASN
38	1g	64	GLN
38	1g	86	GLN
38	1g	96	GLN
40	1i	3	GLN
40	1i	31	GLN

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Mol	Chain	Res	Type
40	1i	73	GLN
40	1i	87	GLN
40	1i	124	GLN
41	1j	13	HIS
41	1j	56	HIS
42	1k	93	GLN
42	1k	117	ASN
43	1l	99	HIS
44	1m	92	HIS
44	1m	106	ASN
46	1o	13	GLN
47	1p	16	HIS
48	1q	16	GLN
50	1s	69	HIS
50	1s	83	HIS
51	1t	18	GLN
51	1t	73	HIS
51	1t	75	ASN
53	1y	38	HIS
53	1y	84	GLN
53	1y	89	GLN
3	2D	87	ASN
3	2D	126	GLN
3	2D	143	HIS
3	2D	253	GLN
4	2E	48	GLN
4	2E	143	ASN
5	2F	204	ASN
6	2G	26	GLN
6	2G	58	GLN
6	2G	79	ASN
7	2H	143	GLN
8	2I	43	ASN
8	2I	105	HIS
8	2I	133	HIS
9	2N	130	HIS
12	2Q	123	HIS
15	2T	38	ASN
15	2T	58	ASN
15	2T	84	GLN
15	2T	123	GLN
16	2U	94	ASN

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Mol	Chain	Res	Type
16	2U	104	GLN
17	2V	64	HIS
19	2X	31	HIS
19	2X	82	GLN
24	22	9	GLN
24	22	56	GLN
26	24	60	GLN
30	28	35	GLN
33	2b	19	HIS
33	2b	25	ASN
33	2b	135	GLN
33	2b	140	HIS
33	2b	212	GLN
33	2b	224	GLN
34	2c	28	GLN
34	2c	139	GLN
34	2c	162	GLN
34	2c	176	HIS
34	2c	181	ASN
35	2d	42	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	123	HIS
35	2d	160	GLN
35	2d	161	ASN
35	2d	201	GLN
36	2e	65	ASN
36	2e	130	ASN
36	2e	141	GLN
37	2f	100	ASN
38	2g	11	GLN
38	2g	13	GLN
38	2g	28	ASN
38	2g	56	GLN
38	2g	64	GLN
39	2h	81	HIS
40	2i	58	HIS
41	2j	62	HIS
41	2j	69	ASN
41	2j	84	GLN
42	2k	38	ASN
42	2k	62	GLN

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Mol	Chain	Res	Type
42	2k	93	GLN
42	2k	116	HIS
42	2k	117	ASN
43	2l	80	HIS
43	2l	99	HIS
44	2m	77	ASN
44	2m	106	ASN
46	2o	9	GLN
46	2o	13	GLN
46	2o	37	ASN
50	2s	14	HIS
50	2s	23	ASN
51	2t	90	GLN
53	2y	38	HIS
53	2y	46	GLN
53	2y	55	ASN
53	2y	84	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	428 (14%)	28 (0%)
1	2A	2858/2915 (98%)	497 (17%)	35 (1%)
2	1B	119/121 (98%)	9 (7%)	0
2	2B	119/121 (98%)	16 (13%)	0
32	1a	1497/1521 (98%)	266 (17%)	0
32	2a	1501/1521 (98%)	290 (19%)	0
54	1w	2/5 (40%)	0	0
54	2w	2/5 (40%)	0	0
55	1x	1/4 (25%)	0	0
55	2x	1/4 (25%)	0	0
All	All	8965/9132 (98%)	1506 (16%)	63 (0%)

All (1506) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	15	G
1	1A	34	C
1	1A	45	C
1	1A	50	U
1	1A	71	A

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Mol	Chain	Res	Type
1	1A	74	A
1	1A	75	G
1	1A	92	A
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	154(A)	C
1	1A	181	A
1	1A	196	A
1	1A	197	A
1	1A	199	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	219	G
1	1A	222	A
1	1A	229	A
1	1A	248	G
1	1A	271(I)	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	271(O)	C
1	1A	271(S)	G
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	272(H)	C
1	1A	275	G
1	1A	279	C
1	1A	280	C
1	1A	283	A
1	1A	311	A
1	1A	330	A
1	1A	346	A
1	1A	352	G
1	1A	363	G
1	1A	363(B)	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G

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Mol	Chain	Res	Type
1	1A	412	A
1	1A	428	A
1	1A	447	A
1	1A	451	C
1	1A	454	A
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	505	A
1	1A	508	G
1	1A	509	C
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	592	G
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	615	G
1	1A	616	G
1	1A	621	A
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(E)	G
1	1A	652(U)	G
1	1A	668	G
1	1A	669	G
1	1A	686	G
1	1A	730	C
1	1A	731	C
1	1A	746	A
1	1A	747	U
1	1A	775	G
1	1A	776	G

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Mol	Chain	Res	Type
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	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	884	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	899	A
1	1A	900	A
1	1A	907	U
1	1A	910	A
1	1A	915	C
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1026	U
1	1A	1033	U
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1058	G
1	1A	1061	U

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Mol	Chain	Res	Type
1	1A	1062	G
1	1A	1063	G
1	1A	1065	U
1	1A	1066	U
1	1A	1067	A
1	1A	1070	A
1	1A	1072	C
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1077	A
1	1A	1079	C
1	1A	1080	C
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	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	1128	A
1	1A	1130	U
1	1A	1135	C
1	1A	1136	G
1	1A	1141	U
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	1218	C

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Mol	Chain	Res	Type
1	1A	1220	A
1	1A	1250	G
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1345	C
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1437	C
1	1A	1445	A
1	1A	1450	G
1	1A	1451	C
1	1A	1455	G
1	1A	1459	G
1	1A	1460	A
1	1A	1467	C
1	1A	1471	A
1	1A	1473	G
1	1A	1478	G
1	1A	1482	G
1	1A	1484	G
1	1A	1490	A
1	1A	1493	C
1	1A	1505	C
1	1A	1508	A
1	1A	1509	C

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Mol	Chain	Res	Type
1	1A	1509(A)	A
1	1A	1523	U
1	1A	1525	G
1	1A	1529	G
1	1A	1531	C
1	1A	1542	A
1	1A	1543	C
1	1A	1558	A
1	1A	1569	A
1	1A	1578	U
1	1A	1579	A
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1616	A
1	1A	1634	A
1	1A	1639	U
1	1A	1648	C
1	1A	1654	A
1	1A	1664	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1717	G
1	1A	1722	A
1	1A	1739	U
1	1A	1740	G
1	1A	1756	G
1	1A	1757	U
1	1A	1758	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	1791	A

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Mol	Chain	Res	Type
1	1A	1800	C
1	1A	1801	G
1	1A	1812	A
1	1A	1816	G
1	1A	1839	G
1	1A	1847	A
1	1A	1877	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1914	C
1	1A	1919	A
1	1A	1929	G
1	1A	1930	G
1	1A	1936	A
1	1A	1938	A
1	1A	1941	C
1	1A	1955	U
1	1A	1963	U
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1985	G
1	1A	1993	U
1	1A	1997	G
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2093	G
1	1A	2103	C
1	1A	2107	C

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Mol	Chain	Res	Type
1	1A	2108	C
1	1A	2110	G
1	1A	2111	C
1	1A	2112	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2126	A
1	1A	2127	G
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2137	C
1	1A	2146	C
1	1A	2148	G
1	1A	2158	A
1	1A	2159	G
1	1A	2164	C
1	1A	2171	A
1	1A	2172	U
1	1A	2181	G
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	2267	A
1	1A	2268	A
1	1A	2269	A
1	1A	2273	A
1	1A	2278	A
1	1A	2280	G
1	1A	2283	C

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Mol	Chain	Res	Type
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2307	G
1	1A	2308	G
1	1A	2318	G
1	1A	2320	A
1	1A	2321	G
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2361	A
1	1A	2383	G
1	1A	2385	C
1	1A	2393	A
1	1A	2406	U
1	1A	2422	A
1	1A	2423	U
1	1A	2424	C
1	1A	2425	A
1	1A	2428	G
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2434	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2476	A
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2520	C
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G

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Mol	Chain	Res	Type
1	1A	2573	C
1	1A	2574	G
1	1A	2585	U
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	2641	G
1	1A	2654	A
1	1A	2662	A
1	1A	2689	U
1	1A	2690	C
1	1A	2691	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2744	G
1	1A	2758	A
1	1A	2764	A
1	1A	2765	A
1	1A	2766	G
1	1A	2769	C
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2794	C
1	1A	2802	G
1	1A	2805	G
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2869	G
1	1A	2872	G
1	1A	2892	A

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Mol	Chain	Res	Type
1	1A	2893	G
1	1A	2894	G
1	1A	2895	U
2	1B	2	C
2	1B	3	C
2	1B	13	A
2	1B	45	A
2	1B	56	G
2	1B	66	A
2	1B	73	A
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	68	G
32	1a	78	G
32	1a	79	G
32	1a	98	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	120	A
32	1a	121	C
32	1a	129(A)	G
32	1a	131	C
32	1a	137	C
32	1a	141	A
32	1a	163	C
32	1a	169	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(D)	C
32	1a	190	U
32	1a	195	A

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Mol	Chain	Res	Type
32	1a	197	A
32	1a	201	C
32	1a	216	G
32	1a	217	C
32	1a	220	G
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	280	C
32	1a	289	G
32	1a	321	A
32	1a	328	C
32	1a	329	A
32	1a	332	G
32	1a	347	G
32	1a	348	G
32	1a	352	C
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	383	A
32	1a	392	G
32	1a	393	A
32	1a	397	A
32	1a	406	G
32	1a	412	A
32	1a	413	G
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	444	C
32	1a	452	A
32	1a	461	A
32	1a	470	C
32	1a	477	A

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Mol	Chain	Res	Type
32	1a	485	G
32	1a	487	A
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	519	C
32	1a	521	G
32	1a	524	G
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	562	C
32	1a	564	C
32	1a	572	A
32	1a	573	A
32	1a	575	G
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	633	G
32	1a	642	A
32	1a	653	A
32	1a	657	G
32	1a	661	G
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	693	G
32	1a	717	C
32	1a	724	G
32	1a	728	A
32	1a	731	G

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Mol	Chain	Res	Type
32	1a	734	G
32	1a	747	C
32	1a	755	G
32	1a	759	A
32	1a	768	A
32	1a	774	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	827	U
32	1a	828	A
32	1a	829	G
32	1a	836	G
32	1a	839	U
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	855	G
32	1a	870	U
32	1a	878	G
32	1a	902	G
32	1a	913	A
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	931	C
32	1a	934	C
32	1a	935	A
32	1a	939	G
32	1a	940	C
32	1a	958	A
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

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Mol	Chain	Res	Type
32	1a	977	A
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	996	A
32	1a	998	G
32	1a	999	C
32	1a	1001(A)	G
32	1a	1004	A
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1017	G
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	1027	C
32	1a	1028	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(B)	C
32	1a	1031	G
32	1a	1032	G
32	1a	1033	G
32	1a	1037	C
32	1a	1044	A
32	1a	1063	C
32	1a	1065	U
32	1a	1066	C
32	1a	1067	A
32	1a	1070	U
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1125	U
32	1a	1127	G
32	1a	1133	G
32	1a	1134	G

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Mol	Chain	Res	Type
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1144	G
32	1a	1145	C
32	1a	1146	A
32	1a	1152	A
32	1a	1155	G
32	1a	1159	U
32	1a	1163	C
32	1a	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1186	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1212	U
32	1a	1213	A
32	1a	1224	G
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	1260	C
32	1a	1270	C
32	1a	1277	C
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1293	G
32	1a	1299	A
32	1a	1300	G
32	1a	1320	C
32	1a	1322	C
32	1a	1340	A
32	1a	1346	A

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Mol	Chain	Res	Type
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1370	G
32	1a	1397	C
32	1a	1398	A
32	1a	1406	U
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1456	G
32	1a	1457	G
32	1a	1469	G
32	1a	1492	A
32	1a	1493	A
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1507	A
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	12	U
1	2A	15	G
1	2A	34	C
1	2A	45	C
1	2A	63	U
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	92	A
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G

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Mol	Chain	Res	Type
1	2A	139	G
1	2A	139(A)	G
1	2A	141	A
1	2A	157	U
1	2A	181	A
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	201	C
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	223	A
1	2A	229	A
1	2A	230	U
1	2A	233	A
1	2A	248	G
1	2A	271(D)	G
1	2A	271(E)	U
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	283	A
1	2A	302	C
1	2A	311	A
1	2A	317	G
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	335	C
1	2A	352	G

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Mol	Chain	Res	Type
1	2A	363	G
1	2A	370	G
1	2A	386	G
1	2A	390	A
1	2A	396	G
1	2A	399	G
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	428	A
1	2A	444	C
1	2A	446	G
1	2A	454	A
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	470	A
1	2A	475	U
1	2A	481	G
1	2A	482	A
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	551	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	614(C)	A
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	652(U)	G
1	2A	653	A
1	2A	669	G
1	2A	686	G
1	2A	701	G
1	2A	730	C
1	2A	740	U
1	2A	752	A
1	2A	753	C
1	2A	771	G
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	827	U
1	2A	828	U
1	2A	847	U
1	2A	857	C
1	2A	859	G
1	2A	869	G
1	2A	880	G
1	2A	882	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	896	A
1	2A	897	C
1	2A	901	A
1	2A	910	A
1	2A	915	C

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Mol	Chain	Res	Type
1	2A	917	A
1	2A	932	G
1	2A	937	U
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	996	A
1	2A	1006	C
1	2A	1012	U
1	2A	1013	C
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
1	2A	1044	G
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1048	A
1	2A	1052	C
1	2A	1054	A
1	2A	1056	G
1	2A	1060	U
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
1	2A	1073	A
1	2A	1074	G
1	2A	1075	C
1	2A	1076	C
1	2A	1077	A

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Mol	Chain	Res	Type
1	2A	1079	C
1	2A	1080	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	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	1106	G
1	2A	1110	G
1	2A	1112	G
1	2A	1116	C
1	2A	1117	G
1	2A	1120	G
1	2A	1129	A
1	2A	1135	C
1	2A	1136	G
1	2A	1171	G
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1244	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1274	A
1	2A	1276	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1321	A

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Mol	Chain	Res	Type
1	2A	1342	A
1	2A	1349	A
1	2A	1352	U
1	2A	1365	A
1	2A	1368	G
1	2A	1372	U
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1414	G
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	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	1507	A
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1511	C
1	2A	1531	C
1	2A	1533	G
1	2A	1542	A
1	2A	1543	C
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1584	C
1	2A	1586	A

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Mol	Chain	Res	Type
1	2A	1590	U
1	2A	1593	G
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1613	G
1	2A	1639	U
1	2A	1648	C
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1741	A
1	2A	1756	G
1	2A	1757	U
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	1829	A
1	2A	1834	U
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1852	C
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1927	A
1	2A	1929	G
1	2A	1930	G

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Mol	Chain	Res	Type
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1984	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2096	U
1	2A	2101	G
1	2A	2103	C
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2110	G
1	2A	2112	G
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
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2130	U
1	2A	2132	U

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Mol	Chain	Res	Type
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2137	C
1	2A	2138	C
1	2A	2140	C
1	2A	2141	G
1	2A	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2150	U
1	2A	2151	G
1	2A	2155	G
1	2A	2158	A
1	2A	2159	G
1	2A	2160	G
1	2A	2161	C
1	2A	2164	C
1	2A	2165	G
1	2A	2166	G
1	2A	2172	U
1	2A	2173	A
1	2A	2174	C
1	2A	2175	C
1	2A	2178	C
1	2A	2182	G
1	2A	2186	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	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2268	A
1	2A	2269	A
1	2A	2273	A

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Mol	Chain	Res	Type
1	2A	2275	C
1	2A	2280	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2294	C
1	2A	2300	G
1	2A	2305	A
1	2A	2308	G
1	2A	2309	A
1	2A	2310	A
1	2A	2311	A
1	2A	2312	U
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	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2366	A
1	2A	2383	G
1	2A	2385	C
1	2A	2396	G
1	2A	2402	C
1	2A	2406	U
1	2A	2410	G
1	2A	2414	G
1	2A	2422	A
1	2A	2423	U
1	2A	2424	C
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2445	G

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Mol	Chain	Res	Type
1	2A	2448	A
1	2A	2468	G
1	2A	2474	C
1	2A	2476	A
1	2A	2487	G
1	2A	2490	G
1	2A	2491	U
1	2A	2498	C
1	2A	2502	G
1	2A	2505	G
1	2A	2518	A
1	2A	2529	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	2582	G
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2629	A
1	2A	2630	G
1	2A	2654	A
1	2A	2663	G
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2752	C
1	2A	2754	U
1	2A	2757	A
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A

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Mol	Chain	Res	Type
1	2A	2769	C
1	2A	2778	A
1	2A	2779	U
1	2A	2789	C
1	2A	2802	G
1	2A	2803	C
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2834	G
1	2A	2835	A
1	2A	2848	G
1	2A	2872	G
1	2A	2880	C
1	2A	2891	G
1	2A	2892	A
1	2A	2894	G
1	2A	2895	U
2	2B	2	C
2	2B	8	U
2	2B	9	G
2	2B	12	C
2	2B	21	G
2	2B	23	G
2	2B	24	G
2	2B	33	G
2	2B	41	U
2	2B	42	C
2	2B	56	G
2	2B	73	A
2	2B	89	G
2	2B	90	A
2	2B	110	G
2	2B	116	G
32	2a	5	U
32	2a	6	G
32	2a	9	G
32	2a	22	G
32	2a	29	G
32	2a	30	U
32	2a	32	A

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Mol	Chain	Res	Type
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	60	A
32	2a	61	G
32	2a	78	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	102	G
32	2a	116	A
32	2a	121	C
32	2a	129(A)	G
32	2a	131	C
32	2a	142	G
32	2a	144	G
32	2a	156	G
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(B)	C
32	2a	189(C)	C
32	2a	189(D)	C
32	2a	189(F)	U
32	2a	189(G)	G
32	2a	194	C
32	2a	195	A
32	2a	196	A
32	2a	201	C
32	2a	202	U
32	2a	204	U
32	2a	216	G
32	2a	220	G
32	2a	223	U
32	2a	240	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C

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Mol	Chain	Res	Type
32	2a	289	G
32	2a	306	G
32	2a	316	G
32	2a	319	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	345	C
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	363	A
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	382	A
32	2a	392	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	409	G
32	2a	412	A
32	2a	413	G
32	2a	423	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	452	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	508	C
32	2a	509	A

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Mol	Chain	Res	Type
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	562	C
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	574	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	630	G
32	2a	631	G
32	2a	632	A
32	2a	648	A
32	2a	651	C
32	2a	653	A
32	2a	665	A
32	2a	685	G
32	2a	687	A
32	2a	688	G
32	2a	702	A
32	2a	703	G
32	2a	712	A
32	2a	723	U
32	2a	731	G
32	2a	734	G
32	2a	735	C
32	2a	742	G
32	2a	746	A
32	2a	749	C
32	2a	753	A
32	2a	755	G
32	2a	777	A
32	2a	784	C
32	2a	793	U
32	2a	794	A

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Mol	Chain	Res	Type
32	2a	802	A
32	2a	805	C
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	851	G
32	2a	854	G
32	2a	859	A
32	2a	872	A
32	2a	902	G
32	2a	914	A
32	2a	916	G
32	2a	920	U
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	939	G
32	2a	955	U
32	2a	960	U
32	2a	961	U
32	2a	966	M2G
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	983	A
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	995	C
32	2a	996	A
32	2a	1000	U
32	2a	1003	G
32	2a	1004	A

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Mol	Chain	Res	Type
32	2a	1005	A
32	2a	1006	C
32	2a	1017	G
32	2a	1020	U
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1030(C)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1034	G
32	2a	1041	A
32	2a	1043	C
32	2a	1053	G
32	2a	1054	C
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1094	G
32	2a	1101	A
32	2a	1113	C
32	2a	1118	C
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1134	G
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1158	C

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Mol	Chain	Res	Type
32	2a	1159	U
32	2a	1161	C
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1201	A
32	2a	1213	A
32	2a	1214	C
32	2a	1215	G
32	2a	1224	G
32	2a	1227	A
32	2a	1228	C
32	2a	1236	A
32	2a	1238	A
32	2a	1246	C
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1281	U
32	2a	1287	A
32	2a	1298	C
32	2a	1299	A
32	2a	1300	G
32	2a	1301	U
32	2a	1302	U
32	2a	1303	C
32	2a	1316	G
32	2a	1317	C
32	2a	1319	A
32	2a	1322	C
32	2a	1323	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1352	C

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Mol	Chain	Res	Type
32	2a	1353	G
32	2a	1363	C
32	2a	1363(A)	A
32	2a	1364	U
32	2a	1370	G
32	2a	1384	C
32	2a	1385	G
32	2a	1397	C
32	2a	1400	5MC
32	2a	1401	G
32	2a	1406	U
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1442(B)	A
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1459	C
32	2a	1487	G
32	2a	1492	A
32	2a	1497	G
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1529	G
32	2a	1530	G

All (63) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	214	G
1	1A	266	G
1	1A	278	A
1	1A	746	A
1	1A	764	A
1	1A	784	A
1	1A	839	U

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Mol	Chain	Res	Type
1	1A	840	C
1	1A	888	C
1	1A	895	U
1	1A	974	G
1	1A	1047	G
1	1A	1089	G
1	1A	1142(A)	A
1	1A	1145	C
1	1A	1175	U
1	1A	1210	A
1	1A	1379	A
1	1A	1442	G
1	1A	1608	A
1	1A	1653	G
1	1A	2126	A
1	1A	2238	G
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2689	U
1	1A	2893	G
1	2A	195	A
1	2A	196	A
1	2A	249	C
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	746	A
1	2A	752	A
1	2A	764	A
1	2A	827	U
1	2A	840	C
1	2A	856	C
1	2A	900	A
1	2A	1047	G
1	2A	1051	G
1	2A	1053	C
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1076	C
1	2A	1210	A

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Mol	Chain	Res	Type
1	2A	1275	A
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	2422	A
1	2A	2689	U
1	2A	2756	U

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

50 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	OMC	2A	1920	1	19,22,23	0.81	0	25,31,34	0.97	1 (4%)
1	2MU	1A	2552	1,57	19,22,24	1.31	3 (15%)	25,31,36	1.84	6 (24%)
1	5MC	1A	1962	1,57	19,22,23	1.62	3 (15%)	26,32,35	1.10	1 (3%)
32	UR3	1a	1498	32	19,22,23	0.99	1 (5%)	26,32,35	1.76	2 (7%)
32	2MG	1a	1207	32	23,26,27	1.22	2 (8%)	33,38,41	2.24	8 (24%)
32	PSU	2a	516	57,32	18,21,22	1.41	3 (16%)	21,30,33	2.12	5 (23%)
1	5MU	2A	1939	1,57	19,22,23	1.38	5 (26%)	27,32,35	2.08	6 (22%)
1	PSU	1A	1911	1	18,21,22	1.38	2 (11%)	21,30,33	2.01	4 (19%)
32	MA6	2a	1518	32	23,26,27	0.40	0	33,38,41	2.01	9 (27%)
1	5MU	2A	1915	1	19,22,23	1.47	4 (21%)	27,32,35	2.12	8 (29%)
1	OMC	1A	1920	1	19,22,23	0.87	0	25,31,34	1.22	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MC	1A	1942	1,57	19,22,23	1.42	3 (15%)	26,32,35	1.08	2 (7%)
32	5MC	2a	1400	32	19,22,23	1.52	3 (15%)	26,32,35	1.24	3 (11%)
32	UR3	2a	1498	32	19,22,23	1.01	2 (10%)	26,32,35	1.70	4 (15%)
32	G7M	1a	527	57,32	23,26,27	1.54	4 (17%)	34,39,42	1.64	4 (11%)
32	2MG	2a	1207	32	23,26,27	1.22	3 (13%)	33,38,41	2.09	8 (24%)
1	PSU	2A	1917	1	18,21,22	1.34	3 (16%)	21,30,33	2.02	3 (14%)
1	5MU	1A	1939	1	19,22,23	1.39	5 (26%)	27,32,35	2.01	7 (25%)
1	2MA	2A	2503	1,57	22,25,26	1.43	3 (13%)	32,37,40	2.38	9 (28%)
32	5MC	1a	1407	32	19,22,23	1.69	2 (10%)	26,32,35	1.16	3 (11%)
1	OMG	2A	2251	55,1,57	23,26,27	1.20	3 (13%)	32,38,41	2.11	7 (21%)
32	4OC	1a	1402	32	20,23,24	0.75	0	25,32,35	0.98	1 (4%)
1	PSU	2A	2605	1	18,21,22	1.37	3 (16%)	21,30,33	1.96	4 (19%)
32	MA6	1a	1519	32	23,26,27	0.45	0	33,38,41	2.06	10 (30%)
32	5MC	2a	967	32	19,22,23	1.69	3 (15%)	26,32,35	1.04	2 (7%)
32	5MC	1a	1400	32	19,22,23	1.62	3 (15%)	26,32,35	1.16	2 (7%)
1	5MU	1A	1915	1	19,22,23	1.41	5 (26%)	27,32,35	2.32	9 (33%)
32	MA6	1a	1518	32	23,26,27	0.40	0	33,38,41	1.93	9 (27%)
32	5MC	2a	1407	32	19,22,23	1.69	2 (10%)	26,32,35	1.19	3 (11%)
1	5MC	2A	1942	1	19,22,23	1.68	3 (15%)	26,32,35	1.16	2 (7%)
32	5MC	1a	1404	32	19,22,23	1.70	2 (10%)	26,32,35	1.19	4 (15%)
1	2MA	1A	2503	1,57	22,25,26	1.44	5 (22%)	32,37,40	2.25	9 (28%)
32	PSU	1a	516	57,32	18,21,22	1.39	2 (11%)	21,30,33	1.90	5 (23%)
1	OMG	1A	2251	55,1	23,26,27	1.27	3 (13%)	32,38,41	2.05	6 (18%)
1	PSU	1A	1917	1	18,21,22	1.35	2 (11%)	21,30,33	1.97	3 (14%)
55	8AN	1x	76	55,56,57	21,24,25	1.37	3 (14%)	26,35,38	2.39	11 (42%)
32	5MC	1a	967	32	19,22,23	1.55	3 (15%)	26,32,35	1.05	2 (7%)
43	0TD	2l	92	43	8,9,10	4.31	1 (12%)	6,11,13	7.37	3 (50%)
1	PSU	1A	2605	1	18,21,22	1.50	4 (22%)	21,30,33	2.12	5 (23%)
1	5MC	2A	1962	1	19,22,23	1.77	3 (15%)	26,32,35	1.21	4 (15%)
32	M2G	2a	966	57,32	24,27,28	1.36	4 (16%)	33,40,43	1.82	5 (15%)
1	2MU	2A	2552	1,57	19,22,24	1.18	2 (10%)	25,31,36	1.83	6 (24%)
55	8AN	2x	76	55,56,57	21,24,25	1.37	3 (14%)	26,35,38	2.21	10 (38%)
32	4OC	2a	1402	32	20,23,24	0.78	0	25,32,35	1.03	1 (4%)
1	PSU	2A	1911	1	18,21,22	1.43	3 (16%)	21,30,33	1.99	5 (23%)
32	MA6	2a	1519	32	23,26,27	0.45	0	33,38,41	2.13	10 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
32	5MC	2a	1404	32	19,22,23	1.67	3 (15%)	26,32,35	1.17	3 (11%)
43	0TD	1l	92	43	8,9,10	4.68	2 (25%)	6,11,13	4.48	3 (50%)
32	G7M	2a	527	32	23,26,27	1.49	3 (13%)	34,39,42	1.70	5 (14%)
32	M2G	1a	966	32	24,27,28	1.29	3 (12%)	33,40,43	1.88	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	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
1	2MU	1A	2552	1,57	-	0/9/27/28	0/2/2/2
1	5MC	1A	1962	1,57	-	2/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	PSU	2a	516	57,32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1,57	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	OMC	1A	1920	1	-	2/9/27/28	0/2/2/2
1	5MC	1A	1942	1,57	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	3/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	57,32	-	1/7/25/26	0/3/3/3
32	2MG	2a	1207	32	-	2/9/27/28	0/3/3/3
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	1	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	1,57	-	1/7/25/26	0/3/3/3
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	55,1,57	-	0/9/27/28	0/3/3/3
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	2/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	2MA	1A	2503	1,57	-	2/7/25/26	0/3/3/3
32	PSU	1a	516	57,32	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	55,1	-	0/9/27/28	0/3/3/3
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
55	8AN	1x	76	55,56,57	-	1/7/25/26	0/3/3/3
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	3/7/12/14	-
1	PSU	1A	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	57,32	-	0/11/29/30	0/3/3/3
1	2MU	2A	2552	1,57	-	0/9/27/28	0/2/2/2
55	8AN	2x	76	55,56,57	-	1/7/25/26	0/3/3/3
32	4OC	2a	1402	32	-	0/9/29/30	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	1/11/29/30	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	4/7/12/14	-
32	G7M	2a	527	32	-	3/7/25/26	0/3/3/3
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3

All (124) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.66	1.69	1.82
43	2l	92	0TD	CB-SB	-11.75	1.70	1.82
1	2A	1962	5MC	C5-C4	6.54	1.49	1.44
32	1a	1404	5MC	C5-C4	6.30	1.48	1.44
32	2a	1407	5MC	C5-C4	6.15	1.48	1.44
32	2a	967	5MC	C5-C4	6.11	1.48	1.44
1	2A	1942	5MC	C5-C4	6.10	1.48	1.44
32	2a	1404	5MC	C5-C4	6.07	1.48	1.44
32	1a	1407	5MC	C5-C4	5.87	1.48	1.44
1	1A	1962	5MC	C5-C4	5.83	1.48	1.44
32	1a	1400	5MC	C5-C4	5.62	1.48	1.44
32	1a	967	5MC	C5-C4	5.46	1.48	1.44
32	2a	1400	5MC	C5-C4	5.33	1.48	1.44
32	1a	527	G7M	C5-N7	-4.95	1.33	1.39
1	1A	1942	5MC	C5-C4	4.64	1.47	1.44
32	2a	527	G7M	C5-N7	-4.54	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2503	2MA	C5-C4	4.31	1.46	1.39
1	1A	2503	2MA	C5-C4	4.30	1.46	1.39
55	1x	76	8AN	C5-N7	-3.92	1.31	1.39
55	2x	76	8AN	C5-N7	-3.75	1.32	1.39
1	2A	1911	PSU	C6-C5	3.73	1.39	1.35
32	1a	516	PSU	C6-C5	3.69	1.39	1.35
1	1A	2605	PSU	C4-N3	-3.62	1.32	1.38
1	1A	1911	PSU	C6-C5	3.44	1.39	1.35
32	1a	1407	5MC	C6-C5	3.35	1.40	1.34
32	2a	966	M2G	C5-C4	3.34	1.47	1.38
1	1A	1917	PSU	C6-C5	3.34	1.39	1.35
1	1A	2251	OMG	C5-C4	3.28	1.47	1.38
32	1a	527	G7M	C5-C4	3.24	1.46	1.38
1	2A	2251	OMG	C5-C4	3.24	1.47	1.38
32	2a	516	PSU	C6-C5	3.21	1.38	1.35
32	1a	966	M2G	C5-C4	3.20	1.47	1.38
32	2a	966	M2G	C2-N2	3.18	1.41	1.35
1	2A	2605	PSU	C6-C5	3.17	1.38	1.35
55	2x	76	8AN	C5-C4	-3.17	1.33	1.39
1	2A	1915	5MU	C6-C5	3.17	1.39	1.34
32	2a	527	G7M	C5-C4	3.09	1.46	1.38
55	1x	76	8AN	C5-C4	-3.05	1.33	1.39
1	2A	1917	PSU	C6-C5	3.03	1.38	1.35
1	1A	1942	5MC	C6-C5	3.02	1.39	1.34
32	2a	1207	2MG	C5-C4	3.02	1.47	1.38
32	2a	1407	5MC	C6-C5	3.01	1.39	1.34
1	1A	1939	5MU	C6-C5	2.99	1.39	1.34
1	1A	1915	5MU	C2-N1	2.96	1.43	1.38
32	2a	967	5MC	C6-C5	2.95	1.39	1.34
32	1a	1207	2MG	C5-C4	2.95	1.46	1.38
32	1a	966	M2G	C2-N2	2.92	1.40	1.35
1	2A	1939	5MU	C6-C5	2.90	1.39	1.34
1	2A	1915	5MU	C2-N1	2.90	1.43	1.38
32	1a	1404	5MC	C6-C5	2.83	1.39	1.34
1	2A	1942	5MC	C6-C5	2.79	1.39	1.34
1	2A	1962	5MC	C6-C5	2.79	1.39	1.34
1	2A	1911	PSU	C4-N3	-2.79	1.33	1.38
1	1A	2552	2MU	C4-N3	-2.78	1.33	1.38
32	2a	1404	5MC	C6-C5	2.75	1.39	1.34
1	1A	2605	PSU	C2-N3	-2.75	1.32	1.37
1	1A	1911	PSU	C4-N3	-2.75	1.33	1.38
32	1a	1400	5MC	C6-N1	-2.73	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2503	2MA	C5-C6	2.73	1.48	1.41
32	1a	1400	5MC	C6-C5	2.70	1.39	1.34
32	1a	967	5MC	C6-C5	2.68	1.39	1.34
32	2a	516	PSU	C4-N3	-2.62	1.33	1.38
55	2x	76	8AN	C5-C6	-2.61	1.33	1.41
1	2A	1939	5MU	C4-N3	-2.56	1.34	1.38
1	1A	1962	5MC	C6-C5	2.56	1.38	1.34
1	2A	1915	5MU	C4-N3	-2.55	1.34	1.38
1	1A	1917	PSU	C4-N3	-2.55	1.34	1.38
1	1A	1962	5MC	C6-N1	-2.55	1.33	1.38
32	2a	1400	5MC	C6-C5	2.53	1.38	1.34
1	1A	1915	5MU	C6-C5	2.53	1.38	1.34
1	2A	1915	5MU	C4-C5	2.51	1.48	1.44
1	1A	1915	5MU	C4-N3	-2.50	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.50	1.34	1.38
1	1A	2605	PSU	C6-C5	2.50	1.38	1.35
1	2A	2605	PSU	C4-N3	-2.48	1.34	1.38
1	1A	2552	2MU	C2-N1	2.45	1.42	1.38
1	1A	1939	5MU	C4-C5	2.45	1.48	1.44
1	2A	2251	OMG	C6-N1	-2.45	1.34	1.38
32	2a	1400	5MC	C6-N1	-2.45	1.33	1.38
1	2A	2251	OMG	C5-N7	-2.44	1.34	1.39
32	2a	1207	2MG	C6-N1	-2.43	1.34	1.38
1	2A	1939	5MU	C4-C5	2.41	1.48	1.44
32	2a	527	G7M	C6-N1	-2.41	1.34	1.38
1	1A	1939	5MU	C4-N3	-2.39	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.39	1.34	1.38
1	2A	2552	2MU	C4-N3	-2.39	1.34	1.38
55	1x	76	8AN	C5-C6	-2.38	1.34	1.41
1	1A	2251	OMG	C5-N7	-2.37	1.34	1.39
32	1a	516	PSU	C4-N3	-2.36	1.34	1.38
32	2a	966	M2G	C6-N1	-2.35	1.34	1.38
1	2A	2503	2MA	C8-N7	2.35	1.36	1.31
1	2A	1917	PSU	C4-N3	-2.34	1.34	1.38
1	1A	2503	2MA	C5-C6	2.33	1.47	1.41
1	2A	1962	5MC	C6-N1	-2.32	1.34	1.38
43	1l	92	0TD	CB-CA	2.26	1.55	1.54
1	1A	2503	2MA	C8-N7	2.26	1.36	1.31
32	1a	966	M2G	C6-N1	-2.26	1.34	1.38
1	1A	2552	2MU	C5-C4	2.25	1.48	1.43
1	2A	1939	5MU	C2-N1	2.23	1.42	1.38
32	2a	1498	UR3	C2-N1	2.23	1.41	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2552	2MU	C5-C4	2.21	1.48	1.43
1	2A	2605	PSU	C2-N3	-2.21	1.33	1.37
32	1a	527	G7M	C6-N1	-2.21	1.34	1.38
32	2a	1404	5MC	C6-N1	-2.20	1.34	1.38
1	1A	2503	2MA	C4-N9	-2.20	1.33	1.37
1	1A	2503	2MA	C5-N7	-2.20	1.35	1.39
1	1A	1915	5MU	C4-C5	2.20	1.48	1.44
32	2a	1207	2MG	C5-N7	-2.16	1.34	1.39
1	2A	1911	PSU	C2-N3	-2.16	1.33	1.37
1	2A	1942	5MC	C6-N1	-2.15	1.34	1.38
1	1A	1939	5MU	C2-N1	2.15	1.41	1.38
1	1A	2605	PSU	C2-N1	-2.15	1.33	1.36
32	2a	966	M2G	C5-N7	-2.10	1.34	1.39
1	1A	1942	5MC	C6-N1	-2.10	1.34	1.38
32	2a	1498	UR3	C6-C5	2.08	1.39	1.35
32	1a	527	G7M	C4-N9	-2.06	1.32	1.38
32	1a	967	5MC	C6-N1	-2.06	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.05	1.34	1.38
32	2a	967	5MC	C6-N1	-2.05	1.34	1.38
32	1a	1498	UR3	C6-C5	2.04	1.39	1.35
32	2a	516	PSU	O4'-C1'	-2.03	1.41	1.43
1	2A	1917	PSU	C2-N1	-2.02	1.34	1.36
1	1A	1939	5MU	C6-N1	-2.01	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.00	1.34	1.38

All (250) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	2l	92	0TD	CSB-SB-CB	17.52	133.86	102.36
43	1l	92	0TD	CSB-SB-CB	10.23	120.76	102.36
1	2A	2503	2MA	C5-C4-N3	-8.00	118.75	127.18
1	1A	2503	2MA	C5-C4-N3	-7.85	118.91	127.18
32	1a	1498	UR3	C4-N3-C2	-7.06	118.90	124.58
32	1a	1207	2MG	C2-N3-C4	7.00	120.76	112.00
1	2A	2251	OMG	C5-C4-N3	-6.92	117.38	128.39
32	2a	516	PSU	N1-C2-N3	6.62	122.15	115.17
32	2a	1498	UR3	C4-N3-C2	-6.61	119.26	124.58
32	2a	1207	2MG	C2-N3-C4	6.60	120.25	112.00
1	1A	2605	PSU	N1-C2-N3	6.59	122.12	115.17
1	1A	2251	OMG	C5-C4-N3	-6.35	118.28	128.39
1	1A	1911	PSU	N1-C2-N3	6.23	121.75	115.17
1	2A	2503	2MA	N3-C4-N9	6.21	134.88	126.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1917	PSU	N1-C2-N3	6.16	121.66	115.17
1	1A	2503	2MA	N3-C4-N9	6.15	134.80	126.99
1	2A	1911	PSU	N1-C2-N3	6.11	121.61	115.17
32	2a	966	M2G	C5-C4-N3	-6.06	118.75	128.39
32	1a	966	M2G	C5-C4-N3	-6.04	118.78	128.39
1	1A	1917	PSU	N1-C2-N3	5.94	121.44	115.17
55	1x	76	8AN	N1-C2-N3	-5.91	119.63	128.58
1	2A	2605	PSU	N1-C2-N3	5.81	121.30	115.17
32	1a	516	PSU	N1-C2-N3	5.74	121.23	115.17
55	2x	76	8AN	N1-C2-N3	-5.66	120.02	128.58
32	2a	1207	2MG	C5-C4-N3	-5.61	119.45	128.39
32	1a	1207	2MG	C5-C4-N3	-5.55	119.56	128.39
1	2A	2251	OMG	N9-C4-N3	5.38	136.71	125.95
32	2a	527	G7M	C5-C4-N3	-5.25	118.22	128.15
32	2a	527	G7M	N9-C4-N3	5.25	136.44	125.95
1	2A	2552	2MU	N3-C2-N1	5.22	121.69	114.89
1	2A	1939	5MU	N3-C2-N1	5.20	121.66	114.89
32	1a	527	G7M	N9-C4-N3	5.20	136.35	125.95
1	1A	2251	OMG	C2-N3-C4	5.20	121.25	112.30
1	2A	1915	5MU	N3-C2-N1	5.20	121.66	114.89
1	2A	2251	OMG	C2-N3-C4	5.10	121.08	112.30
1	2A	1939	5MU	C4-N3-C2	-5.01	120.77	127.34
32	2a	1519	MA6	N1-C2-N3	-4.91	121.14	128.58
55	2x	76	8AN	C5-C4-N3	-4.90	119.98	126.72
32	1a	527	G7M	C5-C4-N3	-4.89	118.92	128.15
55	1x	76	8AN	C5-C4-N3	-4.87	120.01	126.72
32	2a	1518	MA6	N1-C2-N3	-4.85	121.24	128.58
1	1A	2552	2MU	N3-C2-N1	4.85	121.20	114.89
32	1a	1518	MA6	N1-C2-N3	-4.81	121.30	128.58
32	1a	1519	MA6	N1-C2-N3	-4.79	121.33	128.58
1	1A	1939	5MU	C4-N3-C2	-4.77	121.08	127.34
32	2a	527	G7M	C2-N3-C4	4.71	120.41	112.30
32	1a	966	M2G	C2-N3-C4	4.69	121.18	112.51
1	1A	1915	5MU	C1'-N1-C2	4.66	125.96	117.59
1	2A	1915	5MU	C4-N3-C2	-4.65	121.25	127.34
1	1A	1915	5MU	C4-N3-C2	-4.57	121.35	127.34
1	1A	1939	5MU	N3-C2-N1	4.53	120.79	114.89
32	2a	966	M2G	N9-C4-N3	4.52	134.99	125.95
32	1a	1519	MA6	C5-C4-N3	-4.52	120.50	126.72
1	1A	1915	5MU	N3-C2-N1	4.51	120.76	114.89
1	1A	1915	5MU	C5-C4-N3	4.48	119.22	115.32
1	1A	2605	PSU	C4-N3-C2	-4.48	120.20	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1917	PSU	O2-C2-N1	-4.43	118.22	122.79
32	2a	966	M2G	C2-N3-C4	4.43	120.71	112.51
1	1A	1939	5MU	C5-C4-N3	4.42	119.17	115.32
32	2a	1519	MA6	C5-C4-N3	-4.36	120.71	126.72
32	1a	527	G7M	C2-N3-C4	4.34	119.78	112.30
1	2A	1939	5MU	C5-C4-N3	4.29	119.06	115.32
32	2a	1518	MA6	C5-C4-N3	-4.29	120.81	126.72
55	1x	76	8AN	O4'-C1'-N9	4.28	116.31	108.09
32	2a	1519	MA6	C4-C5-N7	-4.27	105.70	110.58
32	1a	966	M2G	N9-C4-N3	4.27	134.49	125.95
1	2A	2552	2MU	C4-N3-C2	-4.27	121.32	126.61
1	1A	2251	OMG	N9-C4-N3	4.25	134.46	125.95
1	1A	1915	5MU	C1'-N1-C6	-4.24	114.17	121.15
1	1A	2552	2MU	C4-N3-C2	-4.24	121.35	126.61
1	1A	1915	5MU	O4-C4-C5	-4.21	120.10	124.92
32	1a	1518	MA6	C5-C4-N3	-4.18	120.96	126.72
32	2a	516	PSU	C4-N3-C2	-4.15	120.65	126.37
1	2A	2605	PSU	C4-N3-C2	-4.10	120.72	126.37
1	1A	1911	PSU	C4-N3-C2	-4.08	120.75	126.37
32	2a	1519	MA6	C5-N7-C8	4.07	109.84	103.45
32	1a	1519	MA6	C4-C5-N7	-4.05	105.95	110.58
32	2a	1518	MA6	C2-N1-C6	4.04	121.70	111.83
1	1A	1917	PSU	C4-N3-C2	-4.03	120.82	126.37
32	1a	1519	MA6	C2-N1-C6	4.01	121.61	111.83
32	2a	1207	2MG	N9-C4-N3	4.00	133.95	125.95
1	2A	1911	PSU	C4-N3-C2	-3.99	120.88	126.37
32	1a	1518	MA6	C2-N1-C6	3.98	121.54	111.83
1	2A	1939	5MU	O4-C4-C5	-3.95	120.40	124.92
32	2a	1519	MA6	C2-N1-C6	3.93	121.43	111.83
1	2A	2503	2MA	C4-C5-N7	-3.90	106.12	110.58
32	1a	1207	2MG	C6-C5-N7	3.89	137.38	130.29
1	2A	1915	5MU	C5-C4-N3	3.89	118.70	115.32
1	2A	1917	PSU	C4-N3-C2	-3.82	121.11	126.37
32	2a	1518	MA6	C5-N7-C8	3.81	109.43	103.45
1	1A	1939	5MU	O4-C4-C5	-3.80	120.56	124.92
32	1a	1400	5MC	C5-C6-N1	-3.79	119.19	123.31
32	1a	1207	2MG	N9-C4-N3	3.79	133.53	125.95
1	2A	1942	5MC	C5-C6-N1	-3.79	119.20	123.31
32	1a	516	PSU	C4-N3-C2	-3.79	121.16	126.37
32	1a	1519	MA6	C5-N7-C8	3.78	109.39	103.45
1	2A	2552	2MU	O2-C2-N1	-3.77	117.88	122.80
32	2a	1518	MA6	C4-C5-N7	-3.74	106.31	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	2552	2MU	C2'-C1'-N1	-3.71	107.20	114.24
1	1A	1917	PSU	O2-C2-N1	-3.70	118.97	122.79
1	1A	2251	OMG	C6-C5-N7	3.66	136.96	130.29
32	2a	516	PSU	O2-C2-N1	-3.64	119.03	122.79
1	1A	1962	5MC	C5-C6-N1	-3.59	119.42	123.31
1	1A	1939	5MU	C5-C6-N1	-3.54	119.47	123.31
1	2A	1915	5MU	O4-C4-C5	-3.49	120.92	124.92
32	2a	1519	MA6	C2-N3-C4	3.48	120.33	111.83
32	1a	1518	MA6	C5-N7-C8	3.45	108.88	103.45
32	1a	966	M2G	C6-C5-N7	3.44	136.55	130.29
1	1A	1911	PSU	O2-C2-N1	-3.42	119.26	122.79
1	2A	1915	5MU	C1'-N1-C2	3.42	123.74	117.59
32	2a	1519	MA6	N9-C8-N7	-3.41	109.10	113.94
32	1a	1519	MA6	C2-N3-C4	3.41	120.16	111.83
55	2x	76	8AN	N9-C8-N7	-3.40	109.12	113.94
55	1x	76	8AN	N9-C8-N7	-3.39	109.13	113.94
32	2a	1400	5MC	C5-C6-N1	-3.36	119.66	123.31
32	2a	1518	MA6	C2-N3-C4	3.36	120.03	111.83
32	2a	1518	MA6	N9-C8-N7	-3.35	109.18	113.94
55	1x	76	8AN	C2-N3-C4	3.34	120.00	111.83
1	1A	2503	2MA	C4-C5-N7	-3.34	106.77	110.58
1	2A	2503	2MA	C4-N9-C8	3.33	109.24	105.74
1	1A	1942	5MC	C5-C6-N1	-3.33	119.69	123.31
55	1x	76	8AN	C4'-O4'-C1'	-3.31	102.16	109.47
32	1a	1518	MA6	C2-N3-C4	3.30	119.90	111.83
32	2a	967	5MC	C5-C6-N1	-3.30	119.73	123.31
32	1a	1498	UR3	C5-C4-N3	3.29	119.38	115.04
55	2x	76	8AN	C2-N3-C4	3.28	119.84	111.83
32	2a	1404	5MC	C5-C6-N1	-3.27	119.76	123.31
32	2a	1207	2MG	C6-C5-N7	3.25	136.20	130.29
1	1A	2251	OMG	C4-C5-N7	-3.24	105.53	110.67
43	2l	92	0TD	OD2-CG-CB	3.21	120.08	113.15
1	2A	2605	PSU	O2-C2-N1	-3.19	119.50	122.79
32	1a	1518	MA6	N9-C8-N7	-3.19	109.41	113.94
32	1a	1518	MA6	C4-C5-N7	-3.14	107.00	110.58
1	1A	1920	OMC	O2-C2-N3	-3.11	117.44	122.33
1	2A	1939	5MU	C5-C6-N1	-3.10	119.95	123.31
1	2A	1962	5MC	C5-C6-N1	-3.10	119.95	123.31
32	1a	1207	2MG	N1-C2-N2	3.09	119.71	116.56
32	2a	1498	UR3	C5-C4-N3	3.09	119.11	115.04
32	1a	1519	MA6	N9-C8-N7	-3.07	109.58	113.94
32	2a	1407	5MC	C5-C4-N3	-3.07	118.61	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2x	76	8AN	C4'-O4'-C1'	-3.06	102.71	109.47
55	1x	76	8AN	C5-N7-C8	3.05	108.24	103.45
1	2A	2503	2MA	N6-C6-N1	3.05	121.14	117.03
32	1a	1404	5MC	C5-C4-N3	-3.03	118.65	121.75
32	2a	966	M2G	C6-C5-N7	3.03	135.81	130.29
32	2a	1407	5MC	C5-C6-N1	-3.01	120.04	123.31
43	1l	92	0TD	OD2-CG-CB	3.00	119.64	113.15
32	2a	1404	5MC	C5-C4-N3	-2.99	118.69	121.75
55	2x	76	8AN	C5-N7-C8	2.98	108.13	103.45
1	2A	2503	2MA	C5-N7-C8	2.98	108.13	103.45
1	1A	2503	2MA	C4-N9-C8	2.97	108.86	105.74
32	1a	1407	5MC	C5-C6-N1	-2.94	120.12	123.31
32	1a	1407	5MC	C5-C4-N3	-2.90	118.78	121.75
32	1a	1207	2MG	C4-C5-N7	-2.89	106.09	110.67
32	1a	967	5MC	C5-C6-N1	-2.87	120.19	123.31
1	1A	2503	2MA	N6-C6-N1	2.84	120.86	117.03
32	1a	1404	5MC	C5-C6-N1	-2.83	120.23	123.31
32	1a	1518	MA6	N3-C4-N9	2.83	131.98	127.17
32	1a	516	PSU	O2-C2-N1	-2.83	119.87	122.79
1	1A	2605	PSU	O2-C2-N1	-2.81	119.89	122.79
1	2A	1911	PSU	O2-C2-N1	-2.75	119.95	122.79
32	1a	967	5MC	C5-C4-N3	-2.74	118.95	121.75
32	1a	1400	5MC	C5-C4-N3	-2.71	118.98	121.75
55	2x	76	8AN	C5-C4-N9	2.70	108.76	105.81
1	1A	2605	PSU	C5-C6-N1	-2.68	118.42	122.14
1	2A	2503	2MA	N9-C8-N7	-2.68	110.14	113.94
1	2A	2552	2MU	O4-C4-C5	-2.67	120.55	125.16
1	1A	2503	2MA	C2-N1-C6	2.67	122.21	118.10
32	1a	966	M2G	C4-C5-N7	-2.67	106.44	110.67
1	2A	1915	5MU	C5-C6-N1	-2.67	120.42	123.31
1	2A	1915	5MU	C1'-N1-C6	-2.63	116.81	121.15
32	2a	1207	2MG	N1-C2-N2	2.62	119.23	116.56
1	2A	1962	5MC	C5-C4-N3	-2.61	119.08	121.75
32	1a	1402	4OC	C6-C5-C4	2.60	120.13	117.00
55	1x	76	8AN	C5-C4-N9	2.59	108.64	105.81
32	2a	1518	MA6	N3-C4-N9	2.59	131.57	127.17
1	1A	1920	OMC	C1'-N1-C2	2.59	124.16	118.44
32	2a	1207	2MG	C4-C5-N7	-2.59	106.57	110.67
32	2a	966	M2G	C4-C5-N7	-2.54	106.64	110.67
1	1A	1939	5MU	O2-C2-N1	-2.53	119.50	122.80
1	2A	2503	2MA	C6-C5-N7	2.51	136.93	132.09
1	1A	2552	2MU	C5-C4-N3	2.51	118.31	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1519	MA6	C4-C5-C6	2.50	118.50	115.91
32	1a	1404	5MC	O2-C2-N3	-2.50	118.39	122.33
32	2a	516	PSU	O4'-C1'-C2'	2.48	108.58	105.15
1	2A	2251	OMG	C4-C5-N7	-2.48	106.74	110.67
1	1A	2552	2MU	O4-C4-C5	-2.48	120.89	125.16
43	2l	92	0TD	OD1-CG-CB	-2.48	117.25	122.44
32	2a	967	5MC	C5-C4-N3	-2.47	119.22	121.75
1	2A	2251	OMG	C6-C5-N7	2.47	134.78	130.29
32	1a	527	G7M	O6-C6-C5	-2.46	122.51	128.01
1	2A	2503	2MA	C2-N1-C6	2.45	121.87	118.10
55	1x	76	8AN	N3-C4-N9	2.45	131.34	127.17
32	2a	1407	5MC	O2-C2-N3	-2.44	118.48	122.33
32	2a	1400	5MC	C5-C4-N3	-2.43	119.26	121.75
1	1A	2503	2MA	C5-N7-C8	2.43	107.27	103.45
32	1a	1519	MA6	N3-C4-N9	2.42	131.28	127.17
55	2x	76	8AN	N3-C4-N9	2.41	131.26	127.17
1	1A	1942	5MC	C5-C4-N3	-2.40	119.29	121.75
1	1A	1915	5MU	O2-C2-N3	-2.39	117.09	121.49
1	2A	2251	OMG	O6-C6-C5	-2.37	120.27	126.53
1	1A	1915	5MU	C5M-C5-C4	2.36	121.30	118.78
1	2A	1942	5MC	C5-C4-N3	-2.35	119.35	121.75
32	2a	1400	5MC	C1'-N1-C6	-2.35	117.28	121.15
32	2a	516	PSU	C5-C6-N1	-2.33	118.90	122.14
32	2a	1207	2MG	N2-C2-N3	-2.33	117.55	120.51
1	2A	1915	5MU	O2-C2-N3	-2.32	117.21	121.49
1	2A	1939	5MU	O2-C2-N1	-2.30	119.80	122.80
1	2A	2552	2MU	C2'-C1'-N1	-2.30	109.88	114.24
32	2a	1519	MA6	N3-C4-N9	2.30	131.07	127.17
32	2a	1518	MA6	C4-C5-C6	2.25	118.24	115.91
1	2A	2605	PSU	C5-C6-N1	-2.25	119.01	122.14
55	2x	76	8AN	C6-C5-C4	2.23	120.22	117.18
32	2a	1402	4OC	C6-C5-C4	2.23	119.69	117.00
1	1A	1915	5MU	C5-C6-N1	-2.23	120.89	123.31
32	1a	1207	2MG	CM2-N2-C2	-2.22	118.88	123.65
1	1A	2251	OMG	C8-N7-C5	2.21	108.19	104.26
32	1a	1519	MA6	C5-C4-N9	2.20	108.21	105.81
32	2a	1519	MA6	C5-C4-N9	2.20	108.21	105.81
1	1A	2503	2MA	N9-C8-N7	-2.20	110.82	113.94
32	2a	527	G7M	O6-C6-C5	-2.20	123.11	128.01
1	2A	1920	OMC	O2-C2-N3	-2.19	118.88	122.33
32	1a	1404	5MC	CM5-C5-C6	-2.18	119.90	122.85
1	1A	2605	PSU	O2-C2-N3	-2.18	117.99	121.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1518	MA6	C4-C5-C6	2.17	118.16	115.91
32	2a	1404	5MC	O2-C2-N3	-2.17	118.91	122.33
1	2A	1962	5MC	C1'-N1-C6	-2.17	117.58	121.15
1	2A	2251	OMG	C2-N1-C6	-2.16	121.19	125.11
55	2x	76	8AN	C4-C5-N7	-2.16	108.11	110.58
32	1a	1207	2MG	N2-C2-N3	-2.15	117.77	120.51
32	2a	1207	2MG	O6-C6-C5	-2.14	120.88	126.53
1	2A	1911	PSU	C6-C5-C4	-2.14	116.73	118.17
55	1x	76	8AN	C4-C5-N7	-2.14	108.14	110.58
1	2A	2552	2MU	C5-C4-N3	2.12	117.77	114.80
32	2a	1498	UR3	C1'-N1-C2	2.12	120.50	117.04
1	1A	2552	2MU	O2-C2-N1	-2.11	120.05	122.80
1	1A	2503	2MA	C6-C5-N7	2.10	136.14	132.09
32	1a	516	PSU	O4'-C1'-C2'	2.10	108.05	105.15
32	2a	527	G7M	C5-C6-N1	2.09	116.17	111.84
1	1A	1911	PSU	O4'-C1'-C2'	2.08	108.03	105.15
55	1x	76	8AN	C6-C5-C4	2.07	120.01	117.18
32	2a	1498	UR3	C6-N1-C2	-2.06	120.11	121.80
32	1a	966	M2G	O6-C6-C5	-2.06	121.11	126.53
1	2A	1962	5MC	O2-C2-N3	-2.03	119.12	122.33
32	1a	1407	5MC	O2-C2-N3	-2.02	119.14	122.33
32	1a	516	PSU	C6-C5-C4	-2.02	116.81	118.17
1	1A	1939	5MU	C5M-C5-C4	2.01	120.93	118.78
32	2a	1519	MA6	C4-C5-C6	2.01	117.99	115.91
1	2A	1911	PSU	C5-C6-N1	-2.01	119.35	122.14
43	1l	92	0TD	OD1-CG-CB	-2.00	118.24	122.44

There are no chirality outliers.

All (35) 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
43	1l	92	0TD	O-C-CA-CB
43	1l	92	0TD	CG-CB-SB-CSB
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
32	2a	1207	2MG	N1-C2-N2-CM2
32	2a	1207	2MG	N3-C2-N2-CM2
43	2l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	SB-CB-CG-OD2
43	2l	92	0TD	SB-CB-CG-OD1

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Mol	Chain	Res	Type	Atoms
32	2a	1400	5MC	C3'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C4'-C5'-O5'
55	1x	76	8AN	C4'-C5'-O5'-P
55	2x	76	8AN	C4'-C5'-O5'-P
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1402	4OC	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD1
1	1A	1920	OMC	C3'-C2'-O2'-CM2
1	1A	1920	OMC	C2'-C1'-N1-C6
1	1A	2503	2MA	C4'-C5'-O5'-P
43	1l	92	0TD	CA-CB-SB-CSB
32	2a	527	G7M	C4'-C5'-O5'-P
1	2A	1920	OMC	C3'-C2'-O2'-CM2
1	1A	1962	5MC	O4'-C1'-N1-C6
1	1A	1962	5MC	C2'-C1'-N1-C6
1	2A	2503	2MA	O4'-C4'-C5'-O5'
1	1A	2503	2MA	O4'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C2'-C1'-N1-C6

There are no ring outliers.

24 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1920	OMC	2	0
1	1A	2552	2MU	2	0
32	1a	1498	UR3	1	0
1	2A	1939	5MU	2	0
32	2a	1518	MA6	1	0
1	1A	1920	OMC	2	0
32	2a	1400	5MC	2	0
32	1a	527	G7M	1	0
32	2a	1207	2MG	1	0
1	2A	1917	PSU	2	0
1	1A	1939	5MU	1	0
1	2A	2251	OMG	1	0
32	1a	1402	4OC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1519	MA6	5	0
32	1a	1518	MA6	2	0
1	1A	2503	2MA	1	0
1	1A	2251	OMG	1	0
32	1a	967	5MC	1	0
43	2l	92	0TD	4	0
1	2A	2552	2MU	1	0
32	2a	1402	4OC	2	0
32	2a	1519	MA6	1	0
32	2a	1404	5MC	1	0
43	1l	92	0TD	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2510 ligands modelled in this entry, 2498 are monoatomic - leaving 12 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	$\#\|Z\| > 2$
58	CLM	2A	3727	-	20,20,20	0.96	1 (5%)	23,27,27	0.90	1 (4%)
62	SF4	2d	501	35	0,12,12	-	-	-		
59	ARG	1B	232	57	10,11,11	0.78	1 (10%)	9,13,13	0.95	1 (11%)
60	MPD	2A	3728	-	7,7,7	0.27	0	9,10,10	0.17	0
60	MPD	1T	207	-	7,7,7	0.29	0	9,10,10	0.19	0
60	MPD	18	103	-	7,7,7	0.29	0	9,10,10	0.24	0
60	MPD	2B	218	-	7,7,7	0.33	0	9,10,10	0.32	0
62	SF4	1d	306	35	0,12,12	-	-	-		
59	ARG	1A	4023	-	10,11,11	0.77	1 (10%)	9,13,13	0.99	1 (11%)
60	MPD	1a	3271	-	7,7,7	0.40	0	9,10,10	0.57	0
60	MPD	1A	4024	-	7,7,7	0.30	0	9,10,10	0.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
58	CLM	1A	4022	-	20,20,20	1.06	2 (10%)	23,27,27	1.17	3 (13%)

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
58	CLM	2A	3727	-	-	0/20/22/22	0/1/1/1
62	SF4	2d	501	35	-	-	0/6/5/5
59	ARG	1B	232	57	-	3/11/11/11	-
60	MPD	2A	3728	-	-	0/5/5/5	-
60	MPD	1T	207	-	-	2/5/5/5	-
60	MPD	18	103	-	-	2/5/5/5	-
60	MPD	2B	218	-	-	4/5/5/5	-
62	SF4	1d	306	35	-	-	0/6/5/5
59	ARG	1A	4023	-	-	1/11/11/11	-
60	MPD	1a	3271	-	-	2/5/5/5	-
60	MPD	1A	4024	-	-	1/5/5/5	-
58	CLM	1A	4022	-	-	4/20/22/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	1A	4022	CLM	C6-C5	-2.39	1.48	1.51
59	1B	232	ARG	OXT-C	-2.38	1.23	1.30
58	2A	3727	CLM	C6-C5	-2.25	1.48	1.51
59	1A	4023	ARG	OXT-C	-2.17	1.23	1.30
58	1A	4022	CLM	C9-N9	-2.05	1.40	1.45

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	1A	4023	ARG	OXT-C-O	-2.82	117.69	124.08
59	1B	232	ARG	OXT-C-O	-2.62	118.14	124.08
58	1A	4022	CLM	C10-C9-N9	2.57	121.58	119.34
58	1A	4022	CLM	C3-N2-C2	-2.31	119.22	123.25
58	1A	4022	CLM	O5-C5-C6	-2.20	106.42	111.20
58	2A	3727	CLM	C8-C9-N9	2.01	121.10	119.34

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	1A	4022	CLM	C5-C3-N2-C2
59	1B	232	ARG	O-C-CA-N
60	2B	218	MPD	C2-C3-C4-C5
59	1A	4023	ARG	CA-CB-CG-CD
58	1A	4022	CLM	C5-C3-C4-O4
58	1A	4022	CLM	N2-C3-C4-O4
58	1A	4022	CLM	CL2-C1-C2-N2
59	1B	232	ARG	OXT-C-CA-N
59	1B	232	ARG	CA-CB-CG-CD
60	1A	4024	MPD	O2-C2-C3-C4
60	18	103	MPD	C2-C3-C4-C5
60	1a	3271	MPD	O2-C2-C3-C4
60	1a	3271	MPD	C2-C3-C4-O4
60	2B	218	MPD	C2-C3-C4-O4
60	1T	207	MPD	C1-C2-C3-C4
60	1T	207	MPD	CM-C2-C3-C4
60	18	103	MPD	C1-C2-C3-C4
60	2B	218	MPD	C1-C2-C3-C4
60	2B	218	MPD	CM-C2-C3-C4

There are no ring outliers.

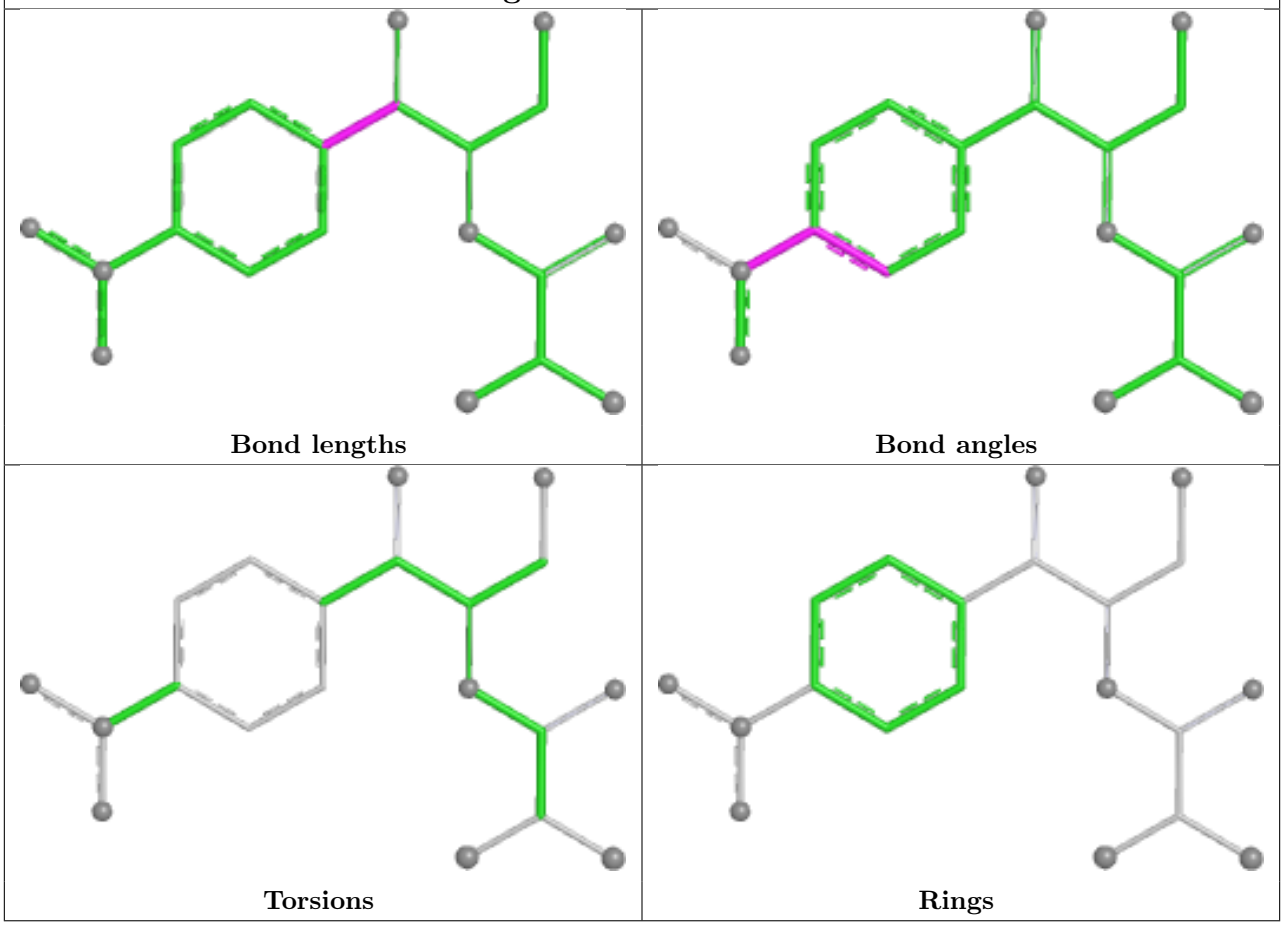
8 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	2A	3727	CLM	1	0
59	1B	232	ARG	1	0
60	1T	207	MPD	1	0
62	1d	306	SF4	2	0
59	1A	4023	ARG	2	0
60	1a	3271	MPD	3	0
60	1A	4024	MPD	1	0
58	1A	4022	CLM	2	0

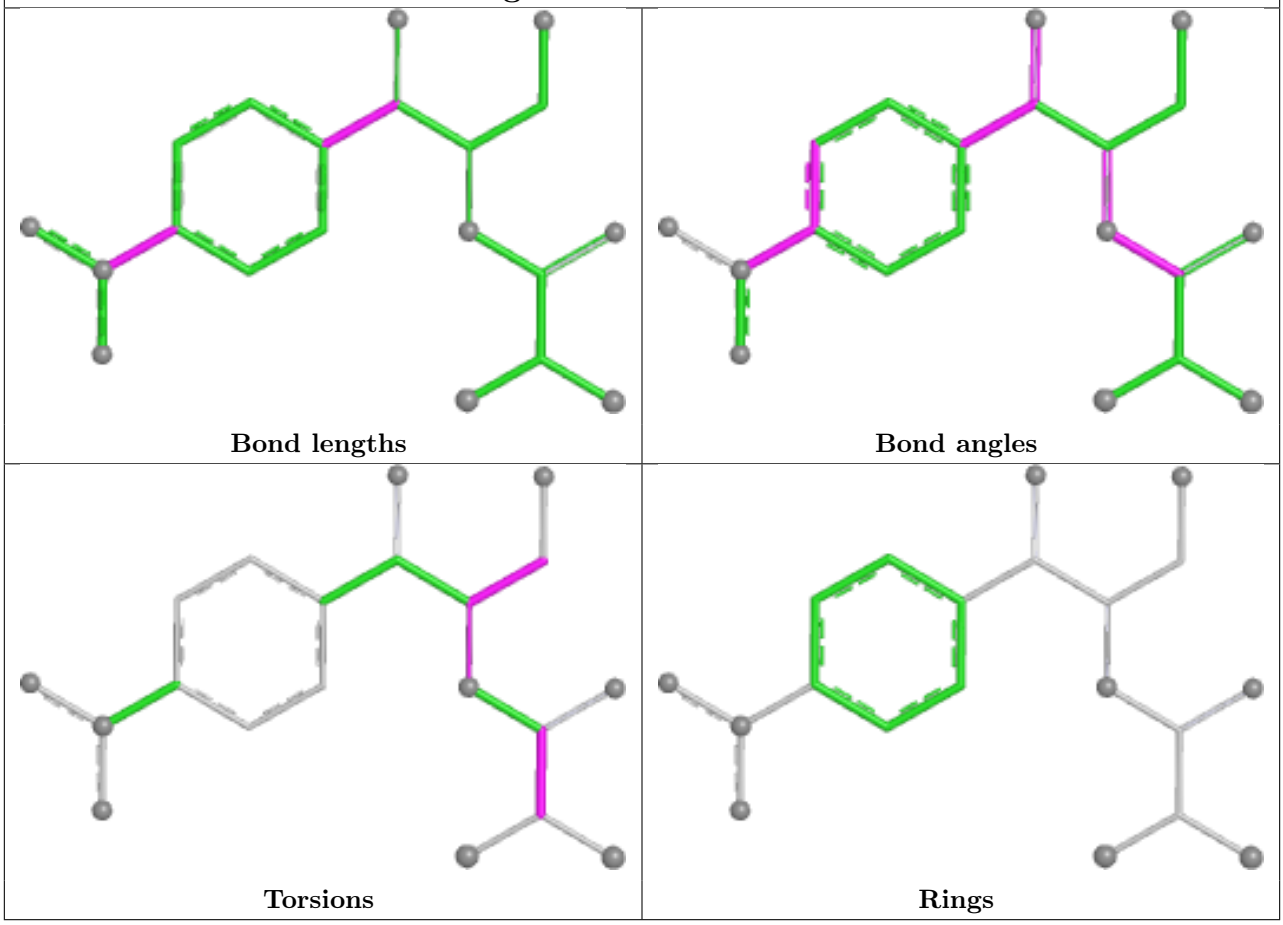
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand CLM 2A 3727



Ligand CLM 1A 4022



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%)	-0.46	116 (4%) 41 37	15, 32, 79, 90	0
1	2A	2856/2915 (97%)	-0.01	141 (4%) 35 31	27, 48, 81, 90	0
2	1B	120/121 (99%)	-0.29	1 (0%) 82 80	24, 43, 54, 68	0
2	2B	120/121 (99%)	0.50	1 (0%) 82 80	49, 64, 71, 75	0
3	1D	275/276 (99%)	-0.11	1 (0%) 88 86	18, 33, 44, 58	0
3	2D	275/276 (99%)	0.18	2 (0%) 84 81	27, 43, 54, 67	0
4	1E	204/206 (99%)	-0.05	0 100 100	16, 36, 52, 64	0
4	2E	204/206 (99%)	0.36	1 (0%) 87 85	25, 48, 62, 68	0
5	1F	203/210 (96%)	0.07	4 (1%) 65 61	14, 36, 58, 74	0
5	2F	203/210 (96%)	0.57	4 (1%) 65 61	28, 55, 65, 73	0
6	1G	181/182 (99%)	0.83	11 (6%) 27 23	40, 56, 66, 72	0
6	2G	181/182 (99%)	1.50	47 (25%) 1 1	58, 68, 74, 77	0
7	1H	174/180 (96%)	0.32	1 (0%) 85 83	30, 45, 55, 58	0
7	2H	173/180 (96%)	1.31	26 (15%) 5 4	58, 66, 72, 76	0
8	1I	147/148 (99%)	0.84	6 (4%) 41 37	37, 61, 70, 76	0
8	2I	146/148 (98%)	1.19	20 (13%) 6 5	46, 64, 72, 76	0
9	1N	140/140 (100%)	-0.09	1 (0%) 84 81	22, 32, 48, 65	0
9	2N	140/140 (100%)	0.58	6 (4%) 40 35	39, 52, 62, 70	0
10	1O	122/122 (100%)	-0.10	0 100 100	23, 35, 50, 57	0
10	2O	122/122 (100%)	0.35	0 100 100	38, 47, 59, 64	0
11	1P	149/150 (99%)	0.16	0 100 100	15, 40, 58, 63	0
11	2P	149/150 (99%)	0.60	5 (3%) 48 43	31, 55, 67, 72	0
12	1Q	141/141 (100%)	0.01	1 (0%) 84 81	22, 34, 45, 51	0
12	2Q	141/141 (100%)	0.77	3 (2%) 63 59	37, 52, 61, 68	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.23	0 100 100	21, 30, 43, 50	0
13	2R	118/118 (100%)	0.30	2 (1%) 69 65	33, 44, 52, 58	0
14	1S	110/112 (98%)	0.30	1 (0%) 81 78	32, 43, 54, 58	0
14	2S	110/112 (98%)	1.11	14 (12%) 8 6	52, 59, 63, 68	0
15	1T	131/146 (89%)	0.13	3 (2%) 61 57	28, 38, 57, 70	0
15	2T	131/146 (89%)	0.48	3 (2%) 61 57	39, 50, 63, 68	0
16	1U	116/118 (98%)	-0.27	0 100 100	17, 26, 40, 51	0
16	2U	116/118 (98%)	0.52	3 (2%) 57 52	33, 48, 61, 68	0
17	1V	101/101 (100%)	-0.09	0 100 100	16, 35, 49, 54	0
17	2V	101/101 (100%)	0.75	4 (3%) 42 38	38, 57, 63, 67	0
18	1W	112/113 (99%)	-0.17	1 (0%) 81 78	18, 26, 45, 62	0
18	2W	112/113 (99%)	0.19	2 (1%) 67 64	32, 42, 57, 76	0
19	1X	95/96 (98%)	0.01	1 (1%) 78 75	22, 33, 52, 63	0
19	2X	95/96 (98%)	0.74	8 (8%) 17 15	38, 52, 64, 69	0
20	1Y	107/110 (97%)	0.21	2 (1%) 66 62	32, 42, 55, 63	0
20	2Y	107/110 (97%)	0.94	8 (7%) 20 18	45, 57, 66, 72	0
21	1Z	203/206 (98%)	0.55	5 (2%) 58 54	32, 49, 61, 71	0
21	2Z	201/206 (97%)	1.12	12 (5%) 27 24	50, 62, 69, 77	0
22	10	83/85 (97%)	0.21	6 (7%) 21 19	23, 32, 58, 68	0
22	20	83/85 (97%)	0.84	6 (7%) 21 19	40, 51, 62, 69	0
23	11	97/98 (98%)	0.18	0 100 100	24, 39, 59, 61	0
23	21	97/98 (98%)	0.47	1 (1%) 79 76	35, 48, 63, 68	0
24	12	70/72 (97%)	0.25	2 (2%) 53 49	30, 43, 51, 62	0
24	22	70/72 (97%)	0.72	0 100 100	46, 58, 62, 65	0
25	13	59/60 (98%)	-0.03	0 100 100	22, 31, 49, 56	0
25	23	59/60 (98%)	0.61	3 (5%) 33 29	41, 49, 63, 72	0
26	14	69/71 (97%)	1.20	11 (15%) 5 4	50, 68, 75, 79	0
26	24	69/71 (97%)	1.78	25 (36%) 1 1	67, 73, 79, 81	0
27	15	59/60 (98%)	-0.11	1 (1%) 69 65	17, 28, 44, 55	0
27	25	59/60 (98%)	0.05	0 100 100	27, 42, 55, 65	0
28	16	53/54 (98%)	-0.14	0 100 100	27, 36, 49, 51	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.35	0 100 100	44, 51, 59, 63	0
29	17	48/49 (97%)	-0.23	0 100 100	16, 23, 48, 51	0
29	27	48/49 (97%)	0.14	2 (4%) 40 36	29, 36, 51, 62	0
30	18	64/65 (98%)	-0.15	0 100 100	22, 29, 36, 50	0
30	28	64/65 (98%)	0.46	2 (3%) 51 47	36, 45, 50, 59	0
31	19	37/37 (100%)	0.18	1 (2%) 56 51	26, 35, 50, 53	0
31	29	37/37 (100%)	0.87	2 (5%) 31 27	46, 54, 64, 66	0
32	1a	1488/1521 (97%)	0.35	33 (2%) 62 58	33, 60, 78, 90	0
32	2a	1492/1521 (98%)	0.53	45 (3%) 52 48	41, 65, 80, 90	0
33	1b	231/256 (90%)	1.25	32 (13%) 6 5	56, 66, 73, 79	0
33	2b	231/256 (90%)	1.46	55 (23%) 2 1	59, 69, 75, 80	0
34	1c	206/239 (86%)	0.97	11 (5%) 32 28	52, 63, 71, 74	0
34	2c	206/239 (86%)	1.46	40 (19%) 3 2	57, 69, 74, 80	0
35	1d	208/209 (99%)	1.01	17 (8%) 17 15	48, 61, 69, 73	0
35	2d	208/209 (99%)	1.03	16 (7%) 19 17	49, 61, 67, 70	0
36	1e	148/162 (91%)	0.64	1 (0%) 84 81	42, 57, 64, 69	0
36	2e	148/162 (91%)	1.00	10 (6%) 23 20	51, 61, 69, 74	0
37	1f	100/101 (99%)	0.71	2 (2%) 65 61	46, 58, 65, 67	0
37	2f	100/101 (99%)	0.65	0 100 100	48, 60, 65, 67	0
38	1g	155/156 (99%)	0.88	4 (2%) 57 52	52, 62, 67, 72	0
38	2g	155/156 (99%)	1.28	27 (17%) 4 3	59, 67, 71, 75	0
39	1h	137/138 (99%)	0.76	3 (2%) 62 58	47, 59, 64, 67	0
39	2h	137/138 (99%)	0.90	4 (2%) 53 49	54, 61, 66, 68	0
40	1i	127/128 (99%)	1.46	24 (18%) 3 2	56, 66, 72, 74	0
40	2i	126/128 (98%)	2.02	64 (50%) 0 0	61, 70, 75, 79	0
41	1j	97/105 (92%)	1.29	13 (13%) 7 5	55, 66, 73, 78	0
41	2j	96/105 (91%)	1.99	44 (45%) 0 0	61, 70, 75, 77	0
42	1k	114/129 (88%)	0.64	4 (3%) 47 42	40, 55, 64, 67	0
42	2k	114/129 (88%)	0.90	6 (5%) 32 28	49, 61, 68, 71	0
43	1l	121/132 (91%)	0.68	4 (3%) 49 45	45, 53, 60, 63	0
43	2l	121/132 (91%)	0.79	4 (3%) 49 45	44, 56, 63, 70	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	116/126 (92%)	1.18	16 (13%) 6 5	54, 65, 70, 77	0
44	2m	114/126 (90%)	1.47	20 (17%) 4 3	61, 69, 73, 76	0
45	1n	60/61 (98%)	1.11	5 (8%) 17 15	54, 61, 66, 71	0
45	2n	60/61 (98%)	1.92	19 (31%) 1 1	60, 68, 73, 79	0
46	1o	88/89 (98%)	0.83	6 (6%) 23 20	38, 55, 66, 72	0
46	2o	88/89 (98%)	1.01	5 (5%) 29 26	51, 61, 67, 74	0
47	1p	82/88 (93%)	1.37	10 (12%) 8 7	50, 61, 67, 74	0
47	2p	82/88 (93%)	1.18	9 (10%) 10 8	54, 60, 66, 70	0
48	1q	99/105 (94%)	1.01	7 (7%) 22 19	45, 58, 64, 69	0
48	2q	99/105 (94%)	0.77	3 (3%) 52 48	47, 59, 66, 70	0
49	1r	68/88 (77%)	0.73	1 (1%) 72 68	48, 57, 66, 73	0
49	2r	68/88 (77%)	0.97	6 (8%) 15 14	52, 61, 69, 74	0
50	1s	83/93 (89%)	1.10	6 (7%) 21 19	56, 65, 70, 76	0
50	2s	83/93 (89%)	1.59	16 (19%) 3 2	59, 70, 74, 78	0
51	1t	96/106 (90%)	1.26	16 (16%) 4 3	53, 61, 68, 70	0
51	2t	98/106 (92%)	1.01	8 (8%) 17 15	50, 60, 66, 71	0
52	1u	23/27 (85%)	1.31	5 (21%) 2 2	59, 62, 66, 69	0
52	2u	23/27 (85%)	2.20	14 (60%) 0 0	62, 68, 70, 71	0
53	1y	97/113 (85%)	0.84	4 (4%) 41 37	47, 56, 67, 71	0
53	2y	96/113 (84%)	2.55	72 (75%) 0 0	66, 74, 80, 82	0
54	1w	4/5 (80%)	0.51	0 100 100	45, 49, 56, 71	0
54	2w	4/5 (80%)	0.76	1 (25%) 2 1	50, 58, 65, 72	0
55	1x	3/4 (75%)	2.18	2 (66%) 0 0	61, 61, 67, 73	0
55	2x	3/4 (75%)	1.38	1 (33%) 1 1	65, 65, 69, 77	0
56	1v	3/3 (100%)	3.05	2 (66%) 0 0	50, 50, 59, 61	0
56	2v	3/3 (100%)	3.58	3 (100%) 0 0	58, 58, 66, 67	0
All	All	20798/21492 (96%)	0.41	1249 (6%) 27 24	14, 54, 74, 90	0

All (1249) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	8.2
1	1A	1087	G	7.2

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Mol	Chain	Res	Type	RSRZ
53	2y	98	ALA	6.6
45	1n	2	ALA	6.0
1	2A	2125	G	5.7
56	2v	3	ILE	5.5
41	2j	34	VAL	5.4
53	1y	98	ALA	5.3
44	1m	2	ALA	5.2
1	1A	1072	C	5.2
7	1H	2	SER	5.2
1	2A	2124	G	5.1
22	10	2	ALA	5.0
22	10	7	LEU	4.9
32	2a	1030(A)	G	4.9
40	1i	106	ALA	4.9
1	1A	1090	U	4.8
21	2Z	192	ALA	4.7
1	2A	2174	C	4.6
26	24	56	VAL	4.6
56	1v	3	ILE	4.6
52	2u	2	GLY	4.5
1	1A	1089	G	4.5
1	2A	2153	G	4.5
53	2y	40	ILE	4.5
1	2A	2139	C	4.5
41	2j	37	PRO	4.5
1	1A	1093	G	4.4
34	2c	77	ILE	4.4
53	2y	78	ILE	4.4
1	1A	1081	U	4.4
1	1A	1076	C	4.3
26	14	56	VAL	4.3
1	2A	2793	G	4.2
53	2y	61	LEU	4.2
53	2y	38	HIS	4.2
1	1A	1094	U	4.2
1	2A	2173	A	4.2
1	1A	1070	A	4.2
1	1A	1092	C	4.2
1	1A	1103	A	4.2
1	2A	2133	G	4.2
21	1Z	192	ALA	4.2
51	1t	103	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
33	1b	214	ILE	4.1
1	2A	2137	C	4.1
6	2G	160	VAL	4.1
1	2A	2803	C	4.1
1	2A	2138	C	4.1
40	2i	69	GLY	4.1
26	14	63	TYR	4.1
1	2A	2804	C	4.0
32	1a	1257	U	4.0
41	2j	24	VAL	4.0
53	2y	81	LEU	4.0
34	2c	8	ILE	4.0
7	2H	21	PRO	4.0
1	1A	1068	G	3.9
32	2a	1036	G	3.9
1	1A	1071	G	3.9
15	1T	131	ALA	3.9
40	2i	105	ASP	3.9
45	2n	13	THR	3.9
1	2A	2147	G	3.9
1	2A	2161	C	3.9
40	2i	102	LEU	3.8
50	2s	33	THR	3.8
1	1A	1099	G	3.8
1	2A	2160	G	3.8
34	1c	2	GLY	3.8
14	2S	22	GLY	3.8
1	2A	2896	C	3.8
1	2A	2132	U	3.8
26	14	49	PHE	3.8
1	1A	1088	A	3.8
5	1F	16	GLY	3.8
1	1A	2794	C	3.8
45	2n	5	ALA	3.7
1	2A	1064	C	3.7
40	2i	109	VAL	3.7
5	1F	208	GLY	3.7
22	20	8	GLY	3.7
1	1A	1066	U	3.7
53	2y	12	ILE	3.7
1	1A	1077	A	3.7
1	2A	1046	A	3.7

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Mol	Chain	Res	Type	RSRZ
40	1i	66	ARG	3.7
1	1A	2793	G	3.7
1	2A	2152	G	3.7
32	1a	1030(A)	G	3.7
41	2j	71	LEU	3.7
1	1A	2167	U	3.7
41	2j	46	ARG	3.7
1	1A	1086	A	3.6
35	1d	179	GLU	3.6
32	1a	1030	C	3.6
32	2a	1030	C	3.6
32	2a	1030(B)	C	3.6
1	1A	1078	U	3.6
1	2A	1085	A	3.6
1	2A	2126	A	3.6
6	2G	159	VAL	3.6
1	2A	2136	C	3.6
1	2A	2146	C	3.6
11	2P	99	LEU	3.6
40	2i	101	PHE	3.6
34	2c	152	ILE	3.6
32	2a	1257	U	3.6
1	1A	1074	G	3.6
6	1G	146	TYR	3.6
40	2i	122	ALA	3.6
38	2g	5	ARG	3.6
53	2y	35	ILE	3.6
53	2y	45	PRO	3.6
1	1A	1080	C	3.6
1	1A	2803	C	3.6
1	1A	1091	G	3.6
1	1A	1176	G	3.6
1	2A	2123	G	3.6
1	2A	2159	G	3.6
35	1d	2	GLY	3.5
40	2i	67	GLY	3.5
53	2y	52	ALA	3.5
1	1A	1064	C	3.5
51	2t	7	LYS	3.5
33	2b	121	LEU	3.5
1	1A	2792	G	3.5
1	2A	2805	G	3.5

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Mol	Chain	Res	Type	RSRZ
40	2i	18	PHE	3.5
38	2g	154	TYR	3.5
1	2A	2169	A	3.5
55	1x	73	A	3.5
32	1a	1036	G	3.5
12	2Q	59	ARG	3.5
1	2A	2145	C	3.5
32	1a	1030(B)	C	3.5
1	1A	1082	U	3.5
1	1A	1083	U	3.5
53	2y	88	LEU	3.5
40	2i	36	TYR	3.5
40	1i	15	ALA	3.5
40	2i	126	SER	3.5
26	24	49	PHE	3.5
8	2I	92	VAL	3.4
1	1A	2804	C	3.4
33	1b	19	HIS	3.4
1	1A	1067	A	3.4
1	1A	1098	A	3.4
1	2A	2131	G	3.4
33	1b	213	LEU	3.4
39	2h	2	LEU	3.4
53	2y	24	LEU	3.4
53	2y	41	LEU	3.4
40	2i	13	ALA	3.4
40	2i	106	ALA	3.4
1	2A	1067	A	3.4
8	1I	85	GLU	3.4
1	1A	1097	U	3.4
15	1T	130	ALA	3.4
53	2y	54	ILE	3.4
1	2A	2154	G	3.3
21	2Z	191	VAL	3.3
45	2n	33	VAL	3.3
40	1i	128	ARG	3.3
1	1A	1175	U	3.3
53	2y	6	THR	3.3
53	2y	62	VAL	3.3
1	1A	2174	C	3.3
6	2G	92	VAL	3.3
33	2b	7	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
47	1p	48	TRP	3.3
33	2b	38	GLY	3.3
38	2g	83	ALA	3.3
53	2y	5	ILE	3.3
1	1A	1095	A	3.3
1	2A	2171	A	3.3
53	2y	9	GLN	3.3
1	1A	1059	G	3.3
1	2A	2140	C	3.3
1	2A	2135	A	3.2
32	1a	1001	A	3.2
50	2s	9	VAL	3.2
46	2o	86	GLY	3.2
1	1A	1063	G	3.2
1	2A	2142	C	3.2
1	2A	2157	G	3.2
41	2j	26	ALA	3.2
1	1A	1057	A	3.2
8	2I	89	TYR	3.2
22	20	3	HIS	3.2
1	1A	2144	U	3.2
53	2y	16	ILE	3.2
21	1Z	188	ALA	3.2
1	2A	2162	G	3.2
33	2b	57	PHE	3.2
41	2j	62	HIS	3.2
50	2s	71	LEU	3.2
33	2b	199	TYR	3.2
56	1v	1	MET	3.2
44	2m	98	VAL	3.2
53	2y	53	THR	3.2
8	2I	146	ALA	3.2
1	2A	1076	C	3.2
1	1A	2116	G	3.2
1	1A	2893	G	3.2
34	1c	12	LEU	3.2
53	2y	27	LEU	3.2
44	1m	24	GLY	3.2
1	2A	2150	U	3.2
47	1p	19	ILE	3.2
51	1t	18	GLN	3.1
46	1o	19	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
52	2u	23	PRO	3.1
19	2X	92	LEU	3.1
1	2A	2106	G	3.1
1	2A	2151	G	3.1
17	2V	5	VAL	3.1
32	1a	1286	A	3.1
45	2n	25	VAL	3.1
40	2i	43	ALA	3.1
26	24	51	ASP	3.1
44	1m	56	LEU	3.1
1	2A	1536	C	3.1
44	2m	6	GLY	3.1
51	2t	103	GLY	3.1
32	2a	1031	G	3.1
53	2y	60	VAL	3.1
53	2y	39	ILE	3.1
1	2A	2122	U	3.1
1	2A	2144	U	3.1
8	1I	147	GLN	3.1
20	2Y	1	MET	3.1
52	2u	14	TRP	3.1
53	2y	55	ASN	3.1
1	1A	1100	C	3.1
1	1A	1104	C	3.1
26	24	43	TYR	3.1
1	2A	2158	A	3.1
6	1G	50	ALA	3.1
1	1A	2118	U	3.1
33	2b	21	ARG	3.1
26	14	50	VAL	3.1
40	2i	14	VAL	3.1
41	1j	4	ILE	3.1
53	2y	49	VAL	3.1
40	1i	94	ALA	3.0
56	2v	1	MET	3.0
1	2A	1091	G	3.0
41	2j	91	PRO	3.0
53	2y	14	PRO	3.0
26	24	9	LEU	3.0
33	1b	10	LEU	3.0
35	1d	157	LEU	3.0
40	2i	96	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
16	2U	73	GLY	3.0
41	2j	72	VAL	3.0
1	1A	888	C	3.0
51	1t	66	ALA	3.0
53	2y	50	ALA	3.0
6	2G	146	TYR	3.0
32	2a	1286	A	3.0
1	2A	2127	G	3.0
1	2A	2148	G	3.0
1	2A	2168	G	3.0
33	1b	136	VAL	3.0
41	2j	74	ILE	3.0
6	2G	145	THR	3.0
1	1A	1102	C	3.0
1	2A	2107	C	3.0
40	2i	62	TYR	3.0
50	2s	2	PRO	3.0
1	1A	1073	A	3.0
32	2a	1030(D)	A	3.0
40	2i	59	PHE	3.0
41	2j	54	PHE	3.0
40	2i	95	LYS	3.0
50	2s	4	SER	3.0
1	1A	1062	G	3.0
1	2A	1056	G	3.0
41	1j	74	ILE	3.0
47	1p	53	VAL	3.0
53	2y	20	VAL	3.0
40	2i	2	GLU	3.0
53	2y	3	MET	3.0
6	2G	2	PRO	3.0
1	2A	2111	C	3.0
22	20	7	LEU	3.0
1	1A	1065	U	3.0
1	2A	1096	A	3.0
50	1s	4	SER	3.0
40	2i	100	GLY	3.0
41	2j	38	ILE	2.9
1	1A	2123	G	2.9
1	2A	2802	G	2.9
1	2A	2894	G	2.9
53	2y	97	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
51	2t	6	PRO	2.9
33	2b	118	LEU	2.9
38	2g	38	LEU	2.9
12	2Q	104	PHE	2.9
53	2y	48	PHE	2.9
1	2A	2109	U	2.9
1	2A	2172	U	2.9
32	1a	1000	U	2.9
32	2a	1035	A	2.9
26	24	18	CYS	2.9
40	2i	6	GLY	2.9
33	2b	164	VAL	2.9
53	2y	13	THR	2.9
1	1A	1173	G	2.9
32	2a	1030(C)	G	2.9
22	10	5	LYS	2.9
51	1t	74	LYS	2.9
38	2g	16	LEU	2.9
26	24	67	TYR	2.9
26	14	51	ASP	2.9
26	14	59	PHE	2.9
32	1a	1029	C	2.9
15	1T	37	GLY	2.9
1	2A	2892	A	2.9
40	2i	74	ILE	2.9
40	2i	10	ARG	2.9
1	1A	2124	G	2.9
32	2a	1033	G	2.9
47	2p	82	GLN	2.9
41	2j	35	SER	2.9
1	1A	2172	U	2.9
1	1A	887	A	2.9
1	2A	2119	A	2.9
1	2A	2176	A	2.9
7	2H	44	VAL	2.9
50	2s	79	THR	2.9
8	2I	55	ALA	2.9
33	1b	29	ALA	2.9
34	2c	113	ALA	2.9
40	2i	56	LEU	2.9
32	1a	1001(A)	G	2.9
34	1c	107	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
40	2i	5	TYR	2.9
47	2p	39	TYR	2.9
33	1b	22	LYS	2.8
46	2o	87	ILE	2.8
51	2t	30	LYS	2.8
1	1A	2175	C	2.8
1	1A	2171	A	2.8
22	20	2	ALA	2.8
34	2c	149	ALA	2.8
40	2i	75	ASP	2.8
25	23	60	GLU	2.8
44	2m	31	LYS	2.8
46	2o	68	ARG	2.8
52	2u	15	ARG	2.8
52	2u	24	ARG	2.8
1	1A	2127	G	2.8
1	2A	1062	G	2.8
26	24	22	ILE	2.8
40	2i	63	ILE	2.8
53	2y	36	ASN	2.8
1	2A	2130	U	2.8
33	1b	229	VAL	2.8
38	2g	80	VAL	2.8
50	2s	41	VAL	2.8
40	1i	21	PRO	2.8
15	2T	130	ALA	2.8
1	1A	1085	A	2.8
39	1h	2	LEU	2.8
51	1t	99	LEU	2.8
18	2W	112	GLY	2.8
7	2H	136	ILE	2.8
34	2c	3	ASN	2.8
33	2b	136	VAL	2.8
1	1A	2159	G	2.8
32	2a	1026	G	2.8
9	2N	132	ALA	2.8
51	1t	49	ALA	2.8
1	1A	2896	C	2.8
1	2A	2108	C	2.8
53	2y	83	ARG	2.8
22	10	6	GLY	2.8
38	1g	156	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
26	14	32	TYR	2.8
53	2y	71	TYR	2.8
53	2y	64	SER	2.8
7	2H	79	VAL	2.8
1	1A	2150	U	2.8
34	2c	180	ALA	2.8
40	2i	46	ALA	2.8
1	1A	1055	G	2.8
1	1A	2112	G	2.8
1	1A	2805	G	2.8
32	1a	1023	G	2.8
32	1a	1024	G	2.8
40	1i	42	ARG	2.8
53	1y	9	GLN	2.8
53	2y	11	GLU	2.8
53	2y	66	LYS	2.8
32	2a	1029	C	2.8
50	2s	69	HIS	2.8
41	2j	36	GLY	2.7
51	2t	102	GLY	2.7
18	2W	60	ASN	2.7
33	1b	94	ASN	2.7
40	2i	125	TYR	2.7
41	2j	41	PRO	2.7
44	1m	113	PRO	2.7
45	2n	21	TYR	2.7
48	1q	99	SER	2.7
51	2t	11	SER	2.7
27	15	60	VAL	2.7
33	1b	218	ALA	2.7
34	2c	160	ALA	2.7
43	1l	26	ALA	2.7
50	2s	77	THR	2.7
1	2A	1081	U	2.7
32	1a	1026	G	2.7
1	1A	1069	A	2.7
1	1A	1075	C	2.7
1	1A	1079	C	2.7
1	1A	2176	A	2.7
1	2A	652(B)	A	2.7
1	2A	1084	A	2.7
1	2A	2143	C	2.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2170	A	2.7
40	2i	91	ASP	2.7
48	2q	71	PHE	2.7
41	2j	75	ILE	2.7
6	2G	139	LEU	2.7
53	2y	77	LEU	2.7
33	1b	188	ALA	2.7
42	2k	31	THR	2.7
32	1a	1020	U	2.7
53	2y	51	ASP	2.7
1	2A	2121	G	2.7
43	1l	63	GLY	2.7
1	1A	889	C	2.7
1	2A	645	C	2.7
1	2A	2175	C	2.7
21	2Z	146	ILE	2.7
36	2e	13	ILE	2.7
41	1j	50	ILE	2.7
47	2p	19	ILE	2.7
8	2I	3	VAL	2.7
23	21	2	SER	2.7
6	1G	152	LEU	2.7
29	27	48	LYS	2.7
40	2i	108	VAL	2.7
33	2b	44	LEU	2.7
33	2b	97	TRP	2.7
41	2j	90	LEU	2.7
33	2b	225	ALA	2.7
41	2j	92	THR	2.7
42	1k	13	GLN	2.7
1	1A	2109	U	2.7
1	2A	1082	U	2.7
41	2j	52	GLY	2.7
45	2n	7	ILE	2.7
1	1A	2126	A	2.7
1	1A	2158	A	2.7
1	1A	2168	G	2.7
1	1A	2170	A	2.7
1	2A	2141	G	2.7
1	2A	2893	G	2.7
32	2a	1277	C	2.7
6	2G	28	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
7	2H	41	MET	2.7
6	2G	76	SER	2.7
20	1Y	23	ARG	2.7
33	2b	142	LEU	2.7
40	2i	66	ARG	2.7
43	2l	18	VAL	2.7
44	2m	87	TYR	2.7
41	1j	20	ALA	2.7
53	2y	44	GLU	2.7
53	2y	82	GLU	2.7
33	2b	40	HIS	2.7
1	2A	2808	U	2.7
50	1s	13	ASP	2.6
6	2G	144	ILE	2.6
40	2i	123	PRO	2.6
40	2i	42	ARG	2.6
43	2l	89	ARG	2.6
1	1A	2892	A	2.6
1	2A	2134	A	2.6
7	2H	45	VAL	2.6
33	2b	10	LEU	2.6
35	1d	112	VAL	2.6
41	1j	44	VAL	2.6
48	2q	98	LEU	2.6
1	1A	2115	G	2.6
1	2A	2178	C	2.6
1	2A	2807	G	2.6
32	1a	306	G	2.6
32	1a	1033	G	2.6
44	2m	58	GLU	2.6
6	1G	151	ALA	2.6
34	2c	48	TYR	2.6
41	2j	67	THR	2.6
45	1n	5	ALA	2.6
47	2p	38	TYR	2.6
1	1A	1101	U	2.6
20	2Y	94	LYS	2.6
51	1t	69	GLY	2.6
7	2H	36	PRO	2.6
33	1b	131	PRO	2.6
35	2d	158	ILE	2.6
40	2i	49	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
20	1Y	1	MET	2.6
8	2I	47	LEU	2.6
6	1G	48	GLU	2.6
40	2i	17	VAL	2.6
40	2i	41	VAL	2.6
40	2i	44	VAL	2.6
1	2A	1073	A	2.6
51	1t	70	SER	2.6
53	2y	7	SER	2.6
1	1A	2107	C	2.6
1	1A	2161	C	2.6
40	1i	43	ALA	2.6
44	1m	28	ALA	2.6
44	2m	116	THR	2.6
1	2A	2165	G	2.6
19	2X	69	TYR	2.6
6	2G	100	TRP	2.6
41	2j	93	GLY	2.6
45	2n	55	GLY	2.6
1	1A	1060	U	2.6
1	2A	1066	U	2.6
21	1Z	1	MET	2.6
35	2d	162	LEU	2.6
45	2n	6	LEU	2.6
14	2S	46	VAL	2.6
33	1b	230	VAL	2.6
5	1F	15	SER	2.6
53	2y	84	GLN	2.6
35	2d	48	ALA	2.6
41	2j	32	ALA	2.6
1	1A	2143	C	2.6
26	24	63	TYR	2.6
32	2a	1260	C	2.6
33	1b	236	TYR	2.6
8	2I	90	GLY	2.6
40	2i	115	GLY	2.6
52	2u	11	GLY	2.6
34	2c	124	ILE	2.6
1	1A	2113	U	2.6
1	2A	2897	U	2.6
34	1c	94	LEU	2.6
21	2Z	161	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
35	1d	8	VAL	2.6
41	2j	44	VAL	2.6
48	1q	85	VAL	2.6
18	1W	111	HIS	2.6
34	2c	53	ALA	2.6
38	2g	128	ALA	2.6
49	2r	67	ALA	2.6
50	2s	63	THR	2.6
53	2y	32	THR	2.6
33	2b	236	TYR	2.6
1	1A	2145	C	2.5
33	1b	232	PRO	2.5
1	1A	2125	G	2.5
1	1A	2894	G	2.5
7	2H	89	ILE	2.5
32	1a	1030(C)	G	2.5
41	2j	23	ILE	2.5
33	2b	163	PHE	2.5
21	2Z	42	VAL	2.5
53	2y	4	ASN	2.5
33	2b	123	ALA	2.5
36	2e	94	ALA	2.5
38	2g	116	ALA	2.5
38	2g	117	ALA	2.5
40	1i	13	ALA	2.5
1	2A	6	A	2.5
32	2a	1004	A	2.5
52	2u	18	TYR	2.5
1	2A	2129	C	2.5
5	1F	131	GLY	2.5
8	2I	20	ASP	2.5
33	2b	39	ILE	2.5
34	2c	167	TRP	2.5
6	2G	3	LEU	2.5
17	2V	94	LEU	2.5
33	1b	17	PHE	2.5
32	1a	1002	G	2.5
32	2a	1003	G	2.5
33	2b	69	LEU	2.5
34	1c	87	LEU	2.5
1	2A	2118	U	2.5
6	2G	15	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
6	2G	109	VAL	2.5
8	2I	131	LYS	2.5
40	1i	14	VAL	2.5
53	2y	8	LYS	2.5
53	2y	79	ASN	2.5
5	2F	128	ALA	2.5
21	1Z	51	ALA	2.5
33	1b	130	ARG	2.5
40	2i	21	PRO	2.5
42	1k	25	TYR	2.5
31	29	37	GLY	2.5
44	1m	112	GLY	2.5
33	1b	128	GLU	2.5
1	1A	2142	C	2.5
1	2A	1509	C	2.5
50	2s	34	TRP	2.5
41	2j	40	LEU	2.5
40	2i	127	LYS	2.5
1	1A	2132	U	2.5
1	2A	2180	U	2.5
33	1b	37	ASN	2.5
33	2b	15	VAL	2.5
45	2n	56	VAL	2.5
32	2a	1032	G	2.5
36	1e	113	ALA	2.5
38	2g	76	ARG	2.5
38	2g	152	ALA	2.5
40	2i	76	ALA	2.5
41	1j	32	ALA	2.5
45	2n	59	ALA	2.5
26	24	66	SER	2.5
49	2r	59	SER	2.5
44	2m	24	GLY	2.5
53	2y	65	GLY	2.5
43	1l	64	TYR	2.5
33	2b	172	ILE	2.5
6	1G	82	LEU	2.5
34	2c	175	LEU	2.5
40	1i	56	LEU	2.5
41	2j	33	GLN	2.5
53	2y	46	GLN	2.5
32	2a	979	C	2.5

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Mol	Chain	Res	Type	RSRZ
8	2I	107	VAL	2.5
33	2b	184	VAL	2.5
1	1A	2130	U	2.5
41	1j	27	ALA	2.5
14	2S	21	THR	2.5
53	1y	70	MET	2.5
41	2j	77	PRO	2.4
44	2m	95	GLY	2.4
50	1s	26	GLY	2.4
6	2G	126	ASP	2.4
38	2g	120	ILE	2.4
41	2j	58	ASP	2.4
44	2m	59	TYR	2.4
6	1G	53	LEU	2.4
33	2b	149	LEU	2.4
33	2b	154	LEU	2.4
50	2s	5	LEU	2.4
1	2A	1445	A	2.4
1	2A	2602	A	2.4
5	2F	129	PHE	2.4
41	2j	69	ASN	2.4
51	2t	9	ASN	2.4
6	2G	155	MET	2.4
53	2y	42	SER	2.4
41	2j	64	GLU	2.4
1	2A	2112	G	2.4
14	2S	45	GLY	2.4
32	1a	1032	G	2.4
32	2a	1373	G	2.4
44	2m	46	LYS	2.4
44	2m	65	LYS	2.4
47	1p	50	LYS	2.4
33	2b	162	ILE	2.4
53	2y	74	ILE	2.4
6	2G	90	LEU	2.4
14	2S	7	TYR	2.4
35	1d	194	LEU	2.4
35	2d	20	TYR	2.4
41	1j	71	LEU	2.4
42	2k	25	TYR	2.4
51	2t	13	LEU	2.4
53	2y	89	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
41	2j	47	PHE	2.4
52	1u	24	ARG	2.4
1	1A	2114	A	2.4
1	1A	2119	A	2.4
1	2A	1088	A	2.4
7	2H	19	VAL	2.4
26	24	50	VAL	2.4
1	1A	34	C	2.4
32	2a	1038	C	2.4
45	2n	10	ALA	2.4
47	2p	70	ALA	2.4
41	2j	48	THR	2.4
53	2y	29	LYS	2.4
30	28	38	GLY	2.4
38	2g	81	GLY	2.4
40	1i	67	GLY	2.4
6	2G	88	ILE	2.4
6	2G	157	ILE	2.4
31	29	17	ILE	2.4
44	2m	4	ILE	2.4
26	24	47	GLN	2.4
32	1a	1021	G	2.4
36	2e	12	LEU	2.4
41	2j	16	LEU	2.4
42	1k	98	LEU	2.4
7	2H	101	ARG	2.4
11	2P	79	ARG	2.4
52	2u	6	ARG	2.4
53	2y	67	HIS	2.4
11	2P	110	TYR	2.4
26	24	35	VAL	2.4
35	2d	203	VAL	2.4
8	2I	74	ASN	2.4
41	2j	76	ASN	2.4
20	2Y	105	ALA	2.4
29	27	45	ALA	2.4
33	1b	34	ALA	2.4
49	2r	60	ALA	2.4
53	2y	21	ALA	2.4
8	1I	70	GLU	2.4
1	2A	1079	C	2.4
6	2G	87	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
40	1i	12	GLU	2.4
40	2i	11	LYS	2.4
47	1p	12	LYS	2.4
2	1B	1	U	2.4
32	2a	1116	C	2.4
12	1Q	33	GLY	2.4
22	20	76	GLY	2.4
35	2d	2	GLY	2.4
21	2Z	125	LEU	2.4
24	12	70	GLN	2.4
33	2b	160	ASP	2.4
22	10	3	HIS	2.4
53	2y	95	ARG	2.4
1	1A	2141	G	2.4
26	24	59	PHE	2.4
50	2s	51	VAL	2.4
1	2A	1095	A	2.4
8	2I	46	ALA	2.4
34	2c	100	ALA	2.4
41	2j	27	ALA	2.4
6	2G	137	GLU	2.4
40	2i	12	GLU	2.4
53	2y	30	TRP	2.4
1	2A	1065	U	2.3
1	2A	34	C	2.3
15	2T	69	GLY	2.3
32	1a	1027	C	2.3
32	2a	970	C	2.3
44	1m	100	GLY	2.3
19	2X	95	LEU	2.3
33	1b	39	ILE	2.3
33	2b	196	LEU	2.3
33	2b	201	ILE	2.3
34	2c	5	ILE	2.3
26	24	65	ASP	2.3
33	1b	40	HIS	2.3
53	2y	10	MET	2.3
52	1u	18	TYR	2.3
14	2S	33	LYS	2.3
22	10	4	LYS	2.3
33	1b	165	VAL	2.3
33	2b	81	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
34	1c	207	VAL	2.3
38	2g	118	VAL	2.3
44	1m	54	VAL	2.3
15	2T	131	ALA	2.3
33	2b	218	ALA	2.3
36	2e	52	PRO	2.3
41	2j	53	PRO	2.3
39	2h	3	THR	2.3
49	2r	25	THR	2.3
1	1A	1084	A	2.3
1	1A	1096	A	2.3
1	1A	2117	A	2.3
1	1A	2801(A)	A	2.3
1	2A	2801(A)	A	2.3
32	1a	1030(D)	A	2.3
6	2G	42	GLY	2.3
26	14	55	ARG	2.3
33	2b	72	GLY	2.3
36	2e	22	GLY	2.3
5	2F	181	LEU	2.3
6	2G	140	ILE	2.3
7	2H	71	LEU	2.3
21	2Z	76	LEU	2.3
33	1b	201	ILE	2.3
35	2d	146	ILE	2.3
35	2d	160	GLN	2.3
1	2A	1072	C	2.3
1	2A	2794	C	2.3
35	2d	144	ASP	2.3
42	2k	110	ASP	2.3
6	2G	117	PHE	2.3
40	1i	37	PHE	2.3
53	2y	91	LYS	2.3
6	2G	131	TYR	2.3
36	2e	67	VAL	2.3
47	1p	38	TYR	2.3
34	2c	163	ALA	2.3
44	2m	5	ALA	2.3
53	2y	37	PRO	2.3
53	2y	94	ALA	2.3
1	2A	2104	G	2.3
1	2A	2110	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2181	G	2.3
1	2A	2792	G	2.3
32	1a	1003	G	2.3
33	2b	67	THR	2.3
38	2g	24	THR	2.3
44	1m	49	THR	2.3
53	1y	2	THR	2.3
1	2A	2310	A	2.3
32	1a	1005	A	2.3
34	1c	148	GLY	2.3
34	2c	145	GLY	2.3
51	1t	96	GLY	2.3
52	2u	16	GLY	2.3
33	1b	187	LEU	2.3
40	2i	81	ILE	2.3
1	1A	1061	U	2.3
6	2G	156	ASP	2.3
40	1i	91	ASP	2.3
1	1A	2146	C	2.3
1	2A	2128	C	2.3
1	2A	2179	C	2.3
32	1a	63	C	2.3
33	2b	22	LYS	2.3
14	2S	29	PHE	2.3
33	1b	122	PHE	2.3
33	2b	181	PHE	2.3
47	2p	80	PHE	2.3
6	2G	149	VAL	2.3
9	2N	9	VAL	2.3
21	2Z	86	VAL	2.3
48	2q	9	VAL	2.3
4	2E	204	ALA	2.3
7	2H	128	PRO	2.3
19	2X	84	ALA	2.3
35	1d	149	ALA	2.3
44	2m	12	ASN	2.3
44	2m	51	ALA	2.3
34	2c	78	GLY	2.3
40	2i	24	GLY	2.3
52	2u	4	GLY	2.3
1	1A	1056	G	2.3
34	2c	14	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
44	2m	90	LEU	2.3
1	1A	2173	A	2.3
1	1A	2602	A	2.3
1	2A	529	A	2.3
32	2a	1001	A	2.3
6	2G	116	ASP	2.3
1	2A	1105	U	2.3
1	2A	2113	U	2.3
1	1A	1509	C	2.3
6	2G	31	VAL	2.3
9	2N	53	VAL	2.3
26	24	33	VAL	2.3
33	2b	230	VAL	2.3
44	2m	54	VAL	2.3
6	1G	21	ARG	2.3
13	2R	68	ARG	2.3
26	24	39	CYS	2.3
6	1G	46	ALA	2.2
6	2G	12	TYR	2.3
35	1d	132	ARG	2.3
35	1d	138	TYR	2.3
44	1m	102	ARG	2.3
35	2d	111	ALA	2.2
44	2m	72	ALA	2.2
46	1o	22	THR	2.2
56	2v	2	THR	2.2
20	2Y	80	GLY	2.2
35	2d	16	GLY	2.2
46	1o	89	GLY	2.2
52	2u	19	GLY	2.2
53	2y	33	HIS	2.2
31	19	17	ILE	2.2
33	2b	222	ILE	2.2
34	2c	39	ILE	2.2
41	2j	55	LYS	2.2
43	2l	124	LYS	2.2
47	1p	43	LYS	2.2
52	2u	13	ILE	2.2
54	2w	73	A	2.2
1	1A	2160	G	2.2
1	2A	1063	G	2.2
1	2A	2155	G	2.2

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Mol	Chain	Res	Type	RSRZ
32	1a	1034	G	2.2
32	2a	1025	U	2.2
26	24	30	GLU	2.2
53	2y	76	GLU	2.2
53	2y	93	GLU	2.2
6	2G	80	PHE	2.2
6	2G	141	PHE	2.2
49	1r	43	PHE	2.2
1	2A	886	C	2.2
1	2A	1118	C	2.2
1	2A	2105	C	2.2
7	2H	39	PRO	2.2
8	2I	18	VAL	2.2
8	2I	82	ARG	2.2
19	2X	68	ARG	2.2
19	2X	83	VAL	2.2
35	2d	105	VAL	2.2
38	1g	23	VAL	2.2
40	1i	49	PRO	2.2
41	1j	72	VAL	2.2
47	2p	26	ARG	2.2
12	2Q	136	ALA	2.2
19	2X	45	THR	2.2
20	2Y	93	GLY	2.2
42	2k	118	GLY	2.2
33	2b	11	LEU	2.2
6	2G	124	SER	2.2
46	2o	21	ASP	2.2
38	2g	156	TRP	2.2
47	1p	59	TRP	2.2
1	2A	1057	A	2.2
1	2A	2114	A	2.2
8	1I	10	GLU	2.2
1	2A	271(N)	U	2.2
32	1a	1040	U	2.2
1	2A	1071	G	2.2
1	2A	1087	G	2.2
1	2A	2182	G	2.2
20	2Y	73	ARG	2.2
26	14	48	ARG	2.2
38	2g	41	ARG	2.2
40	2i	107	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
41	2j	63	PHE	2.2
35	1d	148	VAL	2.2
38	1g	75	VAL	2.2
38	2g	112	PRO	2.2
40	1i	41	VAL	2.2
52	1u	23	PRO	2.2
1	1A	1053	C	2.2
32	2a	1019	C	2.2
32	2a	1039	C	2.2
33	2b	161	ALA	2.2
39	2h	15	ASN	2.2
51	1t	97	ALA	2.2
3	1D	276	LYS	2.2
8	1I	86	THR	2.2
11	2P	68	GLN	2.2
33	2b	148	TYR	2.2
35	1d	4	TYR	2.2
42	2k	75	TYR	2.2
45	2n	9	LYS	2.2
39	1h	24	THR	2.2
52	1u	21	TYR	2.2
8	1I	38	LEU	2.2
34	2c	34	LEU	2.2
35	2d	183	GLY	2.2
41	1j	65	LEU	2.2
48	1q	80	GLY	2.2
49	2r	58	LEU	2.2
44	1m	4	ILE	2.2
46	1o	3	ILE	2.2
40	1i	126	SER	2.2
45	1n	32	SER	2.2
51	1t	11	SER	2.2
34	2c	79	ARG	2.2
47	2p	59	TRP	2.2
1	1A	2629	A	2.2
1	2A	1083	U	2.2
1	2A	1090	U	2.2
6	2G	180	PHE	2.2
34	2c	66	VAL	2.2
1	1A	2133	G	2.2
1	2A	2116	G	2.2
1	2A	2207	G	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1001(A)	G	2.2
32	2a	1017	G	2.2
32	2a	1034	G	2.2
6	2G	46	ALA	2.2
21	2Z	113	ALA	2.2
44	1m	51	ALA	2.2
45	1n	20	ALA	2.2
51	1t	95	ALA	2.2
53	2y	90	HIS	2.2
20	2Y	5	MET	2.2
1	2A	1080	C	2.2
9	2N	73	THR	2.2
14	2S	47	THR	2.2
3	2D	37	LEU	2.2
6	2G	152	LEU	2.2
7	2H	105	LEU	2.2
16	2U	74	LEU	2.2
32	2a	1006	C	2.2
32	2a	1027	C	2.2
35	1d	11	LEU	2.2
40	2i	88	TYR	2.2
51	1t	102	GLY	2.2
53	2y	85	LEU	2.2
33	2b	200	ILE	2.2
39	1h	134	ILE	2.2
46	1o	87	ILE	2.2
34	2c	49	SER	2.2
41	1j	30	SER	2.2
8	2I	85	GLU	2.2
6	2G	122	PRO	2.2
38	2g	14	PRO	2.2
1	2A	1460	A	2.1
2	2B	1	U	2.2
7	2H	175	LYS	2.2
9	2N	104	LYS	2.2
16	2U	90	VAL	2.1
32	2a	202	U	2.2
32	2a	1532	U	2.2
35	2d	75	PHE	2.2
38	2g	62	PHE	2.2
45	2n	4	LYS	2.2
5	2F	21	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	41	GLN	2.1
33	2b	34	ALA	2.1
45	2n	20	ALA	2.1
1	2A	1089	G	2.1
6	2G	43	LEU	2.1
8	2I	106	GLY	2.1
32	2a	1138	G	2.1
34	1c	9	GLY	2.1
40	1i	64	THR	2.1
40	2i	19	LEU	2.1
41	2j	31	GLY	2.1
44	2m	85	GLY	2.1
50	1s	16	LEU	2.1
6	2G	77	ILE	2.1
8	2I	97	ILE	2.1
17	2V	12	TYR	2.1
26	24	5	ILE	2.1
38	2g	85	TYR	2.1
40	2i	4	TYR	2.1
32	2a	1259	C	2.1
24	12	69	ARG	2.1
26	24	55	ARG	2.1
35	1d	3	ARG	2.1
40	1i	10	ARG	2.1
40	2i	9	ARG	2.1
41	2j	19	SER	2.1
3	2D	276	LYS	2.1
6	2G	142	PRO	2.1
26	14	69	LYS	2.1
34	2c	4	LYS	2.1
34	2c	195	VAL	2.1
40	2i	26	VAL	2.1
44	1m	64	TRP	2.1
32	2a	1000	U	2.1
32	2a	1219	U	2.1
40	2i	58	HIS	2.1
1	2A	229	A	2.1
34	2c	200	ALA	2.1
7	2H	7	LEU	2.1
7	2H	67	LEU	2.1
7	2H	106	THR	2.1
8	2I	12	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
19	2X	35	THR	2.1
33	2b	168	THR	2.1
34	1c	194	GLY	2.1
35	1d	108	LEU	2.1
40	2i	8	GLY	2.1
40	2i	30	GLY	2.1
40	2i	57	GLY	2.1
40	2i	64	THR	2.1
40	2i	72	GLY	2.1
50	2s	20	LEU	2.1
33	1b	42	ILE	2.1
34	1c	8	ILE	2.1
1	1A	1058	G	2.1
1	2A	2156	G	2.1
7	2H	104	GLU	2.1
19	1X	69	TYR	2.1
33	1b	36	ARG	2.1
35	2d	4	TYR	2.1
40	1i	51	ARG	2.1
40	2i	114	TYR	2.1
32	1a	630	G	2.1
32	2a	630	G	2.1
32	2a	1124	G	2.1
1	1A	2128	C	2.1
1	2A	2177	C	2.1
33	2b	124	SER	2.1
42	1k	36	ASP	2.1
48	1q	79	SER	2.1
45	2n	11	LYS	2.1
47	1p	46	PRO	2.1
34	2c	10	PHE	2.1
38	2g	43	PHE	2.1
21	2Z	90	VAL	2.1
26	24	10	VAL	2.1
34	1c	138	VAL	2.1
35	2d	74	GLN	2.1
37	1f	16	GLN	2.1
44	1m	117	VAL	2.1
1	2A	2167	U	2.1
7	2H	75	ALA	2.1
7	2H	165	ALA	2.1
34	2c	168	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
36	2e	21	ALA	2.1
36	2e	104	ALA	2.1
53	2y	73	ALA	2.1
34	2c	42	LEU	2.1
40	1i	47	LEU	2.1
43	1l	60	LEU	2.1
55	2x	73	A	2.1
6	2G	129	GLY	2.1
50	1s	39	THR	2.1
14	2S	3	ARG	2.1
14	2S	17	ARG	2.1
40	2i	83	ARG	2.1
48	1q	63	ARG	2.1
52	1u	9	ARG	2.1
35	1d	5	ILE	2.1
41	2j	6	ILE	2.1
39	2h	48	TYR	2.1
20	2Y	88	LYS	2.1
22	20	4	LYS	2.1
26	24	28	LYS	2.1
33	1b	132	LYS	2.1
52	2u	5	ASP	2.1
53	2y	26	LYS	2.1
7	2H	63	SER	2.1
14	2S	53	SER	2.1
34	2c	144	SER	2.1
1	2A	1044	G	2.1
1	2A	1171	G	2.1
1	2A	2149	G	2.1
32	2a	1002	G	2.1
32	1a	1019	C	2.1
32	1a	1037	C	2.1
32	2a	1322	C	2.1
7	2H	15	VAL	2.1
21	2Z	136	PHE	2.1
25	23	59	VAL	2.1
33	2b	17	PHE	2.1
33	2b	165	VAL	2.1
34	2c	99	VAL	2.1
34	2c	138	VAL	2.1
38	2g	9	VAL	2.1
7	2H	145	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
36	2e	30	ALA	2.1
40	2i	82	ALA	2.1
1	1A	9	U	2.1
33	1b	97	TRP	2.1
6	2G	127	GLY	2.1
7	2H	59	ARG	2.1
34	2c	41	GLY	2.1
38	1g	132	GLY	2.1
49	2r	54	ARG	2.1
50	2s	3	ARG	2.1
50	2s	8	GLY	2.1
6	2G	64	THR	2.1
8	2I	78	THR	2.1
26	24	27	THR	2.1
26	24	52	THR	2.1
41	1j	100	THR	2.1
44	1m	50	GLU	2.1
53	2y	56	THR	2.1
1	2A	1070	A	2.1
6	2G	52	ILE	2.1
34	2c	157	ILE	2.1
36	2e	109	ILE	2.1
33	2b	75	LYS	2.1
43	2l	126	LYS	2.1
40	2i	92	TYR	2.1
51	1t	64	ASP	2.1
6	1G	76	SER	2.1
33	2b	233	SER	2.1
38	2g	77	SER	2.1
26	24	7	PRO	2.1
41	2j	39	PRO	2.1
1	1A	2111	C	2.1
1	2A	614(B)	G	2.0
1	2A	2184	G	2.0
32	2a	447	G	2.0
32	2a	1037	C	2.1
46	2o	62	GLN	2.0
50	1s	56	GLN	2.0
33	2b	55	PHE	2.0
33	2b	152	PHE	2.0
48	1q	23	VAL	2.0
7	2H	3	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
21	1Z	187	ALA	2.0
30	28	46	ARG	2.0
33	1b	123	ALA	2.0
33	2b	237	ALA	2.0
45	2n	48	ALA	2.0
48	1q	91	ARG	2.0
6	2G	82	LEU	2.0
8	2I	75	LEU	2.0
14	2S	73	LEU	2.0
33	2b	187	LEU	2.0
37	1f	98	LEU	2.0
33	2b	107	THR	2.0
34	2c	18	TRP	2.0
35	1d	180	GLY	2.0
14	2S	35	ILE	2.0
26	14	52	THR	2.0
32	1a	1025	U	2.0
32	2a	1281	U	2.0
40	1i	95	LYS	2.0
40	2i	7	THR	2.0
47	2p	48	TRP	2.0
40	2i	70	LYS	2.0
51	1t	100	ILE	2.0
52	2u	3	LYS	2.0
33	2b	33	TYR	2.0
45	1n	34	TYR	2.0
47	1p	29	ASP	2.0
9	1N	8	GLN	2.0
1	1A	2108	C	2.0
1	1A	2140	C	2.0
1	2A	652(T)	C	2.0
1	2A	1075	C	2.0
11	2P	15	ARG	2.0
21	2Z	74	VAL	2.0
32	1a	1141	C	2.0
40	1i	104	ARG	2.0
41	2j	49	VAL	2.0
44	2m	102	ARG	2.0
53	2y	96	ARG	2.0
55	1x	74	C	2.0
1	2A	1115	G	2.0
1	2A	2206	G	2.0

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Mol	Chain	Res	Type	RSRZ
6	1G	73	ALA	2.0
32	1a	1010	G	2.0
6	2G	34	LEU	2.0
9	2N	26	LEU	2.0
17	2V	20	LEU	2.0
33	2b	188	ALA	2.0
34	2c	12	LEU	2.0
34	2c	87	LEU	2.0
34	2c	129	ALA	2.0
34	2c	187	ALA	2.0
38	2g	104	LEU	2.0
41	1j	26	ALA	2.0
42	2k	15	ALA	2.0
44	1m	6	GLY	2.0
45	2n	58	LYS	2.0
53	2y	68	GLU	2.0
13	2R	7	GLY	2.0
38	2g	37	ASN	2.0
51	1t	101	GLY	2.0
14	1S	40	ILE	2.0
45	2n	22	THR	2.0
1	1A	1045	A	2.0
25	23	2	PRO	2.0
33	1b	48	MET	2.0
38	2g	93	PRO	2.0
41	2j	17	ASP	2.0
14	2S	92	TYR	2.0
35	1d	71	SER	2.0
46	1o	69	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	0.77	0.14	63,76,78,90	0
1	PSU	2A	1917	20/21	0.85	0.11	63,70,85,92	0
32	M2G	2a	966	25/26	0.85	0.17	57,64,74,84	0
55	8AN	1x	76	22/23	0.85	0.17	42,60,70,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	2MG	2a	1207	24/25	0.87	0.13	67,73,77,83	0
1	PSU	2A	1911	20/21	0.87	0.11	62,67,77,78	0
55	8AN	2x	76	22/23	0.87	0.15	49,64,72,84	0
32	5MC	1a	967	21/22	0.89	0.14	57,62,69,73	0
1	5MU	1A	1915	21/22	0.90	0.11	54,65,69,74	0
32	2MG	1a	1207	24/25	0.91	0.11	54,65,69,72	0
1	PSU	1A	1917	20/21	0.92	0.09	54,62,70,72	0
32	PSU	2a	516	20/21	0.92	0.09	63,68,75,76	0
1	PSU	1A	1911	20/21	0.93	0.09	49,57,64,68	0
43	0TD	2l	92	10/11	0.93	0.12	53,60,62,62	0
1	OMC	2A	1920	21/22	0.93	0.12	52,60,66,69	0
32	5MC	2a	967	21/22	0.93	0.13	60,65,71,72	0
32	5MC	1a	1407	21/22	0.94	0.10	40,50,54,58	0
32	4OC	2a	1402	22/23	0.94	0.11	53,59,65,67	0
32	MA6	2a	1518	24/25	0.94	0.12	52,58,61,64	0
32	G7M	2a	527	24/25	0.94	0.10	53,57,60,66	0
43	0TD	1l	92	10/11	0.94	0.12	45,52,57,58	0
32	PSU	1a	516	20/21	0.94	0.09	54,60,67,78	0
32	5MC	1a	1400	21/22	0.95	0.11	42,50,61,61	0
32	5MC	2a	1404	21/22	0.95	0.09	51,55,58,60	0
32	5MC	2a	1407	21/22	0.95	0.11	50,59,63,67	0
32	UR3	2a	1498	21/22	0.95	0.09	52,56,60,63	0
32	4OC	1a	1402	22/23	0.95	0.09	47,49,53,62	0
32	MA6	2a	1519	24/25	0.95	0.12	46,55,60,63	0
1	5MC	2A	1942	21/22	0.95	0.09	39,46,52,58	0
32	G7M	1a	527	24/25	0.95	0.09	44,51,55,57	0
32	5MC	2a	1400	21/22	0.95	0.13	51,68,74,76	0
32	M2G	1a	966	25/26	0.96	0.09	46,54,61,62	0
32	5MC	1a	1404	21/22	0.96	0.09	40,47,50,53	0
1	PSU	1A	2605	20/21	0.96	0.08	18,26,29,29	0
1	5MU	2A	1939	21/22	0.96	0.09	32,38,43,44	0
32	UR3	1a	1498	21/22	0.96	0.09	38,46,49,62	0
1	5MC	2A	1962	21/22	0.96	0.08	32,41,47,52	0
1	2MU	2A	2552	21/23	0.96	0.08	28,37,42,43	0
32	MA6	1a	1518	24/25	0.96	0.10	36,43,49,55	0
32	MA6	1a	1519	24/25	0.96	0.09	40,43,49,50	0
1	OMC	1A	1920	21/22	0.96	0.10	41,51,58,59	0
1	5MC	1A	1942	21/22	0.96	0.07	28,33,38,42	0
1	2MA	2A	2503	23/24	0.97	0.08	23,29,34,35	0
1	OMG	2A	2251	24/25	0.97	0.08	33,37,42,46	0
1	PSU	2A	2605	20/21	0.97	0.08	26,36,43,44	0
1	5MU	1A	1939	21/22	0.98	0.06	19,24,27,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	5MC	1A	1962	21/22	0.98	0.07	26,30,35,38	0
1	OMG	1A	2251	24/25	0.98	0.07	15,21,32,36	0
1	2MA	1A	2503	23/24	0.98	0.06	14,19,22,23	0
1	2MU	1A	2552	21/23	0.98	0.07	20,28,33,34	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3866	1/1	0.55	0.18	65,65,65,65	0
57	MG	2O	202	1/1	0.58	0.19	73,73,73,73	0
57	MG	1a	3182	1/1	0.62	0.20	77,77,77,77	0
57	MG	2A	3624	1/1	0.63	0.19	70,70,70,70	0
57	MG	1A	3977	1/1	0.64	0.20	34,34,34,34	0
57	MG	2A	3459	1/1	0.64	0.20	53,53,53,53	0
57	MG	1A	3504	1/1	0.65	0.17	50,50,50,50	0
57	MG	2A	3528	1/1	0.66	0.16	64,64,64,64	0
57	MG	1A	3883	1/1	0.67	0.20	57,57,57,57	0
57	MG	1a	3174	1/1	0.68	0.15	75,75,75,75	0
57	MG	1A	3408	1/1	0.68	0.13	71,71,71,71	0
57	MG	1P	203	1/1	0.70	0.25	42,42,42,42	0
57	MG	2A	3559	1/1	0.70	0.19	62,62,62,62	0
57	MG	1A	3803	1/1	0.71	0.16	73,73,73,73	0
57	MG	1A	3437	1/1	0.71	0.24	64,64,64,64	0
57	MG	1a	3228	1/1	0.72	0.15	72,72,72,72	0
57	MG	1A	3852	1/1	0.72	0.14	52,52,52,52	0
57	MG	2A	3240	1/1	0.73	0.14	66,66,66,66	0
57	MG	2G	203	1/1	0.73	0.20	65,65,65,65	0
57	MG	1a	3203	1/1	0.73	0.17	59,59,59,59	0
57	MG	1A	3969	1/1	0.74	0.12	30,30,30,30	0
57	MG	2A	3121	1/1	0.74	0.20	73,73,73,73	0
57	MG	1A	3663	1/1	0.74	0.18	62,62,62,62	0
57	MG	2A	3235	1/1	0.75	0.28	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	3063	1/1	0.75	0.21	69,69,69,69	0
57	MG	1A	3984	1/1	0.75	0.24	38,38,38,38	0
57	MG	1A	3535	1/1	0.75	0.21	71,71,71,71	0
57	MG	2A	3159	1/1	0.76	0.17	63,63,63,63	0
57	MG	2A	3433	1/1	0.76	0.13	76,76,76,76	0
57	MG	1a	3102	1/1	0.77	0.17	61,61,61,61	0
57	MG	1A	3528	1/1	0.77	0.14	44,44,44,44	0
57	MG	2A	3627	1/1	0.77	0.19	58,58,58,58	0
57	MG	1A	3990	1/1	0.77	0.13	82,82,82,82	0
57	MG	2A	3539	1/1	0.77	0.16	56,56,56,56	0
57	MG	2a	3008	1/1	0.77	0.20	63,63,63,63	0
57	MG	2A	3377	1/1	0.78	0.18	70,70,70,70	0
57	MG	1A	3742	1/1	0.78	0.13	74,74,74,74	0
57	MG	1A	3783	1/1	0.78	0.22	59,59,59,59	0
57	MG	1a	3188	1/1	0.78	0.13	68,68,68,68	0
57	MG	1A	3996	1/1	0.78	0.19	83,83,83,83	0
57	MG	1A	3957	1/1	0.78	0.14	67,67,67,67	0
57	MG	2A	3572	1/1	0.78	0.15	42,42,42,42	0
57	MG	1A	3262	1/1	0.78	0.16	68,68,68,68	0
57	MG	1a	3092	1/1	0.78	0.21	68,68,68,68	0
57	MG	2A	3207	1/1	0.78	0.19	64,64,64,64	0
57	MG	1A	3283	1/1	0.78	0.10	66,66,66,66	0
57	MG	1a	3144	1/1	0.78	0.20	78,78,78,78	0
57	MG	1A	3514	1/1	0.79	0.12	53,53,53,53	0
57	MG	1D	315	1/1	0.79	0.16	68,68,68,68	0
57	MG	1A	3939	1/1	0.79	0.17	58,58,58,58	0
57	MG	2A	3509	1/1	0.79	0.20	55,55,55,55	0
57	MG	1A	3361	1/1	0.79	0.10	27,27,27,27	0
57	MG	1a	3229	1/1	0.79	0.19	63,63,63,63	0
57	MG	1a	3239	1/1	0.79	0.21	74,74,74,74	0
57	MG	1A	3785	1/1	0.79	0.17	59,59,59,59	0
57	MG	1A	3413	1/1	0.79	0.14	62,62,62,62	0
57	MG	1A	3594	1/1	0.79	0.24	66,66,66,66	0
57	MG	2E	301	1/1	0.79	0.19	39,39,39,39	0
57	MG	1a	3150	1/1	0.79	0.15	59,59,59,59	0
57	MG	1A	3509	1/1	0.79	0.13	28,28,28,28	0
57	MG	2A	3341	1/1	0.79	0.13	42,42,42,42	0
59	ARG	1A	4023	12/12	0.79	0.18	43,60,64,64	0
57	MG	1A	3705	1/1	0.80	0.13	64,64,64,64	0
57	MG	1A	3940	1/1	0.80	0.11	74,74,74,74	0
57	MG	1A	3881	1/1	0.80	0.15	38,38,38,38	0
57	MG	2A	3486	1/1	0.80	0.16	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	3077	1/1	0.80	0.29	65,65,65,65	0
57	MG	1A	3753	1/1	0.80	0.15	45,45,45,45	0
57	MG	2A	3279	1/1	0.80	0.23	61,61,61,61	0
57	MG	2a	3133	1/1	0.80	0.20	72,72,72,72	0
57	MG	2a	3182	1/1	0.80	0.13	82,82,82,82	0
57	MG	1a	3262	1/1	0.80	0.16	61,61,61,61	0
57	MG	2A	3540	1/1	0.81	0.11	55,55,55,55	0
57	MG	2A	3299	1/1	0.81	0.12	33,33,33,33	0
57	MG	1a	3172	1/1	0.81	0.18	65,65,65,65	0
57	MG	2A	3591	1/1	0.81	0.11	38,38,38,38	0
57	MG	1A	3858	1/1	0.81	0.15	43,43,43,43	0
57	MG	2A	3404	1/1	0.81	0.12	52,52,52,52	0
57	MG	2A	3668	1/1	0.81	0.15	68,68,68,68	0
57	MG	1a	3097	1/1	0.81	0.58	81,81,81,81	0
57	MG	2A	3454	1/1	0.81	0.16	72,72,72,72	0
57	MG	1a	3187	1/1	0.81	0.24	68,68,68,68	0
57	MG	2U	201	1/1	0.81	0.32	72,72,72,72	0
57	MG	1A	3568	1/1	0.81	0.10	71,71,71,71	0
57	MG	2a	3124	1/1	0.81	0.15	64,64,64,64	0
57	MG	1A	3889	1/1	0.81	0.12	52,52,52,52	0
57	MG	1A	3924	1/1	0.81	0.17	57,57,57,57	0
57	MG	2a	3187	1/1	0.81	0.17	57,57,57,57	0
57	MG	1a	3155	1/1	0.81	0.18	73,73,73,73	0
57	MG	1A	3516	1/1	0.82	0.14	52,52,52,52	0
57	MG	2A	3324	1/1	0.82	0.15	58,58,58,58	0
57	MG	2A	3328	1/1	0.82	0.17	59,59,59,59	0
57	MG	1A	3078	1/1	0.82	0.14	54,54,54,54	0
57	MG	2A	3609	1/1	0.82	0.17	51,51,51,51	0
57	MG	2A	3611	1/1	0.82	0.12	33,33,33,33	0
57	MG	1A	3913	1/1	0.82	0.11	27,27,27,27	0
57	MG	1A	3921	1/1	0.82	0.13	58,58,58,58	0
57	MG	2A	3413	1/1	0.82	0.16	55,55,55,55	0
57	MG	2B	207	1/1	0.82	0.16	59,59,59,59	0
57	MG	1A	3604	1/1	0.82	0.14	55,55,55,55	0
57	MG	2A	3439	1/1	0.82	0.15	53,53,53,53	0
57	MG	2A	3441	1/1	0.82	0.14	61,61,61,61	0
57	MG	2A	3191	1/1	0.82	0.25	65,65,65,65	0
57	MG	1A	3634	1/1	0.82	0.21	26,26,26,26	0
57	MG	2a	3034	1/1	0.82	0.27	70,70,70,70	0
57	MG	2A	3477	1/1	0.82	0.13	51,51,51,51	0
57	MG	1a	3199	1/1	0.82	0.12	69,69,69,69	0
57	MG	1B	218	1/1	0.82	0.17	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3418	1/1	0.82	0.11	19,19,19,19	0
57	MG	2A	3297	1/1	0.82	0.13	51,51,51,51	0
60	MPD	1A	4024	8/8	0.82	0.24	46,51,56,64	0
57	MG	1A	3646	1/1	0.83	0.13	59,59,59,59	0
57	MG	1A	3550	1/1	0.83	0.15	58,58,58,58	0
57	MG	1A	3684	1/1	0.83	0.09	54,54,54,54	0
57	MG	1A	3519	1/1	0.83	0.14	51,51,51,51	0
57	MG	1D	312	1/1	0.83	0.29	46,46,46,46	0
57	MG	1A	3355	1/1	0.83	0.06	20,20,20,20	0
57	MG	2A	3311	1/1	0.83	0.11	53,53,53,53	0
57	MG	2A	3312	1/1	0.83	0.19	59,59,59,59	0
57	MG	1A	3598	1/1	0.83	0.12	40,40,40,40	0
57	MG	1A	3533	1/1	0.83	0.19	48,48,48,48	0
57	MG	1a	3073	1/1	0.83	0.15	53,53,53,53	0
57	MG	1A	3611	1/1	0.83	0.25	34,34,34,34	0
57	MG	1a	3236	1/1	0.83	0.16	46,46,46,46	0
57	MG	2A	3405	1/1	0.83	0.16	55,55,55,55	0
57	MG	1A	3620	1/1	0.83	0.12	34,34,34,34	0
57	MG	2A	3424	1/1	0.83	0.13	44,44,44,44	0
57	MG	1A	3848	1/1	0.83	0.17	61,61,61,61	0
57	MG	2A	3054	1/1	0.83	0.23	66,66,66,66	0
57	MG	2a	3024	1/1	0.83	0.11	58,58,58,58	0
57	MG	1A	3966	1/1	0.83	0.17	41,41,41,41	0
57	MG	2A	3446	1/1	0.83	0.16	46,46,46,46	0
57	MG	1A	3478	1/1	0.83	0.14	26,26,26,26	0
57	MG	2a	3135	1/1	0.83	0.22	58,58,58,58	0
57	MG	2A	3167	1/1	0.83	0.18	46,46,46,46	0
57	MG	2A	3190	1/1	0.83	0.27	49,49,49,49	0
57	MG	1A	3644	1/1	0.83	0.15	40,40,40,40	0
57	MG	2A	3499	1/1	0.83	0.16	49,49,49,49	0
57	MG	1A	4012	1/1	0.84	0.15	40,40,40,40	0
57	MG	1A	3178	1/1	0.84	0.20	52,52,52,52	0
57	MG	1a	3105	1/1	0.84	0.30	64,64,64,64	0
57	MG	2A	3564	1/1	0.84	0.11	67,67,67,67	0
57	MG	1a	3126	1/1	0.84	0.17	65,65,65,65	0
57	MG	2A	3576	1/1	0.84	0.12	49,49,49,49	0
57	MG	1a	3255	1/1	0.84	0.12	61,61,61,61	0
57	MG	1B	219	1/1	0.84	0.10	46,46,46,46	0
57	MG	1A	3525	1/1	0.84	0.18	56,56,56,56	0
57	MG	2A	3621	1/1	0.84	0.13	28,28,28,28	0
57	MG	2A	3057	1/1	0.84	0.15	56,56,56,56	0
57	MG	1A	3863	1/1	0.84	0.12	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3659	1/1	0.84	0.16	65,65,65,65	0
57	MG	2A	3126	1/1	0.84	0.18	57,57,57,57	0
57	MG	2A	3725	1/1	0.84	0.27	64,64,64,64	0
57	MG	1G	202	1/1	0.84	0.10	56,56,56,56	0
57	MG	1A	3492	1/1	0.84	0.14	34,34,34,34	0
57	MG	2A	3436	1/1	0.84	0.09	65,65,65,65	0
57	MG	2A	3168	1/1	0.84	0.15	58,58,58,58	0
57	MG	2T	202	1/1	0.84	0.16	61,61,61,61	0
57	MG	1a	3179	1/1	0.84	0.13	55,55,55,55	0
57	MG	10	106	1/1	0.84	0.13	50,50,50,50	0
57	MG	1A	3821	1/1	0.84	0.29	36,36,36,36	0
57	MG	2A	3208	1/1	0.84	0.17	56,56,56,56	0
57	MG	2a	3057	1/1	0.84	0.25	68,68,68,68	0
57	MG	1A	3986	1/1	0.84	0.10	28,28,28,28	0
57	MG	1A	3466	1/1	0.84	0.13	37,37,37,37	0
57	MG	2A	3487	1/1	0.84	0.15	48,48,48,48	0
57	MG	2a	3147	1/1	0.84	0.17	67,67,67,67	0
57	MG	1A	3950	1/1	0.84	0.13	61,61,61,61	0
57	MG	2a	3185	1/1	0.84	0.22	63,63,63,63	0
57	MG	1a	3210	1/1	0.84	0.16	59,59,59,59	0
57	MG	2A	3522	1/1	0.84	0.16	38,38,38,38	0
57	MG	2A	3298	1/1	0.84	0.15	71,71,71,71	0
57	MG	2A	3218	1/1	0.85	0.34	71,71,71,71	0
57	MG	1a	3065	1/1	0.85	0.27	61,61,61,61	0
57	MG	1A	3027	1/1	0.85	0.10	56,56,56,56	0
57	MG	2A	3256	1/1	0.85	0.18	53,53,53,53	0
57	MG	2A	3543	1/1	0.85	0.11	33,33,33,33	0
57	MG	1a	3204	1/1	0.85	0.13	47,47,47,47	0
57	MG	1a	3076	1/1	0.85	0.14	56,56,56,56	0
57	MG	1A	3344	1/1	0.85	0.16	53,53,53,53	0
57	MG	1a	3082	1/1	0.85	0.11	56,56,56,56	0
57	MG	2A	3582	1/1	0.85	0.10	42,42,42,42	0
57	MG	1a	3233	1/1	0.85	0.19	61,61,61,61	0
57	MG	1A	3542	1/1	0.85	0.09	31,31,31,31	0
57	MG	1A	3267	1/1	0.85	0.30	58,58,58,58	0
57	MG	2A	3618	1/1	0.85	0.15	57,57,57,57	0
57	MG	1A	3531	1/1	0.85	0.16	43,43,43,43	0
57	MG	2A	3336	1/1	0.85	0.14	44,44,44,44	0
57	MG	1A	3696	1/1	0.85	0.23	40,40,40,40	0
57	MG	2A	3003	1/1	0.85	0.11	58,58,58,58	0
57	MG	1A	3697	1/1	0.85	0.15	59,59,59,59	0
57	MG	2A	3718	1/1	0.85	0.18	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	3719	1/1	0.85	0.15	47,47,47,47	0
57	MG	1N	204	1/1	0.85	0.10	50,50,50,50	0
57	MG	2B	206	1/1	0.85	0.13	54,54,54,54	0
57	MG	2A	3058	1/1	0.85	0.12	51,51,51,51	0
57	MG	2A	3080	1/1	0.85	0.12	78,78,78,78	0
57	MG	2G	202	1/1	0.85	0.15	70,70,70,70	0
57	MG	2A	3426	1/1	0.85	0.16	57,57,57,57	0
57	MG	1A	3700	1/1	0.85	0.25	40,40,40,40	0
57	MG	1A	3987	1/1	0.85	0.13	47,47,47,47	0
57	MG	2T	204	1/1	0.85	0.11	60,60,60,60	0
57	MG	2A	3136	1/1	0.85	0.18	61,61,61,61	0
57	MG	28	102	1/1	0.85	0.20	45,45,45,45	0
57	MG	2A	3148	1/1	0.85	0.20	57,57,57,57	0
57	MG	1a	3022	1/1	0.85	0.20	55,55,55,55	0
57	MG	1a	3033	1/1	0.85	0.29	60,60,60,60	0
57	MG	1a	3049	1/1	0.85	0.21	63,63,63,63	0
57	MG	2a	3106	1/1	0.85	0.25	52,52,52,52	0
57	MG	2A	3463	1/1	0.85	0.19	58,58,58,58	0
57	MG	2a	3132	1/1	0.85	0.12	58,58,58,58	0
57	MG	2A	3473	1/1	0.85	0.10	58,58,58,58	0
57	MG	2A	3189	1/1	0.85	0.23	59,59,59,59	0
57	MG	2A	3484	1/1	0.85	0.13	57,57,57,57	0
57	MG	2a	3180	1/1	0.85	0.17	63,63,63,63	0
57	MG	1a	3054	1/1	0.85	0.15	62,62,62,62	0
57	MG	1a	3058	1/1	0.85	0.16	61,61,61,61	0
57	MG	2A	3496	1/1	0.85	0.11	65,65,65,65	0
57	MG	2e	201	1/1	0.85	0.21	63,63,63,63	0
57	MG	1A	3631	1/1	0.85	0.10	30,30,30,30	0
57	MG	1a	3197	1/1	0.85	0.13	49,49,49,49	0
57	MG	2A	3400	1/1	0.86	0.10	41,41,41,41	0
57	MG	1B	203	1/1	0.86	0.13	56,56,56,56	0
57	MG	2A	3143	1/1	0.86	0.14	42,42,42,42	0
57	MG	2A	3407	1/1	0.86	0.18	56,56,56,56	0
57	MG	1a	3191	1/1	0.86	0.15	59,59,59,59	0
57	MG	1a	3069	1/1	0.86	0.29	54,54,54,54	0
57	MG	1A	3461	1/1	0.86	0.17	55,55,55,55	0
57	MG	2A	3649	1/1	0.86	0.12	53,53,53,53	0
57	MG	2A	3653	1/1	0.86	0.11	27,27,27,27	0
57	MG	1A	3194	1/1	0.86	0.28	54,54,54,54	0
57	MG	1A	3876	1/1	0.86	0.09	24,24,24,24	0
57	MG	2A	3695	1/1	0.86	0.18	53,53,53,53	0
57	MG	2A	3704	1/1	0.86	0.08	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3714	1/1	0.86	0.13	61,61,61,61	0
57	MG	2A	3717	1/1	0.86	0.15	61,61,61,61	0
57	MG	1A	3878	1/1	0.86	0.08	25,25,25,25	0
57	MG	1a	3217	1/1	0.86	0.19	54,54,54,54	0
57	MG	2A	3442	1/1	0.86	0.15	60,60,60,60	0
57	MG	2A	3194	1/1	0.86	0.18	59,59,59,59	0
57	MG	1A	3669	1/1	0.86	0.19	45,45,45,45	0
57	MG	2B	212	1/1	0.86	0.12	53,53,53,53	0
57	MG	2A	3456	1/1	0.86	0.14	53,53,53,53	0
57	MG	1A	3975	1/1	0.86	0.10	56,56,56,56	0
57	MG	1A	3617	1/1	0.86	0.11	16,16,16,16	0
57	MG	2O	201	1/1	0.86	0.10	47,47,47,47	0
57	MG	2A	3472	1/1	0.86	0.17	59,59,59,59	0
57	MG	2Q	203	1/1	0.86	0.10	55,55,55,55	0
57	MG	1A	3470	1/1	0.86	0.11	41,41,41,41	0
57	MG	2A	3474	1/1	0.86	0.18	61,61,61,61	0
57	MG	1a	3019	1/1	0.86	0.20	53,53,53,53	0
57	MG	20	102	1/1	0.86	0.15	59,59,59,59	0
57	MG	1a	3252	1/1	0.86	0.12	46,46,46,46	0
57	MG	2A	3264	1/1	0.86	0.22	54,54,54,54	0
57	MG	2a	3023	1/1	0.86	0.21	59,59,59,59	0
57	MG	2A	3278	1/1	0.86	0.29	57,57,57,57	0
57	MG	2a	3031	1/1	0.86	0.24	71,71,71,71	0
57	MG	1a	3141	1/1	0.86	0.12	59,59,59,59	0
57	MG	2a	3037	1/1	0.86	0.11	67,67,67,67	0
57	MG	2a	3043	1/1	0.86	0.18	64,64,64,64	0
57	MG	1A	3584	1/1	0.86	0.12	35,35,35,35	0
57	MG	2a	3069	1/1	0.86	0.16	62,62,62,62	0
57	MG	2a	3086	1/1	0.86	0.14	60,60,60,60	0
57	MG	2A	3507	1/1	0.86	0.16	59,59,59,59	0
57	MG	2a	3122	1/1	0.86	0.26	69,69,69,69	0
57	MG	1a	3029	1/1	0.86	0.14	53,53,53,53	0
57	MG	1A	3919	1/1	0.86	0.12	46,46,46,46	0
57	MG	1a	3045	1/1	0.86	0.17	60,60,60,60	0
57	MG	2A	3530	1/1	0.86	0.17	55,55,55,55	0
57	MG	2a	3137	1/1	0.86	0.13	45,45,45,45	0
57	MG	1A	3197	1/1	0.86	0.28	53,53,53,53	0
57	MG	2a	3167	1/1	0.86	0.14	73,73,73,73	0
57	MG	2A	3064	1/1	0.86	0.13	51,51,51,51	0
57	MG	1A	3446	1/1	0.86	0.11	58,58,58,58	0
57	MG	2A	3094	1/1	0.86	0.09	61,61,61,61	0
57	MG	1A	3710	1/1	0.86	0.20	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	4014	1/1	0.86	0.09	27,27,27,27	0
57	MG	2A	3397	1/1	0.86	0.12	50,50,50,50	0
57	MG	2A	3399	1/1	0.86	0.26	66,66,66,66	0
57	MG	1A	3655	1/1	0.87	0.09	40,40,40,40	0
57	MG	2A	3660	1/1	0.87	0.11	58,58,58,58	0
57	MG	1A	3893	1/1	0.87	0.14	47,47,47,47	0
57	MG	2A	3679	1/1	0.87	0.13	58,58,58,58	0
57	MG	2A	3690	1/1	0.87	0.11	50,50,50,50	0
57	MG	2A	3693	1/1	0.87	0.10	50,50,50,50	0
57	MG	2A	3187	1/1	0.87	0.14	52,52,52,52	0
57	MG	1A	3765	1/1	0.87	0.10	25,25,25,25	0
57	MG	2A	3708	1/1	0.87	0.11	62,62,62,62	0
57	MG	1A	3659	1/1	0.87	0.10	36,36,36,36	0
57	MG	2A	3716	1/1	0.87	0.12	45,45,45,45	0
57	MG	1A	3660	1/1	0.87	0.11	18,18,18,18	0
57	MG	1A	3794	1/1	0.87	0.27	39,39,39,39	0
57	MG	2A	3448	1/1	0.87	0.21	43,43,43,43	0
57	MG	2A	3723	1/1	0.87	0.18	58,58,58,58	0
57	MG	2A	3196	1/1	0.87	0.26	55,55,55,55	0
57	MG	1a	3227	1/1	0.87	0.13	62,62,62,62	0
57	MG	1B	227	1/1	0.87	0.10	58,58,58,58	0
57	MG	2B	208	1/1	0.87	0.29	57,57,57,57	0
57	MG	1B	229	1/1	0.87	0.10	46,46,46,46	0
57	MG	2D	306	1/1	0.87	0.25	41,41,41,41	0
57	MG	2A	3226	1/1	0.87	0.11	52,52,52,52	0
57	MG	1a	3232	1/1	0.87	0.11	53,53,53,53	0
57	MG	1a	3085	1/1	0.87	0.08	57,57,57,57	0
57	MG	1A	3359	1/1	0.87	0.10	43,43,43,43	0
57	MG	2A	3479	1/1	0.87	0.17	66,66,66,66	0
57	MG	1A	3665	1/1	0.87	0.11	47,47,47,47	0
57	MG	2A	3275	1/1	0.87	0.14	53,53,53,53	0
57	MG	1E	303	1/1	0.87	0.10	22,22,22,22	0
57	MG	1a	3104	1/1	0.87	0.35	61,61,61,61	0
57	MG	1a	3261	1/1	0.87	0.14	60,60,60,60	0
57	MG	1A	3944	1/1	0.87	0.10	21,21,21,21	0
57	MG	1n	103	1/1	0.87	0.13	60,60,60,60	0
57	MG	2A	3511	1/1	0.87	0.16	61,61,61,61	0
57	MG	1A	3831	1/1	0.87	0.10	25,25,25,25	0
57	MG	2A	3005	1/1	0.87	0.13	58,58,58,58	0
57	MG	2A	3033	1/1	0.87	0.20	58,58,58,58	0
57	MG	1A	3284	1/1	0.87	0.12	64,64,64,64	0
57	MG	1A	3571	1/1	0.87	0.14	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	3149	1/1	0.87	0.10	51,51,51,51	0
57	MG	2a	3058	1/1	0.87	0.27	63,63,63,63	0
57	MG	2A	3350	1/1	0.87	0.08	28,28,28,28	0
57	MG	2a	3079	1/1	0.87	0.14	60,60,60,60	0
57	MG	2a	3085	1/1	0.87	0.13	67,67,67,67	0
57	MG	2A	3359	1/1	0.87	0.09	37,37,37,37	0
57	MG	2A	3568	1/1	0.87	0.11	37,37,37,37	0
57	MG	2a	3107	1/1	0.87	0.16	60,60,60,60	0
57	MG	2a	3110	1/1	0.87	0.35	63,63,63,63	0
57	MG	2A	3371	1/1	0.87	0.16	63,63,63,63	0
57	MG	2A	3375	1/1	0.87	0.11	57,57,57,57	0
57	MG	1a	3009	1/1	0.87	0.18	51,51,51,51	0
57	MG	1A	3403	1/1	0.87	0.07	14,14,14,14	0
57	MG	2A	3398	1/1	0.87	0.13	56,56,56,56	0
57	MG	1A	3419	1/1	0.87	0.17	64,64,64,64	0
57	MG	1A	3641	1/1	0.87	0.12	46,46,46,46	0
57	MG	1A	3642	1/1	0.87	0.15	35,35,35,35	0
57	MG	2A	3623	1/1	0.87	0.16	49,49,49,49	0
57	MG	1a	3034	1/1	0.87	0.21	47,47,47,47	0
57	MG	1A	3406	1/1	0.87	0.15	48,48,48,48	0
57	MG	2A	3633	1/1	0.87	0.18	70,70,70,70	0
57	MG	2A	3646	1/1	0.87	0.10	67,67,67,67	0
57	MG	1A	3479	1/1	0.87	0.08	18,18,18,18	0
57	MG	1A	3747	1/1	0.87	0.16	41,41,41,41	0
57	MG	1A	3373	1/1	0.88	0.12	41,41,41,41	0
57	MG	2A	3239	1/1	0.88	0.21	60,60,60,60	0
57	MG	1a	3201	1/1	0.88	0.10	59,59,59,59	0
57	MG	2A	3569	1/1	0.88	0.14	33,33,33,33	0
57	MG	2A	3254	1/1	0.88	0.26	58,58,58,58	0
57	MG	2A	3575	1/1	0.88	0.12	52,52,52,52	0
57	MG	1A	3574	1/1	0.88	0.08	26,26,26,26	0
57	MG	2A	3257	1/1	0.88	0.12	52,52,52,52	0
57	MG	2A	3589	1/1	0.88	0.13	41,41,41,41	0
57	MG	1A	3971	1/1	0.88	0.09	37,37,37,37	0
57	MG	2A	3600	1/1	0.88	0.12	59,59,59,59	0
57	MG	2A	3602	1/1	0.88	0.11	36,36,36,36	0
57	MG	2A	3271	1/1	0.88	0.09	44,44,44,44	0
57	MG	2A	3274	1/1	0.88	0.22	57,57,57,57	0
57	MG	1A	3392	1/1	0.88	0.07	27,27,27,27	0
57	MG	2A	3620	1/1	0.88	0.12	61,61,61,61	0
57	MG	1a	3216	1/1	0.88	0.18	67,67,67,67	0
57	MG	1A	3587	1/1	0.88	0.12	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	3842	1/1	0.88	0.08	41,41,41,41	0
57	MG	1A	3846	1/1	0.88	0.12	43,43,43,43	0
57	MG	1A	3458	1/1	0.88	0.15	38,38,38,38	0
57	MG	1A	3988	1/1	0.88	0.18	41,41,41,41	0
57	MG	1A	3460	1/1	0.88	0.10	36,36,36,36	0
57	MG	2A	3315	1/1	0.88	0.10	38,38,38,38	0
57	MG	2A	3320	1/1	0.88	0.11	53,53,53,53	0
57	MG	2A	3321	1/1	0.88	0.13	54,54,54,54	0
57	MG	2A	3664	1/1	0.88	0.09	58,58,58,58	0
57	MG	1A	3318	1/1	0.88	0.13	47,47,47,47	0
57	MG	2A	3669	1/1	0.88	0.12	58,58,58,58	0
57	MG	1a	3237	1/1	0.88	0.11	53,53,53,53	0
57	MG	2A	3335	1/1	0.88	0.12	32,32,32,32	0
57	MG	1A	3694	1/1	0.88	0.11	29,29,29,29	0
57	MG	1a	3079	1/1	0.88	0.26	53,53,53,53	0
57	MG	2A	3699	1/1	0.88	0.15	67,67,67,67	0
57	MG	1A	3521	1/1	0.88	0.10	46,46,46,46	0
57	MG	1A	3867	1/1	0.88	0.09	23,23,23,23	0
57	MG	1B	211	1/1	0.88	0.18	62,62,62,62	0
57	MG	1a	3265	1/1	0.88	0.16	56,56,56,56	0
57	MG	1a	3266	1/1	0.88	0.18	67,67,67,67	0
57	MG	2A	3385	1/1	0.88	0.11	71,71,71,71	0
57	MG	2A	3391	1/1	0.88	0.15	57,57,57,57	0
57	MG	1A	3612	1/1	0.88	0.10	48,48,48,48	0
57	MG	1y	201	1/1	0.88	0.16	67,67,67,67	0
57	MG	2B	201	1/1	0.88	0.17	59,59,59,59	0
57	MG	2B	204	1/1	0.88	0.15	69,69,69,69	0
57	MG	1y	202	1/1	0.88	0.12	61,61,61,61	0
57	MG	1A	3613	1/1	0.88	0.19	48,48,48,48	0
57	MG	2A	3403	1/1	0.88	0.11	41,41,41,41	0
57	MG	1A	3702	1/1	0.88	0.29	50,50,50,50	0
57	MG	2A	3016	1/1	0.88	0.18	63,63,63,63	0
57	MG	2A	3406	1/1	0.88	0.14	43,43,43,43	0
57	MG	2A	3019	1/1	0.88	0.21	41,41,41,41	0
57	MG	2A	3408	1/1	0.88	0.23	63,63,63,63	0
57	MG	2A	3031	1/1	0.88	0.20	63,63,63,63	0
57	MG	1A	3329	1/1	0.88	0.08	28,28,28,28	0
57	MG	2A	3052	1/1	0.88	0.17	62,62,62,62	0
57	MG	2A	3428	1/1	0.88	0.15	52,52,52,52	0
57	MG	2A	3430	1/1	0.88	0.38	48,48,48,48	0
57	MG	1a	3106	1/1	0.88	0.17	62,62,62,62	0
57	MG	2A	3434	1/1	0.88	0.10	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	3435	1/1	0.88	0.10	42,42,42,42	0
57	MG	2A	3055	1/1	0.88	0.18	49,49,49,49	0
57	MG	1a	3107	1/1	0.88	0.23	55,55,55,55	0
57	MG	1a	3114	1/1	0.88	0.10	68,68,68,68	0
57	MG	1a	3121	1/1	0.88	0.16	58,58,58,58	0
57	MG	1A	3087	1/1	0.88	0.21	48,48,48,48	0
57	MG	2A	3087	1/1	0.88	0.13	53,53,53,53	0
57	MG	2a	3040	1/1	0.88	0.17	56,56,56,56	0
57	MG	1a	3132	1/1	0.88	0.17	50,50,50,50	0
57	MG	1A	3472	1/1	0.88	0.12	43,43,43,43	0
57	MG	1A	3743	1/1	0.88	0.12	51,51,51,51	0
57	MG	2a	3061	1/1	0.88	0.35	69,69,69,69	0
57	MG	1A	3473	1/1	0.88	0.07	17,17,17,17	0
57	MG	2a	3077	1/1	0.88	0.25	54,54,54,54	0
57	MG	1A	3200	1/1	0.88	0.17	52,52,52,52	0
57	MG	1A	3758	1/1	0.88	0.17	43,43,43,43	0
57	MG	1a	3161	1/1	0.88	0.09	41,41,41,41	0
57	MG	2A	3160	1/1	0.88	0.16	52,52,52,52	0
57	MG	1a	3163	1/1	0.88	0.22	69,69,69,69	0
57	MG	1a	3171	1/1	0.88	0.14	58,58,58,58	0
57	MG	2A	3178	1/1	0.88	0.12	48,48,48,48	0
57	MG	1R	203	1/1	0.88	0.13	39,39,39,39	0
57	MG	1W	204	1/1	0.88	0.14	39,39,39,39	0
57	MG	1A	3155	1/1	0.88	0.18	38,38,38,38	0
57	MG	1A	3778	1/1	0.88	0.13	35,35,35,35	0
57	MG	1A	3484	1/1	0.88	0.09	19,19,19,19	0
57	MG	2A	3510	1/1	0.88	0.15	54,54,54,54	0
57	MG	2a	3151	1/1	0.88	0.13	63,63,63,63	0
57	MG	1A	3286	1/1	0.88	0.12	63,63,63,63	0
57	MG	1a	3190	1/1	0.88	0.14	68,68,68,68	0
57	MG	1a	3028	1/1	0.88	0.24	55,55,55,55	0
57	MG	2A	3212	1/1	0.88	0.14	61,61,61,61	0
57	MG	2A	3531	1/1	0.88	0.12	53,53,53,53	0
57	MG	2A	3216	1/1	0.88	0.24	63,63,63,63	0
57	MG	2j	201	1/1	0.88	0.10	68,68,68,68	0
57	MG	2x	101	1/1	0.88	0.11	62,62,62,62	0
57	MG	1a	3194	1/1	0.88	0.12	65,65,65,65	0
57	MG	1A	3791	1/1	0.88	0.10	70,70,70,70	0
60	MPD	1T	207	8/8	0.88	0.18	56,60,62,64	0
57	MG	1A	3110	1/1	0.89	0.14	25,25,25,25	0
57	MG	1A	4013	1/1	0.89	0.18	57,57,57,57	0
57	MG	1a	3061	1/1	0.89	0.16	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	3429	1/1	0.89	0.12	47,47,47,47	0
57	MG	2A	3182	1/1	0.89	0.12	56,56,56,56	0
57	MG	1A	3907	1/1	0.89	0.16	56,56,56,56	0
57	MG	1A	4016	1/1	0.89	0.15	54,54,54,54	0
57	MG	1B	202	1/1	0.89	0.11	44,44,44,44	0
57	MG	1A	3338	1/1	0.89	0.11	51,51,51,51	0
57	MG	1a	3213	1/1	0.89	0.19	68,68,68,68	0
57	MG	1a	3074	1/1	0.89	0.10	54,54,54,54	0
57	MG	1A	3678	1/1	0.89	0.14	52,52,52,52	0
57	MG	1A	3011	1/1	0.89	0.09	42,42,42,42	0
57	MG	2A	3210	1/1	0.89	0.12	64,64,64,64	0
57	MG	2A	3720	1/1	0.89	0.14	52,52,52,52	0
57	MG	1a	3078	1/1	0.89	0.17	70,70,70,70	0
57	MG	1A	3691	1/1	0.89	0.17	54,54,54,54	0
57	MG	1a	3080	1/1	0.89	0.13	55,55,55,55	0
57	MG	2B	202	1/1	0.89	0.08	69,69,69,69	0
57	MG	1B	222	1/1	0.89	0.12	42,42,42,42	0
57	MG	1A	3933	1/1	0.89	0.09	50,50,50,50	0
57	MG	1A	3345	1/1	0.89	0.10	48,48,48,48	0
57	MG	1A	3353	1/1	0.89	0.08	30,30,30,30	0
57	MG	2A	3253	1/1	0.89	0.11	54,54,54,54	0
57	MG	1A	3549	1/1	0.89	0.10	30,30,30,30	0
57	MG	2D	307	1/1	0.89	0.10	53,53,53,53	0
57	MG	2A	3483	1/1	0.89	0.12	59,59,59,59	0
57	MG	1A	3844	1/1	0.89	0.10	25,25,25,25	0
57	MG	1F	317	1/1	0.89	0.11	52,52,52,52	0
57	MG	1A	3953	1/1	0.89	0.12	48,48,48,48	0
57	MG	2A	3495	1/1	0.89	0.10	55,55,55,55	0
57	MG	1A	3010	1/1	0.89	0.17	57,57,57,57	0
57	MG	1a	3111	1/1	0.89	0.12	60,60,60,60	0
57	MG	1d	301	1/1	0.89	0.13	57,57,57,57	0
57	MG	1i	201	1/1	0.89	0.27	60,60,60,60	0
57	MG	2V	201	1/1	0.89	0.12	53,53,53,53	0
57	MG	1n	102	1/1	0.89	0.08	52,52,52,52	0
57	MG	21	102	1/1	0.89	0.14	48,48,48,48	0
57	MG	2A	3287	1/1	0.89	0.37	63,63,63,63	0
57	MG	2a	3007	1/1	0.89	0.12	53,53,53,53	0
57	MG	1N	205	1/1	0.89	0.07	46,46,46,46	0
57	MG	2A	3527	1/1	0.89	0.10	55,55,55,55	0
57	MG	1o	102	1/1	0.89	0.12	53,53,53,53	0
57	MG	2A	3529	1/1	0.89	0.14	70,70,70,70	0
57	MG	1a	3115	1/1	0.89	0.24	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	3118	1/1	0.89	0.19	55,55,55,55	0
57	MG	2a	3039	1/1	0.89	0.20	59,59,59,59	0
57	MG	1A	3555	1/1	0.89	0.15	43,43,43,43	0
57	MG	1A	3640	1/1	0.89	0.22	59,59,59,59	0
57	MG	2a	3049	1/1	0.89	0.28	61,61,61,61	0
57	MG	2a	3051	1/1	0.89	0.26	59,59,59,59	0
57	MG	2A	3006	1/1	0.89	0.10	54,54,54,54	0
57	MG	2A	3545	1/1	0.89	0.09	38,38,38,38	0
57	MG	1A	3209	1/1	0.89	0.29	67,67,67,67	0
57	MG	1W	205	1/1	0.89	0.08	48,48,48,48	0
57	MG	1A	3973	1/1	0.89	0.10	49,49,49,49	0
57	MG	1a	3147	1/1	0.89	0.12	54,54,54,54	0
57	MG	2A	3042	1/1	0.89	0.24	66,66,66,66	0
57	MG	10	108	1/1	0.89	0.09	51,51,51,51	0
57	MG	2a	3087	1/1	0.89	0.33	69,69,69,69	0
57	MG	1a	3007	1/1	0.89	0.11	56,56,56,56	0
57	MG	1A	3311	1/1	0.89	0.13	62,62,62,62	0
57	MG	2A	3363	1/1	0.89	0.08	50,50,50,50	0
57	MG	2A	3365	1/1	0.89	0.13	56,56,56,56	0
57	MG	1a	3018	1/1	0.89	0.09	56,56,56,56	0
57	MG	2a	3126	1/1	0.89	0.14	64,64,64,64	0
57	MG	1A	3312	1/1	0.89	0.12	37,37,37,37	0
57	MG	1A	3380	1/1	0.89	0.11	43,43,43,43	0
57	MG	2A	3380	1/1	0.89	0.09	49,49,49,49	0
57	MG	2A	3617	1/1	0.89	0.12	37,37,37,37	0
57	MG	2a	3138	1/1	0.89	0.15	54,54,54,54	0
57	MG	2a	3145	1/1	0.89	0.09	52,52,52,52	0
57	MG	2A	3079	1/1	0.89	0.14	50,50,50,50	0
57	MG	2a	3148	1/1	0.89	0.09	39,39,39,39	0
57	MG	1A	3386	1/1	0.89	0.07	20,20,20,20	0
57	MG	2a	3153	1/1	0.89	0.12	61,61,61,61	0
57	MG	1A	3190	1/1	0.89	0.14	52,52,52,52	0
57	MG	2A	3090	1/1	0.89	0.21	48,48,48,48	0
57	MG	2a	3181	1/1	0.89	0.17	62,62,62,62	0
57	MG	1a	3176	1/1	0.89	0.13	63,63,63,63	0
57	MG	1a	3032	1/1	0.89	0.13	43,43,43,43	0
57	MG	1A	3597	1/1	0.89	0.08	38,38,38,38	0
57	MG	1a	3184	1/1	0.89	0.19	56,56,56,56	0
57	MG	1A	3395	1/1	0.89	0.09	34,34,34,34	0
57	MG	2n	101	1/1	0.89	0.19	62,62,62,62	0
57	MG	1a	3041	1/1	0.89	0.17	43,43,43,43	0
57	MG	2A	3150	1/1	0.89	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3779	1/1	0.89	0.12	39,39,39,39	0
57	MG	1A	4009	1/1	0.89	0.11	54,54,54,54	0
60	MPD	1a	3271	8/8	0.89	0.15	49,51,53,60	0
60	MPD	2B	218	8/8	0.89	0.18	44,53,60,60	0
57	MG	1a	3224	1/1	0.90	0.18	68,68,68,68	0
57	MG	1a	3090	1/1	0.90	0.18	54,54,54,54	0
57	MG	2A	3697	1/1	0.90	0.08	73,73,73,73	0
57	MG	2A	3432	1/1	0.90	0.22	44,44,44,44	0
57	MG	1A	3838	1/1	0.90	0.12	53,53,53,53	0
57	MG	2A	3705	1/1	0.90	0.13	55,55,55,55	0
57	MG	1F	313	1/1	0.90	0.36	37,37,37,37	0
57	MG	2A	3712	1/1	0.90	0.09	41,41,41,41	0
57	MG	1a	3230	1/1	0.90	0.14	52,52,52,52	0
57	MG	2A	3715	1/1	0.90	0.16	60,60,60,60	0
57	MG	1a	3098	1/1	0.90	0.17	57,57,57,57	0
57	MG	2A	3437	1/1	0.90	0.10	51,51,51,51	0
57	MG	1a	3100	1/1	0.90	0.17	61,61,61,61	0
57	MG	1A	3946	1/1	0.90	0.11	39,39,39,39	0
57	MG	1A	3948	1/1	0.90	0.11	53,53,53,53	0
57	MG	1A	3949	1/1	0.90	0.08	59,59,59,59	0
57	MG	1a	3243	1/1	0.90	0.13	53,53,53,53	0
57	MG	2A	3452	1/1	0.90	0.15	44,44,44,44	0
57	MG	2A	3215	1/1	0.90	0.13	52,52,52,52	0
57	MG	1a	3251	1/1	0.90	0.12	64,64,64,64	0
57	MG	1A	3096	1/1	0.90	0.20	43,43,43,43	0
57	MG	1O	201	1/1	0.90	0.08	41,41,41,41	0
57	MG	2A	3468	1/1	0.90	0.09	44,44,44,44	0
57	MG	1A	3433	1/1	0.90	0.12	40,40,40,40	0
57	MG	2B	215	1/1	0.90	0.13	61,61,61,61	0
57	MG	1A	3954	1/1	0.90	0.10	49,49,49,49	0
57	MG	1a	3264	1/1	0.90	0.14	72,72,72,72	0
57	MG	1A	3602	1/1	0.90	0.09	24,24,24,24	0
57	MG	1A	3717	1/1	0.90	0.10	45,45,45,45	0
57	MG	1A	3396	1/1	0.90	0.09	28,28,28,28	0
57	MG	1d	302	1/1	0.90	0.09	61,61,61,61	0
57	MG	1a	3124	1/1	0.90	0.11	53,53,53,53	0
57	MG	1A	3854	1/1	0.90	0.08	30,30,30,30	0
57	MG	2R	201	1/1	0.90	0.12	55,55,55,55	0
57	MG	2A	3491	1/1	0.90	0.16	44,44,44,44	0
57	MG	17	104	1/1	0.90	0.13	33,33,33,33	0
57	MG	1a	3134	1/1	0.90	0.07	38,38,38,38	0
57	MG	1A	3856	1/1	0.90	0.11	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3503	1/1	0.90	0.11	41,41,41,41	0
57	MG	1a	3142	1/1	0.90	0.12	62,62,62,62	0
57	MG	25	101	1/1	0.90	0.17	46,46,46,46	0
57	MG	28	101	1/1	0.90	0.13	46,46,46,46	0
57	MG	2A	3280	1/1	0.90	0.26	53,53,53,53	0
57	MG	2a	3005	1/1	0.90	0.22	64,64,64,64	0
57	MG	1y	203	1/1	0.90	0.24	59,59,59,59	0
57	MG	2A	3292	1/1	0.90	0.08	59,59,59,59	0
57	MG	1A	3607	1/1	0.90	0.18	24,24,24,24	0
57	MG	1A	3105	1/1	0.90	0.08	51,51,51,51	0
57	MG	2a	3026	1/1	0.90	0.24	64,64,64,64	0
57	MG	1A	3981	1/1	0.90	0.14	60,60,60,60	0
57	MG	2A	3307	1/1	0.90	0.14	41,41,41,41	0
57	MG	1A	3982	1/1	0.90	0.09	44,44,44,44	0
57	MG	1A	3865	1/1	0.90	0.07	32,32,32,32	0
57	MG	2A	3025	1/1	0.90	0.09	48,48,48,48	0
57	MG	1A	3302	1/1	0.90	0.20	58,58,58,58	0
57	MG	2a	3047	1/1	0.90	0.27	51,51,51,51	0
57	MG	1A	3569	1/1	0.90	0.12	39,39,39,39	0
57	MG	2A	3035	1/1	0.90	0.12	51,51,51,51	0
57	MG	2A	3554	1/1	0.90	0.08	43,43,43,43	0
57	MG	2A	3556	1/1	0.90	0.10	34,34,34,34	0
57	MG	1A	3871	1/1	0.90	0.08	34,34,34,34	0
57	MG	2a	3063	1/1	0.90	0.33	63,63,63,63	0
57	MG	2a	3065	1/1	0.90	0.10	69,69,69,69	0
57	MG	2a	3066	1/1	0.90	0.13	55,55,55,55	0
57	MG	2A	3563	1/1	0.90	0.13	51,51,51,51	0
57	MG	1A	3761	1/1	0.90	0.12	52,52,52,52	0
57	MG	2a	3078	1/1	0.90	0.10	66,66,66,66	0
57	MG	1A	3995	1/1	0.90	0.20	61,61,61,61	0
57	MG	2A	3339	1/1	0.90	0.08	35,35,35,35	0
57	MG	1A	3671	1/1	0.90	0.09	53,53,53,53	0
57	MG	1A	3997	1/1	0.90	0.15	27,27,27,27	0
57	MG	1a	3052	1/1	0.90	0.12	50,50,50,50	0
57	MG	2A	3060	1/1	0.90	0.08	44,44,44,44	0
57	MG	2A	3364	1/1	0.90	0.07	36,36,36,36	0
57	MG	2a	3112	1/1	0.90	0.14	65,65,65,65	0
57	MG	2a	3114	1/1	0.90	0.11	45,45,45,45	0
57	MG	2a	3117	1/1	0.90	0.16	56,56,56,56	0
57	MG	1A	3157	1/1	0.90	0.19	54,54,54,54	0
57	MG	2A	3592	1/1	0.90	0.10	40,40,40,40	0
57	MG	2A	3073	1/1	0.90	0.16	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	3882	1/1	0.90	0.13	52,52,52,52	0
57	MG	2A	3608	1/1	0.90	0.07	32,32,32,32	0
57	MG	1A	3387	1/1	0.90	0.05	15,15,15,15	0
57	MG	1A	3689	1/1	0.90	0.08	40,40,40,40	0
57	MG	1A	3578	1/1	0.90	0.30	36,36,36,36	0
57	MG	2a	3140	1/1	0.90	0.12	54,54,54,54	0
57	MG	2a	3143	1/1	0.90	0.08	62,62,62,62	0
57	MG	1A	3899	1/1	0.90	0.12	21,21,21,21	0
57	MG	2A	3396	1/1	0.90	0.10	29,29,29,29	0
57	MG	2A	3095	1/1	0.90	0.14	48,48,48,48	0
57	MG	2A	3622	1/1	0.90	0.15	57,57,57,57	0
57	MG	2A	3104	1/1	0.90	0.30	54,54,54,54	0
57	MG	2A	3113	1/1	0.90	0.07	49,49,49,49	0
57	MG	1A	3905	1/1	0.90	0.11	37,37,37,37	0
57	MG	1A	3788	1/1	0.90	0.10	42,42,42,42	0
57	MG	2A	3642	1/1	0.90	0.14	46,46,46,46	0
57	MG	1A	3692	1/1	0.90	0.11	50,50,50,50	0
57	MG	1A	3792	1/1	0.90	0.07	34,34,34,34	0
57	MG	1A	3494	1/1	0.90	0.09	45,45,45,45	0
57	MG	1a	3207	1/1	0.90	0.10	63,63,63,63	0
57	MG	2l	201	1/1	0.90	0.13	60,60,60,60	0
57	MG	1A	3499	1/1	0.90	0.13	51,51,51,51	0
57	MG	1A	3593	1/1	0.90	0.12	30,30,30,30	0
57	MG	2A	3415	1/1	0.90	0.08	33,33,33,33	0
57	MG	1A	3829	1/1	0.90	0.10	41,41,41,41	0
57	MG	2A	3673	1/1	0.90	0.09	45,45,45,45	0
57	MG	1A	3343	1/1	0.90	0.15	54,54,54,54	0
60	MPD	2A	3728	8/8	0.90	0.19	50,53,58,58	0
57	MG	1a	3221	1/1	0.90	0.16	62,62,62,62	0
57	MG	2A	3386	1/1	0.91	0.07	56,56,56,56	0
57	MG	1A	3972	1/1	0.91	0.07	45,45,45,45	0
57	MG	2A	3395	1/1	0.91	0.07	27,27,27,27	0
57	MG	2A	3677	1/1	0.91	0.12	33,33,33,33	0
57	MG	1A	3843	1/1	0.91	0.09	44,44,44,44	0
57	MG	2A	3685	1/1	0.91	0.13	38,38,38,38	0
57	MG	1A	3685	1/1	0.91	0.13	51,51,51,51	0
57	MG	1a	3178	1/1	0.91	0.09	51,51,51,51	0
57	MG	1A	3431	1/1	0.91	0.10	22,22,22,22	0
57	MG	2A	3086	1/1	0.91	0.10	44,44,44,44	0
57	MG	1a	3181	1/1	0.91	0.11	51,51,51,51	0
57	MG	1A	3599	1/1	0.91	0.10	39,39,39,39	0
57	MG	2A	3093	1/1	0.91	0.27	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3080	1/1	0.91	0.17	37,37,37,37	0
57	MG	2A	3711	1/1	0.91	0.08	38,38,38,38	0
57	MG	1a	3036	1/1	0.91	0.20	58,58,58,58	0
57	MG	1a	3037	1/1	0.91	0.23	59,59,59,59	0
57	MG	1A	3120	1/1	0.91	0.11	38,38,38,38	0
57	MG	2A	3116	1/1	0.91	0.14	51,51,51,51	0
57	MG	2A	3418	1/1	0.91	0.15	51,51,51,51	0
57	MG	1a	3044	1/1	0.91	0.16	50,50,50,50	0
57	MG	2A	3425	1/1	0.91	0.07	41,41,41,41	0
57	MG	1A	3855	1/1	0.91	0.07	51,51,51,51	0
57	MG	2A	3129	1/1	0.91	0.18	57,57,57,57	0
57	MG	1A	3300	1/1	0.91	0.13	43,43,43,43	0
57	MG	2A	3140	1/1	0.91	0.20	60,60,60,60	0
57	MG	1A	3448	1/1	0.91	0.08	39,39,39,39	0
57	MG	1A	3530	1/1	0.91	0.17	24,24,24,24	0
57	MG	1A	3376	1/1	0.91	0.13	48,48,48,48	0
57	MG	2A	3158	1/1	0.91	0.10	44,44,44,44	0
57	MG	1A	3615	1/1	0.91	0.12	50,50,50,50	0
57	MG	2B	209	1/1	0.91	0.12	70,70,70,70	0
57	MG	1A	3196	1/1	0.91	0.08	40,40,40,40	0
57	MG	1A	4008	1/1	0.91	0.19	39,39,39,39	0
57	MG	2B	216	1/1	0.91	0.09	68,68,68,68	0
57	MG	2A	3440	1/1	0.91	0.08	60,60,60,60	0
57	MG	1a	3211	1/1	0.91	0.17	69,69,69,69	0
57	MG	1A	3303	1/1	0.91	0.13	76,76,76,76	0
57	MG	1A	3724	1/1	0.91	0.10	49,49,49,49	0
57	MG	1A	3732	1/1	0.91	0.08	48,48,48,48	0
57	MG	2I	201	1/1	0.91	0.11	47,47,47,47	0
57	MG	1A	3126	1/1	0.91	0.13	34,34,34,34	0
57	MG	1a	3223	1/1	0.91	0.11	56,56,56,56	0
57	MG	1A	3545	1/1	0.91	0.20	46,46,46,46	0
57	MG	2A	3192	1/1	0.91	0.11	39,39,39,39	0
57	MG	2A	3462	1/1	0.91	0.12	48,48,48,48	0
57	MG	1A	3639	1/1	0.91	0.14	51,51,51,51	0
57	MG	1A	3148	1/1	0.91	0.12	48,48,48,48	0
57	MG	1A	3394	1/1	0.91	0.10	18,18,18,18	0
57	MG	2W	201	1/1	0.91	0.17	51,51,51,51	0
57	MG	2W	202	1/1	0.91	0.07	53,53,53,53	0
57	MG	2Y	201	1/1	0.91	0.24	56,56,56,56	0
57	MG	1A	3203	1/1	0.91	0.13	46,46,46,46	0
57	MG	1A	3902	1/1	0.91	0.11	18,18,18,18	0
57	MG	1a	3087	1/1	0.91	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	25	102	1/1	0.91	0.14	41,41,41,41	0
57	MG	2A	3213	1/1	0.91	0.11	49,49,49,49	0
57	MG	1A	3763	1/1	0.91	0.07	46,46,46,46	0
57	MG	28	103	1/1	0.91	0.11	52,52,52,52	0
57	MG	1A	3041	1/1	0.91	0.14	46,46,46,46	0
57	MG	1a	3093	1/1	0.91	0.29	57,57,57,57	0
57	MG	2A	3223	1/1	0.91	0.13	57,57,57,57	0
57	MG	2A	3490	1/1	0.91	0.09	55,55,55,55	0
57	MG	1A	3397	1/1	0.91	0.08	29,29,29,29	0
57	MG	2A	3233	1/1	0.91	0.14	47,47,47,47	0
57	MG	2a	3028	1/1	0.91	0.14	59,59,59,59	0
57	MG	1A	3650	1/1	0.91	0.12	42,42,42,42	0
57	MG	1a	3099	1/1	0.91	0.10	60,60,60,60	0
57	MG	2a	3036	1/1	0.91	0.21	62,62,62,62	0
57	MG	2A	3502	1/1	0.91	0.11	57,57,57,57	0
57	MG	2a	3038	1/1	0.91	0.12	74,74,74,74	0
57	MG	1A	3227	1/1	0.91	0.17	47,47,47,47	0
57	MG	2A	3243	1/1	0.91	0.23	49,49,49,49	0
57	MG	2A	3508	1/1	0.91	0.08	43,43,43,43	0
57	MG	2a	3046	1/1	0.91	0.19	59,59,59,59	0
57	MG	2A	3249	1/1	0.91	0.12	49,49,49,49	0
57	MG	2A	3252	1/1	0.91	0.11	46,46,46,46	0
57	MG	1a	3260	1/1	0.91	0.08	62,62,62,62	0
57	MG	2A	3520	1/1	0.91	0.14	52,52,52,52	0
57	MG	1a	3101	1/1	0.91	0.29	58,58,58,58	0
57	MG	2a	3060	1/1	0.91	0.23	66,66,66,66	0
57	MG	1A	3658	1/1	0.91	0.09	14,14,14,14	0
57	MG	1E	308	1/1	0.91	0.11	29,29,29,29	0
57	MG	2A	3262	1/1	0.91	0.22	47,47,47,47	0
57	MG	1F	304	1/1	0.91	0.19	27,27,27,27	0
57	MG	1A	3930	1/1	0.91	0.10	48,48,48,48	0
57	MG	1a	3267	1/1	0.91	0.08	52,52,52,52	0
57	MG	1a	3269	1/1	0.91	0.29	48,48,48,48	0
57	MG	1a	3270	1/1	0.91	0.11	46,46,46,46	0
57	MG	2a	3081	1/1	0.91	0.10	52,52,52,52	0
57	MG	1A	3787	1/1	0.91	0.11	49,49,49,49	0
57	MG	1A	3934	1/1	0.91	0.08	22,22,22,22	0
57	MG	2A	3285	1/1	0.91	0.16	54,54,54,54	0
57	MG	2a	3101	1/1	0.91	0.31	57,57,57,57	0
57	MG	2A	3286	1/1	0.91	0.23	61,61,61,61	0
57	MG	1f	201	1/1	0.91	0.23	55,55,55,55	0
57	MG	1g	202	1/1	0.91	0.09	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3235	1/1	0.91	0.11	60,60,60,60	0
57	MG	1A	3251	1/1	0.91	0.09	39,39,39,39	0
57	MG	1A	3662	1/1	0.91	0.13	28,28,28,28	0
57	MG	2A	3302	1/1	0.91	0.07	43,43,43,43	0
57	MG	1A	3945	1/1	0.91	0.08	47,47,47,47	0
57	MG	1t	202	1/1	0.91	0.14	48,48,48,48	0
57	MG	1A	3057	1/1	0.91	0.15	44,44,44,44	0
57	MG	1T	201	1/1	0.91	0.08	40,40,40,40	0
57	MG	1a	3128	1/1	0.91	0.11	52,52,52,52	0
57	MG	1a	3131	1/1	0.91	0.09	43,43,43,43	0
57	MG	2A	3322	1/1	0.91	0.10	45,45,45,45	0
57	MG	2A	3604	1/1	0.91	0.12	72,72,72,72	0
57	MG	1W	201	1/1	0.91	0.13	45,45,45,45	0
57	MG	1A	3586	1/1	0.91	0.12	51,51,51,51	0
57	MG	2A	3012	1/1	0.91	0.14	50,50,50,50	0
57	MG	1a	3140	1/1	0.91	0.08	49,49,49,49	0
57	MG	1A	3804	1/1	0.91	0.14	15,15,15,15	0
57	MG	10	101	1/1	0.91	0.10	36,36,36,36	0
57	MG	1A	3417	1/1	0.91	0.10	14,14,14,14	0
57	MG	1A	3825	1/1	0.91	0.08	32,32,32,32	0
57	MG	2A	3360	1/1	0.91	0.18	77,77,77,77	0
57	MG	2A	3362	1/1	0.91	0.09	37,37,37,37	0
57	MG	1A	3826	1/1	0.91	0.10	42,42,42,42	0
57	MG	2A	3629	1/1	0.91	0.11	54,54,54,54	0
57	MG	2a	3189	1/1	0.91	0.09	51,51,51,51	0
57	MG	2A	3632	1/1	0.91	0.11	59,59,59,59	0
57	MG	2A	3036	1/1	0.91	0.21	59,59,59,59	0
57	MG	2A	3641	1/1	0.91	0.12	60,60,60,60	0
57	MG	1A	3507	1/1	0.91	0.05	17,17,17,17	0
57	MG	2A	3370	1/1	0.91	0.12	44,44,44,44	0
57	MG	1A	3677	1/1	0.91	0.09	64,64,64,64	0
57	MG	1a	3159	1/1	0.91	0.15	64,64,64,64	0
57	MG	1a	3016	1/1	0.91	0.14	54,54,54,54	0
57	MG	1A	3162	1/1	0.91	0.07	37,37,37,37	0
57	MG	2A	3663	1/1	0.91	0.12	61,61,61,61	0
57	MG	1A	3014	1/1	0.91	0.12	46,46,46,46	0
57	MG	2A	3671	1/1	0.92	0.17	65,65,65,65	0
57	MG	2A	3672	1/1	0.92	0.07	60,60,60,60	0
57	MG	2A	3097	1/1	0.92	0.18	48,48,48,48	0
57	MG	1A	3857	1/1	0.92	0.07	41,41,41,41	0
57	MG	2A	3112	1/1	0.92	0.11	52,52,52,52	0
57	MG	1A	3135	1/1	0.92	0.18	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	3042	1/1	0.92	0.15	54,54,54,54	0
57	MG	2A	3119	1/1	0.92	0.07	38,38,38,38	0
57	MG	1A	3859	1/1	0.92	0.06	49,49,49,49	0
57	MG	1A	3862	1/1	0.92	0.12	44,44,44,44	0
57	MG	1a	3048	1/1	0.92	0.20	52,52,52,52	0
57	MG	2A	3132	1/1	0.92	0.17	54,54,54,54	0
57	MG	1A	3991	1/1	0.92	0.07	42,42,42,42	0
57	MG	2A	3137	1/1	0.92	0.26	55,55,55,55	0
57	MG	2A	3138	1/1	0.92	0.10	46,46,46,46	0
57	MG	1A	3992	1/1	0.92	0.08	48,48,48,48	0
57	MG	1A	3316	1/1	0.92	0.15	34,34,34,34	0
57	MG	1A	3245	1/1	0.92	0.23	48,48,48,48	0
57	MG	1A	3328	1/1	0.92	0.10	54,54,54,54	0
57	MG	1A	3249	1/1	0.92	0.09	54,54,54,54	0
57	MG	1A	3749	1/1	0.92	0.09	40,40,40,40	0
57	MG	2A	3431	1/1	0.92	0.10	45,45,45,45	0
57	MG	1A	3330	1/1	0.92	0.07	21,21,21,21	0
57	MG	2A	3164	1/1	0.92	0.23	53,53,53,53	0
57	MG	1a	3218	1/1	0.92	0.19	60,60,60,60	0
57	MG	1A	3754	1/1	0.92	0.09	26,26,26,26	0
57	MG	2A	3175	1/1	0.92	0.10	58,58,58,58	0
57	MG	1A	3880	1/1	0.92	0.06	35,35,35,35	0
57	MG	2A	3180	1/1	0.92	0.12	54,54,54,54	0
57	MG	1A	3647	1/1	0.92	0.09	58,58,58,58	0
57	MG	1A	4018	1/1	0.92	0.14	50,50,50,50	0
57	MG	1B	201	1/1	0.92	0.12	49,49,49,49	0
57	MG	2B	210	1/1	0.92	0.20	52,52,52,52	0
57	MG	2B	211	1/1	0.92	0.09	50,50,50,50	0
57	MG	2A	3443	1/1	0.92	0.17	48,48,48,48	0
57	MG	1A	3760	1/1	0.92	0.17	52,52,52,52	0
57	MG	1A	3033	1/1	0.92	0.09	30,30,30,30	0
57	MG	1A	3340	1/1	0.92	0.07	41,41,41,41	0
57	MG	1B	217	1/1	0.92	0.12	50,50,50,50	0
57	MG	2D	308	1/1	0.92	0.09	34,34,34,34	0
57	MG	2D	309	1/1	0.92	0.20	61,61,61,61	0
57	MG	1a	3234	1/1	0.92	0.10	48,48,48,48	0
57	MG	2E	306	1/1	0.92	0.08	40,40,40,40	0
57	MG	2G	201	1/1	0.92	0.15	63,63,63,63	0
57	MG	2A	3458	1/1	0.92	0.10	48,48,48,48	0
57	MG	1a	3086	1/1	0.92	0.13	50,50,50,50	0
57	MG	1A	3579	1/1	0.92	0.12	37,37,37,37	0
57	MG	1A	3254	1/1	0.92	0.11	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3464	1/1	0.92	0.10	43,43,43,43	0
57	MG	2A	3465	1/1	0.92	0.16	50,50,50,50	0
57	MG	2A	3466	1/1	0.92	0.16	40,40,40,40	0
57	MG	2A	3467	1/1	0.92	0.09	60,60,60,60	0
57	MG	1A	3502	1/1	0.92	0.09	35,35,35,35	0
57	MG	1A	3082	1/1	0.92	0.07	34,34,34,34	0
57	MG	1a	3096	1/1	0.92	0.18	55,55,55,55	0
57	MG	1A	3591	1/1	0.92	0.10	49,49,49,49	0
57	MG	1a	3259	1/1	0.92	0.12	50,50,50,50	0
57	MG	2A	3222	1/1	0.92	0.08	40,40,40,40	0
57	MG	1B	231	1/1	0.92	0.09	60,60,60,60	0
57	MG	1A	3071	1/1	0.92	0.09	41,41,41,41	0
57	MG	1A	3351	1/1	0.92	0.07	30,30,30,30	0
57	MG	1A	3790	1/1	0.92	0.12	44,44,44,44	0
57	MG	2A	3237	1/1	0.92	0.11	52,52,52,52	0
57	MG	1A	3923	1/1	0.92	0.10	50,50,50,50	0
57	MG	2A	3492	1/1	0.92	0.08	47,47,47,47	0
57	MG	2a	3004	1/1	0.92	0.11	46,46,46,46	0
57	MG	1E	309	1/1	0.92	0.08	51,51,51,51	0
57	MG	1A	3352	1/1	0.92	0.13	53,53,53,53	0
57	MG	2A	3246	1/1	0.92	0.19	55,55,55,55	0
57	MG	2a	3014	1/1	0.92	0.18	55,55,55,55	0
57	MG	2a	3015	1/1	0.92	0.17	52,52,52,52	0
57	MG	2a	3018	1/1	0.92	0.16	44,44,44,44	0
57	MG	1A	3271	1/1	0.92	0.07	62,62,62,62	0
57	MG	1F	314	1/1	0.92	0.07	33,33,33,33	0
57	MG	1a	3110	1/1	0.92	0.18	56,56,56,56	0
57	MG	1A	3518	1/1	0.92	0.13	35,35,35,35	0
57	MG	1d	303	1/1	0.92	0.08	45,45,45,45	0
57	MG	1e	201	1/1	0.92	0.15	61,61,61,61	0
57	MG	1A	3124	1/1	0.92	0.10	46,46,46,46	0
57	MG	2A	3517	1/1	0.92	0.08	51,51,51,51	0
57	MG	1G	203	1/1	0.92	0.07	48,48,48,48	0
57	MG	1a	3116	1/1	0.92	0.16	51,51,51,51	0
57	MG	2A	3523	1/1	0.92	0.08	47,47,47,47	0
57	MG	1m	202	1/1	0.92	0.18	58,58,58,58	0
57	MG	2a	3044	1/1	0.92	0.15	61,61,61,61	0
57	MG	1n	101	1/1	0.92	0.36	64,64,64,64	0
57	MG	1A	3164	1/1	0.92	0.05	30,30,30,30	0
57	MG	1A	3814	1/1	0.92	0.11	22,22,22,22	0
57	MG	2a	3050	1/1	0.92	0.22	56,56,56,56	0
57	MG	1A	3815	1/1	0.92	0.10	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	2a	3053	1/1	0.92	0.17	58,58,58,58	0
57	MG	2A	3283	1/1	0.92	0.23	53,53,53,53	0
57	MG	1a	3125	1/1	0.92	0.16	55,55,55,55	0
57	MG	1A	3819	1/1	0.92	0.08	54,54,54,54	0
57	MG	1A	3688	1/1	0.92	0.09	41,41,41,41	0
57	MG	2a	3062	1/1	0.92	0.20	56,56,56,56	0
57	MG	2A	3549	1/1	0.92	0.07	70,70,70,70	0
57	MG	2A	3552	1/1	0.92	0.08	48,48,48,48	0
57	MG	1A	3171	1/1	0.92	0.12	42,42,42,42	0
57	MG	2A	3294	1/1	0.92	0.13	56,56,56,56	0
57	MG	2a	3070	1/1	0.92	0.21	55,55,55,55	0
57	MG	2A	3295	1/1	0.92	0.10	53,53,53,53	0
57	MG	1T	204	1/1	0.92	0.11	52,52,52,52	0
57	MG	1A	3371	1/1	0.92	0.07	44,44,44,44	0
57	MG	1a	3139	1/1	0.92	0.14	62,62,62,62	0
57	MG	2a	3084	1/1	0.92	0.20	51,51,51,51	0
57	MG	2A	3008	1/1	0.92	0.08	36,36,36,36	0
57	MG	1A	3452	1/1	0.92	0.12	60,60,60,60	0
57	MG	1A	3951	1/1	0.92	0.14	36,36,36,36	0
57	MG	2a	3091	1/1	0.92	0.12	53,53,53,53	0
57	MG	2a	3092	1/1	0.92	0.22	47,47,47,47	0
57	MG	2a	3093	1/1	0.92	0.09	45,45,45,45	0
57	MG	2a	3099	1/1	0.92	0.34	46,46,46,46	0
57	MG	1A	3830	1/1	0.92	0.07	41,41,41,41	0
57	MG	2A	3580	1/1	0.92	0.09	36,36,36,36	0
57	MG	2A	3581	1/1	0.92	0.10	62,62,62,62	0
57	MG	2A	3023	1/1	0.92	0.12	56,56,56,56	0
57	MG	1a	3143	1/1	0.92	0.12	56,56,56,56	0
57	MG	10	104	1/1	0.92	0.09	46,46,46,46	0
57	MG	1A	3211	1/1	0.92	0.08	45,45,45,45	0
57	MG	2a	3118	1/1	0.92	0.10	54,54,54,54	0
57	MG	2A	3594	1/1	0.92	0.11	54,54,54,54	0
57	MG	10	107	1/1	0.92	0.09	42,42,42,42	0
57	MG	2A	3601	1/1	0.92	0.08	32,32,32,32	0
57	MG	2a	3130	1/1	0.92	0.12	64,64,64,64	0
57	MG	2a	3131	1/1	0.92	0.15	54,54,54,54	0
57	MG	1A	3214	1/1	0.92	0.08	49,49,49,49	0
57	MG	2A	3603	1/1	0.92	0.07	37,37,37,37	0
57	MG	2A	3332	1/1	0.92	0.12	47,47,47,47	0
57	MG	1A	3960	1/1	0.92	0.06	46,46,46,46	0
57	MG	2A	3045	1/1	0.92	0.16	55,55,55,55	0
57	MG	1a	3005	1/1	0.92	0.08	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	3160	1/1	0.92	0.17	56,56,56,56	0
57	MG	2a	3144	1/1	0.92	0.08	64,64,64,64	0
57	MG	2A	3344	1/1	0.92	0.10	37,37,37,37	0
57	MG	1A	3840	1/1	0.92	0.08	44,44,44,44	0
57	MG	1A	3215	1/1	0.92	0.08	46,46,46,46	0
57	MG	1a	3164	1/1	0.92	0.14	55,55,55,55	0
57	MG	1a	3014	1/1	0.92	0.11	61,61,61,61	0
57	MG	2a	3164	1/1	0.92	0.10	61,61,61,61	0
57	MG	1A	3540	1/1	0.92	0.13	41,41,41,41	0
57	MG	2a	3170	1/1	0.92	0.17	49,49,49,49	0
57	MG	2a	3176	1/1	0.92	0.08	55,55,55,55	0
57	MG	2A	3625	1/1	0.92	0.11	46,46,46,46	0
57	MG	1A	3623	1/1	0.92	0.06	14,14,14,14	0
57	MG	2A	3076	1/1	0.92	0.10	45,45,45,45	0
57	MG	1A	3630	1/1	0.92	0.11	37,37,37,37	0
57	MG	2a	3186	1/1	0.92	0.09	52,52,52,52	0
57	MG	1A	3974	1/1	0.92	0.12	49,49,49,49	0
57	MG	2A	3636	1/1	0.92	0.12	52,52,52,52	0
57	MG	2A	3083	1/1	0.92	0.23	56,56,56,56	0
57	MG	1A	3464	1/1	0.92	0.08	54,54,54,54	0
57	MG	1A	3712	1/1	0.92	0.07	60,60,60,60	0
57	MG	2A	3382	1/1	0.92	0.20	61,61,61,61	0
57	MG	2A	3089	1/1	0.92	0.13	58,58,58,58	0
57	MG	1A	3978	1/1	0.92	0.11	36,36,36,36	0
57	MG	2A	3387	1/1	0.92	0.08	32,32,32,32	0
57	MG	2A	3389	1/1	0.92	0.09	53,53,53,53	0
57	MG	1A	3715	1/1	0.92	0.07	29,29,29,29	0
57	MG	1A	3002	1/1	0.92	0.14	57,57,57,57	0
57	MG	1A	3718	1/1	0.92	0.13	30,30,30,30	0
57	MG	2A	3411	1/1	0.93	0.12	44,44,44,44	0
57	MG	2A	3700	1/1	0.93	0.12	46,46,46,46	0
57	MG	2A	3703	1/1	0.93	0.26	42,42,42,42	0
57	MG	2A	3133	1/1	0.93	0.20	58,58,58,58	0
57	MG	1A	3762	1/1	0.93	0.06	30,30,30,30	0
57	MG	1a	3059	1/1	0.93	0.10	50,50,50,50	0
57	MG	1A	3181	1/1	0.93	0.09	49,49,49,49	0
57	MG	1A	3388	1/1	0.93	0.06	23,23,23,23	0
57	MG	1A	3775	1/1	0.93	0.12	43,43,43,43	0
57	MG	1A	3188	1/1	0.93	0.11	41,41,41,41	0
57	MG	1a	3220	1/1	0.93	0.06	57,57,57,57	0
57	MG	2A	3154	1/1	0.93	0.16	45,45,45,45	0
57	MG	1A	3189	1/1	0.93	0.16	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	3222	1/1	0.93	0.08	75,75,75,75	0
57	MG	1A	3780	1/1	0.93	0.08	43,43,43,43	0
57	MG	2A	3722	1/1	0.93	0.16	54,54,54,54	0
57	MG	2A	3161	1/1	0.93	0.14	52,52,52,52	0
57	MG	2A	3724	1/1	0.93	0.08	50,50,50,50	0
57	MG	1B	204	1/1	0.93	0.11	42,42,42,42	0
57	MG	2A	3165	1/1	0.93	0.07	67,67,67,67	0
57	MG	1A	3324	1/1	0.93	0.10	34,34,34,34	0
57	MG	1B	216	1/1	0.93	0.10	43,43,43,43	0
57	MG	1A	3906	1/1	0.93	0.10	22,22,22,22	0
57	MG	1A	3485	1/1	0.93	0.07	39,39,39,39	0
57	MG	1a	3081	1/1	0.93	0.20	54,54,54,54	0
57	MG	1A	3912	1/1	0.93	0.07	53,53,53,53	0
57	MG	2A	3186	1/1	0.93	0.16	60,60,60,60	0
57	MG	1a	3084	1/1	0.93	0.08	46,46,46,46	0
57	MG	2A	3451	1/1	0.93	0.10	56,56,56,56	0
57	MG	1A	3580	1/1	0.93	0.09	37,37,37,37	0
57	MG	1B	225	1/1	0.93	0.11	47,47,47,47	0
57	MG	1A	3914	1/1	0.93	0.07	34,34,34,34	0
57	MG	1a	3089	1/1	0.93	0.06	43,43,43,43	0
57	MG	1a	3248	1/1	0.93	0.09	45,45,45,45	0
57	MG	2A	3461	1/1	0.93	0.10	53,53,53,53	0
57	MG	2A	3195	1/1	0.93	0.17	41,41,41,41	0
57	MG	1A	3916	1/1	0.93	0.11	52,52,52,52	0
57	MG	2A	3199	1/1	0.93	0.13	55,55,55,55	0
57	MG	2A	3202	1/1	0.93	0.21	62,62,62,62	0
57	MG	1B	230	1/1	0.93	0.08	44,44,44,44	0
57	MG	1A	3664	1/1	0.93	0.08	49,49,49,49	0
57	MG	1a	3094	1/1	0.93	0.10	57,57,57,57	0
57	MG	1A	3583	1/1	0.93	0.05	29,29,29,29	0
57	MG	2P	201	1/1	0.93	0.09	49,49,49,49	0
57	MG	1D	314	1/1	0.93	0.19	33,33,33,33	0
57	MG	2A	3214	1/1	0.93	0.20	51,51,51,51	0
57	MG	2R	202	1/1	0.93	0.12	47,47,47,47	0
57	MG	2A	3476	1/1	0.93	0.09	55,55,55,55	0
57	MG	1A	3486	1/1	0.93	0.08	20,20,20,20	0
57	MG	2A	3478	1/1	0.93	0.15	47,47,47,47	0
57	MG	1A	3004	1/1	0.93	0.11	40,40,40,40	0
57	MG	2A	3482	1/1	0.93	0.07	21,21,21,21	0
57	MG	1A	3927	1/1	0.93	0.09	52,52,52,52	0
57	MG	2A	3221	1/1	0.93	0.08	55,55,55,55	0
57	MG	1A	3929	1/1	0.93	0.17	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	21	101	1/1	0.93	0.22	53,53,53,53	0
57	MG	1A	3674	1/1	0.93	0.07	43,43,43,43	0
57	MG	21	103	1/1	0.93	0.08	54,54,54,54	0
57	MG	1F	309	1/1	0.93	0.15	44,44,44,44	0
57	MG	2A	3228	1/1	0.93	0.24	51,51,51,51	0
57	MG	2A	3232	1/1	0.93	0.19	51,51,51,51	0
57	MG	1A	3932	1/1	0.93	0.07	50,50,50,50	0
57	MG	1A	3801	1/1	0.93	0.09	40,40,40,40	0
57	MG	2a	3002	1/1	0.93	0.22	57,57,57,57	0
57	MG	1A	3676	1/1	0.93	0.06	57,57,57,57	0
57	MG	1A	3130	1/1	0.93	0.10	47,47,47,47	0
57	MG	1d	304	1/1	0.93	0.06	55,55,55,55	0
57	MG	2A	3504	1/1	0.93	0.08	39,39,39,39	0
57	MG	2a	3010	1/1	0.93	0.16	61,61,61,61	0
57	MG	2a	3013	1/1	0.93	0.18	56,56,56,56	0
57	MG	1A	3808	1/1	0.93	0.06	32,32,32,32	0
57	MG	2A	3244	1/1	0.93	0.34	37,37,37,37	0
57	MG	1a	3112	1/1	0.93	0.21	53,53,53,53	0
57	MG	2a	3020	1/1	0.93	0.09	58,58,58,58	0
57	MG	2A	3248	1/1	0.93	0.12	50,50,50,50	0
57	MG	1f	202	1/1	0.93	0.13	45,45,45,45	0
57	MG	2A	3512	1/1	0.93	0.07	43,43,43,43	0
57	MG	2A	3515	1/1	0.93	0.08	67,67,67,67	0
57	MG	2a	3029	1/1	0.93	0.11	57,57,57,57	0
57	MG	2A	3516	1/1	0.93	0.12	61,61,61,61	0
57	MG	2a	3033	1/1	0.93	0.21	48,48,48,48	0
57	MG	1G	204	1/1	0.93	0.13	49,49,49,49	0
57	MG	1h	202	1/1	0.93	0.16	69,69,69,69	0
57	MG	1A	3053	1/1	0.93	0.25	31,31,31,31	0
57	MG	1A	3681	1/1	0.93	0.11	32,32,32,32	0
57	MG	1A	3263	1/1	0.93	0.10	37,37,37,37	0
57	MG	1A	3820	1/1	0.93	0.09	11,11,11,11	0
57	MG	1a	3122	1/1	0.93	0.14	56,56,56,56	0
57	MG	2A	3266	1/1	0.93	0.12	54,54,54,54	0
57	MG	1a	3123	1/1	0.93	0.08	45,45,45,45	0
57	MG	2A	3533	1/1	0.93	0.10	59,59,59,59	0
57	MG	2A	3534	1/1	0.93	0.14	61,61,61,61	0
57	MG	1P	204	1/1	0.93	0.07	59,59,59,59	0
57	MG	1A	3022	1/1	0.93	0.09	43,43,43,43	0
57	MG	2a	3052	1/1	0.93	0.17	51,51,51,51	0
57	MG	1A	3409	1/1	0.93	0.06	18,18,18,18	0
57	MG	2a	3054	1/1	0.93	0.18	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3544	1/1	0.93	0.07	36,36,36,36	0
57	MG	1A	3270	1/1	0.93	0.11	51,51,51,51	0
57	MG	2a	3059	1/1	0.93	0.20	53,53,53,53	0
57	MG	1V	204	1/1	0.93	0.09	46,46,46,46	0
57	MG	1A	3510	1/1	0.93	0.06	14,14,14,14	0
57	MG	1a	3133	1/1	0.93	0.13	61,61,61,61	0
57	MG	1A	3103	1/1	0.93	0.14	34,34,34,34	0
57	MG	2A	3557	1/1	0.93	0.09	54,54,54,54	0
57	MG	1A	3955	1/1	0.93	0.10	42,42,42,42	0
57	MG	2a	3068	1/1	0.93	0.09	60,60,60,60	0
57	MG	2A	3291	1/1	0.93	0.17	33,33,33,33	0
57	MG	1A	3060	1/1	0.93	0.11	47,47,47,47	0
57	MG	2a	3071	1/1	0.93	0.13	58,58,58,58	0
57	MG	2a	3073	1/1	0.93	0.17	58,58,58,58	0
57	MG	1A	3348	1/1	0.93	0.10	43,43,43,43	0
57	MG	1A	3424	1/1	0.93	0.12	30,30,30,30	0
57	MG	2A	3024	1/1	0.93	0.10	58,58,58,58	0
57	MG	2a	3080	1/1	0.93	0.11	47,47,47,47	0
57	MG	1A	3427	1/1	0.93	0.08	22,22,22,22	0
57	MG	2a	3083	1/1	0.93	0.25	54,54,54,54	0
57	MG	1A	3158	1/1	0.93	0.12	52,52,52,52	0
57	MG	2A	3032	1/1	0.93	0.21	51,51,51,51	0
57	MG	2A	3304	1/1	0.93	0.10	37,37,37,37	0
57	MG	1A	3285	1/1	0.93	0.11	29,29,29,29	0
57	MG	2a	3089	1/1	0.93	0.10	54,54,54,54	0
57	MG	1A	3706	1/1	0.93	0.15	52,52,52,52	0
57	MG	1A	3616	1/1	0.93	0.07	32,32,32,32	0
57	MG	2A	3038	1/1	0.93	0.19	46,46,46,46	0
57	MG	2a	3094	1/1	0.93	0.19	60,60,60,60	0
57	MG	2a	3095	1/1	0.93	0.18	67,67,67,67	0
57	MG	1A	3851	1/1	0.93	0.11	15,15,15,15	0
57	MG	2A	3595	1/1	0.93	0.07	61,61,61,61	0
57	MG	2a	3103	1/1	0.93	0.39	61,61,61,61	0
57	MG	2a	3104	1/1	0.93	0.30	48,48,48,48	0
57	MG	1a	3010	1/1	0.93	0.27	63,63,63,63	0
57	MG	2A	3047	1/1	0.93	0.09	52,52,52,52	0
57	MG	2a	3109	1/1	0.93	0.31	50,50,50,50	0
57	MG	1A	3034	1/1	0.93	0.12	47,47,47,47	0
57	MG	2A	3053	1/1	0.93	0.18	58,58,58,58	0
57	MG	1a	3015	1/1	0.93	0.12	59,59,59,59	0
57	MG	2A	3607	1/1	0.93	0.07	42,42,42,42	0
57	MG	1A	3292	1/1	0.93	0.10	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3299	1/1	0.93	0.13	27,27,27,27	0
57	MG	1a	3170	1/1	0.93	0.08	49,49,49,49	0
57	MG	2a	3125	1/1	0.93	0.10	49,49,49,49	0
57	MG	1A	3035	1/1	0.93	0.07	32,32,32,32	0
57	MG	2a	3129	1/1	0.93	0.09	67,67,67,67	0
57	MG	2A	3061	1/1	0.93	0.08	43,43,43,43	0
57	MG	2A	3348	1/1	0.93	0.07	45,45,45,45	0
57	MG	1A	3301	1/1	0.93	0.14	53,53,53,53	0
57	MG	2A	3065	1/1	0.93	0.07	45,45,45,45	0
57	MG	1a	3024	1/1	0.93	0.10	51,51,51,51	0
57	MG	2A	3075	1/1	0.93	0.10	48,48,48,48	0
57	MG	1A	3985	1/1	0.93	0.11	35,35,35,35	0
57	MG	2a	3139	1/1	0.93	0.09	60,60,60,60	0
57	MG	2A	3626	1/1	0.93	0.07	67,67,67,67	0
57	MG	2A	3077	1/1	0.93	0.08	43,43,43,43	0
57	MG	1A	3632	1/1	0.93	0.08	40,40,40,40	0
57	MG	1A	3038	1/1	0.93	0.10	32,32,32,32	0
57	MG	2A	3081	1/1	0.93	0.09	51,51,51,51	0
57	MG	2A	3373	1/1	0.93	0.07	44,44,44,44	0
57	MG	2a	3150	1/1	0.93	0.09	45,45,45,45	0
57	MG	1a	3180	1/1	0.93	0.24	60,60,60,60	0
57	MG	1A	3224	1/1	0.93	0.11	29,29,29,29	0
57	MG	2a	3159	1/1	0.93	0.11	56,56,56,56	0
57	MG	1A	3377	1/1	0.93	0.09	49,49,49,49	0
57	MG	2a	3165	1/1	0.93	0.17	58,58,58,58	0
57	MG	1a	3183	1/1	0.93	0.09	37,37,37,37	0
57	MG	2A	3652	1/1	0.93	0.12	31,31,31,31	0
57	MG	1A	3306	1/1	0.93	0.08	35,35,35,35	0
57	MG	2a	3177	1/1	0.93	0.07	64,64,64,64	0
57	MG	2a	3178	1/1	0.93	0.13	62,62,62,62	0
57	MG	1A	3554	1/1	0.93	0.06	32,32,32,32	0
57	MG	1a	3040	1/1	0.93	0.14	58,58,58,58	0
57	MG	1a	3189	1/1	0.93	0.06	58,58,58,58	0
57	MG	2a	3184	1/1	0.93	0.24	59,59,59,59	0
57	MG	1A	3643	1/1	0.93	0.10	52,52,52,52	0
57	MG	2A	3099	1/1	0.93	0.14	47,47,47,47	0
57	MG	2A	3103	1/1	0.93	0.16	47,47,47,47	0
57	MG	1A	3868	1/1	0.93	0.08	41,41,41,41	0
57	MG	1A	3125	1/1	0.93	0.12	29,29,29,29	0
57	MG	1A	3759	1/1	0.93	0.08	33,33,33,33	0
57	MG	1A	3560	1/1	0.93	0.08	52,52,52,52	0
57	MG	1A	4010	1/1	0.93	0.18	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	4011	1/1	0.93	0.17	64,64,64,64	0
57	MG	2A	3688	1/1	0.93	0.09	49,49,49,49	0
57	MG	2A	3123	1/1	0.93	0.10	33,33,33,33	0
57	MG	1A	3563	1/1	0.93	0.07	34,34,34,34	0
57	MG	1a	3205	1/1	0.93	0.13	59,59,59,59	0
57	MG	1a	3056	1/1	0.93	0.14	51,51,51,51	0
57	MG	2A	3698	1/1	0.93	0.09	63,63,63,63	0
61	ZN	24	501	1/1	0.93	0.17	127,127,127,127	0
57	MG	1a	3006	1/1	0.94	0.10	59,59,59,59	0
57	MG	2A	3706	1/1	0.94	0.08	33,33,33,33	0
57	MG	2A	3707	1/1	0.94	0.07	35,35,35,35	0
57	MG	2A	3088	1/1	0.94	0.10	40,40,40,40	0
57	MG	1A	3562	1/1	0.94	0.17	56,56,56,56	0
57	MG	1A	3182	1/1	0.94	0.09	49,49,49,49	0
57	MG	1A	3670	1/1	0.94	0.15	33,33,33,33	0
57	MG	1A	3824	1/1	0.94	0.09	41,41,41,41	0
57	MG	1A	3564	1/1	0.94	0.09	50,50,50,50	0
57	MG	1A	3673	1/1	0.94	0.09	36,36,36,36	0
57	MG	1A	3566	1/1	0.94	0.07	15,15,15,15	0
57	MG	1A	3360	1/1	0.94	0.12	45,45,45,45	0
57	MG	1A	3976	1/1	0.94	0.07	48,48,48,48	0
57	MG	2A	3109	1/1	0.94	0.15	42,42,42,42	0
57	MG	1A	3222	1/1	0.94	0.15	33,33,33,33	0
57	MG	2A	3412	1/1	0.94	0.06	30,30,30,30	0
57	MG	1a	3026	1/1	0.94	0.21	53,53,53,53	0
57	MG	2A	3115	1/1	0.94	0.20	52,52,52,52	0
57	MG	2A	3416	1/1	0.94	0.07	49,49,49,49	0
57	MG	2B	203	1/1	0.94	0.17	54,54,54,54	0
57	MG	1a	3193	1/1	0.94	0.08	47,47,47,47	0
57	MG	2A	3419	1/1	0.94	0.05	28,28,28,28	0
57	MG	2A	3117	1/1	0.94	0.25	47,47,47,47	0
57	MG	1A	3834	1/1	0.94	0.08	34,34,34,34	0
57	MG	2A	3120	1/1	0.94	0.31	47,47,47,47	0
57	MG	1a	3195	1/1	0.94	0.13	52,52,52,52	0
57	MG	1A	3570	1/1	0.94	0.09	39,39,39,39	0
57	MG	1a	3030	1/1	0.94	0.12	38,38,38,38	0
57	MG	1A	3462	1/1	0.94	0.10	46,46,46,46	0
57	MG	2A	3131	1/1	0.94	0.18	52,52,52,52	0
57	MG	2D	303	1/1	0.94	0.14	44,44,44,44	0
57	MG	2D	305	1/1	0.94	0.10	30,30,30,30	0
57	MG	1a	3202	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	3983	1/1	0.94	0.06	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3363	1/1	0.94	0.07	42,42,42,42	0
57	MG	1A	3370	1/1	0.94	0.09	38,38,38,38	0
57	MG	1A	3686	1/1	0.94	0.10	54,54,54,54	0
57	MG	1a	3038	1/1	0.94	0.10	56,56,56,56	0
57	MG	1A	3467	1/1	0.94	0.06	41,41,41,41	0
57	MG	1a	3212	1/1	0.94	0.07	64,64,64,64	0
57	MG	2A	3149	1/1	0.94	0.13	44,44,44,44	0
57	MG	1A	3183	1/1	0.94	0.19	63,63,63,63	0
57	MG	1a	3215	1/1	0.94	0.09	44,44,44,44	0
57	MG	2A	3157	1/1	0.94	0.11	57,57,57,57	0
57	MG	1A	3581	1/1	0.94	0.08	33,33,33,33	0
57	MG	1A	3226	1/1	0.94	0.09	38,38,38,38	0
57	MG	2A	3453	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3187	1/1	0.94	0.08	47,47,47,47	0
57	MG	2T	201	1/1	0.94	0.18	51,51,51,51	0
57	MG	1A	3476	1/1	0.94	0.06	24,24,24,24	0
57	MG	2T	203	1/1	0.94	0.07	55,55,55,55	0
57	MG	1A	3305	1/1	0.94	0.20	25,25,25,25	0
57	MG	1A	3378	1/1	0.94	0.06	26,26,26,26	0
57	MG	2A	3460	1/1	0.94	0.07	55,55,55,55	0
57	MG	2V	203	1/1	0.94	0.15	53,53,53,53	0
57	MG	2A	3166	1/1	0.94	0.12	59,59,59,59	0
57	MG	1a	3053	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	3999	1/1	0.94	0.08	39,39,39,39	0
57	MG	2A	3169	1/1	0.94	0.24	49,49,49,49	0
57	MG	1A	3481	1/1	0.94	0.07	23,23,23,23	0
57	MG	1A	3114	1/1	0.94	0.15	28,28,28,28	0
57	MG	1A	3861	1/1	0.94	0.07	32,32,32,32	0
57	MG	1A	3595	1/1	0.94	0.09	54,54,54,54	0
57	MG	2A	3183	1/1	0.94	0.12	48,48,48,48	0
57	MG	27	101	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3237	1/1	0.94	0.17	47,47,47,47	0
57	MG	1A	3069	1/1	0.94	0.20	27,27,27,27	0
57	MG	2A	3475	1/1	0.94	0.10	48,48,48,48	0
57	MG	2A	3188	1/1	0.94	0.13	48,48,48,48	0
57	MG	2a	3003	1/1	0.94	0.10	52,52,52,52	0
57	MG	1a	3066	1/1	0.94	0.12	45,45,45,45	0
57	MG	1a	3068	1/1	0.94	0.08	53,53,53,53	0
57	MG	1A	3489	1/1	0.94	0.08	53,53,53,53	0
57	MG	1A	4015	1/1	0.94	0.09	52,52,52,52	0
57	MG	1a	3241	1/1	0.94	0.08	49,49,49,49	0
57	MG	1A	3600	1/1	0.94	0.10	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	3244	1/1	0.94	0.09	56,56,56,56	0
57	MG	1a	3245	1/1	0.94	0.07	52,52,52,52	0
57	MG	2A	3200	1/1	0.94	0.12	57,57,57,57	0
57	MG	1A	3314	1/1	0.94	0.06	32,32,32,32	0
57	MG	2a	3021	1/1	0.94	0.23	58,58,58,58	0
57	MG	2A	3203	1/1	0.94	0.06	40,40,40,40	0
57	MG	2A	3204	1/1	0.94	0.19	43,43,43,43	0
57	MG	2a	3025	1/1	0.94	0.12	57,57,57,57	0
57	MG	1a	3249	1/1	0.94	0.12	51,51,51,51	0
57	MG	1A	4020	1/1	0.94	0.13	48,48,48,48	0
57	MG	1A	3869	1/1	0.94	0.07	20,20,20,20	0
57	MG	1a	3254	1/1	0.94	0.15	45,45,45,45	0
57	MG	1A	3722	1/1	0.94	0.07	35,35,35,35	0
57	MG	1A	3723	1/1	0.94	0.09	39,39,39,39	0
57	MG	1A	3123	1/1	0.94	0.07	64,64,64,64	0
57	MG	1B	207	1/1	0.94	0.15	50,50,50,50	0
57	MG	2A	3217	1/1	0.94	0.09	49,49,49,49	0
57	MG	1a	3083	1/1	0.94	0.15	52,52,52,52	0
57	MG	2A	3220	1/1	0.94	0.13	57,57,57,57	0
57	MG	2a	3041	1/1	0.94	0.27	65,65,65,65	0
57	MG	1B	208	1/1	0.94	0.25	48,48,48,48	0
57	MG	1B	210	1/1	0.94	0.09	46,46,46,46	0
57	MG	1A	3729	1/1	0.94	0.11	42,42,42,42	0
57	MG	2A	3518	1/1	0.94	0.07	58,58,58,58	0
57	MG	2a	3048	1/1	0.94	0.11	58,58,58,58	0
57	MG	1A	3730	1/1	0.94	0.10	47,47,47,47	0
57	MG	2A	3521	1/1	0.94	0.08	49,49,49,49	0
57	MG	1A	3605	1/1	0.94	0.19	43,43,43,43	0
57	MG	2A	3230	1/1	0.94	0.08	43,43,43,43	0
57	MG	2A	3524	1/1	0.94	0.13	50,50,50,50	0
57	MG	1A	3741	1/1	0.94	0.08	47,47,47,47	0
57	MG	2a	3056	1/1	0.94	0.19	49,49,49,49	0
57	MG	1A	3191	1/1	0.94	0.15	53,53,53,53	0
57	MG	2A	3234	1/1	0.94	0.11	40,40,40,40	0
57	MG	1A	3321	1/1	0.94	0.14	48,48,48,48	0
57	MG	2A	3236	1/1	0.94	0.12	38,38,38,38	0
57	MG	2A	3532	1/1	0.94	0.06	53,53,53,53	0
57	MG	1A	3896	1/1	0.94	0.07	36,36,36,36	0
57	MG	1A	3323	1/1	0.94	0.06	26,26,26,26	0
57	MG	2A	3535	1/1	0.94	0.09	47,47,47,47	0
57	MG	1d	305	1/1	0.94	0.07	75,75,75,75	0
57	MG	2a	3067	1/1	0.94	0.20	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	3241	1/1	0.94	0.21	51,51,51,51	0
57	MG	2A	3541	1/1	0.94	0.09	48,48,48,48	0
57	MG	1A	3192	1/1	0.94	0.19	27,27,27,27	0
57	MG	1A	3751	1/1	0.94	0.06	37,37,37,37	0
57	MG	2A	3245	1/1	0.94	0.10	43,43,43,43	0
57	MG	1A	3400	1/1	0.94	0.06	11,11,11,11	0
57	MG	1D	308	1/1	0.94	0.19	44,44,44,44	0
57	MG	1A	3325	1/1	0.94	0.07	46,46,46,46	0
57	MG	1A	3911	1/1	0.94	0.07	52,52,52,52	0
57	MG	1i	202	1/1	0.94	0.13	55,55,55,55	0
57	MG	2A	3558	1/1	0.94	0.10	52,52,52,52	0
57	MG	1l	201	1/1	0.94	0.13	56,56,56,56	0
57	MG	2A	3255	1/1	0.94	0.18	54,54,54,54	0
57	MG	1l	202	1/1	0.94	0.11	64,64,64,64	0
57	MG	1A	3756	1/1	0.94	0.11	48,48,48,48	0
57	MG	2A	3259	1/1	0.94	0.08	43,43,43,43	0
57	MG	1D	316	1/1	0.94	0.07	49,49,49,49	0
57	MG	1A	3327	1/1	0.94	0.14	24,24,24,24	0
57	MG	1E	305	1/1	0.94	0.07	40,40,40,40	0
57	MG	2A	3267	1/1	0.94	0.14	48,48,48,48	0
57	MG	1o	101	1/1	0.94	0.14	49,49,49,49	0
57	MG	2a	3096	1/1	0.94	0.07	55,55,55,55	0
57	MG	1E	307	1/1	0.94	0.08	44,44,44,44	0
57	MG	1A	3093	1/1	0.94	0.07	56,56,56,56	0
57	MG	1A	3915	1/1	0.94	0.08	47,47,47,47	0
57	MG	1A	3517	1/1	0.94	0.07	16,16,16,16	0
57	MG	1A	3032	1/1	0.94	0.17	45,45,45,45	0
57	MG	2A	3002	1/1	0.94	0.06	38,38,38,38	0
57	MG	2A	3597	1/1	0.94	0.08	53,53,53,53	0
57	MG	1A	3040	1/1	0.94	0.10	47,47,47,47	0
57	MG	1a	3117	1/1	0.94	0.19	36,36,36,36	0
57	MG	1A	3269	1/1	0.94	0.06	23,23,23,23	0
57	MG	2a	3116	1/1	0.94	0.08	47,47,47,47	0
57	MG	1a	3119	1/1	0.94	0.32	55,55,55,55	0
57	MG	1A	3168	1/1	0.94	0.17	43,43,43,43	0
57	MG	2a	3119	1/1	0.94	0.10	60,60,60,60	0
57	MG	2a	3121	1/1	0.94	0.14	54,54,54,54	0
57	MG	2A	3014	1/1	0.94	0.09	51,51,51,51	0
57	MG	1F	318	1/1	0.94	0.08	41,41,41,41	0
57	MG	1A	3926	1/1	0.94	0.12	35,35,35,35	0
57	MG	1A	3127	1/1	0.94	0.27	42,42,42,42	0
57	MG	1A	3422	1/1	0.94	0.09	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	1N	203	1/1	0.94	0.08	45,45,45,45	0
57	MG	1a	3127	1/1	0.94	0.19	52,52,52,52	0
57	MG	1A	3276	1/1	0.94	0.10	56,56,56,56	0
57	MG	1A	3532	1/1	0.94	0.09	46,46,46,46	0
57	MG	1A	3207	1/1	0.94	0.16	30,30,30,30	0
57	MG	1A	3173	1/1	0.94	0.07	48,48,48,48	0
57	MG	1A	3349	1/1	0.94	0.08	44,44,44,44	0
57	MG	1a	3137	1/1	0.94	0.09	61,61,61,61	0
57	MG	2A	3043	1/1	0.94	0.09	39,39,39,39	0
57	MG	1A	3434	1/1	0.94	0.10	52,52,52,52	0
57	MG	2A	3327	1/1	0.94	0.14	38,38,38,38	0
57	MG	1A	3942	1/1	0.94	0.06	25,25,25,25	0
57	MG	2a	3146	1/1	0.94	0.09	56,56,56,56	0
57	MG	2A	3634	1/1	0.94	0.10	48,48,48,48	0
57	MG	2A	3049	1/1	0.94	0.18	54,54,54,54	0
57	MG	2A	3050	1/1	0.94	0.06	47,47,47,47	0
57	MG	1A	3543	1/1	0.94	0.12	45,45,45,45	0
57	MG	1T	205	1/1	0.94	0.08	50,50,50,50	0
57	MG	1V	203	1/1	0.94	0.08	31,31,31,31	0
57	MG	2a	3160	1/1	0.94	0.12	52,52,52,52	0
57	MG	1A	3653	1/1	0.94	0.28	42,42,42,42	0
57	MG	1A	3436	1/1	0.94	0.09	44,44,44,44	0
57	MG	2A	3654	1/1	0.94	0.06	29,29,29,29	0
57	MG	2a	3168	1/1	0.94	0.06	45,45,45,45	0
57	MG	1A	3656	1/1	0.94	0.07	17,17,17,17	0
57	MG	2a	3173	1/1	0.94	0.09	64,64,64,64	0
57	MG	2A	3353	1/1	0.94	0.10	54,54,54,54	0
57	MG	1A	3798	1/1	0.94	0.06	46,46,46,46	0
57	MG	1A	3210	1/1	0.94	0.19	26,26,26,26	0
57	MG	2A	3062	1/1	0.94	0.12	40,40,40,40	0
57	MG	2A	3063	1/1	0.94	0.20	43,43,43,43	0
57	MG	1A	3012	1/1	0.94	0.09	32,32,32,32	0
57	MG	1A	3553	1/1	0.94	0.10	49,49,49,49	0
57	MG	2A	3072	1/1	0.94	0.10	44,44,44,44	0
57	MG	1A	3287	1/1	0.94	0.09	48,48,48,48	0
57	MG	1A	3066	1/1	0.94	0.05	32,32,32,32	0
57	MG	2a	3188	1/1	0.94	0.19	57,57,57,57	0
57	MG	2A	3680	1/1	0.94	0.14	39,39,39,39	0
57	MG	13	102	1/1	0.94	0.10	51,51,51,51	0
57	MG	1a	3165	1/1	0.94	0.10	53,53,53,53	0
57	MG	2A	3689	1/1	0.94	0.12	62,62,62,62	0
57	MG	2A	3078	1/1	0.94	0.13	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	2p	101	1/1	0.94	0.17	49,49,49,49	0
57	MG	2t	201	1/1	0.94	0.13	40,40,40,40	0
57	MG	15	105	1/1	0.94	0.11	25,25,25,25	0
58	CLM	2A	3727	20/20	0.94	0.10	33,38,57,59	0
57	MG	15	108	1/1	0.94	0.07	34,34,34,34	0
57	MG	15	109	1/1	0.94	0.07	46,46,46,46	0
57	MG	1A	3455	1/1	0.94	0.07	41,41,41,41	0
57	MG	2A	3388	1/1	0.94	0.10	49,49,49,49	0
57	MG	2A	3084	1/1	0.94	0.07	35,35,35,35	0
57	MG	1A	3958	1/1	0.94	0.16	37,37,37,37	0
61	ZN	14	501	1/1	0.94	0.11	104,104,104,104	0
57	MG	2A	3393	1/1	0.94	0.08	51,51,51,51	0
57	MG	1B	212	1/1	0.95	0.07	45,45,45,45	0
57	MG	1a	3225	1/1	0.95	0.12	60,60,60,60	0
57	MG	1a	3226	1/1	0.95	0.11	49,49,49,49	0
57	MG	1a	3064	1/1	0.95	0.23	57,57,57,57	0
57	MG	1A	3261	1/1	0.95	0.08	40,40,40,40	0
57	MG	2A	3146	1/1	0.95	0.18	45,45,45,45	0
57	MG	1A	3771	1/1	0.95	0.07	12,12,12,12	0
57	MG	1A	3772	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3557	1/1	0.95	0.14	58,58,58,58	0
57	MG	2A	3153	1/1	0.95	0.10	37,37,37,37	0
57	MG	1a	3072	1/1	0.95	0.17	46,46,46,46	0
57	MG	2A	3417	1/1	0.95	0.06	38,38,38,38	0
57	MG	2A	3155	1/1	0.95	0.05	30,30,30,30	0
57	MG	1A	3381	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3383	1/1	0.95	0.06	39,39,39,39	0
57	MG	1B	226	1/1	0.95	0.06	35,35,35,35	0
57	MG	1a	3238	1/1	0.95	0.08	54,54,54,54	0
57	MG	1A	3109	1/1	0.95	0.11	31,31,31,31	0
57	MG	2A	3163	1/1	0.95	0.16	35,35,35,35	0
57	MG	1A	3781	1/1	0.95	0.07	46,46,46,46	0
57	MG	1a	3242	1/1	0.95	0.13	52,52,52,52	0
57	MG	1A	3202	1/1	0.95	0.12	38,38,38,38	0
57	MG	1A	3028	1/1	0.95	0.16	26,26,26,26	0
57	MG	1D	306	1/1	0.95	0.07	45,45,45,45	0
57	MG	1A	3389	1/1	0.95	0.05	22,22,22,22	0
57	MG	2A	3172	1/1	0.95	0.08	34,34,34,34	0
57	MG	2A	3174	1/1	0.95	0.06	44,44,44,44	0
57	MG	2B	213	1/1	0.95	0.08	54,54,54,54	0
57	MG	2A	3438	1/1	0.95	0.06	30,30,30,30	0
57	MG	1A	3111	1/1	0.95	0.11	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	3029	1/1	0.95	0.10	36,36,36,36	0
57	MG	1A	3020	1/1	0.95	0.25	33,33,33,33	0
57	MG	2A	3181	1/1	0.95	0.09	45,45,45,45	0
57	MG	1A	3573	1/1	0.95	0.08	21,21,21,21	0
57	MG	1A	3482	1/1	0.95	0.12	27,27,27,27	0
57	MG	1a	3256	1/1	0.95	0.09	55,55,55,55	0
57	MG	2A	3450	1/1	0.95	0.06	48,48,48,48	0
57	MG	2E	303	1/1	0.95	0.07	36,36,36,36	0
57	MG	1a	3088	1/1	0.95	0.16	46,46,46,46	0
57	MG	2F	303	1/1	0.95	0.11	43,43,43,43	0
57	MG	1A	3795	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3672	1/1	0.95	0.09	52,52,52,52	0
57	MG	1A	3935	1/1	0.95	0.07	42,42,42,42	0
57	MG	1A	3936	1/1	0.95	0.10	36,36,36,36	0
57	MG	2N	201	1/1	0.95	0.06	59,59,59,59	0
57	MG	1A	3577	1/1	0.95	0.11	43,43,43,43	0
57	MG	1A	3074	1/1	0.95	0.07	33,33,33,33	0
57	MG	1A	3941	1/1	0.95	0.07	19,19,19,19	0
57	MG	2Q	201	1/1	0.95	0.14	51,51,51,51	0
57	MG	1a	3268	1/1	0.95	0.14	47,47,47,47	0
57	MG	2A	3198	1/1	0.95	0.06	41,41,41,41	0
57	MG	1A	3334	1/1	0.95	0.05	28,28,28,28	0
57	MG	1F	316	1/1	0.95	0.12	35,35,35,35	0
57	MG	1b	301	1/1	0.95	0.19	52,52,52,52	0
57	MG	1A	3806	1/1	0.95	0.09	22,22,22,22	0
57	MG	1A	3281	1/1	0.95	0.07	48,48,48,48	0
57	MG	1A	3487	1/1	0.95	0.06	19,19,19,19	0
57	MG	2A	3470	1/1	0.95	0.08	60,60,60,60	0
57	MG	2V	202	1/1	0.95	0.17	49,49,49,49	0
57	MG	1A	3046	1/1	0.95	0.11	44,44,44,44	0
57	MG	2A	3209	1/1	0.95	0.09	49,49,49,49	0
57	MG	1A	3341	1/1	0.95	0.06	32,32,32,32	0
57	MG	1A	3079	1/1	0.95	0.19	35,35,35,35	0
57	MG	20	101	1/1	0.95	0.08	41,41,41,41	0
57	MG	1A	3497	1/1	0.95	0.09	40,40,40,40	0
57	MG	1a	3109	1/1	0.95	0.21	46,46,46,46	0
57	MG	1A	3589	1/1	0.95	0.07	16,16,16,16	0
57	MG	1A	3052	1/1	0.95	0.14	33,33,33,33	0
57	MG	1A	3500	1/1	0.95	0.08	38,38,38,38	0
57	MG	1a	3113	1/1	0.95	0.27	45,45,45,45	0
57	MG	25	103	1/1	0.95	0.08	48,48,48,48	0
57	MG	1A	3827	1/1	0.95	0.08	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	27	102	1/1	0.95	0.21	37,37,37,37	0
57	MG	27	103	1/1	0.95	0.17	38,38,38,38	0
57	MG	2A	3485	1/1	0.95	0.07	54,54,54,54	0
57	MG	1Q	201	1/1	0.95	0.09	27,27,27,27	0
57	MG	1A	3021	1/1	0.95	0.10	30,30,30,30	0
57	MG	1A	3415	1/1	0.95	0.07	40,40,40,40	0
57	MG	2A	3224	1/1	0.95	0.07	44,44,44,44	0
57	MG	1T	202	1/1	0.95	0.09	43,43,43,43	0
57	MG	1A	3961	1/1	0.95	0.10	40,40,40,40	0
57	MG	2a	3006	1/1	0.95	0.07	54,54,54,54	0
57	MG	2A	3229	1/1	0.95	0.06	27,27,27,27	0
57	MG	2A	3497	1/1	0.95	0.10	40,40,40,40	0
57	MG	2a	3009	1/1	0.95	0.23	54,54,54,54	0
57	MG	2A	3498	1/1	0.95	0.05	36,36,36,36	0
57	MG	1A	3596	1/1	0.95	0.06	27,27,27,27	0
57	MG	1U	207	1/1	0.95	0.07	37,37,37,37	0
57	MG	1A	3968	1/1	0.95	0.04	21,21,21,21	0
57	MG	2a	3016	1/1	0.95	0.06	50,50,50,50	0
57	MG	2a	3017	1/1	0.95	0.10	46,46,46,46	0
57	MG	1A	3832	1/1	0.95	0.05	33,33,33,33	0
57	MG	2a	3019	1/1	0.95	0.06	64,64,64,64	0
57	MG	1V	205	1/1	0.95	0.06	41,41,41,41	0
57	MG	1A	3833	1/1	0.95	0.10	40,40,40,40	0
57	MG	2A	3001	1/1	0.95	0.22	49,49,49,49	0
57	MG	1A	3085	1/1	0.95	0.06	38,38,38,38	0
57	MG	1A	3699	1/1	0.95	0.07	44,44,44,44	0
57	MG	1Y	201	1/1	0.95	0.06	41,41,41,41	0
57	MG	2A	3242	1/1	0.95	0.15	50,50,50,50	0
57	MG	1A	3291	1/1	0.95	0.10	51,51,51,51	0
57	MG	10	102	1/1	0.95	0.08	31,31,31,31	0
57	MG	2a	3032	1/1	0.95	0.19	55,55,55,55	0
57	MG	2A	3011	1/1	0.95	0.06	27,27,27,27	0
57	MG	10	103	1/1	0.95	0.05	37,37,37,37	0
57	MG	1A	3003	1/1	0.95	0.06	20,20,20,20	0
57	MG	1A	3703	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3511	1/1	0.95	0.06	36,36,36,36	0
57	MG	2A	3022	1/1	0.95	0.25	44,44,44,44	0
57	MG	2A	3525	1/1	0.95	0.05	27,27,27,27	0
57	MG	1A	3421	1/1	0.95	0.08	50,50,50,50	0
57	MG	11	101	1/1	0.95	0.13	42,42,42,42	0
57	MG	11	104	1/1	0.95	0.11	47,47,47,47	0
57	MG	1A	3979	1/1	0.95	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	3145	1/1	0.95	0.07	55,55,55,55	0
57	MG	1A	3228	1/1	0.95	0.24	24,24,24,24	0
57	MG	2A	3263	1/1	0.95	0.09	20,20,20,20	0
57	MG	1A	3849	1/1	0.95	0.06	50,50,50,50	0
57	MG	2A	3265	1/1	0.95	0.33	45,45,45,45	0
57	MG	2A	3536	1/1	0.95	0.06	49,49,49,49	0
57	MG	2A	3538	1/1	0.95	0.11	46,46,46,46	0
57	MG	1A	3229	1/1	0.95	0.27	31,31,31,31	0
57	MG	1a	3151	1/1	0.95	0.09	61,61,61,61	0
57	MG	2A	3040	1/1	0.95	0.12	33,33,33,33	0
57	MG	2A	3542	1/1	0.95	0.05	40,40,40,40	0
57	MG	2A	3272	1/1	0.95	0.12	53,53,53,53	0
57	MG	2A	3273	1/1	0.95	0.26	51,51,51,51	0
57	MG	1a	3152	1/1	0.95	0.10	45,45,45,45	0
57	MG	2A	3546	1/1	0.95	0.11	25,25,25,25	0
57	MG	17	102	1/1	0.95	0.14	26,26,26,26	0
57	MG	2a	3064	1/1	0.95	0.13	47,47,47,47	0
57	MG	2A	3550	1/1	0.95	0.07	51,51,51,51	0
57	MG	1a	3156	1/1	0.95	0.11	39,39,39,39	0
57	MG	2A	3553	1/1	0.95	0.05	39,39,39,39	0
57	MG	1A	3058	1/1	0.95	0.09	21,21,21,21	0
57	MG	2A	3555	1/1	0.95	0.06	65,65,65,65	0
57	MG	18	102	1/1	0.95	0.12	32,32,32,32	0
57	MG	1a	3002	1/1	0.95	0.12	49,49,49,49	0
57	MG	1a	3162	1/1	0.95	0.18	55,55,55,55	0
57	MG	2a	3076	1/1	0.95	0.10	54,54,54,54	0
57	MG	1A	3716	1/1	0.95	0.09	21,21,21,21	0
57	MG	2A	3560	1/1	0.95	0.07	33,33,33,33	0
57	MG	1A	3236	1/1	0.95	0.21	47,47,47,47	0
57	MG	2A	3290	1/1	0.95	0.15	47,47,47,47	0
57	MG	2A	3565	1/1	0.95	0.07	56,56,56,56	0
57	MG	1A	3520	1/1	0.95	0.08	20,20,20,20	0
57	MG	1a	3167	1/1	0.95	0.16	62,62,62,62	0
57	MG	2A	3571	1/1	0.95	0.09	37,37,37,37	0
57	MG	2A	3293	1/1	0.95	0.06	46,46,46,46	0
57	MG	1a	3169	1/1	0.95	0.06	43,43,43,43	0
57	MG	1a	3008	1/1	0.95	0.19	46,46,46,46	0
57	MG	1A	3720	1/1	0.95	0.06	62,62,62,62	0
57	MG	1A	3150	1/1	0.95	0.27	38,38,38,38	0
57	MG	1a	3173	1/1	0.95	0.09	44,44,44,44	0
57	MG	2A	3585	1/1	0.95	0.05	38,38,38,38	0
57	MG	2A	3586	1/1	0.95	0.12	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3300	1/1	0.95	0.12	45,45,45,45	0
57	MG	1a	3013	1/1	0.95	0.08	49,49,49,49	0
57	MG	1A	3304	1/1	0.95	0.26	39,39,39,39	0
57	MG	2A	3306	1/1	0.95	0.09	36,36,36,36	0
57	MG	1A	3435	1/1	0.95	0.07	47,47,47,47	0
57	MG	2A	3308	1/1	0.95	0.16	68,68,68,68	0
57	MG	1A	3151	1/1	0.95	0.08	24,24,24,24	0
57	MG	1a	3017	1/1	0.95	0.09	51,51,51,51	0
57	MG	1A	3364	1/1	0.95	0.07	13,13,13,13	0
57	MG	2A	3317	1/1	0.95	0.07	28,28,28,28	0
57	MG	1A	3444	1/1	0.95	0.17	26,26,26,26	0
57	MG	2a	3115	1/1	0.95	0.11	42,42,42,42	0
57	MG	2A	3605	1/1	0.95	0.11	42,42,42,42	0
57	MG	2A	3606	1/1	0.95	0.07	49,49,49,49	0
57	MG	1a	3021	1/1	0.95	0.09	44,44,44,44	0
57	MG	1A	3733	1/1	0.95	0.08	20,20,20,20	0
57	MG	2A	3323	1/1	0.95	0.06	34,34,34,34	0
57	MG	1A	4000	1/1	0.95	0.08	42,42,42,42	0
57	MG	2A	3613	1/1	0.95	0.08	40,40,40,40	0
57	MG	2A	3615	1/1	0.95	0.12	26,26,26,26	0
57	MG	2A	3616	1/1	0.95	0.10	55,55,55,55	0
57	MG	2a	3128	1/1	0.95	0.07	53,53,53,53	0
57	MG	2A	3325	1/1	0.95	0.16	55,55,55,55	0
57	MG	1A	4004	1/1	0.95	0.07	49,49,49,49	0
57	MG	2A	3082	1/1	0.95	0.13	43,43,43,43	0
57	MG	1A	4007	1/1	0.95	0.06	37,37,37,37	0
57	MG	2A	3334	1/1	0.95	0.05	37,37,37,37	0
57	MG	2a	3134	1/1	0.95	0.12	60,60,60,60	0
57	MG	1A	3625	1/1	0.95	0.08	45,45,45,45	0
57	MG	2a	3136	1/1	0.95	0.06	43,43,43,43	0
57	MG	1A	3368	1/1	0.95	0.06	22,22,22,22	0
57	MG	2A	3337	1/1	0.95	0.07	40,40,40,40	0
57	MG	1a	3192	1/1	0.95	0.16	56,56,56,56	0
57	MG	2A	3340	1/1	0.95	0.11	49,49,49,49	0
57	MG	1A	3008	1/1	0.95	0.08	25,25,25,25	0
57	MG	2A	3342	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3450	1/1	0.95	0.07	20,20,20,20	0
57	MG	1A	3748	1/1	0.95	0.10	48,48,48,48	0
57	MG	2A	3349	1/1	0.95	0.07	38,38,38,38	0
57	MG	2A	3091	1/1	0.95	0.07	44,44,44,44	0
57	MG	1A	3250	1/1	0.95	0.13	50,50,50,50	0
57	MG	2A	3644	1/1	0.95	0.14	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	3152	1/1	0.95	0.10	55,55,55,55	0
57	MG	1a	3198	1/1	0.95	0.10	65,65,65,65	0
57	MG	1A	3879	1/1	0.95	0.07	31,31,31,31	0
57	MG	2A	3651	1/1	0.95	0.08	40,40,40,40	0
57	MG	1A	3061	1/1	0.95	0.12	36,36,36,36	0
57	MG	1a	3039	1/1	0.95	0.08	58,58,58,58	0
57	MG	2A	3101	1/1	0.95	0.10	41,41,41,41	0
57	MG	2A	3102	1/1	0.95	0.14	40,40,40,40	0
57	MG	2a	3169	1/1	0.95	0.13	52,52,52,52	0
57	MG	2A	3366	1/1	0.95	0.13	33,33,33,33	0
57	MG	1A	3752	1/1	0.95	0.05	27,27,27,27	0
57	MG	2a	3174	1/1	0.95	0.09	62,62,62,62	0
57	MG	1A	4017	1/1	0.95	0.07	38,38,38,38	0
57	MG	2A	3108	1/1	0.95	0.15	56,56,56,56	0
57	MG	1A	3544	1/1	0.95	0.05	33,33,33,33	0
57	MG	2A	3670	1/1	0.95	0.09	49,49,49,49	0
57	MG	1A	3253	1/1	0.95	0.12	47,47,47,47	0
57	MG	1A	3548	1/1	0.95	0.16	22,22,22,22	0
57	MG	2A	3114	1/1	0.95	0.09	53,53,53,53	0
57	MG	2A	3674	1/1	0.95	0.09	36,36,36,36	0
57	MG	2A	3383	1/1	0.95	0.17	56,56,56,56	0
57	MG	2A	3384	1/1	0.95	0.10	50,50,50,50	0
57	MG	1A	3459	1/1	0.95	0.04	17,17,17,17	0
57	MG	2A	3681	1/1	0.95	0.06	55,55,55,55	0
57	MG	2A	3684	1/1	0.95	0.06	35,35,35,35	0
57	MG	1A	3065	1/1	0.95	0.08	45,45,45,45	0
57	MG	1A	3551	1/1	0.95	0.14	42,42,42,42	0
57	MG	1a	3214	1/1	0.95	0.10	59,59,59,59	0
57	MG	1B	206	1/1	0.95	0.05	36,36,36,36	0
57	MG	2A	3691	1/1	0.95	0.09	57,57,57,57	0
57	MG	1A	3900	1/1	0.95	0.06	26,26,26,26	0
57	MG	1A	3259	1/1	0.95	0.22	32,32,32,32	0
57	MG	2A	3696	1/1	0.95	0.11	65,65,65,65	0
59	ARG	1B	232	12/12	0.95	0.09	26,36,46,51	0
57	MG	2A	3394	1/1	0.95	0.07	45,45,45,45	0
57	MG	1a	3057	1/1	0.95	0.10	55,55,55,55	0
60	MPD	18	103	8/8	0.95	0.11	25,28,37,43	0
57	MG	2A	3127	1/1	0.95	0.21	41,41,41,41	0
57	MG	1B	209	1/1	0.95	0.09	45,45,45,45	0
57	MG	1A	3648	1/1	0.95	0.08	31,31,31,31	0
57	MG	1a	3060	1/1	0.95	0.09	51,51,51,51	0
57	MG	1A	3379	1/1	0.95	0.08	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	1R	202	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3618	1/1	0.96	0.05	20,20,20,20	0
57	MG	1A	3140	1/1	0.96	0.07	21,21,21,21	0
57	MG	1A	3621	1/1	0.96	0.07	40,40,40,40	0
57	MG	1T	203	1/1	0.96	0.06	39,39,39,39	0
57	MG	2A	3368	1/1	0.96	0.05	34,34,34,34	0
57	MG	1A	3622	1/1	0.96	0.10	35,35,35,35	0
57	MG	1A	3141	1/1	0.96	0.11	47,47,47,47	0
57	MG	2A	3372	1/1	0.96	0.14	43,43,43,43	0
57	MG	1T	206	1/1	0.96	0.06	47,47,47,47	0
57	MG	1U	201	1/1	0.96	0.18	28,28,28,28	0
57	MG	2A	3702	1/1	0.96	0.08	61,61,61,61	0
57	MG	1a	3158	1/1	0.96	0.05	41,41,41,41	0
57	MG	1U	205	1/1	0.96	0.16	34,34,34,34	0
57	MG	2A	3381	1/1	0.96	0.09	47,47,47,47	0
57	MG	1U	206	1/1	0.96	0.10	29,29,29,29	0
57	MG	1A	3757	1/1	0.96	0.10	56,56,56,56	0
57	MG	1A	3184	1/1	0.96	0.06	24,24,24,24	0
57	MG	1A	3626	1/1	0.96	0.05	30,30,30,30	0
57	MG	2A	3096	1/1	0.96	0.07	44,44,44,44	0
57	MG	1A	3356	1/1	0.96	0.09	17,17,17,17	0
57	MG	2A	3098	1/1	0.96	0.07	47,47,47,47	0
57	MG	1A	3118	1/1	0.96	0.06	24,24,24,24	0
57	MG	2A	3100	1/1	0.96	0.10	40,40,40,40	0
57	MG	1W	202	1/1	0.96	0.05	30,30,30,30	0
57	MG	1A	3149	1/1	0.96	0.19	35,35,35,35	0
57	MG	1A	3937	1/1	0.96	0.06	29,29,29,29	0
57	MG	2A	3721	1/1	0.96	0.08	39,39,39,39	0
57	MG	1X	101	1/1	0.96	0.07	32,32,32,32	0
57	MG	2A	3105	1/1	0.96	0.06	46,46,46,46	0
57	MG	1A	3633	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3764	1/1	0.96	0.10	46,46,46,46	0
57	MG	1A	3297	1/1	0.96	0.17	30,30,30,30	0
57	MG	2A	3402	1/1	0.96	0.09	40,40,40,40	0
57	MG	1a	3175	1/1	0.96	0.08	43,43,43,43	0
57	MG	1A	3766	1/1	0.96	0.04	30,30,30,30	0
57	MG	2B	205	1/1	0.96	0.11	50,50,50,50	0
57	MG	1a	3177	1/1	0.96	0.06	50,50,50,50	0
57	MG	1A	3943	1/1	0.96	0.14	18,18,18,18	0
57	MG	10	105	1/1	0.96	0.07	43,43,43,43	0
57	MG	1A	3768	1/1	0.96	0.06	20,20,20,20	0
57	MG	2A	3410	1/1	0.96	0.07	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3637	1/1	0.96	0.15	40,40,40,40	0
57	MG	1A	3119	1/1	0.96	0.21	45,45,45,45	0
57	MG	1A	3774	1/1	0.96	0.05	24,24,24,24	0
57	MG	2A	3125	1/1	0.96	0.12	42,42,42,42	0
57	MG	11	103	1/1	0.96	0.06	37,37,37,37	0
57	MG	2D	301	1/1	0.96	0.08	25,25,25,25	0
57	MG	1a	3185	1/1	0.96	0.06	58,58,58,58	0
57	MG	2D	304	1/1	0.96	0.07	44,44,44,44	0
57	MG	1a	3186	1/1	0.96	0.09	53,53,53,53	0
57	MG	1A	3441	1/1	0.96	0.06	25,25,25,25	0
57	MG	2A	3422	1/1	0.96	0.10	39,39,39,39	0
57	MG	2A	3423	1/1	0.96	0.10	58,58,58,58	0
57	MG	1A	3776	1/1	0.96	0.13	33,33,33,33	0
57	MG	15	102	1/1	0.96	0.06	27,27,27,27	0
57	MG	2A	3134	1/1	0.96	0.07	48,48,48,48	0
57	MG	2E	305	1/1	0.96	0.16	43,43,43,43	0
57	MG	2A	3427	1/1	0.96	0.06	34,34,34,34	0
57	MG	2E	307	1/1	0.96	0.07	48,48,48,48	0
57	MG	2F	302	1/1	0.96	0.05	33,33,33,33	0
57	MG	1A	3777	1/1	0.96	0.06	41,41,41,41	0
57	MG	1A	3442	1/1	0.96	0.08	56,56,56,56	0
57	MG	1A	3232	1/1	0.96	0.13	30,30,30,30	0
57	MG	15	110	1/1	0.96	0.06	57,57,57,57	0
57	MG	2A	3142	1/1	0.96	0.06	42,42,42,42	0
57	MG	1A	3537	1/1	0.96	0.07	34,34,34,34	0
57	MG	2A	3144	1/1	0.96	0.09	40,40,40,40	0
57	MG	17	103	1/1	0.96	0.14	31,31,31,31	0
57	MG	2A	3147	1/1	0.96	0.10	43,43,43,43	0
57	MG	2P	202	1/1	0.96	0.07	56,56,56,56	0
57	MG	1A	3538	1/1	0.96	0.05	17,17,17,17	0
57	MG	2Q	202	1/1	0.96	0.23	52,52,52,52	0
57	MG	17	105	1/1	0.96	0.07	39,39,39,39	0
57	MG	18	101	1/1	0.96	0.07	32,32,32,32	0
57	MG	1a	3200	1/1	0.96	0.07	54,54,54,54	0
57	MG	1A	3645	1/1	0.96	0.11	28,28,28,28	0
57	MG	1a	3001	1/1	0.96	0.10	52,52,52,52	0
57	MG	1A	3959	1/1	0.96	0.08	42,42,42,42	0
57	MG	1a	3004	1/1	0.96	0.14	49,49,49,49	0
57	MG	1A	3784	1/1	0.96	0.07	48,48,48,48	0
57	MG	2A	3449	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3445	1/1	0.96	0.05	46,46,46,46	0
57	MG	1a	3209	1/1	0.96	0.08	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	2A	3162	1/1	0.96	0.16	32,32,32,32	0
57	MG	1A	3963	1/1	0.96	0.09	25,25,25,25	0
57	MG	1A	3366	1/1	0.96	0.11	50,50,50,50	0
57	MG	1A	3043	1/1	0.96	0.07	23,23,23,23	0
57	MG	2A	3457	1/1	0.96	0.07	50,50,50,50	0
57	MG	1A	3122	1/1	0.96	0.15	37,37,37,37	0
57	MG	1a	3011	1/1	0.96	0.11	26,26,26,26	0
57	MG	1a	3012	1/1	0.96	0.12	52,52,52,52	0
57	MG	23	101	1/1	0.96	0.12	42,42,42,42	0
57	MG	1A	3652	1/1	0.96	0.11	46,46,46,46	0
57	MG	1A	3451	1/1	0.96	0.07	19,19,19,19	0
57	MG	1A	3068	1/1	0.96	0.10	38,38,38,38	0
57	MG	1a	3219	1/1	0.96	0.13	56,56,56,56	0
57	MG	1A	3372	1/1	0.96	0.06	40,40,40,40	0
57	MG	1A	3796	1/1	0.96	0.05	32,32,32,32	0
57	MG	1A	3797	1/1	0.96	0.12	41,41,41,41	0
57	MG	1A	3456	1/1	0.96	0.12	49,49,49,49	0
57	MG	1A	3800	1/1	0.96	0.06	35,35,35,35	0
57	MG	29	101	1/1	0.96	0.19	53,53,53,53	0
57	MG	2a	3001	1/1	0.96	0.07	46,46,46,46	0
57	MG	1A	3240	1/1	0.96	0.15	43,43,43,43	0
57	MG	1a	3023	1/1	0.96	0.10	42,42,42,42	0
57	MG	1A	3802	1/1	0.96	0.17	36,36,36,36	0
57	MG	1A	3193	1/1	0.96	0.18	36,36,36,36	0
57	MG	1A	3051	1/1	0.96	0.13	31,31,31,31	0
57	MG	1A	3310	1/1	0.96	0.15	30,30,30,30	0
57	MG	1A	3556	1/1	0.96	0.12	47,47,47,47	0
57	MG	1A	3811	1/1	0.96	0.09	42,42,42,42	0
57	MG	2A	3480	1/1	0.96	0.07	45,45,45,45	0
57	MG	2a	3011	1/1	0.96	0.20	49,49,49,49	0
57	MG	1A	3812	1/1	0.96	0.05	37,37,37,37	0
57	MG	1a	3235	1/1	0.96	0.09	64,64,64,64	0
57	MG	1A	3195	1/1	0.96	0.07	45,45,45,45	0
57	MG	1a	3035	1/1	0.96	0.10	38,38,38,38	0
57	MG	1A	3989	1/1	0.96	0.12	30,30,30,30	0
57	MG	2A	3201	1/1	0.96	0.07	45,45,45,45	0
57	MG	1A	3559	1/1	0.96	0.07	37,37,37,37	0
57	MG	1a	3240	1/1	0.96	0.17	56,56,56,56	0
57	MG	1A	3816	1/1	0.96	0.06	29,29,29,29	0
57	MG	2A	3493	1/1	0.96	0.10	46,46,46,46	0
57	MG	1A	3463	1/1	0.96	0.07	46,46,46,46	0
57	MG	1A	3993	1/1	0.96	0.15	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	3994	1/1	0.96	0.11	42,42,42,42	0
57	MG	1A	3081	1/1	0.96	0.07	24,24,24,24	0
57	MG	1A	3313	1/1	0.96	0.06	30,30,30,30	0
57	MG	2A	3500	1/1	0.96	0.07	53,53,53,53	0
57	MG	1A	3823	1/1	0.96	0.06	15,15,15,15	0
57	MG	1A	3062	1/1	0.96	0.07	35,35,35,35	0
57	MG	1A	3468	1/1	0.96	0.04	27,27,27,27	0
57	MG	2A	3506	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	3675	1/1	0.96	0.11	46,46,46,46	0
57	MG	1A	3469	1/1	0.96	0.06	33,33,33,33	0
57	MG	1A	3384	1/1	0.96	0.11	33,33,33,33	0
57	MG	1a	3258	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3198	1/1	0.96	0.09	42,42,42,42	0
57	MG	2a	3042	1/1	0.96	0.24	48,48,48,48	0
57	MG	1A	3680	1/1	0.96	0.06	37,37,37,37	0
57	MG	2A	3514	1/1	0.96	0.07	58,58,58,58	0
57	MG	2a	3045	1/1	0.96	0.22	54,54,54,54	0
57	MG	1A	3255	1/1	0.96	0.07	66,66,66,66	0
57	MG	1A	3682	1/1	0.96	0.09	43,43,43,43	0
57	MG	2A	3225	1/1	0.96	0.06	44,44,44,44	0
57	MG	1A	3683	1/1	0.96	0.06	29,29,29,29	0
57	MG	2A	3227	1/1	0.96	0.17	38,38,38,38	0
57	MG	1A	3835	1/1	0.96	0.06	29,29,29,29	0
57	MG	1a	3062	1/1	0.96	0.15	47,47,47,47	0
57	MG	1A	3258	1/1	0.96	0.16	35,35,35,35	0
57	MG	2A	3231	1/1	0.96	0.18	45,45,45,45	0
57	MG	1A	3199	1/1	0.96	0.15	32,32,32,32	0
57	MG	1A	3576	1/1	0.96	0.10	32,32,32,32	0
57	MG	1A	3687	1/1	0.96	0.10	36,36,36,36	0
57	MG	1a	3067	1/1	0.96	0.17	64,64,64,64	0
57	MG	1A	3390	1/1	0.96	0.08	38,38,38,38	0
57	MG	1A	3480	1/1	0.96	0.05	35,35,35,35	0
57	MG	2A	3238	1/1	0.96	0.09	50,50,50,50	0
57	MG	1a	3070	1/1	0.96	0.06	41,41,41,41	0
57	MG	1A	3847	1/1	0.96	0.08	41,41,41,41	0
57	MG	1A	3690	1/1	0.96	0.13	39,39,39,39	0
57	MG	1A	3260	1/1	0.96	0.09	25,25,25,25	0
57	MG	1B	205	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3165	1/1	0.96	0.09	43,43,43,43	0
57	MG	1g	201	1/1	0.96	0.19	49,49,49,49	0
57	MG	1A	3483	1/1	0.96	0.06	22,22,22,22	0
57	MG	2A	3247	1/1	0.96	0.10	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	2a	3072	1/1	0.96	0.09	56,56,56,56	0
57	MG	1A	3695	1/1	0.96	0.12	35,35,35,35	0
57	MG	2a	3074	1/1	0.96	0.22	47,47,47,47	0
57	MG	1A	3582	1/1	0.96	0.09	38,38,38,38	0
57	MG	1A	3326	1/1	0.96	0.11	39,39,39,39	0
57	MG	1A	3166	1/1	0.96	0.10	39,39,39,39	0
57	MG	1A	3167	1/1	0.96	0.05	21,21,21,21	0
57	MG	1B	215	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	3266	1/1	0.96	0.05	39,39,39,39	0
57	MG	1A	3588	1/1	0.96	0.12	46,46,46,46	0
57	MG	1A	3204	1/1	0.96	0.18	38,38,38,38	0
57	MG	2A	3260	1/1	0.96	0.13	48,48,48,48	0
57	MG	1A	3590	1/1	0.96	0.12	40,40,40,40	0
57	MG	1A	3708	1/1	0.96	0.07	34,34,34,34	0
57	MG	2a	3088	1/1	0.96	0.13	50,50,50,50	0
57	MG	1t	201	1/1	0.96	0.09	48,48,48,48	0
57	MG	1B	224	1/1	0.96	0.06	38,38,38,38	0
57	MG	1a	3091	1/1	0.96	0.15	39,39,39,39	0
57	MG	1A	3490	1/1	0.96	0.06	23,23,23,23	0
57	MG	2A	3268	1/1	0.96	0.19	49,49,49,49	0
57	MG	2A	3269	1/1	0.96	0.13	43,43,43,43	0
57	MG	1A	3711	1/1	0.96	0.07	28,28,28,28	0
57	MG	2a	3098	1/1	0.96	0.24	42,42,42,42	0
57	MG	1A	3404	1/1	0.96	0.03	16,16,16,16	0
57	MG	2A	3570	1/1	0.96	0.07	51,51,51,51	0
57	MG	1a	3095	1/1	0.96	0.09	52,52,52,52	0
57	MG	1B	228	1/1	0.96	0.08	48,48,48,48	0
57	MG	1A	3405	1/1	0.96	0.14	40,40,40,40	0
57	MG	2A	3276	1/1	0.96	0.30	50,50,50,50	0
57	MG	2a	3108	1/1	0.96	0.23	50,50,50,50	0
57	MG	2A	3577	1/1	0.96	0.06	52,52,52,52	0
57	MG	1A	3268	1/1	0.96	0.05	37,37,37,37	0
57	MG	2a	3111	1/1	0.96	0.07	33,33,33,33	0
57	MG	1A	3872	1/1	0.96	0.05	29,29,29,29	0
57	MG	2a	3113	1/1	0.96	0.13	50,50,50,50	0
57	MG	1D	305	1/1	0.96	0.15	28,28,28,28	0
57	MG	2A	3583	1/1	0.96	0.09	50,50,50,50	0
57	MG	2A	3584	1/1	0.96	0.07	47,47,47,47	0
57	MG	2A	3281	1/1	0.96	0.15	41,41,41,41	0
57	MG	1A	3874	1/1	0.96	0.10	53,53,53,53	0
57	MG	1A	3083	1/1	0.96	0.17	29,29,29,29	0
57	MG	2a	3120	1/1	0.96	0.09	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	3015	1/1	0.96	0.08	31,31,31,31	0
57	MG	1a	3103	1/1	0.96	0.24	44,44,44,44	0
57	MG	2a	3123	1/1	0.96	0.07	42,42,42,42	0
57	MG	2A	3289	1/1	0.96	0.19	45,45,45,45	0
57	MG	2A	3017	1/1	0.96	0.08	48,48,48,48	0
57	MG	2A	3596	1/1	0.96	0.08	56,56,56,56	0
57	MG	2a	3127	1/1	0.96	0.07	53,53,53,53	0
57	MG	2A	3018	1/1	0.96	0.16	34,34,34,34	0
57	MG	1A	3877	1/1	0.96	0.06	38,38,38,38	0
57	MG	1A	3169	1/1	0.96	0.14	21,21,21,21	0
57	MG	1A	3129	1/1	0.96	0.16	32,32,32,32	0
57	MG	1A	3721	1/1	0.96	0.05	25,25,25,25	0
57	MG	2A	3296	1/1	0.96	0.04	30,30,30,30	0
57	MG	1A	3503	1/1	0.96	0.08	20,20,20,20	0
57	MG	2A	3026	1/1	0.96	0.04	24,24,24,24	0
57	MG	1A	3414	1/1	0.96	0.05	26,26,26,26	0
57	MG	1A	3506	1/1	0.96	0.09	43,43,43,43	0
57	MG	1A	3726	1/1	0.96	0.09	49,49,49,49	0
57	MG	2A	3610	1/1	0.96	0.06	53,53,53,53	0
57	MG	1A	3273	1/1	0.96	0.05	32,32,32,32	0
57	MG	2a	3142	1/1	0.96	0.07	60,60,60,60	0
57	MG	1A	3894	1/1	0.96	0.08	45,45,45,45	0
57	MG	2A	3037	1/1	0.96	0.07	39,39,39,39	0
57	MG	1F	307	1/1	0.96	0.15	19,19,19,19	0
57	MG	1A	3072	1/1	0.96	0.09	24,24,24,24	0
57	MG	1F	311	1/1	0.96	0.14	35,35,35,35	0
57	MG	2A	3313	1/1	0.96	0.07	42,42,42,42	0
57	MG	1F	312	1/1	0.96	0.05	24,24,24,24	0
57	MG	2A	3316	1/1	0.96	0.06	34,34,34,34	0
57	MG	1A	3606	1/1	0.96	0.08	24,24,24,24	0
57	MG	2A	3318	1/1	0.96	0.08	28,28,28,28	0
57	MG	2a	3156	1/1	0.96	0.09	52,52,52,52	0
57	MG	2a	3157	1/1	0.96	0.07	54,54,54,54	0
57	MG	2a	3158	1/1	0.96	0.09	57,57,57,57	0
57	MG	2A	3046	1/1	0.96	0.07	53,53,53,53	0
57	MG	1a	3120	1/1	0.96	0.28	50,50,50,50	0
57	MG	2a	3161	1/1	0.96	0.08	51,51,51,51	0
57	MG	1A	3279	1/1	0.96	0.12	21,21,21,21	0
57	MG	1F	315	1/1	0.96	0.09	43,43,43,43	0
57	MG	2A	3630	1/1	0.96	0.07	37,37,37,37	0
57	MG	2A	3631	1/1	0.96	0.09	58,58,58,58	0
57	MG	1A	3736	1/1	0.96	0.05	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	3737	1/1	0.96	0.08	39,39,39,39	0
57	MG	2a	3171	1/1	0.96	0.13	47,47,47,47	0
57	MG	1A	3738	1/1	0.96	0.06	32,32,32,32	0
57	MG	1G	201	1/1	0.96	0.06	63,63,63,63	0
57	MG	2A	3330	1/1	0.96	0.08	39,39,39,39	0
57	MG	2A	3331	1/1	0.96	0.14	43,43,43,43	0
57	MG	1A	3059	1/1	0.96	0.10	35,35,35,35	0
57	MG	2a	3179	1/1	0.96	0.08	56,56,56,56	0
57	MG	1A	3512	1/1	0.96	0.06	42,42,42,42	0
57	MG	2A	3647	1/1	0.96	0.05	40,40,40,40	0
57	MG	1a	3129	1/1	0.96	0.16	48,48,48,48	0
57	MG	2a	3183	1/1	0.96	0.07	65,65,65,65	0
57	MG	1a	3130	1/1	0.96	0.08	47,47,47,47	0
57	MG	1A	3513	1/1	0.96	0.07	10,10,10,10	0
57	MG	2A	3338	1/1	0.96	0.08	35,35,35,35	0
57	MG	1H	201	1/1	0.96	0.10	42,42,42,42	0
57	MG	2A	3656	1/1	0.96	0.06	24,24,24,24	0
57	MG	1H	202	1/1	0.96	0.06	40,40,40,40	0
57	MG	1A	3745	1/1	0.96	0.10	25,25,25,25	0
57	MG	2f	201	1/1	0.96	0.11	50,50,50,50	0
57	MG	2A	3068	1/1	0.96	0.11	47,47,47,47	0
57	MG	2A	3343	1/1	0.96	0.05	27,27,27,27	0
57	MG	2l	202	1/1	0.96	0.18	52,52,52,52	0
57	MG	2A	3070	1/1	0.96	0.13	46,46,46,46	0
57	MG	1A	3746	1/1	0.96	0.07	14,14,14,14	0
57	MG	1A	3136	1/1	0.96	0.10	36,36,36,36	0
57	MG	1A	3216	1/1	0.96	0.12	21,21,21,21	0
58	CLM	1A	4022	20/20	0.96	0.08	18,30,47,48	0
57	MG	2A	3351	1/1	0.96	0.11	40,40,40,40	0
57	MG	2A	3352	1/1	0.96	0.14	42,42,42,42	0
57	MG	1A	3423	1/1	0.96	0.08	27,27,27,27	0
57	MG	2A	3675	1/1	0.96	0.06	43,43,43,43	0
57	MG	2A	3354	1/1	0.96	0.07	27,27,27,27	0
57	MG	2A	3355	1/1	0.96	0.05	34,34,34,34	0
57	MG	2A	3357	1/1	0.96	0.13	56,56,56,56	0
57	MG	1A	3750	1/1	0.96	0.08	33,33,33,33	0
57	MG	1A	3922	1/1	0.96	0.05	30,30,30,30	0
57	MG	2A	3361	1/1	0.96	0.14	35,35,35,35	0
61	ZN	2Y	202	1/1	0.96	0.06	81,81,81,81	0
57	MG	2A	3687	1/1	0.96	0.08	47,47,47,47	0
57	MG	1A	3128	1/1	0.97	0.17	24,24,24,24	0
57	MG	1A	3809	1/1	0.97	0.05	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	3420	1/1	0.97	0.05	42,42,42,42	0
57	MG	2A	3726	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3536	1/1	0.97	0.14	20,20,20,20	0
57	MG	1A	3179	1/1	0.97	0.08	36,36,36,36	0
57	MG	1A	3813	1/1	0.97	0.08	45,45,45,45	0
57	MG	1A	3247	1/1	0.97	0.08	26,26,26,26	0
57	MG	1A	3667	1/1	0.97	0.07	36,36,36,36	0
57	MG	1a	3025	1/1	0.97	0.05	45,45,45,45	0
57	MG	1A	3668	1/1	0.97	0.05	33,33,33,33	0
57	MG	1A	3817	1/1	0.97	0.17	26,26,26,26	0
57	MG	1A	3539	1/1	0.97	0.04	17,17,17,17	0
57	MG	1A	3248	1/1	0.97	0.09	43,43,43,43	0
57	MG	1A	3541	1/1	0.97	0.06	30,30,30,30	0
57	MG	2A	3170	1/1	0.97	0.09	37,37,37,37	0
57	MG	2A	3171	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3024	1/1	0.97	0.05	15,15,15,15	0
57	MG	1a	3231	1/1	0.97	0.07	42,42,42,42	0
57	MG	2B	217	1/1	0.97	0.09	53,53,53,53	0
57	MG	1A	3098	1/1	0.97	0.05	44,44,44,44	0
57	MG	2D	302	1/1	0.97	0.40	40,40,40,40	0
57	MG	1A	3998	1/1	0.97	0.09	12,12,12,12	0
57	MG	2A	3179	1/1	0.97	0.07	55,55,55,55	0
57	MG	1A	3425	1/1	0.97	0.07	21,21,21,21	0
57	MG	1A	3132	1/1	0.97	0.09	23,23,23,23	0
57	MG	1A	4001	1/1	0.97	0.07	30,30,30,30	0
57	MG	1A	3546	1/1	0.97	0.12	54,54,54,54	0
57	MG	2A	3444	1/1	0.97	0.06	27,27,27,27	0
57	MG	2A	3445	1/1	0.97	0.09	49,49,49,49	0
57	MG	2A	3185	1/1	0.97	0.10	44,44,44,44	0
57	MG	2A	3447	1/1	0.97	0.05	23,23,23,23	0
57	MG	1A	4006	1/1	0.97	0.07	38,38,38,38	0
57	MG	1A	3133	1/1	0.97	0.05	34,34,34,34	0
57	MG	2F	301	1/1	0.97	0.22	38,38,38,38	0
57	MG	1A	3331	1/1	0.97	0.12	33,33,33,33	0
57	MG	1a	3043	1/1	0.97	0.12	41,41,41,41	0
57	MG	1A	3185	1/1	0.97	0.14	33,33,33,33	0
57	MG	1A	3335	1/1	0.97	0.10	9,9,9,9	0
57	MG	1a	3047	1/1	0.97	0.12	44,44,44,44	0
57	MG	2A	3455	1/1	0.97	0.04	46,46,46,46	0
57	MG	2A	3193	1/1	0.97	0.06	56,56,56,56	0
57	MG	1A	3552	1/1	0.97	0.07	33,33,33,33	0
57	MG	1a	3247	1/1	0.97	0.06	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	3099	1/1	0.97	0.14	25,25,25,25	0
57	MG	2A	3197	1/1	0.97	0.07	42,42,42,42	0
57	MG	1a	3051	1/1	0.97	0.14	52,52,52,52	0
57	MG	1a	3250	1/1	0.97	0.13	42,42,42,42	0
57	MG	1A	3256	1/1	0.97	0.06	35,35,35,35	0
57	MG	1A	3837	1/1	0.97	0.13	46,46,46,46	0
57	MG	1A	3439	1/1	0.97	0.15	46,46,46,46	0
57	MG	1a	3055	1/1	0.97	0.18	36,36,36,36	0
57	MG	1A	3102	1/1	0.97	0.10	25,25,25,25	0
57	MG	1A	3841	1/1	0.97	0.05	41,41,41,41	0
57	MG	1A	3342	1/1	0.97	0.07	25,25,25,25	0
57	MG	2A	3471	1/1	0.97	0.05	36,36,36,36	0
57	MG	1A	4019	1/1	0.97	0.07	43,43,43,43	0
57	MG	1A	3558	1/1	0.97	0.05	31,31,31,31	0
57	MG	2A	3211	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3138	1/1	0.97	0.09	35,35,35,35	0
57	MG	1a	3263	1/1	0.97	0.09	49,49,49,49	0
57	MG	1A	3054	1/1	0.97	0.13	25,25,25,25	0
57	MG	1A	3104	1/1	0.97	0.11	30,30,30,30	0
57	MG	1A	3447	1/1	0.97	0.07	35,35,35,35	0
57	MG	1A	3347	1/1	0.97	0.08	22,22,22,22	0
57	MG	2A	3481	1/1	0.97	0.05	50,50,50,50	0
57	MG	1A	3850	1/1	0.97	0.06	33,33,33,33	0
57	MG	2A	3219	1/1	0.97	0.05	39,39,39,39	0
57	MG	1A	3449	1/1	0.97	0.08	41,41,41,41	0
57	MG	1A	3567	1/1	0.97	0.05	32,32,32,32	0
57	MG	1A	3853	1/1	0.97	0.09	31,31,31,31	0
57	MG	25	104	1/1	0.97	0.05	40,40,40,40	0
57	MG	1A	3142	1/1	0.97	0.07	45,45,45,45	0
57	MG	1a	3071	1/1	0.97	0.14	56,56,56,56	0
57	MG	1A	3143	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3350	1/1	0.97	0.04	20,20,20,20	0
57	MG	1A	3453	1/1	0.97	0.04	50,50,50,50	0
57	MG	1A	3454	1/1	0.97	0.07	36,36,36,36	0
57	MG	1A	3144	1/1	0.97	0.09	64,64,64,64	0
57	MG	1A	3575	1/1	0.97	0.06	20,20,20,20	0
57	MG	1A	3145	1/1	0.97	0.12	41,41,41,41	0
57	MG	1A	3146	1/1	0.97	0.21	32,32,32,32	0
57	MG	1g	203	1/1	0.97	0.08	55,55,55,55	0
57	MG	2A	3501	1/1	0.97	0.07	49,49,49,49	0
57	MG	1h	201	1/1	0.97	0.15	42,42,42,42	0
57	MG	1A	3864	1/1	0.97	0.08	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	1A	3147	1/1	0.97	0.06	22,22,22,22	0
57	MG	1A	3075	1/1	0.97	0.10	32,32,32,32	0
57	MG	1A	3713	1/1	0.97	0.23	29,29,29,29	0
57	MG	1A	3714	1/1	0.97	0.20	36,36,36,36	0
57	MG	2a	3012	1/1	0.97	0.12	45,45,45,45	0
57	MG	1A	3358	1/1	0.97	0.04	14,14,14,14	0
57	MG	1A	3870	1/1	0.97	0.06	30,30,30,30	0
57	MG	1A	3106	1/1	0.97	0.13	28,28,28,28	0
57	MG	1D	301	1/1	0.97	0.05	38,38,38,38	0
57	MG	1D	303	1/1	0.97	0.11	24,24,24,24	0
57	MG	1A	3108	1/1	0.97	0.09	33,33,33,33	0
57	MG	1A	3274	1/1	0.97	0.20	33,33,33,33	0
57	MG	1D	307	1/1	0.97	0.05	31,31,31,31	0
57	MG	1A	3275	1/1	0.97	0.04	26,26,26,26	0
57	MG	2a	3022	1/1	0.97	0.06	46,46,46,46	0
57	MG	1D	311	1/1	0.97	0.15	28,28,28,28	0
57	MG	2A	3251	1/1	0.97	0.06	47,47,47,47	0
57	MG	1A	3585	1/1	0.97	0.07	42,42,42,42	0
57	MG	1A	3063	1/1	0.97	0.07	31,31,31,31	0
57	MG	1A	3277	1/1	0.97	0.06	19,19,19,19	0
57	MG	1A	3367	1/1	0.97	0.09	23,23,23,23	0
57	MG	2A	3004	1/1	0.97	0.04	39,39,39,39	0
57	MG	1D	317	1/1	0.97	0.09	38,38,38,38	0
57	MG	1A	3278	1/1	0.97	0.09	30,30,30,30	0
57	MG	1A	3471	1/1	0.97	0.06	37,37,37,37	0
57	MG	2A	3261	1/1	0.97	0.12	20,20,20,20	0
57	MG	1E	306	1/1	0.97	0.08	15,15,15,15	0
57	MG	1A	3369	1/1	0.97	0.05	23,23,23,23	0
57	MG	1A	3884	1/1	0.97	0.13	23,23,23,23	0
57	MG	1A	3885	1/1	0.97	0.06	29,29,29,29	0
57	MG	1F	302	1/1	0.97	0.13	25,25,25,25	0
57	MG	2A	3537	1/1	0.97	0.06	44,44,44,44	0
57	MG	1a	3108	1/1	0.97	0.05	37,37,37,37	0
57	MG	1A	3154	1/1	0.97	0.11	19,19,19,19	0
57	MG	1F	306	1/1	0.97	0.05	23,23,23,23	0
57	MG	2A	3270	1/1	0.97	0.05	36,36,36,36	0
57	MG	1A	3891	1/1	0.97	0.06	24,24,24,24	0
57	MG	1A	3892	1/1	0.97	0.04	37,37,37,37	0
57	MG	1A	3475	1/1	0.97	0.06	13,13,13,13	0
57	MG	1A	3734	1/1	0.97	0.07	44,44,44,44	0
57	MG	1A	3895	1/1	0.97	0.07	44,44,44,44	0
57	MG	2A	3548	1/1	0.97	0.06	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3027	1/1	0.97	0.07	39,39,39,39	0
57	MG	2A	3277	1/1	0.97	0.14	33,33,33,33	0
57	MG	2a	3055	1/1	0.97	0.08	53,53,53,53	0
57	MG	2A	3029	1/1	0.97	0.05	31,31,31,31	0
57	MG	1A	3064	1/1	0.97	0.05	46,46,46,46	0
57	MG	1A	3897	1/1	0.97	0.09	22,22,22,22	0
57	MG	1A	3898	1/1	0.97	0.04	14,14,14,14	0
57	MG	2A	3282	1/1	0.97	0.16	45,45,45,45	0
57	MG	2A	3034	1/1	0.97	0.11	45,45,45,45	0
57	MG	2A	3284	1/1	0.97	0.26	51,51,51,51	0
57	MG	1A	3282	1/1	0.97	0.11	40,40,40,40	0
57	MG	1A	3055	1/1	0.97	0.07	21,21,21,21	0
57	MG	1A	3739	1/1	0.97	0.17	44,44,44,44	0
57	MG	2A	3288	1/1	0.97	0.08	37,37,37,37	0
57	MG	1A	3904	1/1	0.97	0.04	11,11,11,11	0
57	MG	1A	3740	1/1	0.97	0.05	47,47,47,47	0
57	MG	1A	3374	1/1	0.97	0.10	27,27,27,27	0
57	MG	1A	3375	1/1	0.97	0.06	29,29,29,29	0
57	MG	2A	3044	1/1	0.97	0.09	44,44,44,44	0
57	MG	1A	3208	1/1	0.97	0.25	27,27,27,27	0
57	MG	1A	3601	1/1	0.97	0.05	45,45,45,45	0
57	MG	1A	3047	1/1	0.97	0.08	18,18,18,18	0
57	MG	2a	3075	1/1	0.97	0.07	43,43,43,43	0
57	MG	1A	3603	1/1	0.97	0.15	20,20,20,20	0
57	MG	1A	3160	1/1	0.97	0.06	35,35,35,35	0
57	MG	2A	3051	1/1	0.97	0.07	34,34,34,34	0
57	MG	1A	3161	1/1	0.97	0.04	19,19,19,19	0
57	MG	2A	3301	1/1	0.97	0.04	26,26,26,26	0
57	MG	1A	3917	1/1	0.97	0.07	57,57,57,57	0
57	MG	2a	3082	1/1	0.97	0.27	46,46,46,46	0
57	MG	1A	3918	1/1	0.97	0.05	38,38,38,38	0
57	MG	1Q	203	1/1	0.97	0.06	31,31,31,31	0
57	MG	2A	3588	1/1	0.97	0.05	50,50,50,50	0
57	MG	2A	3056	1/1	0.97	0.07	29,29,29,29	0
57	MG	1a	3136	1/1	0.97	0.13	44,44,44,44	0
57	MG	2A	3310	1/1	0.97	0.07	35,35,35,35	0
57	MG	1R	201	1/1	0.97	0.09	26,26,26,26	0
57	MG	2a	3090	1/1	0.97	0.21	50,50,50,50	0
57	MG	1a	3138	1/1	0.97	0.07	36,36,36,36	0
57	MG	1A	3288	1/1	0.97	0.10	16,16,16,16	0
57	MG	1A	3290	1/1	0.97	0.08	38,38,38,38	0
57	MG	2A	3599	1/1	0.97	0.05	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3610	1/1	0.97	0.10	32,32,32,32	0
57	MG	1A	3382	1/1	0.97	0.08	45,45,45,45	0
57	MG	2a	3097	1/1	0.97	0.23	51,51,51,51	0
57	MG	1A	3067	1/1	0.97	0.04	24,24,24,24	0
57	MG	2A	3319	1/1	0.97	0.11	49,49,49,49	0
57	MG	2a	3100	1/1	0.97	0.21	37,37,37,37	0
57	MG	2A	3066	1/1	0.97	0.05	34,34,34,34	0
57	MG	1A	3925	1/1	0.97	0.12	27,27,27,27	0
57	MG	2A	3069	1/1	0.97	0.26	41,41,41,41	0
57	MG	2a	3105	1/1	0.97	0.36	51,51,51,51	0
57	MG	1A	3755	1/1	0.97	0.12	22,22,22,22	0
57	MG	1A	3049	1/1	0.97	0.11	28,28,28,28	0
57	MG	1a	3148	1/1	0.97	0.07	35,35,35,35	0
57	MG	2A	3326	1/1	0.97	0.09	42,42,42,42	0
57	MG	1A	3294	1/1	0.97	0.05	36,36,36,36	0
57	MG	2A	3612	1/1	0.97	0.09	31,31,31,31	0
57	MG	1U	204	1/1	0.97	0.14	24,24,24,24	0
57	MG	1A	3295	1/1	0.97	0.12	35,35,35,35	0
57	MG	1A	3931	1/1	0.97	0.04	41,41,41,41	0
57	MG	1a	3153	1/1	0.97	0.05	47,47,47,47	0
57	MG	1A	3296	1/1	0.97	0.08	42,42,42,42	0
57	MG	2A	3619	1/1	0.97	0.08	44,44,44,44	0
57	MG	1A	3036	1/1	0.97	0.06	23,23,23,23	0
57	MG	1A	3218	1/1	0.97	0.09	22,22,22,22	0
57	MG	1A	3391	1/1	0.97	0.04	26,26,26,26	0
57	MG	1A	3220	1/1	0.97	0.14	30,30,30,30	0
57	MG	2A	3085	1/1	0.97	0.21	40,40,40,40	0
57	MG	1A	3505	1/1	0.97	0.05	44,44,44,44	0
57	MG	1A	3938	1/1	0.97	0.06	32,32,32,32	0
57	MG	1A	3624	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3221	1/1	0.97	0.08	32,32,32,32	0
57	MG	1A	3086	1/1	0.97	0.07	22,22,22,22	0
57	MG	2A	3345	1/1	0.97	0.06	31,31,31,31	0
57	MG	2A	3346	1/1	0.97	0.13	42,42,42,42	0
57	MG	2A	3347	1/1	0.97	0.04	24,24,24,24	0
57	MG	1a	3166	1/1	0.97	0.05	48,48,48,48	0
57	MG	2A	3635	1/1	0.97	0.07	54,54,54,54	0
57	MG	2A	3092	1/1	0.97	0.11	41,41,41,41	0
57	MG	1Z	301	1/1	0.97	0.09	51,51,51,51	0
57	MG	1a	3168	1/1	0.97	0.05	41,41,41,41	0
57	MG	1A	3769	1/1	0.97	0.05	32,32,32,32	0
57	MG	2A	3645	1/1	0.97	0.06	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	1A	3627	1/1	0.97	0.05	33,33,33,33	0
57	MG	1A	3508	1/1	0.97	0.07	15,15,15,15	0
57	MG	1A	3773	1/1	0.97	0.07	21,21,21,21	0
57	MG	2a	3141	1/1	0.97	0.15	53,53,53,53	0
57	MG	1A	3070	1/1	0.97	0.09	24,24,24,24	0
57	MG	1A	3225	1/1	0.97	0.12	31,31,31,31	0
57	MG	1A	3092	1/1	0.97	0.07	36,36,36,36	0
57	MG	1A	3401	1/1	0.97	0.11	14,14,14,14	0
57	MG	1A	3635	1/1	0.97	0.04	28,28,28,28	0
57	MG	2A	3657	1/1	0.97	0.05	58,58,58,58	0
57	MG	1A	3952	1/1	0.97	0.07	54,54,54,54	0
57	MG	1A	3636	1/1	0.97	0.11	21,21,21,21	0
57	MG	2A	3661	1/1	0.97	0.06	50,50,50,50	0
57	MG	2A	3107	1/1	0.97	0.09	30,30,30,30	0
57	MG	13	101	1/1	0.97	0.16	28,28,28,28	0
57	MG	2a	3154	1/1	0.97	0.12	32,32,32,32	0
57	MG	2A	3666	1/1	0.97	0.05	42,42,42,42	0
57	MG	1A	3025	1/1	0.97	0.09	27,27,27,27	0
57	MG	2A	3369	1/1	0.97	0.04	21,21,21,21	0
57	MG	2A	3110	1/1	0.97	0.06	45,45,45,45	0
57	MG	13	103	1/1	0.97	0.05	37,37,37,37	0
57	MG	1A	3638	1/1	0.97	0.09	37,37,37,37	0
57	MG	2a	3162	1/1	0.97	0.06	49,49,49,49	0
57	MG	1A	3170	1/1	0.97	0.14	23,23,23,23	0
57	MG	15	106	1/1	0.97	0.09	30,30,30,30	0
57	MG	2a	3166	1/1	0.97	0.07	62,62,62,62	0
57	MG	2A	3376	1/1	0.97	0.12	49,49,49,49	0
57	MG	2A	3676	1/1	0.97	0.04	37,37,37,37	0
57	MG	15	107	1/1	0.97	0.18	24,24,24,24	0
57	MG	1A	3515	1/1	0.97	0.04	38,38,38,38	0
57	MG	2A	3118	1/1	0.97	0.09	47,47,47,47	0
57	MG	2a	3172	1/1	0.97	0.05	50,50,50,50	0
57	MG	1A	3094	1/1	0.97	0.04	23,23,23,23	0
57	MG	1A	3231	1/1	0.97	0.09	35,35,35,35	0
57	MG	17	101	1/1	0.97	0.10	23,23,23,23	0
57	MG	1A	3407	1/1	0.97	0.07	28,28,28,28	0
57	MG	1A	3789	1/1	0.97	0.06	55,55,55,55	0
57	MG	1A	3965	1/1	0.97	0.05	34,34,34,34	0
57	MG	1A	3172	1/1	0.97	0.16	26,26,26,26	0
57	MG	1A	3967	1/1	0.97	0.04	19,19,19,19	0
57	MG	2A	3692	1/1	0.97	0.08	36,36,36,36	0
57	MG	1A	3095	1/1	0.97	0.10	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3694	1/1	0.97	0.06	44,44,44,44	0
57	MG	19	101	1/1	0.97	0.11	41,41,41,41	0
57	MG	1A	3411	1/1	0.97	0.17	36,36,36,36	0
57	MG	1A	3970	1/1	0.97	0.04	39,39,39,39	0
57	MG	2A	3135	1/1	0.97	0.08	23,23,23,23	0
57	MG	1a	3003	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3522	1/1	0.97	0.04	29,29,29,29	0
57	MG	2A	3701	1/1	0.97	0.05	55,55,55,55	0
57	MG	1A	3524	1/1	0.97	0.22	21,21,21,21	0
57	MG	1A	3412	1/1	0.97	0.04	15,15,15,15	0
57	MG	2A	3401	1/1	0.97	0.05	30,30,30,30	0
57	MG	1A	3174	1/1	0.97	0.17	39,39,39,39	0
57	MG	1A	3529	1/1	0.97	0.05	41,41,41,41	0
57	MG	1a	3208	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3799	1/1	0.97	0.07	47,47,47,47	0
57	MG	2A	3709	1/1	0.97	0.11	42,42,42,42	0
57	MG	2A	3710	1/1	0.97	0.07	44,44,44,44	0
57	MG	1A	3317	1/1	0.97	0.12	44,44,44,44	0
57	MG	1A	3175	1/1	0.97	0.11	19,19,19,19	0
57	MG	1A	3416	1/1	0.97	0.07	21,21,21,21	0
57	MG	1A	3980	1/1	0.97	0.07	32,32,32,32	0
57	MG	2A	3151	1/1	0.97	0.05	41,41,41,41	0
57	MG	2A	3152	1/1	0.97	0.06	53,53,53,53	0
57	MG	1A	3238	1/1	0.97	0.22	29,29,29,29	0
57	MG	2A	3414	1/1	0.97	0.04	49,49,49,49	0
57	MG	1A	3534	1/1	0.97	0.08	49,49,49,49	0
57	MG	1A	3661	1/1	0.97	0.04	35,35,35,35	0
57	MG	2A	3156	1/1	0.97	0.21	46,46,46,46	0
57	MG	2A	3519	1/1	0.98	0.07	48,48,48,48	0
57	MG	1A	3910	1/1	0.98	0.07	26,26,26,26	0
57	MG	1A	3307	1/1	0.98	0.09	8,8,8,8	0
57	MG	1A	3309	1/1	0.98	0.26	29,29,29,29	0
57	MG	1A	3152	1/1	0.98	0.23	35,35,35,35	0
57	MG	1a	3046	1/1	0.98	0.17	34,34,34,34	0
57	MG	1A	3015	1/1	0.98	0.06	29,29,29,29	0
57	MG	2A	3526	1/1	0.98	0.05	39,39,39,39	0
57	MG	1A	3782	1/1	0.98	0.04	15,15,15,15	0
57	MG	2A	3106	1/1	0.98	0.04	31,31,31,31	0
57	MG	2A	3309	1/1	0.98	0.13	36,36,36,36	0
57	MG	1A	3666	1/1	0.98	0.04	30,30,30,30	0
57	MG	1a	3050	1/1	0.98	0.05	36,36,36,36	0
57	MG	1D	310	1/1	0.98	0.04	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3050	1/1	0.98	0.32	37,37,37,37	0
57	MG	2A	3314	1/1	0.98	0.04	34,34,34,34	0
57	MG	2A	3111	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3565	1/1	0.98	0.08	29,29,29,29	0
57	MG	1A	3786	1/1	0.98	0.09	27,27,27,27	0
57	MG	1A	3385	1/1	0.98	0.06	15,15,15,15	0
57	MG	1A	3156	1/1	0.98	0.12	29,29,29,29	0
57	MG	1A	3016	1/1	0.98	0.09	28,28,28,28	0
57	MG	1D	318	1/1	0.98	0.05	38,38,38,38	0
57	MG	1E	301	1/1	0.98	0.11	27,27,27,27	0
57	MG	1E	302	1/1	0.98	0.08	26,26,26,26	0
57	MG	1A	3315	1/1	0.98	0.15	24,24,24,24	0
57	MG	1E	304	1/1	0.98	0.08	33,33,33,33	0
57	MG	2A	3122	1/1	0.98	0.08	41,41,41,41	0
57	MG	1A	3474	1/1	0.98	0.05	31,31,31,31	0
57	MG	1A	3121	1/1	0.98	0.05	31,31,31,31	0
57	MG	2A	3329	1/1	0.98	0.06	47,47,47,47	0
57	MG	2A	3551	1/1	0.98	0.04	46,46,46,46	0
57	MG	1A	3793	1/1	0.98	0.06	23,23,23,23	0
57	MG	1A	3572	1/1	0.98	0.06	45,45,45,45	0
57	MG	2A	3128	1/1	0.98	0.09	37,37,37,37	0
57	MG	2A	3333	1/1	0.98	0.07	44,44,44,44	0
57	MG	1A	3159	1/1	0.98	0.06	23,23,23,23	0
57	MG	2A	3130	1/1	0.98	0.13	38,38,38,38	0
57	MG	1F	301	1/1	0.98	0.05	21,21,21,21	0
57	MG	1A	3477	1/1	0.98	0.04	22,22,22,22	0
57	MG	1F	303	1/1	0.98	0.17	28,28,28,28	0
57	MG	2A	3561	1/1	0.98	0.04	18,18,18,18	0
57	MG	1A	3257	1/1	0.98	0.06	35,35,35,35	0
57	MG	1F	305	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3679	1/1	0.98	0.06	15,15,15,15	0
57	MG	2A	3567	1/1	0.98	0.08	49,49,49,49	0
57	MG	1A	3319	1/1	0.98	0.07	37,37,37,37	0
57	MG	1a	3075	1/1	0.98	0.07	40,40,40,40	0
57	MG	2A	3139	1/1	0.98	0.04	33,33,33,33	0
57	MG	1a	3246	1/1	0.98	0.05	55,55,55,55	0
57	MG	2A	3141	1/1	0.98	0.14	43,43,43,43	0
57	MG	2A	3574	1/1	0.98	0.07	33,33,33,33	0
57	MG	1F	308	1/1	0.98	0.08	26,26,26,26	0
57	MG	1A	3393	1/1	0.98	0.08	12,12,12,12	0
57	MG	1F	310	1/1	0.98	0.10	27,27,27,27	0
57	MG	2A	3578	1/1	0.98	0.04	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3579	1/1	0.98	0.06	41,41,41,41	0
57	MG	2A	3145	1/1	0.98	0.12	29,29,29,29	0
57	MG	1A	3320	1/1	0.98	0.05	22,22,22,22	0
57	MG	1A	3088	1/1	0.98	0.10	25,25,25,25	0
57	MG	1A	3322	1/1	0.98	0.08	17,17,17,17	0
57	MG	1A	3201	1/1	0.98	0.16	34,34,34,34	0
57	MG	1A	3805	1/1	0.98	0.04	33,33,33,33	0
57	MG	2a	3027	1/1	0.98	0.07	52,52,52,52	0
57	MG	2A	3356	1/1	0.98	0.08	32,32,32,32	0
57	MG	1A	3398	1/1	0.98	0.03	14,14,14,14	0
57	MG	2a	3030	1/1	0.98	0.12	42,42,42,42	0
57	MG	2A	3358	1/1	0.98	0.07	34,34,34,34	0
57	MG	2A	3590	1/1	0.98	0.09	38,38,38,38	0
57	MG	1a	3257	1/1	0.98	0.06	25,25,25,25	0
57	MG	1A	3399	1/1	0.98	0.06	17,17,17,17	0
57	MG	2a	3035	1/1	0.98	0.07	31,31,31,31	0
57	MG	1A	3089	1/1	0.98	0.15	21,21,21,21	0
57	MG	1A	3810	1/1	0.98	0.07	24,24,24,24	0
57	MG	1A	3090	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3163	1/1	0.98	0.20	23,23,23,23	0
57	MG	2A	3598	1/1	0.98	0.04	36,36,36,36	0
57	MG	1A	3947	1/1	0.98	0.10	46,46,46,46	0
57	MG	1A	3205	1/1	0.98	0.07	33,33,33,33	0
57	MG	2A	3367	1/1	0.98	0.08	40,40,40,40	0
57	MG	1A	3493	1/1	0.98	0.04	39,39,39,39	0
57	MG	1A	3693	1/1	0.98	0.14	30,30,30,30	0
57	MG	1A	3264	1/1	0.98	0.16	29,29,29,29	0
57	MG	1A	3495	1/1	0.98	0.08	21,21,21,21	0
57	MG	1A	3818	1/1	0.98	0.14	19,19,19,19	0
57	MG	1P	201	1/1	0.98	0.15	28,28,28,28	0
57	MG	1P	202	1/1	0.98	0.13	26,26,26,26	0
57	MG	1A	3496	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3265	1/1	0.98	0.22	24,24,24,24	0
57	MG	1A	3498	1/1	0.98	0.06	38,38,38,38	0
57	MG	1Q	202	1/1	0.98	0.05	33,33,33,33	0
57	MG	1A	3822	1/1	0.98	0.06	25,25,25,25	0
57	MG	2A	3614	1/1	0.98	0.04	21,21,21,21	0
57	MG	1Q	204	1/1	0.98	0.06	33,33,33,33	0
57	MG	2A	3173	1/1	0.98	0.04	40,40,40,40	0
57	MG	1A	3206	1/1	0.98	0.07	28,28,28,28	0
57	MG	1A	3026	1/1	0.98	0.15	27,27,27,27	0
57	MG	2A	3176	1/1	0.98	0.05	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	2A	3177	1/1	0.98	0.08	33,33,33,33	0
57	MG	1A	3333	1/1	0.98	0.06	18,18,18,18	0
57	MG	1A	3704	1/1	0.98	0.04	18,18,18,18	0
57	MG	1A	3037	1/1	0.98	0.05	32,32,32,32	0
57	MG	1A	3828	1/1	0.98	0.09	34,34,34,34	0
57	MG	1A	3018	1/1	0.98	0.12	18,18,18,18	0
57	MG	1A	3707	1/1	0.98	0.08	28,28,28,28	0
57	MG	2A	3184	1/1	0.98	0.06	51,51,51,51	0
57	MG	2A	3628	1/1	0.98	0.07	47,47,47,47	0
57	MG	1A	3337	1/1	0.98	0.07	26,26,26,26	0
57	MG	1A	3709	1/1	0.98	0.10	15,15,15,15	0
57	MG	1U	202	1/1	0.98	0.05	30,30,30,30	0
57	MG	1m	201	1/1	0.98	0.05	60,60,60,60	0
57	MG	1A	3039	1/1	0.98	0.11	29,29,29,29	0
57	MG	1A	3339	1/1	0.98	0.05	22,22,22,22	0
57	MG	1A	3056	1/1	0.98	0.07	34,34,34,34	0
57	MG	1A	3836	1/1	0.98	0.05	36,36,36,36	0
57	MG	2A	3639	1/1	0.98	0.07	55,55,55,55	0
57	MG	2A	3640	1/1	0.98	0.05	47,47,47,47	0
57	MG	1V	201	1/1	0.98	0.10	24,24,24,24	0
57	MG	1V	202	1/1	0.98	0.12	20,20,20,20	0
57	MG	1A	3272	1/1	0.98	0.07	41,41,41,41	0
57	MG	2A	3409	1/1	0.98	0.06	38,38,38,38	0
57	MG	1A	3212	1/1	0.98	0.03	12,12,12,12	0
57	MG	1A	3097	1/1	0.98	0.11	21,21,21,21	0
57	MG	2A	3648	1/1	0.98	0.06	47,47,47,47	0
57	MG	1A	3420	1/1	0.98	0.04	23,23,23,23	0
57	MG	2A	3650	1/1	0.98	0.08	36,36,36,36	0
57	MG	1A	3608	1/1	0.98	0.11	26,26,26,26	0
57	MG	1A	3609	1/1	0.98	0.12	22,22,22,22	0
57	MG	1A	3073	1/1	0.98	0.06	30,30,30,30	0
57	MG	1A	3845	1/1	0.98	0.05	36,36,36,36	0
57	MG	2A	3655	1/1	0.98	0.07	32,32,32,32	0
57	MG	1A	3007	1/1	0.98	0.09	24,24,24,24	0
57	MG	1A	3346	1/1	0.98	0.06	43,43,43,43	0
57	MG	2A	3658	1/1	0.98	0.05	42,42,42,42	0
57	MG	2A	3205	1/1	0.98	0.07	39,39,39,39	0
57	MG	2A	3206	1/1	0.98	0.09	39,39,39,39	0
57	MG	2A	3421	1/1	0.98	0.04	36,36,36,36	0
57	MG	2A	3662	1/1	0.98	0.05	37,37,37,37	0
57	MG	2a	3102	1/1	0.98	0.24	52,52,52,52	0
57	MG	1A	3217	1/1	0.98	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	2A	3007	1/1	0.98	0.04	36,36,36,36	0
57	MG	2A	3665	1/1	0.98	0.05	52,52,52,52	0
57	MG	1A	3614	1/1	0.98	0.05	26,26,26,26	0
57	MG	2A	3667	1/1	0.98	0.04	35,35,35,35	0
57	MG	2A	3010	1/1	0.98	0.07	51,51,51,51	0
57	MG	1A	3134	1/1	0.98	0.05	32,32,32,32	0
57	MG	1a	3135	1/1	0.98	0.07	29,29,29,29	0
57	MG	2A	3013	1/1	0.98	0.05	19,19,19,19	0
57	MG	1A	3727	1/1	0.98	0.04	16,16,16,16	0
57	MG	1A	3728	1/1	0.98	0.03	27,27,27,27	0
57	MG	1A	3426	1/1	0.98	0.06	23,23,23,23	0
57	MG	1A	3219	1/1	0.98	0.06	43,43,43,43	0
57	MG	1A	3428	1/1	0.98	0.05	16,16,16,16	0
57	MG	1A	3429	1/1	0.98	0.05	29,29,29,29	0
57	MG	2A	3020	1/1	0.98	0.14	37,37,37,37	0
57	MG	2A	3021	1/1	0.98	0.05	33,33,33,33	0
57	MG	11	102	1/1	0.98	0.08	42,42,42,42	0
57	MG	2A	3682	1/1	0.98	0.09	37,37,37,37	0
57	MG	2A	3683	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3430	1/1	0.98	0.09	44,44,44,44	0
57	MG	1A	3735	1/1	0.98	0.07	15,15,15,15	0
57	MG	2A	3686	1/1	0.98	0.07	45,45,45,45	0
57	MG	11	105	1/1	0.98	0.05	39,39,39,39	0
57	MG	1a	3146	1/1	0.98	0.07	29,29,29,29	0
57	MG	1A	3280	1/1	0.98	0.11	34,34,34,34	0
57	MG	2A	3028	1/1	0.98	0.03	28,28,28,28	0
57	MG	1A	3860	1/1	0.98	0.04	30,30,30,30	0
57	MG	2A	3030	1/1	0.98	0.09	22,22,22,22	0
57	MG	1A	3432	1/1	0.98	0.05	27,27,27,27	0
57	MG	15	101	1/1	0.98	0.07	29,29,29,29	0
57	MG	1A	3526	1/1	0.98	0.04	26,26,26,26	0
57	MG	15	103	1/1	0.98	0.11	34,34,34,34	0
57	MG	1A	3100	1/1	0.98	0.23	27,27,27,27	0
57	MG	1a	3154	1/1	0.98	0.05	47,47,47,47	0
57	MG	1A	3013	1/1	0.98	0.09	21,21,21,21	0
57	MG	1A	4002	1/1	0.98	0.17	42,42,42,42	0
57	MG	2A	3039	1/1	0.98	0.13	34,34,34,34	0
57	MG	1a	3157	1/1	0.98	0.04	49,49,49,49	0
57	MG	2A	3041	1/1	0.98	0.03	21,21,21,21	0
57	MG	1A	4003	1/1	0.98	0.03	27,27,27,27	0
57	MG	1A	3076	1/1	0.98	0.16	24,24,24,24	0
57	MG	1A	4005	1/1	0.98	0.05	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3628	1/1	0.98	0.04	16,16,16,16	0
57	MG	1A	3629	1/1	0.98	0.05	49,49,49,49	0
57	MG	1A	3223	1/1	0.98	0.19	27,27,27,27	0
57	MG	2a	3149	1/1	0.98	0.06	45,45,45,45	0
57	MG	2A	3048	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3176	1/1	0.98	0.07	24,24,24,24	0
57	MG	1A	3438	1/1	0.98	0.03	9,9,9,9	0
57	MG	2A	3713	1/1	0.98	0.06	40,40,40,40	0
57	MG	1A	3177	1/1	0.98	0.41	35,35,35,35	0
57	MG	2a	3155	1/1	0.98	0.07	57,57,57,57	0
57	MG	1A	3440	1/1	0.98	0.06	21,21,21,21	0
57	MG	1A	3139	1/1	0.98	0.06	27,27,27,27	0
57	MG	19	102	1/1	0.98	0.05	44,44,44,44	0
57	MG	1A	3077	1/1	0.98	0.12	25,25,25,25	0
57	MG	1A	3289	1/1	0.98	0.05	8,8,8,8	0
57	MG	2A	3258	1/1	0.98	0.09	41,41,41,41	0
57	MG	1A	3362	1/1	0.98	0.03	10,10,10,10	0
57	MG	1A	3042	1/1	0.98	0.07	16,16,16,16	0
57	MG	1A	3030	1/1	0.98	0.04	31,31,31,31	0
57	MG	1A	3365	1/1	0.98	0.04	18,18,18,18	0
57	MG	1A	3107	1/1	0.98	0.11	23,23,23,23	0
57	MG	1A	4021	1/1	0.98	0.04	41,41,41,41	0
57	MG	1A	3293	1/1	0.98	0.06	27,27,27,27	0
57	MG	1A	3044	1/1	0.98	0.07	14,14,14,14	0
57	MG	1A	3233	1/1	0.98	0.17	27,27,27,27	0
57	MG	2A	3067	1/1	0.98	0.11	40,40,40,40	0
57	MG	1A	3886	1/1	0.98	0.04	30,30,30,30	0
57	MG	1A	3887	1/1	0.98	0.03	34,34,34,34	0
57	MG	1A	3888	1/1	0.98	0.06	34,34,34,34	0
57	MG	1A	3547	1/1	0.98	0.09	33,33,33,33	0
57	MG	2A	3489	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3006	1/1	0.98	0.04	16,16,16,16	0
57	MG	2A	3074	1/1	0.98	0.12	39,39,39,39	0
57	MG	1A	3186	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3649	1/1	0.98	0.10	48,48,48,48	0
57	MG	2B	214	1/1	0.98	0.06	51,51,51,51	0
57	MG	2A	3494	1/1	0.98	0.03	47,47,47,47	0
57	MG	1A	3023	1/1	0.98	0.17	19,19,19,19	0
57	MG	1a	3020	1/1	0.98	0.08	43,43,43,43	0
57	MG	1A	3651	1/1	0.98	0.05	34,34,34,34	0
57	MG	1B	213	1/1	0.98	0.06	33,33,33,33	0
57	MG	1B	214	1/1	0.98	0.04	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3048	1/1	0.98	0.07	42,42,42,42	0
57	MG	1A	3457	1/1	0.98	0.12	40,40,40,40	0
57	MG	1A	3770	1/1	0.98	0.03	28,28,28,28	0
57	MG	1a	3027	1/1	0.98	0.22	55,55,55,55	0
57	MG	1A	3239	1/1	0.98	0.18	32,32,32,32	0
57	MG	2A	3505	1/1	0.98	0.03	38,38,38,38	0
57	MG	1A	3112	1/1	0.98	0.08	28,28,28,28	0
57	MG	2E	302	1/1	0.98	0.05	35,35,35,35	0
57	MG	1B	220	1/1	0.98	0.07	22,22,22,22	0
57	MG	2E	304	1/1	0.98	0.09	37,37,37,37	0
57	MG	1B	221	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3901	1/1	0.98	0.03	49,49,49,49	0
57	MG	1B	223	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3657	1/1	0.98	0.09	45,45,45,45	0
57	MG	1A	3903	1/1	0.98	0.05	27,27,27,27	0
57	MG	2A	3513	1/1	0.98	0.04	49,49,49,49	0
57	MG	2F	304	1/1	0.98	0.16	38,38,38,38	0
57	MG	1A	3244	1/1	0.98	0.15	28,28,28,28	0
57	MG	1A	3084	1/1	0.98	0.19	34,34,34,34	0
57	MG	1A	3115	1/1	0.98	0.06	16,16,16,16	0
61	ZN	1n	104	1/1	0.98	0.04	66,66,66,66	0
57	MG	1A	3117	1/1	0.98	0.04	26,26,26,26	0
57	MG	1A	3909	1/1	0.98	0.05	40,40,40,40	0
62	SF4	1d	306	8/8	0.98	0.05	52,62,71,75	0
62	SF4	2d	501	8/8	0.98	0.05	58,67,74,76	0
57	MG	1A	3956	1/1	0.99	0.04	32,32,32,32	0
57	MG	1V	206	1/1	0.99	0.05	34,34,34,34	0
57	MG	1A	3017	1/1	0.99	0.18	33,33,33,33	0
57	MG	2A	3643	1/1	0.99	0.04	31,31,31,31	0
57	MG	2A	3303	1/1	0.99	0.06	52,52,52,52	0
57	MG	1A	3153	1/1	0.99	0.08	22,22,22,22	0
57	MG	2A	3305	1/1	0.99	0.04	28,28,28,28	0
57	MG	2A	3469	1/1	0.99	0.05	24,24,24,24	0
57	MG	1W	203	1/1	0.99	0.10	16,16,16,16	0
57	MG	1A	3213	1/1	0.99	0.03	15,15,15,15	0
57	MG	1A	3298	1/1	0.99	0.12	31,31,31,31	0
57	MG	2A	3390	1/1	0.99	0.09	29,29,29,29	0
57	MG	1A	3410	1/1	0.99	0.04	35,35,35,35	0
57	MG	2A	3392	1/1	0.99	0.04	38,38,38,38	0
57	MG	1a	3031	1/1	0.99	0.04	33,33,33,33	0
57	MG	2A	3562	1/1	0.99	0.04	42,42,42,42	0
57	MG	2A	3009	1/1	0.99	0.07	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3962	1/1	0.99	0.05	30,30,30,30	0
57	MG	1A	3252	1/1	0.99	0.07	25,25,25,25	0
57	MG	2A	3566	1/1	0.99	0.04	41,41,41,41	0
57	MG	1A	3964	1/1	0.99	0.08	36,36,36,36	0
57	MG	1A	3443	1/1	0.99	0.02	21,21,21,21	0
57	MG	1A	3908	1/1	0.99	0.03	9,9,9,9	0
57	MG	1A	3807	1/1	0.99	0.11	47,47,47,47	0
57	MG	1A	3230	1/1	0.99	0.04	27,27,27,27	0
57	MG	1A	3116	1/1	0.99	0.09	26,26,26,26	0
57	MG	2E	308	1/1	0.99	0.05	24,24,24,24	0
57	MG	2A	3573	1/1	0.99	0.06	43,43,43,43	0
57	MG	1A	3354	1/1	0.99	0.03	15,15,15,15	0
57	MG	1A	3001	1/1	0.99	0.02	31,31,31,31	0
57	MG	2A	3488	1/1	0.99	0.04	34,34,34,34	0
57	MG	1A	3592	1/1	0.99	0.04	33,33,33,33	0
57	MG	1A	3019	1/1	0.99	0.17	22,22,22,22	0
57	MG	1A	3357	1/1	0.99	0.08	20,20,20,20	0
57	MG	1A	3719	1/1	0.99	0.03	35,35,35,35	0
57	MG	1A	3234	1/1	0.99	0.10	25,25,25,25	0
57	MG	1a	3253	1/1	0.99	0.12	44,44,44,44	0
57	MG	2A	3250	1/1	0.99	0.09	33,33,33,33	0
57	MG	1A	3091	1/1	0.99	0.02	12,12,12,12	0
57	MG	2A	3678	1/1	0.99	0.03	33,33,33,33	0
57	MG	1A	3131	1/1	0.99	0.14	23,23,23,23	0
57	MG	1A	3332	1/1	0.99	0.05	23,23,23,23	0
57	MG	2A	3587	1/1	0.99	0.03	42,42,42,42	0
57	MG	1A	3523	1/1	0.99	0.03	23,23,23,23	0
57	MG	1A	3725	1/1	0.99	0.06	19,19,19,19	0
57	MG	2a	3163	1/1	0.99	0.02	48,48,48,48	0
57	MG	1A	3561	1/1	0.99	0.04	31,31,31,31	0
57	MG	15	104	1/1	0.99	0.16	25,25,25,25	0
57	MG	1A	3009	1/1	0.99	0.04	23,23,23,23	0
57	MG	2A	3593	1/1	0.99	0.06	30,30,30,30	0
57	MG	1A	3873	1/1	0.99	0.04	23,23,23,23	0
57	MG	1A	3928	1/1	0.99	0.06	36,36,36,36	0
57	MG	1N	201	1/1	0.99	0.03	31,31,31,31	0
57	MG	1N	202	1/1	0.99	0.10	26,26,26,26	0
57	MG	1A	3488	1/1	0.99	0.03	26,26,26,26	0
57	MG	1a	3196	1/1	0.99	0.10	40,40,40,40	0
57	MG	1A	3875	1/1	0.99	0.06	32,32,32,32	0
57	MG	2a	3175	1/1	0.99	0.06	42,42,42,42	0
57	MG	1A	3308	1/1	0.99	0.06	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3527	1/1	0.99	0.03	17,17,17,17	0
57	MG	1A	3731	1/1	0.99	0.08	24,24,24,24	0
57	MG	1A	3101	1/1	0.99	0.09	23,23,23,23	0
57	MG	1A	3336	1/1	0.99	0.06	35,35,35,35	0
57	MG	1A	3031	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3005	1/1	0.99	0.07	18,18,18,18	0
57	MG	1A	3241	1/1	0.99	0.14	26,26,26,26	0
57	MG	1a	3206	1/1	0.99	0.06	51,51,51,51	0
57	MG	2A	3124	1/1	0.99	0.03	33,33,33,33	0
57	MG	1A	3242	1/1	0.99	0.13	36,36,36,36	0
57	MG	1D	302	1/1	0.99	0.16	25,25,25,25	0
57	MG	1A	3243	1/1	0.99	0.23	35,35,35,35	0
57	MG	1D	304	1/1	0.99	0.06	40,40,40,40	0
57	MG	1A	3113	1/1	0.99	0.10	31,31,31,31	0
57	MG	1A	3137	1/1	0.99	0.03	17,17,17,17	0
57	MG	1A	3654	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3465	1/1	0.99	0.03	37,37,37,37	0
57	MG	1D	309	1/1	0.99	0.02	13,13,13,13	0
57	MG	2A	3059	1/1	0.99	0.06	41,41,41,41	0
57	MG	1A	3890	1/1	0.99	0.03	34,34,34,34	0
57	MG	1A	3839	1/1	0.99	0.03	14,14,14,14	0
57	MG	1A	3501	1/1	0.99	0.04	36,36,36,36	0
57	MG	1D	313	1/1	0.99	0.13	18,18,18,18	0
57	MG	1U	203	1/1	0.99	0.10	30,30,30,30	0
57	MG	1A	3744	1/1	0.99	0.05	16,16,16,16	0
57	MG	1A	3698	1/1	0.99	0.06	21,21,21,21	0
57	MG	1A	3402	1/1	0.99	0.02	11,11,11,11	0
57	MG	1A	3246	1/1	0.99	0.10	24,24,24,24	0
57	MG	1A	3701	1/1	0.99	0.04	31,31,31,31	0
57	MG	2A	3374	1/1	0.99	0.08	38,38,38,38	0
57	MG	1A	3045	1/1	0.99	0.08	14,14,14,14	0
57	MG	2A	3071	1/1	0.99	0.04	20,20,20,20	0
61	ZN	1Y	202	1/1	0.99	0.03	52,52,52,52	0
57	MG	1A	3619	1/1	0.99	0.07	20,20,20,20	0
61	ZN	15	111	1/1	0.99	0.02	37,37,37,37	0
61	ZN	16	501	1/1	0.99	0.04	35,35,35,35	0
61	ZN	19	103	1/1	0.99	0.03	37,37,37,37	0
57	MG	2A	3379	1/1	0.99	0.05	28,28,28,28	0
57	MG	1A	3180	1/1	0.99	0.17	32,32,32,32	0
57	MG	2A	3637	1/1	0.99	0.07	39,39,39,39	0
61	ZN	25	105	1/1	0.99	0.03	47,47,47,47	0
61	ZN	26	501	1/1	0.99	0.03	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
61	ZN	29	102	1/1	0.99	0.04	63,63,63,63	0
61	ZN	2n	102	1/1	0.99	0.03	73,73,73,73	0
57	MG	2A	3638	1/1	0.99	0.04	29,29,29,29	0
57	MG	2A	3547	1/1	0.99	0.03	44,44,44,44	0
57	MG	1A	3920	1/1	1.00	0.04	41,41,41,41	0
57	MG	2A	3378	1/1	1.00	0.03	22,22,22,22	0
57	MG	1A	3491	1/1	1.00	0.03	22,22,22,22	0
57	MG	1A	3767	1/1	1.00	0.02	31,31,31,31	0

6.5 Other polymers (i)

There are no such residues in this entry.