



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 16, 2026 – 02:45 am BST

PDB ID : 5F8K / pdb_00005f8k
Title : Crystal structure of the Bac7(1-16) antimicrobial peptide bound to the *Thermus thermophilus* 70S ribosome
Authors : Seefeldt, A.C.; Graf, M.; Perebaskine, N.; Nguyen, F.; Arenz, S.; Mardirossian, M.; Scocchi, M.; Wilson, D.N.; Innis, C.A.
Deposited on : 2015-12-09
Resolution : 2.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

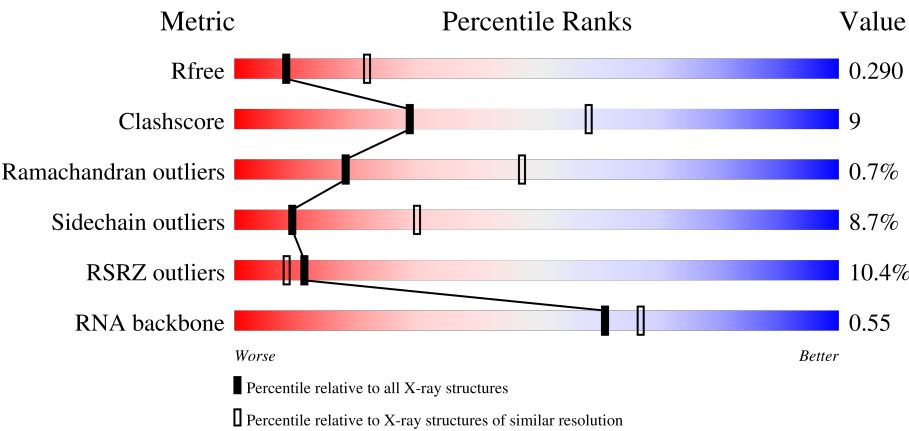
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

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 $\leq 5\%$. 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	
1	2A	2915	
2	1B	120	
2	2B	120	

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Mol	Chain	Length	Quality of chain
3	1D	275	
3	2D	275	
4	1E	204	
4	2E	204	
5	1F	203	
5	2F	203	
6	1G	181	
6	2G	181	
7	1H	174	
7	2H	174	
8	1I	147	
8	2I	147	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	149	
11	2P	149	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	110	
14	2S	110	
15	1T	131	

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Mol	Chain	Length	Quality of chain
15	2T	131	3% 75% 21% .
16	1U	116	79% 19% .
16	2U	116	3% 77% 22% .
17	1V	101	% 78% 19% .
17	2V	101	6% 73% 24% ..
18	1W	112	% 84% 13% .
18	2W	112	6% 76% 22% .
19	1X	95	2% 74% 24% .
19	2X	95	6% 73% 26% .
20	1Y	107	% 71% 28% .
20	2Y	107	17% 75% 25% .
21	1Z	203	12% 67% 30% .
21	2Z	203	16% 61% 33% ..
22	10	77	4% 79% 16% 5%
22	20	77	9% 78% 21% .
23	11	97	6% 77% 22% .
23	21	97	7% 64% 31% 5%
24	12	70	6% 79% 17% .
24	22	70	10% 77% 21% .
25	13	59	71% 29%
25	23	59	7% 58% 37% 5%
26	14	69	23% 52% 39% 7% .
26	24	69	51% 49% 46% .
27	15	59	3% 73% 25% .
27	25	59	7% 80% 20%

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Mol	Chain	Length	Quality of chain
28	16	53	
28	26	53	
29	17	48	
29	27	48	
30	18	64	
30	28	64	
31	19	37	
31	29	37	
32	1a	1520	
32	2a	1520	
33	1b	231	
33	2b	231	
34	1c	206	
34	2c	206	
35	1d	208	
35	2d	208	
36	1e	148	
36	2e	148	
37	1f	100	
37	2f	100	
38	1g	155	
38	2g	155	
39	1h	137	
39	2h	137	
40	1i	127	

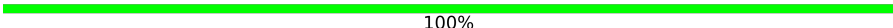
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Mol	Chain	Length	Quality of chain
40	2i	127	
41	1j	97	
41	2j	97	
42	1k	114	
42	2k	114	
43	1l	122	
43	2l	122	
44	1m	116	
44	2m	116	
45	1n	60	
45	2n	60	
46	1o	88	
46	2o	88	
47	1p	82	
47	2p	82	
48	1q	99	
48	2q	99	
49	1r	68	
49	2r	68	
50	1s	83	
50	2s	83	
51	1t	98	
51	2t	98	
52	1u	23	
52	2u	23	

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Mol	Chain	Length	Quality of chain
53	1v	3	
53	2v	3	
54	1x	76	
54	2x	76	
55	1y	16	
55	2y	16	

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
56	MG	2A	3079	-	-	-	X
56	MG	2A	3131	-	-	-	X
56	MG	2A	3719	-	-	-	X
56	MG	2A	3742	-	-	-	X
56	MG	2a	1718	-	-	-	X
56	MG	2a	1752	-	-	-	X

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 296108 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
			61872	27540	11574	19886	2872			
1	2A	2867	Total	C	N	O	P	0	0	0
			61761	27491	11552	19852	2866			

- 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
			2575	1145	476	834	120			
2	2B	120	Total	C	N	O	P	0	0	0
			2571	1146	476	831	118			

- 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	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
22	20	77	Total	C	N	O	S	0	0	0
			608	375	129	103	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 RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	3	Total	C	N	O	P	0	0	0
			65	29	12	21	3			
53	2v	3	Total	C	N	O	P	0	0	0
			65	29	12	21	3			

- Molecule 54 is a RNA chain called tRNAiMet.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
54	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 55 is a protein called Cathelicidin-3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	1y	16	Total	C	N	O	0	0	0
			147	90	40	17			
55	2y	16	Total	C	N	O	0	0	0
			147	90	40	17			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	973	Total	Mg	0	0
			973	973		
56	1B	27	Total	Mg	0	0
			27	27		
56	1D	14	Total	Mg	0	0
			14	14		
56	1E	7	Total	Mg	0	0
			7	7		
56	1F	10	Total	Mg	0	0
			10	10		
56	1G	3	Total	Mg	0	0
			3	3		
56	1H	2	Total	Mg	0	0
			2	2		
56	1N	4	Total	Mg	0	0
			4	4		
56	1P	4	Total	Mg	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1Q	6	Total 6	Mg 6	0	0
56	1R	4	Total 4	Mg 4	0	0
56	1S	1	Total 1	Mg 1	0	0
56	1T	1	Total 1	Mg 1	0	0
56	1U	3	Total 3	Mg 3	0	0
56	1V	3	Total 3	Mg 3	0	0
56	1W	3	Total 3	Mg 3	0	0
56	1X	1	Total 1	Mg 1	0	0
56	10	8	Total 8	Mg 8	0	0
56	11	2	Total 2	Mg 2	0	0
56	13	2	Total 2	Mg 2	0	0
56	15	7	Total 7	Mg 7	0	0
56	17	2	Total 2	Mg 2	0	0
56	18	1	Total 1	Mg 1	0	0
56	19	3	Total 3	Mg 3	0	0
56	1a	240	Total 240	Mg 240	0	0
56	1b	1	Total 1	Mg 1	0	0
56	1d	5	Total 5	Mg 5	0	0
56	1e	1	Total 1	Mg 1	0	0
56	1f	1	Total 1	Mg 1	0	0
56	1g	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1h	1	Total 1	Mg 1	0	0
56	1i	1	Total 1	Mg 1	0	0
56	1l	3	Total 3	Mg 3	0	0
56	1n	1	Total 1	Mg 1	0	0
56	1o	2	Total 2	Mg 2	0	0
56	1q	1	Total 1	Mg 1	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1x	13	Total 13	Mg 13	0	0
56	2A	986	Total 986	Mg 986	0	0
56	2B	25	Total 25	Mg 25	0	0
56	2D	17	Total 17	Mg 17	0	0
56	2E	6	Total 6	Mg 6	0	0
56	2F	9	Total 9	Mg 9	0	0
56	2G	3	Total 3	Mg 3	0	0
56	2H	2	Total 2	Mg 2	0	0
56	2N	3	Total 3	Mg 3	0	0
56	2P	3	Total 3	Mg 3	0	0
56	2Q	4	Total 4	Mg 4	0	0
56	2R	2	Total 2	Mg 2	0	0
56	2S	1	Total 1	Mg 1	0	0
56	2U	7	Total 7	Mg 7	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2V	1	Total 1	Mg 1	0	0
56	2W	1	Total 1	Mg 1	0	0
56	2X	2	Total 2	Mg 2	0	0
56	2Y	2	Total 2	Mg 2	0	0
56	20	5	Total 5	Mg 5	0	0
56	23	2	Total 2	Mg 2	0	0
56	25	3	Total 3	Mg 3	0	0
56	27	2	Total 2	Mg 2	0	0
56	28	1	Total 1	Mg 1	0	0
56	29	2	Total 2	Mg 2	0	0
56	2a	221	Total 221	Mg 221	0	0
56	2b	1	Total 1	Mg 1	0	0
56	2d	4	Total 4	Mg 4	0	0
56	2e	1	Total 1	Mg 1	0	0
56	2f	1	Total 1	Mg 1	0	0
56	2g	1	Total 1	Mg 1	0	0
56	2h	2	Total 2	Mg 2	0	0
56	2i	1	Total 1	Mg 1	0	0
56	2j	1	Total 1	Mg 1	0	0
56	2l	2	Total 2	Mg 2	0	0
56	2n	1	Total 1	Mg 1	0	0

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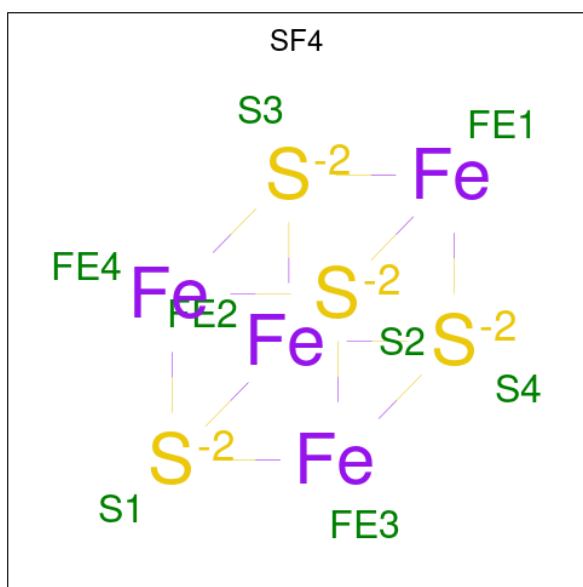
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2o	1	Total 1	Mg 1	0	0
56	2t	1	Total 1	Mg 1	0	0
56	2v	1	Total 1	Mg 1	0	0
56	2x	12	Total 12	Mg 12	0	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1Y	1	Total 1	Zn 1	0	0
57	14	1	Total 1	Zn 1	0	0
57	15	1	Total 1	Zn 1	0	0
57	16	1	Total 1	Zn 1	0	0
57	19	1	Total 1	Zn 1	0	0
57	1n	1	Total 1	Zn 1	0	0
57	2Y	1	Total 1	Zn 1	0	0
57	24	1	Total 1	Zn 1	0	0
57	25	1	Total 1	Zn 1	0	0
57	26	1	Total 1	Zn 1	0	0
57	29	1	Total 1	Zn 1	0	0
57	2n	1	Total 1	Zn 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	1d	1	Total	Fe	S	0	0
			8	4	4		
58	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 59 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1x	1	Total	K	0	0
			1	1		
59	2A	1	Total	K	0	0
			1	1		

- Molecule 60 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1A	1795	Total	O	0	0
			1795	1795		
60	1B	49	Total	O	0	0
			49	49		
60	1D	23	Total	O	0	0
			23	23		
60	1E	16	Total	O	0	0
			16	16		
60	1F	9	Total	O	0	0
			9	9		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1G	2	Total 2	O 2	0	0
60	1H	4	Total 4	O 4	0	0
60	1N	8	Total 8	O 8	0	0
60	1P	14	Total 14	O 14	0	0
60	1Q	6	Total 6	O 6	0	0
60	1R	6	Total 6	O 6	0	0
60	1T	5	Total 5	O 5	0	0
60	1U	3	Total 3	O 3	0	0
60	1V	6	Total 6	O 6	0	0
60	1W	1	Total 1	O 1	0	0
60	1X	6	Total 6	O 6	0	0
60	1Y	4	Total 4	O 4	0	0
60	10	5	Total 5	O 5	0	0
60	11	5	Total 5	O 5	0	0
60	13	1	Total 1	O 1	0	0
60	15	3	Total 3	O 3	0	0
60	16	1	Total 1	O 1	0	0
60	17	2	Total 2	O 2	0	0
60	18	8	Total 8	O 8	0	0
60	19	2	Total 2	O 2	0	0
60	1a	408	Total 408	O 408	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1d	8	Total 8	O 8	0	0
60	1e	3	Total 3	O 3	0	0
60	1f	1	Total 1	O 1	0	0
60	1h	1	Total 1	O 1	0	0
60	1j	1	Total 1	O 1	0	0
60	1l	4	Total 4	O 4	0	0
60	1m	1	Total 1	O 1	0	0
60	1o	2	Total 2	O 2	0	0
60	1p	1	Total 1	O 1	0	0
60	1t	2	Total 2	O 2	0	0
60	1v	2	Total 2	O 2	0	0
60	1x	5	Total 5	O 5	0	0
60	1y	2	Total 2	O 2	0	0
60	2A	1787	Total 1787	O 1787	0	0
60	2B	46	Total 46	O 46	0	0
60	2D	20	Total 20	O 20	0	0
60	2E	15	Total 15	O 15	0	0
60	2F	11	Total 11	O 11	0	0
60	2G	2	Total 2	O 2	0	0
60	2H	4	Total 4	O 4	0	0
60	2N	8	Total 8	O 8	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	2P	17	Total 17	O 17	0	0
60	2Q	4	Total 4	O 4	0	0
60	2R	6	Total 6	O 6	0	0
60	2T	4	Total 4	O 4	0	0
60	2U	5	Total 5	O 5	0	0
60	2V	3	Total 3	O 3	0	0
60	2W	1	Total 1	O 1	0	0
60	2X	5	Total 5	O 5	0	0
60	2Y	8	Total 8	O 8	0	0
60	20	9	Total 9	O 9	0	0
60	21	2	Total 2	O 2	0	0
60	23	2	Total 2	O 2	0	0
60	25	2	Total 2	O 2	0	0
60	26	1	Total 1	O 1	0	0
60	27	2	Total 2	O 2	0	0
60	28	9	Total 9	O 9	0	0
60	29	4	Total 4	O 4	0	0
60	2a	408	Total 408	O 408	0	0
60	2d	7	Total 7	O 7	0	0
60	2e	4	Total 4	O 4	0	0
60	2f	1	Total 1	O 1	0	0

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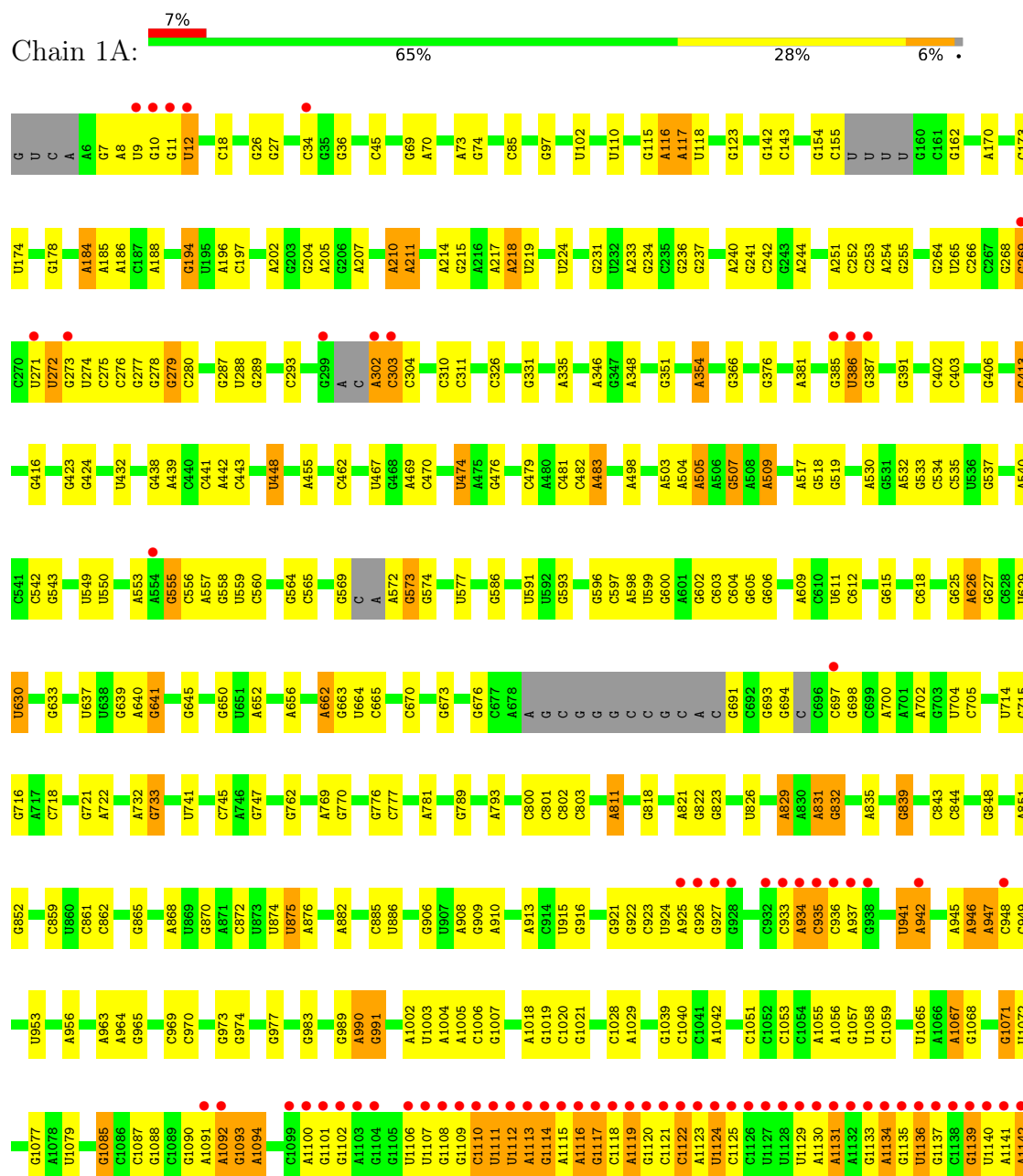
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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60	2j	2	Total 2	O 2	0	0
60	2l	7	Total 7	O 7	0	0
60	2m	1	Total 1	O 1	0	0
60	2n	1	Total 1	O 1	0	0
60	2t	1	Total 1	O 1	0	0
60	2v	3	Total 3	O 3	0	0
60	2x	4	Total 4	O 4	0	0
60	2y	4	Total 4	O 4	0	0

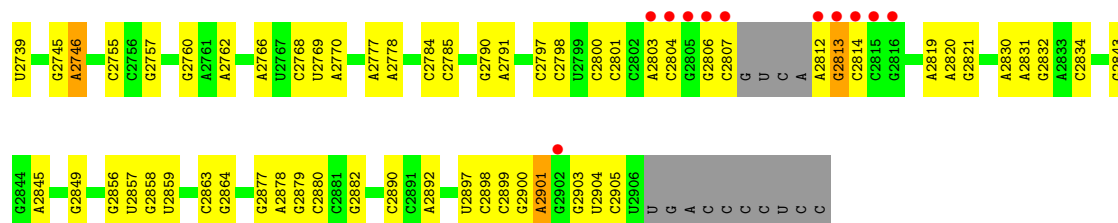
3 Residue-property plots [i](#)

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.

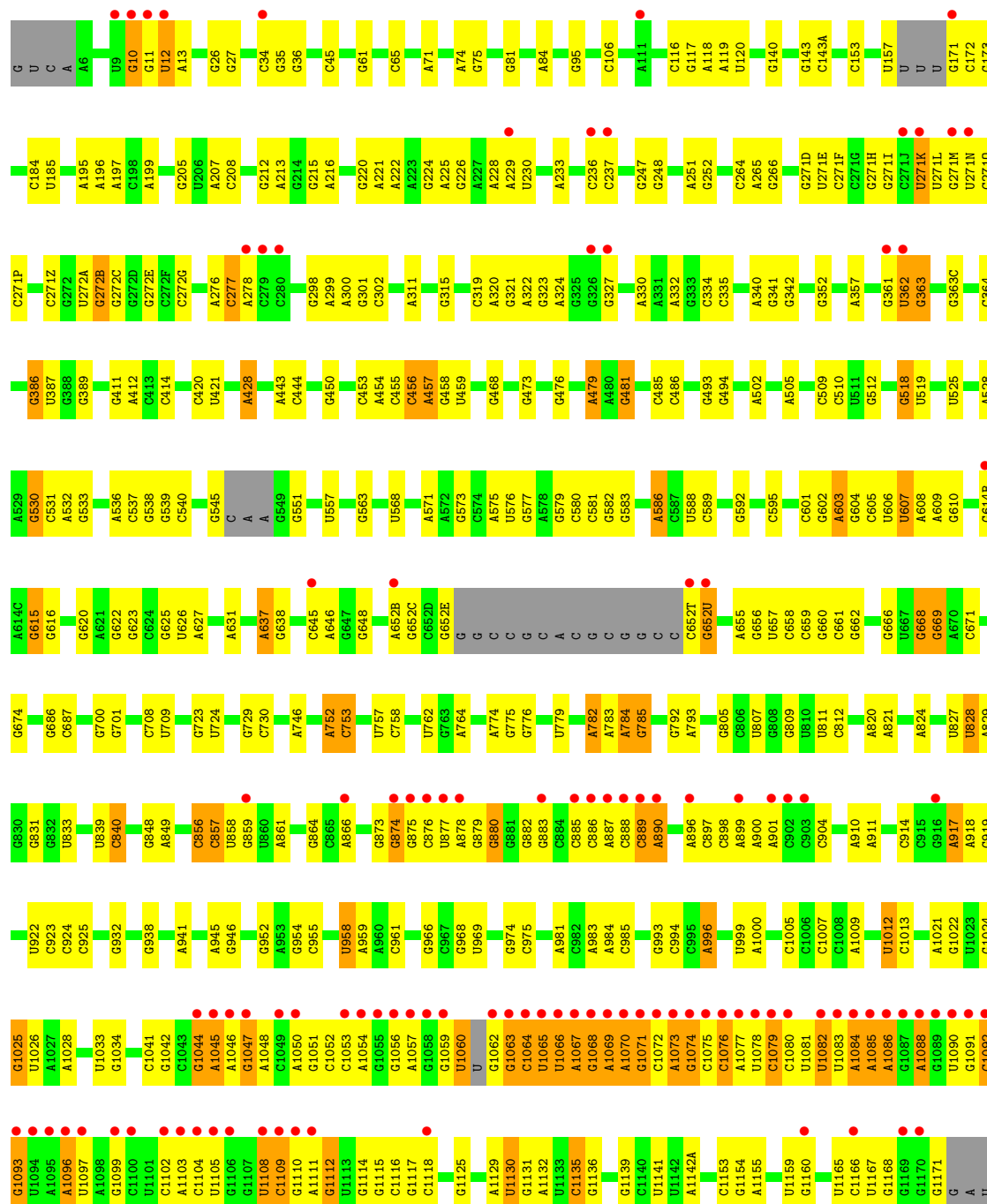
• Molecule 1: 23S ribosomal RNA







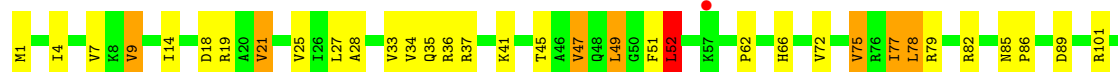
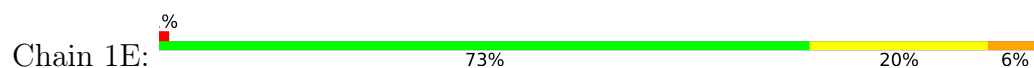
• Molecule 1: 23S ribosomal RNA



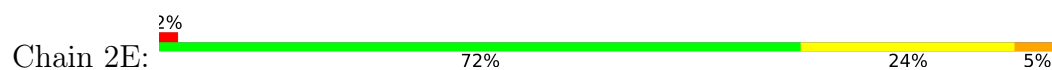




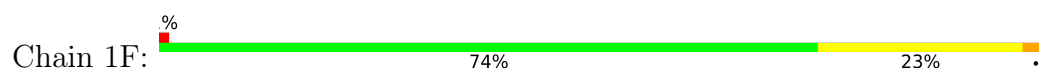
• Molecule 4: 50S ribosomal protein L3



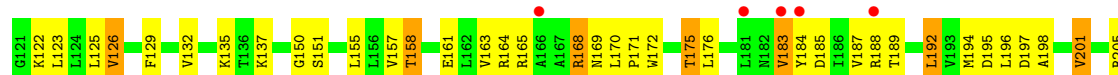
• Molecule 4: 50S ribosomal protein L3



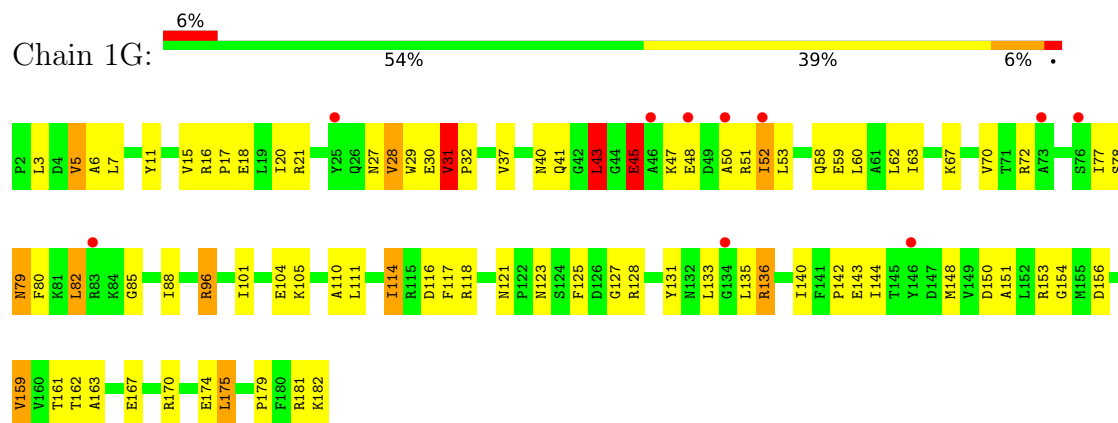
• Molecule 5: 50S ribosomal protein L4



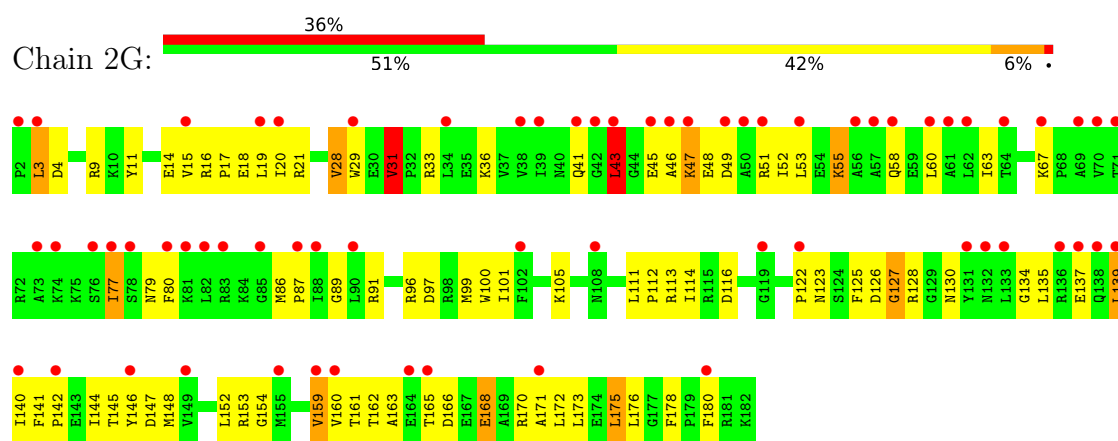
• Molecule 5: 50S ribosomal protein L4



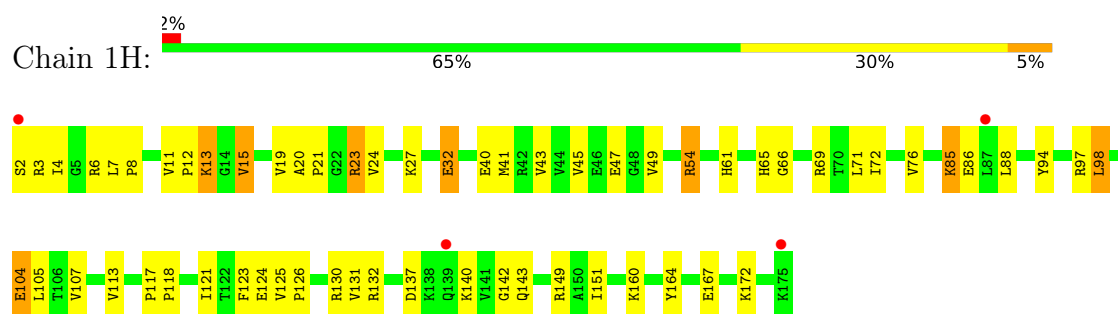
- Molecule 6: 50S ribosomal protein L5



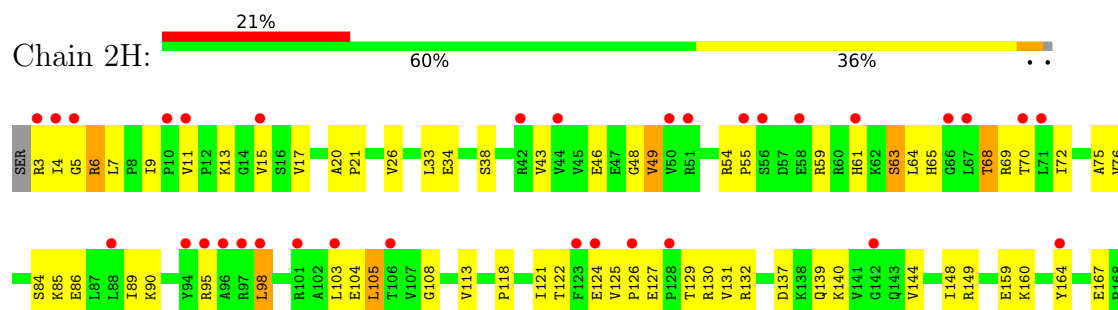
- Molecule 6: 50S ribosomal protein L5

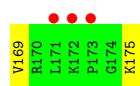


- Molecule 7: 50S ribosomal protein L6

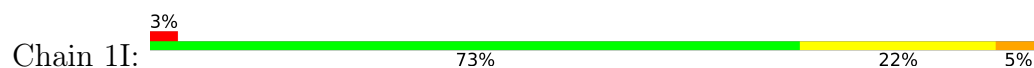


- Molecule 7: 50S ribosomal protein L6

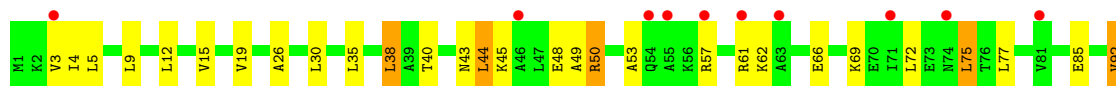




• Molecule 8: 50S ribosomal protein L9



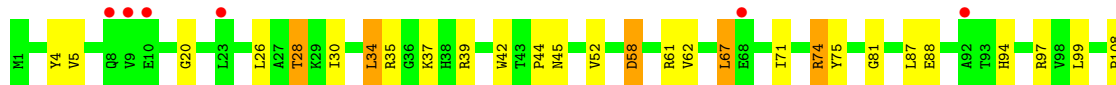
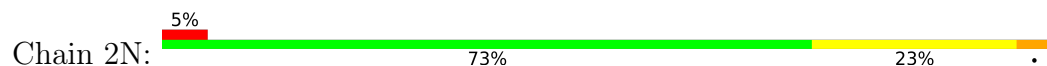
• Molecule 8: 50S ribosomal protein L9



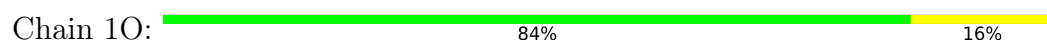
• Molecule 9: 50S ribosomal protein L13



• Molecule 9: 50S ribosomal protein L13

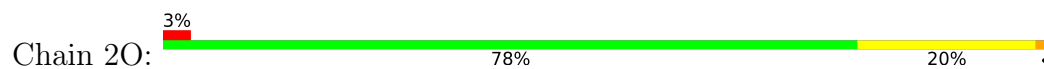


• Molecule 10: 50S ribosomal protein L14

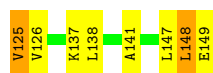




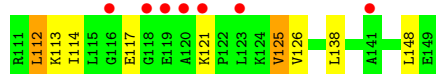
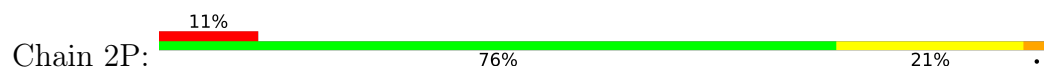
- Molecule 10: 50S ribosomal protein L14



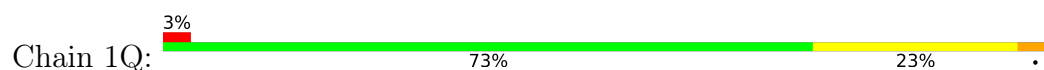
- Molecule 11: 50S ribosomal protein L15



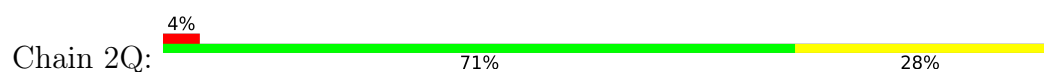
- Molecule 11: 50S ribosomal protein L15



- Molecule 12: 50S ribosomal protein L16

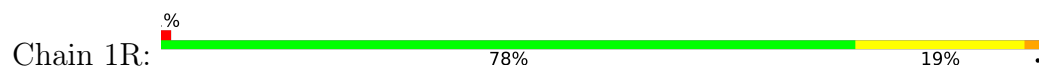


- Molecule 12: 50S ribosomal protein L16

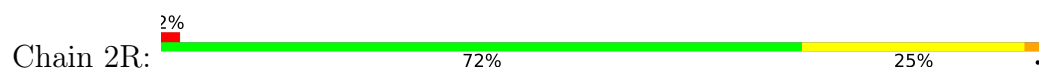




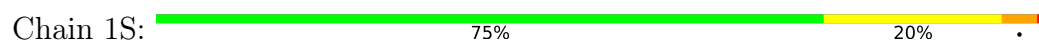
- Molecule 13: 50S ribosomal protein L17



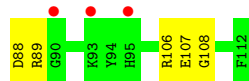
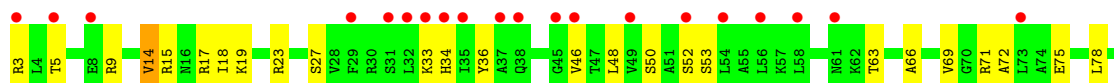
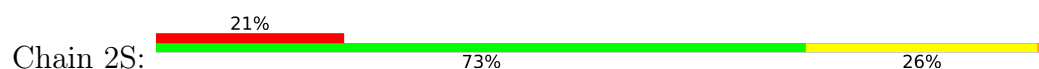
- Molecule 13: 50S ribosomal protein L17



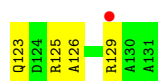
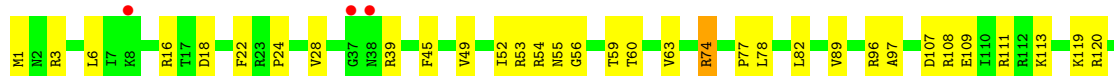
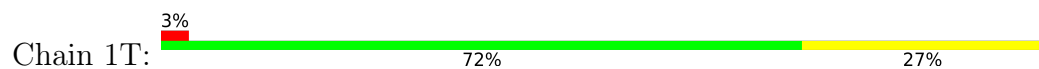
- Molecule 14: 50S ribosomal protein L18



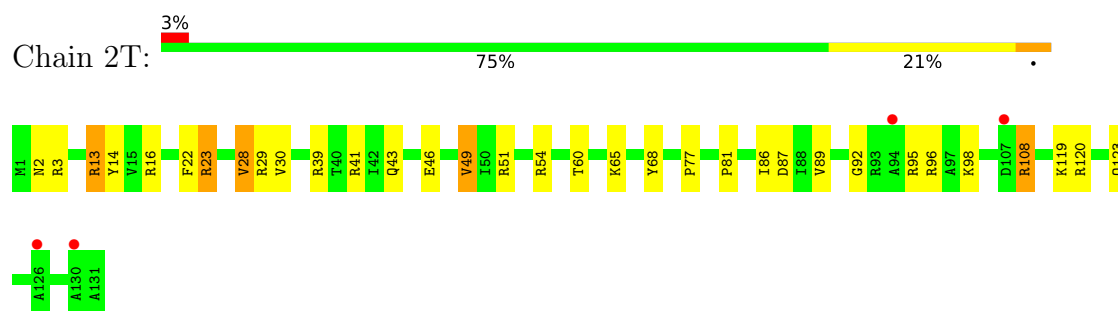
- Molecule 14: 50S ribosomal protein L18



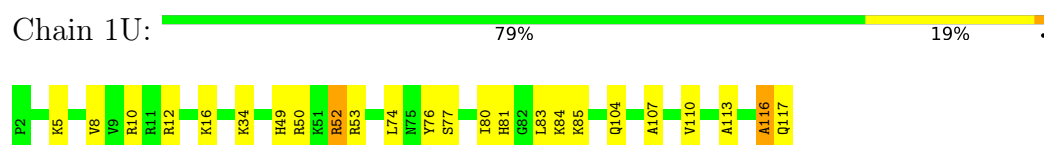
- Molecule 15: 50S ribosomal protein L19



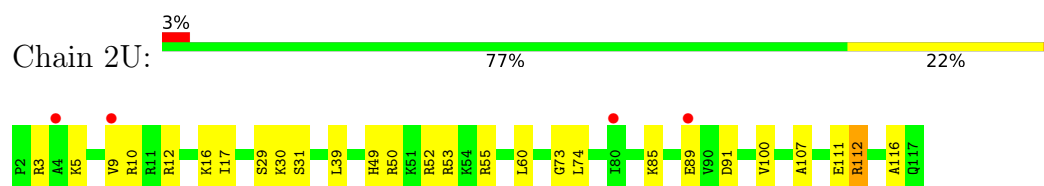
- Molecule 15: 50S ribosomal protein L19



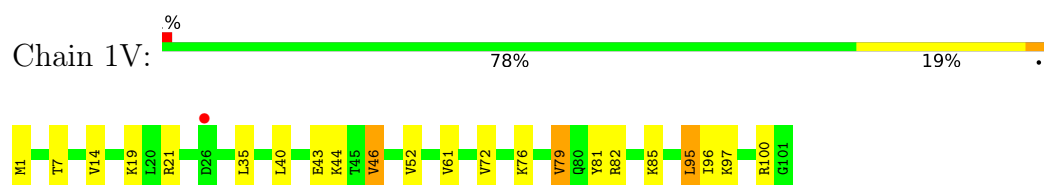
- Molecule 16: 50S ribosomal protein L20



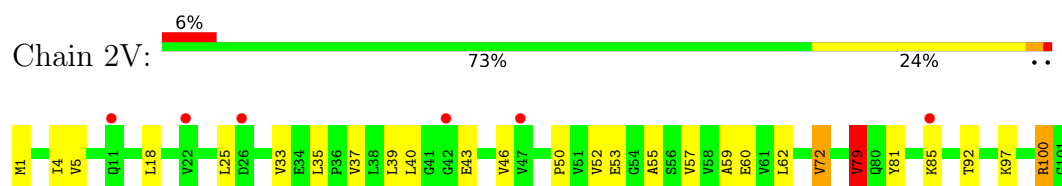
- Molecule 16: 50S ribosomal protein L20



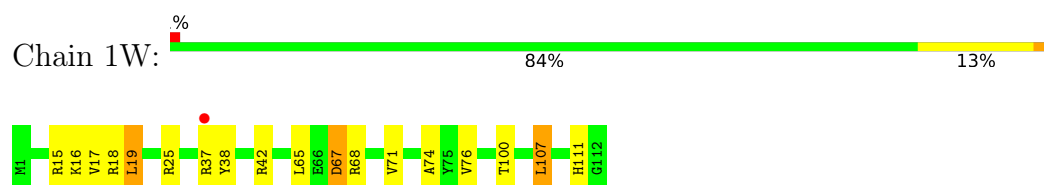
- Molecule 17: 50S ribosomal protein L21



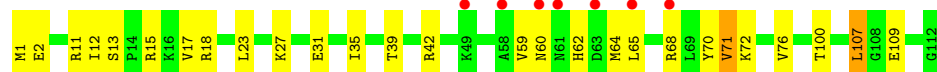
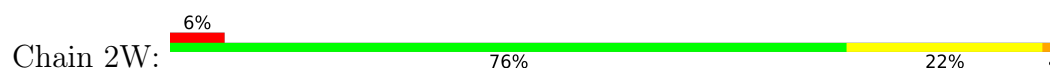
- Molecule 17: 50S ribosomal protein L21



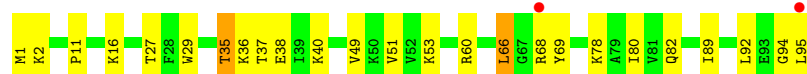
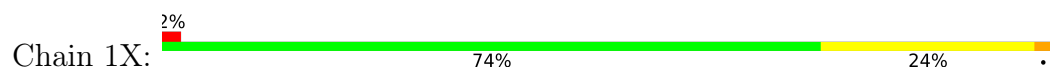
- Molecule 18: 50S ribosomal protein L22



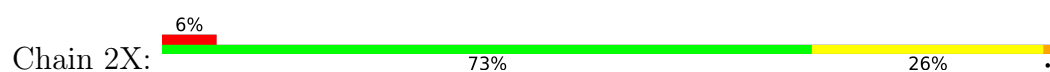
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L23



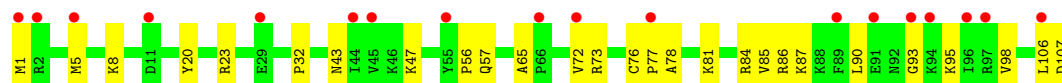
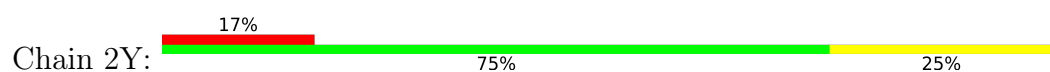
- Molecule 19: 50S ribosomal protein L23



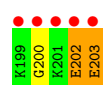
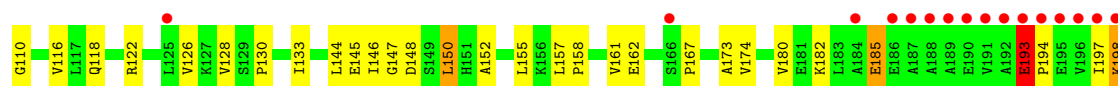
- Molecule 20: 50S ribosomal protein L24



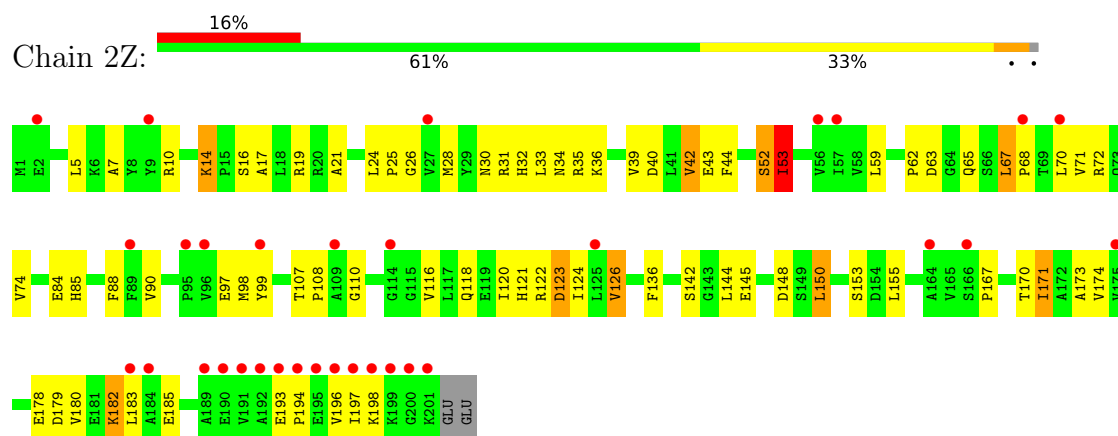
- Molecule 20: 50S ribosomal protein L24



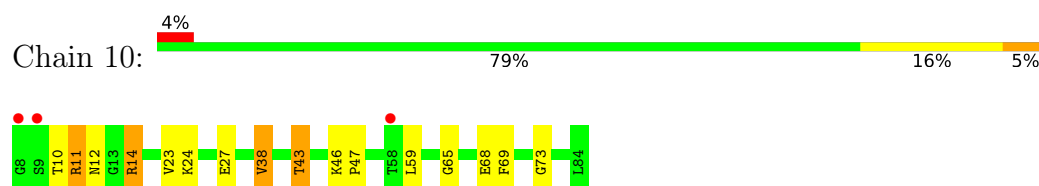
- Molecule 21: 50S ribosomal protein L25



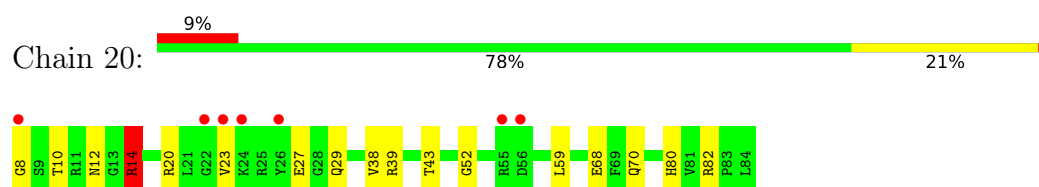
- Molecule 21: 50S ribosomal protein L25



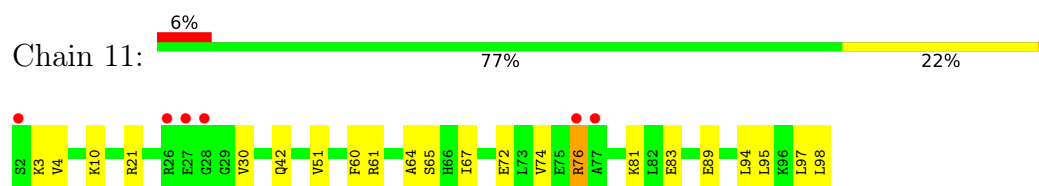
- Molecule 22: 50S ribosomal protein L27



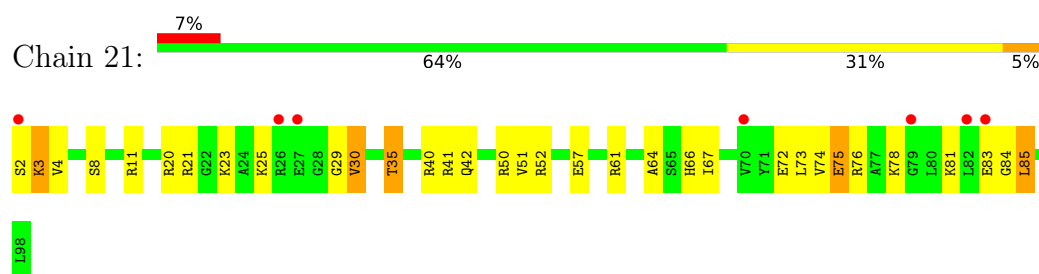
- Molecule 22: 50S ribosomal protein L27



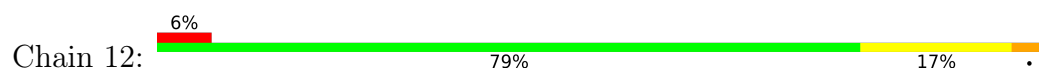
- Molecule 23: 50S ribosomal protein L28



- Molecule 23: 50S ribosomal protein L28

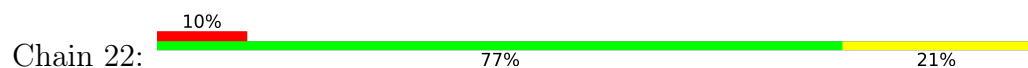


- Molecule 24: 50S ribosomal protein L29





- Molecule 24: 50S ribosomal protein L29



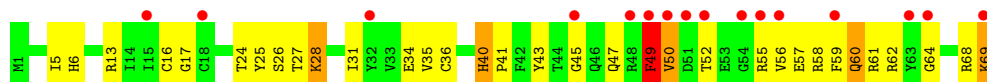
- Molecule 25: 50S ribosomal protein L30



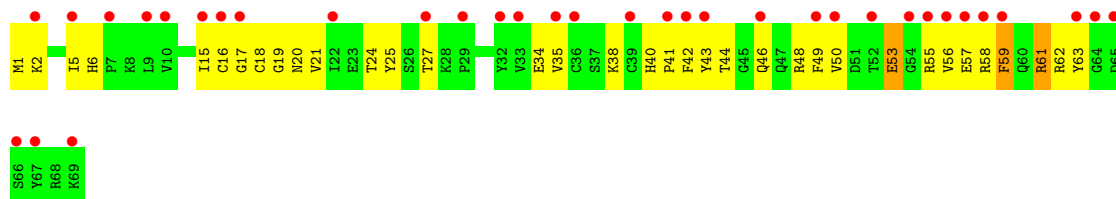
- Molecule 25: 50S ribosomal protein L30



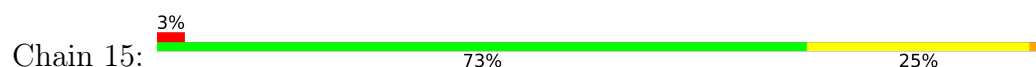
- Molecule 26: 50S ribosomal protein L31



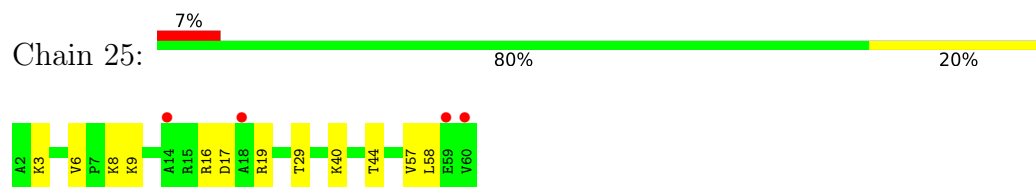
- Molecule 26: 50S ribosomal protein L31



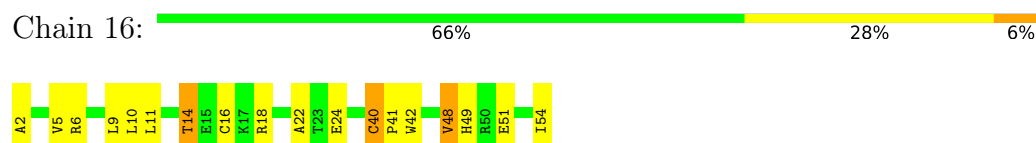
- Molecule 27: 50S ribosomal protein L32



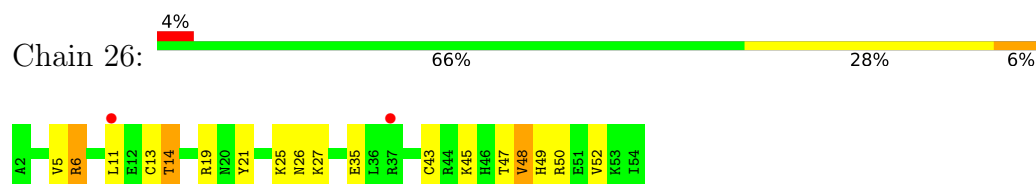
- Molecule 27: 50S ribosomal protein L32



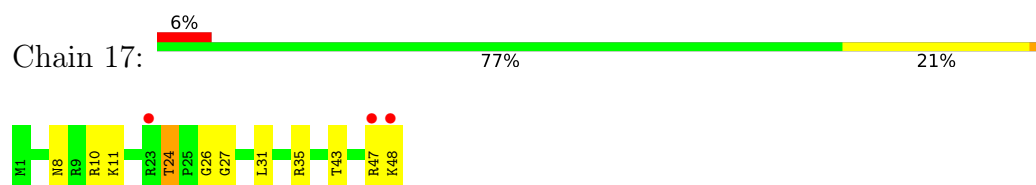
- Molecule 28: 50S ribosomal protein L33



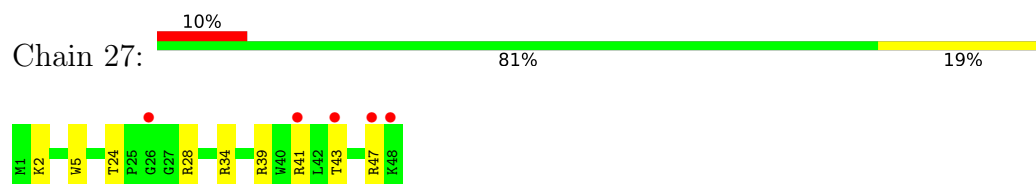
- Molecule 28: 50S ribosomal protein L33



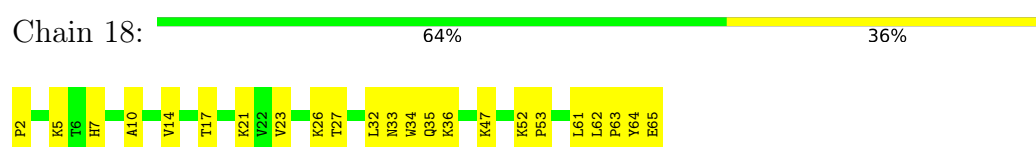
- Molecule 29: 50S ribosomal protein L34



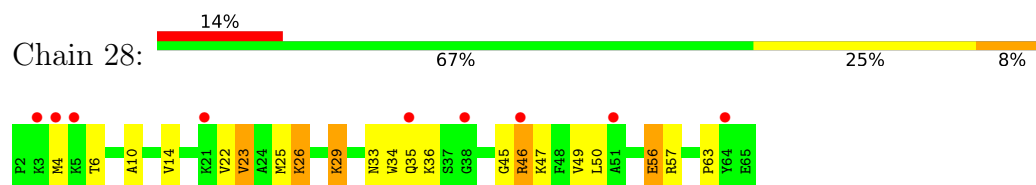
- Molecule 29: 50S ribosomal protein L34



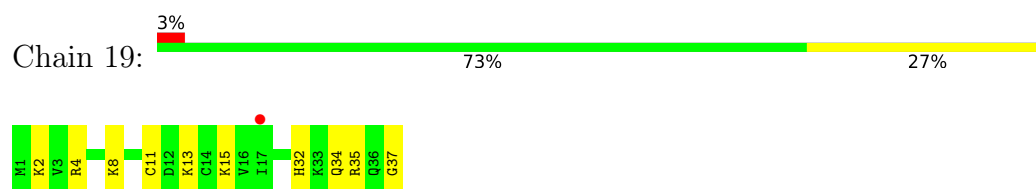
- Molecule 30: 50S ribosomal protein L35



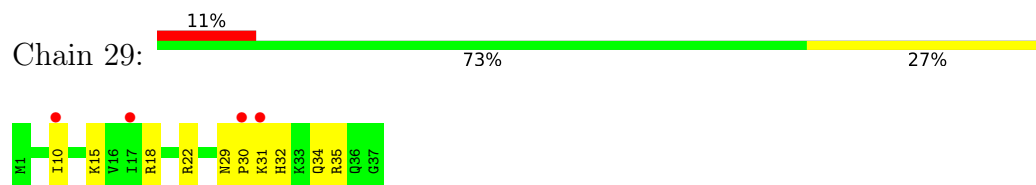
- Molecule 30: 50S ribosomal protein L35



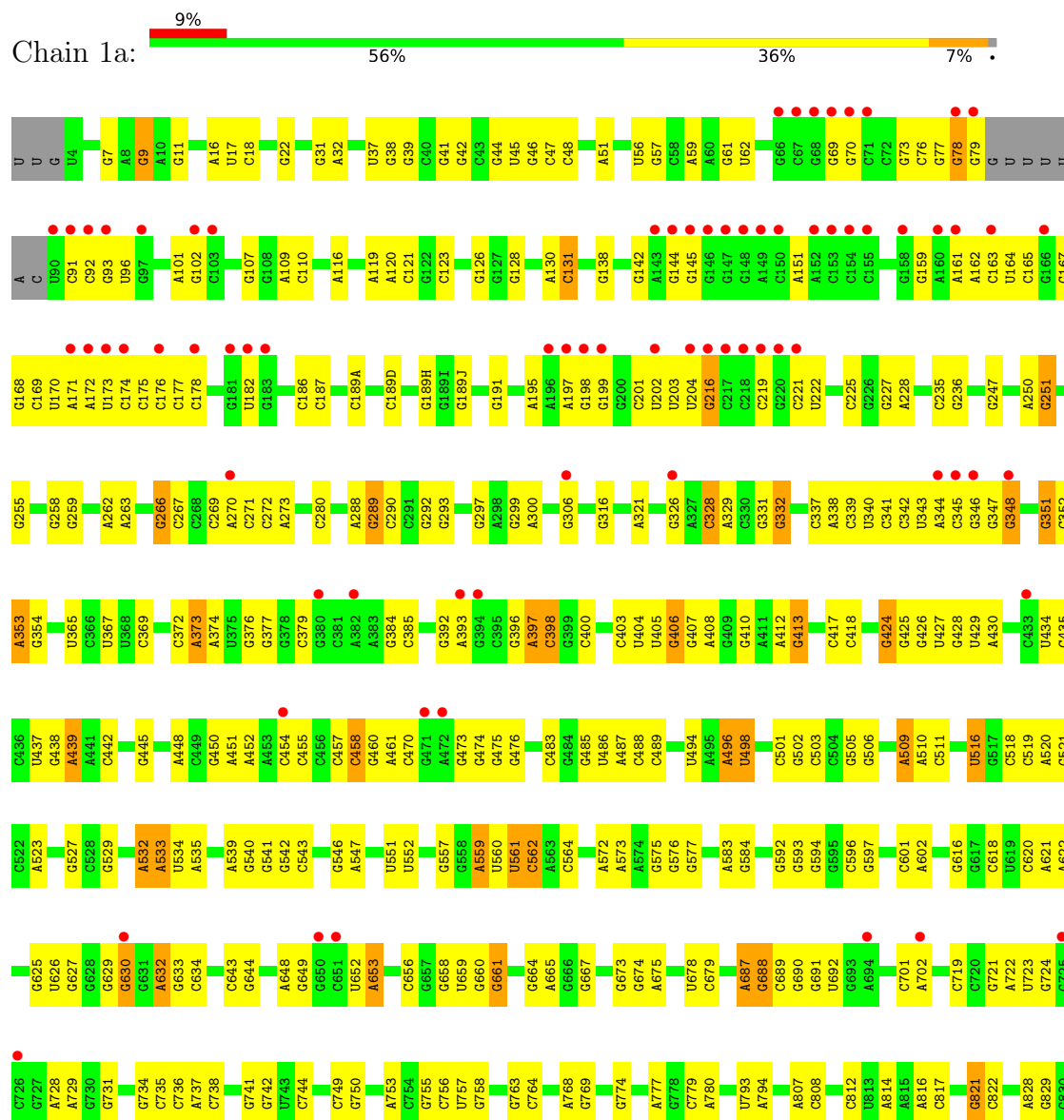
- Molecule 31: 50S ribosomal protein L36



- Molecule 31: 50S ribosomal protein L36

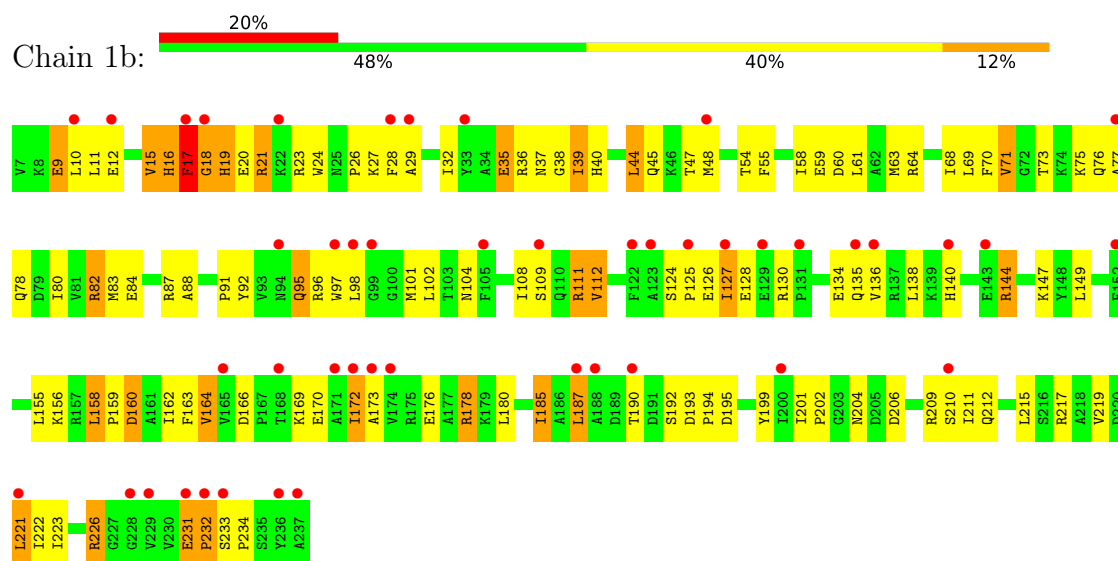


- Molecule 32: 16S ribosomal RNA

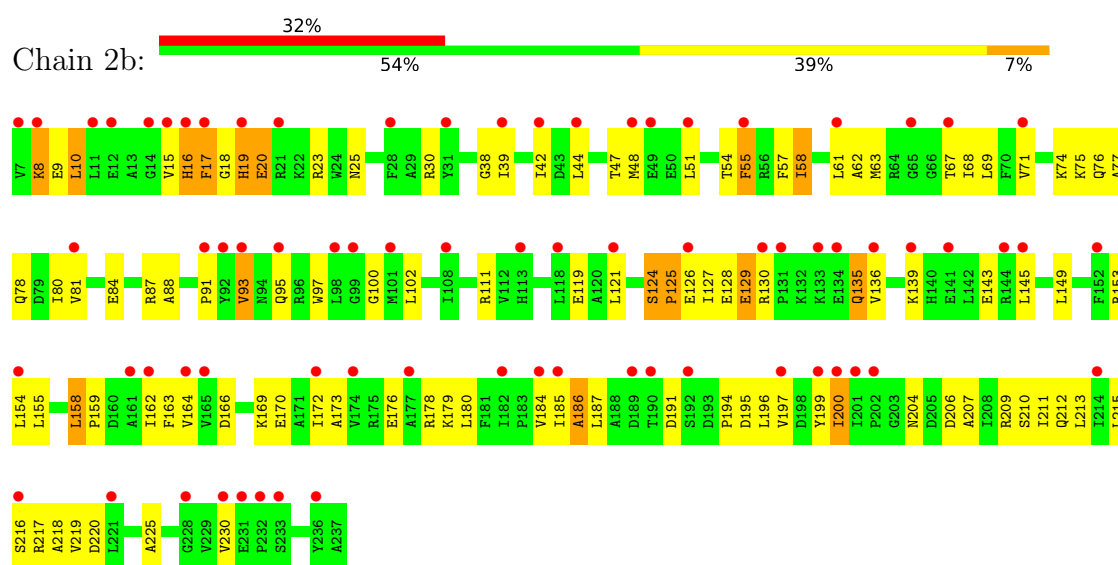


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C	G1442	C1359	G1282	G1212	G1133	G1063	G1003	A935	C808	G688	A583	C503	G408
U	G1442A	A1213	G1283	A1213	G1134	G1064	A1004	C940	C811	G693	C584	C504	G409
C	U1446	G1361	C1284	G1217	U1135	U1065	A1005	G941	A814	A694	G587	C505	G410
U	A1447	C1362	A1285	C1218	U1136	C1066	C1006	G942	A815	A695	C590	A509	A411
U	C1452	C1363	A1286	U1219	G1137	A1067	C1007	G946	A816	A696	C591	A510	A412
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			G1294	G1224	G1142	U1073	G1012	G951	G821	A704	C596	C517	G424
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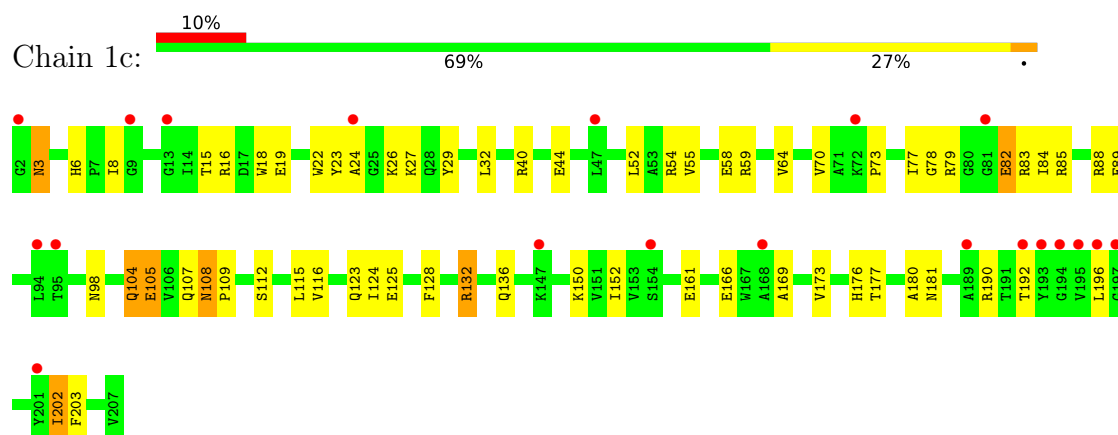
• Molecule 33: 30S ribosomal protein S2



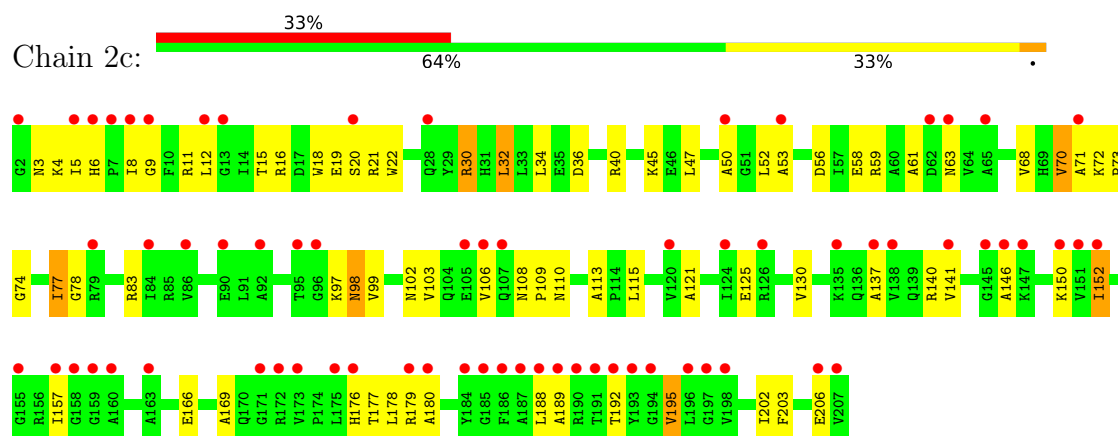
• Molecule 33: 30S ribosomal protein S2



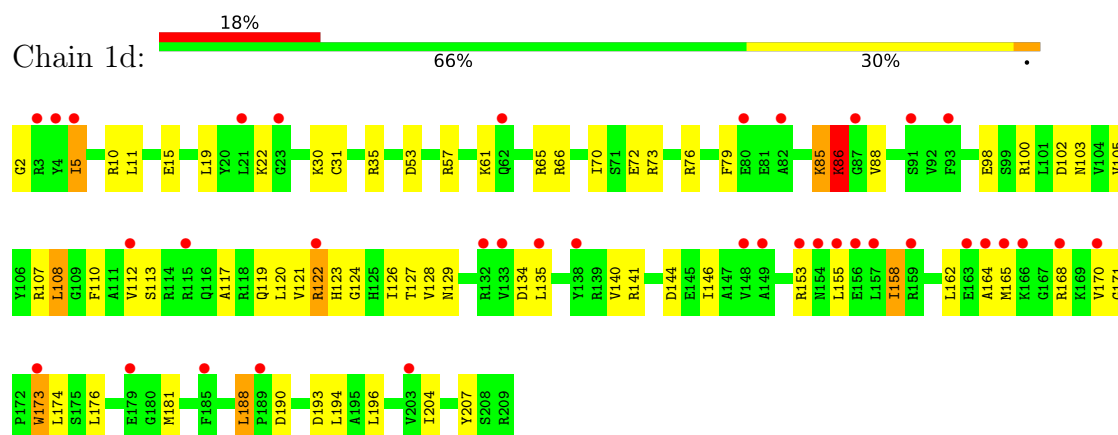
• Molecule 34: 30S ribosomal protein S3



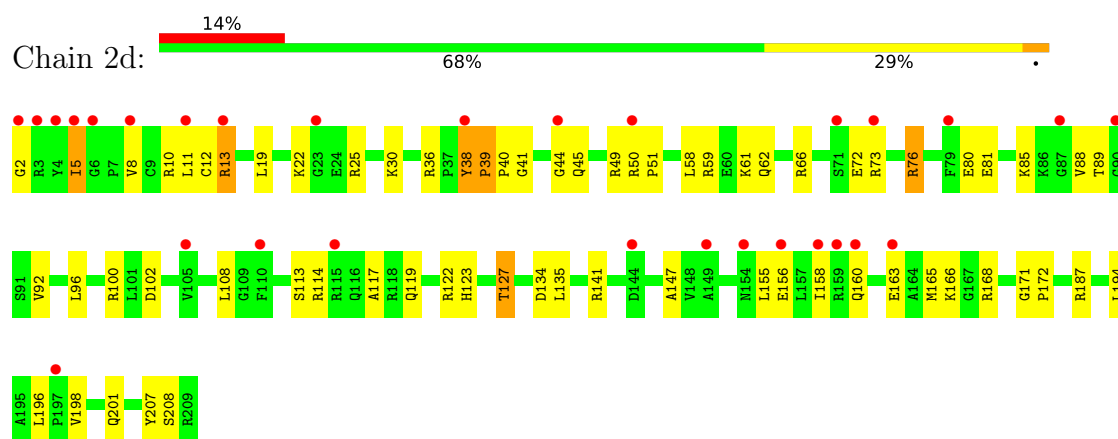
- Molecule 34: 30S ribosomal protein S3



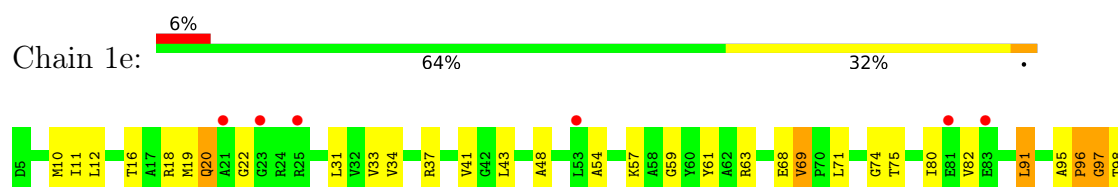
- Molecule 35: 30S ribosomal protein S4



- Molecule 35: 30S ribosomal protein S4



- Molecule 36: 30S ribosomal protein S5

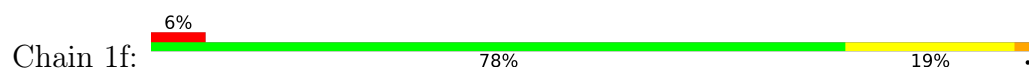




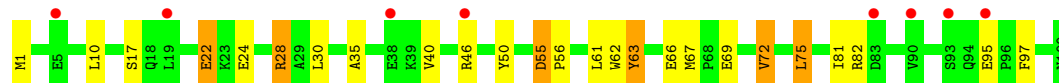
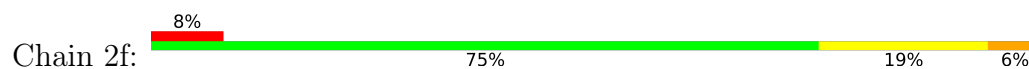
- Molecule 36: 30S ribosomal protein S5



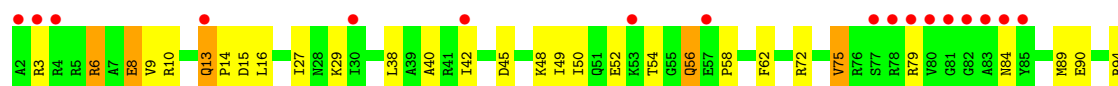
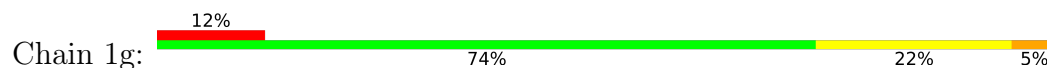
- Molecule 37: 30S ribosomal protein S6



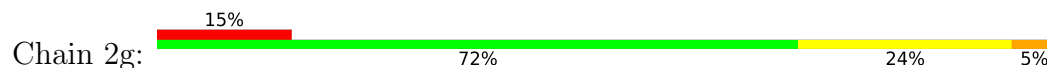
- Molecule 37: 30S ribosomal protein S6

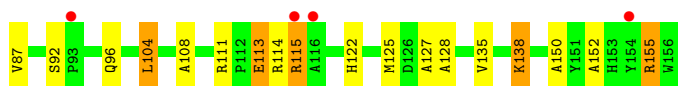


- Molecule 38: 30S ribosomal protein S7

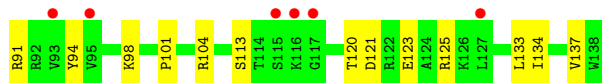


- Molecule 38: 30S ribosomal protein S7

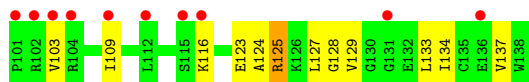
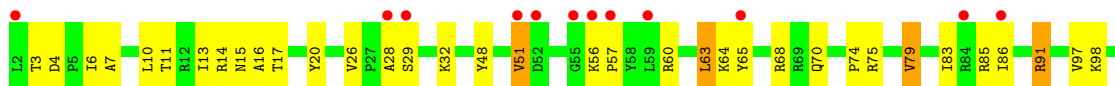




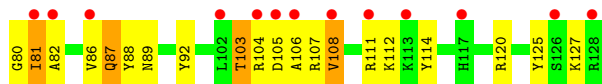
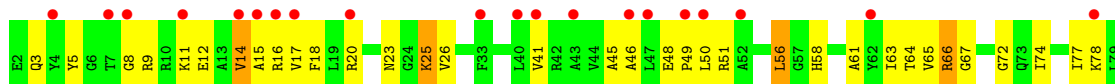
- Molecule 39: 30S ribosomal protein S8



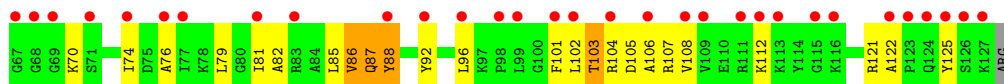
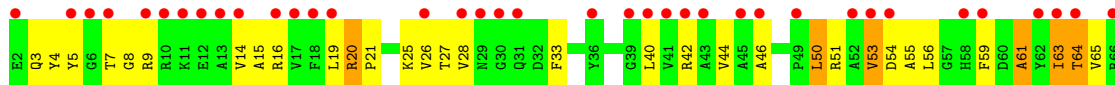
- Molecule 39: 30S ribosomal protein S8



- Molecule 40: 30S ribosomal protein S9

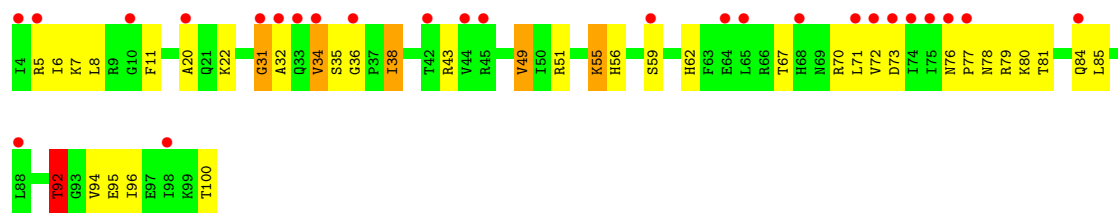


- Molecule 40: 30S ribosomal protein S9

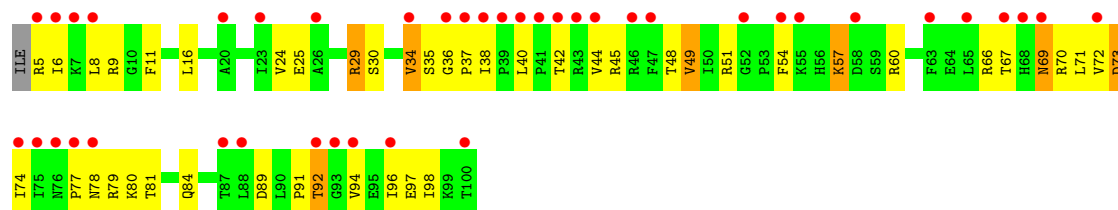
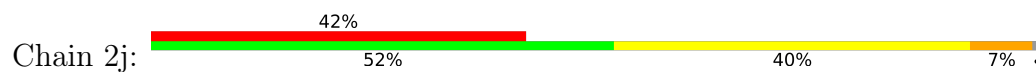


- Molecule 41: 30S ribosomal protein S10

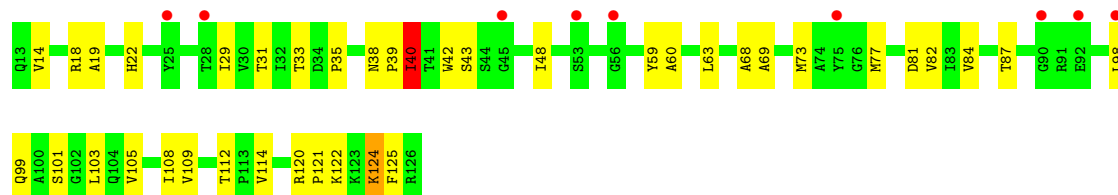




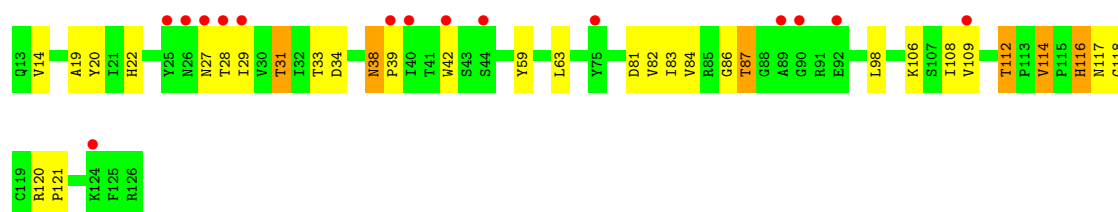
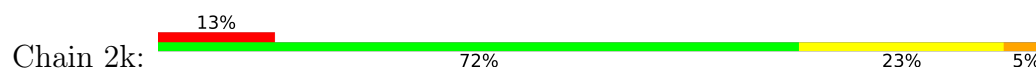
• Molecule 41: 30S ribosomal protein S10



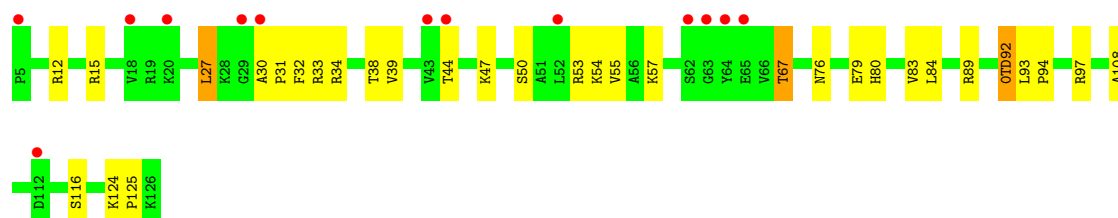
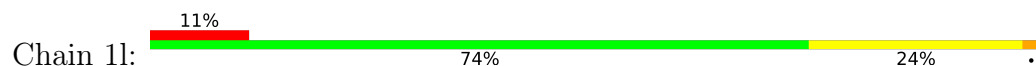
• Molecule 42: 30S ribosomal protein S11



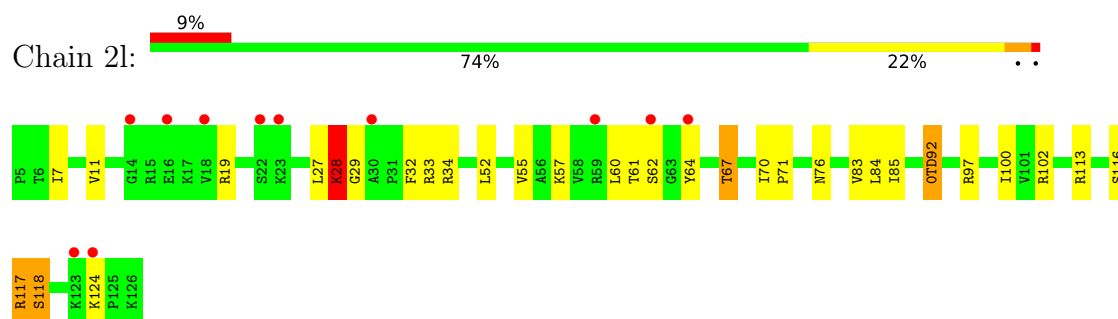
• Molecule 42: 30S ribosomal protein S11



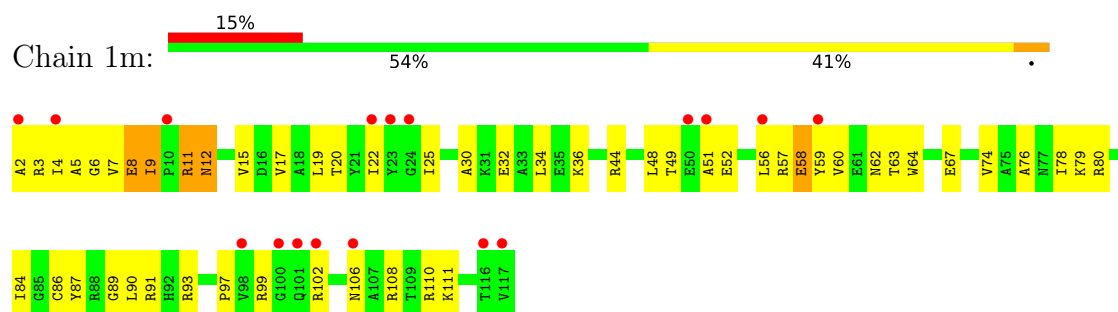
• Molecule 43: 30S ribosomal protein S12



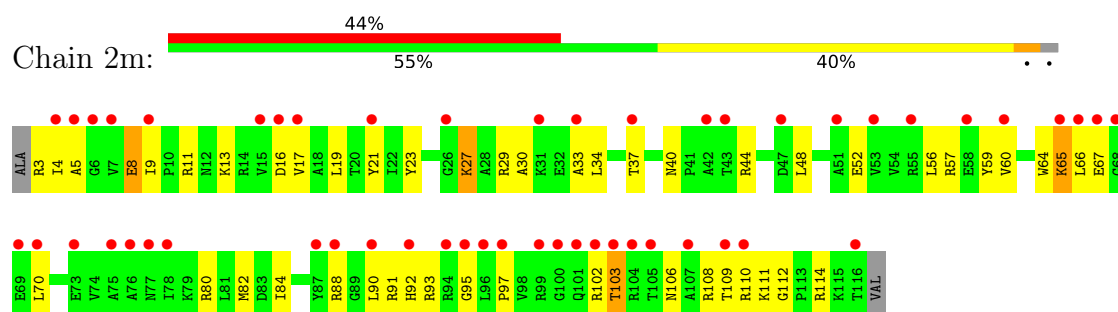
- Molecule 43: 30S ribosomal protein S12



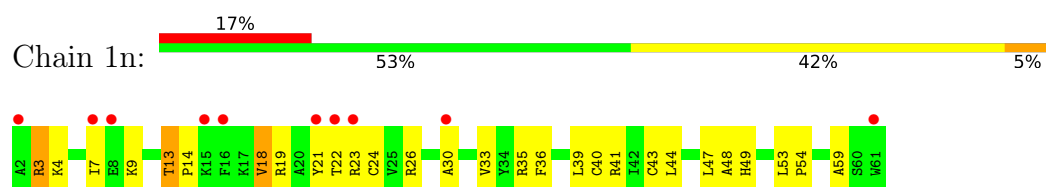
- Molecule 44: 30S ribosomal protein S13



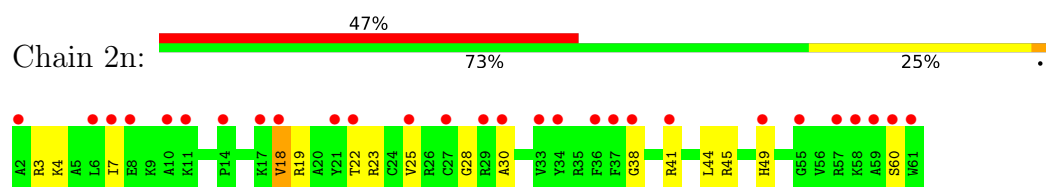
- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14 type Z



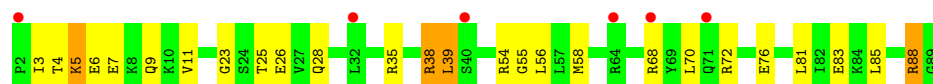
- Molecule 45: 30S ribosomal protein S14 type Z



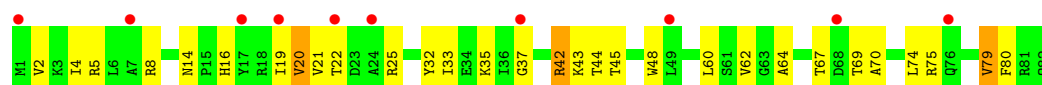
- Molecule 46: 30S ribosomal protein S15



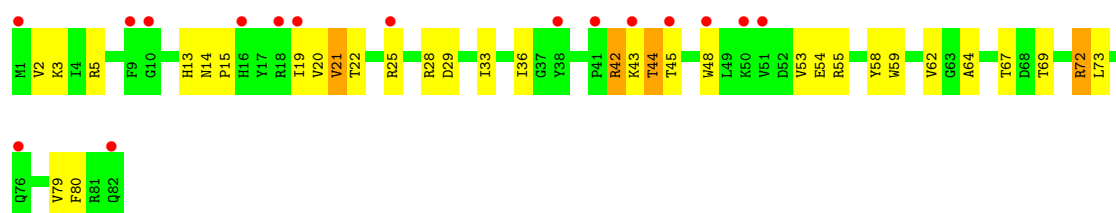
- Molecule 46: 30S ribosomal protein S15



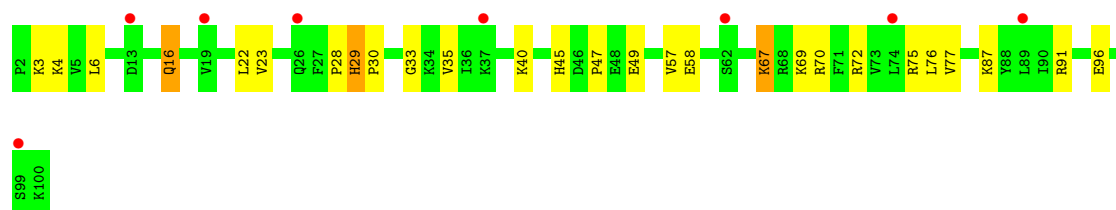
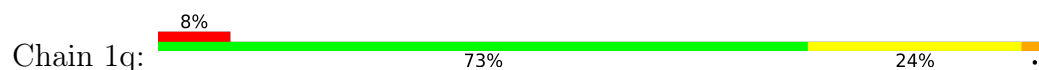
- Molecule 47: 30S ribosomal protein S16



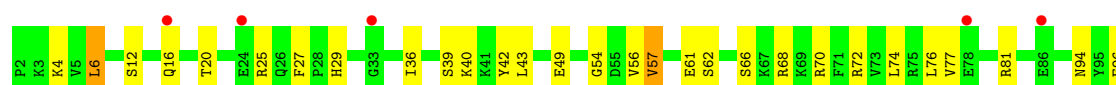
- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17

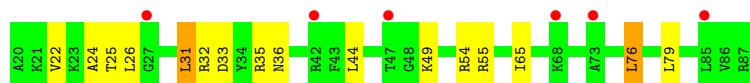
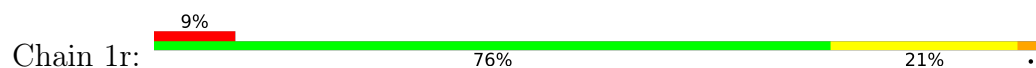


- Molecule 48: 30S ribosomal protein S17

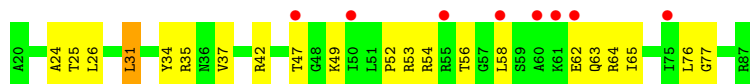




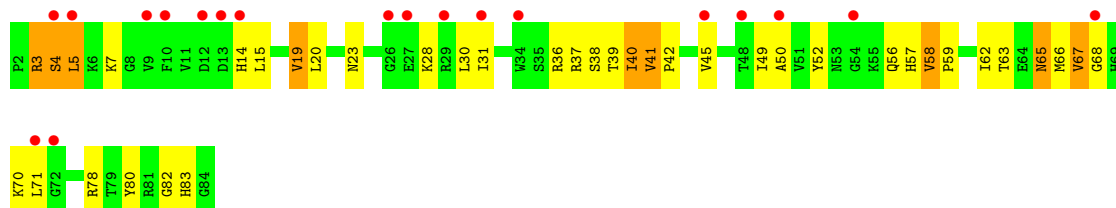
- Molecule 49: 30S ribosomal protein S18



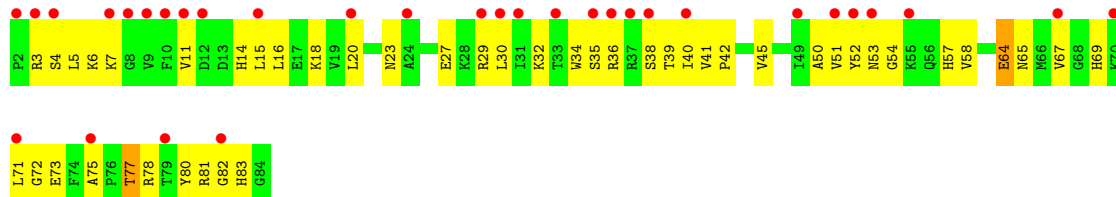
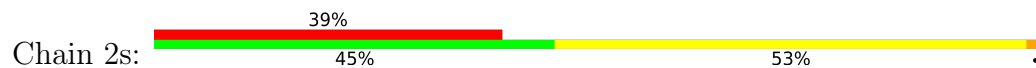
- Molecule 49: 30S ribosomal protein S18



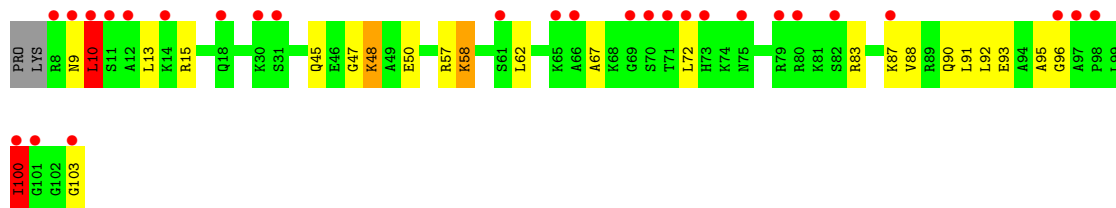
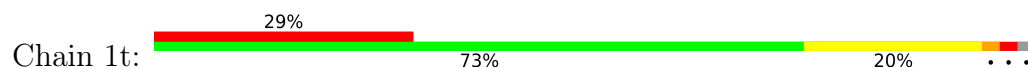
- Molecule 50: 30S ribosomal protein S19



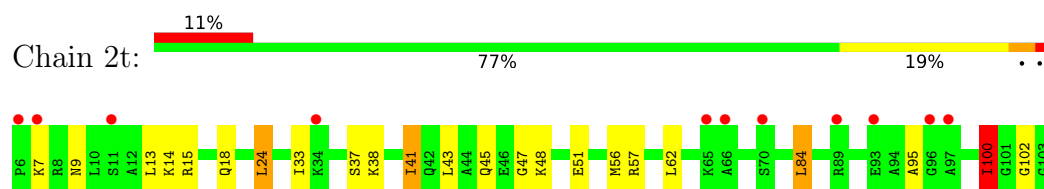
- Molecule 50: 30S ribosomal protein S19



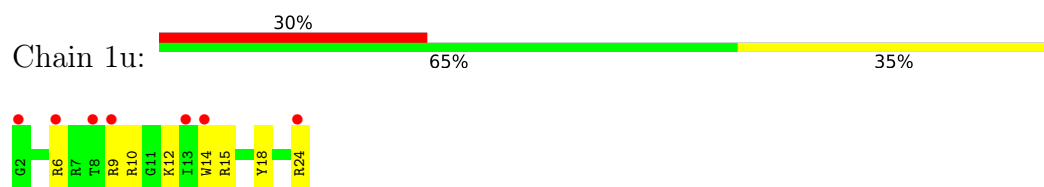
- Molecule 51: 30S ribosomal protein S20



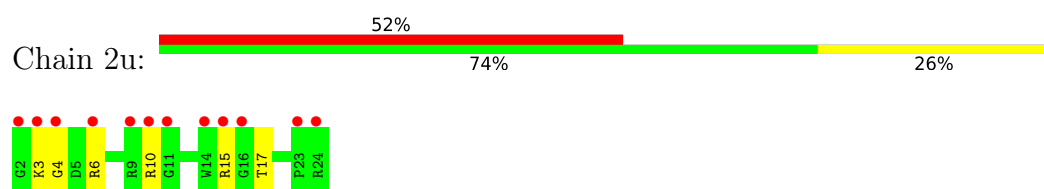
- Molecule 51: 30S ribosomal protein S20



- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx

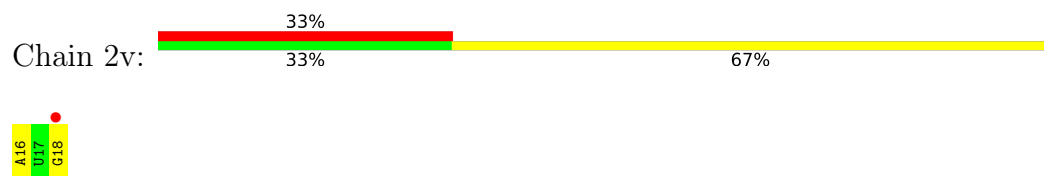


- Molecule 53: mRNA

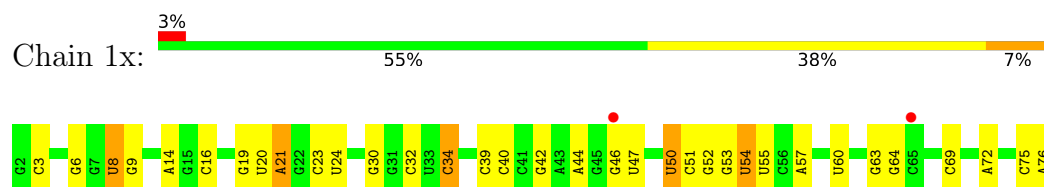


There are no outlier residues recorded for this chain.

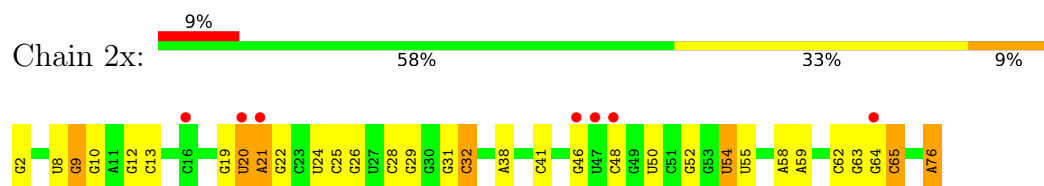
- Molecule 53: mRNA



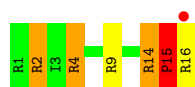
- Molecule 54: tRNAiMet



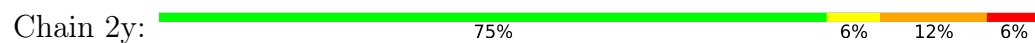
- Molecule 54: tRNAiMet



- Molecule 55: Cathelicidin-3



- Molecule 55: Cathelicidin-3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.96Å 450.13Å 622.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.62 – 2.80 48.62 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.62-2.80) 99.6 (48.62-2.80)	Depositor EDS
R_{merge}	0.51	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.81Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.249 , 0.292 0.248 , 0.290	Depositor DCC
R_{free} test set	70217 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	296108	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: MA6, 2MA, ZN, OMG, UR3, 7MG, SF4, 2MG, PSU, 0TD, OMU, 4SU, 5MC, 5MU, OMC, MG, 4OC, K, M2G

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	0.30	1/69034 (0.0%)	0.52	3/107758 (0.0%)
1	2A	0.25	1/68906 (0.0%)	0.48	1/107556 (0.0%)
2	1B	0.25	0/2879	0.47	0/4490
2	2B	0.22	0/2874	0.44	0/4482
3	1D	0.52	0/2181	0.97	2/2940 (0.1%)
3	2D	0.46	0/2186	0.95	4/2944 (0.1%)
4	1E	0.50	0/1592	0.94	2/2149 (0.1%)
4	2E	0.47	0/1592	0.98	8/2149 (0.4%)
5	1F	0.48	0/1619	0.96	3/2193 (0.1%)
5	2F	0.42	0/1615	0.96	10/2188 (0.5%)
6	1G	0.43	0/1451	0.97	7/1961 (0.4%)
6	2G	0.42	0/1449	1.03	8/1957 (0.4%)
7	1H	0.47	0/1356	0.92	2/1834 (0.1%)
7	2H	0.41	0/1350	0.95	4/1826 (0.2%)
8	1I	0.43	0/1109	0.99	4/1512 (0.3%)
8	2I	0.41	0/1091	0.96	3/1490 (0.2%)
9	1N	0.47	0/1148	0.90	0/1547
9	2N	0.38	0/1144	0.94	6/1543 (0.4%)
10	1O	0.50	0/943	0.93	0/1269
10	2O	0.43	0/943	0.90	0/1269
11	1P	0.47	0/1152	0.92	0/1533
11	2P	0.39	0/1152	0.92	4/1533 (0.3%)
12	1Q	0.55	1/1143 (0.1%)	0.95	1/1527 (0.1%)
12	2Q	0.43	0/1143	0.87	0/1527
13	1R	0.50	0/982	0.88	0/1312
13	2R	0.42	0/982	0.86	0/1312
14	1S	0.41	0/887	0.89	2/1180 (0.2%)
14	2S	0.41	0/880	0.93	0/1172
15	1T	0.43	0/1105	0.93	0/1477
15	2T	0.41	0/1097	0.89	1/1468 (0.1%)
16	1U	0.50	0/977	0.87	1/1301 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.41	0/977	0.87	2/1301 (0.2%)
17	1V	0.47	0/786	0.87	0/1053
17	2V	0.41	0/782	0.85	0/1049
18	1W	0.54	0/897	0.91	1/1205 (0.1%)
18	2W	0.44	0/897	0.90	3/1205 (0.2%)
19	1X	0.48	0/764	0.91	1/1025 (0.1%)
19	2X	0.43	0/764	0.93	1/1025 (0.1%)
20	1Y	0.48	0/823	0.95	0/1099
20	2Y	0.38	0/823	0.92	1/1100 (0.1%)
21	1Z	0.44	0/1620	1.03	9/2200 (0.4%)
21	2Z	0.43	0/1590	1.04	9/2162 (0.4%)
22	10	0.44	0/616	0.91	1/821 (0.1%)
22	20	0.38	0/616	0.91	3/821 (0.4%)
23	11	0.45	0/761	0.85	0/1013
23	21	0.40	0/766	0.85	0/1018
24	12	0.46	0/590	0.96	1/781 (0.1%)
24	22	0.37	0/594	0.86	0/785
25	13	0.49	0/474	0.90	0/635
25	23	0.38	0/469	0.85	0/630
26	14	0.47	0/559	1.14	7/754 (0.9%)
26	24	0.51	0/549	1.13	1/741 (0.1%)
27	15	0.52	0/473	0.88	1/639 (0.2%)
27	25	0.47	0/469	0.90	0/635
28	16	0.47	0/460	0.88	2/613 (0.3%)
28	26	0.42	0/456	0.85	0/608
29	17	0.54	0/426	0.95	0/561
29	27	0.47	0/426	0.88	0/561
30	18	0.50	0/525	0.92	0/691
30	28	0.43	0/525	0.87	0/691
31	19	0.44	0/310	0.87	0/407
31	29	0.38	0/310	0.89	0/407
32	1a	0.23	1/35795 (0.0%)	0.47	4/55864 (0.0%)
32	2a	0.22	1/35890 (0.0%)	0.47	7/56012 (0.0%)
33	1b	0.46	0/1876	1.07	15/2533 (0.6%)
33	2b	0.44	0/1860	1.00	9/2518 (0.4%)
34	1c	0.44	0/1582	0.93	3/2137 (0.1%)
34	2c	0.44	0/1566	1.03	9/2119 (0.4%)
35	1d	0.46	0/1695	1.01	7/2274 (0.3%)
35	2d	0.40	0/1698	0.96	6/2277 (0.3%)
36	1e	0.43	0/1149	0.96	2/1548 (0.1%)
36	2e	0.42	0/1149	1.01	8/1548 (0.5%)
37	1f	0.43	0/827	0.91	2/1120 (0.2%)
37	2f	0.40	0/829	0.91	2/1123 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.40	0/1254	0.89	1/1683 (0.1%)
38	2g	0.39	0/1248	0.89	0/1676
39	1h	0.40	0/1118	0.93	3/1506 (0.2%)
39	2h	0.37	0/1108	0.94	5/1494 (0.3%)
40	1i	0.40	0/1005	0.93	2/1351 (0.1%)
40	2i	0.43	0/985	0.97	4/1329 (0.3%)
41	1j	0.46	0/732	1.07	6/993 (0.6%)
41	2j	0.50	0/723	1.01	2/984 (0.2%)
42	1k	0.49	0/849	0.94	3/1150 (0.3%)
42	2k	0.60	2/848 (0.2%)	0.97	5/1149 (0.4%)
43	1l	0.40	0/937	0.92	5/1260 (0.4%)
43	2l	0.38	0/937	0.93	3/1260 (0.2%)
44	1m	0.39	0/924	0.98	4/1242 (0.3%)
44	2m	0.42	0/905	0.98	4/1217 (0.3%)
45	1n	0.39	0/501	0.92	2/664 (0.3%)
45	2n	0.39	0/501	0.85	0/664
46	1o	0.42	0/739	0.99	3/985 (0.3%)
46	2o	0.37	0/739	0.87	0/985
47	1p	0.40	0/697	0.93	0/939
47	2p	0.42	0/693	0.87	1/935 (0.1%)
48	1q	0.38	0/836	0.90	3/1117 (0.3%)
48	2q	0.37	0/836	0.84	3/1117 (0.3%)
49	1r	0.38	0/560	0.87	1/746 (0.1%)
49	2r	0.40	0/560	0.85	0/746
50	1s	0.40	0/663	1.01	2/895 (0.2%)
50	2s	0.42	0/660	1.00	3/893 (0.3%)
51	1t	0.42	0/734	0.97	1/969 (0.1%)
51	2t	0.42	0/736	0.92	0/976
52	1u	0.36	0/203	0.95	0/266
52	2u	0.40	0/203	1.00	0/266
53	1v	0.23	0/72	0.38	0/110
53	2v	0.26	0/72	0.51	0/110
54	1x	0.24	0/1725	0.41	0/2689
54	2x	0.25	1/1725 (0.1%)	0.40	0/2689
55	1y	0.51	0/152	1.48	3/203 (1.5%)
55	2y	0.45	0/152	1.50	3/203 (1.5%)
All	All	0.32	8/312307 (0.0%)	0.64	265/467169 (0.1%)

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
55	1y	0	1
55	2y	0	1
All	All	0	4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	2k	116	HIS	CE1-NE2	8.01	1.40	1.32
12	1Q	41	TRP	NE1-CE2	7.58	1.45	1.37
42	2k	116	HIS	CD2-NE2	-7.46	1.29	1.37
54	2x	8	4SU	O3'-P	5.76	1.62	1.56
32	2a	1498	UR3	O3'-P	5.49	1.61	1.56
1	1A	2564	OMU	O3'-P	5.39	1.61	1.56
32	1a	1498	UR3	O3'-P	5.29	1.61	1.56
1	2A	2552	OMU	O3'-P	5.02	1.61	1.56

All (265) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1208	C	OP1-P-OP2	-13.64	78.69	119.60
32	1a	1520	G	OP1-P-OP2	-13.18	80.06	119.60
32	2a	1208	C	O5'-P-OP1	-11.76	72.74	108.00
32	1a	1520	G	O5'-P-OP1	-11.15	74.54	108.00
32	2a	1207	2MG	OP2-P-O3'	-10.12	77.64	108.00
46	1o	87	ILE	N-CA-C	9.72	120.29	112.12
55	1y	14	ARG	CA-C-N	9.72	131.99	119.84
55	1y	14	ARG	C-N-CA	9.72	131.99	119.84
24	12	69	ARG	N-CA-C	9.40	124.58	113.20
32	2a	1207	2MG	OP1-P-O3'	9.05	135.16	108.00
55	2y	15	PRO	O-C-N	-8.80	110.76	122.64
55	2y	14	ARG	CA-C-N	8.71	130.72	119.84
55	2y	14	ARG	C-N-CA	8.71	130.72	119.84
32	1a	1520	G	O5'-P-OP2	8.68	134.03	108.00
32	2a	351	G	OP1-P-O3'	-8.56	82.33	108.00
21	2Z	14	LYS	CA-C-N	8.54	129.06	119.32
21	2Z	14	LYS	C-N-CA	8.54	129.06	119.32
35	1d	188	LEU	CA-C-N	8.41	130.35	119.84
35	1d	188	LEU	C-N-CA	8.41	130.35	119.84
26	24	19	GLY	N-CA-C	-8.21	103.16	115.32
42	1k	40	ILE	N-CA-C	-8.20	105.23	112.12
32	2a	1208	C	O5'-P-OP2	8.05	132.16	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	2b	19	HIS	N-CA-C	8.00	120.28	108.60
50	1s	58	VAL	N-CA-C	7.84	114.69	107.56
36	2e	98	THR	N-CA-C	7.71	119.59	111.03
55	1y	15	PRO	O-C-N	-7.60	112.38	122.64
21	2Z	67	LEU	CA-C-N	7.59	129.33	119.84
21	2Z	67	LEU	C-N-CA	7.59	129.33	119.84
33	1b	128	GLU	N-CA-C	-7.57	102.35	114.09
34	2c	125	GLU	N-CA-C	-7.44	103.67	112.89
50	1s	67	VAL	N-CA-C	7.44	118.03	110.82
21	1Z	193	GLU	CA-C-N	7.39	127.15	119.76
21	1Z	193	GLU	C-N-CA	7.39	127.15	119.76
21	2Z	120	ILE	N-CA-C	7.35	117.33	110.42
34	2c	108	ASN	CA-C-N	7.34	126.97	119.56
34	2c	108	ASN	C-N-CA	7.34	126.97	119.56
16	2U	9	VAL	N-CA-C	7.27	117.36	110.53
32	2a	351	G	OP2-P-O3'	-7.26	86.20	108.00
6	2G	144	ILE	N-CA-C	7.20	118.17	106.72
33	2b	25	ASN	CA-C-N	7.18	126.86	119.82
33	2b	25	ASN	C-N-CA	7.18	126.86	119.82
6	1G	96	ARG	CB-CA-C	-7.08	108.40	116.54
18	2W	13	SER	CA-C-N	7.00	128.59	119.84
18	2W	13	SER	C-N-CA	7.00	128.59	119.84
44	2m	112	GLY	CA-C-N	6.98	127.01	119.89
44	2m	112	GLY	C-N-CA	6.98	127.01	119.89
50	2s	29	ARG	N-CA-C	6.92	118.25	108.00
7	2H	9	ILE	N-CA-C	6.91	113.85	107.56
35	1d	190	ASP	N-CA-C	-6.84	100.40	110.52
37	1f	55	ASP	CA-C-N	6.79	126.49	119.56
37	1f	55	ASP	C-N-CA	6.79	126.49	119.56
5	2F	9	ILE	CA-C-N	6.78	126.74	119.76
5	2F	9	ILE	C-N-CA	6.78	126.74	119.76
35	2d	171	GLY	CA-C-N	6.77	128.31	119.84
35	2d	171	GLY	C-N-CA	6.77	128.31	119.84
37	2f	55	ASP	CA-C-N	6.76	126.45	119.56
37	2f	55	ASP	C-N-CA	6.76	126.45	119.56
15	2T	95	ARG	N-CA-C	-6.71	103.47	112.94
7	1H	54	ARG	CA-C-N	6.66	128.16	119.84
7	1H	54	ARG	C-N-CA	6.66	128.16	119.84
8	1I	110	ASP	CA-C-N	6.65	126.15	119.24
8	1I	110	ASP	C-N-CA	6.65	126.15	119.24
3	2D	35	LYS	CA-C-N	-6.65	112.81	119.99
3	2D	35	LYS	C-N-CA	-6.65	112.81	119.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	1b	193	ASP	CA-C-N	6.64	125.87	118.97
33	1b	193	ASP	C-N-CA	6.64	125.87	118.97
35	1d	171	GLY	CA-C-N	6.54	128.01	119.84
35	1d	171	GLY	C-N-CA	6.54	128.01	119.84
41	1j	34	VAL	N-CA-C	6.52	116.11	106.85
48	2q	77	VAL	N-CA-C	-6.51	106.65	112.12
34	2c	59	ARG	N-CA-C	6.50	119.30	109.23
8	2I	124	GLY	N-CA-C	6.49	118.60	110.29
34	2c	72	LYS	CA-C-N	6.49	126.42	119.28
34	2c	72	LYS	C-N-CA	6.49	126.42	119.28
45	1n	13	THR	CA-C-N	6.44	127.89	119.84
45	1n	13	THR	C-N-CA	6.44	127.89	119.84
33	1b	18	GLY	N-CA-C	6.42	118.58	112.04
33	1b	23	ARG	N-CA-C	-6.39	102.73	111.56
36	2e	127	ASN	CA-C-N	6.38	125.87	119.24
36	2e	127	ASN	C-N-CA	6.38	125.87	119.24
5	1F	9	ILE	N-CA-C	6.34	114.96	107.73
33	1b	19	HIS	N-CA-C	6.32	116.78	107.88
3	1D	46	GLN	N-CA-C	-6.31	105.74	113.50
41	1j	92	THR	N-CA-C	6.29	117.80	111.07
35	2d	38	TYR	CA-C-N	6.29	126.86	120.38
35	2d	38	TYR	C-N-CA	6.29	126.86	120.38
21	1Z	198	LYS	N-CA-C	6.24	118.97	110.55
35	1d	19	LEU	N-CA-C	-6.23	100.04	109.95
14	1S	58	LEU	N-CA-C	6.23	118.75	110.53
33	2b	200	ILE	N-CA-C	6.19	116.84	108.17
20	2Y	93	GLY	N-CA-C	-6.18	106.56	113.79
12	1Q	41	TRP	CD2-CE2-CZ2	6.16	128.56	122.40
43	2I	28	LYS	N-CA-C	6.15	119.73	111.24
43	2I	118	SER	N-CA-C	-6.14	104.51	111.14
41	2j	44	VAL	N-CA-C	6.11	116.67	107.80
4	2E	190	GLY	CA-C-N	6.10	127.31	120.66
4	2E	190	GLY	C-N-CA	6.10	127.31	120.66
34	2c	19	GLU	N-CA-C	-6.09	105.43	112.92
21	1Z	53	ILE	N-CA-C	-6.05	105.48	111.77
44	1m	9	ILE	CA-C-N	6.03	127.38	119.84
44	1m	9	ILE	C-N-CA	6.03	127.38	119.84
47	2p	80	PHE	N-CA-C	6.03	120.64	113.28
5	2F	24	LEU	CA-C-N	6.01	126.03	119.90
5	2F	24	LEU	C-N-CA	6.01	126.03	119.90
36	2e	69	VAL	CA-C-N	5.99	127.33	119.84
36	2e	69	VAL	C-N-CA	5.99	127.33	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	1h	44	PHE	N-CA-C	-5.99	106.13	113.50
6	2G	31	VAL	CA-C-N	5.96	127.29	119.84
6	2G	31	VAL	C-N-CA	5.96	127.29	119.84
8	1I	13	GLY	N-CA-C	5.93	118.58	110.69
48	1q	67	LYS	N-CA-C	-5.92	102.67	110.43
6	2G	77	ILE	N-CA-C	5.92	116.65	108.12
21	1Z	157	LEU	CA-C-N	5.92	126.47	120.38
21	1Z	157	LEU	C-N-CA	5.92	126.47	120.38
6	1G	127	GLY	N-CA-C	-5.92	106.87	113.79
34	2c	77	ILE	N-CA-C	5.91	116.69	110.72
4	2E	72	VAL	N-CA-C	5.90	117.25	108.46
21	1Z	133	ILE	CA-C-N	5.88	125.78	119.85
21	1Z	133	ILE	C-N-CA	5.88	125.78	119.85
5	2F	21	ALA	CA-C-N	5.85	132.23	121.70
5	2F	21	ALA	C-N-CA	5.85	132.23	121.70
36	1e	105	VAL	CA-C-N	-5.83	113.67	119.56
36	1e	105	VAL	C-N-CA	-5.83	113.67	119.56
46	1o	21	ASP	N-CA-C	5.82	118.68	109.96
43	2l	19	ARG	N-CA-C	5.81	118.40	110.55
3	2D	251	GLY	N-CA-C	5.78	121.66	114.37
9	2N	94	HIS	CA-C-N	5.78	125.47	119.05
9	2N	94	HIS	C-N-CA	5.78	125.47	119.05
11	2P	26	GLY	N-CA-C	-5.75	107.71	115.36
41	1j	76	ASN	CA-C-N	5.72	127.00	119.84
41	1j	76	ASN	C-N-CA	5.72	127.00	119.84
5	2F	168	ARG	N-CA-C	5.70	117.29	111.14
40	1i	11	LYS	CB-CA-C	-5.69	109.99	116.54
21	1Z	157	LEU	N-CA-C	5.67	116.81	109.72
33	1b	233	SER	CA-C-N	5.67	125.68	119.90
33	1b	233	SER	C-N-CA	5.67	125.68	119.90
6	1G	58	GLN	N-CA-C	-5.66	105.10	112.23
26	14	68	ARG	N-CA-C	5.64	118.83	110.48
26	14	52	THR	N-CA-C	-5.64	103.55	110.65
1	1A	1700	G	P-O3'-C3'	5.63	128.65	120.20
16	1U	116	ALA	N-CA-C	5.62	118.18	111.71
26	14	28	LYS	CA-C-N	5.62	125.47	119.28
26	14	28	LYS	C-N-CA	5.62	125.47	119.28
33	2b	186	ALA	N-CA-C	5.62	117.65	108.55
21	2Z	53	ILE	N-CA-C	-5.61	105.94	111.88
44	1m	58	GLU	N-CA-C	5.61	117.39	111.28
43	1l	44	THR	CA-C-N	5.60	126.07	120.52
43	1l	44	THR	C-N-CA	5.60	126.07	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	1o	23	GLY	N-CA-C	5.60	123.53	114.90
3	1D	229	VAL	CB-CA-C	-5.59	104.60	112.14
4	1E	52	LEU	CA-C-N	5.55	125.46	119.85
4	1E	52	LEU	C-N-CA	5.55	125.46	119.85
39	2h	79	VAL	N-CA-C	-5.55	107.04	111.81
36	2e	92	LYS	CA-C-N	5.53	125.53	119.89
36	2e	92	LYS	C-N-CA	5.53	125.53	119.89
33	2b	129	GLU	N-CA-C	-5.53	106.31	113.16
11	2P	22	GLY	CA-C-N	5.51	124.70	118.97
11	2P	22	GLY	C-N-CA	5.51	124.70	118.97
8	2I	110	ASP	CA-C-N	5.50	124.96	119.24
8	2I	110	ASP	C-N-CA	5.50	124.96	119.24
33	2b	130	ARG	CA-C-N	5.50	125.80	119.92
33	2b	130	ARG	C-N-CA	5.50	125.80	119.92
18	1W	111	HIS	N-CA-C	5.48	117.64	109.25
40	2i	61	ALA	N-CA-C	5.48	118.35	108.48
48	1q	29	HIS	CA-C-N	5.47	125.82	119.47
48	1q	29	HIS	C-N-CA	5.47	125.82	119.47
33	1b	16	HIS	N-CA-C	5.46	122.44	110.80
7	2H	70	THR	N-CA-C	5.46	116.91	111.07
33	2b	23	ARG	N-CA-C	-5.46	104.02	111.56
6	1G	114	ILE	N-CA-C	5.45	116.73	109.37
38	1g	3	ARG	N-CA-C	5.44	117.02	111.14
6	2G	178	PHE	CA-C-N	5.44	126.64	119.84
6	2G	178	PHE	C-N-CA	5.44	126.64	119.84
6	1G	45	GLU	N-CA-C	-5.43	105.92	112.54
41	2j	73	ASP	N-CA-C	5.42	117.51	108.02
5	1F	170	LEU	CA-C-N	5.42	125.24	119.28
5	1F	170	LEU	C-N-CA	5.42	125.24	119.28
28	16	40	CYS	CA-C-N	5.42	125.03	119.56
28	16	40	CYS	C-N-CA	5.42	125.03	119.56
42	1k	38	ASN	CA-C-N	5.41	125.41	119.89
42	1k	38	ASN	C-N-CA	5.41	125.41	119.89
6	1G	31	VAL	CA-C-N	5.40	126.59	119.84
6	1G	31	VAL	C-N-CA	5.40	126.59	119.84
40	2i	63	ILE	N-CA-C	5.39	116.04	108.17
33	1b	17	PHE	N-CA-C	5.38	122.27	110.80
33	1b	149	LEU	N-CA-C	5.38	119.48	113.02
26	14	40	HIS	CA-C-N	5.38	126.57	119.84
26	14	40	HIS	C-N-CA	5.38	126.57	119.84
4	2E	89	ASP	N-CA-C	-5.38	106.76	113.38
16	2U	73	GLY	N-CA-C	5.38	123.28	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	1i	58	HIS	N-CA-C	5.37	118.93	112.38
42	2k	114	VAL	CA-C-N	5.37	125.83	120.14
42	2k	114	VAL	C-N-CA	5.37	125.83	120.14
42	2k	38	ASN	CA-C-N	5.35	125.36	119.90
42	2k	38	ASN	C-N-CA	5.35	125.36	119.90
9	2N	39	ARG	CA-C-N	5.35	125.17	119.28
9	2N	39	ARG	C-N-CA	5.35	125.17	119.28
41	1j	38	ILE	N-CA-C	5.32	112.40	107.56
6	2G	127	GLY	N-CA-C	-5.31	107.58	113.79
21	2Z	107	THR	CA-C-N	5.30	125.20	119.85
21	2Z	107	THR	C-N-CA	5.30	125.20	119.85
5	2F	151	SER	N-CA-C	-5.29	106.83	113.28
43	1l	30	ALA	CA-C-N	5.28	124.61	118.85
43	1l	30	ALA	C-N-CA	5.28	124.61	118.85
14	1S	111	GLU	N-CA-C	5.27	117.22	108.20
34	1c	152	ILE	N-CA-C	5.27	115.71	108.12
34	1c	82	GLU	N-CA-C	5.27	118.04	111.24
4	2E	102	VAL	N-CA-C	5.26	117.20	108.99
22	20	14	ARG	N-CA-C	5.24	118.27	110.14
33	1b	232	PRO	N-CA-C	5.24	118.82	111.33
33	1b	187	LEU	N-CA-C	-5.24	102.11	109.96
49	1r	22	VAL	N-CA-C	5.22	117.58	111.05
39	1h	75	ARG	CA-C-N	5.22	125.15	119.78
39	1h	75	ARG	C-N-CA	5.22	125.15	119.78
5	2F	91	GLY	N-CA-C	-5.21	105.92	112.23
44	2m	40	ASN	CA-C-N	5.20	124.92	119.82
44	2m	40	ASN	C-N-CA	5.20	124.92	119.82
35	1d	86	LYS	N-CA-C	5.19	117.41	110.35
22	20	82	ARG	CA-C-N	5.19	125.19	119.90
22	20	82	ARG	C-N-CA	5.19	125.19	119.90
6	2G	89	GLY	N-CA-C	5.19	118.27	110.18
44	1m	6	GLY	N-CA-C	-5.18	108.48	115.21
32	1a	1442	G	P-O3'-C3'	5.17	125.90	119.70
41	1j	51	ARG	N-CA-C	5.17	116.60	110.97
42	2k	116	HIS	ND1-CG-CD2	-5.16	100.94	106.10
33	1b	164	VAL	N-CA-C	5.14	115.89	108.48
3	2D	229	VAL	CB-CA-C	-5.14	105.19	112.14
39	2h	75	ARG	CA-C-N	5.14	125.08	119.78
39	2h	75	ARG	C-N-CA	5.14	125.08	119.78
26	14	36	CYS	N-CA-C	5.14	114.92	108.45
33	1b	78	GLN	N-CA-C	5.14	116.57	110.97
9	2N	125	GLY	CA-C-N	5.14	125.21	119.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	2N	125	GLY	C-N-CA	5.14	125.21	119.87
27	15	27	PRO	O-C-N	5.13	123.67	121.31
4	2E	76	ARG	N-CA-C	5.13	116.95	111.36
35	2d	208	SER	N-CA-C	-5.13	107.53	112.97
1	1A	1255	A	C4'-C3'-O3'	5.13	117.09	109.40
4	2E	73	GLU	CA-C-N	5.13	125.12	119.89
4	2E	73	GLU	C-N-CA	5.13	125.12	119.89
21	2Z	52	SER	CB-CA-C	-5.12	109.17	116.34
19	1X	69	TYR	N-CA-C	5.11	117.69	107.62
43	1l	38	THR	N-CA-C	-5.10	105.90	112.68
7	2H	38	SER	CA-C-N	5.10	125.39	119.47
7	2H	38	SER	C-N-CA	5.10	125.39	119.47
50	2s	29	ARG	CB-CA-C	-5.09	109.21	116.34
22	10	65	GLY	N-CA-C	5.09	116.81	110.29
8	1I	19	VAL	N-CA-C	5.08	116.22	108.80
50	2s	67	VAL	N-CA-C	5.08	115.37	110.74
39	2h	134	ILE	N-CA-C	5.08	115.31	110.53
48	2q	29	HIS	CA-C-N	5.08	125.36	119.47
48	2q	29	HIS	C-N-CA	5.08	125.36	119.47
1	2A	1992	G	C2'-C3'-O3'	5.07	117.11	109.50
36	2e	48	ALA	N-CA-C	5.06	112.58	108.07
34	1c	202	ILE	N-CA-C	5.05	115.13	107.75
5	2F	9	ILE	N-CA-C	5.05	113.48	107.73
35	2d	39	PRO	N-CA-C	5.05	116.86	110.70
1	1A	1700	G	C2'-C3'-O3'	5.04	117.07	109.50
11	2P	65	ARG	N-CA-C	5.04	117.38	108.75
40	2i	20	ARG	CA-C-N	5.04	125.32	119.93
40	2i	20	ARG	C-N-CA	5.04	125.32	119.93
19	2X	44	GLU	N-CA-C	5.02	116.45	111.07
34	2c	146	ALA	N-CA-C	5.02	117.18	110.35
51	1t	88	VAL	N-CA-C	5.02	115.24	110.42
18	2W	31	GLU	N-CA-C	-5.00	105.91	111.36
39	2h	70	GLN	N-CA-C	-5.00	103.80	110.55

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	1b	231	GLU	Peptide
55	1y	15	PRO	Mainchain
26	24	59	PHE	Peptide
55	2y	15	PRO	Mainchain

5.2 Too-close contacts ⓘ

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	61872	0	31199	610	0
1	2A	61761	0	31142	675	0
2	1B	2575	0	1304	20	0
2	2B	2571	0	1308	30	0
3	1D	2131	0	2207	51	0
3	2D	2136	0	2218	43	0
4	1E	1559	0	1618	36	0
4	2E	1559	0	1618	33	0
5	1F	1584	0	1625	32	0
5	2F	1580	0	1619	49	0
6	1G	1426	0	1445	63	0
6	2G	1424	0	1441	65	0
7	1H	1330	0	1407	39	0
7	2H	1324	0	1402	42	0
8	1I	1094	0	1127	21	0
8	2I	1076	0	1094	26	0
9	1N	1121	0	1195	28	0
9	2N	1117	0	1184	22	0
10	1O	933	0	996	8	0
10	2O	933	0	996	20	0
11	1P	1135	0	1212	30	0
11	2P	1135	0	1212	26	0
12	1Q	1122	0	1179	26	0
12	2Q	1122	0	1178	30	0
13	1R	968	0	1033	15	0
13	2R	968	0	1032	17	0
14	1S	877	0	938	22	0
14	2S	870	0	923	21	0
15	1T	1091	0	1151	30	0
15	2T	1083	0	1136	24	0
16	1U	959	0	1019	16	0
16	2U	959	0	1019	18	0
17	1V	775	0	841	10	0
17	2V	771	0	830	15	0
18	1W	886	0	940	9	0
18	2W	886	0	940	15	0
19	1X	750	0	814	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	15	0
20	1Y	810	0	892	18	0
20	2Y	810	0	887	17	0
21	1Z	1587	0	1598	39	0
21	2Z	1557	0	1564	53	0
22	10	608	0	622	15	0
22	20	608	0	621	11	0
23	11	754	0	823	11	0
23	21	759	0	837	24	0
24	12	588	0	643	10	0
24	22	592	0	654	7	0
25	13	469	0	518	9	0
25	23	464	0	514	12	0
26	14	546	0	522	24	0
26	24	536	0	514	30	0
27	15	459	0	476	12	0
27	25	455	0	465	8	0
28	16	453	0	473	10	0
28	26	449	0	469	10	0
29	17	418	0	467	10	0
29	27	418	0	467	10	0
30	18	517	0	582	17	0
30	28	517	0	582	12	0
31	19	307	0	335	6	0
31	29	307	0	335	7	0
32	1a	32246	0	16295	472	0
32	2a	32331	0	16339	508	0
33	1b	1842	0	1862	76	0
33	2b	1825	0	1828	71	0
34	1c	1558	0	1557	44	0
34	2c	1542	0	1517	47	0
35	1d	1665	0	1687	56	0
35	2d	1668	0	1703	50	0
36	1e	1133	0	1190	34	0
36	2e	1133	0	1191	40	0
37	1f	814	0	808	14	0
37	2f	816	0	808	12	0
38	1g	1235	0	1249	25	0
38	2g	1229	0	1238	33	0
39	1h	1098	0	1143	30	0
39	2h	1088	0	1126	30	0
40	1i	986	0	990	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	966	0	953	35	0
41	1j	719	0	672	26	0
41	2j	710	0	661	36	0
42	1k	834	0	838	22	0
42	2k	833	0	836	17	0
43	1l	932	0	981	18	0
43	2l	932	0	981	20	0
44	1m	914	0	954	31	0
44	2m	895	0	920	34	0
45	1n	492	0	529	18	0
45	2n	492	0	529	13	0
46	1o	728	0	760	19	0
46	2o	728	0	760	17	0
47	1p	681	0	697	22	0
47	2p	677	0	686	23	0
48	1q	823	0	891	22	0
48	2q	823	0	891	16	0
49	1r	555	0	618	11	0
49	2r	555	0	618	14	0
50	1s	648	0	658	26	0
50	2s	645	0	635	37	0
51	1t	732	0	809	15	0
51	2t	733	0	795	13	0
52	1u	199	0	208	9	0
52	2u	199	0	208	5	0
53	1v	65	0	33	0	0
53	2v	65	0	33	3	0
54	1x	1625	0	829	13	0
54	2x	1625	0	829	20	0
55	1y	147	0	170	6	0
55	2y	147	0	170	6	0
56	10	8	0	0	0	0
56	11	2	0	0	0	0
56	13	2	0	0	0	0
56	15	7	0	0	0	0
56	17	2	0	0	0	0
56	18	1	0	0	0	0
56	19	3	0	0	0	0
56	1A	973	0	0	0	0
56	1B	27	0	0	0	0
56	1D	14	0	0	0	0
56	1E	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1F	10	0	0	0	0
56	1G	3	0	0	0	0
56	1H	2	0	0	0	0
56	1N	4	0	0	0	0
56	1P	4	0	0	0	0
56	1Q	6	0	0	0	0
56	1R	4	0	0	0	0
56	1S	1	0	0	0	0
56	1T	1	0	0	0	0
56	1U	3	0	0	0	0
56	1V	3	0	0	0	0
56	1W	3	0	0	0	0
56	1X	1	0	0	0	0
56	1a	240	0	0	0	0
56	1b	1	0	0	0	0
56	1d	5	0	0	0	0
56	1e	1	0	0	0	0
56	1f	1	0	0	0	0
56	1g	1	0	0	0	0
56	1h	1	0	0	0	0
56	1i	1	0	0	0	0
56	1l	3	0	0	0	0
56	1n	1	0	0	0	0
56	1o	2	0	0	0	0
56	1q	1	0	0	0	0
56	1t	1	0	0	0	0
56	1x	13	0	0	0	0
56	20	5	0	0	0	0
56	23	2	0	0	0	0
56	25	3	0	0	0	0
56	27	2	0	0	0	0
56	28	1	0	0	0	0
56	29	2	0	0	0	0
56	2A	986	0	0	0	0
56	2B	25	0	0	0	0
56	2D	17	0	0	0	0
56	2E	6	0	0	0	0
56	2F	9	0	0	0	0
56	2G	3	0	0	0	0
56	2H	2	0	0	0	0
56	2N	3	0	0	0	0
56	2P	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2Q	4	0	0	0	0
56	2R	2	0	0	0	0
56	2S	1	0	0	0	0
56	2U	7	0	0	0	0
56	2V	1	0	0	0	0
56	2W	1	0	0	0	0
56	2X	2	0	0	0	0
56	2Y	2	0	0	0	0
56	2a	221	0	0	0	0
56	2b	1	0	0	0	0
56	2d	4	0	0	0	0
56	2e	1	0	0	0	0
56	2f	1	0	0	0	0
56	2g	1	0	0	0	0
56	2h	2	0	0	0	0
56	2i	1	0	0	0	0
56	2j	1	0	0	0	0
56	2l	2	0	0	0	0
56	2n	1	0	0	0	0
56	2o	1	0	0	0	0
56	2t	1	0	0	0	0
56	2v	1	0	0	0	0
56	2x	12	0	0	0	0
57	14	1	0	0	0	0
57	15	1	0	0	0	0
57	16	1	0	0	0	0
57	19	1	0	0	0	0
57	1Y	1	0	0	0	0
57	1n	1	0	0	0	0
57	24	1	0	0	0	0
57	25	1	0	0	0	0
57	26	1	0	0	0	0
57	29	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2n	1	0	0	0	0
58	1d	8	0	0	0	0
58	2d	8	0	0	0	0
59	1x	1	0	0	0	0
59	2A	1	0	0	0	0
60	10	5	0	0	0	0
60	11	5	0	0	0	0
60	13	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	15	3	0	0	0	0
60	16	1	0	0	0	0
60	17	2	0	0	0	0
60	18	8	0	0	0	0
60	19	2	0	0	0	0
60	1A	1795	0	0	7	0
60	1B	49	0	0	1	0
60	1D	23	0	0	0	0
60	1E	16	0	0	0	0
60	1F	9	0	0	0	0
60	1G	2	0	0	0	0
60	1H	4	0	0	0	0
60	1N	8	0	0	0	0
60	1P	14	0	0	0	0
60	1Q	6	0	0	0	0
60	1R	6	0	0	1	0
60	1T	5	0	0	0	0
60	1U	3	0	0	0	0
60	1V	6	0	0	0	0
60	1W	1	0	0	0	0
60	1X	6	0	0	0	0
60	1Y	4	0	0	0	0
60	1a	408	0	0	2	0
60	1d	8	0	0	0	0
60	1e	3	0	0	0	0
60	1f	1	0	0	0	0
60	1h	1	0	0	0	0
60	1j	1	0	0	0	0
60	1l	4	0	0	1	0
60	1m	1	0	0	0	0
60	1o	2	0	0	0	0
60	1p	1	0	0	0	0
60	1t	2	0	0	0	0
60	1v	2	0	0	0	0
60	1x	5	0	0	0	0
60	1y	2	0	0	0	0
60	20	9	0	0	1	0
60	21	2	0	0	0	0
60	23	2	0	0	0	0
60	25	2	0	0	0	0
60	26	1	0	0	0	0
60	27	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	28	9	0	0	0	0
60	29	4	0	0	0	0
60	2A	1787	0	0	17	0
60	2B	46	0	0	2	0
60	2D	20	0	0	0	0
60	2E	15	0	0	1	0
60	2F	11	0	0	0	0
60	2G	2	0	0	0	0
60	2H	4	0	0	0	0
60	2N	8	0	0	0	0
60	2P	17	0	0	0	0
60	2Q	4	0	0	0	0
60	2R	6	0	0	0	0
60	2T	4	0	0	0	0
60	2U	5	0	0	0	0
60	2V	3	0	0	0	0
60	2W	1	0	0	0	0
60	2X	5	0	0	0	0
60	2Y	8	0	0	0	0
60	2a	408	0	0	7	0
60	2d	7	0	0	1	0
60	2e	4	0	0	0	0
60	2f	1	0	0	0	0
60	2h	1	0	0	0	0
60	2j	2	0	0	0	0
60	2l	7	0	0	0	0
60	2m	1	0	0	1	0
60	2n	1	0	0	0	0
60	2t	1	0	0	0	0
60	2v	3	0	0	0	0
60	2x	4	0	0	0	0
60	2y	4	0	0	0	0
All	All	296108	0	194899	4151	0

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

All (4151) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2564:OMU:C4	1:1A:2564:OMU:C5	1.78	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2552:OMU:C5	1:2A:2552:OMU:C4	1.77	1.56
1:1A:1085:G:H1	1:1A:1162:C:N4	1.37	1.23
1:2A:2119:A:H61	1:2A:2168:G:N2	1.40	1.17
1:2A:2119:A:N6	1:2A:2168:G:H21	1.43	1.14
1:1A:1405:A:N6	1:1A:1418:U:H3	1.46	1.11
32:1a:1005:A:C6	32:1a:1024:G:N2	2.22	1.08
32:2a:516:PSU:HN3	32:2a:533:A:N6	1.52	1.07
1:2A:2131:G:H5''	1:2A:2132:U:H5'	1.38	1.05
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.37	1.00
1:2A:2123:G:H1	1:2A:2175:C:H42	1.08	0.99
1:2A:2102:U:O2	1:2A:2187:G:O6	1.81	0.98
32:1a:189(A):C:N4	32:1a:189(J):G:H1	1.61	0.98
1:1A:1578:C:H42	1:1A:1585:G:H1	1.04	0.97
1:2A:1065:U:H3	1:2A:1073:A:N6	1.61	0.97
21:1Z:198:LYS:HB3	21:1Z:202:GLU:HB2	1.47	0.96
1:2A:1041:C:H42	1:2A:1114:G:H1	1.03	0.96
32:2a:1004:A:H5''	32:2a:1025:U:H5	1.30	0.96
32:1a:516:PSU:HN3	32:1a:533:A:N6	1.64	0.95
32:2a:1244:C:H42	32:2a:1293:G:H1	1.16	0.94
1:1A:1405:A:N1	1:1A:1418:U:O4	2.01	0.94
1:1A:303:C:H42	1:1A:385:G:H1	1.00	0.93
1:2A:1047:G:H21	1:2A:1111:A:H62	0.98	0.93
35:2d:10:ARG:HA	35:2d:13:ARG:HD2	1.49	0.92
32:1a:1005:A:N6	32:1a:1024:G:N2	2.17	0.92
1:1A:354:A:H2	1:1A:1255:A:HO2'	0.97	0.92
1:1A:2331:G:H22	14:1S:3:ARG:HD3	1.35	0.90
1:2A:1064:C:H3'	1:2A:1065:U:H5''	1.53	0.89
1:1A:1110:C:H3'	1:1A:1111:U:H5''	1.53	0.89
32:2a:1125:U:O4	32:2a:1280:A:N7	2.05	0.88
32:2a:975:A:H4'	32:2a:976:G:H5''	1.55	0.88
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.55	0.88
32:1a:78:G:N2	32:1a:91:C:N3	2.20	0.87
32:1a:975:A:H4'	32:1a:976:G:H5''	1.54	0.87
12:1Q:8:LYS:HA	21:1Z:197:ILE:HB	1.56	0.87
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.57	0.87
33:1b:231:GLU:HB3	33:1b:232:PRO:HD3	1.56	0.87
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.39	0.86
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.21	0.86
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.08	0.86
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.38	0.86
1:2A:272(G):C:H42	1:2A:363(C):G:H1	1.23	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:2:LYS:NZ	19:2X:38:GLU:OE2	2.09	0.85
1:2A:2123:G:H1	1:2A:2175:C:N4	1.72	0.85
1:2A:1063:G:N2	1:2A:1076:C:O2'	2.09	0.85
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.58	0.85
1:1A:303:C:N4	1:1A:385:G:H1	1.74	0.84
32:1a:405:U:O4	35:1d:2:GLY:N	2.10	0.84
1:2A:2123:G:N2	1:2A:2175:C:N3	2.25	0.84
32:1a:189(A):C:H42	32:1a:189(J):G:H1	0.87	0.84
32:2a:516:PSU:O2	32:2a:533:A:N7	2.10	0.84
32:2a:817:C:H42	32:2a:1529:G:H1	1.21	0.84
1:1A:922:G:H1	1:1A:948:C:H42	1.21	0.83
32:1a:38:G:H22	32:1a:397:A:H5''	1.41	0.83
1:2A:1065:U:H3	1:2A:1073:A:H61	0.87	0.83
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.44	0.83
32:2a:1440:C:H42	32:2a:1461:G:H1	1.23	0.82
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.13	0.82
32:2a:410:G:OP1	35:2d:30:LYS:NZ	2.13	0.82
32:2a:988:G:H1	32:2a:1217:C:H42	1.27	0.82
1:2A:2111:C:H42	1:2A:2147:G:H22	1.27	0.82
32:1a:404:U:O2	32:1a:498:U:O4	1.98	0.82
32:1a:516:PSU:HN3	32:1a:533:A:H62	0.84	0.81
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.60	0.81
42:2k:82:VAL:HB	42:2k:108:ILE:HG12	1.62	0.81
1:1A:1766:G:H8	1:1A:1770:A:H62	1.28	0.81
1:1A:1847:G:O6	3:1D:35:LYS:NZ	2.13	0.81
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.62	0.81
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.13	0.81
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.62	0.81
33:2b:63:MET:HG3	33:2b:225:ALA:HB1	1.62	0.81
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.61	0.81
40:2i:53:VAL:O	40:2i:55:ALA:N	2.13	0.81
1:1A:11:G:H2'	1:1A:12:U:H5''	1.63	0.80
1:2A:1047:G:N2	1:2A:1111:A:H62	1.77	0.80
2:2B:60:C:N4	60:2B:3101:HOH:O	2.13	0.80
1:1A:1087:C:H42	1:1A:1160:G:H1	1.28	0.80
1:2A:1864:U:OP1	1:2A:2410:G:O2'	1.98	0.80
1:1A:2702:C:OP1	13:1R:17:ARG:NH2	2.15	0.80
1:1A:1578:C:N4	1:1A:1585:G:H1	1.79	0.80
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.63	0.80
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.47	0.80
1:2A:1041:C:N4	1:2A:1114:G:H1	1.79	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HD13	1.63	0.80
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.14	0.79
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.64	0.79
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	1.63	0.79
18:2W:2:GLU:OE2	18:2W:72:LYS:NZ	2.15	0.79
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.64	0.79
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.45	0.79
1:1A:2138:G:OP2	1:1A:2188:G:N2	2.15	0.79
2:2B:16:G:H1	2:2B:68:C:H42	1.26	0.79
1:2A:2141:G:H1	1:2A:2150:U:H3	1.27	0.79
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.65	0.79
2:2B:18:G:H1	2:2B:65:C:H42	1.29	0.79
8:1I:38:LEU:HB3	8:1I:40:THR:HG23	1.65	0.78
32:2a:1129:C:O2	32:2a:1130:A:N6	2.14	0.78
15:1T:39:ARG:HH21	32:1a:345:C:H5''	1.49	0.78
32:2a:38:G:H22	32:2a:397:A:H5''	1.47	0.78
32:2a:1027:C:O2	32:2a:1034:G:N1	2.14	0.78
32:2a:1046:A:N6	32:2a:1211:U:O2	2.16	0.78
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.48	0.78
32:1a:516:PSU:O2	32:1a:533:A:N7	2.17	0.78
1:1A:1039:G:OP1	16:1U:50:ARG:NH2	2.17	0.78
1:1A:1102:G:N1	1:1A:1148:C:OP2	2.13	0.78
32:2a:992:U:H4'	32:2a:993:G:O5'	1.83	0.78
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.17	0.77
2:2B:16:G:H1	2:2B:68:C:N4	1.81	0.77
1:1A:1140:U:H1'	1:1A:1143:U:H5	1.48	0.77
32:1a:138:G:H1	32:1a:225:C:H42	1.32	0.77
12:1Q:21:THR:HG21	12:1Q:101:ARG:HB2	1.66	0.77
36:1e:143:ARG:NH1	39:1h:77:GLU:OE2	2.17	0.77
1:2A:1466:G:HO2'	1:2A:1546:C:HO2'	1.31	0.77
32:2a:411:A:OP2	35:2d:25:ARG:NH2	2.16	0.77
32:1a:455:C:H42	32:1a:476:G:H1	1.33	0.77
1:1A:2188:G:O6	1:1A:2194:U:O4	2.01	0.77
32:1a:343:U:O2	32:1a:346:G:O6	2.01	0.77
32:2a:954:G:H21	32:2a:1227:A:H62	1.32	0.77
1:1A:2798:C:OP1	4:1E:41:LYS:NZ	2.18	0.77
1:2A:1202:C:H42	1:2A:1243:G:H1	1.29	0.77
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.66	0.77
32:2a:343:U:O2	32:2a:346:G:O6	2.02	0.77
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.18	0.76
33:2b:75:LYS:HA	33:2b:78:GLN:HB2	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:664:G:H22	32:1a:741:G:H1	1.31	0.76
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.67	0.76
12:2Q:6:ARG:HE	21:2Z:197:ILE:HD11	1.51	0.76
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.19	0.76
6:2G:3:LEU:HD11	6:2G:97:ASP:HB3	1.68	0.76
54:2x:21:A:H61	54:2x:46:G:H2'	1.50	0.76
1:1A:2188:G:O6	1:1A:2194:U:C4	2.38	0.76
1:2A:65:C:O2	1:2A:456:C:N4	2.18	0.76
38:2g:47:CYS:HB3	38:2g:58:PRO:HB3	1.68	0.76
1:1A:909:G:OP1	12:1Q:18:LYS:NZ	2.18	0.75
21:1Z:202:GLU:HA	54:1x:53:G:O2'	1.86	0.75
26:14:40:HIS:HB3	26:14:43:TYR:HB2	1.68	0.75
35:2d:76:ARG:NH2	35:2d:80:GLU:OE1	2.19	0.75
12:2Q:8:LYS:HA	21:2Z:197:ILE:HB	1.68	0.75
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.17	0.75
1:1A:2188:G:O6	1:1A:2194:U:C5	2.39	0.75
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.69	0.75
1:2A:1359:A:N6	1:2A:1372:U:O4	2.19	0.75
5:1F:120:GLU:HB3	5:1F:122:LYS:HG2	1.67	0.75
1:1A:1121:C:OP1	12:1Q:59:ARG:NE	2.18	0.75
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.68	0.75
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.67	0.75
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.69	0.75
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.50	0.75
1:1A:1310:G:OP1	27:15:19:ARG:NH2	2.18	0.75
1:2A:11:G:H2'	1:2A:12:U:H5''	1.69	0.75
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.51	0.75
1:2A:1047:G:H21	1:2A:1111:A:N6	1.81	0.75
1:1A:2188:G:C6	1:1A:2194:U:O4	2.39	0.74
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.69	0.74
3:2D:164:GLN:OE1	3:2D:176:ARG:NH2	2.19	0.74
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.19	0.74
2:2B:8:U:H3	2:2B:113:G:H1	1.35	0.74
17:2V:100:ARG:HH11	17:2V:100:ARG:HB2	1.51	0.74
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.21	0.74
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.51	0.74
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.53	0.74
33:1b:10:LEU:HA	33:1b:48:MET:HE1	1.67	0.74
41:2j:57:LYS:HD2	41:2j:60:ARG:HH21	1.50	0.74
1:1A:2324:U:H5'	6:1G:88:ILE:HD11	1.69	0.74
19:1X:60:ARG:HH12	29:17:47:ARG:HH22	1.33	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.02	0.74
1:2A:2640:G:O3'	9:2N:74:ARG:NH2	2.21	0.74
12:2Q:59:ARG:HA	21:2Z:180:VAL:HG23	1.69	0.74
26:24:16:CYS:SG	26:24:17:GLY:N	2.60	0.74
33:2b:195:ASP:O	39:2h:68:ARG:NH2	2.20	0.74
1:1A:1071:G:O2'	60:1A:9001:HOH:O	2.05	0.74
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.15	0.74
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.20	0.73
41:1j:38:ILE:HD11	41:1j:71:LEU:HD23	1.70	0.73
1:1A:1112:U:H3	1:1A:1119:A:H62	1.36	0.73
32:2a:442:C:H42	32:2a:492:G:H1	1.34	0.73
33:2b:93:VAL:HG21	33:2b:97:TRP:HD1	1.53	0.73
1:1A:215:G:N2	1:1A:217:A:H62	1.86	0.73
1:1A:2766:A:N3	31:19:15:LYS:NZ	2.33	0.73
3:1D:4:LYS:HB3	3:1D:18:VAL:HG23	1.69	0.73
1:2A:1914:C:O2'	1:2A:1915:5MU:OP1	2.06	0.73
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.22	0.73
26:24:59:PHE:HA	26:24:61:ARG:N	2.03	0.73
4:1E:47:VAL:HG21	4:1E:86:PRO:HD2	1.70	0.73
1:2A:220:G:O2'	1:2A:233:A:N3	2.20	0.73
41:2j:30:SER:OG	41:2j:84:GLN:OE1	2.07	0.73
27:15:33:CYS:HB2	27:15:40:LYS:HD3	1.71	0.73
32:2a:1301:U:O2'	32:2a:1302:U:H5'	1.89	0.73
1:1A:2701:U:H4'	1:1A:2702:C:H5'	1.71	0.72
32:2a:664:G:H22	32:2a:741:G:H1	1.36	0.72
33:2b:84:GLU:HG3	33:2b:215:LEU:HB3	1.71	0.72
32:1a:1158:C:H5	32:1a:1181:G:H1	1.38	0.72
1:1A:1219:A:H1'	1:1A:1220:U:H5''	1.71	0.72
32:2a:404:U:O2	32:2a:498:U:O4	2.07	0.72
38:2g:111:ARG:NH1	38:2g:113:GLU:OE2	2.21	0.72
32:1a:1103:C:OP1	33:1b:96:ARG:NH2	2.23	0.72
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.55	0.72
7:2H:64:LEU:O	7:2H:68:THR:OG1	2.08	0.72
1:1A:1218:G:O2'	1:1A:1219:A:O5'	2.06	0.72
1:1A:215:G:H21	1:1A:217:A:H62	1.36	0.72
35:1d:165:MET:HE2	35:1d:176:LEU:HD23	1.69	0.72
1:2A:2144:U:OP1	1:2A:2145:C:N4	2.23	0.72
1:2A:2224:G:OP1	3:2D:268:ARG:NE	2.23	0.72
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.71	0.72
19:1X:1:MET:HE1	24:12:26:ARG:HH21	1.55	0.71
48:1q:75:ARG:NH1	48:1q:76:LEU:O	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.55	0.71
5:1F:165:ARG:HA	5:1F:168:ARG:HD3	1.72	0.71
41:2j:38:ILE:HG13	41:2j:71:LEU:HB3	1.72	0.71
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.73	0.71
5:1F:28:ILE:HG23	5:1F:112:MET:HB3	1.71	0.71
32:1a:1005:A:N6	32:1a:1024:G:H21	1.88	0.71
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	1.71	0.71
1:2A:568:U:O2'	60:2A:4002:HOH:O	2.06	0.71
1:2A:1430:C:H42	1:2A:1563:G:H1	1.37	0.71
40:2i:40:LEU:HD11	40:2i:70:LYS:HB3	1.72	0.71
32:1a:1414:U:H3	32:1a:1486:G:H1	1.36	0.71
32:2a:425:G:O3'	35:2d:45:GLN:NE2	2.24	0.71
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.24	0.71
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.71	0.71
13:1R:3:HIS:NE2	60:1R:301:HOH:O	2.23	0.71
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.72	0.71
43:1l:34:ARG:NH2	60:1l:301:HOH:O	2.24	0.71
38:2g:114:ARG:HB2	38:2g:115:ARG:NH2	2.05	0.71
13:2R:57:ARG:NE	13:2R:59:ASP:OD2	2.21	0.71
1:2A:1842:G:O2'	3:2D:253:GLN:NE2	2.24	0.70
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.25	0.70
1:2A:1798:U:OP2	3:2D:274:ARG:NH2	2.24	0.70
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.26	0.70
32:2a:343:U:C2	32:2a:346:G:O6	2.44	0.70
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.24	0.70
32:1a:189(A):C:N3	32:1a:189(J):G:N2	2.34	0.70
50:1s:20:LEU:HD23	50:1s:23:ASN:HD22	1.55	0.70
1:2A:2207:G:O2'	1:2A:2208:A:OP1	2.09	0.70
1:2A:2552:OMU:C4	1:2A:2552:OMU:C6	2.46	0.70
28:26:43:CYS:HB3	28:26:45:LYS:HE2	1.73	0.70
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.73	0.70
40:2i:51:ARG:HG2	40:2i:56:LEU:HD21	1.72	0.70
1:1A:2228:G:O2'	1:1A:2229:A:OP1	2.09	0.70
32:1a:1278:U:H5'	32:1a:1279:A:O4'	1.92	0.70
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.72	0.70
21:1Z:202:GLU:OE2	54:1x:52:G:N2	2.25	0.70
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.73	0.70
25:13:29:ARG:HG3	25:13:30:ARG:HG3	1.74	0.70
32:1a:428:G:OP2	35:1d:10:ARG:NH1	2.25	0.70
32:1a:1005:A:C5	32:1a:1024:G:N2	2.60	0.70
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:272(G):C:N4	1:2A:363(C):G:H1	1.90	0.70
32:2a:1194:U:H4'	36:2e:22:GLY:HA2	1.72	0.70
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.73	0.70
34:2c:109:PRO:HB3	34:2c:115:LEU:HD23	1.73	0.70
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.24	0.70
32:2a:79:G:N2	32:2a:90:U:O2	2.17	0.70
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.27	0.69
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.74	0.69
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.25	0.69
1:1A:922:G:H1	1:1A:948:C:N4	1.89	0.69
32:1a:161:A:N1	32:1a:347:G:O2'	2.25	0.69
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.27	0.69
1:2A:2302:G:N2	6:2G:126:ASP:OD1	2.24	0.69
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.72	0.69
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.25	0.69
32:2a:817:C:N4	32:2a:1529:G:H1	1.91	0.69
32:2a:1125:U:C4	32:2a:1280:A:N7	2.59	0.69
36:2e:88:LYS:HB3	36:2e:123:LEU:HB2	1.75	0.69
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.73	0.69
15:1T:1:MET:HE2	15:1T:3:ARG:HG3	1.73	0.69
34:1c:78:GLY:HA3	34:1c:83:ARG:H	1.56	0.69
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.75	0.69
5:2F:32:LEU:HD13	5:2F:112:MET:HE1	1.74	0.69
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	1.74	0.69
18:2W:65:LEU:HD12	18:2W:68:ARG:HE	1.56	0.69
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.26	0.69
40:2i:50:LEU:HD23	40:2i:50:LEU:H	1.58	0.69
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.73	0.69
1:2A:2357:U:OP1	22:20:20:ARG:NE	2.23	0.69
32:2a:67:C:H2'	32:2a:68:G:C8	2.28	0.69
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.73	0.69
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.75	0.69
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.75	0.68
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.58	0.68
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.75	0.68
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.11	0.68
1:1A:2695:C:O2	10:1O:70:LYS:NZ	2.19	0.68
32:1a:191:G:H1'	51:1t:103:GLY:HA3	1.76	0.68
32:1a:1108:G:H5'	34:1c:176:HIS:CD2	2.28	0.68
1:2A:2452:C:OP1	55:2y:4:ARG:NH2	2.26	0.68
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2143:C:N3	1:2A:2148:G:O6	2.26	0.68
32:2a:1244:C:N4	32:2a:1293:G:H1	1.87	0.68
1:1A:1085:G:N2	1:1A:1162:C:N3	2.37	0.68
16:2U:85:LYS:HB3	16:2U:116:ALA:HB1	1.73	0.68
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.10	0.68
1:1A:268:G:HO2'	1:1A:269:G:H8	1.41	0.68
32:1a:62:U:O2'	32:1a:379:C:O2	2.10	0.68
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.76	0.68
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.27	0.68
1:1A:2183:C:H2'	1:1A:2184:G:H5''	1.76	0.68
47:1p:74:LEU:HD23	47:1p:79:VAL:HG11	1.75	0.68
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.08	0.68
17:2V:1:MET:HE3	17:2V:40:LEU:HB3	1.76	0.68
47:2p:14:ASN:HA	47:2p:42:ARG:HH21	1.57	0.68
1:2A:2689:U:H4'	1:2A:2690:C:H5'	1.75	0.68
24:22:35:LEU:HD21	24:22:49:LYS:HE2	1.75	0.68
32:2a:516:PSU:HN3	32:2a:533:A:H62	0.75	0.68
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.75	0.68
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.73	0.68
1:1A:268:G:O2'	1:1A:269:G:H8	1.77	0.68
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.22	0.68
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.27	0.68
39:1h:14:ARG:O	39:1h:18:ARG:HG2	1.94	0.67
6:2G:41:GLN:HB3	6:2G:43:LEU:HD22	1.74	0.67
35:2d:89:THR:OG1	60:2d:601:HOH:O	2.12	0.67
1:1A:921:G:H1	1:1A:949:C:H42	1.42	0.67
1:1A:2304:C:OP1	14:1S:17:ARG:NH2	2.27	0.67
32:1a:404:U:O2	32:1a:498:U:C4	2.46	0.67
32:1a:503:C:OP2	43:1l:116:SER:OG	2.09	0.67
32:1a:272:C:H2'	32:1a:273:A:H8	1.57	0.67
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.75	0.67
32:2a:1101:A:N6	33:2b:176:GLU:OE2	2.27	0.67
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.26	0.67
1:2A:1245:G:OP1	11:2P:13:ASN:ND2	2.23	0.67
32:2a:688:G:H1	32:2a:699:C:H42	1.42	0.67
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.75	0.67
32:1a:458:C:H2'	32:1a:460:G:O4'	1.94	0.67
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.75	0.67
26:24:41:PRO:HG3	26:24:49:PHE:HE2	1.59	0.67
8:1I:72:LEU:O	8:1I:74:ASN:N	2.26	0.67
32:1a:107:G:N7	51:1t:15:ARG:NH2	2.43	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1x:21:A:H61	54:1x:46:G:H2'	1.58	0.67
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.76	0.67
1:1A:467:U:O2	5:1F:46:ARG:NH2	2.27	0.67
1:2A:2134:A:O2'	1:2A:2159:G:N3	2.27	0.67
12:1Q:45:GLN:OE1	12:1Q:45:GLN:N	2.28	0.67
32:2a:1047:G:H5''	45:2n:4:LYS:HD3	1.77	0.67
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.77	0.67
44:1m:32:GLU:OE2	44:1m:36:LYS:NZ	2.28	0.67
32:2a:134:A:H61	47:2p:25:ARG:HH22	1.42	0.67
1:1A:1700:G:H3'	13:1R:2:ARG:HD3	1.77	0.67
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.21	0.67
21:2Z:198:LYS:NZ	54:2x:52:G:N3	2.42	0.67
1:1A:1405:A:H61	1:1A:1418:U:H3	0.73	0.66
1:1A:2391:G:O2'	14:1S:17:ARG:NH1	2.28	0.66
6:1G:67:LYS:HD3	26:14:5:ILE:HB	1.77	0.66
32:1a:259:G:OP2	51:1t:83:ARG:NH1	2.28	0.66
12:2Q:39:PRO:HD3	12:2Q:99:PRO:HG3	1.77	0.66
1:1A:1085:G:H1	1:1A:1162:C:H42	0.70	0.66
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.78	0.66
22:10:10:THR:HG22	22:10:12:ASN:H	1.60	0.66
29:17:24:THR:HG22	29:17:27:GLY:H	1.61	0.66
1:2A:1065:U:O2'	1:2A:1066:U:OP2	2.11	0.66
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.29	0.66
6:2G:122:PRO:HB3	6:2G:170:ARG:HH12	1.59	0.66
32:2a:1004:A:H5''	32:2a:1025:U:C5	2.22	0.66
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.30	0.66
33:2b:15:VAL:HB	33:2b:209:ARG:HB3	1.77	0.66
1:1A:1346:U:H4'	1:1A:1347:A:H5''	1.78	0.66
41:1j:81:THR:HA	41:1j:84:GLN:HE21	1.60	0.66
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.29	0.66
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.26	0.66
27:25:40:LYS:NZ	27:25:44:THR:O	2.23	0.66
1:1A:2877:G:OP2	15:1T:119:LYS:NZ	2.23	0.66
40:2i:105:ASP:HB2	40:2i:107:ARG:HG3	1.77	0.66
1:1A:611:U:H2'	1:1A:612:C:C6	2.30	0.66
23:11:76:ARG:HB3	23:11:97:LEU:HD13	1.76	0.66
1:1A:1873:G:O2'	3:1D:253:GLN:NE2	2.29	0.66
32:2a:1000:U:O4	32:2a:1041:A:N1	2.28	0.66
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.25	0.66
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.28	0.66
34:2c:73:PRO:HB3	34:2c:103:VAL:HG11	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:54:ARG:HA	15:1T:59:THR:HG22	1.78	0.66
32:1a:976:G:H5'	32:1a:1358:U:O2'	1.95	0.66
1:2A:864:G:H1'	1:2A:914:C:H42	1.61	0.66
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	1.78	0.66
1:1A:1261:G:OP2	16:1U:12:ARG:NH2	2.25	0.66
6:1G:136:ARG:HH11	6:1G:136:ARG:HB2	1.60	0.66
1:2A:2111:C:N4	1:2A:2147:G:H22	1.94	0.66
32:2a:1028:C:H2'	32:2a:1033:G:N2	2.11	0.66
32:2a:1402:4OC:HM41	53:2v:18:G:OP2	1.95	0.66
1:1A:2762:A:OP1	7:1H:3:ARG:NH1	2.30	0.65
8:1I:77:LEU:HD12	8:1I:104:GLN:HE21	1.60	0.65
34:1c:124:ILE:HD12	34:1c:196:LEU:HD12	1.79	0.65
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.76	0.65
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.41	0.65
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.29	0.65
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.29	0.65
26:14:58:ARG:HD2	50:1s:68:GLY:H	1.62	0.65
32:1a:1347:G:C8	40:1i:107:ARG:HB3	2.31	0.65
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.78	0.65
32:2a:36:C:O2'	43:2l:117:ARG:NH2	2.29	0.65
32:1a:7:G:H21	36:1e:121:LYS:HG2	1.60	0.65
1:2A:106:C:H1'	20:2Y:1:MET:HG3	1.78	0.65
33:2b:213:LEU:HD23	33:2b:217:ARG:HG3	1.78	0.65
32:1a:1130:A:H5'	40:1i:18:PHE:CE2	2.32	0.65
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.32	0.65
1:1A:2149:G:H21	1:1A:2195:A:H1'	1.61	0.65
32:1a:946:A:H2'	32:1a:947:G:C8	2.31	0.65
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.23	0.65
1:2A:1066:U:O2'	1:2A:1067:A:H5'	1.96	0.65
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.32	0.65
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.79	0.65
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.61	0.65
32:1a:474:G:H2'	32:1a:475:G:H8	1.61	0.65
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.25	0.65
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.29	0.65
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.20	0.65
4:2E:52:LEU:HB3	4:2E:53:PRO:HD2	1.79	0.65
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.30	0.65
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.96	0.65
32:2a:1353:G:OP1	52:2u:10:ARG:NH1	2.28	0.65
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1129:C:H5''	40:1i:16:ARG:HH12	1.61	0.65
42:1k:60:ALA:HA	42:1k:63:LEU:HD12	1.77	0.65
32:2a:673:G:H2'	32:2a:674:G:C8	2.32	0.65
1:1A:1117:G:H1'	1:1A:1135:G:H2'	1.77	0.65
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.79	0.65
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.79	0.65
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.23	0.64
1:2A:2638:G:P	4:2E:82:ARG:HH12	2.20	0.64
32:2a:1438:G:H1	32:2a:1463:C:H42	1.43	0.64
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.79	0.64
1:2A:1041:C:N3	1:2A:1114:G:N2	2.37	0.64
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.78	0.64
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.12	0.64
32:1a:701:C:OP1	32:1a:702:A:O2'	2.14	0.64
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.78	0.64
1:1A:1219:A:H4'	1:1A:1220:U:OP1	1.98	0.64
32:1a:201:C:N3	32:1a:216:G:N2	2.36	0.64
1:2A:276:A:H5''	1:2A:277:C:H5'	1.80	0.64
1:2A:2186:G:H2'	1:2A:2187:G:H5''	1.79	0.64
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.79	0.64
32:2a:405:U:O4	35:2d:2:GLY:N	2.31	0.64
32:1a:1144:G:H21	32:1a:1146:A:H62	1.46	0.64
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.62	0.64
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.62	0.64
48:2q:62:SER:OG	48:2q:72:ARG:NH1	2.30	0.64
32:1a:316:G:OP2	32:1a:351:G:O2'	2.16	0.64
1:2A:2313:C:H5''	6:2G:91:ARG:HD3	1.80	0.64
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.31	0.64
32:2a:45:U:H2'	32:2a:46:G:C8	2.33	0.64
32:2a:272:C:H2'	32:2a:273:A:H8	1.62	0.64
32:2a:1245:A:H2'	32:2a:1246:C:O4'	1.98	0.64
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.79	0.64
1:2A:362:U:O2'	1:2A:363:G:H5''	1.98	0.64
32:2a:948:C:N4	60:2a:1905:HOH:O	2.30	0.64
34:2c:130:VAL:HG21	34:2c:157:ILE:HG23	1.80	0.64
26:14:61:ARG:HG3	26:14:62:ARG:H	1.63	0.64
1:2A:2012:G:OP1	18:2W:11:ARG:NH2	2.30	0.64
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.33	0.64
34:1c:150:LYS:HG3	34:1c:169:ALA:HB2	1.79	0.64
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.31	0.64
32:2a:35:G:O2'	43:2l:118:SER:O	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:9:VAL:HB	15:1T:3:ARG:HG2	1.80	0.64
32:1a:560:U:O2'	32:1a:561:U:OP2	2.16	0.64
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.32	0.64
22:20:10:THR:HG22	22:20:12:ASN:H	1.62	0.64
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.31	0.63
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	1.80	0.63
1:1A:1094:A:OP2	1:1A:1155:C:N4	2.32	0.63
1:1A:2642:G:H21	1:1A:2901:A:H1'	1.62	0.63
44:2m:3:ARG:O	44:2m:57:ARG:NH2	2.31	0.63
1:1A:2658:C:OP2	1:1A:2745:G:O2'	2.11	0.63
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.63	0.63
32:1a:1227:A:OP2	44:1m:111:LYS:NZ	2.31	0.63
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.32	0.63
38:1g:79:ARG:HA	38:1g:84:ASN:HA	1.80	0.63
1:2A:856:C:H2'	1:2A:857:C:C6	2.34	0.63
1:2A:2573:C:C2	55:2y:2:ARG:HG3	2.33	0.63
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.24	0.63
12:2Q:45:GLN:N	12:2Q:45:GLN:OE1	2.30	0.63
32:2a:19:C:OP1	36:2e:130:ASN:ND2	2.31	0.63
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.34	0.63
1:1A:85:C:H4'	1:1A:102:U:H1'	1.80	0.63
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.80	0.63
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.80	0.63
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.80	0.63
4:2E:98:PRO:HG3	4:2E:174:ASP:HA	1.81	0.63
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.31	0.63
1:1A:1474:C:O2'	1:1A:1616:A:OP2	2.14	0.63
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.30	0.63
19:1X:60:ARG:HH22	29:17:47:ARG:HH12	1.46	0.63
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.17	0.63
1:2A:1202:C:N4	1:2A:1243:G:H1	1.95	0.63
32:2a:64:G:H4'	32:2a:65:U:H3'	1.81	0.63
51:2t:43:LEU:HD13	51:2t:51:GLU:HB3	1.79	0.63
34:1c:79:ARG:H	34:1c:82:GLU:HB3	1.64	0.63
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.80	0.63
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.27	0.63
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	1.98	0.63
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.29	0.63
26:14:56:VAL:HB	26:14:60:GLN:HG2	1.81	0.63
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.32	0.63
1:1A:2457:G:OP1	5:1F:74:ARG:NH2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:519:C:OP2	43:1l:50:SER:OG	2.14	0.63
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.13	0.63
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.20	0.62
1:2A:530:G:N1	1:2A:2023:G:OP1	2.27	0.62
1:1A:2757:G:N2	7:1H:143:GLN:OE1	2.32	0.62
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.45	0.62
40:1i:25:LYS:HD2	40:1i:26:VAL:H	1.64	0.62
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.81	0.62
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.79	0.62
32:2a:1183:A:O2'	32:2a:1184:G:OP1	2.15	0.62
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.80	0.62
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.63	0.62
20:2Y:77:PRO:HD2	20:2Y:106:LEU:HD23	1.81	0.62
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	1.81	0.62
1:1A:2156:A:H1'	1:1A:2180:A:H1'	1.80	0.62
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.81	0.62
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	1.81	0.62
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.81	0.62
32:2a:1440:C:N4	32:2a:1461:G:H1	1.95	0.62
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.34	0.62
32:2a:533:A:O2'	32:2a:535:A:OP2	2.17	0.62
1:1A:2160:C:H2'	1:1A:2161:C:C6	2.35	0.62
34:1c:40:ARG:HG2	34:1c:55:VAL:HG11	1.82	0.62
38:1g:48:LYS:O	38:1g:52:GLU:HG2	2.00	0.62
1:2A:528:A:OP2	9:2N:114:ARG:NH2	2.32	0.62
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.82	0.62
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.81	0.62
32:1a:1007:C:N3	32:1a:1022:G:O6	2.33	0.62
1:2A:1081:U:H2'	1:2A:1082:U:H5''	1.81	0.62
32:2a:79:G:H1	32:2a:90:U:H3	1.46	0.62
1:1A:1578:C:N3	1:1A:1585:G:N2	2.40	0.62
33:1b:185:ILE:HG23	33:1b:199:TYR:HB2	1.80	0.62
36:2e:7:GLU:OE1	36:2e:37:ARG:NE	2.29	0.62
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.35	0.62
1:1A:1147:U:H2'	1:1A:1148:C:C6	2.34	0.62
2:2B:5:C:OP1	2:2B:61:G:O2'	2.15	0.62
40:2i:4:TYR:CD1	40:2i:88:TYR:HB2	2.33	0.62
32:2a:1338:G:N3	54:2x:41:C:O2'	2.32	0.61
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.35	0.61
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.81	0.61
32:2a:474:G:H2'	32:2a:475:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1192:C:OP2	34:2c:4:LYS:NZ	2.33	0.61
8:1I:31:LEU:HD21	8:1I:38:LEU:HD13	1.81	0.61
1:2A:1216:G:OP2	16:2U:12:ARG:NH2	2.26	0.61
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.48	0.61
1:1A:559:U:O2'	16:1U:49:HIS:ND1	2.24	0.61
1:1A:630:U:OP1	5:1F:102:PRO:HA	2.00	0.61
1:1A:1087:C:N4	1:1A:1160:G:H1	1.99	0.61
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.36	0.61
33:1b:32:ILE:HG21	33:1b:40:HIS:HD2	1.66	0.61
34:1c:84:ILE:O	34:1c:88:ARG:NH1	2.30	0.61
38:1g:8:GLU:H	38:1g:8:GLU:CD	2.08	0.61
1:2A:2561:A:H2	10:2O:23:ARG:HH21	1.49	0.61
1:1A:941:U:H5'	1:1A:942:A:OP2	2.00	0.61
2:2B:39:A:O2'	2:2B:46:A:N1	2.33	0.61
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.32	0.61
26:24:34:GLU:HG2	26:24:35:VAL:HG12	1.82	0.61
32:2a:7:G:H21	36:2e:121:LYS:HG2	1.65	0.61
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.80	0.61
34:2c:8:ILE:HG23	34:2c:16:ARG:HD3	1.82	0.61
1:1A:242:C:OP2	30:18:5:LYS:NZ	2.27	0.61
1:1A:2149:G:OP2	1:1A:2184:G:N2	2.32	0.61
1:1A:2585:C:C2	55:1y:2:ARG:HG3	2.34	0.61
16:1U:83:LEU:HD12	16:1U:113:ALA:HB2	1.82	0.61
43:2l:33:ARG:HD3	43:2l:62:SER:HB3	1.82	0.61
1:1A:555:G:N1	1:1A:2045:G:OP1	2.28	0.61
8:1I:9:LEU:HD11	8:1I:35:LEU:HD13	1.82	0.61
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.34	0.61
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.36	0.61
32:2a:7:G:O2'	36:2e:120:THR:O	2.18	0.61
32:2a:539:A:H2'	32:2a:540:G:C8	2.36	0.61
32:2a:1352:C:N4	60:2a:1906:HOH:O	2.34	0.61
36:2e:71:LEU:HD21	36:2e:115:VAL:HG22	1.82	0.61
1:1A:2897:U:H2'	1:1A:2898:C:H6	1.66	0.61
11:1P:121:LYS:O	11:1P:123:LEU:N	2.34	0.61
33:1b:223:ILE:HG22	33:1b:226:ARG:HH21	1.65	0.61
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.17	0.61
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.99	0.61
45:2n:23:ARG:NH1	45:2n:28:GLY:O	2.29	0.61
1:1A:769:A:H2'	1:1A:770:G:C8	2.36	0.61
1:1A:1451:U:H2'	1:1A:1452:U:C6	2.35	0.61
11:1P:95:VAL:HA	11:1P:99:LEU:HD12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2543:G:H21	1:2A:2646:C:H5''	1.65	0.61
32:2a:1498:UR3:OP2	53:2v:16:A:O2'	2.19	0.61
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.34	0.61
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.36	0.61
1:1A:2163:G:H1	1:1A:2172:U:H3	1.48	0.61
1:1A:2892:A:OP1	13:1R:96:ARG:NH1	2.33	0.61
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.36	0.61
24:12:23:LYS:O	24:12:27:GLU:HG3	2.01	0.61
32:1a:175:C:H2'	32:1a:176:C:H6	1.65	0.61
33:1b:109:SER:HA	33:1b:112:VAL:HG13	1.82	0.61
32:2a:1075:C:H5''	33:2b:179:LYS:HE2	1.83	0.61
7:1H:27:LYS:HG2	7:1H:32:GLU:HB3	1.83	0.60
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.16	0.60
54:1x:50:U:H3	54:1x:64:G:H1	1.48	0.60
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.35	0.60
1:2A:2585:U:H4'	1:2A:2586:C:OP1	2.01	0.60
5:2F:197:ASP:OD1	5:2F:198:ALA:N	2.33	0.60
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.29	0.60
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.83	0.60
32:2a:973:G:OP1	41:2j:57:LYS:NZ	2.34	0.60
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.36	0.60
36:2e:52:PRO:HG2	36:2e:53:LEU:HD12	1.82	0.60
3:1D:221:VAL:HG22	3:1D:226:MET:HE3	1.83	0.60
32:1a:1347:G:O2'	32:1a:1373:G:O6	2.13	0.60
1:2A:271(K):U:O2	8:2I:50:ARG:NH2	2.34	0.60
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.16	0.60
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.66	0.60
50:2s:20:LEU:HD23	50:2s:23:ASN:HD22	1.65	0.60
1:1A:331:G:H21	1:1A:354:A:H62	1.48	0.60
40:1i:105:ASP:HB2	40:1i:107:ARG:HD3	1.84	0.60
1:2A:1048:A:N1	1:2A:1112:G:O2'	2.33	0.60
1:2A:1069:A:H5'	1:2A:1096:A:H5'	1.84	0.60
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.36	0.60
4:2E:14:ILE:HG13	4:2E:21:VAL:HG23	1.84	0.60
1:1A:406:G:N2	23:11:42:GLN:OE1	2.26	0.60
32:1a:911:U:H2'	32:1a:912:C:C6	2.36	0.60
42:1k:73:MET:HG2	42:1k:103:LEU:HD21	1.82	0.60
1:2A:615:G:OP2	5:2F:43:LYS:NZ	2.29	0.60
1:2A:1268:A:H5'	60:2A:5440:HOH:O	2.01	0.60
1:2A:2390:U:P	30:28:35:GLN:HE22	2.25	0.60
4:2E:98:PRO:HD3	4:2E:175:VAL:HG12	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:113:ARG:HD2	6:2G:140:ILE:HA	1.84	0.60
32:2a:404:U:O2	32:2a:498:U:C4	2.54	0.60
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.36	0.60
1:1A:1110:C:H3'	1:1A:1111:U:C5'	2.31	0.60
37:1f:70:ASP:N	37:1f:70:ASP:OD1	2.27	0.60
1:1A:1218:G:O2'	1:1A:1219:A:O4'	2.18	0.60
32:1a:235:C:H5'	48:1q:70:ARG:HG3	1.83	0.60
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.34	0.60
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	1.83	0.60
32:2a:564:C:O2'	39:2h:91:ARG:NH2	2.34	0.60
41:2j:38:ILE:HD11	41:2j:71:LEU:HD22	1.82	0.60
5:1F:10:PRO:HB3	5:1F:17:ARG:NH2	2.16	0.60
37:1f:41:GLU:OE1	49:1r:35:ARG:NH2	2.30	0.60
43:1l:32:PHE:HB3	43:1l:84:LEU:HD11	1.83	0.60
48:1q:57:VAL:HG12	48:1q:76:LEU:HA	1.83	0.60
3:2D:109:ASP:HB2	3:2D:197:GLY:HA2	1.83	0.60
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.84	0.60
50:2s:36:ARG:NH2	50:2s:72:GLY:O	2.34	0.60
1:1A:747:G:O2'	1:1A:1679:A:N3	2.25	0.60
32:1a:454:C:OP1	47:1p:75:ARG:NH2	2.35	0.60
32:1a:1144:G:N2	32:1a:1146:A:H62	1.99	0.60
43:1l:76:ASN:N	43:1l:76:ASN:OD1	2.34	0.60
32:1a:833:U:H2'	32:1a:834:C:H6	1.66	0.60
35:1d:107:ARG:HH21	35:1d:194:LEU:HD11	1.66	0.60
32:2a:1304:G:H1'	32:2a:1333:A:N6	2.16	0.60
1:1A:302:A:H2'	1:1A:303:C:C6	2.36	0.60
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.37	0.60
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.34	0.60
32:2a:236:G:OP1	48:2q:40:LYS:NZ	2.35	0.60
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.17	0.59
9:1N:73:THR:HG23	9:1N:82:LEU:HD11	1.83	0.59
26:14:24:THR:OG1	26:14:25:TYR:N	2.35	0.59
32:1a:93:G:H2'	32:1a:96:U:O4'	2.02	0.59
33:1b:21:ARG:HB3	33:1b:38:GLY:O	2.02	0.59
1:2A:153:C:OP2	23:21:92:LYS:NZ	2.35	0.59
19:2X:11:PRO:HG2	19:2X:13:LEU:HD21	1.84	0.59
21:2Z:108:PRO:HA	21:2Z:142:SER:HA	1.83	0.59
32:2a:757:U:H2'	32:2a:758:G:O4'	2.02	0.59
1:1A:2240:G:OP1	3:1D:261:LYS:NZ	2.20	0.59
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.83	0.59
37:1f:97:PHE:HD2	49:1r:31:LEU:HD23	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.19	0.59
8:2I:62:LYS:HG2	8:2I:133:HIS:CD2	2.37	0.59
43:2I:117:ARG:NH2	43:2I:124:LYS:HB2	2.17	0.59
1:1A:1116:A:C8	1:1A:1143:U:H4'	2.37	0.59
1:1A:1410:G:N7	23:1I:3:LYS:HE2	2.16	0.59
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.84	0.59
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.84	0.59
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.84	0.59
21:2Z:40:ASP:HB3	21:2Z:43:GLU:HB2	1.85	0.59
32:2a:503:C:OP2	43:2I:116:SER:OG	2.18	0.59
32:2a:1014:A:H4'	50:2s:14:HIS:CE1	2.37	0.59
32:2a:1123:A:H4'	41:2j:36:GLY:HA3	1.85	0.59
1:1A:1911:A:H2'	1:1A:1912:A:C8	2.37	0.59
6:1G:60:LEU:HD23	6:1G:63:ILE:HD12	1.85	0.59
7:1H:20:ALA:HB3	7:1H:23:ARG:HG3	1.83	0.59
21:1Z:198:LYS:CB	21:1Z:202:GLU:HB2	2.27	0.59
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.84	0.59
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.36	0.59
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.02	0.59
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.30	0.59
32:2a:624:C:H2'	32:2a:625:G:H8	1.67	0.59
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.35	0.59
48:2q:54:GLY:O	48:2q:81:ARG:N	2.31	0.59
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.33	0.59
32:1a:418:C:H42	32:1a:425:G:H1	1.49	0.59
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.17	0.59
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.35	0.59
32:1a:509:A:N3	32:1a:543:C:O2'	2.31	0.59
38:1g:75:VAL:HG13	38:1g:145:ALA:HA	1.85	0.59
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.36	0.59
1:2A:2105:C:H42	1:2A:2184:G:H1	1.50	0.59
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.84	0.59
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.67	0.59
32:2a:977:A:N6	32:2a:1224:G:OP1	2.34	0.59
47:2p:42:ARG:HB3	47:2p:44:THR:HG22	1.85	0.59
49:2r:26:LEU:HD11	49:2r:42:ARG:HD2	1.84	0.59
32:1a:911:U:H2'	32:1a:912:C:H6	1.67	0.59
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.84	0.59
33:1b:27:LYS:HB2	33:1b:194:PRO:HD2	1.85	0.59
39:1h:51:VAL:HG21	39:1h:60:ARG:HH11	1.68	0.59
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:184:A:OP1	11:1P:46:LYS:NZ	2.35	0.59
1:1A:2155:G:C2	1:1A:2179:G:H2'	2.38	0.59
6:1G:11:TYR:OH	6:1G:32:PRO:O	2.20	0.59
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.00	0.59
8:1I:4:ILE:HG12	8:1I:18:VAL:HG22	1.84	0.59
22:10:11:ARG:O	22:10:14:ARG:NH2	2.36	0.59
32:1a:1318:A:H5''	50:1s:3:ARG:HH12	1.68	0.59
33:1b:17:PHE:HB3	33:1b:44:LEU:HD21	1.83	0.59
1:2A:1991:U:H2'	1:2A:1992:G:H5''	1.85	0.59
1:2A:2115:G:H1'	1:2A:2171:A:N6	2.18	0.59
1:2A:2406:U:OP1	1:2A:2411:A:N6	2.36	0.59
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.85	0.59
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.83	0.59
1:1A:2650:G:P	4:1E:82:ARG:HH12	2.25	0.59
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.85	0.59
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.68	0.59
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.26	0.59
21:1Z:110:GLY:HA3	21:1Z:174:VAL:HG11	1.84	0.59
32:1a:413:G:N7	35:1d:35:ARG:NH1	2.51	0.59
33:1b:91:PRO:HG2	33:1b:155:LEU:HD13	1.84	0.59
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.85	0.59
1:2A:2126:A:H4'	1:2A:2127:G:O5'	2.01	0.59
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.37	0.59
1:1A:142:G:H4'	19:1X:35:THR:HG21	1.83	0.58
21:1Z:145:GLU:H	21:1Z:148:ASP:HB2	1.66	0.58
32:1a:376:G:O3'	47:1p:5:ARG:NH1	2.32	0.58
32:1a:455:C:N4	32:1a:476:G:H1	2.00	0.58
47:1p:75:ARG:HG3	47:1p:80:PHE:HD2	1.66	0.58
4:2E:201:THR:HG23	4:2E:203:LYS:H	1.67	0.58
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.15	0.58
36:2e:137:GLU:OE1	36:2e:141:GLN:NE2	2.36	0.58
1:2A:481:G:O5'	20:2Y:47:LYS:NZ	2.30	0.58
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.34	0.58
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.04	0.58
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.37	0.58
32:2a:1027:C:H2'	32:2a:1028:C:C6	2.38	0.58
1:1A:2208:G:H2'	1:1A:2209:G:H5''	1.86	0.58
1:1A:2320:G:O2'	1:1A:2322:A:N7	2.34	0.58
21:1Z:118:GLN:N	21:1Z:173:ALA:O	2.36	0.58
33:1b:17:PHE:HA	33:1b:44:LEU:HD11	1.85	0.58
1:2A:671:C:N4	60:2A:4014:HOH:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.84	0.58
32:2a:406:G:H21	35:2d:119:GLN:HE22	1.50	0.58
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.84	0.58
1:1A:196:A:H2'	1:1A:197:C:O4'	2.03	0.58
1:1A:1513:G:HO2'	1:1A:1593:C:HO2'	1.34	0.58
12:1Q:93:TYR:OH	21:1Z:194:PRO:HG2	2.03	0.58
20:1Y:17:SER:OG	20:1Y:71:LYS:NZ	2.28	0.58
1:2A:952:G:OP1	12:2Q:16:ARG:NH2	2.36	0.58
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.28	0.58
1:1A:2108:U:H2'	1:1A:2109:G:C8	2.38	0.58
1:1A:2904:U:H2'	1:1A:2905:C:C6	2.39	0.58
18:1W:65:LEU:HD12	18:1W:68:ARG:HE	1.69	0.58
32:1a:532:A:N6	32:1a:1206:G:O2'	2.35	0.58
1:2A:2816:C:N4	60:2A:4013:HOH:O	2.35	0.58
4:2E:121:ASN:ND2	60:2E:401:HOH:O	2.36	0.58
5:2F:20:LEU:HD23	5:2F:22:ALA:HB2	1.86	0.58
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HB	1.85	0.58
33:2b:80:ILE:HG12	33:2b:215:LEU:HD12	1.85	0.58
1:1A:10:G:N2	1:1A:2813:G:OP1	2.36	0.58
21:1Z:128:VAL:HB	21:1Z:161:VAL:HG23	1.86	0.58
32:1a:171:A:H2'	32:1a:172:A:C8	2.39	0.58
32:1a:1003:G:C2	32:1a:1004:A:H1'	2.38	0.58
32:1a:1027:C:H2'	32:1a:1028:C:C6	2.38	0.58
32:1a:1136:U:H5''	32:1a:1137:C:C2	2.37	0.58
1:2A:226:G:N2	1:2A:228:A:H62	2.02	0.58
6:1G:170:ARG:NH1	6:1G:174:GLU:OE1	2.36	0.58
51:1t:90:GLN:HA	51:1t:93:GLU:HG2	1.84	0.58
23:21:83:GLU:OE1	23:21:83:GLU:N	2.37	0.58
32:2a:988:G:H1	32:2a:1217:C:N4	1.99	0.58
1:1A:2148:A:H4'	1:1A:2149:G:O5'	2.04	0.58
6:1G:16:ARG:HG3	6:1G:16:ARG:HH11	1.69	0.58
32:1a:486:U:H2'	32:1a:487:A:H8	1.69	0.58
1:2A:1915:5MU:H3'	1:2A:1916:A:H8	1.68	0.58
1:2A:2163:C:OP2	1:2A:2164:C:N4	2.36	0.58
32:2a:107:G:N7	51:2t:15:ARG:NH2	2.52	0.58
1:1A:1825:U:H2'	1:1A:1826:C:C6	2.39	0.58
32:1a:1289:A:OP1	52:1u:10:ARG:NH2	2.37	0.58
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.39	0.58
32:2a:76:C:H42	32:2a:93:G:H1	1.51	0.58
50:2s:53:ASN:HB2	50:2s:77:THR:HA	1.85	0.58
1:1A:142:G:H1'	19:1X:37:THR:HG21	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1261:G:P	16:1U:12:ARG:HH21	2.27	0.58
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.86	0.58
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.86	0.58
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.84	0.58
32:1a:1101:A:N6	33:1b:176:GLU:OE2	2.37	0.58
1:2A:1741:A:H2'	1:2A:1742:G:O4'	2.04	0.58
1:2A:2867:G:OP2	15:2T:119:LYS:NZ	2.36	0.58
32:2a:404:U:O2	32:2a:498:U:C5	2.57	0.58
47:2p:72:ARG:HG3	47:2p:73:LEU:N	2.18	0.58
25:13:3:ARG:HD3	25:13:60:GLU:CD	2.29	0.57
32:1a:343:U:C2	32:1a:346:G:O6	2.56	0.57
32:1a:406:G:H4'	35:1d:5:ILE:HD11	1.85	0.57
54:1x:50:U:H5'	54:1x:51:C:OP2	2.04	0.57
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.36	0.57
32:2a:316:G:OP2	32:2a:351:G:O2'	2.21	0.57
32:2a:473:G:H2'	32:2a:474:G:H8	1.69	0.57
35:2d:11:LEU:HG	35:2d:66:ARG:HD3	1.85	0.57
40:2i:53:VAL:HG21	40:2i:92:TYR:CE1	2.39	0.57
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.04	0.57
33:1b:231:GLU:HB3	33:1b:232:PRO:CD	2.32	0.57
50:1s:31:ILE:HD12	50:1s:49:ILE:HG12	1.86	0.57
8:2I:75:LEU:HD11	8:2I:105:HIS:ND1	2.19	0.57
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.69	0.57
33:2b:127:ILE:C	33:2b:129:GLU:H	2.11	0.57
33:1b:178:ARG:NH2	39:1h:68:ARG:HH21	2.01	0.57
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.37	0.57
47:1p:75:ARG:HG3	47:1p:80:PHE:CD2	2.39	0.57
1:2A:2162:G:H4'	1:2A:2172:U:O2'	2.03	0.57
26:24:50:VAL:HG21	44:2m:65:LYS:N	2.20	0.57
39:2h:86:ILE:HG13	39:2h:133:LEU:HD22	1.86	0.57
34:1c:8:ILE:HG23	34:1c:16:ARG:HD3	1.86	0.57
1:2A:302:C:H42	1:2A:315:G:H1	1.51	0.57
1:2A:2430:A:H2'	1:2A:2430:A:N3	2.19	0.57
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.69	0.57
25:23:8:LEU:HG	25:23:31:LEU:HD22	1.87	0.57
32:2a:442:C:N4	32:2a:492:G:H1	2.03	0.57
32:2a:1157:A:H61	32:2a:1178:G:H21	1.51	0.57
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.37	0.57
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.86	0.57
40:2i:50:LEU:HD12	40:2i:56:LEU:HD23	1.86	0.57
1:1A:1091:A:H5'	1:1A:1092:A:H5''	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.38	0.57
2:2B:40:U:H2'	26:24:2:LYS:HE3	1.85	0.57
7:2H:59:ARG:O	7:2H:63:SER:OG	2.23	0.57
32:2a:660:G:H1	32:2a:745:C:H42	1.53	0.57
38:2g:20:ASP:OD2	38:2g:63:LYS:NZ	2.30	0.57
8:1I:4:ILE:HD11	8:1I:44:LEU:HD13	1.85	0.57
32:1a:344:A:H4'	32:1a:345:C:OP2	2.05	0.57
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.38	0.57
35:1d:61:LYS:NZ	35:1d:72:GLU:OE1	2.37	0.57
3:2D:79:VAL:HG21	3:2D:111:LEU:HD11	1.85	0.57
34:2c:97:LYS:O	34:2c:99:VAL:N	2.38	0.57
1:1A:831:A:H5'	1:1A:832:G:OP1	2.05	0.57
1:1A:2136:A:O2'	1:1A:2189:U:H5''	2.04	0.57
2:1B:59:A:N6	60:1B:3101:HOH:O	2.16	0.57
7:1H:85:LYS:HE2	7:1H:142:GLY:HA2	1.87	0.57
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.39	0.57
35:1d:53:ASP:HB3	35:1d:57:ARG:HH12	1.68	0.57
1:1A:953:U:H4'	12:1Q:101:ARG:HH22	1.69	0.57
1:1A:2464:C:OP1	55:1y:4:ARG:NH2	2.38	0.57
11:1P:126:VAL:HG12	11:1P:148:LEU:HD11	1.87	0.57
25:13:44:ARG:O	25:13:48:GLU:HG3	2.04	0.57
32:1a:343:U:H3	32:1a:346:G:H1	1.52	0.57
34:1c:104:GLN:HG3	34:1c:105:GLU:N	2.20	0.57
42:1k:19:ALA:HB3	42:1k:82:VAL:HG22	1.86	0.57
44:1m:60:VAL:HG22	44:1m:64:TRP:HZ3	1.68	0.57
1:2A:1076:C:H4'	1:2A:1077:A:OP1	2.04	0.57
1:2A:2189:U:H2'	1:2A:2190:G:H8	1.68	0.57
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HB2	1.86	0.57
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.85	0.57
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.87	0.57
32:1a:1347:G:H8	40:1i:107:ARG:HB3	1.70	0.57
44:1m:90:LEU:HD23	44:1m:93:ARG:HH21	1.70	0.57
1:2A:2666:C:N4	7:2H:108:GLY:O	2.33	0.57
32:2a:406:G:N2	35:2d:119:GLN:HE22	2.03	0.57
32:2a:1006:C:N4	32:2a:1022:G:O6	2.38	0.57
32:2a:1129:C:OP1	40:2i:16:ARG:NH1	2.37	0.57
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.12	0.57
11:1P:97:PRO:HA	11:1P:112:LEU:HD12	1.87	0.57
32:1a:473:G:H2'	32:1a:474:G:C8	2.39	0.57
33:1b:19:HIS:CE1	33:1b:206:ASP:HB2	2.40	0.57
32:2a:986:A:N3	50:2s:52:TYR:OH	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.22	0.57
1:1A:402:C:H2'	1:1A:403:C:C6	2.40	0.56
1:1A:843:C:H2'	1:1A:844:C:C6	2.39	0.56
1:1A:2710:U:H2'	1:1A:2711:C:C6	2.40	0.56
6:1G:50:ALA:C	6:1G:52:ILE:H	2.13	0.56
32:1a:280:C:OP1	48:1q:91:ARG:NH1	2.37	0.56
44:1m:11:ARG:O	44:1m:12:ASN:HB2	2.04	0.56
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.40	0.56
1:2A:2660:A:N7	7:2H:175:LYS:NZ	2.50	0.56
1:1A:326:C:OP2	20:1Y:73:ARG:NH2	2.38	0.56
9:1N:34:LEU:HD21	9:1N:120:LEU:HB2	1.87	0.56
32:1a:424:G:H2'	32:1a:425:G:H8	1.70	0.56
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.20	0.56
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.37	0.56
7:2H:89:ILE:O	7:2H:129:THR:HG23	2.05	0.56
15:2T:22:PHE:HE1	15:2T:49:VAL:HG11	1.69	0.56
25:23:6:VAL:HG13	25:23:56:VAL:HG13	1.85	0.56
1:1A:7:G:H2'	1:1A:8:A:O4'	2.05	0.56
1:1A:1055:A:OP2	9:1N:37:LYS:NZ	2.39	0.56
1:1A:2858:G:H8	15:1T:97:ALA:HB2	1.70	0.56
3:1D:145:VAL:HG11	3:1D:175:LEU:HD11	1.86	0.56
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	1.87	0.56
5:1F:8:GLN:HE22	5:1F:21:ALA:HB2	1.71	0.56
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.39	0.56
26:14:16:CYS:SG	26:14:17:GLY:N	2.78	0.56
32:1a:966:M2G:HM12	54:1x:34:C:H5'	1.86	0.56
47:1p:21:VAL:HG22	47:1p:33:ILE:HD12	1.86	0.56
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.38	0.56
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.40	0.56
1:2A:2129:C:N3	1:2A:2159:G:O6	2.38	0.56
1:2A:2819:G:H1	1:2A:2827:C:H42	1.51	0.56
28:26:13:CYS:SG	28:26:47:THR:HG21	2.45	0.56
32:2a:986:A:H1'	50:2s:54:GLY:O	2.05	0.56
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.86	0.56
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.21	0.56
36:2e:74:GLY:HA3	36:2e:116:THR:HG22	1.87	0.56
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.87	0.56
38:2g:114:ARG:HB2	38:2g:115:ARG:HH22	1.71	0.56
1:1A:2348:A:H61	22:10:43:THR:CG2	2.18	0.56
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	1.87	0.56
32:1a:673:G:H2'	32:1a:674:G:C8	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:178:ARG:HH22	39:1h:68:ARG:HH21	1.54	0.56
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.41	0.56
1:2A:2657:A:O3'	7:2H:160:LYS:NZ	2.38	0.56
1:1A:989:G:H5''	1:1A:990:A:O5'	2.05	0.56
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.88	0.56
25:13:10:LYS:NZ	25:13:15:TYR:OH	2.38	0.56
32:1a:1276:G:N3	32:1a:1282:C:O2'	2.36	0.56
33:1b:36:ARG:O	33:1b:38:GLY:N	2.35	0.56
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.20	0.56
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.36	0.56
32:2a:979:C:O2	45:2n:19:ARG:NE	2.37	0.56
1:1A:2236:G:OP1	3:1D:268:ARG:NE	2.39	0.56
5:1F:56:GLU:OE1	5:1F:93:LYS:NZ	2.38	0.56
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.24	0.56
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.87	0.56
32:2a:1135:U:H2'	32:2a:1137:C:C4	2.40	0.56
32:2a:1182:G:H4'	32:2a:1183:A:H5'	1.86	0.56
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.38	0.56
1:1A:605:G:H2'	1:1A:606:G:C8	2.40	0.56
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.38	0.56
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.87	0.56
32:1a:11:G:O2'	32:1a:506:G:N2	2.35	0.56
32:1a:1346:A:H61	32:1a:1374:A:H3'	1.71	0.56
32:1a:1402:4OC:CM2	32:1a:1403:C:H5'	2.35	0.56
43:1l:57:LYS:HD2	43:1l:67:THR:HG23	1.87	0.56
1:2A:453:C:O2	1:2A:457:A:O2'	2.23	0.56
26:24:46:GLN:HE21	26:24:48:ARG:HH22	1.53	0.56
32:2a:109:A:H2'	32:2a:326:G:N2	2.20	0.56
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.22	0.56
3:1D:69:ARG:HE	3:1D:130:ALA:HB2	1.71	0.56
32:1a:198:G:H2'	32:1a:199:G:H8	1.71	0.56
33:1b:24:TRP:HZ3	33:1b:29:ALA:HB2	1.71	0.56
1:2A:2137:C:H2'	1:2A:2138:C:O4'	2.05	0.56
7:2H:33:LEU:HD11	7:2H:75:ALA:HB1	1.87	0.56
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.88	0.56
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.38	0.56
32:2a:520:A:H2'	32:2a:521:G:O4'	2.05	0.56
34:2c:20:SER:OG	34:2c:22:TRP:NE1	2.36	0.56
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.88	0.56
32:1a:744:C:O2'	32:1a:851:G:N2	2.38	0.56
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:332:A:O2'	1:2A:334:C:OP2	2.24	0.56
1:2A:1155:A:H5''	16:2U:55:ARG:HD3	1.87	0.56
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.40	0.56
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.05	0.56
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.38	0.56
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	1.88	0.56
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.41	0.56
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.21	0.56
1:1A:1091:A:H1'	1:1A:1093:G:N3	2.21	0.56
32:1a:77:G:C2'	32:1a:78:G:H5'	2.36	0.56
33:1b:158:LEU:HD21	33:1b:180:LEU:HD13	1.88	0.56
34:1c:107:GLN:O	34:1c:108:ASN:HB2	2.06	0.56
46:1o:69:TYR:HA	46:1o:72:ARG:NH2	2.20	0.56
1:2A:1063:G:H1	1:2A:1075:C:H42	1.54	0.56
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.21	0.56
7:2H:17:VAL:HG22	7:2H:26:VAL:HG22	1.88	0.56
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.20	0.56
32:2a:811:C:N4	60:2a:1908:HOH:O	2.38	0.56
32:2a:946:A:H2'	32:2a:947:G:C8	2.41	0.56
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.71	0.56
2:1B:91:C:OP2	12:1Q:16:ARG:NH1	2.39	0.55
6:1G:40:ASN:HB3	6:1G:156:ASP:HB2	1.87	0.55
32:1a:750:G:H1'	46:1o:22:THR:O	2.06	0.55
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.89	0.55
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.39	0.55
1:1A:1186:U:OP1	9:1N:25:ARG:NH1	2.39	0.55
1:1A:2579:G:H2'	1:1A:2580:C:C6	2.41	0.55
1:2A:662:G:H5''	11:2P:16:ARG:HG2	1.88	0.55
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.05	0.55
2:2B:5:C:H42	2:2B:116:G:H1	1.54	0.55
32:2a:376:G:H5''	47:2p:5:ARG:HD2	1.88	0.55
32:2a:501:C:H2'	32:2a:502:G:H8	1.71	0.55
33:2b:47:THR:O	33:2b:51:LEU:N	2.36	0.55
1:1A:1219:A:H1'	1:1A:1220:U:C5'	2.36	0.55
13:1R:97:VAL:HG22	13:1R:114:VAL:HG22	1.88	0.55
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	1.89	0.55
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.06	0.55
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.89	0.55
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.06	0.55
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.89	0.55
1:1A:1766:G:N2	1:1A:1768:U:OP2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.07	0.55
32:1a:473:G:H2'	32:1a:474:G:H8	1.70	0.55
40:1i:5:TYR:H	40:1i:87:GLN:HE22	1.53	0.55
1:2A:2128:C:H2'	1:2A:2129:C:H5''	1.89	0.55
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.07	0.55
32:2a:1125:U:O2'	32:2a:1126:U:H2'	2.06	0.55
47:2p:19:ILE:HG22	47:2p:36:ILE:HG13	1.88	0.55
1:1A:606:G:OP2	16:1U:10:ARG:NH1	2.39	0.55
1:1A:1091:A:H8	1:1A:1157:A:C6	2.25	0.55
1:1A:1855:G:OP1	3:1D:52:ARG:NH1	2.39	0.55
7:1H:72:ILE:O	7:1H:76:VAL:HG23	2.06	0.55
32:1a:138:G:H1	32:1a:225:C:N4	2.03	0.55
32:1a:971:G:N2	32:1a:1363(A):A:OP2	2.35	0.55
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.42	0.55
32:1a:1348:U:H4'	40:1i:120:ARG:HD2	1.86	0.55
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.21	0.55
40:1i:114:TYR:HE1	41:1j:59:SER:HA	1.71	0.55
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.71	0.55
32:2a:1028:C:H1'	32:2a:1034:G:H1'	1.89	0.55
1:1A:733:G:N2	1:1A:835:A:H61	2.05	0.55
33:1b:222:ILE:O	33:1b:226:ARG:HB2	2.07	0.55
34:1c:85:ARG:HA	34:1c:88:ARG:HD2	1.88	0.55
1:2A:1297:C:O2'	1:2A:1302:A:N1	2.34	0.55
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.42	0.55
32:2a:951:G:N7	44:2m:102:ARG:NH2	2.54	0.55
32:2a:1003:G:H2'	32:2a:1004:A:O4'	2.06	0.55
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.22	0.55
1:1A:1562:U:H2'	1:1A:1563:G:H8	1.72	0.55
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.41	0.55
51:1t:9:ASN:HB2	51:1t:13:LEU:HD11	1.88	0.55
8:2I:77:LEU:HD21	8:2I:100:ALA:HB3	1.88	0.55
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.38	0.55
33:2b:19:HIS:CE1	33:2b:206:ASP:HB2	2.42	0.55
41:2j:8:LEU:HD23	41:2j:96:ILE:HG23	1.88	0.55
1:1A:1889:G:N2	1:1A:1905:G:H2'	2.21	0.55
7:1H:88:LEU:HD23	7:1H:130:ARG:HG3	1.89	0.55
32:1a:392:G:H2'	32:1a:393:A:H8	1.71	0.55
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.89	0.55
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.87	0.55
1:2A:2224:G:H4'	1:2A:2226:C:C2	2.41	0.55
6:2G:173:LEU:HA	6:2G:176:LEU:HD12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:163:GLU:O	35:2d:166:LYS:HG2	2.06	0.55
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	1.88	0.55
32:2a:41:G:H2'	32:2a:42:G:H8	1.70	0.55
38:2g:68:ASN:HD22	38:2g:128:ALA:HA	1.72	0.55
40:2i:50:LEU:HB2	40:2i:56:LEU:HA	1.88	0.55
1:1A:240:A:C5	1:1A:241:G:H1'	2.41	0.55
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.71	0.55
2:1B:91:C:H5'	12:1Q:18:LYS:HA	1.88	0.55
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.40	0.55
32:1a:1309:G:OP2	44:1m:99:ARG:NH2	2.39	0.55
7:2H:149:ARG:NH1	7:2H:167:GLU:OE2	2.40	0.55
14:2S:78:LEU:HD11	14:2S:108:GLY:O	2.07	0.55
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.25	0.55
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.39	0.55
35:2d:201:GLN:NE2	36:2e:116:THR:OG1	2.40	0.55
41:2j:49:VAL:HG23	45:2n:41:ARG:HD2	1.89	0.55
9:1N:72:TYR:HE2	9:1N:87:LEU:HD23	1.72	0.54
21:1Z:58:VAL:HG12	21:1Z:68:PRO:HA	1.88	0.54
32:1a:164:U:H2'	32:1a:165:C:C6	2.42	0.54
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	1.88	0.54
35:1d:129:ASN:ND2	35:1d:144:ASP:OD1	2.40	0.54
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.89	0.54
32:2a:501:C:H2'	32:2a:502:G:C8	2.42	0.54
1:1A:385:G:C6	1:1A:386:U:O4	2.60	0.54
1:1A:1114:G:C8	1:1A:1115:A:N7	2.76	0.54
1:1A:2348:A:H61	22:10:43:THR:HG22	1.72	0.54
6:1G:16:ARG:HE	6:1G:31:VAL:HG21	1.71	0.54
11:1P:90:ARG:HH11	11:1P:105:LEU:HD11	1.72	0.54
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.07	0.54
18:1W:18:ARG:NH1	18:1W:76:VAL:O	2.39	0.54
32:1a:269:C:H2'	32:1a:270:A:C8	2.42	0.54
32:1a:404:U:O2	32:1a:498:U:C5	2.60	0.54
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.42	0.54
34:2c:34:LEU:HD13	45:2n:25:VAL:HG21	1.89	0.54
1:1A:1142:A:H8	1:1A:1142:A:OP2	1.91	0.54
32:1a:161:A:H2'	32:1a:162:A:C8	2.43	0.54
32:1a:404:U:C2	32:1a:498:U:O4	2.60	0.54
32:1a:833:U:H2'	32:1a:834:C:C6	2.42	0.54
33:1b:16:HIS:O	33:1b:18:GLY:N	2.38	0.54
33:1b:97:TRP:HZ2	33:1b:102:LEU:HD13	1.72	0.54
36:1e:82:VAL:HG21	36:1e:138:ALA:HA	1.87	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:984:A:H5''	1:2A:985:C:H5	1.72	0.54
1:2A:1430:C:N4	1:2A:1563:G:H1	2.02	0.54
1:2A:2119:A:H61	1:2A:2168:G:H21	0.65	0.54
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.88	0.54
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.33	0.54
7:2H:90:LYS:NZ	7:2H:159:GLU:OE2	2.40	0.54
12:2Q:55:VAL:HG11	21:2Z:183:LEU:HD21	1.89	0.54
32:2a:189(C):C:H2'	32:2a:189(D):C:O4'	2.06	0.54
33:2b:93:VAL:HG21	33:2b:97:TRP:CD1	2.40	0.54
54:2x:31:G:H3'	54:2x:32:5MC:HM53	1.89	0.54
1:1A:591:U:O2'	60:1A:9004:HOH:O	2.18	0.54
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.40	0.54
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.91	0.54
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.08	0.54
32:1a:1372:U:OP1	40:1i:72:GLY:N	2.40	0.54
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.43	0.54
36:1e:11:ILE:HD11	36:1e:108:ALA:HB3	1.89	0.54
52:1u:6:ARG:CZ	52:1u:15:ARG:HH12	2.20	0.54
1:2A:207:A:H2'	1:2A:208:C:O4'	2.08	0.54
1:2A:1210:A:O2'	60:2A:4005:HOH:O	2.17	0.54
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.89	0.54
34:2c:8:ILE:HD12	34:2c:16:ARG:HD2	1.89	0.54
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.43	0.54
40:2i:9:ARG:HB2	40:2i:104:ARG:HE	1.72	0.54
32:1a:757:U:OP1	32:1a:822:C:O2'	2.26	0.54
32:1a:1288:A:N1	32:1a:1371:G:H1'	2.23	0.54
33:1b:130:ARG:O	33:1b:135:GLN:NE2	2.40	0.54
1:2A:1034:G:H5'	31:29:18:ARG:HD3	1.90	0.54
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.06	0.54
32:2a:1183:A:H5''	32:2a:1183:A:C8	2.42	0.54
39:2h:11:THR:O	39:2h:15:ASN:ND2	2.40	0.54
1:1A:509:A:H5''	20:1Y:50:ARG:HD3	1.89	0.54
1:1A:2418:U:H2'	1:1A:2418:U:OP2	2.07	0.54
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.90	0.54
32:1a:41:G:H2'	32:1a:42:G:C8	2.43	0.54
32:1a:1492:A:H4'	32:1a:1493:A:N1	2.22	0.54
47:1p:43:LYS:HG2	47:1p:48:TRP:CD2	2.42	0.54
1:2A:1200:C:H5'	60:2A:4003:HOH:O	2.08	0.54
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.42	0.54
1:2A:1792:G:O2'	1:2A:1830:C:OP1	2.25	0.54
1:2A:2641:G:P	9:2N:74:ARG:HH22	2.31	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:46:VAL:HG12	14:2S:48:LEU:HD12	1.90	0.54
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.90	0.54
20:2Y:20:TYR:CE2	20:2Y:43:ASN:HA	2.42	0.54
39:2h:4:ASP:OD2	39:2h:85:ARG:NH1	2.41	0.54
1:1A:1827:U:H2'	1:1A:1828:C:C6	2.42	0.54
1:1A:2155:G:HO2'	1:1A:2180:A:H2	1.56	0.54
1:1A:2250:G:N3	1:1A:2250:G:H2'	2.23	0.54
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.07	0.54
9:1N:67:LEU:HD12	9:1N:87:LEU:HD12	1.88	0.54
10:1O:68:GLU:HB3	10:1O:78:ARG:HD3	1.90	0.54
21:1Z:182:LYS:O	21:1Z:185:GLU:HG3	2.07	0.54
32:1a:1006:C:H2'	32:1a:1007:C:C6	2.42	0.54
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.73	0.54
1:2A:1069:A:H5'	1:2A:1096:A:C5'	2.38	0.54
17:2V:5:VAL:HG11	17:2V:57:VAL:HG21	1.90	0.54
34:2c:22:TRP:CZ3	34:2c:32:LEU:HD23	2.42	0.54
44:2m:48:LEU:HD22	44:2m:52:GLU:HB3	1.90	0.54
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.89	0.54
1:1A:599:U:H2'	1:1A:600:G:C8	2.43	0.54
32:1a:167:G:H2'	32:1a:168:G:H8	1.72	0.54
32:1a:438:G:O2'	32:1a:494:U:O4	2.17	0.54
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.90	0.54
44:1m:49:THR:HB	44:1m:52:GLU:H	1.73	0.54
44:1m:74:VAL:O	44:1m:78:ILE:HG13	2.07	0.54
54:1x:8:4SU:O5'	54:1x:8:4SU:H6	2.08	0.54
32:2a:954:G:H21	32:2a:1227:A:N6	2.03	0.54
32:2a:976:G:OP2	32:2a:1358:U:O2'	2.21	0.54
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.37	0.54
50:2s:38:SER:HB2	50:2s:71:LEU:HD22	1.90	0.54
1:1A:2156:A:O2'	1:1A:2181:G:N3	2.38	0.54
9:1N:9:VAL:HG21	9:1N:39:ARG:NH2	2.22	0.54
32:1a:38:G:N2	32:1a:397:A:H5''	2.18	0.54
32:1a:198:G:O6	32:1a:219:C:N4	2.41	0.54
41:1j:62:HIS:HB3	45:1n:59:ALA:HB3	1.90	0.54
1:2A:579:G:H2'	1:2A:580:C:C6	2.42	0.54
1:2A:1072:C:N4	1:2A:1093:G:H1	2.06	0.54
2:2B:16:G:N2	2:2B:68:C:N3	2.44	0.54
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.89	0.54
9:2N:34:LEU:HD21	9:2N:120:LEU:HB2	1.90	0.54
20:2Y:5:MET:HE2	20:2Y:32:PRO:HA	1.90	0.54
32:2a:1035:A:HO2'	32:2a:1036:G:H8	1.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:43:LYS:HA	47:2p:48:TRP:HB3	1.89	0.54
1:1A:265:U:H2'	1:1A:266:C:C6	2.43	0.54
1:1A:2149:G:N2	1:1A:2195:A:H1'	2.23	0.54
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.43	0.54
1:1A:2621:U:C5	55:1y:15:PRO:HG2	2.43	0.54
32:1a:1212:U:H5''	32:1a:1213:A:H5'	1.89	0.54
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.73	0.54
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.89	0.54
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.40	0.54
1:2A:1300:U:H4'	1:2A:1301:A:H5'	1.89	0.54
1:2A:1946:U:H2'	1:2A:1947:C:C6	2.43	0.54
6:2G:139:LEU:HD21	6:2G:152:LEU:HD23	1.90	0.54
8:2I:101:LEU:HD21	8:2I:140:LEU:HD11	1.89	0.54
32:2a:664:G:N2	32:2a:741:G:H1	2.03	0.54
32:2a:1302:U:OP2	44:2m:21:TYR:OH	2.22	0.54
33:2b:178:ARG:NH1	33:2b:196:LEU:O	2.41	0.54
1:1A:965:G:N2	1:1A:2281:A:OP2	2.41	0.53
6:1G:62:LEU:HD13	26:14:28:LYS:HZ1	1.73	0.53
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.90	0.53
15:1T:22:PHE:CE1	15:1T:49:VAL:HG11	2.42	0.53
48:1q:6:LEU:HD23	48:1q:23:VAL:HG11	1.90	0.53
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.24	0.53
1:2A:2155:G:H2'	1:2A:2156:G:O4'	2.07	0.53
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.42	0.53
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.16	0.53
2:2B:18:G:H1	2:2B:65:C:N4	2.02	0.53
6:2G:166:ASP:O	6:2G:170:ARG:N	2.40	0.53
32:2a:1148:U:O4'	40:2i:16:ARG:HD2	2.08	0.53
41:2j:77:PRO:O	41:2j:81:THR:OG1	2.26	0.53
32:1a:673:G:O3'	37:1f:87:ARG:NH2	2.41	0.53
40:1i:9:ARG:HG2	40:1i:14:VAL:HG13	1.88	0.53
54:1x:53:G:H2'	54:1x:54:5MU:C6	2.43	0.53
12:2Q:16:ARG:HG3	12:2Q:17:LEU:H	1.74	0.53
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.08	0.53
30:28:26:LYS:HE3	30:28:46:ARG:HH12	1.72	0.53
32:2a:93:G:H2'	32:2a:96:U:O4'	2.08	0.53
32:2a:923:A:O2'	32:2a:1399:C:OP2	2.18	0.53
32:2a:1051:C:H2'	32:2a:1052:U:H6	1.73	0.53
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.72	0.53
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.91	0.53
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:408:A:H4'	35:1d:112:VAL:HG21	1.90	0.53
32:1a:1286:A:H2	52:1u:18:TYR:HH	1.57	0.53
34:1c:109:PRO:HB3	34:1c:115:LEU:HD23	1.90	0.53
36:1e:71:LEU:HD21	36:1e:115:VAL:HG22	1.90	0.53
1:2A:1789:A:N6	60:2A:4018:HOH:O	2.42	0.53
1:2A:1835:G:H5'	1:2A:1836:C:OP2	2.08	0.53
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.43	0.53
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.26	0.53
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.42	0.53
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.08	0.53
32:1a:270:A:H2'	32:1a:271:C:C6	2.43	0.53
50:1s:52:TYR:HA	50:1s:56:GLN:O	2.08	0.53
1:2A:1078:U:O2'	1:2A:1079:C:OP2	2.26	0.53
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.42	0.53
2:2B:22:U:H3	2:2B:61:G:H1	1.56	0.53
14:2S:66:ALA:O	14:2S:69:VAL:HG12	2.08	0.53
32:2a:392:G:H2'	32:2a:393:A:H8	1.72	0.53
32:2a:407:G:H2'	32:2a:408:A:C8	2.44	0.53
1:1A:2185:C:OP2	1:1A:2186:C:N4	2.40	0.53
8:1I:57:ARG:O	8:1I:61:ARG:HG2	2.09	0.53
33:1b:160:ASP:N	33:1b:160:ASP:OD1	2.41	0.53
34:1c:8:ILE:HD12	34:1c:16:ARG:HD2	1.90	0.53
35:1d:11:LEU:HG	35:1d:66:ARG:HD3	1.91	0.53
41:1j:78:ASN:O	41:1j:80:LYS:N	2.42	0.53
1:2A:603:A:N1	1:2A:625:G:O2'	2.40	0.53
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.44	0.53
25:23:5:LYS:HG3	25:23:36:VAL:HG22	1.90	0.53
1:1A:1117:G:H4'	1:1A:1135:G:OP2	2.09	0.53
1:1A:1186:U:OP2	9:1N:63:THR:OG1	2.27	0.53
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.42	0.53
1:1A:2801:C:O2'	1:1A:2819:A:N3	2.40	0.53
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.43	0.53
19:1X:60:ARG:NH1	29:17:47:ARG:HH22	2.04	0.53
34:1c:59:ARG:O	41:1j:92:THR:HG22	2.09	0.53
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	1.89	0.53
1:2A:61:G:OP1	24:22:51:ARG:NH1	2.41	0.53
32:2a:1114:C:H42	32:2a:1186:G:H1	1.55	0.53
36:2e:78:HIS:CE1	36:2e:143:ARG:H	2.13	0.53
1:1A:1085:G:N1	1:1A:1162:C:N4	2.16	0.53
5:1F:95:ARG:HD3	5:1F:97:TYR:CZ	2.43	0.53
18:1W:67:ASP:OD1	18:1W:67:ASP:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:450:G:H1	32:1a:483:C:H42	1.56	0.53
32:1a:1005:A:N6	32:1a:1024:G:C2	2.77	0.53
35:1d:120:LEU:HB3	35:1d:126:ILE:HD11	1.89	0.53
1:2A:1071:G:N2	60:2A:4017:HOH:O	2.42	0.53
1:2A:1296:G:OP1	1:2A:2709:G:O2'	2.22	0.53
32:2a:17:U:O2'	32:2a:1079:G:N3	2.39	0.53
32:2a:814:A:H2'	32:2a:816:A:H5''	1.89	0.53
32:2a:1114:C:H1'	45:2n:60:SER:O	2.08	0.53
42:2k:19:ALA:HB3	42:2k:82:VAL:HG22	1.91	0.53
43:2l:60:LEU:HB2	43:2l:64:TYR:O	2.09	0.53
1:1A:1139:G:C2'	1:1A:1144:A:H61	2.22	0.53
15:1T:96:ARG:HH11	15:1T:96:ARG:HB2	1.74	0.53
17:1V:72:VAL:HG13	17:1V:85:LYS:HB3	1.90	0.53
32:1a:1003:G:N2	32:1a:1004:A:N3	2.57	0.53
33:1b:19:HIS:HE1	33:1b:206:ASP:HB2	1.73	0.53
1:2A:606:U:H4'	1:2A:658:C:H4'	1.91	0.53
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.09	0.53
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.90	0.53
21:2Z:30:ASN:ND2	21:2Z:90:VAL:HB	2.23	0.53
32:2a:1435:G:H2'	32:2a:1436:U:H6	1.73	0.53
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.23	0.53
32:1a:992:U:H4'	32:1a:993:G:O5'	2.09	0.53
1:2A:581:C:H2'	1:2A:582:G:C8	2.44	0.53
1:2A:793:A:OP2	1:2A:2071:A:O2'	2.26	0.53
26:24:24:THR:OG1	26:24:25:TYR:N	2.36	0.53
32:2a:537:G:OP1	43:2l:113:ARG:NH1	2.40	0.53
1:1A:602:G:H2'	1:1A:603:C:C6	2.44	0.53
1:1A:1525:G:O2'	1:1A:1605:A:N7	2.40	0.53
1:1A:1815:A:H4'	1:1A:1816:A:O5'	2.09	0.53
1:1A:2806:G:H2'	1:1A:2807:C:O4'	2.09	0.53
33:1b:71:VAL:HB	33:1b:164:VAL:HG13	1.91	0.53
40:1i:45:ALA:O	40:1i:78:LYS:HE2	2.09	0.53
1:2A:1044:G:H1'	1:2A:1048:A:H1'	1.91	0.53
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.44	0.53
5:2F:135:LYS:HG2	5:2F:137:LYS:HG2	1.90	0.53
8:2I:38:LEU:HB3	8:2I:40:THR:HG23	1.90	0.53
14:2S:71:ARG:NE	14:2S:107:GLU:OE1	2.39	0.53
32:2a:353:A:H5'	32:2a:353:A:H8	1.72	0.53
32:2a:1183:A:H5''	32:2a:1183:A:H8	1.73	0.53
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.23	0.53
1:1A:116:A:C8	1:1A:117:A:C8	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:625:G:O2'	1:1A:702:A:N6	2.42	0.52
7:1H:125:VAL:HG22	7:1H:131:VAL:HG22	1.90	0.52
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HD2	1.91	0.52
32:1a:110:C:O2'	47:1p:25:ARG:O	2.27	0.52
32:1a:841:U:P	32:1a:841:U:H6	2.32	0.52
36:1e:110:LEU:HD13	36:1e:118:ILE:HD13	1.90	0.52
1:2A:1056:G:H5''	1:2A:1057:A:O4'	2.09	0.52
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.44	0.52
1:2A:2602:A:N7	54:2x:76:A:O2'	2.41	0.52
1:2A:2641:G:P	9:2N:74:ARG:HH12	2.32	0.52
5:2F:11:VAL:HB	5:2F:18:ARG:HG2	1.91	0.52
7:2H:55:PRO:HG2	7:2H:61:HIS:CG	2.43	0.52
48:2q:94:ASN:O	48:2q:98:LEU:HD13	2.09	0.52
1:1A:441:C:H2'	1:1A:442:A:C8	2.43	0.52
1:1A:641:G:OP2	5:1F:43:LYS:NZ	2.42	0.52
1:1A:946:A:H2'	1:1A:947:A:H8	1.72	0.52
1:1A:1727:U:O2'	1:1A:1794:G:N7	2.34	0.52
3:1D:69:ARG:C	3:1D:71:ASP:H	2.17	0.52
32:1a:923:A:O2'	32:1a:1399:C:OP2	2.25	0.52
1:2A:2626:C:H2'	1:2A:2627:G:O4'	2.10	0.52
4:2E:21:VAL:HG12	4:2E:185:LYS:HD2	1.92	0.52
6:2G:36:LYS:HE2	6:2G:160:VAL:HG21	1.92	0.52
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.91	0.52
32:2a:344:A:H4'	32:2a:345:C:OP2	2.08	0.52
32:2a:615:C:H2'	32:2a:616:G:O4'	2.09	0.52
49:2r:34:TYR:CD1	49:2r:35:ARG:HG3	2.44	0.52
1:1A:2584:A:N7	4:1E:144:ARG:HD2	2.24	0.52
32:1a:757:U:H2'	32:1a:758:G:O4'	2.10	0.52
32:1a:1320:C:O2	50:1s:36:ARG:NH2	2.41	0.52
33:1b:61:LEU:HD23	33:1b:68:ILE:HD11	1.91	0.52
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.73	0.52
1:2A:2167:U:H2'	1:2A:2168:G:C8	2.45	0.52
33:2b:149:LEU:O	33:2b:153:ARG:N	2.41	0.52
40:2i:8:GLY:O	40:2i:15:ALA:N	2.35	0.52
1:1A:236:G:H4'	1:1A:413:G:C5	2.45	0.52
1:1A:811:A:N3	3:1D:213:ARG:NH1	2.56	0.52
1:1A:1133:G:N2	1:1A:1149:A:H1'	2.24	0.52
9:1N:67:LEU:HA	9:1N:87:LEU:HD12	1.90	0.52
12:1Q:41:TRP:HZ3	12:1Q:74:TYR:HE1	1.58	0.52
32:1a:1004:A:C5	32:1a:1037:C:C2	2.98	0.52
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:140:G:N2	1:2A:1596:A:H4'	2.23	0.52
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.92	0.52
36:2e:110:LEU:HD21	36:2e:139:LEU:HD21	1.91	0.52
38:2g:69:VAL:HG21	38:2g:104:LEU:HD11	1.91	0.52
1:1A:174:U:H4'	1:1A:207:A:H4'	1.90	0.52
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.91	0.52
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.90	0.52
36:1e:102:ALA:HB1	36:1e:106:PRO:HG2	1.92	0.52
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.91	0.52
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.43	0.52
32:2a:458:C:H2'	32:2a:460:G:O4'	2.10	0.52
32:2a:573:A:N3	32:2a:883:C:O2'	2.39	0.52
1:1A:704:U:H2'	1:1A:705:C:C6	2.45	0.52
1:1A:2118:U:H3	1:1A:2215:G:H1	1.57	0.52
1:1A:2182:G:H2'	1:1A:2183:C:C6	2.44	0.52
1:1A:2495:C:N3	12:1Q:124:LYS:NZ	2.53	0.52
12:1Q:6:ARG:C	12:1Q:7:MET:HG3	2.35	0.52
32:1a:533:A:O2'	32:1a:535:A:OP2	2.19	0.52
32:1a:877:C:H5''	39:1h:88:LYS:HD3	1.92	0.52
42:1k:48:ILE:HD13	42:1k:63:LEU:HD13	1.92	0.52
14:2S:36:TYR:HA	14:2S:52:SER:HB3	1.90	0.52
17:2V:33:VAL:HG23	17:2V:59:ALA:HB3	1.91	0.52
1:1A:1121:C:H2'	1:1A:1122:C:H3'	1.91	0.52
4:1E:78:LEU:O	4:1E:79:ARG:NH1	2.43	0.52
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.91	0.52
19:1X:60:ARG:HH12	29:17:47:ARG:NH2	2.04	0.52
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.91	0.52
32:1a:44:G:C2	32:1a:45:U:H1'	2.45	0.52
32:1a:1135:U:H4'	32:1a:1136:U:H5	1.74	0.52
39:1h:44:PHE:HB3	39:1h:80:ILE:HG12	1.92	0.52
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.75	0.52
39:1h:120:THR:N	39:1h:123:GLU:OE1	2.34	0.52
40:1i:45:ALA:O	40:1i:48:GLU:HB2	2.09	0.52
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.92	0.52
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.09	0.52
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.45	0.52
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.09	0.52
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	1.92	0.52
13:2R:79:LEU:HA	13:2R:83:ILE:HD12	1.91	0.52
21:2Z:150:LEU:HB3	21:2Z:171:ILE:HD11	1.92	0.52
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.24	0.52
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.74	0.52
1:1A:2227:G:H5''	1:1A:2228:G:N7	2.24	0.52
15:1T:126:ALA:HA	15:1T:129:ARG:NH1	2.24	0.52
28:16:14:THR:HG21	28:16:48:VAL:HG13	1.92	0.52
32:1a:169:C:H2'	32:1a:170:U:H6	1.73	0.52
32:1a:403:C:O2'	35:1d:122:ARG:NH1	2.42	0.52
32:1a:539:A:H2'	32:1a:540:G:C8	2.45	0.52
33:1b:9:GLU:HG3	33:1b:217:ARG:HH22	1.75	0.52
52:1u:6:ARG:NH2	52:1u:15:ARG:HH12	2.07	0.52
1:2A:588:U:H2'	1:2A:589:C:C6	2.44	0.52
1:2A:762:U:H5''	60:2A:4243:HOH:O	2.09	0.52
1:2A:878:A:H2'	1:2A:879:G:H5'	1.91	0.52
1:2A:1448:G:O2'	1:2A:1528(A):A:N1	2.39	0.52
1:2A:2119:A:N6	1:2A:2168:G:N2	2.21	0.52
1:2A:2318:G:H22	14:2S:3:ARG:NE	2.07	0.52
6:2G:141:PHE:HB3	6:2G:142:PRO:HD2	1.91	0.52
8:2I:26:ALA:HA	8:2I:30:LEU:HB2	1.91	0.52
32:2a:308:C:H2'	32:2a:309:G:C8	2.44	0.52
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.45	0.52
42:2k:20:TYR:CZ	42:2k:83:ILE:HD12	2.44	0.52
11:1P:116:GLY:O	11:1P:137:LYS:NZ	2.37	0.52
21:1Z:24:LEU:HD12	21:1Z:25:PRO:HD2	1.91	0.52
32:1a:1240:U:H4'	38:1g:38:LEU:HD21	1.92	0.52
32:1a:1279:A:O2'	32:1a:1281:U:OP2	2.25	0.52
1:2A:729:G:OP1	3:2D:10:THR:OG1	2.20	0.52
1:2A:1658:C:OP1	4:2E:135:HIS:NE2	2.42	0.52
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	1.91	0.52
1:2A:2471:C:N4	1:2A:2476:A:O2'	2.42	0.52
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.23	0.52
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.92	0.52
32:2a:1304:G:H1'	32:2a:1333:A:H61	1.73	0.52
32:2a:1376:U:O4	38:2g:10:ARG:NH1	2.43	0.52
32:2a:1426:C:H2'	32:2a:1427:U:C6	2.45	0.52
1:1A:2134:G:O6	1:1A:2191:A:N7	2.43	0.52
1:1A:2589:A:O4'	27:15:3:LYS:HB2	2.09	0.52
1:1A:2597:U:H4'	1:1A:2598:C:OP1	2.08	0.52
32:1a:384:G:H2'	32:1a:385:C:C6	2.45	0.52
32:1a:1003:G:N2	32:1a:1004:A:H1'	2.25	0.52
1:2A:458:G:O2'	29:27:39:ARG:HD3	2.10	0.52
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2378:A:O5'	1:2A:2378:A:H8	1.93	0.52
1:2A:2444:G:OP2	5:2F:68:LYS:NZ	2.34	0.52
32:2a:688:G:H1	32:2a:699:C:N4	2.06	0.52
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.45	0.52
33:2b:48:MET:HA	33:2b:51:LEU:HD12	1.92	0.52
34:2c:113:ALA:HB2	34:2c:202:ILE:HG13	1.92	0.52
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.45	0.52
1:1A:721:G:O2'	5:1F:74:ARG:HD3	2.10	0.51
1:1A:1276:C:H2'	1:1A:1277:G:C8	2.45	0.51
1:1A:2879:G:H2'	1:1A:2880:C:O4'	2.10	0.51
30:18:23:VAL:HG22	30:18:47:LYS:HB3	1.92	0.51
30:18:62:LEU:HB3	30:18:65:GLU:HG3	1.92	0.51
47:1p:70:ALA:O	47:1p:74:LEU:HD12	2.11	0.51
54:1x:53:G:H2'	54:1x:54:5MU:H6	1.75	0.51
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.25	0.51
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.46	0.51
6:2G:55:LYS:HZ2	6:2G:153:ARG:HH22	1.58	0.51
32:2a:1034:G:H2'	32:2a:1035:A:O4'	2.10	0.51
34:1c:73:PRO:O	34:1c:77:ILE:HG12	2.10	0.51
1:2A:2316:C:O2'	6:2G:128:ARG:NH1	2.43	0.51
1:2A:2495:G:H5''	12:2Q:82:ARG:HG2	1.91	0.51
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.58	0.51
1:1A:2018:C:H4'	1:1A:2019:G:OP1	2.10	0.51
1:1A:2086:C:H2'	1:1A:2087:C:C6	2.45	0.51
1:1A:2131:U:O2	1:1A:2202:U:O4	2.28	0.51
1:1A:2211:U:H2'	1:1A:2212:G:C8	2.45	0.51
1:1A:2291:G:O6	22:10:14:ARG:HG3	2.10	0.51
32:1a:186:C:H2'	32:1a:187:C:C6	2.45	0.51
32:1a:332:G:OP2	51:1t:10:LEU:HD21	2.10	0.51
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.45	0.51
40:1i:25:LYS:HD2	40:1i:26:VAL:N	2.25	0.51
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.92	0.51
1:2A:226:G:H21	1:2A:228:A:H62	1.56	0.51
1:2A:2172:U:H4'	1:2A:2173:A:OP2	2.11	0.51
5:2F:118:ALA:HA	5:2F:123:LEU:HB3	1.92	0.51
20:2Y:86:ARG:HB2	20:2Y:98:VAL:HG23	1.92	0.51
32:2a:756:C:H2'	32:2a:757:U:O4'	2.11	0.51
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.94	0.51
35:2d:201:GLN:NE2	36:2e:116:THR:O	2.43	0.51
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.92	0.51
51:2t:37:SER:O	51:2t:41:ILE:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:437:U:O2'	35:1d:123:HIS:HD2	1.94	0.51
32:1a:1252:A:H2'	32:1a:1253:G:O4'	2.10	0.51
36:1e:107:ARG:O	36:1e:111:GLU:HB2	2.10	0.51
3:2D:4:LYS:HB3	3:2D:18:VAL:HG23	1.93	0.51
5:2F:197:ASP:O	5:2F:201:VAL:HG12	2.10	0.51
32:2a:17:U:H2'	32:2a:18:C:C6	2.45	0.51
32:2a:300:A:H8	32:2a:300:A:O5'	1.93	0.51
32:2a:560:U:O2'	32:2a:561:U:OP2	2.25	0.51
32:2a:947:G:H2'	32:2a:948:C:O4'	2.09	0.51
32:2a:1150:U:O4	32:2a:1151:A:N6	2.43	0.51
32:2a:1366:C:HO2'	41:2j:60:ARG:HH22	1.53	0.51
36:2e:11:ILE:HD11	36:2e:108:ALA:HB3	1.92	0.51
37:2f:1:MET:HE3	37:2f:66:GLU:HG2	1.93	0.51
1:1A:1140:U:H1'	1:1A:1143:U:C5	2.36	0.51
1:1A:1556:A:H2'	1:1A:1557:A:O4'	2.11	0.51
1:1A:1825:U:H2'	1:1A:1826:C:H6	1.75	0.51
1:1A:2184:G:H4'	1:1A:2194:U:O2'	2.11	0.51
1:1A:2800:C:H1'	4:1E:62:PRO:HG3	1.91	0.51
3:1D:71:ASP:OD2	3:1D:103:ARG:NH2	2.41	0.51
6:1G:135:LEU:O	6:1G:154:GLY:HA3	2.10	0.51
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.91	0.51
21:1Z:152:ALA:HB3	21:1Z:167:PRO:HA	1.92	0.51
32:1a:719:C:O2'	49:1r:49:LYS:HB3	2.11	0.51
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.92	0.51
1:2A:247:G:H4'	1:2A:386:G:C5	2.45	0.51
1:2A:2250:G:C8	1:2A:2496:C:H5''	2.45	0.51
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.90	0.51
5:2F:184:TYR:HE1	11:2P:3:LEU:HD21	1.75	0.51
10:2O:107:ARG:HG2	10:2O:115:VAL:HG21	1.93	0.51
32:2a:474:G:H2'	32:2a:475:G:C8	2.45	0.51
38:2g:78:ARG:HE	38:2g:80:VAL:CG2	2.23	0.51
50:2s:11:VAL:HB	50:2s:16:LEU:HD12	1.91	0.51
1:1A:1119:A:H3'	1:1A:1119:A:N3	2.25	0.51
1:1A:2023:A:H2'	1:1A:2024:G:C8	2.46	0.51
14:1S:15:ARG:O	14:1S:19:LYS:HG2	2.11	0.51
32:1a:77:G:H2'	32:1a:78:G:H5'	1.91	0.51
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.26	0.51
32:1a:1157:A:H4'	32:1a:1158:C:O5'	2.10	0.51
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.41	0.51
34:1c:6:HIS:HB3	45:1n:49:HIS:ND1	2.26	0.51
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2139:C:H42	1:2A:2152:G:H1	1.58	0.51
2:2B:90:A:C5	2:2B:91:C:H1'	2.45	0.51
22:20:8:GLY:N	54:2x:2:G:H5'	2.25	0.51
23:21:75:GLU:O	23:21:78:LYS:HG2	2.11	0.51
32:2a:404:U:H2'	32:2a:405:U:C6	2.46	0.51
34:2c:11:ARG:HD3	34:2c:15:THR:HB	1.93	0.51
38:2g:54:THR:O	38:2g:56:GLN:N	2.43	0.51
47:2p:13:HIS:O	47:2p:42:ARG:NH2	2.44	0.51
1:1A:1316:C:O2'	1:1A:1695:C:OP2	2.25	0.51
1:1A:2623:U:C4	27:15:3:LYS:HG3	2.46	0.51
6:1G:143:GLU:HG3	26:14:31:ILE:HD11	1.93	0.51
8:1I:1:MET:N	8:1I:21:VAL:O	2.41	0.51
23:11:72:GLU:OE2	23:11:76:ARG:NH2	2.44	0.51
32:1a:643:C:H2'	32:1a:644:G:H8	1.75	0.51
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.21	0.51
32:1a:1110:A:H8	32:1a:1110:A:O5'	1.94	0.51
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.36	0.51
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.36	0.51
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.45	0.51
1:2A:2336:A:H61	22:20:43:THR:CG2	2.24	0.51
2:2B:84:C:H42	2:2B:93:G:H1	1.57	0.51
32:2a:975:A:N1	41:2j:48:THR:HB	2.26	0.51
35:2d:127:THR:HG23	35:2d:147:ALA:HB3	1.92	0.51
37:2f:69:GLU:O	37:2f:72:VAL:HG12	2.10	0.51
43:2l:57:LYS:HD2	43:2l:67:THR:HG23	1.93	0.51
47:2p:43:LYS:HG2	47:2p:48:TRP:CG	2.46	0.51
54:2x:21:A:N6	54:2x:46:G:H2'	2.23	0.51
1:1A:2096:U:H2'	1:1A:2097:U:C6	2.46	0.51
1:1A:2328:C:O2'	6:1G:128:ARG:NH2	2.44	0.51
2:1B:24:G:N7	2:1B:56:G:H2'	2.26	0.51
27:15:16:ARG:HG3	27:15:17:ASP:N	2.25	0.51
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.26	0.51
1:2A:876:C:H2'	1:2A:877:U:O4'	2.11	0.51
1:2A:1264:G:H2'	1:2A:2014:A:N6	2.26	0.51
8:2I:98:ALA:HA	8:2I:101:LEU:HD12	1.92	0.51
32:2a:41:G:H2'	32:2a:42:G:C8	2.45	0.51
32:2a:1244:C:N3	32:2a:1293:G:N2	2.51	0.51
35:2d:156:GLU:O	35:2d:160:GLN:HG3	2.11	0.51
1:1A:733:G:H21	1:1A:835:A:H61	1.58	0.51
1:1A:1101:G:N2	1:1A:1150:C:O2	2.34	0.51
1:1A:1362:U:H2'	1:1A:1363:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.11	0.51
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.59	0.51
15:1T:16:ARG:NH2	15:1T:18:ASP:OD2	2.42	0.51
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.91	0.51
32:1a:353:A:H5'	32:1a:353:A:H8	1.75	0.51
32:1a:691:G:H2'	32:1a:692:U:C6	2.45	0.51
32:1a:1128:C:H42	32:1a:1144:G:H1	1.59	0.51
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.44	0.51
34:1c:125:GLU:HG2	34:1c:190:ARG:O	2.11	0.51
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.11	0.51
32:2a:108:G:N1	51:2t:15:ARG:HG2	2.26	0.51
32:2a:554:C:H2'	32:2a:555:C:C6	2.46	0.51
32:2a:693:G:H1'	38:2g:82:GLY:HA3	1.93	0.51
1:1A:826:U:OP1	3:1D:49:ILE:HG13	2.11	0.51
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.10	0.51
1:1A:1879:A:H2'	1:1A:1880:G:H8	1.76	0.51
3:1D:242:ARG:HG3	3:1D:242:ARG:NH1	2.22	0.51
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.11	0.51
48:1q:28:PRO:HA	48:1q:35:VAL:HA	1.92	0.51
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.44	0.51
1:2A:2125:G:H1'	1:2A:2173:A:N6	2.26	0.51
23:21:40:ARG:NH2	23:21:42:GLN:HG2	2.25	0.51
33:2b:74:LYS:NZ	33:2b:206:ASP:OD1	2.42	0.51
39:2h:14:ARG:NH1	39:2h:83:ILE:O	2.44	0.51
42:2k:59:TYR:CE2	42:2k:63:LEU:HD11	2.45	0.51
1:1A:469:A:C6	5:1F:45:ARG:HD2	2.46	0.50
6:1G:82:LEU:HD21	6:1G:88:ILE:HG21	1.93	0.50
12:1Q:93:TYR:CZ	21:1Z:194:PRO:HG2	2.47	0.50
32:1a:1037:C:H2'	32:1a:1038:C:C6	2.45	0.50
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.59	0.50
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.45	0.50
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.94	0.50
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.25	0.50
15:2T:120:ARG:HA	15:2T:123:GLN:HB3	1.92	0.50
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.93	0.50
32:2a:134:A:N6	47:2p:25:ARG:HH22	2.08	0.50
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.39	0.50
1:1A:1077:G:H5''	31:19:8:LYS:HE3	1.93	0.50
1:1A:1338:U:H2'	1:1A:1339:C:C6	2.46	0.50
1:1A:1562:U:H2'	1:1A:1563:G:C8	2.46	0.50
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:396:G:O2'	32:1a:398:C:OP1	2.09	0.50
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.11	0.50
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.00	0.50
1:2A:2324:C:H5''	1:2A:2325:G:H5'	1.93	0.50
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.43	0.50
5:2F:164:ARG:HD2	5:2F:175:THR:HG23	1.93	0.50
22:20:70:GLN:HG2	22:20:80:HIS:HE2	1.76	0.50
32:2a:537:G:H2'	32:2a:538:G:H8	1.76	0.50
35:2d:172:PRO:HB2	35:2d:187:ARG:NH2	2.26	0.50
39:2h:124:ALA:O	39:2h:128:GLY:N	2.44	0.50
1:1A:1112:U:H3	1:1A:1119:A:N6	2.05	0.50
1:1A:1857:G:H4'	3:1D:242:ARG:CZ	2.40	0.50
6:1G:11:TYR:CZ	6:1G:16:ARG:HD3	2.46	0.50
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.77	0.50
32:1a:167:G:H2'	32:1a:168:G:C8	2.46	0.50
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.93	0.50
48:1q:67:LYS:O	48:1q:69:LYS:N	2.40	0.50
49:1r:44:LEU:HD11	49:1r:79:LEU:HD13	1.92	0.50
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.26	0.50
1:2A:2576:G:H1'	60:2A:4759:HOH:O	2.10	0.50
1:2A:2815:C:C5'	27:25:29:THR:HG21	2.41	0.50
5:2F:117:ARG:NH2	5:2F:189:THR:O	2.28	0.50
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.30	0.50
32:2a:1438:G:H1	32:2a:1463:C:N4	2.10	0.50
44:2m:80:ARG:NH2	50:2s:65:ASN:O	2.40	0.50
1:1A:442:A:H2'	1:1A:443:C:H6	1.76	0.50
1:1A:2188:G:O6	1:1A:2194:U:H5	1.93	0.50
2:1B:50:G:OP1	14:1S:63:THR:OG1	2.18	0.50
7:1H:97:ARG:HG2	7:1H:104:GLU:HB3	1.94	0.50
10:1O:64:ARG:NH1	10:1O:81:ASP:OD1	2.45	0.50
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.93	0.50
15:1T:107:ASP:O	15:1T:111:ARG:HG3	2.12	0.50
21:1Z:200:GLY:C	21:1Z:202:GLU:H	2.20	0.50
32:1a:648:A:H2'	32:1a:649:G:H8	1.76	0.50
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.12	0.50
39:1h:14:ARG:NH1	39:1h:83:ILE:O	2.44	0.50
40:1i:5:TYR:HE1	40:1i:16:ARG:HA	1.77	0.50
44:1m:84:ILE:HD11	44:1m:86:CYS:HB2	1.93	0.50
1:2A:586:A:N1	1:2A:809:G:O2'	2.40	0.50
1:2A:774:A:H2'	1:2A:774:A:N3	2.26	0.50
1:2A:1108:U:H2'	1:2A:1109:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1115:G:H2'	1:2A:1116:C:C6	2.46	0.50
6:2G:19:LEU:HD11	6:2G:172:LEU:HA	1.94	0.50
15:2T:51:ARG:HG3	15:2T:98:LYS:HE3	1.93	0.50
32:2a:67:C:H2'	32:2a:68:G:H8	1.75	0.50
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.11	0.50
1:1A:217:A:H8	1:1A:218:A:H5'	1.77	0.50
6:1G:3:LEU:HD22	26:14:25:TYR:CZ	2.47	0.50
8:1I:10:GLU:O	8:1I:12:LEU:N	2.44	0.50
35:1d:100:ARG:HB3	35:1d:102:ASP:OD1	2.11	0.50
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	1.92	0.50
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.42	0.50
4:2E:36:ARG:NH2	4:2E:88:GLY:O	2.44	0.50
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.47	0.50
7:2H:121:ILE:HD11	7:2H:140:LYS:HG2	1.93	0.50
21:2Z:7:ALA:O	21:2Z:62:PRO:HD3	2.10	0.50
32:2a:384:G:H2'	32:2a:385:C:C6	2.47	0.50
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.47	0.50
32:2a:1426:C:H2'	32:2a:1427:U:H6	1.75	0.50
1:1A:801:C:H2'	1:1A:802:C:H6	1.76	0.50
1:1A:1231:G:H2'	1:1A:1232:G:O4'	2.12	0.50
5:1F:30:PRO:HB3	11:1P:1:MET:HE1	1.93	0.50
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.94	0.50
1:2A:783:A:O2'	1:2A:785:G:OP1	2.27	0.50
1:2A:2009:G:N3	13:2R:107:ASP:HA	2.27	0.50
1:1A:9:U:N3	1:1A:2641:A:C2	2.78	0.50
8:1I:117:GLU:HG3	8:1I:118:LYS:N	2.27	0.50
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.92	0.50
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.93	0.50
1:2A:1799:G:O2'	3:2D:183:ARG:NH1	2.43	0.50
1:2A:2138:C:H2'	1:2A:2139:C:C6	2.47	0.50
1:2A:2875:C:O2'	15:2T:2:ASN:OD1	2.30	0.50
32:2a:848:C:H2'	32:2a:849:C:H6	1.77	0.50
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.93	0.50
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.44	0.50
36:1e:59:GLY:O	36:1e:63:ARG:HG3	2.12	0.50
49:1r:24:ALA:C	49:1r:26:LEU:H	2.20	0.50
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.77	0.50
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.29	0.50
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.47	0.50
2:2B:86:G:H1	2:2B:91:C:H42	1.59	0.50
8:2I:77:LEU:HD11	8:2I:100:ALA:HB1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:406:G:H4'	35:2d:5:ILE:HD11	1.93	0.50
32:2a:632:A:H5'	32:2a:633:G:OP2	2.12	0.50
1:1A:714:U:O2	30:18:2:PRO:HD2	2.12	0.50
3:1D:75:ILE:HG21	3:1D:99:ASP:HB2	1.94	0.50
1:2A:26:G:C6	1:2A:27:G:N1	2.80	0.50
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.11	0.50
1:2A:2012:G:P	18:2W:11:ARG:HH22	2.35	0.50
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.12	0.50
32:2a:775:G:N2	32:2a:804:U:O4	2.45	0.50
32:2a:1015:A:O5'	32:2a:1015:A:H8	1.94	0.50
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.12	0.50
34:2c:18:TRP:HE3	34:2c:18:TRP:H	1.58	0.50
34:2c:50:ALA:HB1	34:2c:70:VAL:HG21	1.94	0.50
46:2o:81:LEU:HG	46:2o:85:LEU:HD12	1.94	0.50
1:1A:27:G:N2	1:1A:537:G:H1'	2.27	0.49
1:1A:233:A:C2	1:1A:244:A:C4	3.00	0.49
1:1A:2131:U:H6	1:1A:2131:U:O5'	1.94	0.49
4:1E:18:ASP:HB3	15:1T:82:LEU:HD21	1.94	0.49
32:1a:41:G:H2'	32:1a:42:G:H8	1.76	0.49
32:1a:102:G:O2'	32:1a:151:A:N3	2.39	0.49
1:2A:538:G:H2'	1:2A:539:G:H8	1.76	0.49
1:2A:657:U:H2'	1:2A:658:C:C6	2.46	0.49
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.46	0.49
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.47	0.49
3:2D:275:LYS:HE3	3:2D:276:LYS:HA	1.94	0.49
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.45	0.49
22:20:14:ARG:NE	60:20:201:HOH:O	2.44	0.49
32:2a:272:C:H2'	32:2a:273:A:C8	2.45	0.49
32:2a:984:C:H42	32:2a:1221:G:H1	1.59	0.49
32:2a:1053:G:O5'	32:2a:1054:C:H3'	2.12	0.49
54:2x:28:C:H2'	54:2x:29:G:H8	1.77	0.49
1:1A:2117:C:H2'	1:1A:2118:U:O4'	2.12	0.49
1:1A:2331:G:N1	14:1S:3:ARG:HA	2.27	0.49
7:1H:113:VAL:HG11	7:1H:151:ILE:HD13	1.93	0.49
14:1S:20:ARG:HH21	22:10:47:PRO:HB2	1.77	0.49
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.47	0.49
32:1a:475:G:O2'	32:1a:476:G:H5'	2.12	0.49
32:1a:1086:U:H3	32:1a:1099:G:H22	1.61	0.49
33:1b:36:ARG:C	33:1b:38:GLY:H	2.20	0.49
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.44	0.49
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271(Z):C:H1'	1:2A:272(C):G:H1'	1.94	0.49
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.47	0.49
1:2A:2119:A:N1	1:2A:2170:A:H2'	2.26	0.49
1:2A:2121:G:O6	1:2A:2176:A:N6	2.44	0.49
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.12	0.49
21:2Z:39:VAL:HG21	21:2Z:44:PHE:HB2	1.94	0.49
32:2a:328:C:H4'	32:2a:329:A:H5'	1.94	0.49
32:2a:1157:A:H61	32:2a:1178:G:N2	2.09	0.49
1:1A:173:C:H2'	1:1A:174:U:C6	2.47	0.49
1:1A:1604:C:H5''	1:1A:1605:A:OP2	2.12	0.49
1:1A:1890:A:N6	1:1A:1905:G:O2'	2.45	0.49
1:1A:1936:C:H2'	1:1A:1937:5MU:O4'	2.13	0.49
4:1E:120:TRP:CD1	4:1E:155:LYS:HB3	2.48	0.49
12:1Q:30:GLY:O	12:1Q:134:ARG:NH1	2.45	0.49
12:1Q:109:VAL:HG22	12:1Q:113:GLN:OE1	2.12	0.49
32:1a:601:C:H2'	32:1a:602:A:C8	2.47	0.49
1:2A:576:U:H2'	1:2A:577:G:C8	2.47	0.49
1:2A:1509(A):A:H2'	1:2A:1509(B):A:O4'	2.12	0.49
17:2V:25:LEU:H	17:2V:92:THR:HG1	1.60	0.49
23:21:35:THR:OG1	23:21:35:THR:O	2.31	0.49
32:2a:404:U:C2	32:2a:498:U:O4	2.66	0.49
32:2a:537:G:H5''	43:2l:113:ARG:NH1	2.27	0.49
32:2a:1304:G:C6	32:2a:1305:G:N1	2.79	0.49
1:1A:2402:U:P	30:18:35:GLN:HE22	2.35	0.49
3:1D:37:LEU:HD12	3:1D:62:TYR:HB2	1.92	0.49
17:1V:19:LYS:HG2	17:1V:95:LEU:HD12	1.95	0.49
32:1a:142:G:H1	32:1a:221:C:H42	1.60	0.49
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.45	0.49
32:1a:1207:2MG:H2'	32:1a:1208:C:C6	2.47	0.49
44:1m:2:ALA:HB1	44:1m:7:VAL:C	2.38	0.49
1:2A:922:U:H2'	1:2A:923:C:C6	2.46	0.49
1:2A:1067:A:H4'	1:2A:1068:G:OP2	2.12	0.49
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.30	0.49
7:2H:6:ARG:NH2	7:2H:54:ARG:HH12	2.11	0.49
30:28:22:VAL:HG12	30:28:50:LEU:HD12	1.95	0.49
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.47	0.49
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.47	0.49
32:2a:1428:A:H2'	32:2a:1429:C:O4'	2.13	0.49
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.47	0.49
6:1G:59:GLU:OE1	6:1G:153:ARG:HD2	2.12	0.49
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:128:HIS:O	9:1N:131:GLN:NE2	2.46	0.49
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.11	0.49
16:1U:85:LYS:HB2	16:1U:116:ALA:HB1	1.95	0.49
20:1Y:8:LYS:HA	20:1Y:30:VAL:HG21	1.94	0.49
32:1a:339:C:H2'	32:1a:340:U:C6	2.47	0.49
32:1a:1028:C:H2'	32:1a:1029:C:O4'	2.12	0.49
39:1h:91:ARG:HE	48:1q:33:GLY:HA3	1.77	0.49
1:2A:27:G:N2	1:2A:512:G:H1'	2.28	0.49
1:2A:1791:A:H3'	1:2A:1792:G:H8	1.78	0.49
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.48	0.49
32:2a:841:U:H6	32:2a:841:U:P	2.35	0.49
32:2a:848:C:H2'	32:2a:849:C:C6	2.47	0.49
35:2d:13:ARG:HG2	35:2d:40:PRO:HD3	1.92	0.49
35:2d:196:LEU:O	35:2d:198:VAL:N	2.44	0.49
40:2i:9:ARG:O	40:2i:104:ARG:HG3	2.12	0.49
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.95	0.49
1:1A:178:G:H2'	1:1A:194:G:N2	2.27	0.49
1:1A:2133:C:N3	1:1A:2169:G:N2	2.60	0.49
32:1a:373:A:O2'	32:1a:451:A:N7	2.46	0.49
1:2A:272(B):G:H2'	1:2A:272(C):G:H8	1.78	0.49
1:2A:1069:A:C2	1:2A:1073:A:H5'	2.48	0.49
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.41	0.49
15:2T:22:PHE:CE1	15:2T:49:VAL:HG11	2.47	0.49
21:2Z:24:LEU:HD12	21:2Z:25:PRO:HD2	1.94	0.49
21:2Z:59:LEU:N	21:2Z:67:LEU:O	2.43	0.49
32:2a:601:C:H2'	32:2a:602:A:C8	2.47	0.49
32:2a:735:C:H2'	32:2a:736:C:H6	1.76	0.49
32:2a:1360:A:H8	32:2a:1360:A:OP1	1.95	0.49
33:2b:102:LEU:HB3	33:2b:180:LEU:HD12	1.94	0.49
1:1A:1002:A:H4'	12:1Q:74:TYR:OH	2.13	0.49
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.95	0.49
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.95	0.49
11:1P:89:ALA:O	11:1P:121:LYS:NZ	2.40	0.49
26:14:34:GLU:HG2	26:14:35:VAL:HG12	1.94	0.49
40:1i:49:PRO:HD2	40:1i:81:ILE:HD11	1.95	0.49
42:1k:22:HIS:HB3	42:1k:29:ILE:HB	1.93	0.49
1:2A:622:G:H2'	1:2A:623:G:H8	1.76	0.49
1:2A:637:A:H4'	1:2A:638:G:O5'	2.13	0.49
1:2A:1913:A:H8	32:2a:1494:G:O4'	1.95	0.49
1:2A:2690:C:H5''	1:2A:2872:G:N2	2.28	0.49
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:34:GLU:HA	44:2m:57:ARG:NH1	2.27	0.49
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.46	0.49
32:2a:1005:A:C6	32:2a:1024:G:N2	2.80	0.49
43:2l:7:ILE:O	43:2l:11:VAL:HG23	2.12	0.49
1:1A:27:G:C2	1:1A:537:G:N3	2.81	0.49
1:1A:769:A:H2'	1:1A:770:G:H8	1.78	0.49
1:1A:2291:G:N7	22:10:14:ARG:NH1	2.60	0.49
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.95	0.49
7:1H:41:MET:HE1	7:1H:54:ARG:HB3	1.93	0.49
32:1a:56:U:H2'	32:1a:57:G:C8	2.48	0.49
32:1a:601:C:H2'	32:1a:602:A:H8	1.78	0.49
32:1a:1264:C:H42	32:1a:1271:G:H1	1.60	0.49
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.13	0.49
1:2A:1045:A:N3	1:2A:1045:A:H2'	2.27	0.49
1:2A:1077:A:C5	1:2A:1078:U:O4	2.65	0.49
1:2A:1384:A:N3	1:2A:1405:U:H1'	2.28	0.49
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.13	0.49
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.48	0.49
42:2k:34:ASP:OD2	42:2k:38:ASN:HB2	2.13	0.49
1:1A:1143:U:H2'	1:1A:1144:A:O4'	2.13	0.49
1:1A:1577:C:O2'	1:1A:1578:C:O5'	2.29	0.49
1:1A:2745:G:H3'	1:1A:2746:A:O4'	2.13	0.49
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.95	0.49
32:1a:9:G:OP2	36:1e:121:LYS:NZ	2.39	0.49
32:1a:201:C:H42	32:1a:216:G:H1	1.60	0.49
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.46	0.49
32:1a:1426:C:H2'	32:1a:1427:U:H6	1.77	0.49
39:1h:36:LEU:O	39:1h:40:ALA:N	2.45	0.49
40:1i:9:ARG:HB2	40:1i:104:ARG:HE	1.78	0.49
1:2A:602:G:O2'	1:2A:655:A:N6	2.46	0.49
1:2A:1096:A:C8	1:2A:1097:U:H5	2.30	0.49
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.46	0.49
1:2A:2103:C:O2	1:2A:2186:G:N1	2.44	0.49
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.94	0.49
32:2a:583:A:H2'	32:2a:584:G:O4'	2.12	0.49
32:2a:1027:C:C2	32:2a:1034:G:N1	2.81	0.49
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.78	0.49
50:2s:32:LYS:HE2	50:2s:57:HIS:CD2	2.48	0.49
1:1A:1560:U:H2'	1:1A:1561:C:C6	2.47	0.49
1:1A:1889:G:H22	1:1A:1905:G:H2'	1.78	0.49
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:15:45:VAL:HA	27:15:52:TYR:HB2	1.95	0.49
32:1a:1038:C:H2'	32:1a:1039:C:C6	2.48	0.49
32:1a:1089:G:H1	32:1a:1096:C:H42	1.61	0.49
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.48	0.49
34:1c:22:TRP:CH2	34:1c:32:LEU:HB2	2.48	0.49
1:2A:2064:C:H1'	1:2A:2450:A:C2	2.48	0.49
5:2F:39:TRP:NE1	5:2F:99:TYR:O	2.45	0.49
10:2O:119:PRO:HB2	15:2T:68:TYR:CE2	2.47	0.49
32:2a:88:A:O2'	32:2a:89:C:OP1	2.29	0.49
32:2a:343:U:H3	32:2a:346:G:H1	1.61	0.49
32:2a:434:U:H2'	32:2a:435:C:C6	2.48	0.49
32:2a:1179:A:H4'	40:2i:103:THR:HA	1.95	0.49
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.47	0.49
50:2s:20:LEU:HA	50:2s:23:ASN:HB2	1.93	0.49
1:1A:2135:U:O4	1:1A:2190:G:H4'	2.13	0.48
32:1a:1269:A:H2	32:1a:1312:G:N3	2.11	0.48
46:1o:71:GLN:HA	46:1o:78:TYR:HB2	1.94	0.48
1:2A:10:G:H2'	1:2A:11:G:H8	1.77	0.48
1:2A:272(G):C:N3	1:2A:363(C):G:N2	2.50	0.48
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.48	0.48
1:2A:2166:G:O5'	1:2A:2166:G:H8	1.96	0.48
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.31	0.48
10:2O:34:THR:OG1	10:2O:35:VAL:N	2.45	0.48
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.47	0.48
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.48	0.48
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.48	0.48
34:2c:110:ASN:O	34:2c:141:VAL:HG22	2.13	0.48
35:2d:12:CYS:SG	35:2d:19:LEU:HB2	2.53	0.48
46:2o:6:GLU:OE1	46:2o:6:GLU:N	2.41	0.48
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.43	0.48
21:1Z:54:HIS:HD2	21:1Z:99:TYR:O	1.95	0.48
23:11:95:LEU:O	23:11:98:LEU:HB2	2.13	0.48
32:1a:126:G:H4'	32:1a:634:C:O2	2.13	0.48
40:1i:18:PHE:O	40:1i:61:ALA:HA	2.13	0.48
1:2A:856:C:H2'	1:2A:857:C:H6	1.76	0.48
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.46	0.48
1:2A:2635:C:O2	4:2E:37:ARG:NH2	2.46	0.48
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.48	0.48
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.12	0.48
32:2a:1226:C:H2'	44:2m:103:THR:HB	1.93	0.48
35:2d:165:MET:SD	35:2d:168:ARG:NH1	2.86	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:505:A:N3	1:1A:507:G:H5''	2.28	0.48
1:1A:2141:A:N6	1:1A:2190:G:H1'	2.27	0.48
1:1A:2149:G:H8	1:1A:2149:G:H5''	1.79	0.48
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.94	0.48
36:1e:152:ARG:HB2	39:1h:43:GLY:O	2.13	0.48
1:2A:620:G:N3	1:2A:620:G:H5'	2.29	0.48
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.13	0.48
1:2A:2773:C:H5''	4:2E:164:ARG:HG2	1.95	0.48
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.95	0.48
12:2Q:108:GLY:HA3	21:2Z:116:VAL:HG13	1.96	0.48
32:2a:1015:A:C6	32:2a:1016:A:C6	3.01	0.48
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.48	0.48
43:2l:28:LYS:N	43:2l:29:GLY:HA2	2.28	0.48
1:1A:745:C:O2'	1:1A:781:A:N6	2.47	0.48
1:1A:2032:G:H5''	18:1W:42:ARG:HB2	1.95	0.48
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.13	0.48
32:1a:266:G:O3'	48:1q:67:LYS:HB2	2.14	0.48
32:1a:1289:A:P	52:1u:10:ARG:HH22	2.37	0.48
33:1b:60:ASP:CG	33:1b:64:ARG:HH21	2.21	0.48
36:1e:69:VAL:HG11	36:1e:113:ALA:HB1	1.94	0.48
39:1h:101:PRO:HG3	39:1h:133:LEU:HD11	1.95	0.48
44:1m:80:ARG:O	44:1m:84:ILE:HG23	2.13	0.48
1:2A:658:C:H2'	1:2A:659:C:C6	2.49	0.48
1:2A:1923:U:OP1	54:2x:24:U:O2'	2.29	0.48
1:2A:2156:G:O6	1:2A:2157:G:N2	2.35	0.48
1:2A:2250:G:O2'	1:2A:2496:C:OP1	2.24	0.48
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.48	0.48
7:2H:7:LEU:HB3	7:2H:69:ARG:HH21	1.78	0.48
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.94	0.48
26:24:18:CYS:HB2	26:24:20:ASN:HB2	1.95	0.48
32:2a:1125:U:H2'	32:2a:1127:G:N7	2.28	0.48
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.14	0.48
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.29	0.48
34:2c:36:ASP:O	34:2c:40:ARG:HG2	2.13	0.48
38:2g:70:LYS:HD3	38:2g:96:GLN:OE1	2.14	0.48
43:2l:76:ASN:OD1	43:2l:76:ASN:N	2.46	0.48
1:1A:626:A:N1	1:1A:650:G:O2'	2.44	0.48
15:1T:55:ASN:N	15:1T:59:THR:HG22	2.28	0.48
32:1a:583:A:H2'	32:1a:584:G:O4'	2.13	0.48
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.14	0.48
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:124:LYS:H	42:1k:124:LYS:HG2	1.41	0.48
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.13	0.48
1:2A:2294:C:OP2	14:2S:89:ARG:NH2	2.39	0.48
1:2A:2889:C:H3'	1:2A:2891:G:H8	1.78	0.48
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.96	0.48
6:2G:145:THR:HG22	6:2G:148:MET:HE3	1.94	0.48
33:2b:61:LEU:HD23	33:2b:68:ILE:HD11	1.96	0.48
38:2g:72:ARG:HH12	38:2g:138:LYS:HZ3	1.61	0.48
1:1A:553:A:OP2	9:1N:114:ARG:NH1	2.47	0.48
1:1A:1554:A:H4'	1:1A:1556:A:C5	2.49	0.48
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.34	0.48
32:1a:262:A:H2'	32:1a:263:A:C8	2.49	0.48
34:1c:44:GLU:HG2	34:1c:52:LEU:HD23	1.95	0.48
35:1d:53:ASP:HB3	35:1d:57:ARG:NH1	2.28	0.48
36:1e:96:PRO:O	36:1e:98:THR:N	2.44	0.48
1:2A:848:G:H2'	1:2A:849:A:C8	2.49	0.48
6:2G:122:PRO:HA	6:2G:180:PHE:CD1	2.49	0.48
7:2H:98:LEU:HD22	7:2H:125:VAL:HG23	1.95	0.48
32:2a:1005:A:C5	32:2a:1024:G:N2	2.81	0.48
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	1.95	0.48
50:2s:39:THR:HG22	50:2s:40:ILE:O	2.14	0.48
1:1A:265:U:H2'	1:1A:266:C:H6	1.77	0.48
1:1A:275:C:H2'	1:1A:276:C:C6	2.48	0.48
1:1A:1766:G:H5'	1:1A:1767:A:OP2	2.14	0.48
1:1A:1895:U:OP1	1:1A:2422:G:O2'	2.23	0.48
3:1D:70:TRP:CE2	3:1D:150:LYS:HD3	2.49	0.48
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.77	0.48
32:1a:437:U:H5''	35:1d:155:LEU:HD11	1.94	0.48
32:1a:534:U:O5'	32:1a:534:U:H6	1.95	0.48
32:1a:1051:C:H2'	32:1a:1052:U:H6	1.78	0.48
32:1a:1368:G:OP2	40:1i:112:LYS:HG3	2.14	0.48
33:1b:97:TRP:CH2	33:1b:173:ALA:HA	2.49	0.48
1:2A:320:A:H4'	1:2A:322:A:C8	2.49	0.48
1:2A:1130:U:O2	4:2E:149:ARG:NH2	2.46	0.48
1:2A:1365:A:O4'	23:21:41:ARG:NH2	2.47	0.48
1:2A:1472:A:N6	1:2A:1519:G:H1'	2.28	0.48
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.48	0.48
1:2A:2105:C:N4	1:2A:2184:G:H1	2.11	0.48
6:2G:122:PRO:HA	6:2G:180:PHE:HD1	1.78	0.48
20:2Y:43:ASN:ND2	20:2Y:65:ALA:HB3	2.29	0.48
23:21:72:GLU:HG2	23:21:76:ARG:HD2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:443:C:H2'	32:2a:444:C:H6	1.78	0.48
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.62	0.48
54:2x:58:A:H4'	54:2x:59:A:OP1	2.13	0.48
1:1A:211:A:H5''	1:1A:448:U:OP1	2.14	0.48
1:1A:2136:A:H2'	1:1A:2137:G:O4'	2.14	0.48
12:1Q:110:THR:HG23	12:1Q:113:GLN:OE1	2.14	0.48
27:15:35:GLU:OE1	27:15:35:GLU:N	2.47	0.48
32:1a:1014:A:H4'	50:1s:14:HIS:NE2	2.28	0.48
32:1a:1095:U:H2'	32:1a:1096:C:C6	2.48	0.48
32:1a:1148:U:O3'	40:1i:14:VAL:HG11	2.14	0.48
45:1n:39:LEU:HD11	45:1n:47:LEU:HD12	1.95	0.48
49:1r:24:ALA:O	49:1r:26:LEU:N	2.47	0.48
1:2A:536:A:H2'	1:2A:537:C:C6	2.49	0.48
1:2A:833:U:O2	11:2P:55:ARG:NH1	2.47	0.48
1:2A:923:C:H4'	22:20:29:GLN:HG3	1.94	0.48
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.14	0.48
1:2A:2135:A:H3'	1:2A:2136:C:H5'	1.95	0.48
1:2A:2144:U:H1'	1:2A:2147:G:O6	2.14	0.48
1:2A:2309:A:H61	6:2G:79:ASN:ND2	2.11	0.48
1:2A:2386:C:H2'	1:2A:2387:U:C6	2.48	0.48
32:2a:1014:A:N7	32:2a:1015:A:N6	2.61	0.48
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.78	0.48
36:2e:137:GLU:HG2	36:2e:140:ARG:HH11	1.78	0.48
1:1A:217:A:H2'	1:1A:219:U:O4'	2.13	0.48
1:1A:741:U:OP1	3:1D:59:LYS:NZ	2.44	0.48
1:1A:2236:G:H4'	1:1A:2238:C:C2	2.49	0.48
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.94	0.48
31:19:32:HIS:O	31:19:34:GLN:HG3	2.13	0.48
34:1c:26:LYS:HE3	34:1c:27:LYS:NZ	2.29	0.48
48:1q:45:HIS:O	48:1q:47:PRO:HD3	2.13	0.48
54:1x:23:C:H2'	54:1x:24:U:C6	2.49	0.48
1:2A:479:A:N3	1:2A:481:G:H5''	2.29	0.48
1:2A:2134:A:N6	1:2A:2135:A:H62	2.12	0.48
2:2B:95:C:H2'	2:2B:96:U:C6	2.48	0.48
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.12	0.48
8:2I:45:LYS:O	8:2I:49:ALA:N	2.38	0.48
26:24:1:MET:HB3	26:24:6:HIS:CD2	2.49	0.48
26:24:46:GLN:NE2	26:24:48:ARG:HH12	2.12	0.48
32:2a:1330:U:H2'	32:2a:1331:G:H5'	1.96	0.48
36:2e:43:LEU:HD21	36:2e:132:ALA:HB1	1.96	0.48
38:2g:75:VAL:HG11	38:2g:86:GLN:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:6:ILE:HB	41:2j:72:VAL:HG23	1.95	0.48
1:1A:915:U:C4	1:1A:916:G:N7	2.82	0.48
11:1P:50:ARG:HG3	30:18:61:LEU:HD11	1.94	0.48
12:1Q:108:GLY:HA3	21:1Z:116:VAL:HG13	1.96	0.48
13:1R:72:ASP:O	13:1R:76:VAL:HG23	2.13	0.48
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.20	0.48
32:1a:130:A:O2'	32:1a:131:C:O5'	2.25	0.48
32:1a:221:C:H2'	32:1a:222:U:H6	1.79	0.48
32:1a:597:G:N2	39:1h:94:TYR:OH	2.47	0.48
32:1a:1127:G:H5'	32:1a:1280:A:O2'	2.14	0.48
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.96	0.48
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.95	0.48
51:1t:92:LEU:O	51:1t:96:GLY:N	2.46	0.48
1:2A:1079:C:C4	1:2A:1080:C:H1'	2.49	0.48
1:2A:2573:C:OP1	1:2A:2574:G:H5''	2.13	0.48
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.14	0.48
28:26:25:LYS:HE3	28:26:27:LYS:HA	1.95	0.48
32:2a:106:C:O2	32:2a:379:C:H4'	2.14	0.48
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.27	0.48
36:2e:36:ASP:OD1	36:2e:38:GLN:N	2.42	0.48
1:1A:211:A:H3'	1:1A:448:U:H5'	1.94	0.47
1:1A:921:G:H1	1:1A:949:C:N4	2.10	0.47
1:1A:1040:C:OP1	16:1U:53:ARG:NH2	2.46	0.47
1:1A:1309:U:C4	1:1A:1310:G:C6	3.02	0.47
1:1A:2073:A:H4'	4:1E:141:ILE:HG12	1.95	0.47
1:1A:2760:G:O6	1:1A:2768:C:H5''	2.14	0.47
1:1A:2821:G:N2	1:1A:2900:G:H1'	2.29	0.47
6:1G:143:GLU:O	26:14:28:LYS:NZ	2.45	0.47
11:1P:88:LEU:HD21	11:1P:100:LEU:HD11	1.95	0.47
32:1a:407:G:H2'	32:1a:408:A:C8	2.48	0.47
35:1d:85:LYS:HG3	35:1d:86:LYS:N	2.28	0.47
1:2A:687:C:H5''	29:27:2:LYS:HE2	1.94	0.47
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.14	0.47
1:2A:1903:G:OP1	3:2D:241:PRO:HB2	2.13	0.47
1:2A:2095:C:H2'	1:2A:2096:U:O4'	2.14	0.47
1:2A:2102:U:H2'	1:2A:2103:C:O4'	2.14	0.47
1:2A:2464:C:O2'	60:2A:4001:HOH:O	1.99	0.47
3:2D:112:GLN:O	3:2D:115:GLN:HG2	2.14	0.47
12:2Q:5:ARG:O	21:2Z:194:PRO:HA	2.14	0.47
21:2Z:31:ARG:HG3	21:2Z:32:HIS:CD2	2.49	0.47
24:22:63:VAL:O	24:22:67:LYS:HG2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	1.95	0.47
41:2j:6:ILE:HD13	41:2j:98:ILE:HA	1.94	0.47
44:2m:27:LYS:HD2	44:2m:27:LYS:HA	1.63	0.47
1:1A:1057:G:OP1	16:1U:77:SER:OG	2.20	0.47
1:1A:2078:G:H1	27:15:3:LYS:HB3	1.78	0.47
32:1a:292:G:N7	32:1a:293:G:H1'	2.29	0.47
32:1a:1125:U:H4'	41:1j:5:ARG:HH21	1.79	0.47
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.96	0.47
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.79	0.47
51:1t:50:GLU:O	51:1t:100:ILE:HD11	2.14	0.47
1:2A:605:C:H2'	1:2A:606:U:O4'	2.15	0.47
1:2A:1062:G:O2'	1:2A:1063:G:H5'	2.14	0.47
1:2A:1814:G:H2'	1:2A:1815:A:C8	2.48	0.47
6:2G:18:GLU:CD	6:2G:21:ARG:HH21	2.21	0.47
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.47	0.47
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.42	0.47
32:2a:222:U:H2'	32:2a:223:U:C6	2.48	0.47
32:2a:560:U:H4'	32:2a:561:U:O5'	2.14	0.47
38:2g:76:ARG:N	38:2g:87:VAL:O	2.40	0.47
1:1A:231:G:C8	30:18:5:LYS:HG2	2.49	0.47
1:1A:818:G:OP1	29:17:10:ARG:NH1	2.47	0.47
1:1A:839:G:O2'	1:1A:2452:C:N3	2.43	0.47
1:1A:1125:C:H41	1:1A:1134:A:P	2.37	0.47
1:1A:2139:A:C2	1:1A:2141:A:H5'	2.50	0.47
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.14	0.47
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.13	0.47
11:1P:86:LYS:HB3	11:1P:118:GLY:HA3	1.95	0.47
21:1Z:200:GLY:C	21:1Z:202:GLU:N	2.72	0.47
32:1a:728:A:H2'	32:1a:729:A:C8	2.49	0.47
48:1q:75:ARG:CZ	48:1q:77:VAL:HG22	2.45	0.47
1:2A:299:A:N3	1:2A:319:C:O2'	2.40	0.47
1:2A:857:C:H2'	1:2A:858:U:C6	2.49	0.47
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.49	0.47
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.95	0.47
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.29	0.47
5:2F:29:ASN:H	5:2F:112:MET:HE3	1.79	0.47
6:2G:137:GLU:HG2	6:2G:152:LEU:HD22	1.95	0.47
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.96	0.47
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.95	0.47
32:2a:56:U:H2'	32:2a:57:G:C8	2.49	0.47
32:2a:359:U:H2'	32:2a:360:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1299:A:O2'	32:2a:1300:G:H4'	2.15	0.47
32:2a:1486:G:H2'	32:2a:1487:G:O4'	2.14	0.47
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.47	0.47
40:2i:19:LEU:HD23	40:2i:61:ALA:HB2	1.96	0.47
1:1A:1143:U:H3'	1:1A:1144:A:H8	1.79	0.47
1:1A:1958:A:OP1	1:1A:1959:A:H5'	2.15	0.47
1:1A:2099:A:H2'	1:1A:2100:C:H6	1.79	0.47
6:1G:101:ILE:HG22	6:1G:105:LYS:HE2	1.96	0.47
14:1S:39:ILE:HD11	14:1S:110:LEU:HD21	1.95	0.47
32:1a:981:U:H5'	45:1n:21:TYR:CZ	2.49	0.47
32:1a:1135:U:H4'	32:1a:1136:U:C5	2.49	0.47
60:1a:1904:HOH:O	42:1k:122:LYS:HE2	2.14	0.47
42:1k:59:TYR:CE2	42:1k:63:LEU:HD11	2.49	0.47
43:1l:92:OTD:O	43:1l:94:PRO:HD3	2.14	0.47
1:2A:784:A:H5'	1:2A:785:G:OP1	2.14	0.47
1:2A:1914:C:H2'	1:2A:1915:5MU:O4'	2.14	0.47
1:2A:2319:G:C2	14:2S:3:ARG:HA	2.49	0.47
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.47	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.14	0.47
30:28:56:GLU:HG2	30:28:57:ARG:N	2.30	0.47
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.80	0.47
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.15	0.47
1:1A:479:C:O2	1:1A:483:A:O2'	2.29	0.47
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.33	0.47
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.24	0.47
32:1a:272:C:H2'	32:1a:273:A:C8	2.44	0.47
32:1a:1519:MA6:H8	32:1a:1519:MA6:O5'	2.14	0.47
33:1b:140:HIS:O	33:1b:144:ARG:N	2.43	0.47
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.95	0.47
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.14	0.47
5:2F:126:VAL:O	5:2F:196:LEU:HG	2.15	0.47
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.50	0.47
26:24:62:ARG:H	26:24:62:ARG:NH1	2.11	0.47
32:2a:575:G:O2'	32:2a:821:G:H5'	2.15	0.47
41:2j:89:ASP:O	41:2j:91:PRO:HD3	2.15	0.47
1:1A:215:G:C2	1:1A:217:A:N6	2.82	0.47
1:1A:776:G:OP2	3:1D:13:ARG:NH1	2.47	0.47
1:1A:1102:G:H1'	1:1A:1149:A:H61	1.80	0.47
1:1A:2155:G:O2'	1:1A:2180:A:H2	1.97	0.47
1:1A:2432:C:H5'	28:16:54:ILE:HD11	1.96	0.47
6:1G:111:LEU:HA	6:1G:114:ILE:HD12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:20:ARG:NH2	22:10:47:PRO:HB2	2.30	0.47
26:14:58:ARG:HG3	50:1s:67:VAL:HB	1.96	0.47
32:1a:593:G:H2'	32:1a:594:G:O4'	2.15	0.47
32:1a:921:U:O2'	36:1e:19:MET:O	2.25	0.47
32:1a:1386:G:H2'	32:1a:1387:G:H8	1.80	0.47
33:1b:24:TRP:CH2	33:1b:26:PRO:HA	2.50	0.47
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.15	0.47
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.31	0.47
39:1h:29:SER:HB3	39:1h:32:LYS:HG3	1.96	0.47
1:2A:323:G:H1'	1:2A:1205:U:O2	2.14	0.47
1:2A:485:C:H2'	1:2A:486:C:C6	2.50	0.47
1:2A:2869:G:H2'	1:2A:2870:C:O4'	2.14	0.47
3:2D:228:PRO:HD3	3:2D:235:GLY:HA3	1.96	0.47
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.50	0.47
10:2O:24:VAL:HB	10:2O:33:ALA:HB2	1.96	0.47
12:2Q:141:GLN:HE22	21:2Z:74:VAL:HG13	1.79	0.47
32:2a:5:U:H1'	60:2a:2148:HOH:O	2.13	0.47
32:2a:509:A:HO2'	32:2a:510:A:P	2.37	0.47
32:2a:1124:G:H1	32:2a:1149:C:H42	1.62	0.47
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.49	0.47
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.95	0.47
38:2g:48:LYS:O	38:2g:51:GLN:HB3	2.14	0.47
39:2h:103:VAL:HG21	39:2h:109:ILE:C	2.40	0.47
49:2r:58:LEU:HD23	49:2r:62:GLU:HG3	1.96	0.47
50:2s:23:ASN:HA	50:2s:27:GLU:OE2	2.15	0.47
1:1A:69:G:H5''	1:1A:110:U:O2	2.14	0.47
1:1A:346:A:OP2	5:1F:169:ASN:HB2	2.14	0.47
1:1A:1085:G:C6	1:1A:1162:C:N4	2.78	0.47
1:1A:1113:A:H2'	1:1A:1113:A:N3	2.30	0.47
1:1A:1231:G:C2	1:1A:1232:G:H1'	2.49	0.47
1:1A:1688:A:H2'	1:1A:1689:G:O4'	2.13	0.47
1:1A:1804:A:C5	1:1A:1860:A:H1'	2.49	0.47
1:1A:1857:G:H4'	3:1D:242:ARG:NH1	2.30	0.47
1:1A:1921:G:N3	1:1A:1921:G:H2'	2.29	0.47
4:1E:51:PHE:CD2	4:1E:52:LEU:HG	2.49	0.47
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.97	0.47
13:1R:13:HIS:CE1	13:1R:16:HIS:HB2	2.49	0.47
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.96	0.47
24:12:3:LEU:HD22	24:12:7:ARG:HH21	1.80	0.47
32:1a:144:G:H1	32:1a:178:C:H42	1.62	0.47
32:1a:341:C:H2'	32:1a:342:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:616:G:OP2	35:1d:141:ARG:NH2	2.48	0.47
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.37	0.47
32:1a:1288:A:H2'	32:1a:1289:A:C8	2.49	0.47
32:1a:1377:A:OP2	38:1g:94:ARG:NH2	2.47	0.47
32:1a:1426:C:H2'	32:1a:1427:U:C6	2.49	0.47
38:1g:6:ARG:H	38:1g:6:ARG:HG3	1.52	0.47
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.28	0.47
1:2A:251:A:C5	1:2A:252:G:H1'	2.50	0.47
1:2A:468:G:N7	29:27:39:ARG:NH2	2.57	0.47
1:2A:493:G:H2'	1:2A:494:G:O4'	2.14	0.47
1:2A:882:G:H2'	1:2A:883:G:C8	2.49	0.47
1:2A:1062:G:O6	1:2A:1088:A:H8	1.98	0.47
1:2A:1915:5MU:H3'	1:2A:1916:A:C8	2.48	0.47
1:2A:2111:C:H42	1:2A:2147:G:N2	2.03	0.47
1:2A:2114:A:O2'	1:2A:2167:U:H5''	2.14	0.47
1:2A:2206:G:C3'	1:2A:2207:G:H8	2.26	0.47
1:2A:2331:G:O2'	1:2A:2336:A:N1	2.39	0.47
1:2A:2561:A:H2	10:2O:23:ARG:NH2	2.12	0.47
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.45	0.47
6:2G:165:THR:OG1	6:2G:168:GLU:HG3	2.15	0.47
7:2H:86:GLU:OE1	7:2H:130:ARG:HD2	2.15	0.47
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.49	0.47
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	1.95	0.47
21:2Z:179:ASP:O	21:2Z:182:LYS:HG2	2.15	0.47
24:22:16:LEU:O	24:22:67:LYS:NZ	2.42	0.47
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.95	0.47
32:2a:396:G:O2'	32:2a:398:C:OP1	2.16	0.47
32:2a:431:A:H2'	32:2a:432:A:O4'	2.15	0.47
32:2a:475:G:O2'	32:2a:476:G:H5'	2.14	0.47
32:2a:614:A:H2'	32:2a:615:C:O4'	2.15	0.47
32:2a:955:U:O2'	50:2s:83:HIS:HD2	1.98	0.47
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5''	1.97	0.47
32:2a:1125:U:H6	32:2a:1126:U:H2'	1.79	0.47
32:2a:1269:A:H2	32:2a:1312:G:N3	2.13	0.47
32:2a:1402:4OC:H6	32:2a:1402:4OC:O5'	2.15	0.47
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.97	0.47
35:2d:13:ARG:HH22	35:2d:36:ARG:NE	2.13	0.47
35:2d:50:ARG:HA	35:2d:51:PRO:HD3	1.80	0.47
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.50	0.47
51:2t:56:MET:HG3	51:2t:84:LEU:CD1	2.44	0.47
1:1A:664:U:H2'	1:1A:665:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:61:ASN:O	14:1S:65:VAL:HG23	2.14	0.47
15:1T:96:ARG:HB2	15:1T:96:ARG:NH1	2.29	0.47
22:10:23:VAL:HG22	22:10:38:VAL:HG22	1.96	0.47
28:16:18:ARG:HD3	28:16:42:TRP:CD1	2.49	0.47
32:1a:250:A:H4'	32:1a:251:G:O5'	2.14	0.47
32:1a:1287:A:H61	32:1a:1370:G:H21	1.63	0.47
1:2A:875:G:H2'	1:2A:876:C:O4'	2.14	0.47
6:2G:28:VAL:O	6:2G:31:VAL:HG13	2.15	0.47
6:2G:114:ILE:HG12	6:2G:140:ILE:HD13	1.97	0.47
32:2a:1273:G:H5'	32:2a:1274:G:OP2	2.14	0.47
35:2d:58:LEU:O	35:2d:62:GLN:HG2	2.15	0.47
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.15	0.47
1:1A:1617:A:H2'	1:1A:1618:A:C8	2.50	0.47
1:1A:1925:G:OP1	3:1D:241:PRO:HB2	2.15	0.47
1:1A:2346:G:H5'	14:1S:9:ARG:HG2	1.95	0.47
2:1B:90:A:N7	2:1B:91:C:H1'	2.30	0.47
4:1E:49:LEU:HD12	4:1E:49:LEU:HA	1.74	0.47
6:1G:28:VAL:HG23	6:1G:29:TRP:CD1	2.49	0.47
14:1S:82:ILE:HG22	14:1S:110:LEU:HD11	1.97	0.47
15:1T:49:VAL:HG12	15:1T:63:VAL:HG22	1.96	0.47
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.71	0.47
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.50	0.47
42:1k:31:THR:HG22	42:1k:42:TRP:HB2	1.96	0.47
43:1l:76:ASN:HD21	43:1l:108:ALA:H	1.62	0.47
1:2A:923:C:H2'	1:2A:924:C:C6	2.50	0.47
1:2A:2108:C:H2'	1:2A:2109:U:O4'	2.14	0.47
1:2A:2115:G:N1	1:2A:2119:A:OP2	2.40	0.47
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.14	0.47
2:2B:52:A:N6	14:2S:33:LYS:HG2	2.29	0.47
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.97	0.47
32:2a:1026:G:N7	32:2a:1027:C:O2	2.48	0.47
32:2a:1125:U:O4	32:2a:1280:A:C5	2.68	0.47
44:2m:29:ARG:HD3	44:2m:64:TRP:CE2	2.49	0.47
48:2q:62:SER:OG	48:2q:72:ARG:HG3	2.15	0.47
1:1A:532:A:H5''	1:1A:533:G:H3'	1.97	0.47
1:1A:629:U:H4'	1:1A:705:C:H4'	1.96	0.47
35:1d:107:ARG:HD2	35:1d:107:ARG:HA	1.67	0.47
38:1g:90:GLU:H	38:1g:90:GLU:CD	2.23	0.47
40:1i:3:GLN:NE2	40:1i:20:ARG:HH21	2.12	0.47
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.70	0.47
45:1n:3:ARG:HG3	45:1n:4:LYS:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:1y:14:ARG:HA	55:1y:15:PRO:HD2	1.63	0.47
1:2A:1906:G:H1	1:2A:1924:C:H42	1.63	0.47
1:2A:2124:G:N1	1:2A:2174:C:O2	2.47	0.47
5:2F:195:ASP:OD1	5:2F:196:LEU:N	2.47	0.47
7:2H:72:ILE:O	7:2H:76:VAL:HG23	2.15	0.47
17:2V:4:ILE:HD12	17:2V:39:LEU:HD22	1.97	0.47
19:2X:60:ARG:HH22	29:27:47:ARG:HH22	1.62	0.47
21:2Z:182:LYS:O	21:2Z:185:GLU:HG3	2.14	0.47
32:2a:728:A:H2'	32:2a:729:A:C8	2.49	0.47
32:2a:736:C:H2'	32:2a:737:A:C8	2.50	0.47
32:2a:1044:A:C5	32:2a:1045:C:H1'	2.50	0.47
32:2a:1095:U:C4	32:2a:1096:C:C4	3.02	0.47
33:2b:19:HIS:CG	33:2b:20:GLU:H	2.32	0.47
38:2g:152:ALA:O	38:2g:155:ARG:HG2	2.15	0.47
40:2i:5:TYR:H	40:2i:87:GLN:HE22	1.63	0.47
1:1A:97:G:P	24:12:2:LYS:HG2	2.55	0.46
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.96	0.46
4:1E:19:ARG:NH1	10:1O:72:PRO:HB3	2.29	0.46
12:1Q:59:ARG:HA	21:1Z:180:VAL:HG23	1.96	0.46
19:1X:1:MET:HE1	24:12:26:ARG:NH2	2.28	0.46
26:14:62:ARG:C	26:14:64:GLY:HA2	2.40	0.46
32:1a:975:A:N6	32:1a:1367:C:O4'	2.48	0.46
32:1a:1287:A:N6	32:1a:1370:G:H21	2.13	0.46
34:1c:104:GLN:HE21	34:1c:104:GLN:HB2	1.58	0.46
36:1e:57:LYS:HG2	36:1e:61:TYR:HE2	1.81	0.46
36:1e:151:LEU:HD11	39:1h:77:GLU:CD	2.40	0.46
48:1q:75:ARG:NH2	48:1q:77:VAL:HG22	2.30	0.46
51:1t:45:GLN:HB2	51:1t:91:LEU:HD13	1.98	0.46
1:2A:637:A:H8	11:2P:117:GLU:HG3	1.80	0.46
1:2A:1059:G:C6	1:2A:1060:U:N3	2.83	0.46
1:2A:1365:A:O2'	23:21:11:ARG:NH2	2.48	0.46
1:2A:2321:G:N3	1:2A:2321:G:H2'	2.30	0.46
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.50	0.46
26:24:15:ILE:HG23	26:24:21:VAL:HG22	1.96	0.46
32:2a:516:PSU:N3	32:2a:533:A:N6	2.31	0.46
32:2a:1024:G:H2'	32:2a:1024:G:N3	2.30	0.46
32:2a:1221:G:OP1	50:2s:36:ARG:HD3	2.16	0.46
32:2a:1320:C:H1'	50:2s:73:GLU:HG2	1.97	0.46
32:2a:1442:G:O2'	32:2a:1442(A):G:O5'	2.27	0.46
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.80	0.46
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.15	0.46
1:1A:278:G:H2'	1:1A:279:G:H5''	1.96	0.46
1:1A:597:C:N3	4:1E:145:LYS:NZ	2.62	0.46
1:1A:875:U:H2'	1:1A:876:A:C8	2.49	0.46
1:1A:1541:A:H2'	1:1A:1542:A:C8	2.50	0.46
21:1Z:7:ALA:HB2	21:1Z:59:LEU:HD22	1.97	0.46
32:1a:940:C:H2'	32:1a:941:G:C8	2.50	0.46
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.50	0.46
40:1i:89:ASN:HB3	40:1i:92:TYR:CD2	2.50	0.46
47:1p:5:ARG:HE	47:1p:22:THR:HG21	1.80	0.46
1:2A:729:G:C5	3:2D:208:LYS:HB2	2.51	0.46
6:2G:33:ARG:HH21	6:2G:162:THR:HG21	1.79	0.46
13:2R:98:LEU:HB2	13:2R:113:LEU:HD11	1.96	0.46
32:2a:171:A:H2'	32:2a:172:A:C8	2.50	0.46
32:2a:653:A:OP1	39:2h:56:LYS:NZ	2.32	0.46
32:2a:973:G:N3	41:2j:54:PHE:HE1	2.13	0.46
32:2a:1095:U:H2'	32:2a:1096:C:O4'	2.14	0.46
32:2a:1368:G:OP2	40:2i:112:LYS:HG3	2.15	0.46
40:2i:81:ILE:O	40:2i:85:LEU:HG	2.15	0.46
46:2o:3:ILE:HD11	46:2o:35:ARG:HG2	1.97	0.46
1:1A:1451:U:H2'	1:1A:1452:U:H6	1.78	0.46
1:1A:1495:G:O2'	1:1A:1575:A:N1	2.48	0.46
1:1A:1831:C:OP1	3:1D:260:ARG:NH2	2.48	0.46
1:1A:1957:G:H1'	1:1A:1986:G:N2	2.30	0.46
1:1A:2021:C:H4'	1:1A:2736:C:O2	2.16	0.46
2:1B:55:U:O2'	2:1B:57:A:N7	2.47	0.46
3:1D:111:LEU:HD23	3:1D:111:LEU:HA	1.81	0.46
5:1F:102:PRO:HB2	5:1F:105:VAL:HG23	1.98	0.46
26:14:61:ARG:HH21	50:1s:42:PRO:HD2	1.80	0.46
32:1a:69:G:H2'	32:1a:70:G:C8	2.51	0.46
32:1a:337:C:H2'	32:1a:338:A:C8	2.51	0.46
32:1a:1279:A:H5''	41:1j:7:LYS:HZ1	1.80	0.46
34:1c:19:GLU:OE2	34:1c:54:ARG:HG3	2.16	0.46
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.97	0.46
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	1.96	0.46
18:2W:64:MET:HE2	18:2W:109:GLU:HG3	1.96	0.46
21:2Z:67:LEU:HA	21:2Z:68:PRO:HD3	1.74	0.46
32:2a:531:U:O3'	32:2a:532:A:H4'	2.15	0.46
49:2r:56:THR:HB	49:2r:58:LEU:HD13	1.96	0.46
1:1A:645:G:H5'	1:1A:645:G:N3	2.30	0.46
22:10:43:THR:OG1	22:10:46:LYS:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:123:C:O2'	32:1a:290:C:O2	2.30	0.46
32:1a:661:G:H1	32:1a:744:C:H42	1.63	0.46
1:2A:1117:G:H2'	1:2A:1118:C:C6	2.50	0.46
32:2a:542:G:P	35:2d:10:ARG:HH22	2.38	0.46
32:2a:542:G:H5'	35:2d:41:GLY:HA3	1.97	0.46
36:2e:9:LYS:NZ	36:2e:111:GLU:OE1	2.47	0.46
1:1A:1291:G:OP1	11:1P:13:ASN:ND2	2.42	0.46
1:1A:1496:A:N3	1:1A:1576:G:H1'	2.31	0.46
1:1A:1633:A:H2'	1:1A:1634:C:C6	2.51	0.46
1:1A:1845:G:H4'	3:1D:51:VAL:HG21	1.98	0.46
1:1A:2039:U:O2	27:15:10:LYS:HB2	2.16	0.46
1:1A:2098:U:OP2	1:1A:2250:G:N2	2.43	0.46
32:1a:92:C:H2'	32:1a:93:G:C8	2.49	0.46
32:1a:262:A:C6	32:1a:263:A:C6	3.03	0.46
32:1a:632:A:H5'	32:1a:633:G:OP2	2.16	0.46
32:1a:632:A:OP1	39:1h:98:LYS:NZ	2.48	0.46
32:1a:1017:G:H2'	32:1a:1018:C:C6	2.51	0.46
32:1a:1026:G:H3'	32:1a:1027:C:H6	1.81	0.46
44:1m:4:ILE:HG22	44:1m:57:ARG:HE	1.81	0.46
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.15	0.46
1:2A:1111:A:O2'	1:2A:1112:G:H4'	2.16	0.46
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.98	0.46
7:2H:11:VAL:HB	7:2H:48:GLY:HA2	1.97	0.46
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.15	0.46
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.97	0.46
13:2R:29:LEU:HD11	13:2R:48:VAL:HG13	1.97	0.46
19:2X:95:LEU:H	19:2X:95:LEU:HD12	1.80	0.46
32:2a:664:G:OP1	49:2r:64:ARG:NE	2.33	0.46
32:2a:1139:G:N2	32:2a:1143:G:C6	2.83	0.46
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.97	0.46
38:2g:92:SER:O	38:2g:96:GLN:HG3	2.16	0.46
39:2h:6:ILE:HB	39:2h:85:ARG:HH11	1.80	0.46
1:1A:236:G:H4'	1:1A:413:G:C6	2.50	0.46
1:1A:2108:U:H2'	1:1A:2109:G:H8	1.80	0.46
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.51	0.46
2:1B:78:A:C2	2:1B:100:A:C4	3.03	0.46
13:1R:54:LEU:HD12	13:1R:54:LEU:HA	1.75	0.46
25:13:59:VAL:HG23	25:13:60:GLU:HG2	1.96	0.46
32:1a:266:G:H2'	32:1a:266:G:N3	2.31	0.46
32:1a:520:A:H2'	32:1a:521:G:O4'	2.16	0.46
35:1d:153:ARG:O	35:1d:158:ILE:HD11	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:264:C:O2'	1:2A:265:A:H2'	2.16	0.46
1:2A:981:A:N1	1:2A:2027:G:O2'	2.39	0.46
6:2G:60:LEU:HA	6:2G:63:ILE:HD12	1.98	0.46
12:2Q:54:MET:HE1	12:2Q:104:PHE:HB3	1.98	0.46
18:2W:12:ILE:HD12	18:2W:42:ARG:HD3	1.98	0.46
32:2a:7:G:N2	36:2e:121:LYS:HG2	2.29	0.46
32:2a:280:C:N3	48:2q:39:SER:OG	2.48	0.46
32:2a:406:G:H21	35:2d:119:GLN:NE2	2.14	0.46
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.80	0.46
1:1A:600:G:O2'	1:1A:1300:A:OP1	2.30	0.46
1:1A:2473:C:H2'	1:1A:2474:U:C6	2.51	0.46
2:1B:104:U:O2'	21:1Z:72:ARG:HG2	2.15	0.46
4:1E:35:GLN:OE1	4:1E:66:HIS:HE1	1.98	0.46
4:1E:119:ARG:HG2	4:1E:160:TYR:CG	2.51	0.46
6:1G:143:GLU:OE2	26:14:26:SER:OG	2.21	0.46
16:1U:52:ARG:HE	16:1U:52:ARG:HB2	1.54	0.46
32:1a:768:A:H2'	32:1a:769:G:O4'	2.15	0.46
32:1a:1168:A:H2'	32:1a:1169:A:C8	2.50	0.46
35:1d:76:ARG:HA	35:1d:76:ARG:HD2	1.71	0.46
41:1j:95:GLU:HG2	41:1j:96:ILE:N	2.30	0.46
42:1k:33:THR:HG22	42:1k:39:PRO:HA	1.98	0.46
46:1o:9:GLN:O	46:1o:13:GLN:HG3	2.16	0.46
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.50	0.46
50:1s:71:LEU:HD23	50:1s:71:LEU:HA	1.87	0.46
51:1t:47:GLY:HA2	51:1t:48:LYS:CB	2.46	0.46
1:2A:603:A:O4'	1:2A:655:A:N6	2.48	0.46
1:2A:666:G:H1'	30:28:4:MET:HE3	1.97	0.46
1:2A:879:G:H2'	1:2A:880:G:O4'	2.15	0.46
1:2A:1199:U:O2'	60:2A:4003:HOH:O	2.14	0.46
1:2A:2102:U:H2'	1:2A:2103:C:C1'	2.45	0.46
1:2A:2311:A:H5''	6:2G:77:ILE:HD11	1.97	0.46
1:2A:2370:G:C6	1:2A:2371:G:C6	3.04	0.46
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.47	0.46
18:2W:70:TYR:OH	18:2W:72:LYS:HG3	2.14	0.46
32:2a:964:A:N3	32:2a:969:A:O2'	2.48	0.46
33:2b:16:HIS:CD2	33:2b:210:SER:HB3	2.50	0.46
33:2b:163:PHE:HA	33:2b:185:ILE:O	2.15	0.46
35:2d:196:LEU:H	35:2d:196:LEU:HD12	1.79	0.46
41:2j:9:ARG:HH21	41:2j:97:GLU:HG3	1.81	0.46
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.16	0.46
1:1A:442:A:H2'	1:1A:443:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:73:A:C4	2:1B:105:A:C2	3.04	0.46
2:1B:90:A:C5	2:1B:91:C:H1'	2.50	0.46
30:18:17:THR:OG1	30:18:21:LYS:HB2	2.16	0.46
32:1a:426:G:H2'	32:1a:427:U:C6	2.51	0.46
32:1a:626:U:C2	32:1a:627:G:C8	3.04	0.46
32:1a:652:U:O2'	32:1a:653:A:OP2	2.30	0.46
46:1o:61:GLY:O	46:1o:65:ARG:HG3	2.16	0.46
1:2A:588:U:H1'	5:2F:90:PHE:HB3	1.97	0.46
1:2A:1914:C:P	1:2A:1914:C:H6	2.38	0.46
1:2A:2454:G:P	55:2y:2:ARG:HH22	2.39	0.46
1:2A:2615:U:H2'	1:2A:2616:C:H6	1.81	0.46
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.16	0.46
2:2B:4:C:H42	2:2B:117:G:H1	1.62	0.46
2:2B:78:A:H2'	2:2B:79:C:O4'	2.16	0.46
8:2I:9:LEU:HD11	8:2I:35:LEU:HB3	1.98	0.46
23:21:64:ALA:HA	23:21:67:ILE:HG13	1.96	0.46
23:21:85:LEU:HB3	23:21:89:GLU:HB2	1.98	0.46
32:2a:1372:U:H2'	32:2a:1373:G:O4'	2.15	0.46
32:2a:1439:C:OP1	51:2t:38:LYS:HE2	2.15	0.46
33:2b:80:ILE:HD13	33:2b:211:ILE:HG22	1.97	0.46
33:2b:124:SER:HB2	33:2b:125:PRO:HD3	1.97	0.46
33:2b:145:LEU:HD22	33:2b:149:LEU:HD12	1.98	0.46
44:2m:82:MET:HB3	44:2m:93:ARG:HD3	1.96	0.46
1:1A:2650:G:OP2	4:1E:82:ARG:NH1	2.43	0.46
6:1G:148:MET:H	6:1G:148:MET:HG2	1.62	0.46
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.98	0.46
13:1R:103:ARG:NH1	13:1R:108:GLY:O	2.48	0.46
32:1a:255:G:H1'	48:1q:16:GLN:HE21	1.80	0.46
32:1a:373:A:H2'	32:1a:374:A:H8	1.81	0.46
35:1d:88:VAL:HA	36:1e:97:GLY:HA3	1.98	0.46
38:1g:72:ARG:HH11	38:1g:72:ARG:HG3	1.81	0.46
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	1.97	0.46
41:1j:6:ILE:O	41:1j:71:LEU:HD12	2.15	0.46
47:1p:5:ARG:HE	47:1p:22:THR:CG2	2.28	0.46
1:2A:824:A:H1'	1:2A:2358:G:N7	2.31	0.46
1:2A:2138:C:C2	1:2A:2153:G:N2	2.84	0.46
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.50	0.46
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.81	0.46
1:2A:2410:G:H2'	1:2A:2411:A:O4'	2.16	0.46
2:2B:82:G:H5''	60:2B:3118:HOH:O	2.16	0.46
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.97	0.46
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.16	0.46
19:2X:36:LYS:HG2	19:2X:56:THR:HG23	1.98	0.46
32:2a:1441:G:H5''	32:2a:1442:G:H5'	1.97	0.46
37:2f:97:PHE:O	49:2r:31:LEU:HD12	2.16	0.46
1:1A:1091:A:H1'	1:1A:1093:G:C2	2.49	0.46
1:1A:1314:A:C2	1:1A:2035:A:C4	3.04	0.46
1:1A:2390:A:H8	1:1A:2390:A:O5'	1.98	0.46
1:1A:2463:A:C2	55:1y:9:ARG:HB2	2.51	0.46
32:1a:457:C:H2'	32:1a:458:C:C6	2.50	0.46
42:1k:87:THR:O	42:1k:87:THR:OG1	2.26	0.46
46:1o:28:GLN:HE21	46:1o:66:LEU:HD21	1.80	0.46
50:1s:58:VAL:HA	50:1s:59:PRO:HD3	1.76	0.46
1:2A:224:G:N7	1:2A:420:C:H4'	2.31	0.46
1:2A:668:G:H5'	1:2A:669:G:OP2	2.15	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.65	0.46
32:2a:422:C:H4'	32:2a:423:G:C4	2.51	0.46
33:2b:8:LYS:CG	33:2b:9:GLU:H	2.29	0.46
33:2b:16:HIS:HE1	33:2b:42:ILE:HD12	1.81	0.46
39:2h:7:ALA:HB2	39:2h:85:ARG:HG3	1.98	0.46
41:2j:5:ARG:HA	41:2j:73:ASP:OD1	2.16	0.46
1:1A:1821:C:H5''	1:1A:1822:A:OP1	2.16	0.45
1:1A:1954:A:H2'	1:1A:1955:G:O4'	2.16	0.45
1:1A:2136:A:N3	1:1A:2137:G:H1'	2.31	0.45
4:1E:18:ASP:HA	15:1T:82:LEU:HD11	1.98	0.45
4:1E:51:PHE:H	4:1E:75:VAL:CG1	2.29	0.45
6:1G:161:THR:HG22	6:1G:162:THR:N	2.31	0.45
32:1a:688:G:H2'	32:1a:689:C:H6	1.81	0.45
32:1a:779:C:H2'	32:1a:780:A:O4'	2.17	0.45
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.63	0.45
54:1x:39:C:H2'	54:1x:40:C:H6	1.80	0.45
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.51	0.45
1:2A:1575:C:H2'	1:2A:1576:U:O4'	2.15	0.45
1:2A:1681:G:H8	1:2A:1681:G:O5'	1.99	0.45
1:2A:1930:G:N2	1:2A:1968:G:H2'	2.31	0.45
1:2A:2157:G:C8	1:2A:2157:G:H3'	2.51	0.45
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.16	0.45
29:27:24:THR:O	29:27:28:ARG:HG3	2.17	0.45
32:2a:237:C:H5''	48:2q:25:ARG:CZ	2.46	0.45
32:2a:616:G:OP2	35:2d:141:ARG:NH2	2.48	0.45
40:2i:106:ALA:O	40:2i:108:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	1.98	0.45
1:1A:303:C:N3	1:1A:385:G:N2	2.45	0.45
1:1A:354:A:H2	1:1A:1255:A:O2'	1.78	0.45
1:1A:872:C:O2	11:1P:55:ARG:NH1	2.48	0.45
1:1A:1171:G:H5'	31:19:37:GLY:HA2	1.98	0.45
6:1G:150:ASP:OD1	6:1G:151:ALA:N	2.49	0.45
8:1I:72:LEU:HD12	8:1I:138:ILE:HG21	1.97	0.45
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.99	0.45
1:2A:272(B):G:H2'	1:2A:272(C):G:C8	2.50	0.45
1:2A:608:A:C6	1:2A:609:A:C6	3.04	0.45
1:2A:656:G:H2'	1:2A:657:U:O4'	2.16	0.45
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.97	0.45
1:2A:828:U:H4'	1:2A:831:G:N1	2.30	0.45
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.51	0.45
1:2A:1218:C:H42	1:2A:1231:G:H1	1.63	0.45
7:2H:6:ARG:HE	7:2H:6:ARG:HB2	1.28	0.45
21:2Z:10:ARG:HB2	21:2Z:36:LYS:HB3	1.97	0.45
33:2b:76:GLN:NE2	33:2b:206:ASP:OD1	2.49	0.45
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.97	0.45
38:2g:72:ARG:HH11	38:2g:72:ARG:HG3	1.82	0.45
44:2m:3:ARG:HD2	44:2m:8:GLU:HG3	1.98	0.45
48:2q:4:LYS:HE2	48:2q:6:LEU:HD11	1.97	0.45
54:2x:19:G:H4'	54:2x:20:U:OP2	2.16	0.45
1:1A:416:G:O5'	1:1A:416:G:H8	1.99	0.45
1:1A:1093:G:H2'	1:1A:1156:G:H1	1.81	0.45
1:1A:2156:A:C5	1:1A:2179:G:H4'	2.51	0.45
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	1.99	0.45
19:1X:27:THR:HG23	19:1X:80:ILE:HG12	1.98	0.45
32:1a:620:C:H2'	32:1a:621:A:O4'	2.16	0.45
32:1a:1240:U:OP1	38:1g:119:ARG:NH2	2.42	0.45
32:1a:1352:C:H2'	32:1a:1353:G:C8	2.51	0.45
1:2A:752:A:H4'	1:2A:753:C:H5'	1.97	0.45
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.26	0.45
1:2A:1919:A:O3'	32:2a:1517:G:H1'	2.16	0.45
1:2A:2395:C:O2'	23:21:30:VAL:HG23	2.17	0.45
1:2A:2809:A:OP2	1:2A:2891:G:N1	2.47	0.45
2:2B:59:A:H2'	2:2B:60:C:O4'	2.17	0.45
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.50	0.45
21:2Z:70:LEU:HD11	21:2Z:98:MET:SD	2.56	0.45
32:2a:1118:C:OP1	40:2i:9:ARG:HD2	2.17	0.45
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1315:U:H2'	32:2a:1316:G:O4'	2.16	0.45
32:2a:1456:G:N1	51:2t:51:GLU:OE2	2.22	0.45
33:2b:135:GLN:HE21	33:2b:135:GLN:HB3	1.51	0.45
42:2k:81:ASP:OD1	42:2k:106:LYS:HE3	2.17	0.45
1:1A:517:A:H2'	1:1A:518:G:O4'	2.16	0.45
1:1A:2119:C:H2'	1:1A:2120:U:O4'	2.17	0.45
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.98	0.45
11:1P:96:THR:H	11:1P:99:LEU:HD12	1.81	0.45
18:1W:37:ARG:HG2	18:1W:38:TYR:CE2	2.51	0.45
32:1a:618:C:H3'	32:1a:620:C:OP2	2.15	0.45
32:1a:1117:G:H4'	40:1i:104:ARG:NH1	2.32	0.45
32:1a:1286:A:H2	52:1u:18:TYR:OH	1.99	0.45
33:1b:10:LEU:C	33:1b:12:GLU:H	2.25	0.45
33:1b:83:MET:SD	33:1b:234:PRO:HB2	2.57	0.45
44:1m:76:ALA:HA	44:1m:79:LYS:HB3	1.98	0.45
44:1m:89:GLY:O	44:1m:93:ARG:HG3	2.16	0.45
1:2A:918:A:OP2	1:2A:2268:A:N6	2.45	0.45
1:2A:1450:G:H2'	1:2A:1450(A):C:H6	1.81	0.45
1:2A:2494:G:OP2	55:2y:4:ARG:NH1	2.49	0.45
1:2A:2615:U:H2'	1:2A:2616:C:C6	2.51	0.45
6:2G:77:ILE:HG22	6:2G:80:PHE:H	1.81	0.45
21:2Z:150:LEU:HD12	21:2Z:150:LEU:HA	1.84	0.45
26:24:46:GLN:C	26:24:48:ARG:H	2.23	0.45
32:2a:164:U:H2'	32:2a:165:C:C6	2.51	0.45
32:2a:716:A:N3	42:2k:118:GLY:HA2	2.31	0.45
32:2a:1223:C:P	50:2s:78:ARG:HH21	2.40	0.45
36:2e:69:VAL:HA	36:2e:70:PRO:HD3	1.66	0.45
50:2s:15:LEU:HD22	50:2s:35:SER:HB2	1.97	0.45
1:1A:276:C:H2'	1:1A:277:G:O4'	2.17	0.45
1:1A:1709:C:O2'	1:1A:2699:U:OP1	2.33	0.45
1:1A:1732:C:H2'	1:1A:1733:C:H6	1.81	0.45
1:1A:2208:G:C2	1:1A:2209:G:C8	3.04	0.45
4:1E:51:PHE:HB3	4:1E:77:ILE:HD12	1.98	0.45
32:1a:328:C:H4'	32:1a:329:A:H5'	1.99	0.45
32:1a:520:A:N6	32:1a:529:G:H1'	2.31	0.45
32:1a:1027:C:H3'	32:1a:1028:C:H5''	1.98	0.45
32:1a:1143:G:H2'	32:1a:1144:G:H8	1.81	0.45
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.50	0.45
35:1d:168:ARG:HD3	35:1d:168:ARG:HA	1.76	0.45
40:1i:66:ARG:HH21	40:1i:66:ARG:HB2	1.81	0.45
1:2A:1167:U:H2'	1:2A:1168:G:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1889:A:C6	1:2A:1890:A:C6	3.04	0.45
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.52	0.45
5:2F:34:TRP:NE1	11:2P:8:PRO:HD3	2.31	0.45
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.99	0.45
31:29:10:ILE:HD12	31:29:32:HIS:HA	1.97	0.45
32:2a:28:G:O2'	32:2a:296:U:OP1	2.28	0.45
32:2a:46:G:O2'	32:2a:365:U:H1'	2.16	0.45
32:2a:141:A:H1'	32:2a:182:U:O2	2.17	0.45
32:2a:299:G:H8	32:2a:299:G:O5'	2.00	0.45
32:2a:520:A:N1	32:2a:536:C:H1'	2.30	0.45
32:2a:1278:U:H5'	32:2a:1279:A:O4'	2.16	0.45
33:2b:16:HIS:CE1	33:2b:42:ILE:HD12	2.52	0.45
33:2b:74:LYS:HG3	33:2b:77:ALA:HB3	1.98	0.45
33:2b:155:LEU:HD21	33:2b:159:PRO:HG3	1.99	0.45
38:2g:69:VAL:HG21	38:2g:104:LEU:CD1	2.46	0.45
39:2h:63:LEU:HD23	39:2h:65:TYR:OH	2.17	0.45
1:1A:518:G:H2'	1:1A:519:G:O4'	2.16	0.45
1:1A:2167:C:H6	1:1A:2167:C:OP1	1.99	0.45
1:1A:2797:C:H1'	4:1E:37:ARG:HH12	1.82	0.45
3:1D:61:LEU:O	3:1D:63:ARG:NH1	2.45	0.45
6:1G:7:LEU:HD23	6:1G:7:LEU:HA	1.75	0.45
6:1G:43:LEU:C	6:1G:45:GLU:H	2.25	0.45
21:1Z:30:ASN:HD22	21:1Z:90:VAL:HB	1.81	0.45
23:11:3:LYS:HB3	23:11:61:ARG:HH22	1.82	0.45
32:1a:46:G:O2'	32:1a:365:U:H1'	2.17	0.45
32:1a:109:A:H2'	32:1a:326:G:N2	2.31	0.45
32:1a:407:G:H2'	32:1a:408:A:H8	1.81	0.45
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.16	0.45
38:1g:110:GLN:HA	38:1g:110:GLN:HE21	1.81	0.45
51:1t:58:LYS:HD2	51:1t:58:LYS:HA	1.53	0.45
1:2A:1077:A:C6	1:2A:1078:U:O4	2.70	0.45
5:2F:107:LYS:NZ	5:2F:205:ARG:O	2.29	0.45
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.64	0.45
20:2Y:81:LYS:HE3	20:2Y:81:LYS:HB3	1.85	0.45
25:23:57:GLU:HG2	25:23:59:VAL:HG13	1.99	0.45
32:2a:1125:U:HO2'	32:2a:1126:U:H2'	1.82	0.45
32:2a:1183:A:HO2'	32:2a:1184:G:P	2.37	0.45
34:2c:47:LEU:HD13	34:2c:68:VAL:HG11	1.98	0.45
35:2d:36:ARG:HD2	35:2d:38:TYR:OH	2.16	0.45
47:2p:44:THR:O	47:2p:44:THR:OG1	2.35	0.45
50:2s:51:VAL:HB	50:2s:75:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1188:A:C4	1:1A:1190:G:N7	2.85	0.45
15:1T:120:ARG:HA	15:1T:123:GLN:HB3	1.98	0.45
28:16:10:LEU:HD23	28:16:22:ALA:HB2	1.98	0.45
32:1a:145:G:H1	32:1a:177:C:H42	1.64	0.45
32:1a:974:A:H8	32:1a:974:A:OP1	1.99	0.45
32:1a:1158:C:H5	32:1a:1181:G:N1	2.08	0.45
32:1a:1239:A:H62	32:1a:1299:A:N6	2.14	0.45
32:1a:1435:G:H2'	32:1a:1436:U:H6	1.80	0.45
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.16	0.45
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.17	0.45
1:2A:1472:A:H61	1:2A:1519:G:H1'	1.81	0.45
1:2A:1799:G:O3'	3:2D:183:ARG:NH1	2.48	0.45
1:2A:1935:G:H1'	1:2A:1964:G:N2	2.31	0.45
4:2E:50:GLY:O	4:2E:51:PHE:HB2	2.15	0.45
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.97	0.45
9:2N:20:GLY:O	9:2N:61:ARG:NE	2.48	0.45
20:2Y:20:TYR:HB3	20:2Y:23:ARG:HG3	1.99	0.45
32:2a:413:G:N2	32:2a:428:G:O2'	2.49	0.45
32:2a:977:A:O3'	32:2a:980:C:N4	2.49	0.45
32:2a:988:G:N2	32:2a:1217:C:N3	2.50	0.45
32:2a:1263:C:H2'	32:2a:1264:C:H6	1.80	0.45
32:2a:1517:G:H2'	32:2a:1518:MA6:H8	1.98	0.45
48:2q:12:SER:HB3	48:2q:20:THR:HB	1.99	0.45
51:2t:24:LEU:HD13	51:2t:24:LEU:HA	1.83	0.45
1:1A:27:G:H22	1:1A:537:G:H1'	1.82	0.45
1:1A:1405:A:N1	1:1A:1418:U:C4	2.81	0.45
1:1A:2157:A:N6	1:1A:2178:G:O2'	2.49	0.45
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.16	0.45
26:14:62:ARG:O	26:14:64:GLY:HA2	2.17	0.45
26:14:69:LYS:HB2	50:1s:20:LEU:HD13	1.99	0.45
32:1a:17:U:H2'	32:1a:18:C:C6	2.52	0.45
32:1a:130:A:N3	32:1a:263:A:O2'	2.45	0.45
32:1a:266:G:N3	32:1a:266:G:H5'	2.31	0.45
32:1a:1051:C:H2'	32:1a:1052:U:C6	2.52	0.45
32:1a:1330:U:H2'	32:1a:1331:G:H5'	1.98	0.45
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.16	0.45
1:2A:272(E):G:C2	1:2A:364:C:C2	3.05	0.45
1:2A:361:G:O2'	1:2A:362:U:H5'	2.17	0.45
1:2A:1784:A:H4'	1:2A:1785:A:O5'	2.17	0.45
1:2A:1914:C:H2'	1:2A:1915:5MU:O2	2.17	0.45
7:2H:118:PRO:HD2	7:2H:121:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:60:LEU:HD21	43:2l:85:ILE:HD11	1.99	0.45
1:1A:1968:U:H2'	1:1A:1969:C:C6	2.51	0.45
1:1A:2648:U:H2'	1:1A:2649:U:C6	2.52	0.45
2:1B:41:U:C4	6:1G:70:VAL:HB	2.52	0.45
6:1G:45:GLU:H	6:1G:45:GLU:HG2	1.44	0.45
16:1U:16:LYS:HB3	16:1U:16:LYS:HE2	1.63	0.45
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.82	0.45
32:1a:940:C:OP1	38:1g:29:LYS:NZ	2.47	0.45
32:1a:979:C:N3	45:1n:19:ARG:HG2	2.32	0.45
32:1a:1170:A:H8	32:1a:1170:A:O5'	2.00	0.45
33:1b:55:PHE:CD1	33:1b:58:ILE:HD12	2.52	0.45
38:1g:89:MET:SD	38:1g:155:ARG:HB3	2.57	0.45
1:2A:1418:G:H8	1:2A:1418:G:O5'	2.00	0.45
1:2A:1857:G:C6	1:2A:1858:G:C6	3.04	0.45
1:2A:2139:C:N4	1:2A:2152:G:H1	2.15	0.45
11:2P:70:GLN:O	11:2P:73:GLY:N	2.42	0.45
18:2W:59:VAL:HG12	18:2W:60:ASN:ND2	2.32	0.45
26:24:46:GLN:HE21	26:24:48:ARG:HH12	1.64	0.45
32:2a:109:A:H2'	32:2a:326:G:H21	1.81	0.45
32:2a:487:A:H2'	32:2a:488:C:O4'	2.16	0.45
32:2a:510:A:H5''	32:2a:511:C:P	2.57	0.45
32:2a:859:A:H2'	32:2a:860:A:O4'	2.17	0.45
32:2a:1015:A:H1'	32:2a:1219:U:H5'	1.99	0.45
32:2a:1035:A:O2'	32:2a:1036:G:H8	2.00	0.45
32:2a:1125:U:C5	32:2a:1280:A:N7	2.85	0.45
33:2b:216:SER:O	33:2b:220:ASP:N	2.49	0.45
1:1A:722:A:C8	1:1A:851:A:C6	3.05	0.45
1:1A:1386:U:OP1	19:1X:16:LYS:NZ	2.46	0.45
1:1A:2023:A:H4'	1:1A:2701:U:H2'	1.99	0.45
1:1A:2148:A:H1'	1:1A:2184:G:N2	2.32	0.45
9:1N:26:LEU:HG	9:1N:30:ILE:HD11	2.00	0.45
32:1a:376:G:H5''	47:1p:5:ARG:HD2	1.98	0.45
42:1k:98:LEU:O	42:1k:101:SER:OG	2.28	0.45
1:2A:236:C:H2'	1:2A:237:C:C6	2.52	0.45
1:2A:1009:A:OP2	9:2N:37:LYS:NZ	2.43	0.45
1:2A:1246:A:OP1	5:2F:38:ARG:NH1	2.46	0.45
1:2A:1721:G:O6	1:2A:1739:U:H5''	2.17	0.45
1:2A:2462:U:H1'	1:2A:2491:U:O4	2.16	0.45
1:2A:2585:U:O2'	60:2A:4007:HOH:O	2.21	0.45
1:2A:2711:A:OP1	1:2A:2712:U:H3'	2.17	0.45
7:2H:149:ARG:HD3	7:2H:164:TYR:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:104:GLN:HG2	8:2I:105:HIS:CD2	2.52	0.45
25:23:10:LYS:NZ	25:23:15:TYR:OH	2.50	0.45
31:29:22:ARG:HD3	31:29:35:ARG:HD2	1.97	0.45
32:2a:376:G:O3'	47:2p:5:ARG:NH1	2.41	0.45
32:2a:865:A:H5'	32:2a:1078:U:C5	2.52	0.45
32:2a:1402:4OC:HM41	53:2v:18:G:P	2.57	0.45
34:2c:152:ILE:O	34:2c:152:ILE:HG13	2.17	0.45
1:1A:154:G:C6	1:1A:155:C:N4	2.85	0.44
1:1A:718:C:N4	60:1A:9031:HOH:O	2.50	0.44
1:1A:1750:G:H2'	1:1A:1751:G:C8	2.52	0.44
1:1A:1849:U:H4'	1:1A:1852:A:H1'	1.99	0.44
1:1A:2319:G:H4'	1:1A:2320:G:O5'	2.17	0.44
1:1A:2531:U:C6	1:1A:2554:A:N6	2.85	0.44
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.33	0.44
32:1a:1227:A:H5'	44:1m:111:LYS:HZ1	1.83	0.44
33:1b:28:PHE:O	33:1b:32:ILE:HG13	2.17	0.44
33:1b:35:GLU:O	33:1b:35:GLU:HG3	2.17	0.44
33:1b:166:ASP:O	33:1b:170:GLU:N	2.43	0.44
34:1c:18:TRP:H	34:1c:18:TRP:HE3	1.65	0.44
38:1g:54:THR:O	38:1g:56:GLN:NE2	2.49	0.44
1:2A:35:G:H1'	1:2A:454:A:C4	2.53	0.44
1:2A:340:A:H2'	1:2A:341:G:O4'	2.17	0.44
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.52	0.44
1:2A:1068:G:H3'	1:2A:1096:A:OP2	2.17	0.44
9:2N:130:HIS:O	9:2N:133:GLN:HG2	2.16	0.44
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.98	0.44
32:2a:98:G:C6	32:2a:99:U:C4	3.05	0.44
32:2a:948:C:H2'	32:2a:949:A:H8	1.82	0.44
32:2a:1176:A:H2'	32:2a:1177:G:H8	1.79	0.44
35:2d:39:PRO:O	35:2d:44:GLY:HA3	2.17	0.44
39:2h:13:ILE:O	39:2h:17:THR:HG23	2.17	0.44
1:1A:385:G:N1	1:1A:386:U:C4	2.85	0.44
1:1A:1952:G:O2'	1:1A:1990:G:O6	2.29	0.44
1:1A:2639:G:N2	1:1A:2790:G:OP2	2.47	0.44
1:1A:2713:C:H2'	1:1A:2714:U:H2'	1.99	0.44
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.99	0.44
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.82	0.44
32:1a:337:C:H2'	32:1a:338:A:H8	1.82	0.44
32:1a:342:C:H2'	32:1a:343:U:O4'	2.17	0.44
32:1a:540:G:H2'	32:1a:541:G:O4'	2.18	0.44
32:1a:673:G:N2	32:1a:674:G:C2	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1016:A:H8	32:1a:1016:A:O5'	2.00	0.44
33:1b:47:THR:HA	33:1b:202:PRO:HG2	1.99	0.44
44:1m:15:VAL:O	44:1m:19:LEU:HD13	2.16	0.44
1:2A:212:G:H2'	1:2A:213:A:O4'	2.17	0.44
1:2A:1007:C:H5''	9:2N:35:ARG:HH11	1.82	0.44
1:2A:1050:A:H2'	1:2A:1051:G:O4'	2.16	0.44
1:2A:1085:A:H2'	1:2A:1086:A:C2	2.53	0.44
1:2A:2788:C:O2'	1:2A:2809:A:N3	2.51	0.44
2:2B:42:C:C4	2:2B:43:C:C4	3.05	0.44
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.57	0.44
19:2X:35:THR:HG22	19:2X:38:GLU:H	1.82	0.44
23:21:50:ARG:NH1	23:21:57:GLU:OE2	2.50	0.44
32:2a:554:C:H2'	32:2a:555:C:H6	1.82	0.44
32:2a:841:U:H3'	32:2a:848:C:O4'	2.18	0.44
33:2b:186:ALA:HB3	33:2b:197:VAL:HG21	1.98	0.44
34:2c:121:ALA:HB1	34:2c:189:ALA:HB2	1.98	0.44
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	1.99	0.44
1:1A:1094:A:N1	1:1A:1158:G:O2'	2.44	0.44
1:1A:1809:U:H2'	1:1A:1815:A:N6	2.33	0.44
1:1A:2073:A:H8	1:1A:2073:A:OP2	2.00	0.44
1:1A:2137:G:N2	1:1A:2141:A:C8	2.85	0.44
1:1A:2612:A:N6	60:1A:9038:HOH:O	2.50	0.44
32:1a:501:C:H2'	32:1a:502:G:C8	2.53	0.44
32:1a:737:A:H2'	32:1a:738:C:C6	2.52	0.44
32:1a:1530:G:H4'	32:1a:1530:G:OP1	2.17	0.44
46:1o:9:GLN:HA	46:1o:12:ILE:HD12	1.98	0.44
1:2A:299:A:N1	1:2A:322:A:O2'	2.43	0.44
1:2A:1115:G:H2'	1:2A:1116:C:H6	1.82	0.44
1:2A:1131:G:C2	1:2A:1132:A:C4	3.05	0.44
1:2A:1297:C:OP1	1:2A:2710:C:H4'	2.17	0.44
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.17	0.44
1:2A:2489:G:C6	1:2A:2490:G:C6	3.06	0.44
1:2A:2602:A:H4'	1:2A:2603:G:C5'	2.47	0.44
3:2D:155:LEU:HD23	3:2D:177:LEU:HD21	1.99	0.44
21:2Z:14:LYS:HE3	21:2Z:16:SER:OG	2.17	0.44
32:2a:44:G:C2	32:2a:45:U:H1'	2.53	0.44
32:2a:1067:A:N3	32:2a:1068:G:H1'	2.32	0.44
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.52	0.44
32:2a:1125:U:O2'	32:2a:1126:U:O5'	2.28	0.44
33:2b:58:ILE:O	33:2b:62:ALA:N	2.48	0.44
35:2d:22:LYS:O	35:2d:113:SER:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:8:LEU:CD2	41:2j:96:ILE:HG23	2.47	0.44
1:1A:564:G:H2'	1:1A:565:C:H6	1.81	0.44
1:1A:1822:A:H3'	1:1A:1823:G:H8	1.81	0.44
1:1A:2053:A:C6	1:1A:2510:C:H1'	2.51	0.44
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.53	0.44
14:1S:58:LEU:HA	14:1S:58:LEU:HD23	1.74	0.44
17:1V:76:LYS:HD2	17:1V:81:TYR:CD2	2.51	0.44
32:1a:369:C:H42	32:1a:392:G:H1	1.65	0.44
32:1a:539:A:H2'	32:1a:540:G:H8	1.82	0.44
32:1a:658:G:C2	32:1a:749:C:N3	2.85	0.44
32:1a:807:A:H2'	32:1a:808:C:C6	2.52	0.44
32:1a:812:C:OP1	32:1a:903:G:H1'	2.18	0.44
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.82	0.44
32:1a:1073:U:O2'	33:1b:104:ASN:OD1	2.29	0.44
32:1a:1346:A:N1	32:1a:1374:A:H5''	2.33	0.44
33:1b:172:ILE:H	33:1b:172:ILE:HG13	1.51	0.44
35:1d:22:LYS:O	35:1d:113:SER:HB3	2.17	0.44
35:1d:155:LEU:HB3	35:1d:158:ILE:HD13	1.99	0.44
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.50	0.44
42:1k:120:ARG:HA	42:1k:121:PRO:HD3	1.88	0.44
50:1s:41:VAL:HG22	50:1s:42:PRO:HD2	1.99	0.44
1:2A:708:C:H2'	1:2A:709:U:C6	2.52	0.44
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.52	0.44
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.33	0.44
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.32	0.44
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	1.98	0.44
16:2U:17:ILE:HG23	16:2U:39:LEU:HD12	2.00	0.44
16:2U:49:HIS:HA	16:2U:52:ARG:HB3	2.00	0.44
20:2Y:76:CYS:SG	20:2Y:78:ALA:HB3	2.56	0.44
30:28:29:LYS:NZ	30:28:45:GLY:HA2	2.32	0.44
32:2a:377:G:OP1	47:2p:3:LYS:HD3	2.16	0.44
32:2a:766:A:H2'	32:2a:767:A:O4'	2.17	0.44
32:2a:833:U:H2'	32:2a:834:C:H6	1.83	0.44
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.53	0.44
32:2a:1182:G:H5'	32:2a:1184:G:H5'	2.00	0.44
47:2p:21:VAL:HG22	47:2p:33:ILE:HD12	1.99	0.44
1:1A:801:C:H2'	1:1A:802:C:C6	2.52	0.44
1:1A:2211:U:H2'	1:1A:2212:G:H8	1.82	0.44
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.52	0.44
1:1A:2368:C:H2'	1:1A:2369:U:O4'	2.17	0.44
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:77:ASP:OD2	21:1Z:80:ARG:NH1	2.46	0.44
32:1a:269:C:H2'	32:1a:270:A:H8	1.79	0.44
32:1a:392:G:H2'	32:1a:393:A:C8	2.51	0.44
37:1f:2:ARG:HB2	37:1f:4:TYR:CE2	2.53	0.44
45:1n:7:ILE:HA	45:1n:23:ARG:HD2	2.00	0.44
1:2A:861:A:C6	1:2A:917:A:C8	3.06	0.44
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.17	0.44
1:2A:2305:A:H5''	6:2G:134:GLY:HA3	1.99	0.44
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.52	0.44
1:2A:2649:U:H2'	1:2A:2650:U:C6	2.53	0.44
1:2A:2660:A:H2'	1:2A:2661:G:O4'	2.18	0.44
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.99	0.44
10:2O:53:LYS:HE3	10:2O:56:ASP:OD2	2.18	0.44
12:2Q:2:LEU:HD12	12:2Q:2:LEU:HA	1.72	0.44
26:24:40:HIS:O	26:24:44:THR:HG22	2.17	0.44
32:2a:19:C:H2'	32:2a:20:U:H6	1.82	0.44
32:2a:397:A:H3'	32:2a:397:A:N3	2.32	0.44
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.30	0.44
32:2a:449:C:O2	47:2p:42:ARG:HD2	2.17	0.44
32:2a:1003:G:C6	32:2a:1004:A:C2	3.05	0.44
39:2h:51:VAL:HG11	39:2h:60:ARG:NH1	2.32	0.44
41:2j:78:ASN:O	41:2j:80:LYS:N	2.51	0.44
42:2k:33:THR:HG22	42:2k:39:PRO:HA	1.99	0.44
46:2o:7:GLU:O	46:2o:11:VAL:HG23	2.17	0.44
50:2s:64:GLU:H	50:2s:64:GLU:HG3	1.50	0.44
54:2x:54:5MU:O5'	54:2x:54:5MU:H6	2.00	0.44
1:1A:142:G:H2'	1:1A:143:C:C6	2.53	0.44
1:1A:233:A:H2'	1:1A:234:G:O4'	2.17	0.44
1:1A:253:C:O2'	1:1A:254:A:H2'	2.17	0.44
1:1A:302:A:H2'	1:1A:303:C:H6	1.80	0.44
1:1A:865:G:H4'	1:1A:885:C:O3'	2.17	0.44
1:1A:1102:G:H21	1:1A:1149:A:H62	1.65	0.44
1:1A:1314:A:H2'	1:1A:1315:A:O4'	2.18	0.44
1:1A:1732:C:H2'	1:1A:1733:C:C6	2.53	0.44
1:1A:2136:A:H2	1:1A:2189:U:O2'	1.99	0.44
6:1G:114:ILE:HG12	6:1G:140:ILE:HD13	1.98	0.44
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.42	0.44
16:1U:107:ALA:O	16:1U:110:VAL:HB	2.18	0.44
32:1a:44:G:C6	32:1a:45:U:C2	3.06	0.44
32:1a:542:G:P	35:1d:10:ARG:HH22	2.41	0.44
32:1a:1364:U:C6	52:1u:14:TRP:HH2	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:18:ARG:NH2	42:1k:35:PRO:O	2.45	0.44
1:2A:1633:G:C6	1:2A:1635:G:C4	3.06	0.44
1:2A:1800:C:P	3:2D:183:ARG:HH12	2.40	0.44
1:2A:2113:U:H2'	1:2A:2114:A:O4'	2.17	0.44
6:2G:55:LYS:NZ	6:2G:153:ARG:HH22	2.15	0.44
18:2W:18:ARG:HG2	18:2W:76:VAL:HB	1.98	0.44
32:2a:269:C:H2'	32:2a:270:A:C8	2.52	0.44
42:2k:31:THR:HG23	42:2k:42:TRP:HB3	2.00	0.44
44:2m:60:VAL:HG23	44:2m:64:TRP:CZ3	2.53	0.44
1:1A:207:A:C2	1:1A:224:U:H4'	2.52	0.44
1:1A:572:A:O2'	1:1A:573:G:OP1	2.33	0.44
1:1A:2418:U:C2	11:1P:72:PRO:HG2	2.52	0.44
2:1B:2:C:H2'	2:1B:3:C:C6	2.52	0.44
23:11:10:LYS:NZ	23:11:65:SER:OG	2.49	0.44
32:1a:486:U:H2'	32:1a:487:A:C8	2.49	0.44
32:1a:892:A:O2'	32:1a:1415:G:H4'	2.17	0.44
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.83	0.44
32:1a:1397:C:O2	32:1a:1397:C:H2'	2.18	0.44
33:1b:54:THR:O	33:1b:58:ILE:HG13	2.18	0.44
47:1p:4:ILE:HG13	47:1p:64:ALA:HB1	2.00	0.44
47:1p:42:ARG:HB3	47:1p:44:THR:HG23	1.99	0.44
1:2A:298:G:H5''	1:2A:299:A:OP1	2.18	0.44
1:2A:622:G:H2'	1:2A:623:G:C8	2.51	0.44
1:2A:897:C:H2'	1:2A:898:C:C6	2.52	0.44
1:2A:2186:G:C2	1:2A:2187:G:C5	3.06	0.44
2:2B:75:G:O2'	21:2Z:85:HIS:NE2	2.47	0.44
3:2D:37:LEU:HB2	3:2D:62:TYR:HB2	2.00	0.44
4:2E:7:VAL:HG12	4:2E:27:LEU:HB3	2.00	0.44
7:2H:98:LEU:HD13	7:2H:103:LEU:HD13	2.00	0.44
11:2P:27:HIS:O	11:2P:31:ALA:HA	2.18	0.44
31:29:32:HIS:O	31:29:34:GLN:HG3	2.17	0.44
32:2a:15:G:C4'	36:2e:24:ARG:HH21	2.31	0.44
32:2a:718:G:H4'	42:2k:117:ASN:HD21	1.83	0.44
32:2a:942:G:C2	32:2a:1342:C:C2	3.06	0.44
32:2a:979:C:H42	45:2n:18:VAL:HB	1.83	0.44
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.31	0.44
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.48	0.44
39:2h:48:TYR:HA	39:2h:60:ARG:O	2.17	0.44
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.99	0.44
43:2l:33:ARG:O	43:2l:85:ILE:HG12	2.18	0.44
1:1A:762:G:C2	46:1o:56:LEU:HD21	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1140:U:H2'	1:1A:1142:A:OP2	2.18	0.44
1:1A:1223:C:H2'	1:1A:1224:C:H6	1.82	0.44
1:1A:2357:G:N3	1:1A:2393:C:H2'	2.33	0.44
4:1E:14:ILE:HG13	4:1E:21:VAL:HG23	1.99	0.44
15:1T:125:ARG:NH1	32:1a:1442(B):A:H4'	2.33	0.44
32:1a:963:G:H4'	60:1a:2024:HOH:O	2.17	0.44
32:1a:1034:G:H2'	32:1a:1035:A:O4'	2.18	0.44
32:1a:1151:A:O2'	32:1a:1152:A:O5'	2.35	0.44
32:1a:1207:2MG:HO2'	32:1a:1208:C:P	2.41	0.44
34:1c:150:LYS:HE3	34:1c:173:VAL:HG21	2.00	0.44
41:1j:55:LYS:HD2	41:1j:56:HIS:CE1	2.53	0.44
1:2A:322:A:OP1	5:2F:168:ARG:NH1	2.45	0.44
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.51	0.44
1:2A:1637:A:H5'	1:2A:1760:A:O2'	2.18	0.44
1:2A:2057:A:H2'	1:2A:2058:A:C8	2.53	0.44
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.99	0.44
13:2R:72:ASP:O	13:2R:76:VAL:HG23	2.18	0.44
18:2W:1:MET:HE2	18:2W:62:HIS:ND1	2.32	0.44
21:2Z:144:LEU:HD11	21:2Z:150:LEU:HD22	2.00	0.44
32:2a:148:G:H2'	32:2a:149:A:H8	1.83	0.44
32:2a:342:C:H2'	32:2a:343:U:O4'	2.18	0.44
37:2f:22:GLU:OE2	37:2f:82:ARG:NE	2.50	0.44
49:2r:24:ALA:C	49:2r:26:LEU:H	2.26	0.44
1:1A:1067:A:H3'	1:1A:1067:A:N3	2.33	0.44
1:1A:1476:C:H2'	1:1A:1477:U:C6	2.53	0.44
1:1A:2156:A:N7	1:1A:2179:G:H4'	2.33	0.44
1:1A:2240:G:P	3:1D:263:ARG:HH12	2.41	0.44
1:1A:2728:C:H2'	1:1A:2729:U:H6	1.83	0.44
1:1A:2863:C:H2'	1:1A:2864:G:C8	2.53	0.44
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	2.00	0.44
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	1.99	0.44
12:1Q:29:PHE:O	21:1Z:122:ARG:NH2	2.50	0.44
19:1X:49:VAL:HG11	19:1X:89:ILE:HG12	2.00	0.44
32:1a:73:G:H2'	32:1a:76:C:C6	2.52	0.44
32:1a:201:C:N4	32:1a:216:G:H1	2.15	0.44
32:1a:546:G:OP1	35:1d:73:ARG:HG2	2.18	0.44
32:1a:763:G:H2'	32:1a:764:C:C6	2.53	0.44
32:1a:814:A:N7	32:1a:816:A:C4	2.86	0.44
32:1a:1123:A:O3'	41:1j:36:GLY:HA3	2.18	0.44
32:1a:1164:G:O2'	32:1a:1165:C:H5'	2.18	0.44
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:6:ILE:HD11	39:1h:31:PHE:CD2	2.53	0.44
1:2A:571:A:N6	1:2A:2499:C:O3'	2.51	0.44
1:2A:1064:C:OP2	1:2A:1065:U:H5'	2.17	0.44
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.18	0.44
3:2D:275:LYS:HD2	3:2D:275:LYS:HA	1.77	0.44
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	2.00	0.44
25:23:7:LYS:HE3	25:23:32:GLN:HE21	1.83	0.44
32:2a:593:G:H2'	32:2a:594:G:O4'	2.18	0.44
32:2a:1326:C:OP1	52:2u:17:THR:OG1	2.31	0.44
36:2e:137:GLU:HA	36:2e:140:ARG:HB3	2.00	0.44
39:2h:51:VAL:HG11	39:2h:60:ARG:HH11	1.82	0.44
44:2m:3:ARG:HD3	44:2m:9:ILE:N	2.33	0.44
44:2m:80:ARG:O	44:2m:84:ILE:HG23	2.18	0.44
50:2s:80:TYR:CZ	50:2s:82:GLY:HA2	2.53	0.44
1:1A:776:G:C6	3:1D:208:LYS:HB2	2.53	0.43
1:1A:2812:A:N3	1:1A:2904:U:H1'	2.32	0.43
2:1B:45:A:OP2	6:1G:96:ARG:NH2	2.39	0.43
6:1G:5:VAL:HG12	26:14:25:TYR:CE2	2.53	0.43
7:1H:4:ILE:O	7:1H:69:ARG:HD2	2.18	0.43
9:1N:102:ALA:O	9:1N:106:MET:HG3	2.18	0.43
32:1a:857:C:H2'	32:1a:858:G:O4'	2.18	0.43
32:1a:1066:C:O2'	32:1a:1067:A:H5'	2.18	0.43
35:1d:173:TRP:HE1	35:1d:193:ASP:HB3	1.83	0.43
36:1e:43:LEU:HD21	36:1e:132:ALA:HB1	2.00	0.43
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	2.00	0.43
1:2A:323:G:O2'	1:2A:1205:U:N3	2.48	0.43
1:2A:1069:A:O2'	1:2A:1073:A:N7	2.34	0.43
1:2A:1566:A:OP1	3:2D:211:ARG:NH1	2.51	0.43
4:2E:11:MET:HG2	4:2E:24:THR:HB	1.99	0.43
19:2X:31:HIS:HA	19:2X:32:PRO:HD3	1.84	0.43
32:2a:558:G:O2'	60:2a:1901:HOH:O	2.21	0.43
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.53	0.43
32:2a:1511:G:H2'	32:2a:1512:U:O4'	2.18	0.43
33:2b:127:ILE:C	33:2b:129:GLU:N	2.76	0.43
37:2f:55:ASP:HA	37:2f:56:PRO:HD3	1.80	0.43
39:2h:29:SER:OG	39:2h:32:LYS:N	2.41	0.43
1:1A:800:C:O2'	1:1A:801:C:H5'	2.18	0.43
1:1A:1310:G:H2'	1:1A:2036:A:N6	2.33	0.43
32:1a:981:U:OP1	45:1n:9:LYS:NZ	2.50	0.43
32:1a:1176:A:H2'	32:1a:1177:G:C8	2.52	0.43
33:1b:16:HIS:C	33:1b:18:GLY:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:20:GLU:N	33:1b:39:ILE:HD12	2.33	0.43
48:1q:22:LEU:HD12	48:1q:40:LYS:O	2.17	0.43
1:2A:1062:G:C8	1:2A:1070:A:H1'	2.53	0.43
1:2A:1203:G:C6	1:2A:1204:A:N6	2.86	0.43
1:2A:1430:C:N3	1:2A:1563:G:N2	2.58	0.43
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.32	0.43
1:2A:2130:U:H3'	1:2A:2130:U:C6	2.52	0.43
7:2H:55:PRO:HG2	7:2H:61:HIS:ND1	2.32	0.43
7:2H:126:PRO:HB2	7:2H:127:GLU:HG3	2.00	0.43
12:2Q:10:ARG:HB2	21:2Z:196:VAL:HG21	2.00	0.43
15:2T:29:ARG:HB3	15:2T:87:ASP:HB2	2.00	0.43
32:2a:220:G:H2'	32:2a:221:C:H5'	1.99	0.43
32:2a:418:C:H1'	32:2a:540:G:O2'	2.18	0.43
32:2a:971:G:OP1	32:2a:972:C:H5''	2.18	0.43
33:2b:15:VAL:HA	33:2b:209:ARG:HD2	1.99	0.43
34:2c:21:ARG:HH22	34:2c:56:ASP:HB3	1.83	0.43
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.18	0.43
42:2k:87:THR:O	42:2k:87:THR:OG1	2.25	0.43
44:2m:114:ARG:NH1	60:2m:201:HOH:O	2.50	0.43
1:1A:402:C:H2'	1:1A:403:C:H6	1.80	0.43
1:1A:1374:G:O2'	1:1A:1375:U:H2'	2.18	0.43
1:1A:1634:C:H2'	1:1A:1635:C:C6	2.52	0.43
1:1A:2045:G:H5'	1:1A:2629:C:H4'	1.99	0.43
1:1A:2623:U:H6	1:1A:2623:U:H5'	1.83	0.43
1:1A:2724:U:O2'	1:1A:2726:A:H5'	2.19	0.43
1:1A:2735:G:H2'	1:1A:2736:C:C6	2.53	0.43
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.49	0.43
6:1G:11:TYR:CE2	6:1G:16:ARG:HD3	2.54	0.43
7:1H:118:PRO:HG2	7:1H:121:ILE:HG13	2.01	0.43
20:1Y:38:ILE:HD11	20:1Y:66:PRO:HG3	2.00	0.43
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	2.00	0.43
32:1a:814:A:H2'	32:1a:816:A:H5''	2.00	0.43
32:1a:1070:U:OP1	36:1e:18:ARG:NH2	2.51	0.43
32:1a:1143:G:H2'	32:1a:1144:G:C8	2.53	0.43
40:1i:23:ASN:OD1	40:1i:25:LYS:N	2.51	0.43
1:2A:839:U:H2'	1:2A:840:C:C6	2.52	0.43
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.82	0.43
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.83	0.43
21:2Z:40:ASP:OD2	21:2Z:42:VAL:HG13	2.18	0.43
21:2Z:123:ASP:OD1	21:2Z:123:ASP:N	2.51	0.43
26:24:57:GLU:HA	26:24:58:ARG:HA	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:148:G:H2'	32:2a:149:A:C8	2.54	0.43
32:2a:309:G:H2'	32:2a:310:G:H8	1.83	0.43
32:2a:392:G:H2'	32:2a:393:A:C8	2.52	0.43
32:2a:1014:A:OP1	50:2s:18:LYS:NZ	2.31	0.43
32:2a:1126:U:O2	32:2a:1280:A:H2'	2.18	0.43
32:2a:1288:A:H2'	32:2a:1289:A:C8	2.53	0.43
34:2c:20:SER:HB2	34:2c:40:ARG:NH2	2.33	0.43
1:1A:469:A:H5''	1:1A:470:C:O5'	2.18	0.43
1:1A:503:A:H2'	1:1A:504:A:C8	2.53	0.43
1:1A:1501:U:O2'	1:1A:1502:G:N7	2.46	0.43
1:1A:2432:C:O5'	1:1A:2432:C:H6	2.02	0.43
6:1G:50:ALA:O	6:1G:52:ILE:N	2.46	0.43
6:1G:118:ARG:O	6:1G:181:ARG:HB3	2.17	0.43
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.33	0.43
26:14:49:PHE:HB3	26:14:50:VAL:H	1.37	0.43
29:17:24:THR:HG23	29:17:26:GLY:H	1.84	0.43
32:1a:297:G:H4'	32:1a:557:G:H4'	2.00	0.43
32:1a:1194:U:H4'	36:1e:22:GLY:HA2	2.00	0.43
32:1a:1346:A:H5''	40:1i:120:ARG:HH12	1.84	0.43
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	2.00	0.43
38:1g:54:THR:CB	38:1g:56:GLN:HE22	2.30	0.43
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.18	0.43
42:1k:43:SER:HB3	42:1k:68:ALA:HB2	2.00	0.43
46:1o:81:LEU:HG	46:1o:85:LEU:HD12	2.01	0.43
50:1s:42:PRO:O	50:1s:45:VAL:HG23	2.18	0.43
1:2A:300:A:N3	1:2A:319:C:H1'	2.33	0.43
1:2A:1028:A:H61	1:2A:1125:G:H2'	1.80	0.43
1:2A:1248:G:C2	16:2U:3:ARG:HD2	2.54	0.43
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.54	0.43
1:2A:2186:G:N1	1:2A:2187:G:C6	2.86	0.43
6:2G:4:ASP:OD2	6:2G:9:ARG:NH2	2.48	0.43
8:2I:95:LYS:O	8:2I:99:GLU:HG3	2.18	0.43
8:2I:130:TYR:HD2	8:2I:138:ILE:HD12	1.83	0.43
12:2Q:42:ILE:HD13	12:2Q:97:VAL:HG21	2.00	0.43
32:2a:60:A:H4'	32:2a:61:G:O5'	2.18	0.43
33:2b:30:ARG:NH2	33:2b:194:PRO:HB2	2.33	0.43
35:2d:61:LYS:NZ	35:2d:72:GLU:OE1	2.50	0.43
35:2d:76:ARG:HD2	35:2d:76:ARG:HA	1.62	0.43
42:2k:86:GLY:N	42:2k:112:THR:OG1	2.39	0.43
42:2k:120:ARG:HA	42:2k:121:PRO:HD3	1.87	0.43
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:20:LEU:HA	50:2s:23:ASN:HD22	1.83	0.43
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.18	0.43
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.82	0.43
1:1A:559:U:H2'	1:1A:560:C:C6	2.53	0.43
1:1A:1124:U:C5	1:1A:1134:A:H5''	2.54	0.43
1:1A:1613:A:OP1	3:1D:211:ARG:NH1	2.51	0.43
1:1A:2182:G:H2'	1:1A:2183:C:H6	1.82	0.43
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.19	0.43
18:1W:16:LYS:O	18:1W:19:LEU:HB2	2.18	0.43
28:16:2:ALA:HB2	30:18:34:TRP:CZ2	2.54	0.43
32:1a:434:U:H2'	32:1a:435:C:C6	2.53	0.43
32:1a:516:PSU:N3	32:1a:533:A:N6	2.39	0.43
32:1a:523:A:N1	43:1l:92:OTD:H6	2.33	0.43
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.54	0.43
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.54	0.43
37:1f:21:LEU:O	37:1f:24:GLU:HB3	2.19	0.43
44:1m:20:THR:HA	44:1m:25:ILE:O	2.18	0.43
47:1p:74:LEU:O	47:1p:79:VAL:HG13	2.18	0.43
1:2A:539:G:H2'	1:2A:540:C:C6	2.54	0.43
1:2A:1214:A:H61	1:2A:1235:G:H1'	1.83	0.43
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	2.00	0.43
7:2H:61:HIS:O	7:2H:65:HIS:HB2	2.19	0.43
11:2P:97:PRO:HG3	11:2P:112:LEU:HD12	2.00	0.43
12:2Q:52:VAL:HA	12:2Q:55:VAL:HG12	1.99	0.43
14:2S:69:VAL:HA	14:2S:72:ALA:HB3	2.00	0.43
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.19	0.43
32:2a:857:C:H2'	32:2a:858:G:O4'	2.17	0.43
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.54	0.43
32:2a:1203:C:OP1	45:2n:3:ARG:HD3	2.19	0.43
44:2m:33:ALA:HA	44:2m:59:TYR:CE2	2.53	0.43
51:2t:47:GLY:HA2	51:2t:48:LYS:CB	2.48	0.43
54:2x:10:G:N2	54:2x:26:G:H1'	2.34	0.43
1:1A:861:C:H2'	1:1A:862:C:H6	1.83	0.43
1:1A:1750:G:H2'	1:1A:1751:G:H8	1.82	0.43
1:1A:1785:C:OP1	15:1T:96:ARG:NH1	2.52	0.43
1:1A:1836:U:O2	3:1D:50:THR:HB	2.19	0.43
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.77	0.43
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.17	0.43
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.18	0.43
21:1Z:10:ARG:HG3	21:1Z:36:LYS:HB3	2.00	0.43
21:1Z:193:GLU:HA	21:1Z:194:PRO:HD3	1.74	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:17:31:LEU:O	29:17:35:ARG:HB2	2.18	0.43
32:1a:175:C:H2'	32:1a:176:C:C6	2.51	0.43
32:1a:722:A:N6	32:1a:724:G:C2	2.86	0.43
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.50	0.43
32:1a:1298:C:H4'	32:1a:1299:A:C4	2.53	0.43
35:1d:79:PHE:HE1	35:1d:204:ILE:HD13	1.83	0.43
35:1d:164:ALA:O	35:1d:168:ARG:HG2	2.19	0.43
42:1k:124:LYS:HG3	42:1k:125:PHE:CD2	2.54	0.43
1:2A:81:G:C2	1:2A:106:C:N3	2.87	0.43
1:2A:459:U:OP2	29:27:39:ARG:NH1	2.50	0.43
1:2A:924:C:H2'	1:2A:925:C:C6	2.54	0.43
1:2A:1180:C:H2'	1:2A:1181:C:H6	1.84	0.43
1:2A:1991:U:C2'	1:2A:1992:G:H5''	2.47	0.43
1:2A:2122:U:H2'	1:2A:2123:G:O4'	2.18	0.43
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.17	0.43
1:2A:2822:G:O2'	1:2A:2824:C:OP2	2.30	0.43
6:2G:171:ALA:O	6:2G:175:LEU:HD22	2.18	0.43
12:2Q:17:LEU:HD13	12:2Q:39:PRO:HB2	2.01	0.43
13:2R:65:LEU:HD12	13:2R:65:LEU:HA	1.85	0.43
17:2V:60:GLU:HB2	17:2V:97:LYS:HG2	2.01	0.43
21:2Z:30:ASN:HD22	21:2Z:90:VAL:HB	1.83	0.43
33:2b:57:PHE:CE2	33:2b:185:ILE:HD11	2.53	0.43
33:2b:97:TRP:CH2	33:2b:173:ALA:HA	2.53	0.43
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.19	0.43
41:2j:24:VAL:O	41:2j:34:VAL:HG11	2.18	0.43
1:1A:549:U:H2'	1:1A:550:U:C6	2.53	0.43
1:1A:865:G:H5'	1:1A:886:U:OP1	2.18	0.43
1:1A:2813:G:H2'	1:1A:2814:C:C6	2.53	0.43
25:13:3:ARG:HD3	25:13:60:GLU:OE2	2.17	0.43
32:1a:756:C:H2'	32:1a:757:U:O4'	2.19	0.43
32:1a:1129:C:H4'	40:1i:16:ARG:HH22	1.83	0.43
32:1a:1179:A:O3'	40:1i:103:THR:HB	2.18	0.43
32:1a:1236:A:H4'	32:1a:1304:G:H4'	1.99	0.43
33:1b:70:PHE:CD1	33:1b:163:PHE:HB3	2.53	0.43
37:1f:78:GLU:O	37:1f:81:ILE:HG22	2.18	0.43
40:1i:49:PRO:CG	40:1i:82:ALA:HB2	2.49	0.43
44:1m:108:ARG:HA	44:1m:108:ARG:HD3	1.76	0.43
1:2A:700:G:H2'	1:2A:701:G:O4'	2.19	0.43
1:2A:782:A:H5''	60:2A:4830:HOH:O	2.17	0.43
1:2A:889:C:O2'	1:2A:890:A:O5'	2.36	0.43
1:2A:2519:U:C6	1:2A:2542:A:N6	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2650:U:H2'	1:2A:2651:C:C6	2.54	0.43
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.48	0.43
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.25	0.43
32:2a:109:A:N7	32:2a:326:G:H2'	2.34	0.43
32:2a:297:G:H4'	32:2a:557:G:H4'	2.00	0.43
32:2a:1237:C:O2'	32:2a:1300:G:N2	2.44	0.43
35:2d:13:ARG:HG3	35:2d:38:TYR:O	2.19	0.43
41:2j:69:ASN:O	41:2j:70:ARG:NH1	2.44	0.43
1:1A:123:G:H1'	29:17:48:LYS:HE3	1.99	0.43
1:1A:1159:U:H2'	1:1A:1160:G:C8	2.53	0.43
1:1A:1232:G:H5''	17:1V:81:TYR:CE1	2.54	0.43
1:1A:2697:G:H5'	10:1O:68:GLU:OE2	2.18	0.43
3:1D:69:ARG:C	3:1D:71:ASP:N	2.76	0.43
7:1H:121:ILE:HD11	7:1H:140:LYS:HG2	1.99	0.43
9:1N:72:TYR:CE2	9:1N:87:LEU:HD23	2.52	0.43
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.86	0.43
19:1X:95:LEU:H	19:1X:95:LEU:HD12	1.84	0.43
28:16:9:LEU:HD13	28:16:51:GLU:HG3	2.00	0.43
32:1a:227:G:H2'	32:1a:228:A:C8	2.53	0.43
32:1a:926:G:C6	32:1a:1505:G:C6	3.06	0.43
32:1a:1201:A:H1'	32:1a:1202:G:OP2	2.18	0.43
33:1b:32:ILE:HG21	33:1b:40:HIS:CD2	2.52	0.43
34:1c:123:GLN:O	34:1c:128:PHE:HB2	2.19	0.43
35:1d:76:ARG:HD3	35:1d:207:TYR:CE1	2.54	0.43
40:1i:12:GLU:O	40:1i:67:GLY:HA3	2.19	0.43
1:2A:387:U:P	23:21:20:ARG:HH12	2.41	0.43
1:2A:476:G:H4'	1:2A:502:A:N1	2.34	0.43
1:2A:866:A:N6	1:2A:914:C:C4	2.87	0.43
1:2A:996:A:H4'	16:2U:91:ASP:OD2	2.19	0.43
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.99	0.43
1:2A:1798:U:H5'	3:2D:259:THR:HG22	2.01	0.43
5:2F:24:LEU:HD21	5:2F:114:VAL:HG12	2.01	0.43
6:2G:77:ILE:HG21	6:2G:80:PHE:CD2	2.53	0.43
12:2Q:55:VAL:HG23	21:2Z:178:GLU:HB3	2.01	0.43
21:2Z:97:GLU:HA	21:2Z:126:VAL:O	2.19	0.43
31:29:29:ASN:HA	31:29:30:PRO:HD3	1.89	0.43
32:2a:73:G:H2'	32:2a:76:C:H6	1.84	0.43
32:2a:682:G:H2'	32:2a:683:G:O4'	2.19	0.43
32:2a:1106:G:H2'	32:2a:1107:C:H6	1.83	0.43
37:2f:35:ALA:HA	37:2f:67:MET:HB3	2.01	0.43
47:2p:5:ARG:HE	47:2p:22:THR:HG21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:36:ARG:HD2	50:2s:52:TYR:O	2.19	0.43
51:2t:33:ILE:O	51:2t:37:SER:OG	2.29	0.43
1:1A:564:G:H2'	1:1A:565:C:C6	2.54	0.43
1:1A:923:C:H2'	1:1A:924:U:O4'	2.18	0.43
1:1A:964:A:N3	2:1B:80:U:O2'	2.43	0.43
1:1A:1116:A:N7	1:1A:1143:U:H4'	2.34	0.43
1:1A:1431:G:O2'	1:1A:1442:U:O2	2.35	0.43
1:1A:2832:G:O2'	1:1A:2834:C:OP2	2.26	0.43
24:12:8:LYS:HA	24:12:8:LYS:HD2	1.90	0.43
32:1a:341:C:H42	32:1a:348:G:H1	1.67	0.43
32:1a:448:A:C4	32:1a:487:A:C2	3.06	0.43
32:1a:841:U:H6	32:1a:841:U:OP2	2.01	0.43
36:1e:48:ALA:HB3	36:1e:54:ALA:HB2	1.99	0.43
40:1i:87:GLN:HG2	40:1i:88:TYR:N	2.34	0.43
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.78	0.43
48:1q:4:LYS:HG3	48:1q:6:LEU:CD1	2.48	0.43
1:2A:518:G:H2'	1:2A:519:U:C6	2.53	0.43
1:2A:601:C:OP1	5:2F:108:LYS:NZ	2.44	0.43
1:2A:616:G:H5'	5:2F:205:ARG:HD3	2.00	0.43
1:2A:783:A:H2'	1:2A:783:A:N3	2.33	0.43
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.19	0.43
1:2A:2125:G:H1'	1:2A:2173:A:H61	1.82	0.43
6:2G:86:MET:HA	6:2G:87:PRO:HD3	1.85	0.43
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	2.01	0.43
20:2Y:86:ARG:HB2	20:2Y:98:VAL:CG2	2.48	0.43
26:24:42:PHE:HD2	26:24:43:TYR:CD1	2.37	0.43
26:24:62:ARG:HA	26:24:62:ARG:HD3	1.77	0.43
28:26:6:ARG:HH12	28:26:26:ASN:HB2	1.82	0.43
32:2a:179:A:H2'	32:2a:180:U:H6	1.84	0.43
32:2a:189:G:H2'	32:2a:189(A):C:C6	2.54	0.43
32:2a:1014:A:C5	32:2a:1015:A:C6	3.07	0.43
32:2a:1489:G:C6	32:2a:1490:C:C4	3.07	0.43
33:2b:139:LYS:NZ	33:2b:143:GLU:OE1	2.52	0.43
38:2g:108:ALA:HA	38:2g:111:ARG:HD2	2.00	0.43
39:2h:16:ALA:HB1	39:2h:63:LEU:HD21	2.01	0.43
46:2o:38:ARG:HE	46:2o:38:ARG:HB2	1.38	0.43
49:2r:35:ARG:O	49:2r:37:VAL:N	2.52	0.43
50:2s:50:ALA:CB	50:2s:57:HIS:HB3	2.47	0.43
55:2y:14:ARG:HA	55:2y:15:PRO:HD2	1.67	0.43
1:1A:36:G:N3	1:1A:476:G:O2'	2.51	0.43
1:1A:302:A:O2'	1:1A:303:C:O5'	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1131:A:H1'	1:1A:1151:U:H1'	2.00	0.43
1:1A:1594:C:H2'	1:1A:1595:C:C6	2.54	0.43
1:1A:1821:C:H2'	1:1A:1822:A:C5	2.53	0.43
1:1A:2303:U:H2'	1:1A:2304:C:H6	1.81	0.43
1:1A:2899:C:H2'	1:1A:2900:G:O4'	2.19	0.43
3:1D:166:GLN:HB2	3:1D:174:ILE:HG22	2.00	0.43
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.19	0.43
6:1G:123:ASN:C	6:1G:125:PHE:H	2.27	0.43
6:1G:143:GLU:O	6:1G:144:ILE:HD13	2.19	0.43
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.54	0.43
32:1a:45:U:H2'	32:1a:46:G:C8	2.54	0.43
32:1a:417:C:H42	32:1a:426:G:H1	1.67	0.43
32:1a:516:PSU:C4	32:1a:533:A:N6	2.85	0.43
32:1a:763:G:H2'	32:1a:764:C:H6	1.84	0.43
34:1c:26:LYS:HA	45:1n:36:PHE:HE1	1.84	0.43
35:1d:11:LEU:O	35:1d:15:GLU:HG2	2.19	0.43
50:1s:38:SER:O	50:1s:70:LYS:HD2	2.18	0.43
1:2A:674:G:N2	1:2A:2444:G:O3'	2.52	0.43
1:2A:968:G:H2'	1:2A:969:U:C6	2.54	0.43
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.18	0.43
1:2A:2001:A:H4'	1:2A:2689:U:H2'	2.01	0.43
5:2F:158:THR:HB	5:2F:195:ASP:HB2	2.01	0.43
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.19	0.43
16:2U:29:SER:C	16:2U:30:LYS:HD2	2.44	0.43
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.83	0.43
34:2c:30:ARG:NH2	45:2n:38:GLY:HA2	2.34	0.43
1:1A:1124:U:H4'	1:1A:1125:C:H5'	2.00	0.42
1:1A:1640:G:H2'	1:1A:1641:G:O4'	2.19	0.42
1:1A:1715:A:O2'	1:1A:1721:G:N7	2.41	0.42
3:1D:206:LEU:HD23	3:1D:206:LEU:HA	1.90	0.42
11:1P:107:LYS:O	11:1P:110:TYR:HB2	2.18	0.42
32:1a:162:A:H8	32:1a:162:A:O5'	2.02	0.42
34:1c:6:HIS:CD2	34:1c:8:ILE:HB	2.54	0.42
34:1c:79:ARG:N	34:1c:82:GLU:HB3	2.33	0.42
36:1e:12:LEU:CB	36:1e:31:LEU:HB2	2.49	0.42
45:1n:13:THR:HA	45:1n:14:PRO:HD3	1.90	0.42
55:1y:16:ARG:HE	55:1y:16:ARG:HB3	1.69	0.42
1:2A:873:G:H1	1:2A:904:C:H42	1.67	0.42
1:2A:1782:C:O2'	1:2A:2609:U:H5''	2.19	0.42
6:2G:145:THR:HG22	6:2G:148:MET:HG2	2.01	0.42
10:2O:120:GLU:OE2	10:2O:122:LEU:HD21	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:302:G:N3	32:2a:556:C:H4'	2.34	0.42
32:2a:424:G:H2'	32:2a:425:G:H8	1.84	0.42
32:2a:662:G:H2'	32:2a:663:A:C8	2.54	0.42
32:2a:696:A:H8	32:2a:696:A:O5'	2.02	0.42
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.53	0.42
32:2a:1193:G:O2'	36:2e:25:ARG:NH2	2.52	0.42
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.54	0.42
47:2p:59:TRP:HB3	47:2p:64:ALA:HB2	2.00	0.42
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	2.00	0.42
1:1A:1347:A:H2	1:1A:1672:G:N3	2.16	0.42
1:1A:2258:G:H2'	1:1A:2259:A:C8	2.54	0.42
4:1E:1:MET:HE1	4:1E:200:GLU:O	2.19	0.42
7:1H:13:LYS:H	7:1H:13:LYS:HG2	1.64	0.42
32:1a:16:A:O2'	36:1e:16:THR:HB	2.19	0.42
32:1a:288:A:H2'	32:1a:289:G:H4'	2.01	0.42
32:1a:487:A:H2'	32:1a:488:C:O4'	2.19	0.42
32:1a:667:G:H4'	46:1o:51:HIS:ND1	2.35	0.42
32:1a:924:C:O2'	32:1a:1502:A:N1	2.47	0.42
39:1h:113:SER:HB2	39:1h:134:ILE:HD11	2.01	0.42
40:1i:106:ALA:O	40:1i:108:VAL:HG23	2.18	0.42
43:1l:27:LEU:HD13	43:1l:27:LEU:HA	1.84	0.42
44:1m:30:ALA:O	44:1m:34:LEU:HG	2.20	0.42
47:1p:74:LEU:HB3	47:1p:79:VAL:CG2	2.49	0.42
48:1q:4:LYS:HG3	48:1q:6:LEU:HD11	2.00	0.42
49:1r:33:ASP:OD2	49:1r:36:ASN:HB2	2.19	0.42
1:2A:184:C:H2'	1:2A:185:U:C6	2.54	0.42
1:2A:1202:C:N3	1:2A:1243:G:N2	2.59	0.42
1:2A:2115:G:H4'	1:2A:2166:G:O2'	2.20	0.42
6:2G:127:GLY:H	6:2G:166:ASP:CG	2.26	0.42
8:2I:123:LEU:HD12	8:2I:144:VAL:HB	2.01	0.42
13:2R:90:ARG:CZ	13:2R:117:VAL:HG11	2.49	0.42
21:2Z:17:ALA:O	21:2Z:21:ALA:N	2.47	0.42
25:23:48:GLU:HA	25:23:51:ALA:HB2	2.00	0.42
32:2a:10:A:OP2	36:2e:126:ARG:HD2	2.19	0.42
35:2d:119:GLN:HG3	35:2d:123:HIS:CD2	2.53	0.42
43:2l:34:ARG:O	43:2l:61:THR:HG23	2.20	0.42
54:2x:25:C:H2'	54:2x:26:G:O4'	2.19	0.42
1:1A:293:C:H42	1:1A:391:G:H1	1.67	0.42
1:1A:1675:U:H2'	1:1A:1676:G:C8	2.54	0.42
1:1A:1879:A:H2'	1:1A:1880:G:C8	2.52	0.42
1:1A:1976:G:O2'	1:1A:1978:U:O4	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2205:C:H2'	1:1A:2206:G:C8	2.54	0.42
1:1A:2479:C:H4'	12:1Q:123:HIS:CD2	2.54	0.42
1:1A:2679:C:H2'	1:1A:2680:G:O4'	2.19	0.42
3:1D:8:PRO:HB3	3:1D:14:ARG:HG3	2.02	0.42
15:1T:45:PHE:CE2	15:1T:74:ARG:HB2	2.54	0.42
32:1a:953:G:C2	32:1a:954:G:H1'	2.54	0.42
32:1a:1304:G:H1'	32:1a:1333:A:H61	1.83	0.42
32:1a:1317:C:OP1	45:1n:18:VAL:HG22	2.18	0.42
42:1k:124:LYS:HG3	42:1k:125:PHE:CE2	2.54	0.42
44:1m:49:THR:HG22	44:1m:51:ALA:H	1.84	0.42
1:2A:321:G:OP2	5:2F:135:LYS:HG3	2.19	0.42
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.54	0.42
1:2A:1288:U:C2	1:2A:1327:C:O2	2.72	0.42
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.54	0.42
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.67	0.42
1:2A:2506:U:H5'	60:2A:4356:HOH:O	2.19	0.42
1:2A:2684:U:O2'	10:2O:68:GLU:OE2	2.34	0.42
9:2N:42:TRP:CH2	9:2N:44:PRO:HB3	2.55	0.42
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.19	0.42
16:2U:16:LYS:HB3	16:2U:16:LYS:HE2	1.84	0.42
21:2Z:63:ASP:OD1	21:2Z:65:GLN:HG3	2.20	0.42
26:24:40:HIS:CG	26:24:41:PRO:HD2	2.54	0.42
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	2.02	0.42
33:2b:158:LEU:HA	33:2b:159:PRO:HD3	1.93	0.42
36:2e:95:ALA:HB1	36:2e:96:PRO:HD2	2.01	0.42
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.52	0.42
42:2k:98:LEU:HD23	42:2k:98:LEU:HA	1.88	0.42
44:2m:108:ARG:NH1	44:2m:111:LYS:HD2	2.35	0.42
45:2n:7:ILE:HA	45:2n:23:ARG:HD2	2.00	0.42
1:1A:602:G:H2'	1:1A:603:C:H6	1.83	0.42
1:1A:1053:C:OP1	9:1N:37:LYS:NZ	2.50	0.42
1:1A:1556:A:H2'	1:1A:1557:A:C8	2.54	0.42
1:1A:1645:C:OP1	19:1X:36:LYS:HG3	2.19	0.42
1:1A:1805:C:H6	1:1A:1805:C:O5'	2.02	0.42
1:1A:1814:A:H5'	1:1A:2620:G:H4'	2.01	0.42
6:1G:72:ARG:HD3	6:1G:85:GLY:O	2.19	0.42
7:1H:124:GLU:OE2	7:1H:132:ARG:HD2	2.20	0.42
30:18:52:LYS:HB3	30:18:53:PRO:HD3	2.00	0.42
32:1a:59:A:H3'	32:1a:331:G:H22	1.85	0.42
32:1a:437:U:O2	35:1d:119:GLN:NE2	2.51	0.42
32:1a:1026:G:H3'	32:1a:1027:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1054:C:H4'	32:1a:1055:A:O5'	2.19	0.42
32:1a:1162:C:H2'	32:1a:1163:C:H6	1.83	0.42
37:1f:97:PHE:HB2	49:1r:32:ARG:NH1	2.34	0.42
48:1q:29:HIS:HA	48:1q:30:PRO:HD2	1.86	0.42
1:2A:13:A:N1	1:2A:525:U:H2'	2.35	0.42
1:2A:36:G:N3	1:2A:450:G:O2'	2.52	0.42
1:2A:264:C:H4'	1:2A:428:A:C2	2.54	0.42
1:2A:1359:A:N1	1:2A:1372:U:O4	2.52	0.42
2:2B:17:C:H2'	2:2B:18:G:O4'	2.20	0.42
6:2G:33:ARG:NH2	6:2G:162:THR:HG21	2.34	0.42
8:2I:69:LYS:HE3	8:2I:69:LYS:HB2	1.86	0.42
17:2V:37:VAL:O	17:2V:52:VAL:HG22	2.19	0.42
26:24:53:GLU:H	26:24:53:GLU:CD	2.27	0.42
32:2a:73:G:H2'	32:2a:76:C:C6	2.54	0.42
32:2a:411:A:C6	32:2a:429:U:C4	3.07	0.42
32:2a:523:A:H61	43:2l:92:0TD:CG	2.32	0.42
32:2a:562:C:H4'	32:2a:563:A:O5'	2.19	0.42
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.54	0.42
32:2a:1122:U:O4	32:2a:1123:A:N6	2.52	0.42
33:2b:74:LYS:O	33:2b:78:GLN:N	2.52	0.42
35:2d:81:GLU:O	35:2d:85:LYS:HG3	2.19	0.42
35:2d:88:VAL:O	35:2d:92:VAL:HG23	2.19	0.42
36:2e:82:VAL:HG21	36:2e:138:ALA:HA	2.01	0.42
52:2u:6:ARG:HE	52:2u:15:ARG:HH12	1.67	0.42
1:1A:676:G:OP2	30:18:21:LYS:NZ	2.48	0.42
1:1A:821:A:H2'	1:1A:821:A:N3	2.35	0.42
1:1A:973:G:H2'	1:1A:974:G:O4'	2.19	0.42
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.84	0.42
1:1A:2450:U:O2'	1:1A:2452:C:OP1	2.24	0.42
1:1A:2589:A:H5'	27:15:3:LYS:HD3	2.01	0.42
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.53	0.42
5:1F:10:PRO:HB3	5:1F:17:ARG:CZ	2.50	0.42
11:1P:125:VAL:HG13	11:1P:138:LEU:HD21	2.01	0.42
15:1T:111:ARG:NE	32:1a:1463:C:OP1	2.46	0.42
23:11:3:LYS:HG3	23:11:4:VAL:H	1.85	0.42
28:16:11:LEU:HB3	28:16:49:HIS:HB3	2.02	0.42
32:1a:1164:G:H2'	32:1a:1165:C:C6	2.55	0.42
33:1b:28:PHE:CD1	33:1b:190:THR:HG22	2.55	0.42
34:1c:82:GLU:CD	34:1c:85:ARG:HH12	2.27	0.42
35:1d:122:ARG:HA	35:1d:122:ARG:HD2	1.80	0.42
39:1h:13:ILE:O	39:1h:16:ALA:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:8:LEU:HD13	41:1j:20:ALA:HA	2.02	0.42
51:1t:67:ALA:HA	51:1t:72:LEU:O	2.19	0.42
1:2A:116:C:H2'	1:2A:117:G:O4'	2.19	0.42
1:2A:774:A:OP1	3:2D:48:ARG:NH2	2.46	0.42
1:2A:954:G:C5	1:2A:955:C:C5	3.07	0.42
1:2A:2461:C:H2'	1:2A:2462:U:H6	1.85	0.42
1:2A:2864:G:OP1	32:2a:1442(A):G:N2	2.38	0.42
6:2G:11:TYR:OH	6:2G:33:ARG:HG2	2.19	0.42
6:2G:55:LYS:O	6:2G:58:GLN:HB3	2.20	0.42
7:2H:105:LEU:HD12	7:2H:105:LEU:HA	1.84	0.42
12:2Q:130:LYS:HB3	12:2Q:130:LYS:HE3	1.88	0.42
17:2V:100:ARG:HH11	17:2V:100:ARG:CB	2.27	0.42
32:2a:952:U:H4'	32:2a:964:A:N1	2.34	0.42
32:2a:1018:C:H2'	32:2a:1019:C:O4'	2.19	0.42
32:2a:1236:A:O2'	32:2a:1304:G:H4'	2.20	0.42
32:2a:1261:A:C6	32:2a:1262:C:C2	3.08	0.42
32:2a:1399:C:H4'	32:2a:1400:5MC:O5'	2.18	0.42
32:2a:1496:C:H2'	32:2a:1497:G:O4'	2.19	0.42
33:2b:121:LEU:O	33:2b:127:ILE:HG23	2.19	0.42
35:2d:100:ARG:HB3	35:2d:102:ASP:OD1	2.20	0.42
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	2.02	0.42
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.18	0.42
40:2i:82:ALA:O	40:2i:86:VAL:HG23	2.19	0.42
44:2m:30:ALA:O	44:2m:34:LEU:HG	2.19	0.42
1:1A:310:C:H2'	1:1A:311:C:H6	1.85	0.42
1:1A:2161:C:O5'	1:1A:2161:C:H6	2.01	0.42
1:1A:2484:G:C5	1:1A:2487:C:C4	3.07	0.42
1:1A:2849:G:H5'	13:1R:46:GLY:HA2	2.00	0.42
9:1N:34:LEU:HD12	9:1N:34:LEU:HA	1.86	0.42
32:1a:189(D):C:H1'	32:1a:189(H):G:N2	2.35	0.42
32:1a:632:A:H3'	32:1a:633:G:H8	1.85	0.42
32:1a:831:U:H2'	32:1a:832:C:C6	2.53	0.42
33:1b:98:LEU:HG	33:1b:101:MET:HE3	2.02	0.42
36:1e:96:PRO:C	36:1e:98:THR:H	2.28	0.42
37:1f:40:VAL:HG23	37:1f:63:TYR:HD1	1.85	0.42
37:1f:99:ALA:HB2	49:1r:31:LEU:HD21	2.01	0.42
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	2.01	0.42
43:1l:31:PRO:HB2	43:1l:32:PHE:CD2	2.54	0.42
50:1s:62:ILE:HA	50:1s:66:MET:SD	2.59	0.42
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.55	0.42
1:2A:1421:G:C2	1:2A:1422:G:C8	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2186:G:N1	1:2A:2187:G:C5	2.88	0.42
1:2A:2406:U:OP2	1:2A:2406:U:H2'	2.20	0.42
2:2B:11:C:OP2	2:2B:12:C:N4	2.38	0.42
6:2G:67:LYS:HE3	26:24:5:ILE:HD12	2.01	0.42
6:2G:113:ARG:HG3	26:24:34:GLU:OE2	2.20	0.42
9:2N:26:LEU:HG	9:2N:30:ILE:HD11	2.01	0.42
16:2U:89:GLU:HG3	17:2V:50:PRO:HB3	2.01	0.42
21:2Z:5:LEU:HD21	21:2Z:39:VAL:HG11	2.02	0.42
21:2Z:24:LEU:HA	21:2Z:25:PRO:HD3	1.86	0.42
32:2a:685:G:N1	32:2a:704:A:OP2	2.42	0.42
32:2a:817:C:N3	32:2a:1529:G:N2	2.64	0.42
32:2a:918:A:H2'	32:2a:919:A:O4'	2.20	0.42
32:2a:1003:G:H2'	32:2a:1004:A:C4'	2.49	0.42
32:2a:1170:A:H8	32:2a:1170:A:O5'	2.03	0.42
33:2b:76:GLN:HE21	33:2b:206:ASP:HA	1.84	0.42
39:2h:123:GLU:O	39:2h:127:LEU:N	2.30	0.42
1:1A:1056:A:N3	1:1A:1199:C:H1'	2.34	0.42
1:1A:1110:C:OP2	1:1A:1111:U:H5'	2.20	0.42
1:1A:1275:G:C6	1:1A:1276:C:C4	3.08	0.42
1:1A:1490:G:H2'	1:1A:1492:C:C5	2.55	0.42
1:1A:1547:C:O4'	3:1D:100:GLY:HA2	2.20	0.42
1:1A:2156:A:H2'	1:1A:2181:G:H1'	2.02	0.42
3:1D:13:ARG:HD2	3:1D:13:ARG:HA	1.40	0.42
3:1D:17:THR:HG23	3:1D:205:VAL:HB	2.02	0.42
3:1D:85:ASP:HA	3:1D:86:PRO:HD2	1.92	0.42
4:1E:21:VAL:HG12	4:1E:185:LYS:HD2	2.00	0.42
12:1Q:51:ARG:HD3	12:1Q:66:ILE:HD11	2.01	0.42
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.73	0.42
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.53	0.42
26:14:40:HIS:HA	26:14:41:PRO:HD3	1.94	0.42
32:1a:42:G:O2'	32:1a:622:A:N1	2.42	0.42
32:1a:439:A:N1	32:1a:496:A:H1'	2.35	0.42
32:1a:658:G:C6	32:1a:659:U:C4	3.07	0.42
32:1a:660:G:OP1	46:1o:5:LYS:NZ	2.52	0.42
32:1a:1004:A:N7	32:1a:1036:G:C2	2.87	0.42
32:1a:1207:2MG:H2'	32:1a:1208:C:H6	1.84	0.42
32:1a:1521:G:H2'	32:1a:1522:U:C6	2.55	0.42
33:1b:80:ILE:HD11	33:1b:212:GLN:CA	2.49	0.42
35:1d:76:ARG:HD3	35:1d:207:TYR:CZ	2.54	0.42
41:1j:85:LEU:HD23	41:1j:85:LEU:HA	1.91	0.42
1:2A:335:C:H4'	20:2Y:73:ARG:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1059:G:C2	1:2A:1060:U:O4	2.73	0.42
1:2A:2845:G:H5''	15:2T:54:ARG:O	2.19	0.42
5:2F:74:ARG:H	5:2F:74:ARG:HG3	1.48	0.42
32:2a:659:U:H2'	32:2a:660:G:O4'	2.20	0.42
32:2a:774:G:H1	32:2a:805:C:H42	1.67	0.42
32:2a:1210:C:N4	32:2a:1211:U:O4	2.52	0.42
33:2b:100:GLY:N	33:2b:176:GLU:OE2	2.51	0.42
33:2b:119:GLU:HG3	33:2b:153:ARG:HH22	1.85	0.42
39:2h:17:THR:HA	39:2h:65:TYR:OH	2.19	0.42
44:2m:16:ASP:HB3	44:2m:34:LEU:HD12	2.00	0.42
48:2q:4:LYS:N	48:2q:61:GLU:HG2	2.35	0.42
1:1A:474:U:H5'	60:1A:9159:HOH:O	2.19	0.42
1:1A:691:G:N2	1:1A:700:A:H1'	2.34	0.42
1:1A:1110:C:C4	1:1A:1120:G:O6	2.73	0.42
1:1A:1405:A:H2'	1:1A:1406:A:H5'	2.01	0.42
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.35	0.42
1:1A:2342:G:H2'	1:1A:2343:G:O4'	2.20	0.42
5:1F:125:LEU:HD21	5:1F:199:TRP:CD2	2.55	0.42
7:1H:94:TYR:N	7:1H:94:TYR:CD1	2.87	0.42
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.19	0.42
21:1Z:35:ARG:HA	21:1Z:35:ARG:HD2	1.89	0.42
22:10:12:ASN:O	22:10:14:ARG:NH2	2.53	0.42
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.32	0.42
32:1a:977:A:H2'	32:1a:978:A:H5''	2.02	0.42
32:1a:1005:A:H4'	32:1a:1037:C:O2'	2.20	0.42
32:1a:1279:A:O2'	32:1a:1282:C:N4	2.53	0.42
34:1c:132:ARG:HD3	34:1c:136:GLN:NE2	2.35	0.42
38:1g:13:GLN:HA	38:1g:14:PRO:HD3	1.93	0.42
38:1g:16:LEU:HD12	40:1i:41:VAL:O	2.20	0.42
1:2A:455:C:N3	1:2A:473:G:H5'	2.35	0.42
1:2A:779:U:OP1	3:2D:49:ILE:HG13	2.19	0.42
1:2A:1116:C:H2'	1:2A:1117:G:O4'	2.19	0.42
1:2A:1588:C:H2'	1:2A:1589:C:C6	2.55	0.42
1:2A:1686:C:H2'	1:2A:1687:G:O4'	2.20	0.42
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.84	0.42
1:2A:2319:G:N1	14:2S:3:ARG:HA	2.35	0.42
1:2A:2348:U:H5'	28:26:21:TYR:OH	2.19	0.42
1:2A:2464:C:H1'	60:2A:4675:HOH:O	2.20	0.42
18:2W:27:LYS:O	18:2W:71:VAL:HG23	2.20	0.42
19:2X:61:GLY:HA3	19:2X:73:ARG:O	2.20	0.42
21:2Z:118:GLN:N	21:2Z:173:ALA:O	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:27:34:ARG:NH1	29:27:41:ARG:O	2.52	0.42
32:2a:911:U:H2'	32:2a:912:C:C6	2.55	0.42
32:2a:949:A:H2'	32:2a:950:U:C6	2.55	0.42
33:2b:55:PHE:CE1	33:2b:218:ALA:HA	2.54	0.42
34:2c:5:ILE:HG13	34:2c:6:HIS:N	2.35	0.42
35:2d:38:TYR:HA	35:2d:39:PRO:HD3	1.89	0.42
37:2f:62:TRP:C	37:2f:63:TYR:HD2	2.27	0.42
41:2j:25:GLU:O	41:2j:29:ARG:HG2	2.20	0.42
1:1A:1686:U:O2'	1:1A:1687:C:H5'	2.20	0.42
1:1A:2131:U:H1'	1:1A:2203:G:N2	2.35	0.42
1:1A:2136:A:C2	1:1A:2137:G:H1'	2.55	0.42
1:1A:2333:G:H2'	1:1A:2333:G:N3	2.35	0.42
1:1A:2899:C:H3'	1:1A:2900:G:H8	1.84	0.42
6:1G:117:PHE:HZ	6:1G:179:PRO:HG2	1.84	0.42
32:1a:42:G:H1	32:1a:400:C:H42	1.68	0.42
32:1a:455:C:N3	32:1a:476:G:N2	2.57	0.42
32:1a:836:G:C6	32:1a:851:G:C6	3.08	0.42
32:1a:1002:G:C6	32:1a:1003:G:C2	3.07	0.42
35:1d:194:LEU:HD12	35:1d:194:LEU:HA	1.93	0.42
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	2.02	0.42
40:1i:46:ALA:HA	40:1i:78:LYS:HB2	2.01	0.42
48:1q:58:GLU:OE1	48:1q:75:ARG:NE	2.52	0.42
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.19	0.42
1:2A:1099:G:H8	1:2A:1099:G:O5'	2.03	0.42
1:2A:1805:U:C2	1:2A:1813:G:N2	2.88	0.42
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	2.02	0.42
15:2T:46:GLU:O	15:2T:65:LYS:HD2	2.20	0.42
15:2T:92:GLY:O	15:2T:120:ARG:NH2	2.53	0.42
32:2a:192:U:H2'	32:2a:193:C:C6	2.55	0.42
32:2a:807:A:H2'	32:2a:808:C:C6	2.55	0.42
32:2a:1521:G:H2'	32:2a:1522:U:O4'	2.20	0.42
46:2o:68:ARG:O	46:2o:72:ARG:HG3	2.20	0.42
47:2p:14:ASN:N	47:2p:15:PRO:HD3	2.34	0.42
1:1A:540:A:H1'	1:1A:604:C:H1'	2.02	0.42
1:1A:637:U:H4'	1:1A:640:A:C6	2.55	0.42
1:1A:800:C:H2'	1:1A:801:C:C6	2.55	0.42
1:1A:1362:U:H2'	1:1A:1363:A:H8	1.85	0.42
1:1A:1756:U:H2'	1:1A:1757:C:C6	2.54	0.42
1:1A:2343:G:O2'	1:1A:2348:A:N1	2.44	0.42
1:1A:2564:OMU:C4	1:1A:2564:OMU:C6	2.47	0.42
1:1A:2797:C:H1'	4:1E:37:ARG:NH1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:29:A:C2	2:1B:30:C:C2	3.08	0.42
3:1D:4:LYS:HB3	3:1D:18:VAL:CG2	2.45	0.42
6:1G:181:ARG:HG3	6:1G:182:LYS:N	2.35	0.42
15:1T:39:ARG:NH2	32:1a:345:C:H5'	2.25	0.42
19:1X:66:LEU:HA	19:1X:66:LEU:HD23	1.72	0.42
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.53	0.42
32:1a:128:G:O2'	48:1q:3:LYS:HE2	2.20	0.42
32:1a:299:G:H2'	32:1a:300:A:C8	2.55	0.42
32:1a:735:C:H2'	32:1a:736:C:C6	2.55	0.42
34:1c:23:TYR:CG	34:1c:24:ALA:N	2.87	0.42
35:1d:196:LEU:HD12	35:1d:196:LEU:H	1.84	0.42
40:1i:17:VAL:HA	40:1i:63:ILE:HG12	2.02	0.42
43:1l:79:GLU:HG2	43:1l:80:HIS:CD2	2.54	0.42
44:1m:97:PRO:HA	44:1m:110:ARG:HG3	2.02	0.42
49:1r:76:LEU:HD12	49:1r:76:LEU:HA	1.76	0.42
1:2A:389:G:H1	11:2P:70:GLN:HB3	1.85	0.42
1:2A:729:G:H2'	1:2A:1775:U:H1'	2.02	0.42
1:2A:2065:C:H4'	1:2A:2251:OMG:HM22	2.01	0.42
1:2A:2511:U:O4	1:2A:2575:C:N3	2.53	0.42
1:2A:2705:A:O2'	1:2A:2852:G:OP1	2.31	0.42
1:2A:2809:A:H2'	1:2A:2810:A:C8	2.55	0.42
5:2F:29:ASN:H	5:2F:112:MET:CE	2.32	0.42
12:2Q:39:PRO:HA	12:2Q:97:VAL:O	2.20	0.42
16:2U:112:ARG:HE	16:2U:112:ARG:HB3	1.37	0.42
21:2Z:53:ILE:H	21:2Z:53:ILE:HG13	1.72	0.42
32:2a:250:A:H4'	32:2a:251:G:O5'	2.20	0.42
32:2a:514:C:H2'	32:2a:515:G:H8	1.84	0.42
32:2a:540:G:H2'	32:2a:541:G:O4'	2.20	0.42
32:2a:974:A:H8	32:2a:974:A:OP1	2.02	0.42
32:2a:1233:G:C6	32:2a:1234:C:C4	3.08	0.42
32:2a:1272:G:H2'	32:2a:1273:G:O4'	2.19	0.42
32:2a:1319:A:P	50:2s:3:ARG:HD2	2.60	0.42
33:2b:42:ILE:HG13	33:2b:42:ILE:H	1.70	0.42
34:2c:58:GLU:HG2	41:2j:92:THR:OG1	2.20	0.42
44:2m:64:TRP:HB2	44:2m:66:LEU:HD21	2.02	0.42
44:2m:82:MET:HE3	44:2m:92:HIS:HB3	2.01	0.42
46:2o:26:GLU:HG3	46:2o:81:LEU:HD13	2.02	0.42
1:1A:1147:U:H2'	1:1A:1148:C:H6	1.80	0.41
1:1A:1270:C:H2'	1:1A:1271:G:O4'	2.20	0.41
1:1A:2538:G:H5'	1:1A:2755:C:O2'	2.20	0.41
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:19:2:LYS:HD3	31:19:4:ARG:NH2	2.35	0.41
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.50	0.41
32:1a:921:U:O2	36:1e:19:MET:HB2	2.19	0.41
32:1a:1194:U:H2'	32:1a:1195:C:C6	2.55	0.41
39:1h:44:PHE:HB3	39:1h:80:ILE:CG1	2.50	0.41
1:2A:952:G:C6	1:2A:966:G:C6	3.08	0.41
1:2A:1075:C:H2'	1:2A:1076:C:H5'	2.02	0.41
1:2A:1159:U:H2'	1:2A:1160:G:H8	1.84	0.41
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.20	0.41
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.55	0.41
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.20	0.41
2:2B:2:C:H2'	2:2B:3:C:H6	1.84	0.41
2:2B:18:G:H2'	2:2B:19:G:C8	2.55	0.41
6:2G:123:ASN:C	6:2G:125:PHE:H	2.28	0.41
7:2H:125:VAL:HG22	7:2H:131:VAL:HG22	2.02	0.41
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.20	0.41
25:23:16:PRO:HB2	25:23:18:ASP:OD1	2.19	0.41
32:2a:175:C:H2'	32:2a:176:C:H6	1.85	0.41
32:2a:1502:A:C8	32:2a:1505:G:N2	2.87	0.41
34:2c:53:ALA:HB2	34:2c:115:LEU:HD13	2.02	0.41
34:2c:178:LEU:C	34:2c:180:ALA:H	2.28	0.41
36:2e:72:GLN:O	36:2e:75:THR:HG22	2.19	0.41
39:2h:125:ARG:HE	39:2h:125:ARG:HB2	1.49	0.41
48:2q:27:PHE:CE1	48:2q:36:ILE:HD11	2.55	0.41
1:1A:272:U:H5'	8:1I:50:ARG:NH1	2.35	0.41
1:1A:287:G:N7	1:1A:448:U:H2'	2.36	0.41
1:1A:934:A:O2'	1:1A:935:C:H5''	2.20	0.41
1:1A:1101:G:O2'	1:1A:1131:A:N1	2.40	0.41
1:1A:1554:A:H4'	1:1A:1556:A:C6	2.55	0.41
1:1A:2125:C:N4	1:1A:2126:G:O6	2.53	0.41
1:1A:2151:C:C4	1:1A:2152:U:C4	3.07	0.41
1:1A:2672:A:H2'	1:1A:2673:G:O4'	2.19	0.41
2:1B:78:A:H2'	2:1B:79:C:O4'	2.19	0.41
5:1F:9:ILE:HA	5:1F:10:PRO:HD2	1.91	0.41
9:1N:33:LEU:HD12	9:1N:33:LEU:HA	1.91	0.41
21:1Z:14:LYS:HA	21:1Z:15:PRO:HD3	1.95	0.41
21:1Z:203:GLU:H	54:1x:53:G:H4'	1.85	0.41
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.76	0.41
31:19:11:CYS:SG	31:19:13:LYS:HB2	2.60	0.41
32:1a:678:U:H2'	32:1a:679:C:C6	2.55	0.41
32:1a:1083:U:C5	32:1a:1084:G:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:117:ALA:O	35:1d:121:VAL:HG23	2.20	0.41
39:1h:65:TYR:HA	39:1h:79:VAL:HG23	2.01	0.41
45:1n:24:CYS:HB2	45:1n:40:CYS:HB3	2.01	0.41
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.20	0.41
3:2D:70:TRP:CZ2	3:2D:150:LYS:HA	2.55	0.41
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.55	0.41
4:2E:16:ARG:NH1	4:2E:173:VAL:HG13	2.35	0.41
6:2G:112:PRO:HB2	26:24:35:VAL:HG13	2.02	0.41
22:20:23:VAL:HA	22:20:38:VAL:HG22	2.00	0.41
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.85	0.41
30:28:23:VAL:HG23	30:28:49:VAL:HG22	2.02	0.41
32:2a:587:G:N1	32:2a:754:C:OP2	2.46	0.41
32:2a:1309:G:C6	32:2a:1329:A:C6	3.07	0.41
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.85	0.41
35:2d:59:ARG:HA	35:2d:59:ARG:HD3	1.79	0.41
38:2g:113:GLU:H	38:2g:113:GLU:HG2	1.54	0.41
44:2m:60:VAL:HG23	44:2m:64:TRP:HZ3	1.85	0.41
48:2q:56:VAL:HG23	48:2q:81:ARG:HG3	2.02	0.41
50:2s:6:LYS:HB3	50:2s:6:LYS:HE2	1.84	0.41
1:1A:385:G:C2	1:1A:386:U:N3	2.88	0.41
1:1A:800:C:H2'	1:1A:801:C:H6	1.85	0.41
1:1A:1102:G:N2	1:1A:1149:A:H62	2.18	0.41
1:1A:1653:C:H4'	1:1A:1654:A:O5'	2.20	0.41
1:1A:2466:G:H1'	60:1A:9637:HOH:O	2.19	0.41
6:1G:60:LEU:HD23	6:1G:60:LEU:HA	1.92	0.41
9:1N:70:LYS:HE3	9:1N:72:TYR:CE1	2.55	0.41
20:1Y:14:LEU:HD11	20:1Y:22:GLY:HA2	2.01	0.41
20:1Y:90:LEU:HD21	20:1Y:96:ILE:HG23	2.00	0.41
32:1a:940:C:H2'	32:1a:941:G:H8	1.86	0.41
32:1a:955:U:O2'	50:1s:83:HIS:HD2	2.04	0.41
32:1a:1124:G:H1	32:1a:1149:C:H42	1.68	0.41
32:1a:1187:G:H4'	40:1i:111:ARG:NH1	2.35	0.41
35:1d:124:GLY:C	35:1d:126:ILE:H	2.28	0.41
41:1j:78:ASN:C	41:1j:80:LYS:H	2.28	0.41
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.20	0.41
1:2A:10:G:H2'	1:2A:11:G:C8	2.55	0.41
1:2A:1510:G:H2'	1:2A:1511:C:C6	2.55	0.41
1:2A:1937:A:O2'	1:2A:1939:5MU:OP2	2.30	0.41
1:2A:2207:G:H2'	1:2A:2208:A:C2	2.54	0.41
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.55	0.41
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2748:A:H5'	7:2H:4:ILE:CD1	2.49	0.41
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.20	0.41
32:2a:33:A:N3	43:2l:32:PHE:HE2	2.19	0.41
32:2a:73:G:C6	32:2a:97:G:C6	3.09	0.41
32:2a:1220:G:H5'	50:2s:34:TRP:O	2.20	0.41
32:2a:1255:G:OP1	41:2j:45:ARG:NH2	2.54	0.41
32:2a:1256:A:H61	32:2a:1278:U:C1'	2.21	0.41
33:2b:19:HIS:CG	33:2b:20:GLU:N	2.88	0.41
35:2d:36:ARG:HB3	35:2d:38:TYR:CE2	2.56	0.41
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.21	0.41
1:1A:251:A:H2'	1:1A:252:C:O4'	2.20	0.41
1:1A:310:C:H2'	1:1A:311:C:C6	2.55	0.41
1:1A:2169:G:H2'	1:1A:2170:G:O4'	2.20	0.41
7:1H:94:TYR:N	7:1H:94:TYR:HD1	2.18	0.41
8:1I:52:ARG:HB2	8:1I:52:ARG:NH2	2.36	0.41
9:1N:99:LEU:O	9:1N:103:VAL:HG23	2.20	0.41
15:1T:125:ARG:HH12	32:1a:1442(B):A:H4'	1.84	0.41
32:1a:109:A:H4'	32:1a:110:C:OP2	2.20	0.41
32:1a:1263:C:H2'	32:1a:1264:C:H6	1.84	0.41
35:1d:108:LEU:HD23	35:1d:110:PHE:CZ	2.56	0.41
35:1d:170:VAL:HG12	35:1d:174:LEU:HB2	2.03	0.41
36:1e:80:ILE:HG22	36:1e:91:LEU:HB2	2.02	0.41
44:1m:9:ILE:HD13	44:1m:19:LEU:HD12	2.02	0.41
50:1s:39:THR:HG22	50:1s:40:ILE:O	2.20	0.41
1:2A:1297:C:H5''	60:2A:4143:HOH:O	2.20	0.41
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.55	0.41
1:2A:2089:U:H2'	1:2A:2090:G:C8	2.55	0.41
1:2A:2206:G:C3'	1:2A:2207:G:C8	3.00	0.41
1:2A:2674:G:H2'	1:2A:2675:A:C8	2.56	0.41
7:2H:104:GLU:HA	7:2H:113:VAL:O	2.20	0.41
11:2P:47:ASP:HA	11:2P:48:PRO:HD3	1.92	0.41
15:2T:119:LYS:HB2	32:2a:1442(A):G:N2	2.36	0.41
23:21:73:LEU:HD23	23:21:73:LEU:HA	1.87	0.41
27:25:8:LYS:O	27:25:9:LYS:HD2	2.20	0.41
32:2a:601:C:H2'	32:2a:602:A:H8	1.84	0.41
33:2b:97:TRP:HZ2	33:2b:102:LEU:HD13	1.86	0.41
33:2b:166:ASP:O	33:2b:170:GLU:N	2.50	0.41
34:2c:74:GLY:HA2	34:2c:77:ILE:HG12	2.02	0.41
39:2h:116:LYS:HD2	39:2h:129:VAL:HG11	2.01	0.41
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.52	0.41
1:1A:1270:C:O2'	17:1V:85:LYS:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1532:A:H2'	1:1A:1533:G:H8	1.85	0.41
1:1A:2327:G:H2'	1:1A:2328:C:C6	2.55	0.41
5:1F:108:LYS:HE2	5:1F:112:MET:HE3	2.02	0.41
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.36	0.41
9:1N:62:VAL:CG2	9:1N:66:LYS:HD2	2.50	0.41
14:1S:59:LYS:HB2	14:1S:60:GLY:H	1.46	0.41
20:1Y:92:ASN:CB	20:1Y:94:LYS:HG2	2.51	0.41
32:1a:445:G:H1	32:1a:489:C:H42	1.67	0.41
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.20	0.41
40:1i:8:GLY:O	40:1i:15:ALA:N	2.52	0.41
43:1l:89:ARG:HA	43:1l:97:ARG:HA	2.01	0.41
45:1n:26:ARG:NH1	45:1n:43:CYS:SG	2.92	0.41
48:1q:72:ARG:HH11	48:1q:72:ARG:HG3	1.85	0.41
1:2A:828:U:H2'	1:2A:829:A:C8	2.56	0.41
1:2A:1359:A:C6	1:2A:1372:U:O4	2.73	0.41
1:2A:2128:C:O2'	1:2A:2174:C:H4'	2.20	0.41
5:2F:80:ALA:HB3	5:2F:83:PHE:HD2	1.85	0.41
6:2G:43:LEU:HD11	6:2G:153:ARG:HB3	2.02	0.41
6:2G:46:ALA:O	6:2G:51:ARG:HG3	2.20	0.41
11:2P:125:VAL:HG13	11:2P:138:LEU:HD21	2.02	0.41
18:2W:35:ILE:O	18:2W:39:THR:OG1	2.35	0.41
20:2Y:56:PRO:O	20:2Y:57:GLN:HB2	2.19	0.41
28:26:14:THR:OG1	28:26:48:VAL:HG13	2.20	0.41
32:2a:438:G:O2'	32:2a:494:U:O4	2.30	0.41
32:2a:878:G:H1'	39:2h:3:THR:HG21	2.01	0.41
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.55	0.41
32:2a:1104:G:O3'	33:2b:111:ARG:NH2	2.54	0.41
32:2a:1221:G:O3'	50:2s:77:THR:OG1	2.35	0.41
32:2a:1227:A:C8	32:2a:1227:A:H3'	2.56	0.41
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.35	0.41
33:2b:97:TRP:HZ3	33:2b:172:ILE:HG22	1.85	0.41
33:2b:125:PRO:HB2	33:2b:126:GLU:H	1.42	0.41
34:2c:188:LEU:HD11	34:2c:195:VAL:HG13	2.01	0.41
38:2g:47:CYS:O	38:2g:50:ILE:HG12	2.21	0.41
38:2g:122:HIS:HA	38:2g:125:MET:HB2	2.01	0.41
1:1A:210:A:C4	1:1A:255:G:N7	2.88	0.41
1:1A:509:A:O4'	20:1Y:48:ALA:HB1	2.20	0.41
1:1A:925:A:H2'	1:1A:926:G:H5'	2.03	0.41
1:1A:1159:U:H2'	1:1A:1160:G:H8	1.86	0.41
1:1A:2207:C:C4	1:1A:2208:G:N7	2.89	0.41
1:1A:2398:C:H2'	1:1A:2399:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:12:C:H2'	22:10:73:GLY:HA3	2.03	0.41
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.64	0.41
5:1F:178:PRO:HB2	5:1F:201:VAL:CG2	2.50	0.41
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.01	0.41
11:1P:98:GLU:O	11:1P:101:VAL:HB	2.21	0.41
32:1a:474:G:H2'	32:1a:475:G:C8	2.49	0.41
32:1a:629:G:H2'	32:1a:630:G:O4'	2.20	0.41
32:1a:1061:G:H1'	41:1j:56:HIS:CE1	2.56	0.41
32:1a:1256:A:OP1	34:1c:26:LYS:NZ	2.49	0.41
1:2A:626:U:O2	11:2P:105:LEU:HD23	2.20	0.41
1:2A:885:C:H2'	1:2A:886:C:O4'	2.21	0.41
1:2A:1683:C:H2'	1:2A:1684:C:C6	2.56	0.41
1:2A:1946:U:H2'	1:2A:1947:C:H6	1.83	0.41
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.86	0.41
9:2N:75:TYR:HA	9:2N:81:GLY:O	2.21	0.41
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	2.03	0.41
15:2T:13:ARG:HG2	15:2T:14:TYR:CE2	2.55	0.41
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.20	0.41
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.85	0.41
32:2a:439:A:H2'	32:2a:441:A:O4'	2.20	0.41
32:2a:625:G:H2'	32:2a:626:U:H6	1.85	0.41
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.21	0.41
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.56	0.41
34:2c:137:ALA:HA	34:2c:140:ARG:NH2	2.36	0.41
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.21	0.41
38:2g:69:VAL:HG22	38:2g:135:VAL:HG22	2.02	0.41
41:2j:35:SER:HB3	41:2j:73:ASP:CB	2.49	0.41
45:2n:23:ARG:CZ	45:2n:30:ALA:HB2	2.51	0.41
1:1A:870:G:C2	1:1A:882:A:C2	3.09	0.41
1:1A:1230:C:H5''	1:1A:1231:G:OP1	2.21	0.41
1:1A:1303:C:H4'	5:1F:83:PHE:CD1	2.56	0.41
1:1A:1896:G:N2	1:1A:1898:A:H3'	2.35	0.41
1:1A:1948:U:O2'	1:1A:1950:A:N7	2.47	0.41
1:1A:2156:A:C2	1:1A:2180:A:H4'	2.56	0.41
1:1A:2216:G:H2'	1:1A:2217:C:O4'	2.19	0.41
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.21	0.41
6:1G:18:GLU:O	6:1G:21:ARG:HB3	2.20	0.41
12:1Q:137:TYR:O	12:1Q:141:GLN:HG2	2.20	0.41
17:1V:97:LYS:HA	17:1V:97:LYS:HD3	1.72	0.41
19:1X:35:THR:O	19:1X:38:GLU:HB3	2.20	0.41
21:1Z:145:GLU:N	21:1Z:148:ASP:HB2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:3:LEU:HD22	24:12:7:ARG:NH2	2.36	0.41
32:1a:300:A:H8	32:1a:300:A:O5'	2.03	0.41
32:1a:674:G:H2'	32:1a:675:A:H8	1.85	0.41
32:1a:1149:C:O2'	32:1a:1280:A:N1	2.50	0.41
33:1b:59:GLU:HB2	33:1b:221:LEU:HD11	2.02	0.41
50:1s:30:LEU:HD12	50:1s:30:LEU:HA	1.88	0.41
51:1t:91:LEU:HD23	51:1t:91:LEU:HA	1.87	0.41
1:2A:2126:A:H4'	1:2A:2127:G:C4'	2.51	0.41
1:2A:2134:A:N1	1:2A:2135:A:N6	2.69	0.41
1:2A:2298:A:N6	1:2A:2318:G:C8	2.88	0.41
1:2A:2577:A:O4'	27:25:3:LYS:HB2	2.21	0.41
1:2A:2819:G:H1	1:2A:2827:C:N4	2.18	0.41
3:2D:16:MET:HB2	3:2D:207:GLY:HA3	2.03	0.41
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	2.03	0.41
3:2D:264:LYS:HA	3:2D:265:PRO:HD3	1.91	0.41
6:2G:126:ASP:CG	6:2G:130:ASN:HD22	2.28	0.41
6:2G:145:THR:HG23	6:2G:147:ASP:H	1.86	0.41
10:2O:121:VAL:O	15:2T:43:GLN:NE2	2.51	0.41
13:2R:82:GLU:O	13:2R:85:PRO:HD2	2.20	0.41
16:2U:5:LYS:H	16:2U:5:LYS:HG2	1.67	0.41
19:2X:35:THR:HG22	19:2X:37:THR:N	2.35	0.41
28:26:11:LEU:HB3	28:26:49:HIS:HB3	2.03	0.41
32:2a:96:U:H2'	32:2a:97:G:H8	1.86	0.41
32:2a:298:A:C6	32:2a:299:G:C2	3.09	0.41
32:2a:325:A:H2'	32:2a:326:G:O4'	2.20	0.41
32:2a:679:C:H2'	32:2a:680:C:C6	2.55	0.41
32:2a:1026:G:N7	32:2a:1027:C:C2	2.89	0.41
32:2a:1057:G:H2'	32:2a:1058:G:O4'	2.20	0.41
32:2a:1236:A:OP2	52:2u:3:LYS:HE2	2.21	0.41
50:2s:42:PRO:O	50:2s:45:VAL:HG23	2.20	0.41
1:1A:831:A:C5	3:1D:229:VAL:HG21	2.56	0.41
1:1A:848:G:O6	5:1F:53:THR:OG1	2.36	0.41
1:1A:1302:G:O2'	5:1F:75:HIS:HE1	2.04	0.41
1:1A:1854:G:OP1	3:1D:54:ARG:NH1	2.53	0.41
1:1A:2418:U:OP1	1:1A:2423:A:N6	2.54	0.41
1:1A:2545:A:H2'	1:1A:2546:A:O4'	2.21	0.41
1:1A:2820:A:H61	1:1A:2900:G:C2'	2.34	0.41
5:1F:200:GLU:O	5:1F:203:GLN:HB2	2.20	0.41
19:1X:29:TRP:CE3	19:1X:78:LYS:HB3	2.56	0.41
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.36	0.41
30:18:63:PRO:HG2	30:18:64:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:37:U:H2'	32:1a:38:G:O4'	2.21	0.41
32:1a:922:G:C6	32:1a:923:A:C6	3.09	0.41
32:1a:1239:A:O2'	38:1g:114:ARG:O	2.35	0.41
32:1a:1256:A:OP1	34:1c:27:LYS:NZ	2.54	0.41
42:1k:77:MET:HE2	42:1k:77:MET:HB2	1.97	0.41
1:2A:874:G:C6	1:2A:875:G:C5	3.08	0.41
1:2A:1021:A:H3'	1:2A:1021:A:N3	2.36	0.41
1:2A:1612:C:O2'	29:27:5:TRP:O	2.32	0.41
1:2A:1847:A:H3'	1:2A:1848:A:H5'	2.02	0.41
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.36	0.41
1:2A:2130:U:O2'	1:2A:2133:G:H4'	2.21	0.41
1:2A:2157:G:H3'	1:2A:2157:G:H8	1.84	0.41
1:2A:2360:A:C2	1:2A:2361:A:H1'	2.56	0.41
1:2A:2439:A:H1'	1:2A:2587:A:OP1	2.21	0.41
3:2D:43:ARG:HA	3:2D:48:ARG:O	2.20	0.41
4:2E:101:ARG:HD3	4:2E:101:ARG:HA	1.69	0.41
6:2G:16:ARG:NH1	6:2G:31:VAL:HG22	2.36	0.41
7:2H:124:GLU:OE1	7:2H:132:ARG:HD2	2.20	0.41
10:2O:61:VAL:HG11	10:2O:114:ILE:CD1	2.51	0.41
21:2Z:35:ARG:HA	21:2Z:35:ARG:HD2	1.89	0.41
21:2Z:193:GLU:HA	21:2Z:194:PRO:HD3	1.88	0.41
32:2a:977:A:H1'	32:2a:982:U:O4	2.21	0.41
32:2a:1125:U:C5	32:2a:1280:A:C8	3.09	0.41
32:2a:1243:C:H2'	32:2a:1244:C:H6	1.85	0.41
32:2a:1436:U:H2'	32:2a:1437:C:O4'	2.21	0.41
33:2b:38:GLY:C	33:2b:39:ILE:HG13	2.45	0.41
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	2.02	0.41
36:2e:6:PHE:HD2	36:2e:63:ARG:NH1	2.19	0.41
49:2r:53:ARG:HA	49:2r:56:THR:OG1	2.21	0.41
54:2x:64:G:H2'	54:2x:65:C:C6	2.55	0.41
1:1A:276:C:OP1	8:1I:45:LYS:HD3	2.21	0.41
1:1A:424:G:H1'	1:1A:2243:C:O2'	2.20	0.41
1:1A:789:G:H4'	1:1A:1723:A:H5'	2.03	0.41
1:1A:1136:U:C2	1:1A:1148:C:O2	2.74	0.41
1:1A:1324:A:OP1	13:1R:36:THR:HG23	2.21	0.41
1:1A:1404:G:O2'	1:1A:1405:A:H5''	2.21	0.41
1:1A:1497:G:H2'	1:1A:1498:C:H6	1.85	0.41
1:1A:1588:G:H3'	1:1A:1589:A:H2'	2.03	0.41
1:1A:1961:5MU:OP1	1:1A:2616:U:O2'	2.35	0.41
1:1A:2125:C:C2	1:1A:2126:G:N7	2.88	0.41
1:1A:2156:A:N3	1:1A:2180:A:H4'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2167:C:OP1	1:1A:2167:C:C6	2.74	0.41
1:1A:2476:C:H1'	60:1A:9872:HOH:O	2.20	0.41
1:1A:2573:A:H2	10:1O:23:ARG:HH21	1.67	0.41
1:1A:2734:A:H2'	1:1A:2735:G:O4'	2.21	0.41
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	2.03	0.41
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	2.02	0.41
6:1G:121:ASN:O	6:1G:131:TYR:OH	2.30	0.41
7:1H:126:PRO:HD2	7:1H:130:ARG:O	2.21	0.41
8:1I:72:LEU:C	8:1I:74:ASN:N	2.78	0.41
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.20	0.41
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.56	0.41
15:1T:53:ARG:HB3	15:1T:53:ARG:CZ	2.51	0.41
16:1U:34:LYS:HD3	16:1U:34:LYS:HA	1.91	0.41
16:1U:81:HIS:O	16:1U:85:LYS:HG3	2.21	0.41
21:1Z:158:PRO:O	21:1Z:161:VAL:HG12	2.20	0.41
22:10:24:LYS:HA	22:10:24:LYS:HD3	1.82	0.41
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.50	0.41
32:1a:551:U:H2'	32:1a:552:U:C6	2.55	0.41
32:1a:735:C:H2'	32:1a:736:C:H6	1.86	0.41
32:1a:1036:G:H5'	32:1a:1037:C:OP2	2.21	0.41
32:1a:1169:A:H2'	32:1a:1170:A:C8	2.56	0.41
32:1a:1298:C:C5	38:1g:114:ARG:HD3	2.55	0.41
32:1a:1313:U:P	50:1s:5:LEU:HB2	2.60	0.41
32:1a:1405:G:H1'	32:1a:1519:MA6:O4'	2.21	0.41
32:1a:1518:MA6:O5'	32:1a:1518:MA6:H8	2.20	0.41
33:1b:108:ILE:O	33:1b:111:ARG:HB3	2.21	0.41
33:1b:134:GLU:O	33:1b:138:LEU:HG	2.21	0.41
35:1d:108:LEU:HD12	35:1d:108:LEU:HA	1.85	0.41
35:1d:108:LEU:HD11	35:1d:174:LEU:HB3	2.03	0.41
39:1h:104:ARG:HA	39:1h:104:ARG:HD3	1.83	0.41
44:1m:20:THR:C	44:1m:22:ILE:H	2.29	0.41
47:1p:14:ASN:HA	47:1p:42:ARG:HH21	1.86	0.41
1:2A:583:G:OP2	16:2U:10:ARG:NH1	2.54	0.41
1:2A:2392:A:N3	11:2P:61:ARG:HG2	2.35	0.41
1:2A:2650:U:H2'	1:2A:2651:C:H6	1.85	0.41
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.86	0.41
5:2F:184:TYR:CE1	11:2P:3:LEU:HD21	2.55	0.41
6:2G:135:LEU:O	6:2G:154:GLY:HA3	2.21	0.41
7:2H:3:ARG:NH1	7:2H:4:ILE:H	2.19	0.41
15:2T:108:ARG:HB2	32:2a:1432:G:OP1	2.21	0.41
24:22:32:LEU:HD22	24:22:36:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:23:26:LEU:HD21	25:23:46:ASN:HB2	2.03	0.41
26:24:58:ARG:HA	26:24:58:ARG:HD2	1.91	0.41
26:24:62:ARG:H	26:24:62:ARG:HH11	1.68	0.41
32:2a:414:A:N6	32:2a:431:A:N3	2.69	0.41
32:2a:443:C:H2'	32:2a:444:C:C6	2.55	0.41
32:2a:1054:C:H4'	32:2a:1055:A:O5'	2.21	0.41
32:2a:1158:C:H42	32:2a:1181:G:H1	1.68	0.41
32:2a:1226:C:O4'	50:2s:83:HIS:HE1	2.04	0.41
32:2a:1377:A:H2'	38:2g:7:ALA:HB2	2.03	0.41
32:2a:1517:G:H3'	32:2a:1518:MA6:H8	2.03	0.41
34:2c:9:GLY:HA2	34:2c:12:LEU:HG	2.02	0.41
34:2c:18:TRP:HB3	34:2c:20:SER:H	1.85	0.41
36:2e:18:ARG:HG2	36:2e:25:ARG:O	2.20	0.41
40:2i:26:VAL:HB	40:2i:33:PHE:HB2	2.03	0.41
44:2m:90:LEU:CD2	44:2m:93:ARG:HH21	2.34	0.41
46:2o:4:THR:HG23	46:2o:7:GLU:H	1.84	0.41
1:1A:593:G:C6	1:1A:2052:A:C2	3.09	0.41
1:1A:662:A:H4'	1:1A:663:G:O5'	2.21	0.41
1:1A:802:C:H2'	1:1A:803:C:C6	2.56	0.41
1:1A:868:A:O2'	1:1A:991:G:OP2	2.37	0.41
1:1A:1117:G:C6	1:1A:1118:C:C4	3.09	0.41
1:1A:1874:C:H5'	3:1D:253:GLN:NE2	2.36	0.41
1:1A:1911:A:N1	1:1A:2246:G:H1'	2.36	0.41
7:1H:19:VAL:HA	7:1H:24:VAL:HG12	2.02	0.41
9:1N:33:LEU:HD12	9:1N:38:HIS:CE1	2.56	0.41
11:1P:2:LYS:HD2	11:1P:4:SER:H	1.86	0.41
32:1a:235:C:C5'	48:1q:70:ARG:HG3	2.50	0.41
32:1a:377:G:H5'	47:1p:5:ARG:HH12	1.86	0.41
32:1a:690:G:C6	32:1a:691:G:C6	3.09	0.41
32:1a:1005:A:H5'	32:1a:1038:C:H1'	2.03	0.41
35:1d:65:ARG:NH1	35:1d:70:ILE:O	2.54	0.41
37:1f:95:GLU:HA	37:1f:96:PRO:HD3	1.84	0.41
44:1m:36:LYS:HD2	44:1m:59:TYR:CE1	2.55	0.41
47:1p:19:ILE:HG22	47:1p:37:GLY:C	2.46	0.41
1:2A:271(O):C:H2'	1:2A:271(P):C:C6	2.56	0.41
1:2A:601:C:O2'	1:2A:605:C:OP1	2.32	0.41
1:2A:999:U:O2'	1:2A:1000:A:H5'	2.21	0.41
1:2A:1024:G:C6	1:2A:1025:G:C6	3.09	0.41
1:2A:2342:C:O2'	1:2A:2374:C:OP1	2.29	0.41
1:2A:2740:A:C6	1:2A:2764:A:C8	3.09	0.41
2:2B:29:A:C6	2:2B:30:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:167:VAL:CG1	4:2E:189:PRO:HD3	2.51	0.41
6:2G:52:ILE:O	6:2G:53:LEU:HD23	2.21	0.41
7:2H:126:PRO:HD2	7:2H:130:ARG:O	2.21	0.41
8:2I:116:LEU:HD11	8:2I:119:PRO:HA	2.03	0.41
19:2X:60:ARG:NH2	29:27:47:ARG:HH22	2.18	0.41
21:2Z:52:SER:HB3	21:2Z:53:ILE:H	1.62	0.41
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.86	0.41
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.56	0.41
32:2a:266:G:H2'	32:2a:266:G:N3	2.36	0.41
32:2a:926:G:C6	32:2a:1505:G:C6	3.09	0.41
32:2a:940:C:H2'	32:2a:941:G:C8	2.55	0.41
32:2a:1004:A:N7	32:2a:1037:C:C2	2.89	0.41
35:2d:38:TYR:CE1	35:2d:45:GLN:HG2	2.56	0.41
38:2g:68:ASN:ND2	38:2g:128:ALA:HA	2.36	0.41
41:2j:16:LEU:HA	41:2j:16:LEU:HD23	1.83	0.41
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.56	0.41
54:2x:21:A:O3'	54:2x:22:G:H8	2.04	0.41
1:1A:304:C:C2	1:1A:385:G:C2	3.09	0.40
1:1A:2054:G:H1'	4:1E:145:LYS:HD3	2.03	0.40
1:1A:2150:C:H2'	1:1A:2151:C:C6	2.56	0.40
1:1A:2331:G:H1	14:1S:3:ARG:HA	1.86	0.40
1:1A:2856:G:H2'	1:1A:2857:U:O4'	2.21	0.40
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.54	0.40
6:1G:78:SER:OG	54:1x:57:A:O4'	2.15	0.40
7:1H:3:ARG:HG2	7:1H:6:ARG:NE	2.36	0.40
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	2.01	0.40
11:1P:90:ARG:NH1	11:1P:105:LEU:HD11	2.35	0.40
13:1R:17:ARG:O	13:1R:20:LEU:HB3	2.21	0.40
18:1W:107:LEU:HD12	18:1W:107:LEU:HA	1.91	0.40
23:11:60:PHE:HZ	23:11:94:LEU:HD12	1.86	0.40
24:12:35:LEU:HD23	24:12:35:LEU:HA	1.92	0.40
27:15:8:LYS:O	27:15:9:LYS:HD2	2.21	0.40
32:1a:831:U:H2'	32:1a:832:C:H6	1.86	0.40
32:1a:1111:A:N1	34:1c:177:THR:OG1	2.50	0.40
32:1a:1236:A:H2'	32:1a:1237:C:C6	2.56	0.40
32:1a:1517:G:H3'	32:1a:1518:MA6:H8	2.03	0.40
42:1k:69:ALA:O	42:1k:73:MET:HG3	2.22	0.40
1:2A:171:G:H2'	1:2A:172:C:C6	2.56	0.40
1:2A:1065:U:HO2'	1:2A:1066:U:P	2.41	0.40
1:2A:1141:U:O2	1:2A:1142(A):A:N6	2.54	0.40
1:2A:1364:G:P	23:21:3:LYS:HG3	2.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2100:G:C6	1:2A:2101:G:C8	3.09	0.40
1:2A:2138:C:N3	1:2A:2153:G:N2	2.69	0.40
1:2A:2259:G:C2	1:2A:2282:G:C6	3.09	0.40
3:2D:70:TRP:HB3	3:2D:190:TYR:CE2	2.57	0.40
4:2E:51:PHE:CE1	4:2E:52:LEU:HD23	2.56	0.40
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.86	0.40
22:20:52:GLY:O	22:20:59:LEU:HA	2.21	0.40
32:2a:97:G:H2'	32:2a:98:G:C8	2.56	0.40
32:2a:155:C:H2'	32:2a:156:G:O4'	2.21	0.40
32:2a:790:A:OP1	54:2x:38:A:O2'	2.34	0.40
32:2a:922:G:C2	32:2a:923:A:C4	3.09	0.40
32:2a:1053:G:N2	60:2a:1910:HOH:O	2.48	0.40
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.56	0.40
32:2a:1415:G:C6	32:2a:1486:G:C6	3.10	0.40
32:2a:1422:G:C2	32:2a:1479:C:C2	3.10	0.40
32:2a:1498:UR3:H1'	32:2a:1499:A:N7	2.36	0.40
33:2b:207:ALA:O	33:2b:211:ILE:HG13	2.20	0.40
48:2q:40:LYS:HD3	48:2q:42:TYR:CZ	2.56	0.40
1:1A:26:G:C6	1:1A:27:G:N1	2.89	0.40
1:1A:908:A:C2	1:1A:963:A:C4	3.09	0.40
1:1A:1005:A:C8	1:1A:1007:G:C8	3.10	0.40
1:1A:1524:A:C2	1:1A:1563:G:C2	3.09	0.40
1:1A:1785:C:H2'	1:1A:1786:A:O4'	2.21	0.40
1:1A:2302:G:H2'	1:1A:2303:U:O4'	2.21	0.40
11:1P:79:ARG:HA	11:1P:79:ARG:HD3	1.94	0.40
29:17:8:ASN:HB3	29:17:11:LYS:HB3	2.02	0.40
32:1a:450:G:H1	32:1a:483:C:N4	2.17	0.40
32:1a:687:A:H4'	32:1a:688:G:O5'	2.21	0.40
32:1a:721:G:H4'	32:1a:722:A:O4'	2.21	0.40
32:1a:1250:A:O3'	40:1i:67:GLY:HA2	2.21	0.40
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.56	0.40
32:1a:1442:G:O2'	32:1a:1442(A):G:O5'	2.39	0.40
38:1g:45:ASP:O	38:1g:49:ILE:HG13	2.22	0.40
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.36	0.40
46:1o:26:GLU:OE2	46:1o:77:ARG:HG2	2.21	0.40
1:2A:539:G:H2'	1:2A:540:C:H6	1.87	0.40
1:2A:557:U:O2	9:2N:45:ASN:HB2	2.22	0.40
1:2A:581:C:H2'	1:2A:582:G:H8	1.85	0.40
1:2A:700:G:O2'	1:2A:1632:A:N3	2.51	0.40
1:2A:820:A:H2'	1:2A:821:A:O4'	2.21	0.40
1:2A:1528(A):A:H2'	1:2A:1529:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2133:G:N2	1:2A:2158:A:OP2	2.54	0.40
1:2A:2134:A:C4	1:2A:2157:G:H4'	2.56	0.40
8:2I:53:ALA:O	8:2I:57:ARG:HG2	2.21	0.40
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.21	0.40
11:2P:95:VAL:HA	11:2P:99:LEU:HD22	2.02	0.40
21:2Z:145:GLU:HB2	21:2Z:148:ASP:OD2	2.21	0.40
26:24:2:LYS:O	26:24:6:HIS:HD2	2.04	0.40
32:2a:618:C:N4	60:2a:1904:HOH:O	2.30	0.40
32:2a:678:U:O2	32:2a:777:A:H4'	2.21	0.40
32:2a:984:C:H2'	32:2a:985:C:C6	2.55	0.40
32:2a:1072:G:H2'	32:2a:1073:U:H6	1.86	0.40
47:2p:28:ARG:NH1	47:2p:29:ASP:OD2	2.54	0.40
49:2r:53:ARG:HG3	49:2r:63:GLN:HG2	2.02	0.40
1:1A:170:A:H1'	1:1A:462:C:H5'	2.02	0.40
1:1A:264:G:H1	1:1A:280:C:H42	1.69	0.40
1:1A:481:C:N3	1:1A:498:A:H2'	2.36	0.40
1:1A:1550:C:H2'	1:1A:1551:C:C6	2.57	0.40
1:1A:2054:G:N2	1:1A:2584:A:OP2	2.54	0.40
1:1A:2196:C:H2'	1:1A:2197:C:H6	1.85	0.40
6:1G:6:ALA:HB3	6:1G:104:GLU:OE2	2.22	0.40
14:1S:25:ARG:O	14:1S:39:ILE:HA	2.20	0.40
32:1a:198:G:H2'	32:1a:199:G:C8	2.55	0.40
32:1a:575:G:O2'	32:1a:821:G:H5'	2.20	0.40
32:1a:1084:G:C5	32:1a:1085:U:C4	3.09	0.40
32:1a:1120:G:H2'	32:1a:1121:U:C6	2.56	0.40
32:1a:1325:C:H2'	32:1a:1326:C:H6	1.86	0.40
42:1k:40:ILE:HA	42:1k:40:ILE:HD13	1.82	0.40
1:2A:660:G:C6	1:2A:661:C:C4	3.09	0.40
1:2A:723:G:H2'	1:2A:724:U:O4'	2.22	0.40
1:2A:1059:G:C5	1:2A:1060:U:N3	2.90	0.40
1:2A:1721:G:H5'	1:2A:1722:A:OP2	2.21	0.40
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.55	0.40
1:2A:2127:G:N2	1:2A:2173:A:H1'	2.37	0.40
1:2A:2302:G:C6	1:2A:2315:G:C6	3.10	0.40
1:2A:2432:A:C6	1:2A:2433:A:C6	3.10	0.40
1:2A:2609:U:C5	55:2y:15:PRO:HG2	2.56	0.40
1:2A:2810:A:H2'	1:2A:2811:G:O4'	2.22	0.40
4:2E:14:ILE:HD11	4:2E:173:VAL:HG11	2.03	0.40
4:2E:15:PHE:CD2	15:2T:81:PRO:HD3	2.56	0.40
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.56	0.40
6:2G:36:LYS:O	6:2G:159:VAL:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:43:LEU:C	6:2G:45:GLU:H	2.28	0.40
9:2N:110:GLY:O	9:2N:114:ARG:HG3	2.21	0.40
21:2Z:28:MET:HA	21:2Z:88:PHE:O	2.21	0.40
25:23:12:PRO:HB2	25:23:20:LYS:HG2	2.04	0.40
32:2a:96:U:H2'	32:2a:97:G:C8	2.57	0.40
32:2a:407:G:H2'	32:2a:408:A:H8	1.87	0.40
35:2d:76:ARG:HD3	35:2d:207:TYR:CZ	2.55	0.40
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	2.03	0.40
38:2g:150:ALA:HA	42:2k:59:TYR:HB3	2.03	0.40
40:2i:50:LEU:CD1	40:2i:56:LEU:HD23	2.50	0.40
40:2i:96:LEU:HD22	40:2i:101:PHE:HB2	2.03	0.40
44:2m:13:LYS:HA	44:2m:44:ARG:NH1	2.36	0.40
46:2o:3:ILE:H	46:2o:3:ILE:HD12	1.84	0.40
48:2q:43:LEU:HD12	48:2q:68:ARG:HB2	2.03	0.40
54:2x:54:5MU:OP2	54:2x:54:5MU:H71	2.21	0.40
1:1A:910:A:H8	1:1A:910:A:O5'	2.04	0.40
1:1A:969:C:H2'	1:1A:970:C:C6	2.57	0.40
1:1A:1018:A:OP1	1:1A:1018:A:H8	2.04	0.40
1:1A:2382:G:C6	1:1A:2383:G:C6	3.09	0.40
1:1A:2401:G:H5''	1:1A:2402:U:O4'	2.22	0.40
1:1A:2451:A:C8	1:1A:2451:A:H5'	2.56	0.40
1:1A:2658:C:H2'	1:1A:2659:U:O4'	2.21	0.40
1:1A:2669:A:O3'	7:1H:160:LYS:NZ	2.55	0.40
4:1E:4:ILE:HD13	4:1E:28:ALA:HB1	2.02	0.40
6:1G:37:VAL:HG22	6:1G:159:VAL:HB	2.04	0.40
9:1N:1:MET:O	9:1N:1:MET:HG3	2.22	0.40
20:1Y:56:PRO:C	20:1Y:58:GLY:N	2.79	0.40
32:1a:625:G:H4'	47:1p:16:HIS:CD2	2.56	0.40
32:1a:1468:A:H8	32:1a:1468:A:O5'	2.04	0.40
33:1b:95:GLN:HG3	33:1b:147:LYS:O	2.21	0.40
34:1c:112:SER:O	34:1c:116:VAL:HG23	2.21	0.40
40:1i:5:TYR:CE1	40:1i:16:ARG:HA	2.55	0.40
49:1r:54:ARG:HG3	49:1r:55:ARG:HG2	2.03	0.40
1:2A:271(K):U:O2	8:2I:50:ARG:HD2	2.21	0.40
1:2A:919:G:N2	1:2A:2269:A:OP2	2.54	0.40
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.22	0.40
1:2A:1494:A:H2'	1:2A:1495:A:C8	2.57	0.40
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.56	0.40
1:2A:1923:U:O2'	54:2x:12:G:H1'	2.22	0.40
1:2A:2489:G:C6	1:2A:2490:G:N1	2.90	0.40
6:2G:146:TYR:HB3	44:2m:11:ARG:HH12	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:68:GLU:HB3	10:2O:78:ARG:HD3	2.03	0.40
21:2Z:28:MET:O	21:2Z:34:ASN:HA	2.22	0.40
32:2a:19:C:H2'	32:2a:20:U:C6	2.56	0.40
32:2a:514:C:H2'	32:2a:515:G:C8	2.57	0.40
32:2a:629:G:H2'	32:2a:630:G:O4'	2.20	0.40
32:2a:682:G:C6	32:2a:709:G:C6	3.10	0.40
32:2a:1070:U:H2'	32:2a:1071:C:H6	1.87	0.40
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.21	0.40
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.89	0.40
37:2f:24:GLU:O	37:2f:28:ARG:HB2	2.22	0.40
41:2j:42:THR:HG21	41:2j:66:ARG:HB3	2.03	0.40
47:2p:55:ARG:O	47:2p:58:TYR:HB3	2.21	0.40
54:2x:9:G:O2'	54:2x:10:G:N7	2.40	0.40
1:1A:18:C:O2'	1:1A:577:U:OP1	2.34	0.40
1:1A:142:G:H1'	19:1X:37:THR:CG2	2.51	0.40
1:1A:178:G:O6	1:1A:194:G:O2'	2.37	0.40
1:1A:829:A:C2	3:1D:226:MET:HG2	2.56	0.40
1:1A:1259:A:H2'	1:1A:1260:G:O4'	2.22	0.40
1:1A:1513:G:H2'	1:1A:1594:C:N4	2.36	0.40
1:1A:2163:G:C6	1:1A:2173:G:C6	3.09	0.40
6:1G:110:ALA:HB1	6:1G:140:ILE:HG22	2.04	0.40
7:1H:11:VAL:HA	7:1H:12:PRO:HD2	1.98	0.40
7:1H:117:PRO:HG3	7:1H:123:PHE:CD2	2.56	0.40
11:1P:141:ALA:HA	25:23:38:GLU:CG	2.51	0.40
16:1U:81:HIS:CE1	16:1U:85:LYS:HD2	2.57	0.40
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.22	0.40
28:16:16:CYS:SG	28:16:18:ARG:HD2	2.61	0.40
32:1a:31:G:H5'	32:1a:306:G:N2	2.36	0.40
32:1a:119:A:H4'	32:1a:120:A:C8	2.56	0.40
37:1f:2:ARG:HD2	37:1f:4:TYR:OH	2.22	0.40
43:1l:39:VAL:HB	43:1l:57:LYS:HB2	2.03	0.40
52:1u:18:TYR:CE1	52:1u:24:ARG:HB3	2.57	0.40
1:2A:265:A:N6	1:2A:428:A:H1'	2.37	0.40
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.56	0.40
1:2A:414:C:H1'	1:2A:1864:U:H1'	2.04	0.40
1:2A:757:U:H2'	1:2A:758:C:O4'	2.21	0.40
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.21	0.40
6:2G:43:LEU:HD12	6:2G:43:LEU:HA	1.77	0.40
7:2H:103:LEU:HG	7:2H:105:LEU:HD13	2.03	0.40
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.56	0.40
32:2a:25:C:H5'	32:2a:524:G:H1'	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:132:C:H42	32:2a:230:G:H1	1.70	0.40
32:2a:437:U:H5'	35:2d:155:LEU:HD21	2.03	0.40
32:2a:1004:A:N6	32:2a:1037:C:C4	2.90	0.40
32:2a:1442:G:HO2'	32:2a:1442(A):G:P	2.42	0.40
34:2c:21:ARG:HH21	34:2c:58:GLU:CD	2.29	0.40
41:2j:9:ARG:NH2	41:2j:97:GLU:HG3	2.36	0.40
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	2.03	0.40
51:2t:9:ASN:O	51:2t:13:LEU:HG	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/275 (99%)	259 (95%)	13 (5%)	1 (0%)	30	60
3	2D	273/275 (99%)	261 (96%)	12 (4%)	0	100	100
4	1E	202/204 (99%)	193 (96%)	8 (4%)	1 (0%)	24	55
4	2E	202/204 (99%)	192 (95%)	9 (4%)	1 (0%)	24	55
5	1F	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
5	2F	201/203 (99%)	192 (96%)	8 (4%)	1 (0%)	24	55
6	1G	179/181 (99%)	161 (90%)	16 (9%)	2 (1%)	11	36
6	2G	179/181 (99%)	164 (92%)	14 (8%)	1 (1%)	21	51
7	1H	172/174 (99%)	161 (94%)	11 (6%)	0	100	100
7	2H	171/174 (98%)	161 (94%)	10 (6%)	0	100	100
8	1I	145/147 (99%)	130 (90%)	12 (8%)	3 (2%)	5	20
8	2I	144/147 (98%)	131 (91%)	13 (9%)	0	100	100
9	1N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	2N	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
10	1O	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16	44
10	2O	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16	44
11	1P	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
11	2P	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
12	1Q	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
12	2Q	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
13	1R	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
13	2R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
14	1S	108/110 (98%)	102 (94%)	5 (5%)	1 (1%)	14	41
14	2S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
15	1T	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
15	2T	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
16	1U	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
16	2U	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
17	1V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12	38
17	2V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12	38
18	1W	110/112 (98%)	106 (96%)	4 (4%)	0	100	100
18	2W	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
19	1X	93/95 (98%)	90 (97%)	2 (2%)	1 (1%)	11	36
19	2X	93/95 (98%)	88 (95%)	4 (4%)	1 (1%)	11	36
20	1Y	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
20	2Y	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
21	1Z	201/203 (99%)	186 (92%)	15 (8%)	0	100	100
21	2Z	199/203 (98%)	184 (92%)	15 (8%)	0	100	100
22	10	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
22	20	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
23	11	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
23	21	95/97 (98%)	93 (98%)	1 (1%)	1 (1%)	11	36
24	12	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
24	22	68/70 (97%)	66 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	13	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
25	23	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
26	14	67/69 (97%)	55 (82%)	8 (12%)	4 (6%)	1	3
26	24	67/69 (97%)	52 (78%)	14 (21%)	1 (2%)	8	28
27	15	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
27	25	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
28	16	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
28	26	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
29	17	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
29	27	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
30	18	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
30	28	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/231 (99%)	201 (88%)	20 (9%)	8 (4%)	3	10
33	2b	229/231 (99%)	198 (86%)	24 (10%)	7 (3%)	3	12
34	1c	204/206 (99%)	185 (91%)	17 (8%)	2 (1%)	12	38
34	2c	204/206 (99%)	186 (91%)	16 (8%)	2 (1%)	12	38
35	1d	206/208 (99%)	188 (91%)	18 (9%)	0	100	100
35	2d	206/208 (99%)	188 (91%)	18 (9%)	0	100	100
36	1e	146/148 (99%)	138 (94%)	6 (4%)	2 (1%)	9	30
36	2e	146/148 (99%)	139 (95%)	7 (5%)	0	100	100
37	1f	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
37	2f	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
38	1g	153/155 (99%)	148 (97%)	5 (3%)	0	100	100
38	2g	153/155 (99%)	145 (95%)	7 (5%)	1 (1%)	18	47
39	1h	135/137 (98%)	130 (96%)	5 (4%)	0	100	100
39	2h	135/137 (98%)	129 (96%)	6 (4%)	0	100	100
40	1i	125/127 (98%)	112 (90%)	12 (10%)	1 (1%)	16	44
40	2i	124/127 (98%)	109 (88%)	13 (10%)	2 (2%)	7	27
41	1j	95/97 (98%)	82 (86%)	10 (10%)	3 (3%)	3	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	2j	94/97 (97%)	83 (88%)	9 (10%)	2 (2%)	5	20
42	1k	112/114 (98%)	100 (89%)	12 (11%)	0	100	100
42	2k	112/114 (98%)	100 (89%)	12 (11%)	0	100	100
43	1l	119/122 (98%)	114 (96%)	5 (4%)	0	100	100
43	2l	119/122 (98%)	115 (97%)	4 (3%)	0	100	100
44	1m	114/116 (98%)	102 (90%)	9 (8%)	3 (3%)	4	15
44	2m	112/116 (97%)	96 (86%)	13 (12%)	3 (3%)	4	15
45	1n	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
45	2n	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
46	1o	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
46	2o	86/88 (98%)	81 (94%)	3 (4%)	2 (2%)	5	18
47	1p	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
47	2p	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
48	1q	97/99 (98%)	89 (92%)	7 (7%)	1 (1%)	12	38
48	2q	97/99 (98%)	90 (93%)	6 (6%)	1 (1%)	12	38
49	1r	66/68 (97%)	60 (91%)	5 (8%)	1 (2%)	8	28
49	2r	66/68 (97%)	61 (92%)	4 (6%)	1 (2%)	8	28
50	1s	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	10	34
50	2s	81/83 (98%)	73 (90%)	7 (9%)	1 (1%)	10	34
51	1t	94/98 (96%)	85 (90%)	6 (6%)	3 (3%)	3	11
51	2t	96/98 (98%)	87 (91%)	5 (5%)	4 (4%)	2	7
52	1u	21/23 (91%)	19 (90%)	2 (10%)	0	100	100
52	2u	21/23 (91%)	19 (90%)	2 (10%)	0	100	100
55	1y	14/16 (88%)	13 (93%)	0	1 (7%)	1	2
55	2y	14/16 (88%)	13 (93%)	0	1 (7%)	1	2
All	All	11468/11680 (98%)	10719 (94%)	673 (6%)	76 (1%)	18	47

All (76) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	1I	11	ASN
14	1S	59	LYS
33	1b	17	PHE

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Mol	Chain	Res	Type
33	1b	21	ARG
33	1b	37	ASN
34	1c	108	ASN
36	1e	96	PRO
40	1i	127	LYS
41	1j	79	ARG
44	1m	67	GLU
48	1q	49	GLU
51	1t	95	ALA
4	2E	51	PHE
5	2F	21	ALA
6	2G	43	LEU
23	2I	3	LYS
33	2b	8	LYS
33	2b	17	PHE
33	2b	124	SER
34	2c	98	ASN
40	2i	44	VAL
40	2i	54	ASP
51	2t	95	ALA
3	1D	274	ARG
6	1G	43	LEU
8	1I	72	LEU
8	1I	73	GLU
19	1X	94	GLY
26	14	45	GLY
26	14	47	GLN
26	14	49	PHE
26	14	55	ARG
33	1b	95	GLN
33	1b	127	ILE
44	1m	12	ASN
49	1r	25	THR
55	1y	15	PRO
17	2V	79	VAL
19	2X	94	GLY
26	24	55	ARG
33	2b	10	LEU
33	2b	125	PRO
34	2c	61	ALA
41	2j	79	ARG
44	2m	67	GLU

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Mol	Chain	Res	Type
49	2r	25	THR
55	2y	15	PRO
4	1E	52	LEU
6	1G	51	ARG
17	1V	79	VAL
33	1b	125	PRO
44	1m	106	ASN
50	1s	7	LYS
10	2O	5	GLN
44	2m	106	ASN
51	2t	7	LYS
10	1O	5	GLN
33	1b	11	LEU
34	1c	98	ASN
51	1t	10	LEU
33	2b	20	GLU
33	2b	95	GLN
48	2q	49	GLU
50	2s	7	LYS
38	2g	6	ARG
44	2m	5	ALA
46	2o	88	ARG
51	2t	100	ILE
41	1j	77	PRO
51	1t	100	ILE
36	1e	97	GLY
46	2o	23	GLY
33	1b	124	SER
41	1j	31	GLY
51	2t	102	GLY
41	2j	37	PRO

5.3.2 Protein sidechains ⓘ

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	214/217 (99%)	193 (90%)	21 (10%)	7	25
3	2D	215/217 (99%)	195 (91%)	20 (9%)	8	27
4	1E	164/165 (99%)	142 (87%)	22 (13%)	4	13
4	2E	164/165 (99%)	145 (88%)	19 (12%)	5	18
5	1F	160/161 (99%)	145 (91%)	15 (9%)	8	27
5	2F	159/161 (99%)	146 (92%)	13 (8%)	10	33
6	1G	144/155 (93%)	129 (90%)	15 (10%)	7	22
6	2G	142/155 (92%)	129 (91%)	13 (9%)	8	27
7	1H	144/145 (99%)	128 (89%)	16 (11%)	6	20
7	2H	143/145 (99%)	128 (90%)	15 (10%)	6	22
8	1I	111/123 (90%)	100 (90%)	11 (10%)	7	24
8	2I	108/123 (88%)	90 (83%)	18 (17%)	2	8
9	1N	119/119 (100%)	105 (88%)	14 (12%)	5	17
9	2N	118/119 (99%)	103 (87%)	15 (13%)	4	15
10	1O	100/100 (100%)	92 (92%)	8 (8%)	11	34
10	2O	100/100 (100%)	96 (96%)	4 (4%)	28	63
11	1P	115/116 (99%)	106 (92%)	9 (8%)	11	35
11	2P	115/116 (99%)	110 (96%)	5 (4%)	26	60
12	1Q	111/111 (100%)	98 (88%)	13 (12%)	5	18
12	2Q	111/111 (100%)	102 (92%)	9 (8%)	11	33
13	1R	101/101 (100%)	91 (90%)	10 (10%)	7	24
13	2R	101/101 (100%)	91 (90%)	10 (10%)	7	24
14	1S	87/87 (100%)	81 (93%)	6 (7%)	14	41
14	2S	85/87 (98%)	80 (94%)	5 (6%)	18	48
15	1T	115/115 (100%)	110 (96%)	5 (4%)	26	60
15	2T	113/115 (98%)	105 (93%)	8 (7%)	13	39
16	1U	93/93 (100%)	86 (92%)	7 (8%)	12	37
16	2U	93/93 (100%)	89 (96%)	4 (4%)	26	60
17	1V	81/82 (99%)	69 (85%)	12 (15%)	3	10
17	2V	80/82 (98%)	72 (90%)	8 (10%)	7	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	1W	90/91 (99%)	84 (93%)	6 (7%)	15	42
18	2W	90/91 (99%)	85 (94%)	5 (6%)	19	50
19	1X	77/77 (100%)	74 (96%)	3 (4%)	28	64
19	2X	77/77 (100%)	72 (94%)	5 (6%)	15	43
20	1Y	86/88 (98%)	81 (94%)	5 (6%)	18	49
20	2Y	86/88 (98%)	81 (94%)	5 (6%)	18	49
21	1Z	169/176 (96%)	150 (89%)	19 (11%)	6	19
21	2Z	165/176 (94%)	152 (92%)	13 (8%)	11	35
22	10	61/62 (98%)	56 (92%)	5 (8%)	10	33
22	20	61/62 (98%)	59 (97%)	2 (3%)	33	69
23	11	79/82 (96%)	73 (92%)	6 (8%)	12	36
23	21	81/82 (99%)	74 (91%)	7 (9%)	10	31
24	12	65/66 (98%)	60 (92%)	5 (8%)	12	36
24	22	66/66 (100%)	61 (92%)	5 (8%)	12	36
25	13	51/51 (100%)	46 (90%)	5 (10%)	7	25
25	23	50/51 (98%)	45 (90%)	5 (10%)	7	24
26	14	58/62 (94%)	51 (88%)	7 (12%)	5	16
26	24	54/62 (87%)	48 (89%)	6 (11%)	6	20
27	15	51/51 (100%)	47 (92%)	4 (8%)	11	35
27	25	50/51 (98%)	48 (96%)	2 (4%)	28	63
28	16	51/51 (100%)	48 (94%)	3 (6%)	18	48
28	26	50/51 (98%)	44 (88%)	6 (12%)	5	17
29	17	41/41 (100%)	39 (95%)	2 (5%)	22	55
29	27	41/41 (100%)	40 (98%)	1 (2%)	43	77
30	18	54/54 (100%)	51 (94%)	3 (6%)	19	50
30	28	54/54 (100%)	47 (87%)	7 (13%)	4	14
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	73
31	29	34/34 (100%)	34 (100%)	0	100	100
33	1b	191/199 (96%)	164 (86%)	27 (14%)	3	12
33	2b	187/199 (94%)	167 (89%)	20 (11%)	6	21
34	1c	144/160 (90%)	134 (93%)	10 (7%)	14	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	2c	140/160 (88%)	130 (93%)	10 (7%)	13	39
35	1d	171/180 (95%)	160 (94%)	11 (6%)	16	44
35	2d	172/180 (96%)	161 (94%)	11 (6%)	16	44
36	1e	114/114 (100%)	105 (92%)	9 (8%)	11	35
36	2e	114/114 (100%)	106 (93%)	8 (7%)	14	40
37	1f	85/90 (94%)	80 (94%)	5 (6%)	18	48
37	2f	85/90 (94%)	74 (87%)	11 (13%)	4	14
38	1g	120/126 (95%)	106 (88%)	14 (12%)	5	18
38	2g	119/126 (94%)	111 (93%)	8 (7%)	15	42
39	1h	116/118 (98%)	110 (95%)	6 (5%)	21	53
39	2h	114/118 (97%)	106 (93%)	8 (7%)	14	40
40	1i	91/98 (93%)	79 (87%)	12 (13%)	4	14
40	2i	88/98 (90%)	74 (84%)	14 (16%)	2	9
41	1j	68/87 (78%)	60 (88%)	8 (12%)	5	17
41	2j	68/87 (78%)	60 (88%)	8 (12%)	5	17
42	1k	83/86 (96%)	75 (90%)	8 (10%)	8	26
42	2k	83/86 (96%)	75 (90%)	8 (10%)	8	26
43	1l	96/102 (94%)	89 (93%)	7 (7%)	13	38
43	2l	96/102 (94%)	88 (92%)	8 (8%)	10	32
44	1m	90/94 (96%)	84 (93%)	6 (7%)	15	42
44	2m	87/94 (93%)	79 (91%)	8 (9%)	8	27
45	1n	49/49 (100%)	44 (90%)	5 (10%)	7	23
45	2n	49/49 (100%)	46 (94%)	3 (6%)	17	46
46	1o	78/79 (99%)	74 (95%)	4 (5%)	21	54
46	2o	78/79 (99%)	72 (92%)	6 (8%)	12	36
47	1p	69/71 (97%)	59 (86%)	10 (14%)	3	11
47	2p	68/71 (96%)	57 (84%)	11 (16%)	2	8
48	1q	94/94 (100%)	91 (97%)	3 (3%)	34	70
48	2q	94/94 (100%)	89 (95%)	5 (5%)	20	52
49	1r	59/59 (100%)	56 (95%)	3 (5%)	21	54
49	2r	59/59 (100%)	56 (95%)	3 (5%)	21	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	1s	68/72 (94%)	59 (87%)	9 (13%)	4	14
50	2s	67/72 (93%)	62 (92%)	5 (8%)	12	37
51	1t	71/76 (93%)	66 (93%)	5 (7%)	14	40
51	2t	70/76 (92%)	64 (91%)	6 (9%)	10	31
52	1u	18/18 (100%)	17 (94%)	1 (6%)	19	50
52	2u	18/18 (100%)	18 (100%)	0	100	100
55	1y	16/16 (100%)	14 (88%)	2 (12%)	4	15
55	2y	16/16 (100%)	15 (94%)	1 (6%)	16	45
All	All	9395/9728 (97%)	8575 (91%)	820 (9%)	9	30

All (820) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	13	ARG
3	1D	37	LEU
3	1D	61	LEU
3	1D	94	LEU
3	1D	103	ARG
3	1D	111	LEU
3	1D	113	VAL
3	1D	138	VAL
3	1D	141	VAL
3	1D	155	LEU
3	1D	162	SER
3	1D	173	VAL
3	1D	193	VAL
3	1D	200	ASP
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	253	GLN
4	1E	9	VAL
4	1E	21	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	45	THR

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Mol	Chain	Res	Type
4	1E	47	VAL
4	1E	49	LEU
4	1E	72	VAL
4	1E	75	VAL
4	1E	77	ILE
4	1E	78	LEU
4	1E	89	ASP
4	1E	101	ARG
4	1E	116	VAL
4	1E	119	ARG
4	1E	127	ASP
4	1E	144	ARG
4	1E	154	LYS
4	1E	175	VAL
4	1E	178	GLU
4	1E	181	LEU
4	1E	184	VAL
5	1F	18	ARG
5	1F	33	LEU
5	1F	53	THR
5	1F	60	SER
5	1F	74	ARG
5	1F	88	VAL
5	1F	110	LEU
5	1F	126	VAL
5	1F	132	VAL
5	1F	170	LEU
5	1F	175	THR
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU
5	1F	201	VAL
6	1G	5	VAL
6	1G	28	VAL
6	1G	31	VAL
6	1G	43	LEU
6	1G	45	GLU
6	1G	52	ILE
6	1G	53	LEU
6	1G	79	ASN
6	1G	82	LEU
6	1G	116	ASP

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Mol	Chain	Res	Type
6	1G	133	LEU
6	1G	136	ARG
6	1G	159	VAL
6	1G	167	GLU
6	1G	175	LEU
7	1H	2	SER
7	1H	13	LYS
7	1H	15	VAL
7	1H	23	ARG
7	1H	32	GLU
7	1H	43	VAL
7	1H	45	VAL
7	1H	47	GLU
7	1H	49	VAL
7	1H	71	LEU
7	1H	85	LYS
7	1H	98	LEU
7	1H	104	GLU
7	1H	105	LEU
7	1H	107	VAL
7	1H	172	LYS
8	1I	9	LEU
8	1I	12	LEU
8	1I	38	LEU
8	1I	44	LEU
8	1I	75	LEU
8	1I	92	VAL
8	1I	101	LEU
8	1I	103	ARG
8	1I	109	ILE
8	1I	140	LEU
8	1I	144	VAL
9	1N	1	MET
9	1N	5	VAL
9	1N	8	GLN
9	1N	15	LEU
9	1N	33	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	71	ILE
9	1N	73	THR
9	1N	83	LYS

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Mol	Chain	Res	Type
9	1N	87	LEU
9	1N	99	LEU
9	1N	133	GLN
9	1N	140	VAL
10	1O	8	LEU
10	1O	10	VAL
10	1O	20	MET
10	1O	24	VAL
10	1O	26	LYS
10	1O	69	ILE
10	1O	80	ASP
10	1O	94	ARG
11	1P	2	LYS
11	1P	59	LEU
11	1P	76	LYS
11	1P	83	VAL
11	1P	112	LEU
11	1P	125	VAL
11	1P	147	LEU
11	1P	148	LEU
11	1P	149	GLU
12	1Q	2	LEU
12	1Q	7	MET
12	1Q	12	GLN
12	1Q	18	LYS
12	1Q	22	LYS
12	1Q	35	VAL
12	1Q	42	ILE
12	1Q	55	VAL
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	98	LYS
12	1Q	109	VAL
12	1Q	110	THR
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	75	LEU

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Mol	Chain	Res	Type
13	1R	100	LEU
13	1R	111	LEU
14	1S	14	VAL
14	1S	17	ARG
14	1S	46	VAL
14	1S	49	VAL
14	1S	59	LYS
14	1S	75	GLU
15	1T	6	LEU
15	1T	28	VAL
15	1T	74	ARG
15	1T	78	LEU
15	1T	89	VAL
16	1U	5	LYS
16	1U	8	VAL
16	1U	52	ARG
16	1U	74	LEU
16	1U	84	LYS
16	1U	104	GLN
16	1U	117	GLN
17	1V	1	MET
17	1V	7	THR
17	1V	21	ARG
17	1V	35	LEU
17	1V	44	LYS
17	1V	46	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	79	VAL
17	1V	82	ARG
17	1V	95	LEU
17	1V	100	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	67	ASP
18	1W	100	THR
18	1W	107	LEU
19	1X	35	THR
19	1X	66	LEU
19	1X	68	ARG
20	1Y	43	ASN

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Mol	Chain	Res	Type
20	1Y	47	LYS
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	107	ASP
21	1Z	11	GLU
21	1Z	18	LEU
21	1Z	20	ARG
21	1Z	28	MET
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	61	LEU
21	1Z	76	LEU
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	103	ARG
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	162	GLU
21	1Z	185	GLU
21	1Z	193	GLU
21	1Z	202	GLU
21	1Z	203	GLU
22	10	11	ARG
22	10	14	ARG
22	10	38	VAL
22	10	43	THR
22	10	59	LEU
23	11	21	ARG
23	11	30	VAL
23	11	76	ARG
23	11	81	LYS
23	11	83	GLU
23	11	89	GLU
24	12	2	LYS
24	12	3	LEU
24	12	32	LEU
24	12	53	LEU
24	12	70	GLN
25	13	6	VAL
25	13	8	LEU
25	13	23	LEU

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Mol	Chain	Res	Type
25	13	54	VAL
25	13	56	VAL
26	14	13	ARG
26	14	27	THR
26	14	49	PHE
26	14	50	VAL
26	14	59	PHE
26	14	60	GLN
26	14	69	LYS
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
27	15	58	LEU
28	16	5	VAL
28	16	14	THR
28	16	48	VAL
29	17	24	THR
29	17	43	THR
30	18	14	VAL
30	18	26	LYS
30	18	32	LEU
31	19	35	ARG
33	1b	9	GLU
33	1b	15	VAL
33	1b	17	PHE
33	1b	35	GLU
33	1b	39	ILE
33	1b	44	LEU
33	1b	45	GLN
33	1b	63	MET
33	1b	71	VAL
33	1b	73	THR
33	1b	75	LYS
33	1b	76	GLN
33	1b	82	ARG
33	1b	111	ARG
33	1b	112	VAL
33	1b	126	GLU
33	1b	127	ILE
33	1b	136	VAL
33	1b	144	ARG
33	1b	156	LYS

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Mol	Chain	Res	Type
33	1b	158	LEU
33	1b	160	ASP
33	1b	172	ILE
33	1b	178	ARG
33	1b	185	ILE
33	1b	221	LEU
33	1b	226	ARG
34	1c	3	ASN
34	1c	64	VAL
34	1c	70	VAL
34	1c	89	GLU
34	1c	104	GLN
34	1c	105	GLU
34	1c	132	ARG
34	1c	161	GLU
34	1c	166	GLU
34	1c	192	THR
35	1d	5	ILE
35	1d	31	CYS
35	1d	85	LYS
35	1d	86	LYS
35	1d	108	LEU
35	1d	122	ARG
35	1d	127	THR
35	1d	135	LEU
35	1d	158	ILE
35	1d	173	TRP
35	1d	188	LEU
36	1e	10	MET
36	1e	20	GLN
36	1e	34	VAL
36	1e	41	VAL
36	1e	68	GLU
36	1e	69	VAL
36	1e	75	THR
36	1e	91	LEU
36	1e	150	ARG
37	1f	40	VAL
37	1f	46	ARG
37	1f	63	TYR
37	1f	70	ASP
37	1f	72	VAL

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Mol	Chain	Res	Type
38	1g	6	ARG
38	1g	8	GLU
38	1g	9	VAL
38	1g	10	ARG
38	1g	13	GLN
38	1g	15	ASP
38	1g	42	ILE
38	1g	56	GLN
38	1g	75	VAL
38	1g	104	LEU
38	1g	113	GLU
38	1g	136	LYS
38	1g	143	ARG
38	1g	155	ARG
39	1h	26	VAL
39	1h	39	LEU
39	1h	51	VAL
39	1h	52	ASP
39	1h	63	LEU
39	1h	137	VAL
40	1i	14	VAL
40	1i	25	LYS
40	1i	51	ARG
40	1i	56	LEU
40	1i	65	VAL
40	1i	66	ARG
40	1i	81	ILE
40	1i	86	VAL
40	1i	87	GLN
40	1i	103	THR
40	1i	108	VAL
40	1i	125	TYR
41	1j	22	LYS
41	1j	34	VAL
41	1j	49	VAL
41	1j	55	LYS
41	1j	72	VAL
41	1j	92	THR
41	1j	94	VAL
41	1j	100	THR
42	1k	14	VAL
42	1k	40	ILE

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Mol	Chain	Res	Type
42	1k	81	ASP
42	1k	84	VAL
42	1k	109	VAL
42	1k	112	THR
42	1k	114	VAL
42	1k	124	LYS
43	1l	12	ARG
43	1l	27	LEU
43	1l	33	ARG
43	1l	47	LYS
43	1l	55	VAL
43	1l	67	THR
43	1l	83	VAL
44	1m	8	GLU
44	1m	11	ARG
44	1m	17	VAL
44	1m	56	LEU
44	1m	63	THR
44	1m	102	ARG
45	1n	3	ARG
45	1n	18	VAL
45	1n	22	THR
45	1n	33	VAL
45	1n	44	LEU
46	1o	3	ILE
46	1o	26	GLU
46	1o	39	LEU
46	1o	68	ARG
47	1p	2	VAL
47	1p	8	ARG
47	1p	20	VAL
47	1p	42	ARG
47	1p	45	THR
47	1p	60	LEU
47	1p	62	VAL
47	1p	67	THR
47	1p	69	THR
47	1p	79	VAL
48	1q	16	GLN
48	1q	87	LYS
48	1q	96	GLU
49	1r	31	LEU

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Mol	Chain	Res	Type
49	1r	65	ILE
49	1r	76	LEU
50	1s	3	ARG
50	1s	4	SER
50	1s	5	LEU
50	1s	19	VAL
50	1s	28	LYS
50	1s	37	ARG
50	1s	40	ILE
50	1s	41	VAL
50	1s	65	ASN
51	1t	10	LEU
51	1t	48	LYS
51	1t	58	LYS
51	1t	62	LEU
51	1t	100	ILE
52	1u	9	ARG
55	1y	2	ARG
55	1y	4	ARG
3	2D	3	VAL
3	2D	37	LEU
3	2D	61	LEU
3	2D	94	LEU
3	2D	103	ARG
3	2D	109	ASP
3	2D	111	LEU
3	2D	113	VAL
3	2D	141	VAL
3	2D	155	LEU
3	2D	193	VAL
3	2D	200	ASP
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	253	GLN
3	2D	274	ARG
3	2D	276	LYS
4	2E	9	VAL
4	2E	21	VAL
4	2E	24	THR

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Mol	Chain	Res	Type
4	2E	33	VAL
4	2E	34	VAL
4	2E	73	GLU
4	2E	75	VAL
4	2E	78	LEU
4	2E	97	LYS
4	2E	101	ARG
4	2E	116	VAL
4	2E	144	ARG
4	2E	154	LYS
4	2E	167	VAL
4	2E	170	LEU
4	2E	175	VAL
4	2E	181	LEU
4	2E	184	VAL
4	2E	202	LYS
5	2F	33	LEU
5	2F	57	VAL
5	2F	74	ARG
5	2F	88	VAL
5	2F	112	MET
5	2F	126	VAL
5	2F	132	VAL
5	2F	158	THR
5	2F	170	LEU
5	2F	175	THR
5	2F	183	VAL
5	2F	192	LEU
5	2F	201	VAL
6	2G	3	LEU
6	2G	28	VAL
6	2G	31	VAL
6	2G	43	LEU
6	2G	47	LYS
6	2G	49	ASP
6	2G	55	LYS
6	2G	111	LEU
6	2G	116	ASP
6	2G	139	LEU
6	2G	159	VAL
6	2G	168	GLU
6	2G	175	LEU

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Mol	Chain	Res	Type
7	2H	6	ARG
7	2H	13	LYS
7	2H	15	VAL
7	2H	34	GLU
7	2H	43	VAL
7	2H	49	VAL
7	2H	63	SER
7	2H	68	THR
7	2H	84	SER
7	2H	85	LYS
7	2H	95	ARG
7	2H	98	LEU
7	2H	105	LEU
7	2H	122	THR
7	2H	139	GLN
8	2I	5	LEU
8	2I	15	VAL
8	2I	38	LEU
8	2I	43	ASN
8	2I	44	LEU
8	2I	48	GLU
8	2I	50	ARG
8	2I	66	GLU
8	2I	75	LEU
8	2I	85	GLU
8	2I	92	VAL
8	2I	101	LEU
8	2I	116	LEU
8	2I	123	LEU
8	2I	127	VAL
8	2I	129	THR
8	2I	140	LEU
8	2I	144	VAL
9	2N	5	VAL
9	2N	28	THR
9	2N	34	LEU
9	2N	58	ASP
9	2N	62	VAL
9	2N	67	LEU
9	2N	71	ILE
9	2N	74	ARG
9	2N	87	LEU

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Mol	Chain	Res	Type
9	2N	97	ARG
9	2N	99	LEU
9	2N	119	ARG
9	2N	131	GLN
9	2N	133	GLN
9	2N	140	VAL
10	2O	10	VAL
10	2O	24	VAL
10	2O	53	LYS
10	2O	108	GLU
11	2P	3	LEU
11	2P	76	LYS
11	2P	112	LEU
11	2P	125	VAL
11	2P	148	LEU
12	2Q	2	LEU
12	2Q	7	MET
12	2Q	16	ARG
12	2Q	75	THR
12	2Q	85	LYS
12	2Q	98	LYS
12	2Q	106	VAL
12	2Q	109	VAL
12	2Q	112	GLU
13	2R	18	LEU
13	2R	36	THR
13	2R	44	LEU
13	2R	65	LEU
13	2R	67	LEU
13	2R	75	LEU
13	2R	79	LEU
13	2R	96	ARG
13	2R	100	LEU
13	2R	111	LEU
14	2S	5	THR
14	2S	14	VAL
14	2S	23	ARG
14	2S	50	SER
14	2S	75	GLU
15	2T	13	ARG
15	2T	16	ARG
15	2T	23	ARG

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Mol	Chain	Res	Type
15	2T	28	VAL
15	2T	49	VAL
15	2T	89	VAL
15	2T	96	ARG
15	2T	108	ARG
16	2U	31	SER
16	2U	60	LEU
16	2U	74	LEU
16	2U	112	ARG
17	2V	18	LEU
17	2V	35	LEU
17	2V	46	VAL
17	2V	53	GLU
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	100	ARG
18	2W	17	VAL
18	2W	23	LEU
18	2W	71	VAL
18	2W	100	THR
18	2W	107	LEU
19	2X	35	THR
19	2X	57	LEU
19	2X	66	LEU
19	2X	81	VAL
19	2X	83	VAL
20	2Y	8	LYS
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	90	LEU
20	2Y	107	ASP
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	53	ILE
21	2Z	72	ARG
21	2Z	121	HIS
21	2Z	123	ASP
21	2Z	126	VAL
21	2Z	136	PHE
21	2Z	150	LEU
21	2Z	155	LEU

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Mol	Chain	Res	Type
21	2Z	170	THR
21	2Z	171	ILE
21	2Z	182	LYS
22	20	14	ARG
22	20	39	ARG
23	21	2	SER
23	21	4	VAL
23	21	30	VAL
23	21	35	THR
23	21	75	GLU
23	21	81	LYS
23	21	85	LEU
24	22	3	LEU
24	22	26	ARG
24	22	32	LEU
24	22	40	SER
24	22	53	LEU
25	23	6	VAL
25	23	31	LEU
25	23	54	VAL
25	23	55	ARG
25	23	56	VAL
26	24	27	THR
26	24	38	LYS
26	24	53	GLU
26	24	56	VAL
26	24	61	ARG
26	24	63	TYR
27	25	6	VAL
27	25	58	LEU
28	26	5	VAL
28	26	6	ARG
28	26	14	THR
28	26	19	ARG
28	26	48	VAL
28	26	52	VAL
29	27	43	THR
30	28	14	VAL
30	28	23	VAL
30	28	26	LYS
30	28	29	LYS
30	28	34	TRP

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Mol	Chain	Res	Type
30	28	46	ARG
30	28	56	GLU
33	2b	10	LEU
33	2b	16	HIS
33	2b	44	LEU
33	2b	55	PHE
33	2b	58	ILE
33	2b	67	THR
33	2b	71	VAL
33	2b	81	VAL
33	2b	87	ARG
33	2b	93	VAL
33	2b	128	GLU
33	2b	135	GLN
33	2b	136	VAL
33	2b	154	LEU
33	2b	158	LEU
33	2b	164	VAL
33	2b	187	LEU
33	2b	191	ASP
33	2b	200	ILE
33	2b	230	VAL
34	2c	30	ARG
34	2c	32	LEU
34	2c	45	LYS
34	2c	52	LEU
34	2c	70	VAL
34	2c	102	ASN
34	2c	152	ILE
34	2c	166	GLU
34	2c	192	THR
34	2c	195	VAL
35	2d	5	ILE
35	2d	8	VAL
35	2d	13	ARG
35	2d	49	ARG
35	2d	76	ARG
35	2d	96	LEU
35	2d	108	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	158	ILE

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Mol	Chain	Res	Type
35	2d	194	LEU
36	2e	31	LEU
36	2e	34	VAL
36	2e	41	VAL
36	2e	68	GLU
36	2e	69	VAL
36	2e	72	GLN
36	2e	75	THR
36	2e	91	LEU
37	2f	10	LEU
37	2f	17	SER
37	2f	22	GLU
37	2f	28	ARG
37	2f	40	VAL
37	2f	46	ARG
37	2f	63	TYR
37	2f	72	VAL
37	2f	75	LEU
37	2f	81	ILE
37	2f	95	GLU
38	2g	6	ARG
38	2g	53	LYS
38	2g	75	VAL
38	2g	104	LEU
38	2g	113	GLU
38	2g	115	ARG
38	2g	138	LYS
38	2g	155	ARG
39	2h	26	VAL
39	2h	51	VAL
39	2h	63	LEU
39	2h	91	ARG
39	2h	97	VAL
39	2h	98	LYS
39	2h	125	ARG
39	2h	137	VAL
40	2i	7	THR
40	2i	25	LYS
40	2i	27	THR
40	2i	42	ARG
40	2i	50	LEU
40	2i	53	VAL

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Mol	Chain	Res	Type
40	2i	64	THR
40	2i	65	VAL
40	2i	86	VAL
40	2i	87	GLN
40	2i	88	TYR
40	2i	102	LEU
40	2i	103	THR
40	2i	125	TYR
41	2j	29	ARG
41	2j	34	VAL
41	2j	49	VAL
41	2j	57	LYS
41	2j	69	ASN
41	2j	74	ILE
41	2j	92	THR
41	2j	94	VAL
42	2k	14	VAL
42	2k	31	THR
42	2k	84	VAL
42	2k	87	THR
42	2k	109	VAL
42	2k	112	THR
42	2k	114	VAL
42	2k	116	HIS
43	2l	27	LEU
43	2l	28	LYS
43	2l	52	LEU
43	2l	55	VAL
43	2l	67	THR
43	2l	83	VAL
43	2l	97	ARG
43	2l	117	ARG
44	2m	4	ILE
44	2m	8	GLU
44	2m	17	VAL
44	2m	27	LYS
44	2m	65	LYS
44	2m	70	LEU
44	2m	88	ARG
44	2m	103	THR
45	2n	18	VAL
45	2n	22	THR

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Mol	Chain	Res	Type
45	2n	44	LEU
46	2o	5	LYS
46	2o	38	ARG
46	2o	39	LEU
46	2o	76	GLU
46	2o	83	GLU
46	2o	88	ARG
47	2p	2	VAL
47	2p	20	VAL
47	2p	21	VAL
47	2p	42	ARG
47	2p	44	THR
47	2p	45	THR
47	2p	54	GLU
47	2p	62	VAL
47	2p	67	THR
47	2p	69	THR
47	2p	72	ARG
48	2q	6	LEU
48	2q	16	GLN
48	2q	57	VAL
48	2q	74	LEU
48	2q	96	GLU
49	2r	31	LEU
49	2r	65	ILE
49	2r	76	LEU
50	2s	5	LEU
50	2s	41	VAL
50	2s	64	GLU
50	2s	77	THR
50	2s	81	ARG
51	2t	24	LEU
51	2t	41	ILE
51	2t	45	GLN
51	2t	62	LEU
51	2t	84	LEU
51	2t	100	ILE
55	2y	4	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (139) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	201	HIS
3	1D	253	GLN
4	1E	48	GLN
4	1E	55	ASN
5	1F	8	GLN
5	1F	75	HIS
5	1F	203	GLN
6	1G	40	ASN
6	1G	108	ASN
6	1G	132	ASN
8	1I	104	GLN
9	1N	133	GLN
12	1Q	89	ASN
13	1R	13	HIS
13	1R	24	GLN
13	1R	71	GLN
15	1T	58	ASN
18	1W	60	ASN
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	43	ASN
20	1Y	92	ASN
21	1Z	34	ASN
21	1Z	54	HIS
21	1Z	73	GLN
24	12	70	GLN
25	13	32	GLN
26	14	60	GLN
28	16	20	ASN
28	16	49	HIS
30	18	35	GLN
33	1b	78	GLN
33	1b	140	HIS
34	1c	6	HIS
34	1c	104	GLN
34	1c	118	GLN
34	1c	123	GLN
35	1d	77	ASN
35	1d	123	HIS
36	1e	20	GLN
37	1f	57	GLN
37	1f	73	ASN
37	1f	100	ASN

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Mol	Chain	Res	Type
38	1g	28	ASN
38	1g	56	GLN
38	1g	106	GLN
38	1g	110	GLN
39	1h	81	HIS
40	1i	34	ASN
40	1i	73	GLN
40	1i	87	GLN
40	1i	117	HIS
41	1j	56	HIS
41	1j	84	GLN
43	1l	80	HIS
43	1l	99	HIS
46	1o	28	GLN
48	1q	16	GLN
50	1s	23	ASN
50	1s	69	HIS
50	1s	83	HIS
51	1t	75	ASN
3	2D	126	GLN
3	2D	143	HIS
3	2D	253	GLN
4	2E	180	ASN
5	2F	69	HIS
5	2F	203	GLN
6	2G	40	ASN
6	2G	79	ASN
6	2G	130	ASN
8	2I	133	HIS
10	2O	90	GLN
12	2Q	12	GLN
12	2Q	89	ASN
12	2Q	141	GLN
13	2R	13	HIS
17	2V	64	HIS
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	6	HIS
21	2Z	32	HIS
21	2Z	34	ASN
21	2Z	73	GLN

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Mol	Chain	Res	Type
21	2Z	75	ASN
21	2Z	121	HIS
21	2Z	151	HIS
22	20	70	GLN
24	22	46	GLN
24	22	56	GLN
25	23	32	GLN
26	24	20	ASN
26	24	46	GLN
28	26	20	ASN
30	28	35	GLN
33	2b	19	HIS
33	2b	76	GLN
33	2b	135	GLN
33	2b	212	GLN
34	2c	6	HIS
34	2c	102	ASN
34	2c	104	GLN
34	2c	136	GLN
34	2c	176	HIS
35	2d	77	ASN
35	2d	116	GLN
35	2d	119	GLN
35	2d	123	HIS
35	2d	160	GLN
35	2d	161	ASN
35	2d	201	GLN
36	2e	78	HIS
36	2e	141	GLN
37	2f	73	ASN
37	2f	100	ASN
38	2g	11	GLN
38	2g	37	ASN
38	2g	86	GLN
38	2g	106	GLN
39	2h	81	HIS
40	2i	3	GLN
40	2i	31	GLN
40	2i	34	ASN
40	2i	73	GLN
40	2i	117	HIS
41	2j	13	HIS

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Mol	Chain	Res	Type
41	2j	69	ASN
42	2k	22	HIS
42	2k	38	ASN
42	2k	93	GLN
43	2l	80	HIS
43	2l	99	HIS
44	2m	62	ASN
46	2o	28	GLN
50	2s	23	ASN
50	2s	47	HIS
50	2s	69	HIS
50	2s	83	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	409 (14%)	38 (1%)
1	2A	2858/2915 (98%)	410 (14%)	33 (1%)
2	1B	119/120 (99%)	5 (4%)	0
2	2B	118/120 (98%)	6 (5%)	0
32	1a	1497/1520 (98%)	209 (13%)	0
32	2a	1501/1520 (98%)	222 (14%)	0
53	1v	2/3 (66%)	0	0
53	2v	2/3 (66%)	0	0
54	1x	75/76 (98%)	20 (26%)	0
54	2x	75/76 (98%)	10 (13%)	0
All	All	9112/9268 (98%)	1291 (14%)	71 (0%)

All (1291) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	34	C
1	1A	45	C
1	1A	70	A
1	1A	73	A
1	1A	74	G
1	1A	116	A
1	1A	117	A
1	1A	118	U
1	1A	162	G

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Mol	Chain	Res	Type
1	1A	185	A
1	1A	186	A
1	1A	188	A
1	1A	194	G
1	1A	202	A
1	1A	204	G
1	1A	205	A
1	1A	210	A
1	1A	211	A
1	1A	214	A
1	1A	218	A
1	1A	237	G
1	1A	269	G
1	1A	271	U
1	1A	272	U
1	1A	273	G
1	1A	274	U
1	1A	279	G
1	1A	288	U
1	1A	289	G
1	1A	303	C
1	1A	335	A
1	1A	348	A
1	1A	351	G
1	1A	354	A
1	1A	366	G
1	1A	376	G
1	1A	381	A
1	1A	386	U
1	1A	387	G
1	1A	413	G
1	1A	423	G
1	1A	432	U
1	1A	438	G
1	1A	439	A
1	1A	448	U
1	1A	455	A
1	1A	474	U
1	1A	482	C
1	1A	483	A
1	1A	505	A
1	1A	507	G

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Mol	Chain	Res	Type
1	1A	530	A
1	1A	534	C
1	1A	535	C
1	1A	543	G
1	1A	555	G
1	1A	556	C
1	1A	557	A
1	1A	558	G
1	1A	569	G
1	1A	573	G
1	1A	574	G
1	1A	586	G
1	1A	596	G
1	1A	598	A
1	1A	609	A
1	1A	615	G
1	1A	618	C
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	633	G
1	1A	639	G
1	1A	641	G
1	1A	652	A
1	1A	662	A
1	1A	670	C
1	1A	673	G
1	1A	693	G
1	1A	694	G
1	1A	697	C
1	1A	698	G
1	1A	715	G
1	1A	716	G
1	1A	733	G
1	1A	777	C
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	831	A
1	1A	832	G
1	1A	839	G
1	1A	852	G

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Mol	Chain	Res	Type
1	1A	859	C
1	1A	874	U
1	1A	875	U
1	1A	906	G
1	1A	927	G
1	1A	933	C
1	1A	934	A
1	1A	935	C
1	1A	936	C
1	1A	937	A
1	1A	942	A
1	1A	945	A
1	1A	946	A
1	1A	947	A
1	1A	956	A
1	1A	977	G
1	1A	983	G
1	1A	990	A
1	1A	991	G
1	1A	1003	U
1	1A	1004	A
1	1A	1006	C
1	1A	1019	G
1	1A	1020	C
1	1A	1021	G
1	1A	1029	A
1	1A	1042	A
1	1A	1051	C
1	1A	1058	U
1	1A	1059	C
1	1A	1068	G
1	1A	1071	G
1	1A	1072	U
1	1A	1079	U
1	1A	1085	G
1	1A	1088	G
1	1A	1090	G
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A
1	1A	1100	A
1	1A	1106	U

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Mol	Chain	Res	Type
1	1A	1107	U
1	1A	1108	G
1	1A	1109	G
1	1A	1110	C
1	1A	1111	U
1	1A	1112	U
1	1A	1113	A
1	1A	1114	G
1	1A	1116	A
1	1A	1117	G
1	1A	1119	A
1	1A	1122	C
1	1A	1123	A
1	1A	1124	U
1	1A	1129	U
1	1A	1130	A
1	1A	1131	A
1	1A	1134	A
1	1A	1136	U
1	1A	1137	G
1	1A	1139	G
1	1A	1141	A
1	1A	1142	A
1	1A	1143	U
1	1A	1155	C
1	1A	1156	G
1	1A	1158	G
1	1A	1162	C
1	1A	1175	A
1	1A	1176	U
1	1A	1180	C
1	1A	1181	G
1	1A	1217	G
1	1A	1218	G
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1222	A
1	1A	1223	C
1	1A	1256	U
1	1A	1265	A
1	1A	1287	A

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Mol	Chain	Res	Type
1	1A	1299	A
1	1A	1302	G
1	1A	1317	G
1	1A	1318	A
1	1A	1319	U
1	1A	1346	U
1	1A	1347	A
1	1A	1349	G
1	1A	1354	A
1	1A	1398	U
1	1A	1405	A
1	1A	1406	A
1	1A	1411	A
1	1A	1416	C
1	1A	1430	A
1	1A	1431	G
1	1A	1432	C
1	1A	1462	G
1	1A	1463	C
1	1A	1466	U
1	1A	1467	G
1	1A	1474	C
1	1A	1491	A
1	1A	1497	G
1	1A	1500	A
1	1A	1514	C
1	1A	1518	A
1	1A	1529	G
1	1A	1539	C
1	1A	1543	U
1	1A	1554	A
1	1A	1555	C
1	1A	1578	C
1	1A	1589	A
1	1A	1590	C
1	1A	1594	C
1	1A	1605	A
1	1A	1613	A
1	1A	1616	A
1	1A	1625	U
1	1A	1626	A
1	1A	1628	G

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Mol	Chain	Res	Type
1	1A	1631	C
1	1A	1632	A
1	1A	1654	A
1	1A	1655	A
1	1A	1695	C
1	1A	1701	A
1	1A	1721	G
1	1A	1743	G
1	1A	1747	A
1	1A	1748	A
1	1A	1767	A
1	1A	1787	G
1	1A	1793	A
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1811	A
1	1A	1813	C
1	1A	1822	A
1	1A	1831	C
1	1A	1832	G
1	1A	1847	G
1	1A	1860	A
1	1A	1870	G
1	1A	1878	A
1	1A	1899	A
1	1A	1900	G
1	1A	1911	A
1	1A	1918	G
1	1A	1922	A
1	1A	1927	C
1	1A	1928	G
1	1A	1935	A
1	1A	1936	C
1	1A	1951	G
1	1A	1952	G
1	1A	1959	A
1	1A	1960	A
1	1A	1977	U
1	1A	1985	U
1	1A	1989	C
1	1A	1992	A

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Mol	Chain	Res	Type
1	1A	1993	A
1	1A	1994	A
1	1A	2015	U
1	1A	2019	G
1	1A	2042	A
1	1A	2045	G
1	1A	2053	A
1	1A	2055	A
1	1A	2061	C
1	1A	2065	C
1	1A	2077	C
1	1A	2078	G
1	1A	2082	A
1	1A	2083	G
1	1A	2084	A
1	1A	2091	G
1	1A	2115	G
1	1A	2121	U
1	1A	2125	C
1	1A	2126	G
1	1A	2129	C
1	1A	2130	C
1	1A	2132	G
1	1A	2133	C
1	1A	2134	G
1	1A	2137	G
1	1A	2138	G
1	1A	2139	A
1	1A	2140	U
1	1A	2141	A
1	1A	2142	G
1	1A	2148	A
1	1A	2149	G
1	1A	2154	U
1	1A	2155	G
1	1A	2156	A
1	1A	2158	C
1	1A	2160	C
1	1A	2164	C
1	1A	2166	U
1	1A	2167	C
1	1A	2168	C

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Mol	Chain	Res	Type
1	1A	2169	G
1	1A	2170	G
1	1A	2174	G
1	1A	2180	A
1	1A	2181	G
1	1A	2182	G
1	1A	2184	G
1	1A	2194	U
1	1A	2195	A
1	1A	2200	C
1	1A	2208	G
1	1A	2209	G
1	1A	2211	U
1	1A	2212	G
1	1A	2214	G
1	1A	2220	A
1	1A	2227	G
1	1A	2228	G
1	1A	2229	A
1	1A	2237	A
1	1A	2250	G
1	1A	2251	G
1	1A	2280	A
1	1A	2281	A
1	1A	2291	G
1	1A	2295	C
1	1A	2298	A
1	1A	2299	A
1	1A	2301	G
1	1A	2317	A
1	1A	2320	G
1	1A	2324	U
1	1A	2332	A
1	1A	2337	G
1	1A	2346	G
1	1A	2347	A
1	1A	2348	A
1	1A	2359	C
1	1A	2395	G
1	1A	2397	C
1	1A	2408	G
1	1A	2418	U

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Mol	Chain	Res	Type
1	1A	2419	G
1	1A	2426	G
1	1A	2434	A
1	1A	2435	U
1	1A	2437	A
1	1A	2441	G
1	1A	2442	A
1	1A	2443	U
1	1A	2447	A
1	1A	2451	A
1	1A	2453	C
1	1A	2460	A
1	1A	2481	A
1	1A	2486	C
1	1A	2488	A
1	1A	2514	G
1	1A	2517	G
1	1A	2518	U
1	1A	2530	A
1	1A	2532	C
1	1A	2537	G
1	1A	2541	G
1	1A	2566	U
1	1A	2578	A
1	1A	2579	G
1	1A	2585	C
1	1A	2594	G
1	1A	2597	U
1	1A	2598	C
1	1A	2614	A
1	1A	2615	G
1	1A	2621	U
1	1A	2623	U
1	1A	2624	C
1	1A	2642	G
1	1A	2666	A
1	1A	2674	A
1	1A	2675	G
1	1A	2694	U
1	1A	2701	U
1	1A	2702	C
1	1A	2714	U

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Mol	Chain	Res	Type
1	1A	2715	C
1	1A	2725	A
1	1A	2726	A
1	1A	2727	G
1	1A	2739	U
1	1A	2746	A
1	1A	2770	A
1	1A	2777	A
1	1A	2778	A
1	1A	2791	A
1	1A	2803	A
1	1A	2804	C
1	1A	2813	G
1	1A	2830	A
1	1A	2831	A
1	1A	2843	G
1	1A	2845	A
1	1A	2882	G
1	1A	2890	C
1	1A	2901	A
1	1A	2903	G
2	1B	2	C
2	1B	30	C
2	1B	56	G
2	1B	73	A
2	1B	110	G
32	1a	9	G
32	1a	22	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	78	G
32	1a	79	G
32	1a	101	A
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	159	G
32	1a	163	C

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Mol	Chain	Res	Type
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	195	A
32	1a	197	A
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	348	G
32	1a	351	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	424	G
32	1a	429	U
32	1a	430	A
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	485	G
32	1a	496	A

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Mol	Chain	Res	Type
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	532	A
32	1a	533	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	576	G
32	1a	577	G
32	1a	592	G
32	1a	596	C
32	1a	630	G
32	1a	632	A
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	731	G
32	1a	734	G
32	1a	753	A
32	1a	755	G
32	1a	774	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	829	G
32	1a	838	G
32	1a	840	C
32	1a	841	U

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Mol	Chain	Res	Type
32	1a	848	C
32	1a	851	G
32	1a	859	A
32	1a	874	G
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	935	A
32	1a	960	U
32	1a	961	U
32	1a	967	5MC
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	972	C
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	994	A
32	1a	1002	G
32	1a	1003	G
32	1a	1004	A
32	1a	1005	A
32	1a	1006	C
32	1a	1009	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	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1033	G

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Mol	Chain	Res	Type
32	1a	1044	A
32	1a	1053	G
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1125	U
32	1a	1130	A
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1152	A
32	1a	1159	U
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1213	A
32	1a	1224	G
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1250	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1270	C
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U

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Mol	Chain	Res	Type
32	1a	1317	C
32	1a	1320	C
32	1a	1338	G
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1370	G
32	1a	1397	C
32	1a	1402	4OC
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1487	G
32	1a	1493	A
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1517	G
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
54	1x	3	C
54	1x	6	G
54	1x	9	G
54	1x	14	A
54	1x	16	C
54	1x	19	G
54	1x	20	U
54	1x	21	A
54	1x	30	G
54	1x	34	C
54	1x	42	G
54	1x	44	A
54	1x	47	U
54	1x	50	U
54	1x	60	U
54	1x	63	G
54	1x	69	C

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Mol	Chain	Res	Type
54	1x	72	A
54	1x	75	C
54	1x	76	A
1	2A	10	G
1	2A	12	U
1	2A	34	C
1	2A	45	C
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	95	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	157	U
1	2A	173	G
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	225	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	272(A)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	311	A
1	2A	324	A
1	2A	327	G
1	2A	330	A
1	2A	342	G

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Mol	Chain	Res	Type
1	2A	352	G
1	2A	357	A
1	2A	362	U
1	2A	363	G
1	2A	386	G
1	2A	411	G
1	2A	412	A
1	2A	421	U
1	2A	428	A
1	2A	444	C
1	2A	456	C
1	2A	457	A
1	2A	479	A
1	2A	481	G
1	2A	505	A
1	2A	509	C
1	2A	510	C
1	2A	518	G
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	592	G
1	2A	595	C
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	610	G
1	2A	614(B)	G
1	2A	615	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	648	G
1	2A	652(B)	A

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Mol	Chain	Res	Type
1	2A	652(C)	G
1	2A	652(E)	G
1	2A	652(U)	G
1	2A	668	G
1	2A	669	G
1	2A	686	G
1	2A	730	C
1	2A	753	C
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	857	C
1	2A	859	G
1	2A	874	G
1	2A	880	G
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	896	A
1	2A	899	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	958	U
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C

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Mol	Chain	Res	Type
1	2A	983	A
1	2A	996	A
1	2A	1005	C
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1033	U
1	2A	1042	G
1	2A	1044	G
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1052	C
1	2A	1053	C
1	2A	1054	A
1	2A	1060	U
1	2A	1063	G
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1068	G
1	2A	1069	A
1	2A	1070	A
1	2A	1071	G
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1079	C
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	1096	A
1	2A	1108	U

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Mol	Chain	Res	Type
1	2A	1109	C
1	2A	1110	G
1	2A	1112	G
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1171	G
1	2A	1211	U
1	2A	1220	A
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1300	U
1	2A	1301	A
1	2A	1308	A
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1370	C
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C

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Mol	Chain	Res	Type
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1533	G
1	2A	1537	G
1	2A	1542	A
1	2A	1547	C
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1579	A
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1609	A
1	2A	1640	C
1	2A	1648	C
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1722	A
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1829	A
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1896	G
1	2A	1900	A
1	2A	1905	C
1	2A	1906	G

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Mol	Chain	Res	Type
1	2A	1914	C
1	2A	1915	5MU
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2039	C
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2096	U
1	2A	2101	G
1	2A	2103	C
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2110	G
1	2A	2111	C
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2120	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C

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Mol	Chain	Res	Type
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2136	C
1	2A	2138	C
1	2A	2142	C
1	2A	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2151	G
1	2A	2152	G
1	2A	2158	A
1	2A	2159	G
1	2A	2160	G
1	2A	2162	G
1	2A	2172	U
1	2A	2173	A
1	2A	2186	G
1	2A	2187	G
1	2A	2189	U
1	2A	2190	G
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2268	A
1	2A	2269	A
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2286	A
1	2A	2287	A
1	2A	2305	A
1	2A	2308	G
1	2A	2311	A

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Mol	Chain	Res	Type
1	2A	2312	U
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2347	C
1	2A	2383	G
1	2A	2385	C
1	2A	2396	G
1	2A	2406	U
1	2A	2407	G
1	2A	2414	G
1	2A	2422	A
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2431	U
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2474	C
1	2A	2476	A
1	2A	2502	G
1	2A	2503	2MA
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2582	G
1	2A	2585	U
1	2A	2586	C
1	2A	2602	A

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Mol	Chain	Res	Type
1	2A	2603	G
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	2662	A
1	2A	2663	G
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2702	U
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2757	A
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2789	C
1	2A	2802	G
1	2A	2811	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
2	2B	8	U
2	2B	30	C
2	2B	56	G
2	2B	73	A
2	2B	84	C
2	2B	110	G
32	2a	5	U

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Mol	Chain	Res	Type
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	61	G
32	2a	66	G
32	2a	80	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	348	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C

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Mol	Chain	Res	Type
32	2a	373	A
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	527	7MG
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	561	U
32	2a	562	C
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	592	G
32	2a	596	C
32	2a	630	G
32	2a	632	A
32	2a	653	A
32	2a	661	G
32	2a	665	A
32	2a	687	A

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Mol	Chain	Res	Type
32	2a	688	G
32	2a	695	A
32	2a	723	U
32	2a	731	G
32	2a	753	A
32	2a	755	G
32	2a	774	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	815	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G
32	2a	838	G
32	2a	840	C
32	2a	841	U
32	2a	848	C
32	2a	851	G
32	2a	859	A
32	2a	874	G
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	934	C
32	2a	935	A
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	1003	G

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Mol	Chain	Res	Type
32	2a	1005	A
32	2a	1006	C
32	2a	1009	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	1036	G
32	2a	1041	A
32	2a	1044	A
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	1095	U
32	2a	1101	A
32	2a	1117	G
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1134	G
32	2a	1136	U
32	2a	1137	C
32	2a	1139	G
32	2a	1140	C
32	2a	1147	C
32	2a	1152	A
32	2a	1158	C
32	2a	1159	U
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U

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Mol	Chain	Res	Type
32	2a	1197	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1224	G
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
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	1282	C
32	2a	1287	A
32	2a	1299	A
32	2a	1300	G
32	2a	1302	U
32	2a	1305	G
32	2a	1317	C
32	2a	1320	C
32	2a	1338	G
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1370	G
32	2a	1397	C
32	2a	1400	5MC
32	2a	1402	4OC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1487	G
32	2a	1492	A
32	2a	1493	A
32	2a	1497	G

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Mol	Chain	Res	Type
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1505	G
32	2a	1506	U
32	2a	1517	G
32	2a	1528	U
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
54	2x	9	G
54	2x	13	C
54	2x	20	U
54	2x	21	A
54	2x	48	C
54	2x	50	U
54	2x	62	C
54	2x	63	G
54	2x	65	C
54	2x	76	A

All (71) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	115	G
1	1A	184	A
1	1A	185	A
1	1A	188	A
1	1A	302	A
1	1A	386	U
1	1A	509	A
1	1A	732	A
1	1A	793	A
1	1A	811	A
1	1A	874	U
1	1A	913	A
1	1A	934	A
1	1A	935	C
1	1A	941	U
1	1A	1019	G
1	1A	1065	U

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Mol	Chain	Res	Type
1	1A	1067	A
1	1A	1093	G
1	1A	1116	A
1	1A	1157	A
1	1A	1201	A
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1255	A
1	1A	1286	U
1	1A	1466	U
1	1A	1654	A
1	1A	1700	G
1	1A	2148	A
1	1A	2227	G
1	1A	2418	U
1	1A	2434	A
1	1A	2442	A
1	1A	2623	U
1	1A	2701	U
1	1A	2769	U
1	2A	195	A
1	2A	196	A
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	974	G
1	2A	1053	C
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1210	A
1	2A	1399	C
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G

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Mol	Chain	Res	Type
1	2A	1608	A
1	2A	1992	G
1	2A	2126	A
1	2A	2172	U
1	2A	2206	G
1	2A	2321	G
1	2A	2406	U
1	2A	2430	A
1	2A	2585	U
1	2A	2611	U
1	2A	2689	U
1	2A	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
32	MA6	1a	1518	32	23,26,27	1.03	3 (13%)	34,38,41	4.36	14 (41%)
32	5MC	2a	1407	32	18,22,23	1.13	3 (16%)	26,32,35	1.16	3 (11%)
1	OMC	1A	1942	1	19,22,23	2.45	7 (36%)	26,31,34	0.91	1 (3%)
1	PSU	1A	2617	1	18,21,22	1.16	1 (5%)	22,30,33	1.53	4 (18%)
43	0TD	1l	92	43	7,9,10	2.23	2 (28%)	6,11,13	2.83	4 (66%)
1	OMC	2A	1920	1	19,22,23	2.48	7 (36%)	26,31,34	0.94	1 (3%)
32	MA6	2a	1519	32	23,26,27	1.00	1 (4%)	34,38,41	4.62	12 (35%)
32	4OC	2a	1402	32	20,23,24	2.51	8 (40%)	26,32,35	1.58	3 (11%)
1	PSU	2A	1911	1	18,21,22	1.32	3 (16%)	22,30,33	1.59	2 (9%)
1	OMG	1A	2263	1,54	23,26,27	1.71	5 (21%)	33,38,41	1.98	13 (39%)
1	5MC	2A	1942	1	18,22,23	1.08	1 (5%)	26,32,35	1.32	5 (19%)
32	7MG	1a	527	56,32	22,26,27	2.33	7 (31%)	29,39,42	1.94	9 (31%)
32	5MC	2a	1400	32	18,22,23	1.08	1 (5%)	26,32,35	1.27	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	7MG	2a	527	32	22,26,27	2.46	7 (31%)	29,39,42	1.86	8 (27%)
32	4OC	1a	1402	32	20,23,24	2.47	8 (40%)	26,32,35	0.97	2 (7%)
1	5MC	1A	1984	56,1	18,22,23	1.01	1 (5%)	26,32,35	1.39	5 (19%)
32	5MC	2a	967	32	18,22,23	0.88	0	26,32,35	1.31	4 (15%)
32	5MC	1a	1400	32	18,22,23	0.91	0	26,32,35	1.26	4 (15%)
54	PSU	1x	55	54	18,21,22	1.51	3 (16%)	22,30,33	1.50	1 (4%)
32	MA6	2a	1518	32	23,26,27	1.01	1 (4%)	34,38,41	4.53	13 (38%)
1	5MU	1A	1937	1	19,22,23	1.15	1 (5%)	28,32,35	1.48	5 (17%)
1	PSU	2A	1917	1	18,21,22	1.32	3 (16%)	22,30,33	1.53	3 (13%)
1	5MU	1A	1961	1	19,22,23	0.71	0	28,32,35	1.14	4 (14%)
1	OMU	2A	2552	56,1	19,22,23	6.66	10 (52%)	26,31,34	2.28	7 (26%)
32	M2G	2a	966	32	24,27,28	2.13	6 (25%)	35,40,43	1.77	7 (20%)
1	2MA	1A	2515	56,1	22,25,26	2.69	8 (36%)	33,37,40	3.01	10 (30%)
1	5MC	2A	1962	56,1	18,22,23	1.07	2 (11%)	26,32,35	1.13	3 (11%)
1	PSU	1A	1933	1	18,21,22	1.10	2 (11%)	22,30,33	1.65	4 (18%)
1	5MC	1A	1964	56,1	18,22,23	0.94	1 (5%)	26,32,35	1.30	3 (11%)
32	UR3	1a	1498	32	19,22,23	2.02	3 (15%)	26,32,35	1.51	3 (11%)
32	M2G	1a	966	32	24,27,28	2.02	5 (20%)	35,40,43	1.56	6 (17%)
32	PSU	1a	516	32	18,21,22	1.47	3 (16%)	22,30,33	2.31	6 (27%)
32	UR3	2a	1498	32	19,22,23	2.05	4 (21%)	26,32,35	1.34	3 (11%)
54	5MC	2x	32	54	18,22,23	1.09	2 (11%)	26,32,35	1.22	4 (15%)
32	5MC	1a	1407	32	18,22,23	1.07	1 (5%)	26,32,35	1.33	5 (19%)
54	PSU	2x	55	56,54	18,21,22	1.53	3 (16%)	22,30,33	1.55	4 (18%)
1	5MU	2A	1939	1	19,22,23	1.05	2 (10%)	28,32,35	1.24	3 (10%)
32	5MC	1a	1404	32	18,22,23	0.98	1 (5%)	26,32,35	1.16	4 (15%)
54	5MC	1x	32	54	18,22,23	1.13	3 (16%)	26,32,35	1.28	3 (11%)
54	5MU	2x	54	54	19,22,23	0.97	2 (10%)	28,32,35	1.07	2 (7%)
32	2MG	1a	1207	32	23,26,27	2.18	6 (26%)	32,38,41	2.36	12 (37%)
32	MA6	1a	1519	32	23,26,27	1.00	1 (4%)	34,38,41	4.67	13 (38%)
1	PSU	2A	2605	1	18,21,22	1.01	2 (11%)	22,30,33	1.56	3 (13%)
32	2MG	2a	1207	32	23,26,27	2.10	6 (26%)	32,38,41	2.13	10 (31%)
1	2MA	2A	2503	56,1	22,25,26	2.73	8 (36%)	33,37,40	2.94	10 (30%)
1	OMU	1A	2564	56,1	19,22,23	6.67	10 (52%)	26,31,34	2.34	7 (26%)
32	5MC	2a	1404	32	18,22,23	0.93	1 (5%)	26,32,35	1.27	5 (19%)
1	5MU	2A	1915	1	19,22,23	1.25	2 (10%)	28,32,35	1.36	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
43	0TD	2l	92	43	7,9,10	1.97	1 (14%)	6,11,13	2.86	4 (66%)
54	4SU	2x	8	54	18,21,22	1.24	3 (16%)	26,30,33	1.07	1 (3%)
54	5MU	1x	54	54	19,22,23	0.86	1 (5%)	28,32,35	1.14	2 (7%)
1	OMG	2A	2251	1,54	23,26,27	1.73	4 (17%)	33,38,41	2.15	10 (30%)
54	4SU	1x	8	54	18,21,22	1.19	1 (5%)	26,30,33	0.89	1 (3%)
32	5MC	1a	967	32	18,22,23	1.14	2 (11%)	26,32,35	1.22	4 (15%)
1	PSU	1A	1939	56,1	18,21,22	1.40	3 (16%)	22,30,33	1.53	3 (13%)
32	PSU	2a	516	32	18,21,22	1.34	3 (16%)	22,30,33	1.92	5 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	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
1	OMC	1A	1942	1	-	1/9/27/28	0/2/2/2
1	PSU	1A	2617	1	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	2/7/12/14	-
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
32	MA6	2a	1519	32	-	2/11/29/30	0/3/3/3
32	4OC	2a	1402	32	-	2/9/29/30	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2263	1,54	-	2/9/27/28	0/3/3/3
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	7MG	1a	527	56,32	-	2/7/37/38	0/3/3/3
32	5MC	2a	1400	32	-	2/7/25/26	0/2/2/2
32	7MG	2a	527	32	-	2/7/37/38	0/3/3/3
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
1	5MC	1A	1984	56,1	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
54	PSU	1x	55	54	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
1	5MU	1A	1937	1	-	2/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1961	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	2A	2552	56,1	-	1/9/27/28	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	2MA	1A	2515	56,1	-	1/7/25/26	0/3/3/3
1	5MC	2A	1962	56,1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1964	56,1	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	PSU	1a	516	32	-	1/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
54	5MC	2x	32	54	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
54	PSU	2x	55	56,54	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
54	5MC	1x	32	54	-	0/7/25/26	0/2/2/2
54	5MU	2x	54	54	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	MA6	1a	1519	32	-	4/11/29/30	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
1	2MA	2A	2503	56,1	-	2/7/25/26	0/3/3/3
1	OMU	1A	2564	56,1	-	0/9/27/28	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	5/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	5/7/12/14	-
54	4SU	2x	8	54	-	0/7/25/26	0/2/2/2
54	5MU	1x	54	54	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	1,54	-	1/9/27/28	0/3/3/3
54	4SU	1x	8	54	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	2/7/25/26	0/2/2/2
1	PSU	1A	1939	56,1	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32	-	1/7/25/26	0/2/2/2

All (185) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2564	OMU	C5-C4	15.74	1.78	1.43
1	2A	2552	OMU	C5-C4	15.47	1.77	1.43
1	2A	2552	OMU	C4-N3	-14.70	1.12	1.38
1	1A	2564	OMU	C4-N3	-14.50	1.12	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2552	OMU	C6-C5	-10.23	1.11	1.35
1	1A	2564	OMU	C6-C5	-10.16	1.11	1.35
1	1A	2564	OMU	C6-N1	8.61	1.58	1.38
1	1A	2564	OMU	C3'-C2'	-8.56	1.33	1.52
1	2A	2552	OMU	C6-N1	8.52	1.58	1.38
1	2A	2552	OMU	C3'-C2'	-8.32	1.34	1.52
1	2A	2503	2MA	C4-N3	7.82	1.44	1.34
1	1A	2515	2MA	C4-N3	7.18	1.43	1.34
1	2A	2552	OMU	O4'-C1'	6.46	1.57	1.42
1	2A	2552	OMU	O4'-C4'	-6.38	1.30	1.45
1	1A	2564	OMU	O4'-C4'	-6.21	1.31	1.45
1	1A	2564	OMU	O4'-C1'	6.18	1.56	1.42
32	2a	527	7MG	C5-N7	6.07	1.42	1.35
32	1a	527	7MG	C5-N7	5.94	1.42	1.35
1	2A	1920	OMC	C4-N4	5.93	1.47	1.33
1	1A	1942	OMC	C4-N4	5.61	1.47	1.33
32	2a	966	M2G	C4-N3	5.53	1.47	1.34
32	1a	1207	2MG	C2-N3	5.52	1.42	1.31
1	1A	2515	2MA	C2-N1	5.50	1.43	1.34
32	2a	966	M2G	C2-N3	5.30	1.45	1.32
1	1A	2564	OMU	C1'-N1	-5.29	1.32	1.47
32	2a	1498	UR3	C6-C5	5.28	1.47	1.35
32	2a	1207	2MG	C2-N3	5.27	1.42	1.31
1	2A	2503	2MA	C2-N1	5.24	1.43	1.34
32	1a	1402	4OC	C4-N4	5.20	1.46	1.35
32	2a	1402	4OC	C4-N4	5.17	1.46	1.35
1	2A	2552	OMU	C1'-N1	-5.13	1.32	1.47
32	1a	966	M2G	C4-N3	5.04	1.46	1.34
32	1a	1498	UR3	C6-C5	5.01	1.46	1.35
32	1a	1498	UR3	C2-N1	4.99	1.45	1.38
1	2A	2251	OMG	C4-N3	4.93	1.46	1.34
32	2a	966	M2G	C2-N2	4.89	1.44	1.35
43	1l	92	0TD	CB-SB	-4.82	1.77	1.82
32	1a	966	M2G	C2-N3	4.82	1.44	1.32
1	2A	2503	2MA	C2-N3	4.80	1.42	1.34
32	1a	1207	2MG	C2-N1	4.77	1.44	1.36
1	1A	1942	OMC	C2-N3	4.75	1.46	1.36
32	2a	1498	UR3	C2-N1	4.70	1.45	1.38
1	1A	1942	OMC	C6-C5	4.69	1.45	1.35
32	2a	1207	2MG	C2-N1	4.64	1.44	1.36
32	1a	966	M2G	C2-N2	4.63	1.44	1.35
1	2A	1920	OMC	C2-N3	4.63	1.45	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	527	7MG	C4-N3	4.62	1.45	1.34
32	2a	1402	4OC	C2-N3	4.62	1.45	1.36
1	1A	2515	2MA	C2-N3	4.58	1.42	1.34
1	2A	1920	OMC	C6-C5	4.57	1.45	1.35
32	2a	527	7MG	C2-N3	4.55	1.44	1.33
54	1x	8	4SU	C4-S4	-4.52	1.59	1.68
32	1a	1207	2MG	C4-N3	4.52	1.45	1.34
32	1a	1402	4OC	C6-C5	4.48	1.45	1.35
32	1a	527	7MG	C8-N9	4.45	1.48	1.46
32	2a	527	7MG	C8-N9	4.45	1.48	1.46
1	1A	2263	OMG	C4-N3	4.42	1.44	1.34
1	1A	2515	2MA	C6-N1	4.42	1.41	1.35
1	2A	2251	OMG	C2-N3	4.39	1.43	1.33
32	1a	1207	2MG	C2-N2	4.35	1.43	1.33
32	1a	1402	4OC	C2-N3	4.28	1.45	1.36
32	2a	1207	2MG	C4-N3	4.28	1.44	1.34
1	1A	2564	OMU	C3'-C4'	4.25	1.63	1.53
54	1x	55	PSU	C2-N1	4.24	1.42	1.36
1	2A	1915	5MU	C2-N1	4.21	1.45	1.38
32	1a	527	7MG	C4-N3	4.20	1.44	1.34
32	2a	1402	4OC	C4-N3	4.19	1.40	1.32
32	1a	527	7MG	C2-N3	4.19	1.43	1.33
1	1A	1937	5MU	C2-N1	4.18	1.45	1.38
32	2a	1207	2MG	C2-N2	4.10	1.42	1.33
1	2A	2503	2MA	C6-N1	4.06	1.40	1.35
1	1A	1939	PSU	C2-N1	4.04	1.42	1.36
32	1a	1402	4OC	C4-N3	4.00	1.39	1.32
43	2l	92	0TD	CB-SB	-3.99	1.78	1.82
32	1a	516	PSU	C2-N1	3.98	1.42	1.36
32	2a	516	PSU	C2-N1	3.98	1.42	1.36
1	1A	2263	OMG	C2-N3	3.98	1.42	1.33
32	1a	1498	UR3	C2-N3	3.93	1.46	1.39
32	2a	1402	4OC	C6-C5	3.93	1.44	1.35
54	2x	55	PSU	C2-N1	3.89	1.42	1.36
1	2A	2552	OMU	C3'-C4'	3.89	1.62	1.53
32	2a	1498	UR3	C2-N3	3.77	1.46	1.39
1	2A	1917	PSU	C2-N1	3.73	1.41	1.36
32	2a	1402	4OC	C5-C4	3.69	1.48	1.40
1	1A	1942	OMC	C2-N1	3.57	1.47	1.40
1	2A	1920	OMC	C2-N1	3.54	1.47	1.40
32	2a	1402	4OC	C2-N1	3.45	1.47	1.40
32	1a	1402	4OC	C5-C4	3.42	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2617	PSU	C2-N1	3.30	1.41	1.36
1	2A	1911	PSU	C2-N1	3.26	1.41	1.36
54	2x	55	PSU	C4-N3	3.22	1.44	1.38
32	2a	527	7MG	C2-N2	3.20	1.41	1.34
32	1a	527	7MG	C5-C6	3.20	1.51	1.43
1	2A	2503	2MA	C5-C6	3.16	1.49	1.41
32	2a	527	7MG	C5-C6	3.15	1.51	1.43
1	1A	2515	2MA	C5-C6	3.14	1.49	1.41
1	2A	1920	OMC	O2-C2	-3.10	1.18	1.23
32	1a	1402	4OC	C2-N1	3.07	1.46	1.40
1	1A	2515	2MA	C8-N7	3.07	1.37	1.31
32	1a	967	5MC	C2-N1	3.05	1.46	1.40
1	2A	1939	5MU	C2-N1	3.04	1.43	1.38
32	1a	1402	4OC	O2-C2	-3.02	1.18	1.23
1	2A	1942	5MC	C2-N1	3.00	1.46	1.40
32	2a	1402	4OC	O2-C2	-2.98	1.18	1.23
54	2x	8	4SU	C2-N1	2.97	1.43	1.38
32	2a	1519	MA6	C6-N6	2.95	1.45	1.36
32	2a	1400	5MC	C2-N1	2.89	1.46	1.40
32	2a	1402	4OC	CM4-N4	-2.89	1.40	1.45
54	1x	55	PSU	C6-N1	2.87	1.41	1.36
32	2a	1518	MA6	C6-N6	2.86	1.45	1.36
1	2A	2552	OMU	O2'-C2'	2.84	1.49	1.42
1	2A	1920	OMC	C4-N3	2.83	1.40	1.34
1	2A	1911	PSU	C4-N3	2.82	1.44	1.38
32	1a	527	7MG	C2-N2	2.80	1.40	1.34
54	2x	8	4SU	C2-N3	2.79	1.42	1.38
54	1x	55	PSU	C4-N3	2.76	1.44	1.38
1	1A	1942	OMC	C4-N3	2.76	1.40	1.34
32	1a	966	M2G	C2-N1	2.75	1.43	1.36
32	1a	1519	MA6	C6-N6	2.74	1.44	1.36
1	2A	2503	2MA	C8-N7	2.74	1.36	1.31
32	1a	1402	4OC	CM4-N4	-2.74	1.40	1.45
32	2a	527	7MG	C2-N1	2.70	1.44	1.37
1	1A	1942	OMC	O2-C2	-2.68	1.18	1.23
54	2x	32	5MC	C2-N1	2.66	1.45	1.40
32	1a	516	PSU	C6-N1	2.66	1.40	1.36
54	2x	8	4SU	C4-S4	-2.64	1.63	1.68
1	1A	1933	PSU	C2-N1	2.64	1.40	1.36
32	1a	1407	5MC	C2-N1	2.64	1.45	1.40
32	2a	966	M2G	C2-N1	2.63	1.43	1.36
54	2x	55	PSU	C6-N1	2.62	1.40	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	516	PSU	O4'-C1'	-2.60	1.40	1.43
1	1A	1984	5MC	C2-N1	2.59	1.45	1.40
1	1A	1939	PSU	C4-N3	2.58	1.43	1.38
1	1A	1942	OMC	C5-C4	2.58	1.48	1.42
54	2x	54	5MU	C2-N1	2.57	1.42	1.38
1	1A	2515	2MA	C4-N9	-2.57	1.32	1.37
1	2A	2503	2MA	C4-N9	-2.52	1.32	1.37
54	1x	32	5MC	C2-N1	2.51	1.45	1.40
32	2a	1407	5MC	C2-N1	2.49	1.45	1.40
32	2a	516	PSU	C6-N1	2.48	1.40	1.36
32	1a	1518	MA6	C6-N6	2.47	1.44	1.36
1	2A	1920	OMC	C5-C4	2.47	1.48	1.42
1	1A	1939	PSU	C6-N1	2.46	1.40	1.36
1	2A	1962	5MC	C2-N3	2.45	1.41	1.36
1	2A	1917	PSU	C6-N1	2.41	1.40	1.36
1	1A	2564	OMU	O2'-C2'	2.38	1.48	1.42
32	1a	967	5MC	C2-N3	2.37	1.41	1.36
54	1x	54	5MU	C2-N1	2.36	1.42	1.38
1	2A	1915	5MU	C2-N3	2.36	1.42	1.38
32	2a	516	PSU	O4'-C1'	-2.35	1.40	1.43
1	1A	1964	5MC	C2-N1	2.35	1.45	1.40
32	1a	1518	MA6	C5-C6	-2.33	1.35	1.41
32	1a	527	7MG	C2-N1	2.32	1.43	1.37
54	2x	54	5MU	C2-N3	2.30	1.42	1.38
32	2a	1207	2MG	CM2-N2	-2.28	1.41	1.45
1	2A	1911	PSU	C6-N1	2.27	1.40	1.36
1	2A	1962	5MC	C2-N1	2.27	1.44	1.40
54	1x	32	5MC	C2-N3	2.26	1.40	1.36
1	2A	1939	5MU	C2-N3	2.24	1.42	1.38
1	1A	2263	OMG	C8-N7	2.24	1.38	1.32
1	1A	2263	OMG	C2-N1	2.22	1.43	1.37
32	2a	966	M2G	C5-N7	-2.21	1.34	1.39
1	2A	1917	PSU	C4-N3	2.16	1.42	1.38
1	1A	2263	OMG	C2-N2	2.16	1.39	1.34
32	2a	1207	2MG	C5-N7	-2.16	1.34	1.39
54	2x	32	5MC	C6-C5	2.14	1.38	1.34
1	1A	2515	2MA	C5-C4	-2.14	1.35	1.39
1	2A	2605	PSU	C4-N3	2.12	1.42	1.38
32	1a	966	M2G	C5-N7	-2.12	1.35	1.39
1	1A	1933	PSU	C4-N3	2.11	1.42	1.38
32	1a	1207	2MG	CM2-N2	-2.09	1.41	1.45
54	1x	32	5MC	C6-C5	2.08	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1407	5MC	C2-N3	2.08	1.40	1.36
1	2A	2503	2MA	C5-C4	-2.07	1.35	1.39
1	2A	2605	PSU	C2-N1	2.07	1.39	1.36
32	1a	1207	2MG	C5-N7	-2.06	1.35	1.39
32	1a	1518	MA6	C5-C4	-2.06	1.35	1.39
43	1l	92	0TD	CA-N	-2.05	1.41	1.47
1	2A	2251	OMG	C8-N7	2.05	1.38	1.32
32	2a	1407	5MC	C6-C5	2.04	1.37	1.34
1	2A	2251	OMG	C2-N2	2.03	1.39	1.34
32	1a	1404	5MC	C2-N3	2.03	1.40	1.36
32	2a	1498	UR3	O2-C2	-2.03	1.18	1.22
32	2a	966	M2G	C5-C6	2.03	1.51	1.44
32	2a	1404	5MC	C4-N4	2.02	1.39	1.34

All (295) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1519	MA6	N1-C6-N6	-20.19	95.00	117.08
32	2a	1519	MA6	N1-C6-N6	-19.87	95.36	117.08
32	2a	1518	MA6	N1-C6-N6	-19.33	95.95	117.08
32	1a	1518	MA6	N1-C6-N6	-18.51	96.85	117.08
32	1a	1519	MA6	C5-C6-N6	11.62	145.53	125.30
32	2a	1519	MA6	C5-C6-N6	11.55	145.41	125.30
32	2a	1518	MA6	C5-C6-N6	11.10	144.63	125.30
32	1a	1518	MA6	C5-C6-N6	10.45	143.50	125.30
1	1A	2515	2MA	C1'-N9-C8	-9.85	104.90	127.14
1	2A	2503	2MA	C1'-N9-C8	-9.84	104.92	127.14
32	1a	516	PSU	C6-C5-C4	8.15	123.89	118.20
1	1A	2515	2MA	C4-N9-C1'	7.42	144.26	126.59
1	1A	2564	OMU	C5-C4-N3	7.18	125.58	114.84
1	2A	2552	OMU	C5-C4-N3	7.02	125.33	114.84
1	2A	2503	2MA	C4-N9-C1'	6.98	143.23	126.59
1	2A	2503	2MA	N9-C8-N7	-6.54	104.97	113.91
32	1a	1207	2MG	C2-N3-C4	6.40	119.98	112.04
1	1A	2515	2MA	N9-C8-N7	-6.32	105.26	113.91
32	2a	516	PSU	C6-C5-C4	6.31	122.61	118.20
32	2a	1207	2MG	C2-N3-C4	6.31	119.86	112.04
32	2a	1519	MA6	C5-C4-N3	-6.20	118.66	126.75
32	2a	966	M2G	C5-C4-N3	-5.97	118.77	128.46
32	1a	1519	MA6	C5-C4-N3	-5.93	119.02	126.75
32	2a	1518	MA6	C5-C4-N3	-5.72	119.29	126.75
1	2A	2503	2MA	C4-N9-C8	5.64	111.84	105.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2564	OMU	C4-N3-C2	-5.57	119.24	126.58
32	1a	1518	MA6	C5-C4-N3	-5.44	119.65	126.75
32	2a	1518	MA6	N1-C2-N3	-5.31	120.29	128.60
1	2A	2552	OMU	C4-N3-C2	-5.25	119.66	126.58
32	2a	1402	4OC	CM4-N4-C4	-5.22	112.25	122.45
32	2a	1207	2MG	C5-C4-N3	-5.21	120.01	128.46
32	2a	1519	MA6	N1-C2-N3	-5.20	120.47	128.60
32	1a	1518	MA6	N1-C2-N3	-5.15	120.55	128.60
32	1a	1519	MA6	N1-C2-N3	-5.13	120.58	128.60
32	1a	1207	2MG	C5-C4-N3	-5.13	120.14	128.46
1	1A	1933	PSU	C6-C5-C4	5.08	121.75	118.20
1	2A	2251	OMG	C1'-N9-C8	-5.06	112.31	126.70
32	1a	966	M2G	C5-C4-N3	-5.02	120.31	128.46
32	2a	1519	MA6	C4-C5-C6	4.98	121.46	115.88
54	1x	55	PSU	C6-C5-C4	4.95	121.66	118.20
32	1a	1498	UR3	C4-N3-C2	-4.91	119.94	124.56
1	2A	1911	PSU	C6-C5-C4	4.89	121.61	118.20
1	1A	1939	PSU	C6-C5-C4	4.80	121.55	118.20
32	1a	527	7MG	C5-C6-N1	4.80	119.44	110.99
32	1a	1519	MA6	C4-C5-C6	4.78	121.23	115.88
1	2A	2251	OMG	C5-C4-N3	-4.73	120.79	128.46
43	2l	92	0TD	OD2-CG-CB	4.73	123.36	113.15
1	1A	2515	2MA	C4-N9-C8	4.70	110.82	105.73
32	2a	527	7MG	C5-C6-N1	4.69	119.26	110.99
32	1a	1518	MA6	C4-C5-C6	4.68	121.12	115.88
1	1A	2515	2MA	CM2-C2-N1	4.61	124.35	117.15
32	2a	1518	MA6	C4-C5-C6	4.57	120.99	115.88
32	1a	1518	MA6	C4-N9-C1'	-4.46	115.98	126.59
54	2x	55	PSU	C6-C5-C4	4.44	121.31	118.20
1	2A	2605	PSU	C6-C5-C4	4.40	121.27	118.20
32	2a	1518	MA6	N9-C8-N7	-4.39	107.91	113.91
1	2A	1917	PSU	C6-C5-C4	4.39	121.27	118.20
32	1a	1519	MA6	C4-N9-C1'	-4.29	116.37	126.59
1	1A	2263	OMG	N9-C8-N7	-4.28	105.32	113.39
32	1a	527	7MG	C2-N3-C4	4.26	119.88	112.30
32	2a	1518	MA6	C4-N9-C1'	-4.25	116.47	126.59
32	2a	966	M2G	C2-N3-C4	4.23	120.34	112.51
1	2A	2251	OMG	C2-N3-C4	4.22	119.83	112.30
1	1A	2617	PSU	C6-C5-C4	4.22	121.15	118.20
32	2a	1498	UR3	C4-N3-C2	-4.20	120.61	124.56
32	2a	527	7MG	C2-N3-C4	4.15	119.70	112.30
32	1a	1518	MA6	N9-C8-N7	-4.05	108.38	113.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1518	MA6	N3-C4-N9	4.05	133.75	127.08
32	1a	1518	MA6	N3-C4-N9	4.04	133.73	127.08
32	2a	966	M2G	N9-C4-N3	4.03	134.02	125.94
32	1a	1519	MA6	N9-C8-N7	-4.02	108.42	113.91
32	2a	1519	MA6	N3-C4-N9	3.99	133.66	127.08
32	1a	527	7MG	C5-C4-N9	3.93	111.44	106.35
1	2A	2251	OMG	C1'-N9-C4	3.93	138.16	126.50
43	1l	92	0TD	OD2-CG-CB	3.89	121.54	113.15
1	1A	2263	OMG	C2-N3-C4	3.86	119.18	112.30
32	1a	1519	MA6	N3-C4-N9	3.86	133.44	127.08
32	1a	1207	2MG	C1'-N9-C4	-3.80	115.20	126.50
32	1a	1207	2MG	C2-N1-C6	-3.80	120.11	124.48
32	2a	1519	MA6	C4-N9-C1'	-3.78	117.58	126.59
32	1a	1519	MA6	C1'-N9-C8	3.78	135.67	127.14
32	1a	1518	MA6	C1'-N9-C8	3.78	135.66	127.14
1	1A	2263	OMG	C1'-N9-C8	-3.76	115.99	126.70
1	1A	2564	OMU	N3-C2-N1	3.75	119.87	114.89
32	2a	1519	MA6	N9-C8-N7	-3.74	108.80	113.91
43	1l	92	0TD	CSB-SB-CB	3.70	109.13	102.44
1	2A	2552	OMU	N3-C2-N1	3.65	119.74	114.89
32	1a	966	M2G	C2-N3-C4	3.64	119.24	112.51
32	2a	1207	2MG	C2-N1-C6	-3.61	120.32	124.48
1	1A	1984	5MC	C5-C4-N3	3.60	125.56	121.67
32	2a	1518	MA6	C2-N1-C6	3.60	120.25	111.75
1	2A	1939	5MU	C6-C5-C4	3.58	121.03	118.03
32	1a	527	7MG	C5-C4-N3	-3.56	121.34	128.13
32	2a	1519	MA6	C2-N1-C6	3.55	120.14	111.75
32	1a	1518	MA6	C2-N1-C6	3.54	120.10	111.75
32	1a	1519	MA6	C2-N1-C6	3.53	120.09	111.75
32	2a	1519	MA6	C2-N3-C4	3.52	120.06	111.75
32	2a	967	5MC	C5-C4-N3	3.49	125.44	121.67
32	2a	1519	MA6	C1'-N9-C8	3.49	135.00	127.14
1	1A	1964	5MC	C5-C4-N3	3.47	125.41	121.67
32	2a	1518	MA6	C1'-N9-C8	3.46	134.94	127.14
32	2a	527	7MG	C5-C4-N3	-3.45	121.56	128.13
32	1a	1207	2MG	C1'-N9-C8	3.43	136.47	126.70
32	2a	967	5MC	C5-C6-N1	-3.43	119.81	123.34
32	2a	1400	5MC	C5-C4-N3	3.41	125.36	121.67
32	1a	516	PSU	C6-N1-C2	-3.40	119.20	122.68
32	1a	967	5MC	C5-C4-N3	3.39	125.34	121.67
32	2a	1518	MA6	C2-N3-C4	3.39	119.76	111.75
32	2a	1402	4OC	C5-C4-N4	-3.38	115.72	122.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1400	5MC	C5-C6-N1	-3.37	119.87	123.34
1	2A	2251	OMG	N9-C8-N7	-3.37	107.05	113.39
54	1x	32	5MC	C5-C6-N1	-3.35	119.89	123.34
32	1a	516	PSU	N1-C2-N3	3.35	118.93	115.13
32	2a	1404	5MC	C5-C6-N1	-3.35	119.89	123.34
1	1A	2515	2MA	C5-N7-C8	3.34	108.25	103.51
32	1a	1519	MA6	C2-N3-C4	3.34	119.64	111.75
32	2a	1518	MA6	C5-N7-C8	3.29	108.19	103.51
1	2A	1939	5MU	C4-N3-C2	-3.28	123.11	127.35
1	1A	1964	5MC	C5-C6-N1	-3.27	119.97	123.34
32	2a	527	7MG	C5-C4-N9	3.27	110.59	106.35
32	1a	1400	5MC	C5-C4-N3	3.27	125.20	121.67
1	2A	2503	2MA	C5-N7-C8	3.27	108.15	103.51
1	1A	2263	OMG	C5-C4-N3	-3.25	123.18	128.46
32	1a	1407	5MC	C5-C6-N1	-3.25	120.00	123.34
1	2A	1942	5MC	C5-C4-N3	3.23	125.16	121.67
54	2x	54	5MU	C6-C5-C4	3.23	120.73	118.03
32	1a	1498	UR3	C1'-N1-C2	3.22	122.43	116.99
1	2A	1915	5MU	C6-C5-C4	3.20	120.71	118.03
1	1A	1937	5MU	C6-C5-C4	3.19	120.70	118.03
1	1A	2515	2MA	N6-C6-N1	3.19	121.54	117.03
1	1A	2515	2MA	N3-C2-N1	-3.18	119.86	125.72
1	2A	2503	2MA	CM2-C2-N1	3.18	122.11	117.15
1	1A	2564	OMU	O4-C4-C5	-3.17	119.59	125.16
1	1A	2515	2MA	C5-C4-N3	-3.16	123.64	127.19
54	2x	32	5MC	C5-C4-N3	3.16	125.08	121.67
54	1x	8	4SU	C4-N3-C2	-3.15	124.28	127.34
1	1A	1984	5MC	C5-C6-N1	-3.14	120.11	123.34
32	2a	1207	2MG	C1'-N9-C4	-3.13	117.22	126.50
1	2A	2251	OMG	C2-N1-C6	-3.11	119.42	125.10
32	1a	1407	5MC	C5-C4-N3	3.10	125.02	121.67
32	1a	1519	MA6	C5-N7-C8	3.10	107.91	103.51
1	1A	1961	5MU	C4-N3-C2	-3.09	123.36	127.35
32	2a	1519	MA6	C5-N7-C8	3.09	107.89	103.51
1	2A	2251	OMG	N9-C4-N3	3.08	132.13	125.94
32	1a	1404	5MC	C5-C4-N3	3.08	125.00	121.67
32	1a	1207	2MG	N9-C4-N3	3.06	132.07	125.94
54	1x	32	5MC	C4-N3-C2	-3.05	116.56	120.69
1	1A	2564	OMU	O4-C4-N3	-3.05	114.83	119.31
1	1A	1937	5MU	C4-N3-C2	-3.05	123.41	127.35
32	2a	1400	5MC	C5-C6-N1	-3.05	120.20	123.34
43	2l	92	0TD	CSB-SB-CB	3.04	107.94	102.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1518	MA6	C2-N3-C4	3.04	118.93	111.75
1	2A	2552	OMU	O4-C4-C5	-3.04	119.82	125.16
54	2x	8	4SU	C6-C5-C4	3.04	122.58	119.95
1	2A	2552	OMU	O4-C4-N3	-3.03	114.85	119.31
1	2A	2552	OMU	C6-C5-C4	-3.02	115.39	119.52
32	1a	1207	2MG	N9-C8-N7	-3.00	107.74	113.39
54	1x	32	5MC	C5-C4-N3	3.00	124.91	121.67
1	2A	1962	5MC	C5-C4-N3	3.00	124.91	121.67
1	1A	1933	PSU	O2-C2-N1	-2.99	119.50	122.79
54	1x	54	5MU	C6-C5-C4	2.98	120.53	118.03
1	2A	2503	2MA	N6-C6-N1	2.97	121.23	117.03
54	2x	32	5MC	C5-C6-N1	-2.96	120.29	123.34
1	2A	1942	5MC	C5-C6-N1	-2.96	120.30	123.34
32	2a	1207	2MG	N9-C4-N3	2.95	131.86	125.94
32	2a	1207	2MG	C1'-N9-C8	2.94	135.06	126.70
1	2A	2503	2MA	C5-C4-N3	-2.93	123.89	127.19
32	1a	966	M2G	N9-C4-N3	2.91	131.78	125.94
32	2a	1407	5MC	C5-C6-N1	-2.90	120.36	123.34
32	1a	1404	5MC	C5-C6-N1	-2.89	120.36	123.34
1	2A	2251	OMG	C5-C6-N1	2.89	120.52	113.19
43	1l	92	0TD	CB-CA-N	-2.88	102.96	109.10
1	2A	2251	OMG	O6-C6-C5	-2.87	118.97	126.60
32	2a	516	PSU	N1-C2-N3	2.86	118.37	115.13
54	2x	54	5MU	C4-N3-C2	-2.85	123.66	127.35
1	1A	1964	5MC	C4-N3-C2	-2.84	116.85	120.69
1	2A	2503	2MA	N3-C2-N1	-2.83	120.52	125.72
1	2A	1942	5MC	C4-N3-C2	-2.81	116.88	120.69
32	2a	1404	5MC	C5-C4-N3	2.81	124.70	121.67
32	1a	967	5MC	C5-C6-N1	-2.80	120.45	123.34
1	1A	2564	OMU	C6-C5-C4	-2.80	115.69	119.52
1	1A	1984	5MC	C4-N3-C2	-2.80	116.90	120.69
32	2a	1407	5MC	C5-C4-N3	2.80	124.69	121.67
43	2l	92	0TD	OD2-CG-OD1	-2.79	117.75	124.09
54	1x	54	5MU	C4-N3-C2	-2.78	123.76	127.35
1	1A	2263	OMG	C2-N1-C6	-2.74	120.10	125.10
32	2a	1400	5MC	C4-N3-C2	-2.72	117.01	120.69
32	2a	966	M2G	C5-C6-N1	2.71	120.08	113.19
1	1A	2263	OMG	N2-C2-N1	2.71	122.48	116.71
32	1a	966	M2G	N9-C8-N7	-2.70	108.30	113.39
32	2a	966	M2G	N9-C8-N7	-2.70	108.31	113.39
32	2a	1207	2MG	N9-C8-N7	-2.69	108.32	113.39
32	2a	1498	UR3	C1'-N1-C2	2.69	121.53	116.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1962	5MC	C5-C6-N1	-2.69	120.57	123.34
54	2x	55	PSU	O2-C2-N1	-2.68	119.84	122.79
1	1A	1937	5MU	C1'-N1-C2	2.68	122.42	117.57
1	2A	1911	PSU	O2-C2-N1	-2.68	119.84	122.79
32	1a	1518	MA6	C5-N7-C8	2.67	107.30	103.51
1	2A	1915	5MU	C4-N3-C2	-2.66	123.90	127.35
32	2a	967	5MC	C4-N3-C2	-2.66	117.09	120.69
32	2a	1404	5MC	C4-N3-C2	-2.65	117.10	120.69
1	2A	2605	PSU	O2-C2-N1	-2.65	119.87	122.79
1	1A	2263	OMG	C8-N9-C4	2.65	111.09	106.05
32	2a	527	7MG	C4-C5-N7	2.65	109.21	105.53
32	1a	967	5MC	C4-N3-C2	-2.64	117.11	120.69
54	2x	32	5MC	C4-N3-C2	-2.64	117.12	120.69
32	2a	1518	MA6	C4-N9-C8	2.64	108.59	105.73
32	1a	1400	5MC	C4-N3-C2	-2.64	117.12	120.69
1	1A	2617	PSU	O4-C4-N3	-2.64	115.06	120.12
32	1a	1407	5MC	C4-N3-C2	-2.62	117.15	120.69
32	2a	1498	UR3	C6-N1-C2	-2.61	119.45	121.79
1	1A	2263	OMG	C5-C6-N1	2.56	119.69	113.19
1	1A	1961	5MU	C6-C5-C4	2.55	120.16	118.03
32	1a	1402	4OC	CM4-N4-C4	-2.54	117.48	122.45
32	1a	1207	2MG	N1-C2-N3	-2.52	120.05	123.95
32	1a	1207	2MG	C5-C6-N1	2.51	119.57	113.19
32	2a	516	PSU	O4'-C1'-C2'	2.48	108.64	105.14
1	2A	2552	OMU	O2-C2-N1	-2.47	119.50	122.79
1	1A	2263	OMG	C8-N7-C5	2.47	108.71	104.24
32	2a	1402	4OC	C6-C5-C4	2.46	119.97	116.96
32	1a	1402	4OC	CM2-O2'-C2'	2.46	120.98	114.52
32	1a	1407	5MC	N4-C4-N3	-2.45	114.00	118.48
1	2A	1917	PSU	O4-C4-N3	-2.44	115.44	120.12
32	1a	516	PSU	O4'-C1'-C2'	2.44	108.58	105.14
32	1a	966	M2G	C5-C6-N1	2.44	119.38	113.19
32	1a	1518	MA6	C4-N9-C8	2.43	108.36	105.73
32	1a	527	7MG	C4-C5-N7	2.42	108.89	105.53
1	2A	1962	5MC	C4-N3-C2	-2.42	117.41	120.69
1	1A	2263	OMG	O6-C6-C5	-2.42	120.18	126.60
1	2A	1917	PSU	O2-C2-N1	-2.42	120.13	122.79
32	1a	527	7MG	N9-C8-N7	2.41	106.82	103.38
32	2a	1404	5MC	CM5-C5-C6	-2.40	119.64	122.85
1	1A	2263	OMG	C6-C5-N7	2.40	134.71	130.25
1	2A	1915	5MU	C1'-N1-C2	2.40	121.91	117.57
32	1a	1404	5MC	C4-N3-C2	-2.40	117.45	120.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	966	M2G	O6-C6-C5	-2.39	120.27	126.60
1	1A	2515	2MA	C4-C5-N7	-2.36	107.74	110.62
32	1a	1207	2MG	O6-C6-C5	-2.35	120.36	126.60
32	2a	966	M2G	O6-C6-C5	-2.34	120.39	126.60
32	1a	527	7MG	C2-N1-C6	-2.33	120.84	125.10
1	1A	1937	5MU	C1'-N1-C6	-2.33	117.24	121.12
43	1l	92	0TD	OD2-CG-OD1	-2.32	118.82	124.09
1	2A	1942	5MC	CM5-C5-C6	-2.32	119.75	122.85
32	2a	1407	5MC	C4-N3-C2	-2.31	117.56	120.69
32	2a	1207	2MG	N1-C2-N3	-2.31	120.38	123.95
32	1a	1207	2MG	C8-N7-C5	2.29	108.38	104.24
1	1A	2564	OMU	O2-C2-N1	-2.28	119.75	122.79
32	2a	516	PSU	C6-N1-C2	-2.26	120.37	122.68
32	2a	1207	2MG	C5-C6-N1	2.24	118.88	113.19
32	1a	1518	MA6	C6-C5-N7	-2.24	129.53	133.28
54	2x	55	PSU	O4-C4-N3	-2.23	115.84	120.12
1	2A	1920	OMC	O2-C2-N3	-2.23	118.71	122.33
1	1A	1984	5MC	N4-C4-N3	-2.22	114.42	118.48
32	2a	516	PSU	O4-C4-N3	-2.21	115.88	120.12
32	1a	527	7MG	N2-C2-N1	2.19	121.39	116.71
43	2l	92	0TD	CB-CA-N	-2.19	104.42	109.10
32	2a	1404	5MC	N4-C4-N3	-2.19	114.48	118.48
32	2a	527	7MG	O6-C6-C5	-2.19	122.17	127.54
1	1A	1939	PSU	O2-C2-N1	-2.18	120.39	122.79
1	1A	2263	OMG	C4-C5-N7	-2.18	107.26	110.72
32	2a	967	5MC	N4-C4-N3	-2.17	114.51	118.48
32	1a	1404	5MC	N4-C4-N3	-2.16	114.53	118.48
1	1A	2263	OMG	C1'-N9-C4	2.16	132.92	126.50
32	2a	1207	2MG	C8-N7-C5	2.15	108.13	104.24
32	1a	1407	5MC	CM5-C5-C6	-2.15	119.98	122.85
32	1a	516	PSU	C5-C6-N1	-2.15	118.89	122.11
1	1A	1984	5MC	CM5-C5-C6	-2.14	119.99	122.85
32	1a	1207	2MG	O3'-C3'-C2'	2.14	118.75	111.82
1	1A	1937	5MU	C5-C4-N3	2.13	117.13	115.31
1	1A	1961	5MU	C5-C6-N1	-2.12	121.15	123.34
32	2a	966	M2G	C8-N7-C5	2.12	108.08	104.24
32	1a	516	PSU	O4-C4-N3	-2.11	116.07	120.12
32	1a	527	7MG	C6-C5-C4	-2.11	118.27	122.62
32	1a	1400	5MC	N4-C4-N3	-2.09	114.66	118.48
1	1A	1939	PSU	O4-C4-N3	-2.09	116.11	120.12
1	2A	2605	PSU	O4-C4-N3	-2.09	116.11	120.12
1	1A	2617	PSU	O2-C2-N1	-2.09	120.49	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	527	7MG	C2-N1-C6	-2.09	121.30	125.10
1	1A	1933	PSU	N1-C2-N3	2.08	117.49	115.13
1	1A	1933	PSU	O4'-C1'-C2'	2.08	108.08	105.14
1	2A	2251	OMG	C8-N7-C5	2.08	108.00	104.24
1	1A	1942	OMC	O2-C2-N3	-2.07	118.97	122.33
1	1A	2617	PSU	C4-N3-C2	-2.07	123.36	126.34
1	2A	1939	5MU	C5-C6-N1	-2.06	121.21	123.34
54	2x	32	5MC	N4-C4-N3	-2.06	114.71	118.48
54	2x	55	PSU	C4-N3-C2	-2.06	123.36	126.34
32	1a	1498	UR3	C3U-N3-C4	2.06	120.83	117.89
1	2A	2503	2MA	C5-C6-N6	-2.05	118.98	123.43
32	1a	967	5MC	N4-C4-N3	-2.04	114.75	118.48
1	1A	1961	5MU	C5-C4-N3	2.04	117.05	115.31
1	2A	1942	5MC	N4-C4-N3	-2.03	114.77	118.48
1	2A	1915	5MU	O2-C2-N1	2.03	125.48	122.79
32	2a	1400	5MC	N4-C4-N3	-2.03	114.78	118.48
32	2a	527	7MG	N2-C2-N1	2.02	121.02	116.71
32	1a	1519	MA6	C4-N9-C8	2.02	107.92	105.73

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1937	5MU	O4'-C1'-N1-C2
1	1A	1937	5MU	O4'-C1'-N1-C6
1	1A	2263	OMG	C1'-C2'-O2'-CM2
32	1a	967	5MC	O4'-C4'-C5'-O5'
32	1a	967	5MC	C3'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
1	2A	1915	5MU	C3'-C4'-C5'-O5'
1	2A	1915	5MU	O4'-C4'-C5'-O5'
32	2a	527	7MG	C3'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
43	2l	92	0TD	CA-CB-CG-OD2
43	2l	92	0TD	CA-CB-CG-OD1
43	2l	92	0TD	SB-CB-CG-OD2
32	1a	527	7MG	C3'-C4'-C5'-O5'
32	1a	1402	4OC	C3'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	2A	2503	2MA	O4'-C4'-C5'-O5'
1	2A	2503	2MA	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	527	7MG	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	7MG	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C5-C6-N6-C9
43	1l	92	0TD	CA-CB-CG-OD2
1	2A	1915	5MU	C4'-C5'-O5'-P
1	1A	2515	2MA	O4'-C4'-C5'-O5'
1	2A	2552	OMU	O4'-C4'-C5'-O5'
43	2l	92	0TD	CA-CB-SB-CSB
1	2A	2251	OMG	C4'-C5'-O5'-P
32	1a	1400	5MC	O4'-C4'-C5'-O5'
1	1A	1942	OMC	C2'-C1'-N1-C2
32	1a	516	PSU	O4'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
32	1a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	516	PSU	O4'-C4'-C5'-O5'
1	1A	2263	OMG	C4'-C5'-O5'-P
32	1a	1519	MA6	C4'-C5'-O5'-P

There are no ring outliers.

25 monomers are involved in 50 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1518	MA6	2	0
43	1l	92	0TD	2	0
32	2a	1519	MA6	1	0
32	2a	1402	4OC	3	0
32	2a	1400	5MC	1	0
32	1a	1402	4OC	2	0
32	2a	1518	MA6	2	0
1	1A	1937	5MU	1	0
1	1A	1961	5MU	1	0
1	2A	2552	OMU	2	0
32	1a	966	M2G	1	0
32	1a	516	PSU	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1498	UR3	2	0
54	2x	32	5MC	1	0
1	2A	1939	5MU	1	0
54	2x	54	5MU	2	0
32	1a	1207	2MG	3	0
32	1a	1519	MA6	2	0
1	1A	2564	OMU	2	0
1	2A	1915	5MU	5	0
43	2l	92	0TD	1	0
54	1x	54	5MU	2	0
1	2A	2251	OMG	1	0
54	1x	8	4SU	1	0
32	2a	516	PSU	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2719 ligands modelled in this entry, 2717 are monoatomic - leaving 2 for Mogul analysis.

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

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

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

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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%)	0.04	208 (7%) 21 15	6, 22, 80, 93	0
1	2A	2856/2915 (97%)	0.57	249 (8%) 16 11	19, 41, 80, 92	0
2	1B	120/120 (100%)	0.24	2 (1%) 69 60	18, 35, 49, 69	0
2	2B	120/120 (100%)	1.28	19 (15%) 5 4	43, 60, 69, 73	0
3	1D	275/275 (100%)	-0.06	3 (1%) 78 70	7, 23, 36, 52	0
3	2D	275/275 (100%)	0.38	7 (2%) 58 48	19, 36, 47, 63	0
4	1E	204/204 (100%)	0.04	3 (1%) 72 63	7, 29, 47, 56	0
4	2E	204/204 (100%)	0.39	4 (1%) 65 56	19, 41, 55, 63	0
5	1F	203/203 (100%)	0.08	2 (0%) 79 72	7, 28, 53, 70	0
5	2F	203/203 (100%)	0.77	9 (4%) 39 31	24, 50, 63, 73	0
6	1G	181/181 (100%)	0.71	10 (5%) 30 23	28, 44, 55, 69	0
6	2G	181/181 (100%)	1.86	65 (35%) 1 0	56, 65, 74, 77	0
7	1H	174/174 (100%)	0.35	4 (2%) 61 51	23, 38, 49, 54	0
7	2H	173/174 (99%)	1.41	36 (20%) 2 2	50, 62, 69, 71	0
8	1I	147/147 (100%)	0.79	4 (2%) 56 46	31, 54, 66, 70	0
8	2I	146/147 (99%)	1.11	15 (10%) 12 9	39, 58, 68, 76	0
9	1N	140/140 (100%)	0.15	3 (2%) 63 54	14, 26, 44, 58	0
9	2N	140/140 (100%)	0.66	7 (5%) 34 26	28, 47, 59, 63	0
10	1O	122/122 (100%)	0.03	0 100 100	14, 26, 41, 49	0
10	2O	122/122 (100%)	0.61	4 (3%) 49 39	30, 40, 51, 56	0
11	1P	149/149 (100%)	0.14	2 (1%) 75 66	7, 32, 48, 64	0
11	2P	149/149 (100%)	1.05	17 (11%) 10 7	24, 50, 64, 71	0
12	1Q	141/141 (100%)	0.21	4 (2%) 55 45	14, 26, 42, 59	0
12	2Q	141/141 (100%)	0.93	6 (4%) 40 31	31, 47, 57, 65	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.00	1 (0%) 82 75	14, 22, 36, 47	0
13	2R	118/118 (100%)	0.50	2 (1%) 69 60	25, 37, 46, 55	0
14	1S	110/110 (100%)	0.33	0 100 100	24, 36, 45, 51	0
14	2S	110/110 (100%)	1.44	23 (20%) 2 2	46, 55, 62, 66	0
15	1T	131/131 (100%)	0.41	4 (3%) 51 41	20, 33, 52, 64	0
15	2T	131/131 (100%)	0.55	4 (3%) 51 41	36, 44, 59, 65	0
16	1U	116/116 (100%)	-0.19	0 100 100	9, 17, 35, 49	0
16	2U	116/116 (100%)	0.80	4 (3%) 48 39	26, 45, 55, 66	0
17	1V	101/101 (100%)	0.06	1 (0%) 79 72	8, 29, 44, 54	0
17	2V	101/101 (100%)	0.89	6 (5%) 28 21	32, 51, 59, 67	0
18	1W	112/112 (100%)	-0.09	1 (0%) 81 74	10, 17, 36, 66	0
18	2W	112/112 (100%)	0.50	7 (6%) 26 19	25, 34, 48, 60	0
19	1X	95/95 (100%)	0.17	2 (2%) 63 54	13, 24, 43, 59	0
19	2X	95/95 (100%)	0.77	6 (6%) 26 19	35, 44, 57, 60	0
20	1Y	107/107 (100%)	0.42	1 (0%) 81 74	24, 34, 49, 61	0
20	2Y	107/107 (100%)	1.33	18 (16%) 4 3	44, 54, 62, 73	0
21	1Z	203/203 (100%)	1.05	24 (11%) 9 7	28, 47, 62, 78	0
21	2Z	201/203 (99%)	1.46	32 (15%) 5 4	46, 60, 68, 71	0
22	10	77/77 (100%)	0.47	3 (3%) 43 34	17, 23, 37, 41	0
22	20	77/77 (100%)	1.15	7 (9%) 15 11	39, 45, 54, 63	0
23	11	97/97 (100%)	0.56	6 (6%) 26 20	11, 31, 54, 58	0
23	21	97/97 (100%)	0.78	7 (7%) 21 16	28, 40, 58, 64	0
24	12	70/70 (100%)	0.38	4 (5%) 29 22	24, 34, 46, 56	0
24	22	70/70 (100%)	1.11	7 (10%) 12 9	42, 53, 63, 64	0
25	13	59/59 (100%)	0.23	0 100 100	15, 26, 49, 59	0
25	23	59/59 (100%)	0.71	4 (6%) 23 17	37, 46, 57, 63	0
26	14	69/69 (100%)	1.41	16 (23%) 2 1	35, 60, 72, 81	0
26	24	69/69 (100%)	2.06	35 (50%) 0 0	64, 72, 81, 84	0
27	15	59/59 (100%)	0.07	2 (3%) 48 39	8, 23, 42, 51	0
27	25	59/59 (100%)	0.50	4 (6%) 23 17	23, 38, 52, 58	0
28	16	53/53 (100%)	0.08	0 100 100	24, 29, 41, 50	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/53 (100%)	0.71	2 (3%) 44 35	34, 47, 56, 58	0
29	17	48/48 (100%)	0.12	3 (6%) 26 19	8, 13, 34, 42	0
29	27	48/48 (100%)	0.54	5 (10%) 11 8	21, 28, 44, 58	0
30	18	64/64 (100%)	-0.07	0 100 100	15, 20, 28, 37	0
30	28	64/64 (100%)	0.97	9 (14%) 6 5	31, 39, 49, 54	0
31	19	37/37 (100%)	0.17	1 (2%) 56 46	19, 28, 43, 49	0
31	29	37/37 (100%)	1.08	4 (10%) 11 8	39, 47, 54, 57	0
32	1a	1488/1520 (97%)	0.89	139 (9%) 14 10	20, 53, 76, 91	0
32	2a	1492/1520 (98%)	1.11	184 (12%) 8 6	32, 59, 77, 90	0
33	1b	231/231 (100%)	1.45	46 (19%) 3 2	50, 60, 69, 74	0
33	2b	231/231 (100%)	1.74	74 (32%) 1 1	54, 66, 71, 81	0
34	1c	206/206 (100%)	1.11	20 (9%) 13 10	47, 57, 66, 69	0
34	2c	206/206 (100%)	1.71	68 (33%) 1 1	53, 65, 71, 74	0
35	1d	208/208 (100%)	1.31	37 (17%) 4 3	41, 56, 67, 70	0
35	2d	208/208 (100%)	1.35	29 (13%) 6 5	48, 57, 64, 69	0
36	1e	148/148 (100%)	0.80	9 (6%) 27 20	33, 49, 58, 69	0
36	2e	148/148 (100%)	1.23	20 (13%) 7 5	48, 56, 63, 76	0
37	1f	100/100 (100%)	0.97	6 (6%) 27 21	46, 53, 60, 64	0
37	2f	100/100 (100%)	0.99	8 (8%) 18 13	38, 54, 62, 67	0
38	1g	155/155 (100%)	1.16	19 (12%) 8 6	47, 55, 69, 76	0
38	2g	155/155 (100%)	1.38	24 (15%) 5 4	53, 62, 71, 80	0
39	1h	137/137 (100%)	1.16	17 (12%) 8 6	40, 51, 58, 65	0
39	2h	137/137 (100%)	1.30	22 (16%) 4 4	46, 56, 62, 65	0
40	1i	127/127 (100%)	1.56	33 (25%) 1 1	40, 61, 68, 72	0
40	2i	126/127 (99%)	2.14	68 (53%) 0 0	55, 65, 72, 79	0
41	1j	97/97 (100%)	1.64	26 (26%) 1 1	44, 61, 73, 78	0
41	2j	96/97 (98%)	1.91	41 (42%) 0 0	52, 66, 72, 74	0
42	1k	114/114 (100%)	0.92	9 (7%) 18 13	29, 50, 61, 65	0
42	2k	114/114 (100%)	1.22	15 (13%) 7 6	45, 57, 64, 68	0
43	1l	121/122 (99%)	0.94	13 (10%) 11 8	32, 43, 56, 61	0
43	2l	121/122 (99%)	1.00	11 (9%) 15 11	41, 52, 60, 63	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	116/116 (100%)	1.22	17 (14%) 6 4	45, 55, 64, 67	0
44	2m	114/116 (98%)	1.87	51 (44%) 0 0	56, 65, 72, 76	0
45	1n	60/60 (100%)	1.39	10 (16%) 4 3	47, 53, 59, 62	0
45	2n	60/60 (100%)	2.17	28 (46%) 0 0	58, 64, 69, 72	0
46	1o	88/88 (100%)	0.79	4 (4%) 38 30	36, 46, 58, 65	0
46	2o	88/88 (100%)	0.90	6 (6%) 23 17	45, 52, 61, 69	0
47	1p	82/82 (100%)	1.42	10 (12%) 8 6	43, 55, 62, 64	0
47	2p	82/82 (100%)	1.35	16 (19%) 3 2	46, 54, 61, 68	0
48	1q	99/99 (100%)	1.05	8 (8%) 18 13	36, 51, 61, 65	0
48	2q	99/99 (100%)	1.06	7 (7%) 22 16	43, 53, 60, 65	0
49	1r	68/68 (100%)	1.07	6 (8%) 15 11	43, 52, 62, 69	0
49	2r	68/68 (100%)	1.11	8 (11%) 9 7	48, 55, 64, 67	0
50	1s	83/83 (100%)	1.43	19 (22%) 2 1	50, 60, 67, 73	0
50	2s	83/83 (100%)	1.88	32 (38%) 1 0	55, 67, 75, 77	0
51	1t	96/98 (97%)	1.52	28 (29%) 1 1	45, 56, 64, 68	0
51	2t	98/98 (100%)	1.15	11 (11%) 10 7	46, 53, 64, 68	0
52	1u	23/23 (100%)	1.56	7 (30%) 1 1	48, 52, 57, 58	0
52	2u	23/23 (100%)	2.30	12 (52%) 0 0	58, 62, 67, 68	0
53	1v	3/3 (100%)	0.64	0 100 100	37, 37, 39, 40	0
53	2v	3/3 (100%)	1.02	1 (33%) 1 1	53, 53, 57, 62	0
54	1x	72/76 (94%)	0.37	2 (2%) 55 45	15, 41, 61, 71	0
54	2x	72/76 (94%)	1.01	7 (9%) 13 10	32, 57, 68, 75	0
55	1y	16/16 (100%)	0.11	1 (6%) 26 19	14, 20, 32, 39	0
55	2y	16/16 (100%)	0.44	0 100 100	28, 33, 48, 48	0
All	All	20755/20948 (99%)	0.75	2167 (10%) 11 8	6, 47, 71, 93	0

All (2167) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1A	1133	G	14.6
21	1Z	192	ALA	12.0
1	1A	1135	G	11.3
21	1Z	193	GLU	11.1
1	2A	2128	C	10.4

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Mol	Chain	Res	Type	RSRZ
1	1A	2139	A	10.2
1	2A	2147	G	10.1
1	1A	1149	A	9.9
1	1A	1150	C	9.1
1	2A	2112	G	8.9
1	2A	2127	G	8.7
1	1A	2155	G	8.6
1	1A	2149	G	8.2
1	2A	2123	G	8.0
1	2A	2119	A	7.9
1	2A	2124	G	7.9
1	1A	1121	C	7.8
38	1g	83	ALA	7.8
1	1A	2152	U	7.8
1	1A	1137	G	7.7
20	2Y	1	MET	7.7
1	2A	2118	U	7.6
1	2A	2107	C	7.6
1	1A	1123	A	7.3
21	2Z	193	GLU	7.2
21	1Z	202	GLU	7.2
1	1A	1132	A	7.2
21	1Z	194	PRO	7.2
1	1A	2154	U	7.1
1	1A	2180	A	6.9
1	2A	2159	G	6.8
1	1A	2150	C	6.8
1	1A	1134	A	6.7
1	1A	1112	U	6.7
1	1A	1118	C	6.6
1	1A	1139	G	6.6
1	1A	2169	G	6.6
21	1Z	191	VAL	6.5
21	2Z	192	ALA	6.5
1	2A	2148	G	6.5
1	1A	1151	U	6.5
1	1A	1120	G	6.4
1	1A	2145	G	6.4
1	1A	2153	G	6.4
1	2A	1076	C	6.4
21	1Z	195	GLU	6.4
21	1Z	197	ILE	6.3

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Mol	Chain	Res	Type	RSRZ
1	1A	1138	C	6.3
1	2A	2111	C	6.2
1	1A	2142	G	6.2
1	1A	2179	G	6.2
21	1Z	203	GLU	6.2
1	1A	1113	A	6.2
1	1A	1117	G	6.2
1	2A	2117	A	6.2
1	2A	2179	C	6.2
1	1A	2178	G	6.2
22	10	8	GLY	6.2
1	1A	2130	C	6.1
1	1A	2141	A	6.1
1	1A	1110	C	6.1
1	2A	2173	A	6.1
32	2a	1002	G	6.1
1	1A	2151	C	6.0
1	1A	1136	U	5.9
1	2A	2110	G	5.9
1	2A	2120	G	5.9
1	2A	2174	C	5.9
1	2A	2106	G	5.9
39	1h	117	GLY	5.8
1	2A	2168	G	5.8
32	2a	1030(A)	G	5.8
43	1l	29	GLY	5.8
1	2A	1075	C	5.8
1	1A	1148	C	5.8
32	1a	1030	C	5.8
1	1A	1124	U	5.7
21	2Z	194	PRO	5.7
1	2A	2108	C	5.7
33	1b	232	PRO	5.7
1	1A	2140	U	5.6
1	2A	2129	C	5.6
1	2A	2162	G	5.6
1	1A	1109	G	5.6
1	1A	2134	G	5.6
1	2A	2172	U	5.5
1	1A	2171	G	5.5
1	2A	2133	G	5.5
44	2m	6	GLY	5.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1101	G	5.5
1	1A	1114	G	5.5
1	1A	2146	G	5.5
50	2s	35	SER	5.4
1	1A	1103	A	5.4
1	2A	1067	A	5.4
1	1A	2181	G	5.3
32	2a	1003	G	5.3
1	1A	2128	G	5.3
1	1A	2806	G	5.2
1	1A	1122	C	5.2
1	1A	2194	U	5.2
1	1A	2807	C	5.2
32	1a	1027	C	5.2
32	2a	1249	C	5.2
1	2A	2169	A	5.2
1	1A	1104	G	5.2
1	2A	2157	G	5.2
35	2d	44	GLY	5.2
1	2A	2105	C	5.2
45	1n	2	ALA	5.2
45	2n	2	ALA	5.1
6	2G	76	SER	5.1
1	1A	2170	G	5.1
1	1A	1108	G	5.0
21	2Z	201	LYS	5.0
1	2A	2152	G	5.0
1	1A	1111	U	5.0
26	24	56	VAL	5.0
1	1A	1147	U	4.9
1	1A	1146	C	4.9
1	1A	2148	A	4.9
1	2A	2125	G	4.9
22	20	8	GLY	4.9
33	2b	232	PRO	4.9
1	1A	1126	C	4.9
21	1Z	200	GLY	4.9
1	2A	2132	U	4.9
1	1A	2159	C	4.9
32	2a	1027	C	4.9
39	2h	56	LYS	4.9
1	2A	2151	G	4.8

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Mol	Chain	Res	Type	RSRZ
1	2A	1095	A	4.8
1	1A	2198	A	4.8
38	2g	83	ALA	4.8
38	2g	154	TYR	4.8
1	1A	2129	C	4.8
39	2h	55	GLY	4.8
38	2g	4	ARG	4.7
1	1A	2147	G	4.7
1	1A	2177	G	4.7
1	2A	2137	C	4.7
1	2A	1089	G	4.7
32	2a	1001(A)	G	4.7
1	1A	2191	A	4.7
23	1l	26	ARG	4.7
21	2Z	191	VAL	4.7
35	1d	4	TYR	4.7
40	2i	29	ASN	4.7
42	2k	90	GLY	4.7
1	2A	2178	C	4.7
21	2Z	195	GLU	4.6
1	2A	1073	A	4.6
1	2A	1064	C	4.6
1	2A	2150	U	4.6
1	2A	2164	C	4.6
1	1A	1102	G	4.6
1	2A	2131	G	4.6
1	2A	2145	C	4.6
44	2m	66	LEU	4.6
1	2A	2130	U	4.6
1	2A	2136	C	4.6
1	1A	2126	G	4.6
38	2g	84	ASN	4.6
1	1A	2131	U	4.5
34	1c	194	GLY	4.5
1	2A	2163	C	4.5
1	2A	1087	G	4.5
15	1T	38	ASN	4.5
12	2Q	59	ARG	4.5
38	2g	82	GLY	4.5
1	2A	1536	C	4.5
26	24	67	TYR	4.5
38	1g	81	GLY	4.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2134	A	4.5
1	2A	2158	A	4.5
26	24	66	SER	4.5
1	1A	936	C	4.5
1	2A	2155	G	4.5
1	1A	1131	A	4.5
40	2i	126	SER	4.5
1	2A	1467	C	4.4
9	1N	140	VAL	4.4
52	2u	2	GLY	4.4
33	2b	145	LEU	4.4
42	2k	25	TYR	4.4
43	2l	64	TYR	4.4
26	14	50	VAL	4.4
1	1A	1127	U	4.4
1	2A	1099	G	4.4
32	1a	1031	G	4.4
50	2s	4	SER	4.4
52	2u	14	TRP	4.4
1	1A	2183	C	4.4
21	1Z	196	VAL	4.3
32	1a	1028	C	4.3
1	1A	2173	G	4.3
38	2g	81	GLY	4.3
42	1k	56	GLY	4.3
23	1l	27	GLU	4.3
33	1b	188	ALA	4.3
1	2A	2160	G	4.3
51	1t	71	THR	4.3
1	1A	2144	U	4.3
1	2A	2138	C	4.3
18	2W	63	ASP	4.3
1	1A	2195	A	4.2
32	2a	1026	G	4.2
38	1g	85	TYR	4.2
1	2A	1509	C	4.2
1	2A	2146	C	4.2
32	1a	1447	A	4.2
6	2G	149	VAL	4.2
1	1A	2201	C	4.2
1	2A	279	C	4.2
38	1g	84	ASN	4.2

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Mol	Chain	Res	Type	RSRZ
1	1A	2202	U	4.2
21	1Z	198	LYS	4.2
40	2i	62	TYR	4.2
7	2H	95	ARG	4.2
21	2Z	196	VAL	4.2
1	1A	932	C	4.2
1	1A	2132	G	4.2
1	1A	2182	G	4.2
32	2a	1030	C	4.2
51	1t	103	GLY	4.2
45	2n	7	ILE	4.2
26	24	49	PHE	4.2
1	1A	2196	C	4.1
39	2h	116	LYS	4.1
6	2G	60	LEU	4.1
1	1A	1130	A	4.1
23	2l	83	GLU	4.1
6	2G	81	LYS	4.1
1	2A	2121	G	4.1
26	24	41	PRO	4.1
1	1A	1119	A	4.1
40	1i	128	ARG	4.1
1	1A	2184	G	4.1
26	14	49	PHE	4.1
1	2A	2802	G	4.1
33	1b	190	THR	4.0
1	1A	2156	A	4.0
32	1a	91	C	4.0
1	2A	2104	G	4.0
1	2A	2181	G	4.0
40	2i	13	ALA	4.0
41	2j	75	ILE	4.0
45	1n	7	ILE	4.0
1	2A	2189	U	4.0
32	2a	932	C	4.0
32	2a	1286	A	4.0
1	1A	2203	G	4.0
1	2A	1058	G	4.0
1	2A	2149	G	4.0
39	1h	115	SER	4.0
1	1A	933	C	4.0
1	1A	1099	C	4.0

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Mol	Chain	Res	Type	RSRZ
1	1A	2158	C	4.0
35	1d	5	ILE	4.0
42	2k	26	ASN	4.0
6	2G	3	LEU	4.0
1	1A	2190	G	4.0
1	2A	1056	G	4.0
1	2A	1533	G	4.0
6	2G	74	LYS	4.0
32	1a	1024	G	4.0
32	2a	1032	G	4.0
40	2i	123	PRO	4.0
1	2A	2113	U	3.9
1	2A	2122	U	3.9
34	2c	2	GLY	3.9
1	2A	2103	C	3.9
16	2U	89	GLU	3.9
33	2b	17	PHE	3.9
1	1A	2209	G	3.9
1	2A	2154	G	3.9
1	1A	1140	U	3.9
44	2m	102	ARG	3.9
35	2d	11	LEU	3.9
1	1A	2210	C	3.9
1	1A	2176	G	3.9
1	2A	1093	G	3.9
26	14	59	PHE	3.9
1	2A	1528	A	3.9
43	1l	63	GLY	3.9
6	2G	90	LEU	3.9
41	1j	34	VAL	3.9
1	2A	2156	G	3.9
6	2G	39	ILE	3.9
1	1A	2197	C	3.9
34	1c	192	THR	3.9
6	2G	42	GLY	3.8
33	2b	12	GLU	3.8
1	2A	1046	A	3.8
1	2A	2109	U	3.8
32	1a	1032	G	3.8
39	2h	29	SER	3.8
34	2c	175	LEU	3.8
32	1a	163	C	3.8

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Mol	Chain	Res	Type	RSRZ
41	2j	47	PHE	3.8
1	2A	652(B)	A	3.8
51	2t	6	PRO	3.8
29	27	48	LYS	3.8
1	1A	2805	G	3.8
1	2A	1450	G	3.8
32	1a	1034	G	3.8
1	1A	1125	C	3.8
1	1A	2133	C	3.8
32	1a	1029	C	3.8
41	1j	72	VAL	3.8
47	1p	19	ILE	3.8
1	2A	2126	A	3.8
34	2c	184	TYR	3.8
41	2j	40	LEU	3.8
33	1b	48	MET	3.8
47	2p	9	PHE	3.8
23	2l	2	SER	3.8
50	1s	4	SER	3.8
14	2S	35	ILE	3.8
34	2c	5	ILE	3.8
1	2A	10	G	3.8
1	2A	2153	G	3.8
32	2a	1033	G	3.8
27	25	60	VAL	3.7
1	2A	889	C	3.7
33	2b	118	LEU	3.7
38	2g	28	ASN	3.7
1	1A	2138	G	3.7
1	2A	1077	A	3.7
1	2A	2135	A	3.7
35	2d	71	SER	3.7
24	22	46	GLN	3.7
21	1Z	70	LEU	3.7
1	1A	1143	U	3.7
1	2A	1090	U	3.7
44	1m	24	GLY	3.7
1	2A	2188	C	3.7
2	1B	3	C	3.7
2	2B	4	C	3.7
1	2A	1538	G	3.7
1	1A	2193	A	3.7

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Mol	Chain	Res	Type	RSRZ
12	2Q	28	ALA	3.7
21	1Z	189	ALA	3.7
26	24	65	ASP	3.7
42	2k	89	ALA	3.7
26	24	63	TYR	3.7
39	2h	131	GLY	3.7
41	2j	96	ILE	3.7
1	2A	875	G	3.7
32	1a	1030(A)	G	3.7
45	2n	49	HIS	3.7
33	1b	237	ALA	3.7
43	1l	64	TYR	3.7
1	2A	2180	U	3.7
33	2b	172	ILE	3.7
1	1A	2125	C	3.6
1	1A	2199	C	3.6
48	1q	26	GLN	3.6
1	1A	1116	A	3.6
32	2a	1102	A	3.6
33	1b	29	ALA	3.6
39	2h	28	ALA	3.6
52	2u	23	PRO	3.6
35	1d	164	ALA	3.6
1	1A	935	C	3.6
32	1a	92	C	3.6
38	1g	79	ARG	3.6
26	14	45	GLY	3.6
34	2c	185	GLY	3.6
1	2A	1055	G	3.6
1	2A	1071	G	3.6
1	2A	2115	G	3.6
34	2c	189	ALA	3.6
1	1A	2167	C	3.6
1	1A	2168	C	3.6
1	2A	888	C	3.6
1	2A	2143	C	3.6
32	2a	995	C	3.6
1	2A	1084	A	3.6
1	2A	2170	A	3.6
10	2O	57	VAL	3.6
38	1g	80	VAL	3.6
40	2i	5	TYR	3.6

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Mol	Chain	Res	Type	RSRZ
50	2s	79	THR	3.6
35	1d	155	LEU	3.6
1	1A	11	G	3.6
1	1A	2211	U	3.6
3	2D	170	GLY	3.6
44	2m	100	GLY	3.6
41	1j	98	ILE	3.6
47	2p	51	VAL	3.6
1	1A	2127	C	3.6
1	2A	1057	A	3.6
32	1a	152	A	3.6
26	14	52	THR	3.6
6	2G	2	PRO	3.6
1	2A	1066	U	3.5
41	1j	5	ARG	3.5
45	2n	10	ALA	3.5
32	1a	1001(A)	G	3.5
9	2N	9	VAL	3.5
41	2j	44	VAL	3.5
6	2G	82	LEU	3.5
50	1s	71	LEU	3.5
1	2A	2176	A	3.5
34	2c	190	ARG	3.5
35	2d	110	PHE	3.5
45	2n	8	GLU	3.5
32	2a	1084	G	3.5
35	2d	149	ALA	3.5
44	2m	75	ALA	3.5
1	1A	2192	A	3.5
1	2A	1449	A	3.5
1	2A	1083	U	3.5
7	2H	66	GLY	3.5
21	2Z	200	GLY	3.5
32	1a	1025	U	3.5
33	1b	18	GLY	3.5
34	2c	159	GLY	3.5
38	1g	82	GLY	3.5
26	14	56	VAL	3.5
7	2H	124	GLU	3.5
33	2b	48	MET	3.5
21	2Z	199	LYS	3.5
26	14	48	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	1A	10	G	3.5
1	1A	1221	G	3.5
32	1a	70	G	3.5
32	1a	1026	G	3.5
32	2a	1202	G	3.5
40	1i	15	ALA	3.5
1	2A	2161	C	3.5
21	2Z	2	GLU	3.5
34	2c	137	ALA	3.5
34	2c	107	GLN	3.4
1	1A	1145	G	3.4
1	2A	2805	G	3.4
34	2c	13	GLY	3.4
39	1h	90	GLY	3.4
52	2u	16	GLY	3.4
14	2S	33	LYS	3.4
45	1n	15	LYS	3.4
32	1a	1030(D)	A	3.4
1	1A	2172	U	3.4
1	2A	645	C	3.4
1	2A	1102	C	3.4
1	2A	2142	C	3.4
20	2Y	2	ARG	3.4
33	2b	202	PRO	3.4
33	2b	233	SER	3.4
39	2h	52	ASP	3.4
50	1s	13	ASP	3.4
41	2j	76	ASN	3.4
45	1n	8	GLU	3.4
1	1A	2137	G	3.4
1	1A	2208	G	3.4
1	2A	2116	G	3.4
1	2A	2165	G	3.4
32	2a	1034	G	3.4
45	2n	29	ARG	3.4
1	1A	934	A	3.4
1	1A	1141	A	3.4
1	2A	1054	A	3.4
32	2a	88	A	3.4
14	2S	34	HIS	3.4
11	2P	24	GLY	3.4
39	1h	93	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
22	20	55	ARG	3.4
1	1A	1129	U	3.4
43	2l	62	SER	3.4
1	1A	1879	A	3.4
1	1A	2902	G	3.4
1	2A	1074	G	3.4
1	2A	1460	A	3.4
7	2H	106	THR	3.4
1	1A	2186	C	3.4
1	2A	902	C	3.4
21	1Z	201	LYS	3.4
11	2P	123	LEU	3.4
33	1b	221	LEU	3.4
23	1l	28	GLY	3.4
33	1b	229	VAL	3.4
52	2u	10	ARG	3.4
41	2j	77	PRO	3.4
1	1A	1556	A	3.4
1	1A	2123	G	3.3
1	2A	1068	G	3.3
1	2A	2141	G	3.3
32	1a	147	G	3.3
32	1a	725	G	3.3
1	1A	2815	C	3.3
1	2A	2896	C	3.3
40	2i	6	GLY	3.3
21	1Z	190	GLU	3.3
37	2f	93	SER	3.3
40	2i	64	THR	3.3
50	2s	20	LEU	3.3
35	1d	3	ARG	3.3
38	2g	5	ARG	3.3
40	2i	9	ARG	3.3
32	2a	1447	A	3.3
32	1a	178	C	3.3
1	2A	2793	G	3.3
32	1a	1033	G	3.3
51	2t	65	LYS	3.3
21	2Z	197	ILE	3.3
26	24	42	PHE	3.3
44	2m	109	THR	3.3
23	2l	26	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
34	2c	145	GLY	3.3
40	1i	62	TYR	3.3
1	1A	1142	A	3.3
34	2c	71	ALA	3.3
32	2a	1017	G	3.3
20	2Y	106	LEU	3.3
45	2n	6	LEU	3.3
6	2G	70	VAL	3.3
15	1T	37	GLY	3.3
43	1l	62	SER	3.3
1	2A	271(N)	U	3.3
32	1a	1001	A	3.3
35	1d	157	LEU	3.3
41	1j	88	LEU	3.3
40	2i	109	VAL	3.3
6	2G	64	THR	3.3
1	1A	2143	G	3.3
2	2B	117	G	3.3
32	1a	69	G	3.3
32	1a	1002	G	3.3
45	2n	61	TRP	3.3
34	1c	193	TYR	3.2
35	2d	4	TYR	3.2
26	24	57	GLU	3.2
6	2G	20	ILE	3.2
1	1A	2136	A	3.2
1	2A	1103	A	3.2
44	2m	53	VAL	3.2
1	1A	2185	C	3.2
33	1b	228	GLY	3.2
21	2Z	198	LYS	3.2
47	1p	17	TYR	3.2
32	2a	1036	G	3.2
33	1b	94	ASN	3.2
54	2x	46	G	3.2
40	1i	117	HIS	3.2
51	1t	10	LEU	3.2
43	2l	18	VAL	3.2
44	1m	117	VAL	3.2
34	1c	2	GLY	3.2
35	1d	80	GLU	3.2
48	2q	86	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2175	C	3.2
30	28	64	TYR	3.2
41	1j	4	ILE	3.2
1	1A	1220	U	3.2
19	1X	95	LEU	3.2
40	2i	66	ARG	3.2
41	2j	5	ARG	3.2
1	1A	2163	G	3.2
43	1l	18	VAL	3.2
43	1l	43	VAL	3.2
30	28	21	LYS	3.2
35	2d	23	GLY	3.2
40	2i	7	THR	3.2
44	2m	116	THR	3.2
1	2A	2171	A	3.2
23	2l	27	GLU	3.2
32	1a	197	A	3.2
7	1H	2	SER	3.2
40	1i	81	ILE	3.2
44	2m	97	PRO	3.2
45	2n	21	TYR	3.2
46	1o	3	ILE	3.2
41	2j	58	ASP	3.2
1	2A	1104	C	3.2
32	1a	1030(B)	C	3.2
40	2i	111	ARG	3.2
52	2u	15	ARG	3.2
1	2A	877	U	3.2
1	2A	2144	U	3.2
16	2U	4	ALA	3.2
6	2G	47	LYS	3.2
29	17	48	LYS	3.2
1	2A	11	G	3.2
2	2B	118	G	3.2
26	14	54	GLY	3.2
32	2a	1310	G	3.2
45	2n	55	GLY	3.2
34	2c	124	ILE	3.2
38	1g	156	TRP	3.2
6	2G	146	TYR	3.1
8	2I	61	ARG	3.1
40	2i	10	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
41	2j	68	HIS	3.1
51	1t	73	HIS	3.1
1	2A	1108	U	3.1
1	2A	2139	C	3.1
32	1a	726	C	3.1
32	2a	1020	U	3.1
32	2a	1030(B)	C	3.1
38	2g	9	VAL	3.1
40	2i	28	VAL	3.1
35	1d	165	MET	3.1
32	2a	1031	G	3.1
44	2m	90	LEU	3.1
3	2D	38	LYS	3.1
11	2P	121	LYS	3.1
40	2i	11	LYS	3.1
1	2A	896	A	3.1
1	2A	1088	A	3.1
1	2A	1445	A	3.1
1	2A	2629	A	3.1
8	2I	74	ASN	3.1
17	2V	26	ASP	3.1
32	2a	1001	A	3.1
34	2c	86	VAL	3.1
1	1A	386	U	3.1
6	2G	41	GLN	3.1
34	1c	81	GLY	3.1
35	1d	179	GLU	3.1
41	1j	74	ILE	3.1
41	2j	74	ILE	3.1
7	2H	173	PRO	3.1
50	2s	2	PRO	3.1
38	2g	78	ARG	3.1
1	1A	2174	G	3.1
1	2A	2833	G	3.1
18	2W	60	ASN	3.1
32	1a	630	G	3.1
32	2a	963	G	3.1
33	2b	165	VAL	3.1
1	1A	937	A	3.1
32	2a	1287	A	3.1
1	1A	9	U	3.1
40	2i	31	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
35	1d	156	GLU	3.1
35	2d	5	ILE	3.1
35	2d	158	ILE	3.1
32	1a	1043	C	3.1
32	2a	1103	C	3.1
32	2a	1129	C	3.1
6	2G	62	LEU	3.1
21	2Z	125	LEU	3.1
38	1g	78	ARG	3.1
41	1j	77	PRO	3.1
41	2j	42	THR	3.1
44	1m	116	THR	3.1
44	2m	103	THR	3.1
50	2s	30	LEU	3.1
33	1b	28	PHE	3.1
45	1n	21	TYR	3.1
50	2s	52	TYR	3.1
34	2c	9	GLY	3.1
34	2c	158	GLY	3.1
1	2A	1063	G	3.1
1	2A	1096	A	3.1
1	2A	2100	G	3.1
32	2a	994	A	3.1
32	2a	1104	G	3.1
1	2A	2167	U	3.1
32	1a	90	U	3.1
32	2a	1126	U	3.1
26	24	55	ARG	3.1
50	1s	29	ARG	3.1
30	28	5	LYS	3.1
41	2j	37	PRO	3.1
1	1A	2200	C	3.1
6	2G	56	ALA	3.0
34	2c	187	ALA	3.0
7	2H	56	SER	3.0
6	2G	119	GLY	3.0
11	2P	118	GLY	3.0
35	2d	90	GLY	3.0
44	2m	95	GLY	3.0
6	2G	77	ILE	3.0
29	27	41	ARG	3.0
33	2b	133	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
7	2H	55	PRO	3.0
7	2H	67	LEU	3.0
21	2Z	70	LEU	3.0
34	1c	196	LEU	3.0
43	2l	123	LYS	3.0
50	2s	71	LEU	3.0
1	2A	2114	A	3.0
32	2a	1021	G	3.0
27	25	18	ALA	3.0
33	2b	16	HIS	3.0
50	2s	9	VAL	3.0
13	2R	69	ASP	3.0
35	1d	154	ASN	3.0
40	2i	124	GLN	3.0
38	1g	4	ARG	3.0
44	2m	70	LEU	3.0
12	1Q	80	GLU	3.0
35	2d	156	GLU	3.0
42	1k	92	GLU	3.0
1	1A	2189	U	3.0
32	1a	1257	U	3.0
45	1n	22	THR	3.0
1	1A	2641	A	3.0
1	2A	890	A	3.0
47	1p	24	ALA	3.0
32	1a	1042	G	3.0
40	2i	36	TYR	3.0
1	2A	1531	C	3.0
21	1Z	199	LYS	3.0
32	1a	217	C	3.0
32	2a	1354	C	3.0
33	1b	99	GLY	3.0
34	2c	8	ILE	3.0
40	2i	116	LYS	3.0
6	2G	139	LEU	3.0
43	2l	22	SER	3.0
49	2r	58	LEU	3.0
51	1t	61	SER	3.0
14	2S	8	GLU	3.0
21	2Z	95	PRO	3.0
27	15	59	GLU	3.0
32	1a	1532	U	3.0

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Mol	Chain	Res	Type	RSRZ
38	2g	2	ALA	3.0
33	1b	136	VAL	3.0
45	2n	25	VAL	3.0
1	1A	1144	A	3.0
14	2S	93	LYS	3.0
20	2Y	55	TYR	3.0
20	2Y	94	LYS	3.0
40	2i	125	TYR	3.0
24	12	70	GLN	3.0
33	2b	44	LEU	3.0
1	1A	2816	G	3.0
2	2B	2	C	3.0
4	2E	87	GLU	3.0
42	2k	28	THR	3.0
34	2c	173	VAL	3.0
41	1j	44	VAL	3.0
41	2j	72	VAL	3.0
7	2H	61	HIS	3.0
3	2D	275	LYS	2.9
40	1i	78	LYS	2.9
52	2u	6	ARG	2.9
1	2A	2892	A	2.9
16	2U	80	ILE	2.9
32	2a	1183	A	2.9
32	2a	1531	A	2.9
33	2b	108	ILE	2.9
36	2e	13	ILE	2.9
14	2S	54	LEU	2.9
33	1b	187	LEU	2.9
35	2d	6	GLY	2.9
51	1t	11	SER	2.9
1	2A	1047	G	2.9
1	2A	2166	G	2.9
26	14	18	CYS	2.9
26	24	39	CYS	2.9
32	2a	630	G	2.9
1	1A	2164	C	2.9
1	2A	886	C	2.9
1	2A	2177	C	2.9
32	2a	1322	C	2.9
34	2c	160	ALA	2.9
41	1j	20	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
45	2n	30	ALA	2.9
26	24	33	VAL	2.9
33	2b	190	THR	2.9
50	2s	33	THR	2.9
6	2G	83	ARG	2.9
44	2m	96	LEU	2.9
26	24	32	TYR	2.9
38	1g	154	TYR	2.9
40	2i	67	GLY	2.9
41	1j	10	GLY	2.9
41	2j	93	GLY	2.9
1	1A	1100	A	2.9
32	2a	1035	A	2.9
32	2a	1236	A	2.9
39	2h	115	SER	2.9
18	2W	58	ALA	2.9
26	24	35	VAL	2.9
33	1b	105	PHE	2.9
45	2n	18	VAL	2.9
39	1h	116	LYS	2.9
32	1a	153	C	2.9
32	1a	1137	C	2.9
32	1a	1023	G	2.9
37	1f	25	ILE	2.9
1	2A	9	U	2.9
1	2A	271(K)	U	2.9
32	1a	1000	U	2.9
22	20	22	GLY	2.9
27	25	59	GLU	2.9
1	2A	1085	A	2.9
10	2O	73	ASP	2.9
8	1I	19	VAL	2.9
36	2e	105	VAL	2.9
41	2j	34	VAL	2.9
48	1q	37	LYS	2.9
41	2j	38	ILE	2.9
35	1d	21	LEU	2.9
47	1p	49	LEU	2.9
32	1a	1217	C	2.9
32	2a	1363	C	2.9
32	2a	1000	U	2.9
41	1j	36	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	2A	171	G	2.9
9	2N	8	GLN	2.9
32	1a	220	G	2.9
11	2P	119	GLU	2.9
40	2i	2	GLU	2.9
51	1t	75	ASN	2.9
27	15	60	VAL	2.9
35	1d	170	VAL	2.9
51	2t	97	ALA	2.9
33	1b	210	SER	2.9
40	2i	18	PHE	2.9
1	1A	1115	A	2.9
1	1A	2812	A	2.9
6	1G	83	ARG	2.9
32	1a	1493	A	2.9
7	2H	71	LEU	2.9
48	2q	98	LEU	2.9
26	24	54	GLY	2.8
34	2c	96	GLY	2.8
1	1A	1106	U	2.8
5	2F	184	TYR	2.8
32	1a	174	C	2.8
32	2a	1029	C	2.8
54	2x	47	U	2.8
26	14	69	LYS	2.8
40	2i	92	TYR	2.8
1	1A	2187	G	2.8
1	1A	2212	G	2.8
1	2A	2184	G	2.8
6	2G	73	ALA	2.8
32	1a	1036	G	2.8
26	14	55	ARG	2.8
45	2n	37	PHE	2.8
26	14	51	ASP	2.8
6	1G	76	SER	2.8
34	1c	154	SER	2.8
51	1t	70	SER	2.8
6	2G	140	ILE	2.8
39	1h	127	LEU	2.8
40	2i	19	LEU	2.8
41	2j	6	ILE	2.8
50	2s	15	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	2A	901	A	2.8
30	28	4	MET	2.8
40	1i	8	GLY	2.8
6	2G	45	GLU	2.8
37	2f	38	GLU	2.8
44	2m	73	GLU	2.8
32	2a	1235	U	2.8
35	2d	38	TYR	2.8
1	2A	1053	C	2.8
1	2A	2185	C	2.8
52	2u	24	ARG	2.8
46	2o	40	SER	2.8
1	1A	2204	G	2.8
32	1a	102	G	2.8
1	1A	925	A	2.8
1	1A	2157	A	2.8
12	2Q	100	GLY	2.8
17	2V	42	GLY	2.8
32	1a	1286	A	2.8
33	2b	95	GLN	2.8
39	2h	57	PRO	2.8
15	1T	129	ARG	2.8
1	2A	362	U	2.8
33	1b	165	VAL	2.8
45	2n	34	TYR	2.8
44	2m	78	ILE	2.8
6	2G	108	ASN	2.8
36	2e	130	ASN	2.8
1	1A	34	C	2.8
20	2Y	11	ASP	2.8
50	2s	12	ASP	2.8
45	2n	17	LYS	2.8
7	2H	128	PRO	2.8
6	2G	164	GLU	2.8
32	1a	160	A	2.8
32	2a	1030(D)	A	2.8
32	2a	1250	A	2.8
32	2a	1268	A	2.8
7	2H	101	ARG	2.8
39	1h	75	ARG	2.8
35	2d	8	VAL	2.8
39	1h	26	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
6	2G	69	ALA	2.8
11	2P	91	PHE	2.8
21	2Z	164	ALA	2.8
37	1f	63	TYR	2.8
45	1n	16	PHE	2.8
6	2G	34	LEU	2.8
32	1a	921	U	2.8
32	2a	1257	U	2.8
40	2i	63	ILE	2.8
42	2k	27	ASN	2.8
17	2V	85	LYS	2.8
45	2n	11	LYS	2.8
1	1A	1555	C	2.8
1	1A	2804	C	2.8
1	1A	2814	C	2.8
1	2A	1100	C	2.8
32	1a	219	C	2.8
32	1a	345	C	2.8
32	1a	651	C	2.8
32	2a	1019	C	2.8
32	2a	1260	C	2.8
48	2q	99	SER	2.8
26	24	64	GLY	2.8
44	1m	100	GLY	2.8
50	1s	72	GLY	2.8
47	2p	41	PRO	2.8
35	2d	160	GLN	2.7
6	1G	48	GLU	2.7
28	26	37	ARG	2.7
29	27	47	ARG	2.7
51	1t	80	ARG	2.7
6	2G	159	VAL	2.7
1	1A	273	G	2.7
1	1A	938	G	2.7
1	1A	2803	A	2.7
1	2A	614(B)	G	2.7
1	2A	1070	A	2.7
1	2A	1537	G	2.7
14	2S	29	PHE	2.7
32	2a	1004	A	2.7
51	2t	66	ALA	2.7
5	2F	181	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
7	2H	94	TYR	2.7
32	2a	1190	G	2.7
32	2a	1353	G	2.7
33	2b	92	TYR	2.7
33	2b	162	ILE	2.7
34	2c	135	LYS	2.7
17	1V	26	ASP	2.7
34	2c	62	ASP	2.7
11	2P	116	GLY	2.7
34	1c	9	GLY	2.7
35	1d	23	GLY	2.7
45	2n	38	GLY	2.7
51	1t	69	GLY	2.7
51	1t	82	SER	2.7
1	1A	2207	C	2.7
1	2A	2803	C	2.7
32	2a	1038	C	2.7
33	2b	231	GLU	2.7
20	2Y	89	PHE	2.7
27	25	14	ALA	2.7
34	2c	163	ALA	2.7
38	2g	22	LEU	2.7
43	1l	30	ALA	2.7
3	1D	275	LYS	2.7
32	2a	1492	A	2.7
1	1A	2175	G	2.7
32	1a	1082	G	2.7
41	2j	69	ASN	2.7
40	2i	49	PRO	2.7
38	1g	77	SER	2.7
40	2i	14	VAL	2.7
1	2A	1546	C	2.7
32	2a	1158	C	2.7
33	2b	51	LEU	2.7
34	2c	92	ALA	2.7
40	1i	47	LEU	2.7
51	2t	7	LYS	2.7
1	2A	229	A	2.7
1	2A	2102	U	2.7
14	2S	5	THR	2.7
32	1a	1446	U	2.7
44	2m	37	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	1A	1512	G	2.7
1	1A	1905	G	2.7
1	2A	271(M)	G	2.7
1	2A	874	G	2.7
1	2A	2187	G	2.7
32	1a	97	G	2.7
32	1a	148	G	2.7
32	2a	1224	G	2.7
7	2H	15	VAL	2.7
25	23	60	GLU	2.7
37	2f	90	VAL	2.7
37	2f	95	GLU	2.7
40	2i	96	LEU	2.7
41	2j	65	LEU	2.7
5	2F	22	ALA	2.7
6	2G	88	ILE	2.7
36	2e	94	ALA	2.7
45	2n	36	PHE	2.7
44	2m	65	LYS	2.7
45	2n	58	LYS	2.7
1	1A	2160	C	2.7
1	2A	1445(A)	C	2.7
1	2A	1532	C	2.7
32	2a	962	C	2.7
33	1b	236	TYR	2.7
35	2d	73	ARG	2.7
38	2g	115	ARG	2.7
7	2H	126	PRO	2.7
36	1e	114	GLY	2.7
51	1t	9	ASN	2.7
1	1A	12	U	2.7
1	1A	1092	A	2.7
1	1A	1128	U	2.7
1	1A	1466	U	2.7
32	1a	172	A	2.7
32	2a	1319	A	2.7
6	2G	58	GLN	2.7
35	1d	62	GLN	2.7
6	2G	15	VAL	2.7
34	2c	138	VAL	2.7
38	2g	80	VAL	2.7
41	1j	71	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
40	2i	127	LYS	2.6
49	2r	61	LYS	2.6
14	2S	37	ALA	2.6
1	2A	1091	G	2.6
1	2A	1541	G	2.6
32	1a	93	G	2.6
32	2a	1138	G	2.6
6	2G	136	ARG	2.6
35	2d	115	ARG	2.6
1	1A	2161	C	2.6
1	1A	2165	C	2.6
32	2a	1321	C	2.6
40	2i	39	GLY	2.6
40	2i	115	GLY	2.6
34	2c	191	THR	2.6
50	2s	53	ASN	2.6
11	2P	3	LEU	2.6
21	2Z	56	VAL	2.6
21	2Z	183	LEU	2.6
37	2f	83	ASP	2.6
40	2i	26	VAL	2.6
40	2i	40	LEU	2.6
40	2i	102	LEU	2.6
41	2j	55	LYS	2.6
43	1l	52	LEU	2.6
44	2m	101	GLN	2.6
1	2A	878	A	2.6
1	2A	1069	A	2.6
33	1b	172	ILE	2.6
50	2s	70	LYS	2.6
11	2P	120	ALA	2.6
13	2R	41	ALA	2.6
33	2b	152	PHE	2.6
35	1d	149	ALA	2.6
44	2m	107	ALA	2.6
1	1A	269	G	2.6
1	2A	2190	G	2.6
32	2a	993	G	2.6
32	2a	1042	G	2.6
32	2a	1142	G	2.6
32	2a	1220	G	2.6
26	24	17	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
34	2c	7	PRO	2.6
1	2A	1914	C	2.6
4	2E	69	LYS	2.6
14	2S	49	VAL	2.6
18	2W	65	LEU	2.6
32	2a	848	C	2.6
32	2a	979	C	2.6
32	2a	1149	C	2.6
32	2a	1359	C	2.6
32	2a	1397	C	2.6
33	2b	164	VAL	2.6
40	2i	17	VAL	2.6
40	2i	108	VAL	2.6
33	2b	200	ILE	2.6
41	1j	33	GLN	2.6
44	2m	4	ILE	2.6
1	2A	1094	U	2.6
6	2G	46	ALA	2.6
40	2i	45	ALA	2.6
14	2S	31	SER	2.6
32	2a	1493	A	2.6
24	12	69	ARG	2.6
35	1d	115	ARG	2.6
35	2d	159	ARG	2.6
39	1h	37	ARG	2.6
41	2j	43	ARG	2.6
41	2j	46	ARG	2.6
50	2s	3	ARG	2.6
5	1F	16	GLY	2.6
6	2G	142	PRO	2.6
21	2Z	68	PRO	2.6
33	2b	131	PRO	2.6
3	2D	276	LYS	2.6
7	2H	88	LEU	2.6
7	2H	103	LEU	2.6
8	2I	3	VAL	2.6
32	2a	1013	G	2.6
32	2a	1024	G	2.6
32	2a	1355	G	2.6
33	2b	121	LEU	2.6
34	2c	12	LEU	2.6
40	1i	7	THR	2.6

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Mol	Chain	Res	Type	RSRZ
44	2m	105	THR	2.6
34	2c	157	ILE	2.6
50	2s	51	VAL	2.6
6	1G	73	ALA	2.6
11	2P	12	ALA	2.6
34	2c	186	PHE	2.6
38	2g	116	ALA	2.6
1	1A	1936	C	2.6
32	2a	91	C	2.6
32	2a	1043	C	2.6
41	1j	59	SER	2.6
51	1t	31	SER	2.6
11	2P	15	ARG	2.6
40	2i	16	ARG	2.6
1	1A	1491	A	2.6
32	1a	344	A	2.6
32	1a	702	A	2.6
32	1a	1531	A	2.6
40	2i	99	LEU	2.6
16	2U	9	VAL	2.6
20	1Y	1	MET	2.6
25	23	59	VAL	2.6
34	2c	141	VAL	2.6
47	1p	22	THR	2.6
9	2N	92	ALA	2.6
36	1e	21	ALA	2.6
38	2g	65	ALA	2.6
40	2i	43	ALA	2.6
40	2i	101	PHE	2.6
44	1m	2	ALA	2.6
44	1m	51	ALA	2.6
51	1t	66	ALA	2.6
1	2A	361	G	2.5
5	1F	195	ASP	2.6
32	1a	1166	G	2.5
1	2A	2897	U	2.5
23	11	2	SER	2.5
32	2a	1096	C	2.5
50	2s	38	SER	2.5
6	2G	29	TRP	2.5
32	1a	161	A	2.5
32	1a	393	A	2.5

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Mol	Chain	Res	Type	RSRZ
32	1a	694	A	2.5
32	2a	1005	A	2.5
33	2b	228	GLY	2.5
42	1k	90	GLY	2.5
51	1t	101	GLY	2.5
52	2u	11	GLY	2.5
8	2I	136	VAL	2.5
20	2Y	45	VAL	2.5
31	29	17	ILE	2.5
33	2b	136	VAL	2.5
42	2k	109	VAL	2.5
13	1R	102	GLU	2.5
43	1l	65	GLU	2.5
44	2m	67	GLU	2.5
49	2r	47	THR	2.5
26	24	59	PHE	2.5
34	2c	146	ALA	2.5
40	2i	52	ALA	2.5
40	2i	59	PHE	2.5
14	2S	61	ASN	2.5
41	1j	76	ASN	2.5
7	2H	42	ARG	2.5
14	2S	3	ARG	2.5
50	1s	14	HIS	2.5
1	2A	1078	U	2.5
2	2B	1	U	2.5
6	2G	78	SER	2.5
32	2a	1446	U	2.5
2	2B	23	G	2.5
32	1a	144	G	2.5
32	1a	198	G	2.5
1	1A	1595	C	2.5
2	2B	5	C	2.5
32	2a	1119	C	2.5
32	2a	1325	C	2.5
12	2Q	79	LEU	2.5
37	1f	19	LEU	2.5
1	1A	554	A	2.5
1	1A	1091	A	2.5
1	2A	2801(A)	A	2.5
41	1j	64	GLU	2.5
47	2p	45	THR	2.5

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Mol	Chain	Res	Type	RSRZ
48	2q	16	GLN	2.5
33	1b	171	ALA	2.5
33	2b	161	ALA	2.5
40	1i	16	ARG	2.5
44	1m	102	ARG	2.5
44	2m	94	ARG	2.5
30	28	3	LYS	2.5
33	2b	189	ASP	2.5
1	1A	1107	U	2.5
32	2a	952	U	2.5
32	2a	992	U	2.5
40	1i	126	SER	2.5
6	2G	133	LEU	2.5
33	1b	98	LEU	2.5
4	1E	193	GLY	2.5
33	2b	201	ILE	2.5
40	2i	68	GLY	2.5
51	1t	100	ILE	2.5
2	2B	70	C	2.5
32	2a	1128	C	2.5
32	2a	1369	C	2.5
1	1A	1152	G	2.5
1	2A	652(U)	G	2.5
32	1a	346	G	2.5
32	1a	1009	G	2.5
32	2a	988	G	2.5
32	2a	1022	G	2.5
9	2N	68	GLU	2.5
33	1b	12	GLU	2.5
48	2q	78	GLU	2.5
38	2g	7	ALA	2.5
44	2m	76	ALA	2.5
1	1A	302	A	2.5
1	2A	278	A	2.5
5	2F	188	ARG	2.5
32	1a	1503	A	2.5
32	2a	532	A	2.5
32	2a	1092	A	2.5
32	2a	1248	A	2.5
35	1d	132	ARG	2.5
35	1d	159	ARG	2.5
47	2p	18	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
52	1u	9	ARG	2.5
34	1c	72	LYS	2.5
44	1m	106	ASN	2.5
51	1t	14	LYS	2.5
51	1t	30	LYS	2.5
47	2p	16	HIS	2.5
38	2g	12	LEU	2.5
39	2h	2	LEU	2.5
35	2d	197	PRO	2.5
46	2o	2	PRO	2.5
33	2b	15	VAL	2.5
34	2c	106	VAL	2.5
38	2g	17	VAL	2.5
44	2m	60	VAL	2.5
6	2G	102	PHE	2.5
33	1b	17	PHE	2.5
33	1b	33	TYR	2.5
33	1b	129	GLU	2.5
36	2e	83	GLU	2.5
37	2f	5	GLU	2.5
35	2d	50	ARG	2.5
46	2o	68	ARG	2.5
51	1t	12	ALA	2.5
1	2A	1049	C	2.5
1	2A	1080	C	2.5
2	2B	6	C	2.5
2	2B	28	C	2.5
19	2X	33	LYS	2.5
32	1a	221	C	2.5
32	2a	999	C	2.5
52	2u	3	LYS	2.5
1	2A	326	G	2.5
1	2A	2186	G	2.5
1	2A	2894	G	2.5
32	1a	145	G	2.5
32	1a	993	G	2.5
32	2a	971	G	2.5
32	2a	1087	G	2.5
32	2a	1094	G	2.5
32	2a	1294	G	2.5
32	2a	996	A	2.5
34	2c	176	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
26	24	16	CYS	2.5
7	2H	98	LEU	2.4
33	2b	101	MET	2.4
20	2Y	96	ILE	2.4
34	2c	84	ILE	2.4
40	2i	77	ILE	2.4
47	2p	19	ILE	2.4
50	1s	31	ILE	2.4
14	2S	90	GLY	2.4
33	2b	93	VAL	2.4
44	1m	98	VAL	2.4
8	1I	10	GLU	2.4
34	2c	90	GLU	2.4
36	2e	45	PHE	2.4
50	2s	29	ARG	2.4
6	2G	50	ALA	2.4
34	1c	189	ALA	2.4
42	2k	124	LYS	2.4
44	2m	33	ALA	2.4
47	1p	7	ALA	2.4
51	1t	97	ALA	2.4
1	2A	1092	C	2.4
1	2A	1166	C	2.4
33	2b	221	LEU	2.4
37	2f	19	LEU	2.4
44	1m	56	LEU	2.4
32	1a	1035	A	2.4
1	1A	299	G	2.4
1	1A	2122	G	2.4
1	2A	1527	G	2.4
32	1a	394	G	2.4
32	2a	1361	G	2.4
40	2i	98	PRO	2.4
44	2m	16	ASP	2.4
50	1s	12	ASP	2.4
9	2N	140	VAL	2.4
38	2g	21	VAL	2.4
40	1i	14	VAL	2.4
41	1j	31	GLY	2.4
47	2p	10	GLY	2.4
48	2q	33	GLY	2.4
7	2H	97	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
29	17	23	ARG	2.4
33	2b	216	SER	2.4
34	2c	179	ARG	2.4
35	1d	122	ARG	2.4
12	1Q	85	LYS	2.4
32	1a	173	U	2.4
32	2a	991	U	2.4
35	2d	163	GLU	2.4
43	2l	23	LYS	2.4
6	2G	138	GLN	2.4
17	2V	11	GLN	2.4
43	2l	30	ALA	2.4
21	2Z	99	TYR	2.4
48	1q	89	LEU	2.4
51	1t	72	LEU	2.4
1	2A	1072	C	2.4
2	2B	62	C	2.4
32	2a	1039	C	2.4
32	2a	1097	C	2.4
41	2j	39	PRO	2.4
6	1G	134	GLY	2.4
20	2Y	93	GLY	2.4
33	2b	7	VAL	2.4
34	1c	195	VAL	2.4
36	2e	5	ASP	2.4
40	2i	54	ASP	2.4
43	1l	112	ASP	2.4
44	2m	7	VAL	2.4
1	2A	899	A	2.4
1	2A	1045	A	2.4
1	2A	1086	A	2.4
45	2n	41	ARG	2.4
46	1o	88	ARG	2.4
52	1u	6	ARG	2.4
1	1A	1153	G	2.4
1	1A	1513	G	2.4
1	1A	1584	G	2.4
1	2A	1044	G	2.4
32	1a	326	G	2.4
32	2a	1182	G	2.4
33	1b	233	SER	2.4
33	2b	49	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
51	2t	11	SER	2.4
6	2G	57	ALA	2.4
21	1Z	188	ALA	2.4
45	2n	59	ALA	2.4
8	2I	54	GLN	2.4
1	1A	2166	U	2.4
1	2A	1082	U	2.4
32	2a	1219	U	2.4
47	2p	38	TYR	2.4
22	10	58	THR	2.4
33	2b	67	THR	2.4
14	2S	95	HIS	2.4
6	2G	53	LEU	2.4
41	1j	65	LEU	2.4
5	2F	206	ILE	2.4
33	2b	214	ILE	2.4
41	2j	41	PRO	2.4
11	2P	71	VAL	2.4
18	2W	49	LYS	2.4
21	2Z	114	GLY	2.4
33	2b	14	GLY	2.4
33	2b	184	VAL	2.4
39	1h	66	GLY	2.4
49	1r	27	GLY	2.4
51	1t	96	GLY	2.4
33	2b	144	ARG	2.4
34	2c	126	ARG	2.4
1	1A	2162	C	2.4
1	1A	2205	C	2.4
2	1B	2	C	2.4
2	2B	12	C	2.4
32	1a	454	C	2.4
32	2a	1145	C	2.4
6	2G	80	PHE	2.4
50	1s	27	GLU	2.4
6	1G	46	ALA	2.4
15	2T	126	ALA	2.4
21	2Z	184	ALA	2.4
40	1i	82	ALA	2.4
34	2c	20	SER	2.4
1	1A	387	G	2.4
1	1A	2124	U	2.4

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Mol	Chain	Res	Type	RSRZ
32	1a	78	G	2.4
32	2a	1065	U	2.4
34	1c	201	TYR	2.4
46	1o	69	TYR	2.4
39	2h	112	LEU	2.4
33	2b	39	ILE	2.4
34	2c	207	VAL	2.3
35	2d	13	ARG	2.3
40	1i	17	VAL	2.3
40	1i	108	VAL	2.3
41	2j	78	ASN	2.3
44	2m	15	VAL	2.3
6	2G	49	ASP	2.3
41	2j	54	PHE	2.3
47	1p	68	ASP	2.3
21	2Z	190	GLU	2.3
33	1b	77	ALA	2.3
33	1b	123	ALA	2.3
33	2b	141	GLU	2.3
1	2A	652(T)	C	2.3
30	28	35	GLN	2.3
32	1a	1008	C	2.3
32	2a	501	C	2.3
32	2a	1045	C	2.3
34	2c	28	GLN	2.3
41	1j	84	GLN	2.3
32	2a	1044	A	2.3
32	2a	1225	A	2.3
32	2a	1357	A	2.3
36	2e	10	MET	2.3
50	1s	34	TRP	2.3
33	2b	31	TYR	2.3
35	1d	138	TYR	2.3
38	2g	16	LEU	2.3
41	2j	100	THR	2.3
42	1k	25	TYR	2.3
44	2m	92	HIS	2.3
52	1u	8	THR	2.3
32	2a	1040	U	2.3
49	2r	50	ILE	2.3
50	2s	7	LYS	2.3
51	1t	65	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	926	G	2.3
1	2A	1110	G	2.3
1	2A	2792	G	2.3
8	2I	57	ARG	2.3
11	2P	90	ARG	2.3
32	2a	1323	G	2.3
34	2c	198	VAL	2.3
39	2h	102	ARG	2.3
51	1t	8	ARG	2.3
51	1t	79	ARG	2.3
52	1u	24	ARG	2.3
54	1x	46	G	2.3
35	1d	87	GLY	2.3
35	2d	2	GLY	2.3
19	2X	75	ASP	2.3
5	2F	166	ALA	2.3
11	2P	141	ALA	2.3
33	1b	231	GLU	2.3
40	1i	46	ALA	2.3
44	2m	51	ALA	2.3
44	1m	101	GLN	2.3
51	1t	18	GLN	2.3
7	2H	171	LEU	2.3
34	1c	47	LEU	2.3
36	2e	53	LEU	2.3
42	1k	53	SER	2.3
6	2G	165	THR	2.3
32	1a	103	C	2.3
32	1a	150	C	2.3
32	2a	1234	C	2.3
41	2j	67	THR	2.3
1	2A	866	A	2.3
2	2B	58	A	2.3
32	2a	1041	A	2.3
42	2k	29	ILE	2.3
51	2t	34	LYS	2.3
32	1a	182	U	2.3
32	2a	1085	U	2.3
33	1b	131	PRO	2.3
38	1g	3	ARG	2.3
22	20	23	VAL	2.3
34	2c	120	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
50	1s	9	VAL	2.3
50	2s	11	VAL	2.3
11	1P	118	GLY	2.3
34	2c	63	ASN	2.3
35	2d	79	PHE	2.3
1	1A	1218	G	2.3
1	1A	2813	G	2.3
7	2H	96	ALA	2.3
30	28	51	ALA	2.3
32	1a	68	G	2.3
32	2a	428	G	2.3
32	2a	1184	G	2.3
32	2a	1283	G	2.3
36	1e	138	ALA	2.3
37	1f	38	GLU	2.3
45	1n	30	ALA	2.3
49	2r	60	ALA	2.3
41	1j	73	ASP	2.3
38	1g	13	GLN	2.3
41	2j	88	LEU	2.3
12	2Q	22	LYS	2.3
26	24	15	ILE	2.3
42	2k	42	TRP	2.3
45	2n	60	SER	2.3
12	1Q	10	ARG	2.3
12	1Q	59	ARG	2.3
34	2c	172	ARG	2.3
35	1d	153	ARG	2.3
38	2g	3	ARG	2.3
40	1i	104	ARG	2.3
41	1j	45	ARG	2.3
44	1m	23	TYR	2.3
44	2m	88	ARG	2.3
50	2s	36	ARG	2.3
55	1y	16	ARG	2.3
7	2H	10	PRO	2.3
20	2Y	77	PRO	2.3
1	2A	271(J)	C	2.3
1	1A	271	U	2.3
1	1A	1507	A	2.3
1	2A	1079	C	2.3
1	2A	1109	C	2.3

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Mol	Chain	Res	Type	RSRZ
32	1a	71	C	2.3
32	1a	143	A	2.3
32	1a	171	A	2.3
32	2a	1269	A	2.3
33	2b	230	VAL	2.3
35	1d	112	VAL	2.3
42	2k	39	PRO	2.3
54	2x	16	C	2.3
32	2a	1390	U	2.3
3	1D	28	GLU	2.3
6	1G	50	ALA	2.3
6	2G	61	ALA	2.3
9	1N	47	ALA	2.3
11	1P	117	GLU	2.3
36	2e	81	GLU	2.3
38	1g	57	GLU	2.3
19	2X	92	LEU	2.3
23	2l	82	LEU	2.3
40	2i	112	LYS	2.3
49	1r	68	LYS	2.3
1	2A	1059	G	2.3
1	2A	2321	G	2.3
26	24	5	ILE	2.3
32	1a	66	G	2.3
32	1a	166	G	2.3
32	1a	1010	G	2.3
32	1a	1331	G	2.3
32	2a	73	G	2.3
38	1g	42	ILE	2.3
6	2G	71	THR	2.3
8	1I	61	ARG	2.3
9	1N	115	ARG	2.3
19	2X	68	ARG	2.3
23	1l	76	ARG	2.3
24	22	26	ARG	2.3
40	2i	71	SER	2.3
42	1k	28	THR	2.3
6	2G	87	PRO	2.3
40	2i	88	TYR	2.3
17	2V	22	VAL	2.3
21	2Z	96	VAL	2.3
23	2l	70	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
26	24	29	PRO	2.3
33	1b	174	VAL	2.3
52	2u	4	GLY	2.3
32	2a	90	U	2.3
32	2a	723	U	2.3
1	2A	236	C	2.2
1	2A	2804	C	2.2
32	1a	1041	A	2.2
32	1a	1262	C	2.2
32	2a	1209	C	2.2
7	2H	58	GLU	2.2
33	2b	134	GLU	2.2
34	2c	180	ALA	2.2
38	1g	2	ALA	2.2
44	2m	42	ALA	2.2
49	2r	62	GLU	2.2
41	2j	8	LEU	2.2
48	1q	74	LEU	2.2
14	2S	38	GLN	2.2
35	1d	166	LYS	2.2
44	2m	31	LYS	2.2
47	2p	82	GLN	2.2
6	1G	52	ILE	2.2
34	2c	152	ILE	2.2
24	12	51	ARG	2.2
33	2b	19	HIS	2.2
33	2b	21	ARG	2.2
43	2l	59	ARG	2.2
47	2p	25	ARG	2.2
5	2F	14	PRO	2.2
26	24	52	THR	2.2
34	2c	95	THR	2.2
21	2Z	175	VAL	2.2
6	1G	146	TYR	2.2
22	10	9	SER	2.2
26	14	32	TYR	2.2
33	1b	109	SER	2.2
40	1i	49	PRO	2.2
41	2j	94	VAL	2.2
39	1h	20	TYR	2.2
40	1i	4	TYR	2.2
1	1A	385	G	2.2

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Mol	Chain	Res	Type	RSRZ
2	2B	24	G	2.2
32	1a	146	G	2.2
32	1a	158	G	2.2
32	2a	973	G	2.2
32	2a	1089	G	2.2
7	2H	5	GLY	2.2
34	2c	155	GLY	2.2
52	1u	2	GLY	2.2
7	2H	123	PHE	2.2
1	2A	1105	U	2.2
32	2a	1095	U	2.2
32	2a	1532	U	2.2
8	2I	63	ALA	2.2
9	2N	10	GLU	2.2
20	2Y	91	GLU	2.2
24	12	66	GLU	2.2
33	1b	143	GLU	2.2
34	2c	50	ALA	2.2
40	1i	106	ALA	2.2
40	2i	106	ALA	2.2
41	1j	32	ALA	2.2
1	2A	1111	A	2.2
1	2A	1220	A	2.2
1	2A	1224	C	2.2
3	2D	154	LYS	2.2
32	1a	218	C	2.2
32	1a	1019	C	2.2
32	1a	1151	A	2.2
32	2a	1028	C	2.2
32	2a	1093	A	2.2
32	2a	1141	C	2.2
34	2c	147	LYS	2.2
34	2c	150	LYS	2.2
40	1i	40	LEU	2.2
54	2x	21	A	2.2
33	2b	182	ILE	2.2
50	2s	49	ILE	2.2
7	2H	3	ARG	2.2
8	2I	133	HIS	2.2
35	1d	168	ARG	2.2
39	2h	104	ARG	2.2
44	2m	104	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
21	2Z	27	VAL	2.2
11	2P	110	TYR	2.2
35	1d	91	SER	2.2
51	2t	70	SER	2.2
34	2c	194	GLY	2.2
36	2e	23	GLY	2.2
44	2m	26	GLY	2.2
1	2A	1106	G	2.2
15	2T	94	ALA	2.2
21	1Z	125	LEU	2.2
21	2Z	189	ALA	2.2
32	1a	79	G	2.2
32	1a	348	G	2.2
32	1a	380	G	2.2
32	1a	1143	G	2.2
32	2a	933	G	2.2
32	2a	1233	G	2.2
36	1e	83	GLU	2.2
39	2h	136	GLU	2.2
40	1i	50	LEU	2.2
40	2i	122	ALA	2.2
41	2j	20	ALA	2.2
42	2k	92	GLU	2.2
1	1A	2597	U	2.2
2	2B	41	U	2.2
3	1D	262	ARG	2.2
6	2G	51	ARG	2.2
8	2I	71	ILE	2.2
33	1b	200	ILE	2.2
33	2b	42	ILE	2.2
40	1i	111	ARG	2.2
50	2s	37	ARG	2.2
1	1A	1222	A	2.2
1	2A	1050	A	2.2
32	1a	270	A	2.2
32	1a	1092	A	2.2
32	1a	1183	A	2.2
32	2a	1067	A	2.2
1	1A	697	C	2.2
1	1A	1511	C	2.2
1	2A	280	C	2.2
1	2A	2294	C	2.2

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Mol	Chain	Res	Type	RSRZ
32	1a	1141	C	2.2
32	2a	488	C	2.2
54	1x	65	C	2.2
6	2G	122	PRO	2.2
45	2n	33	VAL	2.2
29	27	43	THR	2.2
26	24	36	CYS	2.2
33	1b	97	TRP	2.2
44	2m	43	THR	2.2
7	2H	164	TYR	2.2
26	24	43	TYR	2.2
39	1h	58	TYR	2.2
41	2j	36	GLY	2.2
47	1p	37	GLY	2.2
48	1q	99	SER	2.2
4	1E	57	LYS	2.2
10	2O	99	PHE	2.2
39	1h	56	LYS	2.2
4	1E	195	LEU	2.2
6	2G	43	LEU	2.2
7	1H	87	LEU	2.2
14	2S	56	LEU	2.2
24	22	3	LEU	2.2
24	22	60	LEU	2.2
33	2b	61	LEU	2.2
33	2b	177	ALA	2.2
40	1i	52	ALA	2.2
40	2i	46	ALA	2.2
50	1s	50	ALA	2.2
36	1e	25	ARG	2.2
39	2h	84	ARG	2.2
40	2i	42	ARG	2.2
40	2i	74	ILE	2.2
46	1o	82	ILE	2.2
52	1u	13	ILE	2.2
3	2D	45	ASN	2.2
26	24	46	GLN	2.2
33	1b	135	GLN	2.2
1	2A	327	G	2.2
1	2A	859	G	2.2
1	2A	2891	G	2.2
32	1a	306	G	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	79	G	2.2
1	1A	942	A	2.2
8	2I	81	VAL	2.2
14	2S	46	VAL	2.2
19	2X	81	VAL	2.2
32	1a	149	A	2.2
32	2a	1288	A	2.2
33	2b	197	VAL	2.2
40	2i	41	VAL	2.2
50	2s	67	VAL	2.2
1	1A	1594	C	2.2
1	2A	1547	C	2.2
32	1a	932	C	2.2
32	2a	826	C	2.2
32	2a	1037	C	2.2
33	1b	168	THR	2.2
41	2j	87	THR	2.2
23	21	79	GLY	2.2
24	22	8	LYS	2.2
33	2b	99	GLY	2.2
40	2i	30	GLY	2.2
42	1k	45	GLY	2.2
45	1n	61	TRP	2.2
6	1G	25	TYR	2.2
6	2G	180	PHE	2.2
22	20	26	TYR	2.2
14	2S	52	SER	2.2
14	2S	73	LEU	2.2
21	1Z	166	SER	2.2
26	24	9	LEU	2.2
33	2b	192	SER	2.2
40	1i	33	PHE	2.2
34	2c	188	LEU	2.2
34	2c	196	LEU	2.2
36	1e	53	LEU	2.2
42	1k	98	LEU	2.2
34	2c	65	ALA	2.2
36	2e	21	ALA	2.2
48	2q	24	GLU	2.2
29	17	47	ARG	2.1
30	28	46	ARG	2.1
33	2b	185	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
39	1h	84	ARG	2.1
39	1h	86	ILE	2.1
41	1j	75	ILE	2.1
44	1m	22	ILE	2.1
44	2m	99	ARG	2.1
32	1a	202	U	2.1
32	2a	982	U	2.1
34	2c	6	HIS	2.1
20	2Y	66	PRO	2.1
33	2b	91	PRO	2.1
35	1d	133	VAL	2.1
40	2i	53	VAL	2.1
43	1l	5	PRO	2.1
44	2m	17	VAL	2.1
45	2n	14	PRO	2.1
3	2D	171	ASP	2.1
10	2O	56	ASP	2.1
20	2Y	5	MET	2.1
22	20	56	ASP	2.1
44	2m	47	ASP	2.1
48	1q	13	ASP	2.1
1	1A	927	G	2.1
1	2A	1466	G	2.1
1	2A	2893	G	2.1
6	2G	67	LYS	2.1
2	2B	26	A	2.1
2	2B	63	G	2.1
32	1a	183	G	2.1
32	1a	199	G	2.1
32	1a	216	G	2.1
32	1a	650	G	2.1
32	1a	1003	G	2.1
32	1a	1030(C)	G	2.1
32	1a	1144	G	2.1
32	2a	644	G	2.1
32	2a	731	G	2.1
32	2a	975	A	2.1
32	2a	987	G	2.1
32	2a	1171	G	2.1
33	2b	139	LYS	2.1
41	1j	42	THR	2.1
45	2n	22	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	1A	303	C	2.1
1	1A	948	C	2.1
1	2A	876	C	2.1
1	2A	2789	C	2.1
2	2B	3	C	2.1
14	2S	58	LEU	2.1
6	2G	131	TYR	2.1
32	1a	154	C	2.1
32	2a	590	C	2.1
32	2a	1137	C	2.1
33	1b	10	LEU	2.1
33	2b	28	PHE	2.1
33	2b	154	LEU	2.1
35	1d	185	PHE	2.1
52	1u	14	TRP	2.1
33	2b	199	TYR	2.1
36	2e	60	TYR	2.1
42	2k	75	TYR	2.1
44	2m	87	TYR	2.1
8	2I	46	ALA	2.1
8	2I	55	ALA	2.1
21	2Z	166	SER	2.1
40	1i	43	ALA	2.1
42	2k	44	SER	2.1
6	2G	137	GLU	2.1
34	2c	105	GLU	2.1
40	2i	83	ARG	2.1
44	2m	55	ARG	2.1
49	2r	55	ARG	2.1
33	2b	113	HIS	2.1
32	2a	1150	U	2.1
35	1d	203	VAL	2.1
36	2e	128	PRO	2.1
39	1h	95	VAL	2.1
40	1i	86	VAL	2.1
51	1t	98	PRO	2.1
7	1H	175	LYS	2.1
35	2d	144	ASP	2.1
11	2P	26	GLY	2.1
12	2Q	30	GLY	2.1
14	2S	45	GLY	2.1
34	1c	13	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
43	1l	44	THR	2.1
33	2b	98	LEU	2.1
40	1i	102	LEU	2.1
50	1s	5	LEU	2.1
20	2Y	97	ARG	2.1
21	1Z	187	ALA	2.1
26	24	58	ARG	2.1
32	1a	382	A	2.1
32	1a	1093	A	2.1
37	1f	76	ALA	2.1
49	1r	42	ARG	2.1
1	1A	2188	G	2.1
1	1A	2206	G	2.1
1	1A	2213	G	2.1
1	2A	916	G	2.1
1	2A	1062	G	2.1
1	2A	1160	G	2.1
32	1a	1021	G	2.1
32	2a	413	G	2.1
32	2a	548	G	2.1
32	2a	1124	G	2.1
32	2a	1131	G	2.1
32	2a	1435	G	2.1
33	2b	126	GLU	2.1
42	2k	40	ILE	2.1
50	2s	40	ILE	2.1
54	2x	64	G	2.1
1	2A	34	C	2.1
2	2B	60	C	2.1
32	1a	155	C	2.1
32	1a	1007	C	2.1
32	1a	1038	C	2.1
32	2a	1007	C	2.1
32	2a	1254	C	2.1
36	2e	20	GLN	2.1
46	2o	71	GLN	2.1
33	1b	140	HIS	2.1
40	2i	58	HIS	2.1
41	1j	68	HIS	2.1
7	2H	44	VAL	2.1
18	2W	61	ASN	2.1
36	2e	90	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
40	1i	41	VAL	2.1
47	1p	1	MET	2.1
31	29	30	PRO	2.1
33	1b	125	PRO	2.1
1	2A	12	U	2.1
1	2A	1065	U	2.1
32	1a	841	U	2.1
32	2a	1083	U	2.1
9	2N	23	LEU	2.1
21	1Z	33	LEU	2.1
33	2b	11	LEU	2.1
34	2c	171	GLY	2.1
34	2c	197	GLY	2.1
50	1s	68	GLY	2.1
8	2I	108	THR	2.1
26	24	27	THR	2.1
33	1b	122	PHE	2.1
33	2b	55	PHE	2.1
41	2j	92	THR	2.1
49	1r	47	THR	2.1
50	2s	10	PHE	2.1
18	2W	68	ARG	2.1
19	1X	68	ARG	2.1
36	2e	25	ARG	2.1
45	1n	23	ARG	2.1
6	2G	171	ALA	2.1
23	1l	77	ALA	2.1
8	1I	99	GLU	2.1
20	2Y	44	ILE	2.1
21	1Z	186	GLU	2.1
33	1b	127	ILE	2.1
35	1d	82	ALA	2.1
39	2h	86	ILE	2.1
41	2j	23	ILE	2.1
44	1m	50	GLU	2.1
44	2m	9	ILE	2.1
49	2r	75	ILE	2.1
50	2s	75	ALA	2.1
51	2t	93	GLU	2.1
1	2A	887	A	2.1
11	2P	25	SER	2.1
32	2a	10	A	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1201	A	2.1
32	2a	1285	A	2.1
45	2n	27	CYS	2.1
48	1q	62	SER	2.1
1	2A	885	C	2.1
1	2A	2101	G	2.1
5	2F	183	VAL	2.1
6	2G	38	VAL	2.1
15	1T	8	LYS	2.1
17	2V	47	VAL	2.1
20	2Y	72	VAL	2.1
32	2a	70	G	2.1
32	2a	485	G	2.1
32	2a	657	G	2.1
32	2a	717	C	2.1
32	2a	990	C	2.1
32	2a	1030(C)	G	2.1
32	2a	1108	G	2.1
32	2a	1282	C	2.1
33	2b	174	VAL	2.1
38	1g	53	LYS	2.1
43	1l	20	LYS	2.1
50	1s	45	VAL	2.1
53	2v	18	G	2.1
39	2h	101	PRO	2.1
35	2d	154	ASN	2.1
28	26	11	LEU	2.1
36	2e	123	LEU	2.1
6	2G	85	GLY	2.1
30	28	38	GLY	2.1
32	1a	204	U	2.1
34	1c	197	GLY	2.1
41	2j	52	GLY	2.1
41	2j	63	PHE	2.1
43	2l	14	GLY	2.1
44	2m	68	GLY	2.1
50	1s	26	GLY	2.1
7	2H	70	THR	2.1
24	22	55	ARG	2.1
34	2c	79	ARG	2.1
35	2d	3	ARG	2.1
37	2f	46	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
40	2i	104	ARG	2.1
46	2o	64	ARG	2.1
52	2u	9	ARG	2.1
8	2I	146	ALA	2.1
19	2X	22	ALA	2.1
34	1c	24	ALA	2.1
34	1c	168	ALA	2.1
34	2c	53	ALA	2.1
36	2e	109	ILE	2.1
40	2i	76	ALA	2.1
40	2i	81	ILE	2.1
44	2m	69	GLU	2.1
4	2E	151	TYR	2.1
39	2h	65	TYR	2.1
6	2G	155	MET	2.0
7	1H	139	GLN	2.0
33	1b	22	LYS	2.0
40	1i	11	LYS	2.0
40	1i	113	LYS	2.0
41	2j	7	LYS	2.0
47	1p	76	GLN	2.0
47	2p	76	GLN	2.0
50	2s	55	LYS	2.0
1	2A	111	A	2.0
1	2A	1508	A	2.0
6	2G	160	VAL	2.0
32	1a	472	A	2.0
26	24	7	PRO	2.0
35	1d	189	PRO	2.0
44	1m	10	PRO	2.0
1	2A	237	C	2.0
1	2A	1118	C	2.0
1	2A	1446	C	2.0
1	2A	1584	C	2.0
32	1a	433	C	2.0
32	2a	71	C	2.0
32	2a	984	C	2.0
32	2a	1218	C	2.0
39	1h	2	LEU	2.0
44	2m	77	ASN	2.0
49	1r	85	LEU	2.0
1	1A	928	G	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	883	G	2.0
1	2A	1169	G	2.0
1	2A	1170	G	2.0
1	2A	1447	G	2.0
1	2A	1465	G	2.0
1	2A	2191	G	2.0
7	2H	51	ARG	2.0
7	2H	142	GLY	2.0
21	2Z	89	PHE	2.0
24	22	7	ARG	2.0
32	1a	1156	G	2.0
32	2a	77	G	2.0
32	2a	922	G	2.0
32	2a	1134	G	2.0
32	2a	1221	G	2.0
33	1b	152	PHE	2.0
35	2d	87	GLY	2.0
36	1e	23	GLY	2.0
50	2s	8	GLY	2.0
1	2A	2585	U	2.0
26	14	15	ILE	2.0
31	19	17	ILE	2.0
32	2a	65	U	2.0
34	1c	95	THR	2.0
38	1g	30	ILE	2.0
21	1Z	184	ALA	2.0
25	23	51	ALA	2.0
40	1i	105	ASP	2.0
44	1m	4	ILE	2.0
50	2s	31	ILE	2.0
41	2j	26	ALA	2.0
44	2m	5	ALA	2.0
49	1r	73	ALA	2.0
8	2I	135	GLU	2.0
20	2Y	29	GLU	2.0
34	2c	206	GLU	2.0
36	1e	81	GLU	2.0
40	2i	12	GLU	2.0
43	2l	16	GLU	2.0
7	2H	172	LYS	2.0
26	24	2	LYS	2.0
26	24	69	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
33	2b	8	LYS	2.0
33	2b	236	TYR	2.0
34	1c	147	LYS	2.0
44	1m	59	TYR	2.0
44	2m	21	TYR	2.0
47	2p	50	LYS	2.0
47	2p	1	MET	2.0
4	2E	72	VAL	2.0
7	2H	11	VAL	2.0
7	2H	50	VAL	2.0
39	2h	51	VAL	2.0
38	2g	47	CYS	2.0
38	2g	93	PRO	2.0
1	2A	1509(A)	A	2.0
6	2G	19	LEU	2.0
14	2S	32	LEU	2.0
32	1a	196	A	2.0
32	2a	1130	A	2.0
32	2a	1252	A	2.0
32	2a	1363(A)	A	2.0
34	1c	94	LEU	2.0
35	1d	135	LEU	2.0
36	2e	119	LEU	2.0
39	2h	59	LEU	2.0
46	2o	32	LEU	2.0
6	2G	132	ASN	2.0
18	1W	37	ARG	2.0
33	2b	130	ARG	2.0
40	1i	20	ARG	2.0
44	2m	110	ARG	2.0
45	2n	57	ARG	2.0
51	2t	89	ARG	2.0
26	14	64	GLY	2.0
29	27	26	GLY	2.0
33	2b	65	GLY	2.0
35	1d	93	PHE	2.0
40	2i	69	GLY	2.0
50	1s	10	PHE	2.0
50	1s	54	GLY	2.0
50	2s	82	GLY	2.0
51	2t	96	GLY	2.0
1	1A	2486	C	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	903	C	2.0
1	2A	2140	C	2.0
7	2H	4	ILE	2.0
21	2Z	57	ILE	2.0
26	24	22	ILE	2.0
31	29	10	ILE	2.0
32	1a	67	C	2.0
32	1a	176	C	2.0
32	1a	840	C	2.0
32	1a	1037	C	2.0
32	2a	217	C	2.0
39	2h	109	ILE	2.0
54	2x	48	C	2.0
15	2T	130	ALA	2.0
21	1Z	107	THR	2.0
21	2Z	109	ALA	2.0
33	1b	173	ALA	2.0
34	2c	192	THR	2.0
50	1s	48	THR	2.0
50	2s	24	ALA	2.0
1	2A	1097	U	2.0
32	2a	1086	U	2.0
1	2A	1719	G	2.0
1	2A	2207	G	2.0
5	2F	27	GLU	2.0
15	2T	107	ASP	2.0
32	1a	992	U	2.0
32	1a	1212	U	2.0
22	20	24	LYS	2.0
25	23	48	GLU	2.0
31	29	31	LYS	2.0
32	1a	181	G	2.0
32	1a	471	G	2.0
32	1a	933	G	2.0
35	1d	163	GLU	2.0
36	1e	117	ASP	2.0
44	2m	58	GLU	2.0
54	2x	20	U	2.0
32	2a	505	G	2.0
32	2a	1139	G	2.0
32	2a	1316	G	2.0
32	2a	1356	G	2.0

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Mol	Chain	Res	Type	RSRZ
40	2i	113	LYS	2.0
43	2l	124	LYS	2.0
47	2p	43	LYS	2.0
51	1t	87	LYS	2.0
35	1d	173	TRP	2.0
47	2p	48	TRP	2.0
21	2Z	9	TYR	2.0
26	14	63	TYR	2.0
34	2c	193	TYR	2.0
42	1k	75	TYR	2.0
26	24	10	VAL	2.0
26	24	50	VAL	2.0
33	2b	71	VAL	2.0
33	2b	81	VAL	2.0
34	2c	151	VAL	2.0
35	1d	148	VAL	2.0
35	2d	105	VAL	2.0
37	1f	37	VAL	2.0
39	2h	103	VAL	2.0
48	1q	19	VAL	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
54	PSU	2x	55	20/21	0.78	0.17	54,59,67,69	0
1	5MU	2A	1915	21/22	0.79	0.15	58,65,81,94	0
32	2MG	2a	1207	24/25	0.81	0.14	58,64,73,77	0
32	PSU	2a	516	20/21	0.83	0.15	58,63,69,71	0
1	5MU	1A	1937	21/22	0.84	0.18	50,57,72,76	0
54	5MU	2x	54	21/22	0.85	0.14	56,60,63,66	0
1	PSU	1A	1939	20/21	0.86	0.15	34,47,52,52	0
43	0TD	2l	92	10/11	0.86	0.14	50,53,56,61	0
1	PSU	2A	1917	20/21	0.87	0.14	46,58,67,72	0
32	7MG	2a	527	24/25	0.87	0.14	52,56,62,67	0
32	2MG	1a	1207	24/25	0.88	0.14	54,58,61,69	0
32	5MC	2a	967	21/22	0.88	0.15	52,56,63,69	0
32	M2G	2a	966	25/26	0.89	0.14	48,53,60,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	5MC	1a	1400	21/22	0.90	0.13	39,42,46,48	0
32	5MC	2a	1400	21/22	0.91	0.12	54,59,62,64	0
1	OMC	2A	1920	21/22	0.91	0.13	39,46,48,50	0
54	4SU	2x	8	20/21	0.91	0.13	51,57,61,61	0
54	5MC	2x	32	21/22	0.91	0.12	46,55,57,59	0
32	PSU	1a	516	20/21	0.91	0.11	39,48,50,50	0
1	PSU	2A	1911	20/21	0.91	0.12	45,51,57,60	0
54	5MC	1x	32	21/22	0.92	0.11	36,39,43,49	0
32	4OC	2a	1402	22/23	0.92	0.13	44,50,53,56	0
32	7MG	1a	527	24/25	0.92	0.12	33,38,43,46	0
32	5MC	1a	1404	21/22	0.92	0.11	27,31,34,45	0
32	M2G	1a	966	25/26	0.93	0.11	34,37,46,48	0
43	0TD	1l	92	10/11	0.93	0.11	41,43,47,48	0
54	5MU	1x	54	21/22	0.93	0.11	43,48,53,60	0
54	4SU	1x	8	20/21	0.93	0.11	36,42,44,45	0
54	PSU	1x	55	20/21	0.93	0.10	37,44,48,52	0
1	5MC	2A	1942	21/22	0.93	0.11	35,37,40,45	0
32	5MC	2a	1407	21/22	0.94	0.12	35,44,46,47	0
32	UR3	2a	1498	21/22	0.94	0.13	39,44,48,51	0
32	MA6	2a	1518	24/25	0.94	0.11	41,45,47,48	0
32	5MC	1a	1407	21/22	0.94	0.11	27,31,35,36	0
32	5MC	1a	967	21/22	0.94	0.10	35,43,47,49	0
32	5MC	2a	1404	21/22	0.94	0.10	36,41,44,47	0
32	4OC	1a	1402	22/23	0.95	0.11	31,35,37,39	0
1	PSU	1A	1933	20/21	0.95	0.11	31,43,46,49	0
32	MA6	2a	1519	24/25	0.95	0.12	37,43,46,49	0
1	5MC	1A	1964	21/22	0.95	0.11	25,29,33,40	0
1	5MC	2A	1962	21/22	0.96	0.09	30,33,36,42	0
1	2MA	2A	2503	23/24	0.96	0.10	18,21,24,27	0
1	OMU	2A	2552	21/22	0.96	0.09	26,27,29,31	0
1	OMC	1A	1942	21/22	0.96	0.10	26,34,40,42	0
1	5MU	2A	1939	21/22	0.96	0.08	26,28,30,31	0
32	MA6	1a	1518	24/25	0.96	0.10	23,27,28,29	0
1	OMU	1A	2564	21/22	0.97	0.09	14,18,20,21	0
32	UR3	1a	1498	21/22	0.97	0.07	26,29,32,33	0
1	PSU	2A	2605	20/21	0.97	0.09	22,26,27,27	0
1	PSU	1A	2617	20/21	0.97	0.08	10,12,14,16	0
32	MA6	1a	1519	24/25	0.97	0.08	24,28,29,31	0
1	OMG	2A	2251	24/25	0.97	0.09	19,25,27,28	0
1	2MA	1A	2515	23/24	0.98	0.07	5,9,11,15	0
1	5MU	1A	1961	21/22	0.98	0.08	12,16,19,21	0
1	5MC	1A	1984	21/22	0.98	0.07	19,23,25,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	OMG	1A	2263	24/25	0.98	0.07	9,10,12,12	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3477	1/1	0.12	0.39	62,62,62,62	0
56	MG	2a	1667	1/1	0.25	0.28	79,79,79,79	0
56	MG	2a	1725	1/1	0.33	0.27	71,71,71,71	0
56	MG	1a	1748	1/1	0.34	0.21	65,65,65,65	0
56	MG	2a	1805	1/1	0.34	0.38	94,94,94,94	0
56	MG	2a	1780	1/1	0.46	0.38	77,77,77,77	0
56	MG	2l	201	1/1	0.46	0.17	65,65,65,65	0
56	MG	2a	1716	1/1	0.47	0.22	65,65,65,65	0
56	MG	2A	3872	1/1	0.49	0.22	69,69,69,69	0
56	MG	2a	1758	1/1	0.52	0.29	83,83,83,83	0
56	MG	2a	1807	1/1	0.53	0.15	58,58,58,58	0
56	MG	2a	1713	1/1	0.53	0.19	59,59,59,59	0
56	MG	1a	1796	1/1	0.54	0.27	58,58,58,58	0
56	MG	2A	3690	1/1	0.55	0.31	67,67,67,67	0
56	MG	2A	3362	1/1	0.55	0.27	61,61,61,61	0
56	MG	2H	8002	1/1	0.55	0.23	79,79,79,79	0
56	MG	1a	1768	1/1	0.56	0.15	53,53,53,53	0
56	MG	2a	1676	1/1	0.56	0.17	65,65,65,65	0
56	MG	2A	3684	1/1	0.58	0.21	68,68,68,68	0
56	MG	2A	3098	1/1	0.58	0.33	62,62,62,62	0
56	MG	2d	504	1/1	0.60	0.13	64,64,64,64	0
56	MG	2B	3002	1/1	0.60	0.21	60,60,60,60	0
56	MG	2D	316	1/1	0.61	0.15	47,47,47,47	0
56	MG	2A	3532	1/1	0.61	0.25	54,54,54,54	0
56	MG	2a	1705	1/1	0.61	0.17	63,63,63,63	0
56	MG	2a	1806	1/1	0.62	0.20	65,65,65,65	0
56	MG	2A	3482	1/1	0.62	0.20	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3504	1/1	0.62	0.16	45,45,45,45	0
56	MG	2a	1711	1/1	0.62	0.16	64,64,64,64	0
56	MG	2A	3905	1/1	0.63	0.23	56,56,56,56	0
56	MG	2h	3002	1/1	0.63	0.22	64,64,64,64	0
56	MG	2a	1718	1/1	0.63	0.42	72,72,72,72	0
56	MG	2D	317	1/1	0.64	0.29	59,59,59,59	0
56	MG	2A	3702	1/1	0.64	0.21	55,55,55,55	0
56	MG	2A	3763	1/1	0.64	0.35	51,51,51,51	0
56	MG	2a	1752	1/1	0.65	0.41	71,71,71,71	0
56	MG	2B	3014	1/1	0.65	0.18	66,66,66,66	0
56	MG	2A	3605	1/1	0.65	0.15	35,35,35,35	0
56	MG	2A	3057	1/1	0.66	0.16	42,42,42,42	0
56	MG	2A	3061	1/1	0.66	0.17	68,68,68,68	0
56	MG	1A	8250	1/1	0.66	0.14	50,50,50,50	0
56	MG	2G	3003	1/1	0.66	0.13	59,59,59,59	0
56	MG	2A	3757	1/1	0.66	0.18	32,32,32,32	0
56	MG	2a	1715	1/1	0.66	0.17	50,50,50,50	0
56	MG	2a	1769	1/1	0.67	0.19	59,59,59,59	0
56	MG	2A	3535	1/1	0.67	0.15	55,55,55,55	0
56	MG	2A	3563	1/1	0.67	0.22	51,51,51,51	0
56	MG	2B	3015	1/1	0.67	0.14	59,59,59,59	0
56	MG	2B	3017	1/1	0.67	0.22	74,74,74,74	0
56	MG	2A	3326	1/1	0.67	0.17	55,55,55,55	0
56	MG	2a	1710	1/1	0.67	0.21	55,55,55,55	0
56	MG	2A	3744	1/1	0.67	0.32	45,45,45,45	0
56	MG	1a	1759	1/1	0.68	0.23	63,63,63,63	0
56	MG	2A	3079	1/1	0.68	0.48	61,61,61,61	0
56	MG	25	104	1/1	0.68	0.20	53,53,53,53	0
56	MG	2a	1635	1/1	0.68	0.23	69,69,69,69	0
56	MG	2A	3728	1/1	0.69	0.13	56,56,56,56	0
56	MG	2a	1726	1/1	0.69	0.17	51,51,51,51	0
56	MG	2H	8001	1/1	0.69	0.13	71,71,71,71	0
56	MG	1B	3016	1/1	0.69	0.25	51,51,51,51	0
56	MG	1x	3005	1/1	0.69	0.13	51,51,51,51	0
56	MG	2a	1625	1/1	0.69	0.24	63,63,63,63	0
56	MG	2x	104	1/1	0.69	0.26	68,68,68,68	0
56	MG	2A	3524	1/1	0.70	0.18	59,59,59,59	0
56	MG	2A	3281	1/1	0.70	0.19	52,52,52,52	0
56	MG	1a	1775	1/1	0.70	0.15	41,41,41,41	0
56	MG	2B	3021	1/1	0.70	0.18	50,50,50,50	0
56	MG	2A	3551	1/1	0.70	0.15	34,34,34,34	0
56	MG	2a	1611	1/1	0.70	0.13	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3914	1/1	0.71	0.25	51,51,51,51	0
56	MG	1A	8798	1/1	0.71	0.16	24,24,24,24	0
56	MG	2a	1672	1/1	0.71	0.13	64,64,64,64	0
56	MG	2A	3037	1/1	0.71	0.17	50,50,50,50	0
56	MG	2A	3252	1/1	0.71	0.19	53,53,53,53	0
56	MG	2A	3846	1/1	0.71	0.19	38,38,38,38	0
56	MG	2A	3679	1/1	0.71	0.18	60,60,60,60	0
56	MG	2A	3742	1/1	0.71	0.41	35,35,35,35	0
56	MG	2A	3958	1/1	0.72	0.20	51,51,51,51	0
56	MG	2A	3664	1/1	0.72	0.13	25,25,25,25	0
56	MG	1a	1726	1/1	0.72	0.20	56,56,56,56	0
56	MG	1a	1733	1/1	0.72	0.13	58,58,58,58	0
56	MG	1A	8628	1/1	0.72	0.28	62,62,62,62	0
56	MG	2A	3866	1/1	0.72	0.23	84,84,84,84	0
56	MG	2A	3480	1/1	0.72	0.19	63,63,63,63	0
56	MG	1A	8689	1/1	0.72	0.22	33,33,33,33	0
56	MG	1B	3027	1/1	0.72	0.18	66,66,66,66	0
56	MG	2a	1679	1/1	0.72	0.16	51,51,51,51	0
56	MG	1A	8921	1/1	0.73	0.16	52,52,52,52	0
56	MG	1a	1670	1/1	0.73	0.28	44,44,44,44	0
56	MG	1a	1791	1/1	0.73	0.14	56,56,56,56	0
56	MG	2a	1812	1/1	0.73	0.15	64,64,64,64	0
56	MG	2a	1816	1/1	0.73	0.14	56,56,56,56	0
56	MG	2A	3864	1/1	0.73	0.14	39,39,39,39	0
56	MG	2A	3967	1/1	0.73	0.30	55,55,55,55	0
56	MG	1A	8784	1/1	0.73	0.14	38,38,38,38	0
56	MG	2a	1784	1/1	0.73	0.21	64,64,64,64	0
56	MG	1a	1735	1/1	0.74	0.13	54,54,54,54	0
56	MG	1G	3002	1/1	0.74	0.18	44,44,44,44	0
56	MG	2A	3520	1/1	0.74	0.13	74,74,74,74	0
56	MG	2D	301	1/1	0.74	0.21	52,52,52,52	0
56	MG	2a	1660	1/1	0.74	0.28	59,59,59,59	0
56	MG	2A	3699	1/1	0.74	0.17	46,46,46,46	0
56	MG	2A	3799	1/1	0.74	0.12	54,54,54,54	0
56	MG	2A	3840	1/1	0.74	0.14	42,42,42,42	0
56	MG	1a	1749	1/1	0.74	0.26	54,54,54,54	0
56	MG	2a	1702	1/1	0.74	0.11	54,54,54,54	0
56	MG	1A	8468	1/1	0.74	0.13	29,29,29,29	0
56	MG	1A	8616	1/1	0.75	0.19	61,61,61,61	0
56	MG	2A	3314	1/1	0.75	0.14	22,22,22,22	0
56	MG	1A	8742	1/1	0.75	0.18	50,50,50,50	0
56	MG	2A	3686	1/1	0.75	0.13	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3865	1/1	0.75	0.11	48,48,48,48	0
56	MG	1a	1667	1/1	0.76	0.30	59,59,59,59	0
56	MG	1A	8701	1/1	0.76	0.19	49,49,49,49	0
56	MG	2A	3755	1/1	0.76	0.12	50,50,50,50	0
56	MG	1A	8291	1/1	0.76	0.34	13,13,13,13	0
56	MG	1A	8159	1/1	0.76	0.13	21,21,21,21	0
56	MG	2a	1707	1/1	0.76	0.23	61,61,61,61	0
56	MG	2A	3962	1/1	0.76	0.33	54,54,54,54	0
56	MG	1F	301	1/1	0.76	0.20	21,21,21,21	0
56	MG	2A	3806	1/1	0.76	0.21	65,65,65,65	0
56	MG	2a	1620	1/1	0.76	0.21	69,69,69,69	0
56	MG	1a	1801	1/1	0.76	0.15	60,60,60,60	0
56	MG	1A	8615	1/1	0.76	0.20	13,13,13,13	0
56	MG	1a	1636	1/1	0.76	0.13	56,56,56,56	0
56	MG	1a	1751	1/1	0.76	0.12	59,59,59,59	0
56	MG	1A	8888	1/1	0.77	0.29	62,62,62,62	0
56	MG	1a	1731	1/1	0.77	0.16	64,64,64,64	0
56	MG	1A	8413	1/1	0.77	0.15	44,44,44,44	0
56	MG	2A	3201	1/1	0.77	0.13	51,51,51,51	0
56	MG	2a	1775	1/1	0.77	0.23	68,68,68,68	0
56	MG	2a	1695	1/1	0.77	0.19	53,53,53,53	0
56	MG	2A	3049	1/1	0.77	0.14	43,43,43,43	0
56	MG	2A	3267	1/1	0.77	0.22	58,58,58,58	0
56	MG	2A	3603	1/1	0.77	0.19	53,53,53,53	0
56	MG	2A	3484	1/1	0.77	0.24	57,57,57,57	0
56	MG	2A	3637	1/1	0.77	0.22	48,48,48,48	0
56	MG	2A	3660	1/1	0.77	0.11	51,51,51,51	0
56	MG	2A	3503	1/1	0.77	0.17	47,47,47,47	0
56	MG	2A	3798	1/1	0.77	0.14	59,59,59,59	0
56	MG	2A	3667	1/1	0.77	0.11	58,58,58,58	0
56	MG	1A	8177	1/1	0.77	0.13	55,55,55,55	0
56	MG	2A	3072	1/1	0.78	0.12	36,36,36,36	0
56	MG	1f	8001	1/1	0.78	0.14	36,36,36,36	0
56	MG	1a	1671	1/1	0.78	0.21	39,39,39,39	0
56	MG	2a	1753	1/1	0.78	0.11	57,57,57,57	0
56	MG	2A	3591	1/1	0.78	0.11	51,51,51,51	0
56	MG	2A	3131	1/1	0.78	0.73	33,33,33,33	0
56	MG	2A	3706	1/1	0.78	0.14	32,32,32,32	0
56	MG	2A	3719	1/1	0.78	0.49	37,37,37,37	0
56	MG	2A	3144	1/1	0.78	0.25	63,63,63,63	0
56	MG	2E	303	1/1	0.78	0.12	64,64,64,64	0
56	MG	1a	1642	1/1	0.78	0.16	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3367	1/1	0.78	0.14	55,55,55,55	0
56	MG	2A	3368	1/1	0.78	0.28	54,54,54,54	0
56	MG	2a	1712	1/1	0.78	0.19	64,64,64,64	0
56	MG	2A	3917	1/1	0.78	0.35	49,49,49,49	0
56	MG	2A	3527	1/1	0.78	0.20	42,42,42,42	0
56	MG	2A	3428	1/1	0.78	0.13	30,30,30,30	0
56	MG	2A	3782	1/1	0.78	0.15	60,60,60,60	0
56	MG	2A	3923	1/1	0.79	0.14	39,39,39,39	0
56	MG	27	102	1/1	0.79	0.18	56,56,56,56	0
56	MG	2A	3202	1/1	0.79	0.33	42,42,42,42	0
56	MG	2A	3576	1/1	0.79	0.15	47,47,47,47	0
56	MG	1a	1618	1/1	0.79	0.19	57,57,57,57	0
56	MG	2a	1744	1/1	0.79	0.15	43,43,43,43	0
56	MG	2A	3596	1/1	0.79	0.13	35,35,35,35	0
56	MG	2a	1640	1/1	0.79	0.17	64,64,64,64	0
56	MG	2a	1656	1/1	0.79	0.10	65,65,65,65	0
56	MG	1A	8058	1/1	0.79	0.17	44,44,44,44	0
56	MG	1a	1686	1/1	0.79	0.17	46,46,46,46	0
56	MG	1E	306	1/1	0.79	0.09	41,41,41,41	0
56	MG	2A	3657	1/1	0.79	0.20	33,33,33,33	0
56	MG	2B	3025	1/1	0.79	0.12	52,52,52,52	0
56	MG	1H	202	1/1	0.79	0.12	39,39,39,39	0
56	MG	2A	3870	1/1	0.79	0.16	63,63,63,63	0
56	MG	1a	1753	1/1	0.79	0.14	54,54,54,54	0
56	MG	2A	3539	1/1	0.79	0.15	47,47,47,47	0
56	MG	2G	3002	1/1	0.79	0.16	63,63,63,63	0
56	MG	2A	3490	1/1	0.79	0.12	39,39,39,39	0
56	MG	2A	3683	1/1	0.79	0.12	73,73,73,73	0
56	MG	2A	3921	1/1	0.79	0.22	19,19,19,19	0
56	MG	2x	109	1/1	0.79	0.21	56,56,56,56	0
56	MG	1A	8220	1/1	0.80	0.16	52,52,52,52	0
56	MG	1x	3007	1/1	0.80	0.20	37,37,37,37	0
56	MG	2a	1717	1/1	0.80	0.22	54,54,54,54	0
56	MG	2A	3985	1/1	0.80	0.12	39,39,39,39	0
56	MG	2a	1720	1/1	0.80	0.11	43,43,43,43	0
56	MG	2a	1622	1/1	0.80	0.16	59,59,59,59	0
56	MG	2A	3174	1/1	0.80	0.22	40,40,40,40	0
56	MG	2A	3180	1/1	0.80	0.12	46,46,46,46	0
56	MG	2a	1638	1/1	0.80	0.26	54,54,54,54	0
56	MG	2A	3433	1/1	0.80	0.15	43,43,43,43	0
56	MG	2a	1646	1/1	0.80	0.32	48,48,48,48	0
56	MG	1N	203	1/1	0.80	0.11	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2B	3020	1/1	0.80	0.14	54,54,54,54	0
56	MG	2a	1779	1/1	0.80	0.14	48,48,48,48	0
56	MG	2A	3479	1/1	0.80	0.10	26,26,26,26	0
56	MG	1A	8800	1/1	0.80	0.14	44,44,44,44	0
56	MG	1A	8871	1/1	0.80	0.23	38,38,38,38	0
56	MG	1A	8636	1/1	0.80	0.12	45,45,45,45	0
56	MG	1a	1825	1/1	0.80	0.14	43,43,43,43	0
56	MG	1d	502	1/1	0.80	0.23	56,56,56,56	0
56	MG	2A	3317	1/1	0.80	0.14	68,68,68,68	0
56	MG	2A	3509	1/1	0.80	0.24	66,66,66,66	0
56	MG	1A	8339	1/1	0.80	0.11	32,32,32,32	0
56	MG	2A	3523	1/1	0.80	0.16	38,38,38,38	0
56	MG	2R	201	1/1	0.80	0.16	42,42,42,42	0
56	MG	2A	3781	1/1	0.80	0.15	51,51,51,51	0
59	K	2A	3001	1/1	0.80	0.23	65,65,65,65	0
56	MG	2a	1699	1/1	0.81	0.23	68,68,68,68	0
56	MG	2A	3720	1/1	0.81	0.19	60,60,60,60	0
56	MG	1A	8172	1/1	0.81	0.30	53,53,53,53	0
56	MG	2A	3069	1/1	0.81	0.29	36,36,36,36	0
56	MG	2A	3553	1/1	0.81	0.16	52,52,52,52	0
56	MG	1A	8803	1/1	0.81	0.16	59,59,59,59	0
56	MG	1A	8536	1/1	0.81	0.11	54,54,54,54	0
56	MG	2A	3587	1/1	0.81	0.56	39,39,39,39	0
56	MG	2a	1714	1/1	0.81	0.12	60,60,60,60	0
56	MG	2A	3370	1/1	0.81	0.10	21,21,21,21	0
56	MG	2A	3091	1/1	0.81	0.18	50,50,50,50	0
56	MG	1a	1797	1/1	0.81	0.18	47,47,47,47	0
56	MG	2A	3114	1/1	0.81	0.12	33,33,33,33	0
56	MG	2A	3606	1/1	0.81	0.13	42,42,42,42	0
56	MG	2A	3823	1/1	0.81	0.15	43,43,43,43	0
56	MG	2A	3833	1/1	0.81	0.15	28,28,28,28	0
56	MG	2a	1735	1/1	0.81	0.12	51,51,51,51	0
56	MG	2A	3633	1/1	0.81	0.18	44,44,44,44	0
56	MG	2Y	201	1/1	0.81	0.35	85,85,85,85	0
56	MG	2A	3124	1/1	0.81	0.14	46,46,46,46	0
56	MG	2A	3863	1/1	0.81	0.20	54,54,54,54	0
56	MG	1A	8629	1/1	0.81	0.10	45,45,45,45	0
56	MG	1A	8915	1/1	0.81	0.15	38,38,38,38	0
56	MG	1a	1614	1/1	0.81	0.24	52,52,52,52	0
56	MG	2A	3666	1/1	0.81	0.11	48,48,48,48	0
56	MG	1d	506	1/1	0.81	0.12	77,77,77,77	0
56	MG	2A	3673	1/1	0.81	0.15	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8753	1/1	0.81	0.21	13,13,13,13	0
56	MG	1l	203	1/1	0.81	0.18	56,56,56,56	0
56	MG	2A	3224	1/1	0.81	0.25	48,48,48,48	0
56	MG	1a	1629	1/1	0.81	0.19	36,36,36,36	0
56	MG	2a	1666	1/1	0.81	0.13	55,55,55,55	0
56	MG	2A	3261	1/1	0.81	0.37	42,42,42,42	0
56	MG	1A	8419	1/1	0.81	0.13	31,31,31,31	0
56	MG	1B	3017	1/1	0.81	0.11	44,44,44,44	0
56	MG	2x	105	1/1	0.81	0.31	59,59,59,59	0
56	MG	1B	3026	1/1	0.81	0.10	35,35,35,35	0
56	MG	1A	8683	1/1	0.81	0.14	30,30,30,30	0
56	MG	1a	1746	1/1	0.82	0.10	44,44,44,44	0
56	MG	1a	1639	1/1	0.82	0.24	50,50,50,50	0
56	MG	2G	3001	1/1	0.82	0.10	67,67,67,67	0
56	MG	1A	8717	1/1	0.82	0.11	16,16,16,16	0
56	MG	1n	101	1/1	0.82	0.29	51,51,51,51	0
56	MG	1a	1661	1/1	0.82	0.14	48,48,48,48	0
56	MG	1A	8527	1/1	0.82	0.08	11,11,11,11	0
56	MG	2P	203	1/1	0.82	0.12	63,63,63,63	0
56	MG	10	101	1/1	0.82	0.22	42,42,42,42	0
56	MG	2U	204	1/1	0.82	0.24	52,52,52,52	0
56	MG	15	106	1/1	0.82	0.24	20,20,20,20	0
56	MG	23	101	1/1	0.82	0.22	51,51,51,51	0
56	MG	2A	3899	1/1	0.82	0.27	62,62,62,62	0
56	MG	2A	3726	1/1	0.82	0.11	50,50,50,50	0
56	MG	29	502	1/1	0.82	0.15	53,53,53,53	0
56	MG	1A	8745	1/1	0.82	0.18	17,17,17,17	0
56	MG	2A	3620	1/1	0.82	0.14	61,61,61,61	0
56	MG	1a	1777	1/1	0.82	0.16	56,56,56,56	0
56	MG	1a	1789	1/1	0.82	0.23	61,61,61,61	0
56	MG	1a	1692	1/1	0.82	0.13	40,40,40,40	0
56	MG	2A	3761	1/1	0.82	0.16	43,43,43,43	0
56	MG	1A	8362	1/1	0.82	0.21	52,52,52,52	0
56	MG	2A	3768	1/1	0.82	0.13	42,42,42,42	0
56	MG	1a	1729	1/1	0.82	0.15	52,52,52,52	0
56	MG	2B	3006	1/1	0.82	0.11	48,48,48,48	0
56	MG	2A	3339	1/1	0.82	0.11	35,35,35,35	0
56	MG	2a	1809	1/1	0.82	0.17	81,81,81,81	0
56	MG	2A	3786	1/1	0.82	0.14	62,62,62,62	0
56	MG	1B	3001	1/1	0.82	0.16	37,37,37,37	0
56	MG	2A	3668	1/1	0.82	0.33	57,57,57,57	0
56	MG	1a	1635	1/1	0.82	0.16	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1680	1/1	0.82	0.20	59,59,59,59	0
56	MG	2B	3024	1/1	0.82	0.14	61,61,61,61	0
56	MG	1A	8853	1/1	0.82	0.14	50,50,50,50	0
56	MG	2A	3125	1/1	0.82	0.46	39,39,39,39	0
56	MG	2x	111	1/1	0.82	0.17	67,67,67,67	0
56	MG	2A	3835	1/1	0.82	0.13	40,40,40,40	0
56	MG	1a	1707	1/1	0.83	0.14	51,51,51,51	0
56	MG	2a	1610	1/1	0.83	0.36	63,63,63,63	0
56	MG	2B	3009	1/1	0.83	0.14	67,67,67,67	0
56	MG	2a	1615	1/1	0.83	0.26	50,50,50,50	0
56	MG	2A	3837	1/1	0.83	0.12	21,21,21,21	0
56	MG	1A	8559	1/1	0.83	0.14	43,43,43,43	0
56	MG	2A	3724	1/1	0.83	0.19	50,50,50,50	0
56	MG	1A	8593	1/1	0.83	0.22	16,16,16,16	0
56	MG	18	101	1/1	0.83	0.22	49,49,49,49	0
56	MG	2A	3232	1/1	0.83	0.13	46,46,46,46	0
56	MG	2a	1643	1/1	0.83	0.30	57,57,57,57	0
56	MG	2A	3468	1/1	0.83	0.11	47,47,47,47	0
56	MG	2a	1655	1/1	0.83	0.09	48,48,48,48	0
56	MG	2A	3248	1/1	0.83	0.18	34,34,34,34	0
56	MG	2D	313	1/1	0.83	0.17	32,32,32,32	0
56	MG	1A	8759	1/1	0.83	0.17	15,15,15,15	0
56	MG	2A	3879	1/1	0.83	0.14	36,36,36,36	0
56	MG	2A	3893	1/1	0.83	0.14	44,44,44,44	0
56	MG	2a	1795	1/1	0.83	0.14	65,65,65,65	0
56	MG	1a	1779	1/1	0.83	0.13	50,50,50,50	0
56	MG	1A	8813	1/1	0.83	0.10	11,11,11,11	0
56	MG	1A	8498	1/1	0.83	0.14	34,34,34,34	0
56	MG	2a	1683	1/1	0.83	0.20	61,61,61,61	0
56	MG	2a	1690	1/1	0.83	0.10	57,57,57,57	0
56	MG	2A	3681	1/1	0.83	0.20	57,57,57,57	0
56	MG	2A	3590	1/1	0.83	0.12	65,65,65,65	0
56	MG	1A	8859	1/1	0.83	0.16	37,37,37,37	0
56	MG	1A	8864	1/1	0.83	0.11	26,26,26,26	0
56	MG	2A	3598	1/1	0.83	0.22	50,50,50,50	0
56	MG	2A	3052	1/1	0.83	0.23	37,37,37,37	0
56	MG	2A	3151	1/1	0.83	0.31	32,32,32,32	0
56	MG	1a	1701	1/1	0.83	0.11	44,44,44,44	0
56	MG	2B	3005	1/1	0.83	0.12	55,55,55,55	0
56	MG	1a	1758	1/1	0.84	0.12	38,38,38,38	0
56	MG	2N	201	1/1	0.84	0.19	50,50,50,50	0
56	MG	2N	202	1/1	0.84	0.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3239	1/1	0.84	0.18	51,51,51,51	0
56	MG	1A	8140	1/1	0.84	0.20	52,52,52,52	0
56	MG	2A	3731	1/1	0.84	0.15	63,63,63,63	0
56	MG	1A	8484	1/1	0.84	0.24	17,17,17,17	0
56	MG	20	105	1/1	0.84	0.15	50,50,50,50	0
56	MG	1P	204	1/1	0.84	0.07	62,62,62,62	0
56	MG	2A	3752	1/1	0.84	0.29	39,39,39,39	0
56	MG	2A	3927	1/1	0.84	0.12	30,30,30,30	0
56	MG	2A	3111	1/1	0.84	0.27	47,47,47,47	0
56	MG	1a	1776	1/1	0.84	0.12	35,35,35,35	0
56	MG	1a	1677	1/1	0.84	0.20	49,49,49,49	0
56	MG	2a	1731	1/1	0.84	0.13	56,56,56,56	0
56	MG	2a	1734	1/1	0.84	0.10	59,59,59,59	0
56	MG	1D	312	1/1	0.84	0.09	41,41,41,41	0
56	MG	2A	3658	1/1	0.84	0.11	29,29,29,29	0
56	MG	2B	3003	1/1	0.84	0.14	37,37,37,37	0
56	MG	1A	8390	1/1	0.84	0.22	41,41,41,41	0
56	MG	2A	3327	1/1	0.84	0.10	61,61,61,61	0
56	MG	2A	3138	1/1	0.84	0.12	31,31,31,31	0
56	MG	2a	1772	1/1	0.84	0.09	57,57,57,57	0
56	MG	1A	8880	1/1	0.84	0.23	46,46,46,46	0
56	MG	2A	3528	1/1	0.84	0.10	40,40,40,40	0
56	MG	2B	3016	1/1	0.84	0.19	55,55,55,55	0
56	MG	2a	1649	1/1	0.84	0.26	48,48,48,48	0
56	MG	2A	3530	1/1	0.84	0.46	45,45,45,45	0
56	MG	2a	1796	1/1	0.84	0.16	53,53,53,53	0
56	MG	2A	3675	1/1	0.84	0.15	44,44,44,44	0
56	MG	2A	3364	1/1	0.84	0.15	42,42,42,42	0
56	MG	2A	3365	1/1	0.84	0.13	47,47,47,47	0
56	MG	1a	1792	1/1	0.84	0.19	41,41,41,41	0
56	MG	2A	3547	1/1	0.84	0.10	43,43,43,43	0
56	MG	1a	1659	1/1	0.84	0.22	50,50,50,50	0
56	MG	2b	3001	1/1	0.84	0.20	56,56,56,56	0
56	MG	1A	8585	1/1	0.84	0.08	29,29,29,29	0
56	MG	2A	3372	1/1	0.84	0.12	48,48,48,48	0
56	MG	1a	1754	1/1	0.84	0.17	59,59,59,59	0
56	MG	2A	3063	1/1	0.84	0.13	38,38,38,38	0
56	MG	2a	1692	1/1	0.84	0.11	44,44,44,44	0
56	MG	2x	108	1/1	0.84	0.20	53,53,53,53	0
56	MG	2A	3709	1/1	0.84	0.15	40,40,40,40	0
56	MG	2A	3457	1/1	0.84	0.12	50,50,50,50	0
56	MG	1a	1807	1/1	0.84	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8277	1/1	0.85	0.28	50,50,50,50	0
56	MG	1A	8840	1/1	0.85	0.13	9,9,9,9	0
56	MG	2a	1697	1/1	0.85	0.08	54,54,54,54	0
56	MG	1B	3003	1/1	0.85	0.10	43,43,43,43	0
56	MG	2A	3856	1/1	0.85	0.26	53,53,53,53	0
56	MG	2A	3857	1/1	0.85	0.16	40,40,40,40	0
56	MG	1A	8282	1/1	0.85	0.10	45,45,45,45	0
56	MG	1A	8221	1/1	0.85	0.22	43,43,43,43	0
56	MG	2A	3203	1/1	0.85	0.26	28,28,28,28	0
56	MG	2A	3205	1/1	0.85	0.85	44,44,44,44	0
56	MG	1A	8488	1/1	0.85	0.11	46,46,46,46	0
56	MG	2A	3378	1/1	0.85	0.19	41,41,41,41	0
56	MG	2A	3379	1/1	0.85	0.19	36,36,36,36	0
56	MG	2A	3892	1/1	0.85	0.10	34,34,34,34	0
56	MG	2A	3554	1/1	0.85	0.19	37,37,37,37	0
56	MG	2A	3415	1/1	0.85	0.11	34,34,34,34	0
56	MG	2U	206	1/1	0.85	0.16	38,38,38,38	0
56	MG	2a	1722	1/1	0.85	0.11	61,61,61,61	0
56	MG	2A	3425	1/1	0.85	0.10	25,25,25,25	0
56	MG	20	104	1/1	0.85	0.09	55,55,55,55	0
56	MG	2a	1728	1/1	0.85	0.14	64,64,64,64	0
56	MG	2a	1729	1/1	0.85	0.14	62,62,62,62	0
56	MG	1A	8866	1/1	0.85	0.10	32,32,32,32	0
56	MG	2A	3431	1/1	0.85	0.09	39,39,39,39	0
56	MG	1A	8795	1/1	0.85	0.25	21,21,21,21	0
56	MG	1D	314	1/1	0.85	0.10	31,31,31,31	0
56	MG	2A	3924	1/1	0.85	0.17	26,26,26,26	0
56	MG	2a	1607	1/1	0.85	0.25	55,55,55,55	0
56	MG	1a	1771	1/1	0.85	0.16	46,46,46,46	0
56	MG	2a	1763	1/1	0.85	0.13	81,81,81,81	0
56	MG	2A	3929	1/1	0.85	0.14	48,48,48,48	0
56	MG	2A	3953	1/1	0.85	0.12	37,37,37,37	0
56	MG	2a	1774	1/1	0.85	0.15	54,54,54,54	0
56	MG	1A	8495	1/1	0.85	0.09	14,14,14,14	0
56	MG	1A	8409	1/1	0.85	0.15	35,35,35,35	0
56	MG	2A	3964	1/1	0.85	0.15	37,37,37,37	0
56	MG	2a	1626	1/1	0.85	0.17	63,63,63,63	0
56	MG	2A	3280	1/1	0.85	0.11	35,35,35,35	0
56	MG	1A	8899	1/1	0.85	0.08	37,37,37,37	0
56	MG	2A	3987	1/1	0.85	0.18	28,28,28,28	0
56	MG	2A	3629	1/1	0.85	0.15	25,25,25,25	0
56	MG	2A	3483	1/1	0.85	0.13	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3287	1/1	0.85	0.17	53,53,53,53	0
56	MG	2a	1650	1/1	0.85	0.23	46,46,46,46	0
56	MG	2a	1813	1/1	0.85	0.16	42,42,42,42	0
56	MG	2A	3778	1/1	0.85	0.17	46,46,46,46	0
56	MG	2A	3486	1/1	0.85	0.22	47,47,47,47	0
56	MG	2A	3295	1/1	0.85	0.11	43,43,43,43	0
56	MG	2A	3491	1/1	0.85	0.12	27,27,27,27	0
56	MG	1a	1652	1/1	0.85	0.18	47,47,47,47	0
56	MG	1x	3012	1/1	0.85	0.10	38,38,38,38	0
56	MG	2A	3320	1/1	0.85	0.12	27,27,27,27	0
56	MG	2A	3030	1/1	0.85	0.27	47,47,47,47	0
56	MG	2B	3023	1/1	0.85	0.13	41,41,41,41	0
56	MG	2A	3671	1/1	0.85	0.17	45,45,45,45	0
56	MG	1A	8323	1/1	0.85	0.11	20,20,20,20	0
56	MG	2A	3873	1/1	0.86	0.20	74,74,74,74	0
56	MG	2A	3421	1/1	0.86	0.10	49,49,49,49	0
56	MG	1H	201	1/1	0.86	0.12	38,38,38,38	0
56	MG	2A	3245	1/1	0.86	0.09	46,46,46,46	0
56	MG	1A	8264	1/1	0.86	0.22	37,37,37,37	0
56	MG	1A	8197	1/1	0.86	0.09	42,42,42,42	0
56	MG	2A	3908	1/1	0.86	0.55	57,57,57,57	0
56	MG	1a	1800	1/1	0.86	0.11	31,31,31,31	0
56	MG	2A	3462	1/1	0.86	0.13	26,26,26,26	0
56	MG	2A	3264	1/1	0.86	0.11	65,65,65,65	0
56	MG	1A	8804	1/1	0.86	0.12	31,31,31,31	0
56	MG	2A	3739	1/1	0.86	0.11	46,46,46,46	0
56	MG	1A	8732	1/1	0.86	0.11	33,33,33,33	0
56	MG	2a	1723	1/1	0.86	0.16	50,50,50,50	0
56	MG	2a	1724	1/1	0.86	0.10	56,56,56,56	0
56	MG	1A	8417	1/1	0.86	0.10	37,37,37,37	0
56	MG	1A	8627	1/1	0.86	0.11	48,48,48,48	0
56	MG	1A	8087	1/1	0.86	0.28	45,45,45,45	0
56	MG	1a	1765	1/1	0.86	0.08	44,44,44,44	0
56	MG	2A	3963	1/1	0.86	0.16	53,53,53,53	0
56	MG	2a	1612	1/1	0.86	0.15	43,43,43,43	0
56	MG	2A	3623	1/1	0.86	0.11	53,53,53,53	0
56	MG	2A	3624	1/1	0.86	0.20	52,52,52,52	0
56	MG	2A	3766	1/1	0.86	0.10	41,41,41,41	0
56	MG	1i	3001	1/1	0.86	0.14	46,46,46,46	0
56	MG	2B	3001	1/1	0.86	0.19	59,59,59,59	0
56	MG	1a	1615	1/1	0.86	0.17	51,51,51,51	0
56	MG	1A	8754	1/1	0.86	0.24	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3493	1/1	0.86	0.11	32,32,32,32	0
56	MG	2a	1641	1/1	0.86	0.20	59,59,59,59	0
56	MG	2a	1642	1/1	0.86	0.19	51,51,51,51	0
56	MG	2A	3500	1/1	0.86	0.26	45,45,45,45	0
56	MG	1x	3002	1/1	0.86	0.15	44,44,44,44	0
56	MG	1a	1619	1/1	0.86	0.19	45,45,45,45	0
56	MG	2a	1785	1/1	0.86	0.15	70,70,70,70	0
56	MG	2a	1788	1/1	0.86	0.10	50,50,50,50	0
56	MG	1A	8367	1/1	0.86	0.09	33,33,33,33	0
56	MG	1A	8552	1/1	0.86	0.16	23,23,23,23	0
56	MG	1A	8788	1/1	0.86	0.09	34,34,34,34	0
56	MG	2A	3670	1/1	0.86	0.14	32,32,32,32	0
56	MG	2a	1662	1/1	0.86	0.13	48,48,48,48	0
56	MG	2A	3034	1/1	0.86	0.08	23,23,23,23	0
56	MG	1a	1781	1/1	0.86	0.15	68,68,68,68	0
56	MG	1a	1783	1/1	0.86	0.13	60,60,60,60	0
56	MG	2A	3847	1/1	0.86	0.30	53,53,53,53	0
56	MG	2A	3529	1/1	0.86	0.12	44,44,44,44	0
56	MG	2A	3221	1/1	0.86	0.36	29,29,29,29	0
56	MG	2d	505	1/1	0.86	0.17	73,73,73,73	0
56	MG	2A	3223	1/1	0.86	0.15	52,52,52,52	0
56	MG	2a	1687	1/1	0.86	0.10	58,58,58,58	0
56	MG	1A	8482	1/1	0.86	0.12	31,31,31,31	0
56	MG	2A	3536	1/1	0.86	0.10	31,31,31,31	0
56	MG	2E	305	1/1	0.86	0.11	60,60,60,60	0
56	MG	2A	3398	1/1	0.86	0.12	39,39,39,39	0
56	MG	1A	8263	1/1	0.86	0.09	26,26,26,26	0
56	MG	2A	3700	1/1	0.86	0.11	42,42,42,42	0
56	MG	2A	3787	1/1	0.87	0.20	41,41,41,41	0
56	MG	1a	1773	1/1	0.87	0.10	44,44,44,44	0
56	MG	1A	8704	1/1	0.87	0.14	34,34,34,34	0
56	MG	1l	202	1/1	0.87	0.13	38,38,38,38	0
56	MG	1A	8416	1/1	0.87	0.13	36,36,36,36	0
56	MG	2A	3832	1/1	0.87	0.17	31,31,31,31	0
56	MG	1A	8015	1/1	0.87	0.14	28,28,28,28	0
56	MG	1a	1740	1/1	0.87	0.18	54,54,54,54	0
56	MG	2A	3139	1/1	0.87	0.23	45,45,45,45	0
56	MG	2A	3838	1/1	0.87	0.18	44,44,44,44	0
56	MG	2A	3510	1/1	0.87	0.13	54,54,54,54	0
56	MG	2F	306	1/1	0.87	0.08	30,30,30,30	0
56	MG	2A	3517	1/1	0.87	0.21	47,47,47,47	0
56	MG	1a	1780	1/1	0.87	0.18	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1x	3006	1/1	0.87	0.24	47,47,47,47	0
56	MG	1a	1742	1/1	0.87	0.13	32,32,32,32	0
56	MG	1A	8372	1/1	0.87	0.19	51,51,51,51	0
56	MG	2A	3182	1/1	0.87	0.12	34,34,34,34	0
56	MG	2A	3006	1/1	0.87	0.11	45,45,45,45	0
56	MG	2A	3018	1/1	0.87	0.24	55,55,55,55	0
56	MG	1a	1785	1/1	0.87	0.10	74,74,74,74	0
56	MG	2A	3685	1/1	0.87	0.18	50,50,50,50	0
56	MG	2U	205	1/1	0.87	0.13	49,49,49,49	0
56	MG	1A	8237	1/1	0.87	0.07	41,41,41,41	0
56	MG	1A	8802	1/1	0.87	0.10	26,26,26,26	0
56	MG	2A	3041	1/1	0.87	0.10	39,39,39,39	0
56	MG	2A	3541	1/1	0.87	0.09	24,24,24,24	0
56	MG	2A	3546	1/1	0.87	0.10	54,54,54,54	0
56	MG	1a	1682	1/1	0.87	0.35	45,45,45,45	0
56	MG	2A	3548	1/1	0.87	0.12	52,52,52,52	0
56	MG	2A	3912	1/1	0.87	0.29	49,49,49,49	0
56	MG	2a	1747	1/1	0.87	0.18	39,39,39,39	0
56	MG	2A	3716	1/1	0.87	0.08	37,37,37,37	0
56	MG	2A	3915	1/1	0.87	0.12	42,42,42,42	0
56	MG	2A	3916	1/1	0.87	0.16	86,86,86,86	0
56	MG	2a	1761	1/1	0.87	0.10	42,42,42,42	0
56	MG	2A	3717	1/1	0.87	0.13	24,24,24,24	0
56	MG	2a	1766	1/1	0.87	0.21	67,67,67,67	0
56	MG	1A	8687	1/1	0.87	0.17	46,46,46,46	0
56	MG	1A	8124	1/1	0.87	0.07	16,16,16,16	0
56	MG	2A	3721	1/1	0.87	0.22	47,47,47,47	0
56	MG	2a	1624	1/1	0.87	0.34	48,48,48,48	0
56	MG	2a	1778	1/1	0.87	0.12	42,42,42,42	0
56	MG	1A	8255	1/1	0.87	0.28	33,33,33,33	0
56	MG	1a	1704	1/1	0.87	0.13	47,47,47,47	0
56	MG	2a	1630	1/1	0.87	0.16	50,50,50,50	0
56	MG	1a	1764	1/1	0.87	0.15	54,54,54,54	0
56	MG	2a	1637	1/1	0.87	0.19	36,36,36,36	0
56	MG	2A	3584	1/1	0.87	0.12	30,30,30,30	0
56	MG	2A	3254	1/1	0.87	0.08	38,38,38,38	0
56	MG	2a	1799	1/1	0.87	0.17	57,57,57,57	0
56	MG	2A	3459	1/1	0.87	0.15	33,33,33,33	0
56	MG	1a	1643	1/1	0.87	0.17	53,53,53,53	0
56	MG	2A	3749	1/1	0.87	0.14	50,50,50,50	0
56	MG	2A	3982	1/1	0.87	0.15	26,26,26,26	0
56	MG	2A	3263	1/1	0.87	0.19	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1828	1/1	0.87	0.13	52,52,52,52	0
56	MG	2a	1654	1/1	0.87	0.29	62,62,62,62	0
56	MG	2A	3478	1/1	0.87	0.14	38,38,38,38	0
56	MG	1a	1647	1/1	0.87	0.23	53,53,53,53	0
56	MG	2A	3268	1/1	0.87	0.24	42,42,42,42	0
56	MG	2A	3614	1/1	0.87	0.12	42,42,42,42	0
56	MG	2a	1664	1/1	0.87	0.11	44,44,44,44	0
56	MG	2A	3092	1/1	0.87	0.34	48,48,48,48	0
56	MG	2A	3775	1/1	0.87	0.23	51,51,51,51	0
56	MG	1A	8903	1/1	0.87	0.12	19,19,19,19	0
56	MG	2A	3282	1/1	0.87	0.11	63,63,63,63	0
56	MG	2A	3628	1/1	0.87	0.09	59,59,59,59	0
56	MG	2A	3285	1/1	0.87	0.11	30,30,30,30	0
56	MG	1a	1739	1/1	0.88	0.23	50,50,50,50	0
56	MG	1A	8602	1/1	0.88	0.14	47,47,47,47	0
56	MG	1A	8317	1/1	0.88	0.10	35,35,35,35	0
56	MG	1A	8196	1/1	0.88	0.14	49,49,49,49	0
56	MG	2A	3257	1/1	0.88	0.13	44,44,44,44	0
56	MG	2A	3966	1/1	0.88	0.11	50,50,50,50	0
56	MG	1A	8907	1/1	0.88	0.15	26,26,26,26	0
56	MG	2A	3722	1/1	0.88	0.15	42,42,42,42	0
56	MG	2A	3983	1/1	0.88	0.09	23,23,23,23	0
56	MG	1a	1623	1/1	0.88	0.15	47,47,47,47	0
56	MG	2a	1681	1/1	0.88	0.12	45,45,45,45	0
56	MG	1A	8909	1/1	0.88	0.13	15,15,15,15	0
56	MG	2A	3014	1/1	0.88	0.22	39,39,39,39	0
56	MG	1A	8617	1/1	0.88	0.12	43,43,43,43	0
56	MG	2A	3736	1/1	0.88	0.24	51,51,51,51	0
56	MG	1A	8782	1/1	0.88	0.15	24,24,24,24	0
56	MG	2A	3032	1/1	0.88	0.18	43,43,43,43	0
56	MG	2B	3007	1/1	0.88	0.12	42,42,42,42	0
56	MG	1a	1757	1/1	0.88	0.21	44,44,44,44	0
56	MG	1A	8948	1/1	0.88	0.15	35,35,35,35	0
56	MG	1A	8325	1/1	0.88	0.09	21,21,21,21	0
56	MG	1A	8787	1/1	0.88	0.10	8,8,8,8	0
56	MG	2A	3296	1/1	0.88	0.09	49,49,49,49	0
56	MG	1A	8516	1/1	0.88	0.17	34,34,34,34	0
56	MG	2A	3315	1/1	0.88	0.13	44,44,44,44	0
56	MG	2A	3552	1/1	0.88	0.10	47,47,47,47	0
56	MG	1A	8519	1/1	0.88	0.14	29,29,29,29	0
56	MG	1a	1656	1/1	0.88	0.14	51,51,51,51	0
56	MG	2A	3777	1/1	0.88	0.26	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	3020	1/1	0.88	0.10	23,23,23,23	0
56	MG	2A	3064	1/1	0.88	0.09	34,34,34,34	0
56	MG	1a	1660	1/1	0.88	0.19	39,39,39,39	0
56	MG	1A	8522	1/1	0.88	0.11	34,34,34,34	0
56	MG	1A	8650	1/1	0.88	0.10	39,39,39,39	0
56	MG	2A	3087	1/1	0.88	0.21	54,54,54,54	0
56	MG	2F	309	1/1	0.88	0.14	58,58,58,58	0
56	MG	1A	8674	1/1	0.88	0.14	35,35,35,35	0
56	MG	1A	8328	1/1	0.88	0.17	38,38,38,38	0
56	MG	2a	1730	1/1	0.88	0.10	71,71,71,71	0
56	MG	2A	3810	1/1	0.88	0.10	53,53,53,53	0
56	MG	2A	3817	1/1	0.88	0.36	52,52,52,52	0
56	MG	1A	8685	1/1	0.88	0.10	51,51,51,51	0
56	MG	2a	1743	1/1	0.88	0.25	41,41,41,41	0
56	MG	2A	3105	1/1	0.88	0.14	46,46,46,46	0
56	MG	1a	1680	1/1	0.88	0.12	27,27,27,27	0
56	MG	1a	1681	1/1	0.88	0.14	52,52,52,52	0
56	MG	2Q	203	1/1	0.88	0.11	33,33,33,33	0
56	MG	2A	3119	1/1	0.88	0.09	35,35,35,35	0
56	MG	2A	3406	1/1	0.88	0.11	51,51,51,51	0
56	MG	2A	3121	1/1	0.88	0.17	42,42,42,42	0
56	MG	1a	1787	1/1	0.88	0.28	47,47,47,47	0
56	MG	1A	8273	1/1	0.88	0.08	32,32,32,32	0
56	MG	1a	1684	1/1	0.88	0.10	35,35,35,35	0
56	MG	1a	1685	1/1	0.88	0.12	51,51,51,51	0
56	MG	2A	3858	1/1	0.88	0.13	46,46,46,46	0
56	MG	2A	3646	1/1	0.88	0.11	51,51,51,51	0
56	MG	1A	8831	1/1	0.88	0.10	41,41,41,41	0
56	MG	2A	3434	1/1	0.88	0.10	34,34,34,34	0
56	MG	2A	3446	1/1	0.88	0.15	29,29,29,29	0
56	MG	2A	3869	1/1	0.88	0.13	38,38,38,38	0
56	MG	1A	8550	1/1	0.88	0.12	35,35,35,35	0
56	MG	2a	1794	1/1	0.88	0.18	71,71,71,71	0
56	MG	1A	8027	1/1	0.88	0.12	38,38,38,38	0
56	MG	2A	3153	1/1	0.88	0.12	39,39,39,39	0
56	MG	2A	3165	1/1	0.88	0.11	42,42,42,42	0
56	MG	2A	3885	1/1	0.88	0.12	55,55,55,55	0
56	MG	2a	1623	1/1	0.88	0.30	41,41,41,41	0
56	MG	1A	8262	1/1	0.88	0.11	58,58,58,58	0
56	MG	1A	8711	1/1	0.88	0.13	27,27,27,27	0
56	MG	1a	1823	1/1	0.88	0.12	42,42,42,42	0
56	MG	2A	3199	1/1	0.88	0.20	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1815	1/1	0.88	0.13	58,58,58,58	0
56	MG	1a	1716	1/1	0.88	0.19	52,52,52,52	0
56	MG	1a	1721	1/1	0.88	0.09	49,49,49,49	0
56	MG	1a	1829	1/1	0.88	0.08	36,36,36,36	0
56	MG	1A	8200	1/1	0.88	0.15	46,46,46,46	0
56	MG	1a	1727	1/1	0.88	0.10	32,32,32,32	0
56	MG	1A	8592	1/1	0.88	0.09	24,24,24,24	0
56	MG	2l	202	1/1	0.88	0.18	50,50,50,50	0
56	MG	1A	8385	1/1	0.88	0.10	15,15,15,15	0
56	MG	1a	1601	1/1	0.88	0.11	43,43,43,43	0
56	MG	2x	106	1/1	0.88	0.26	52,52,52,52	0
56	MG	1a	1604	1/1	0.88	0.10	50,50,50,50	0
56	MG	2A	3242	1/1	0.88	0.18	30,30,30,30	0
56	MG	2x	110	1/1	0.88	0.06	42,42,42,42	0
56	MG	2A	3505	1/1	0.88	0.13	43,43,43,43	0
56	MG	2A	3934	1/1	0.88	0.13	32,32,32,32	0
56	MG	2A	3394	1/1	0.89	0.12	65,65,65,65	0
56	MG	2A	3581	1/1	0.89	0.12	31,31,31,31	0
56	MG	1A	8666	1/1	0.89	0.10	18,18,18,18	0
56	MG	2A	3402	1/1	0.89	0.10	39,39,39,39	0
56	MG	2a	1682	1/1	0.89	0.10	53,53,53,53	0
56	MG	1q	201	1/1	0.89	0.07	37,37,37,37	0
56	MG	1A	8009	1/1	0.89	0.13	20,20,20,20	0
56	MG	1A	8333	1/1	0.89	0.13	39,39,39,39	0
56	MG	2A	3774	1/1	0.89	0.18	56,56,56,56	0
56	MG	2B	3011	1/1	0.89	0.10	73,73,73,73	0
56	MG	2a	1696	1/1	0.89	0.12	36,36,36,36	0
56	MG	1A	8542	1/1	0.89	0.12	40,40,40,40	0
56	MG	1E	305	1/1	0.89	0.12	12,12,12,12	0
56	MG	1A	8549	1/1	0.89	0.09	38,38,38,38	0
56	MG	2A	3003	1/1	0.89	0.10	42,42,42,42	0
56	MG	2B	3018	1/1	0.89	0.10	57,57,57,57	0
56	MG	2A	3612	1/1	0.89	0.10	40,40,40,40	0
56	MG	1a	1664	1/1	0.89	0.10	38,38,38,38	0
56	MG	2A	3618	1/1	0.89	0.10	43,43,43,43	0
56	MG	2A	3012	1/1	0.89	0.18	41,41,41,41	0
56	MG	1A	8201	1/1	0.89	0.11	45,45,45,45	0
56	MG	2A	3804	1/1	0.89	0.31	33,33,33,33	0
56	MG	2A	3229	1/1	0.89	0.10	30,30,30,30	0
56	MG	2A	3461	1/1	0.89	0.10	30,30,30,30	0
56	MG	2A	3813	1/1	0.89	0.12	64,64,64,64	0
56	MG	2A	3814	1/1	0.89	0.12	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1669	1/1	0.89	0.24	42,42,42,42	0
56	MG	1A	8425	1/1	0.89	0.10	12,12,12,12	0
56	MG	1A	8554	1/1	0.89	0.12	34,34,34,34	0
56	MG	1A	8556	1/1	0.89	0.11	17,17,17,17	0
56	MG	1A	8436	1/1	0.89	0.11	7,7,7,7	0
56	MG	2a	1727	1/1	0.89	0.30	49,49,49,49	0
56	MG	2A	3040	1/1	0.89	0.19	53,53,53,53	0
56	MG	1A	8464	1/1	0.89	0.13	7,7,7,7	0
56	MG	1Q	201	1/1	0.89	0.10	17,17,17,17	0
56	MG	1S	201	1/1	0.89	0.08	23,23,23,23	0
56	MG	1U	201	1/1	0.89	0.07	26,26,26,26	0
56	MG	1A	8734	1/1	0.89	0.12	22,22,22,22	0
56	MG	2a	1740	1/1	0.89	0.14	62,62,62,62	0
56	MG	10	106	1/1	0.89	0.17	46,46,46,46	0
56	MG	1a	1700	1/1	0.89	0.11	45,45,45,45	0
56	MG	1a	1788	1/1	0.89	0.12	42,42,42,42	0
56	MG	2A	3502	1/1	0.89	0.11	47,47,47,47	0
56	MG	1A	8356	1/1	0.89	0.10	9,9,9,9	0
56	MG	2a	1755	1/1	0.89	0.12	52,52,52,52	0
56	MG	2W	3001	1/1	0.89	0.10	45,45,45,45	0
56	MG	2A	3680	1/1	0.89	0.20	38,38,38,38	0
56	MG	2A	3076	1/1	0.89	0.60	44,44,44,44	0
56	MG	15	107	1/1	0.89	0.06	17,17,17,17	0
56	MG	2a	1768	1/1	0.89	0.23	57,57,57,57	0
56	MG	1A	8152	1/1	0.89	0.10	28,28,28,28	0
56	MG	2A	3294	1/1	0.89	0.12	50,50,50,50	0
56	MG	2A	3514	1/1	0.89	0.12	36,36,36,36	0
56	MG	2A	3689	1/1	0.89	0.10	32,32,32,32	0
56	MG	2a	1777	1/1	0.89	0.09	45,45,45,45	0
56	MG	2A	3888	1/1	0.89	0.10	41,41,41,41	0
56	MG	2A	3889	1/1	0.89	0.23	63,63,63,63	0
56	MG	1a	1713	1/1	0.89	0.16	39,39,39,39	0
56	MG	2A	3698	1/1	0.89	0.10	35,35,35,35	0
56	MG	1A	8598	1/1	0.89	0.13	43,43,43,43	0
56	MG	2a	1787	1/1	0.89	0.15	49,49,49,49	0
56	MG	2A	3093	1/1	0.89	0.17	61,61,61,61	0
56	MG	2A	3907	1/1	0.89	0.12	23,23,23,23	0
56	MG	1A	8295	1/1	0.89	0.07	21,21,21,21	0
56	MG	2A	3910	1/1	0.89	0.20	60,60,60,60	0
56	MG	1A	8155	1/1	0.89	0.17	24,24,24,24	0
56	MG	1A	8768	1/1	0.89	0.12	12,12,12,12	0
56	MG	2a	1628	1/1	0.89	0.26	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3710	1/1	0.89	0.10	39,39,39,39	0
56	MG	1A	8379	1/1	0.89	0.22	19,19,19,19	0
56	MG	2a	1810	1/1	0.89	0.27	53,53,53,53	0
56	MG	1A	8931	1/1	0.89	0.09	18,18,18,18	0
56	MG	2A	3920	1/1	0.89	0.09	43,43,43,43	0
56	MG	2A	3332	1/1	0.89	0.11	69,69,69,69	0
56	MG	1A	8320	1/1	0.89	0.10	7,7,7,7	0
56	MG	2A	3343	1/1	0.89	0.12	35,35,35,35	0
56	MG	1a	1625	1/1	0.89	0.15	47,47,47,47	0
56	MG	1a	1838	1/1	0.89	0.13	46,46,46,46	0
56	MG	2e	201	1/1	0.89	0.26	56,56,56,56	0
56	MG	1a	1840	1/1	0.89	0.15	55,55,55,55	0
56	MG	1A	8508	1/1	0.89	0.10	34,34,34,34	0
56	MG	2A	3730	1/1	0.89	0.10	50,50,50,50	0
56	MG	1A	8228	1/1	0.89	0.16	13,13,13,13	0
56	MG	1B	3014	1/1	0.89	0.10	31,31,31,31	0
56	MG	2A	3737	1/1	0.89	0.10	44,44,44,44	0
56	MG	1A	8324	1/1	0.89	0.13	17,17,17,17	0
56	MG	2A	3741	1/1	0.89	0.13	69,69,69,69	0
56	MG	1A	8128	1/1	0.89	0.10	40,40,40,40	0
56	MG	1A	8523	1/1	0.89	0.10	23,23,23,23	0
56	MG	2A	3390	1/1	0.89	0.16	45,45,45,45	0
56	MG	1e	201	1/1	0.90	0.12	28,28,28,28	0
56	MG	1A	8651	1/1	0.90	0.10	23,23,23,23	0
56	MG	1a	1612	1/1	0.90	0.25	52,52,52,52	0
56	MG	2A	3123	1/1	0.90	0.08	41,41,41,41	0
56	MG	1a	1613	1/1	0.90	0.25	15,15,15,15	0
56	MG	1A	8398	1/1	0.90	0.12	41,41,41,41	0
56	MG	1A	8467	1/1	0.90	0.13	9,9,9,9	0
56	MG	2a	1700	1/1	0.90	0.13	51,51,51,51	0
56	MG	1A	8284	1/1	0.90	0.21	50,50,50,50	0
56	MG	2D	307	1/1	0.90	0.10	33,33,33,33	0
56	MG	1a	1769	1/1	0.90	0.08	46,46,46,46	0
56	MG	2A	3329	1/1	0.90	0.13	30,30,30,30	0
56	MG	1A	8776	1/1	0.90	0.15	35,35,35,35	0
56	MG	2A	3525	1/1	0.90	0.09	25,25,25,25	0
56	MG	1A	8471	1/1	0.90	0.07	17,17,17,17	0
56	MG	1a	1774	1/1	0.90	0.12	59,59,59,59	0
56	MG	2A	3156	1/1	0.90	0.07	33,33,33,33	0
56	MG	2A	3693	1/1	0.90	0.12	34,34,34,34	0
56	MG	1x	3011	1/1	0.90	0.15	34,34,34,34	0
56	MG	2A	3172	1/1	0.90	0.12	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1719	1/1	0.90	0.24	39,39,39,39	0
56	MG	1A	8872	1/1	0.90	0.19	59,59,59,59	0
56	MG	1A	8234	1/1	0.90	0.14	32,32,32,32	0
56	MG	2A	3704	1/1	0.90	0.07	53,53,53,53	0
56	MG	1A	8023	1/1	0.90	0.06	21,21,21,21	0
56	MG	2A	3191	1/1	0.90	0.08	35,35,35,35	0
56	MG	2Q	201	1/1	0.90	0.12	38,38,38,38	0
56	MG	2A	3880	1/1	0.90	0.11	32,32,32,32	0
56	MG	2A	3373	1/1	0.90	0.09	29,29,29,29	0
56	MG	2A	3714	1/1	0.90	0.10	39,39,39,39	0
56	MG	1A	8082	1/1	0.90	0.09	27,27,27,27	0
56	MG	1A	8900	1/1	0.90	0.11	13,13,13,13	0
56	MG	2a	1732	1/1	0.90	0.10	77,77,77,77	0
56	MG	2A	3385	1/1	0.90	0.10	24,24,24,24	0
56	MG	1a	1640	1/1	0.90	0.14	47,47,47,47	0
56	MG	2A	3902	1/1	0.90	0.11	39,39,39,39	0
56	MG	1A	8490	1/1	0.90	0.09	18,18,18,18	0
56	MG	1A	8129	1/1	0.90	0.06	19,19,19,19	0
56	MG	2A	3206	1/1	0.90	0.20	48,48,48,48	0
56	MG	2A	3564	1/1	0.90	0.27	51,51,51,51	0
56	MG	1A	8387	1/1	0.90	0.15	28,28,28,28	0
56	MG	2A	3729	1/1	0.90	0.13	76,76,76,76	0
56	MG	2A	3222	1/1	0.90	0.19	48,48,48,48	0
56	MG	1a	1728	1/1	0.90	0.07	38,38,38,38	0
56	MG	1a	1650	1/1	0.90	0.22	42,42,42,42	0
56	MG	2a	1613	1/1	0.90	0.23	46,46,46,46	0
56	MG	1a	1730	1/1	0.90	0.12	43,43,43,43	0
56	MG	2a	1617	1/1	0.90	0.20	50,50,50,50	0
56	MG	2a	1771	1/1	0.90	0.15	55,55,55,55	0
56	MG	1A	8913	1/1	0.90	0.08	48,48,48,48	0
56	MG	2a	1621	1/1	0.90	0.17	49,49,49,49	0
56	MG	2A	3922	1/1	0.90	0.21	65,65,65,65	0
56	MG	2A	3050	1/1	0.90	0.14	39,39,39,39	0
56	MG	1a	1655	1/1	0.90	0.14	28,28,28,28	0
56	MG	1A	8727	1/1	0.90	0.09	36,36,36,36	0
56	MG	1A	8048	1/1	0.90	0.08	22,22,22,22	0
56	MG	2a	1783	1/1	0.90	0.10	59,59,59,59	0
56	MG	1A	8458	1/1	0.90	0.09	53,53,53,53	0
56	MG	2A	3937	1/1	0.90	0.16	38,38,38,38	0
56	MG	1A	8944	1/1	0.90	0.14	24,24,24,24	0
56	MG	1a	1810	1/1	0.90	0.15	52,52,52,52	0
56	MG	2A	3616	1/1	0.90	0.10	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1744	1/1	0.90	0.11	59,59,59,59	0
56	MG	2A	3473	1/1	0.90	0.10	51,51,51,51	0
56	MG	1A	8646	1/1	0.90	0.12	30,30,30,30	0
56	MG	2a	1803	1/1	0.90	0.09	41,41,41,41	0
56	MG	1A	8973	1/1	0.90	0.13	12,12,12,12	0
56	MG	2a	1645	1/1	0.90	0.12	53,53,53,53	0
56	MG	2A	3977	1/1	0.90	0.15	30,30,30,30	0
56	MG	2A	3980	1/1	0.90	0.09	51,51,51,51	0
56	MG	2A	3265	1/1	0.90	0.08	56,56,56,56	0
56	MG	2a	1651	1/1	0.90	0.15	48,48,48,48	0
56	MG	1a	1668	1/1	0.90	0.14	47,47,47,47	0
56	MG	1a	1834	1/1	0.90	0.19	46,46,46,46	0
56	MG	2A	3636	1/1	0.90	0.11	48,48,48,48	0
56	MG	2a	1819	1/1	0.90	0.14	59,59,59,59	0
56	MG	2A	3273	1/1	0.90	0.09	44,44,44,44	0
56	MG	2a	1661	1/1	0.90	0.16	43,43,43,43	0
56	MG	2A	3785	1/1	0.90	0.12	29,29,29,29	0
56	MG	2a	1663	1/1	0.90	0.16	43,43,43,43	0
56	MG	2f	8001	1/1	0.90	0.10	43,43,43,43	0
56	MG	2A	3640	1/1	0.90	0.14	26,26,26,26	0
56	MG	2A	3274	1/1	0.90	0.09	42,42,42,42	0
56	MG	2A	3789	1/1	0.90	0.09	48,48,48,48	0
56	MG	2A	3654	1/1	0.90	0.36	41,41,41,41	0
56	MG	2a	1675	1/1	0.90	0.14	42,42,42,42	0
56	MG	2B	3008	1/1	0.90	0.19	52,52,52,52	0
56	MG	1A	8814	1/1	0.90	0.09	62,62,62,62	0
56	MG	1a	1839	1/1	0.90	0.09	48,48,48,48	0
56	MG	1A	8572	1/1	0.90	0.10	5,5,5,5	0
56	MG	1A	8839	1/1	0.90	0.15	31,31,31,31	0
56	MG	1a	1756	1/1	0.90	0.11	51,51,51,51	0
56	MG	1a	1626	1/1	0.91	0.11	38,38,38,38	0
56	MG	1A	8182	1/1	0.91	0.06	12,12,12,12	0
56	MG	1A	8911	1/1	0.91	0.18	32,32,32,32	0
56	MG	1A	8370	1/1	0.91	0.11	10,10,10,10	0
56	MG	2A	3550	1/1	0.91	0.22	50,50,50,50	0
56	MG	2A	3279	1/1	0.91	0.09	49,49,49,49	0
56	MG	2A	3827	1/1	0.91	0.17	66,66,66,66	0
56	MG	2A	3830	1/1	0.91	0.11	42,42,42,42	0
56	MG	1a	1638	1/1	0.91	0.11	27,27,27,27	0
56	MG	2A	3035	1/1	0.91	0.08	37,37,37,37	0
56	MG	1A	8470	1/1	0.91	0.11	39,39,39,39	0
56	MG	2a	1629	1/1	0.91	0.20	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8183	1/1	0.91	0.07	24,24,24,24	0
56	MG	1A	8473	1/1	0.91	0.18	35,35,35,35	0
56	MG	2A	3567	1/1	0.91	0.09	43,43,43,43	0
56	MG	2A	3572	1/1	0.91	0.12	56,56,56,56	0
56	MG	2A	3574	1/1	0.91	0.10	31,31,31,31	0
56	MG	2A	3575	1/1	0.91	0.10	42,42,42,42	0
56	MG	1A	8478	1/1	0.91	0.37	9,9,9,9	0
56	MG	1A	8374	1/1	0.91	0.11	41,41,41,41	0
56	MG	1A	8972	1/1	0.91	0.21	20,20,20,20	0
56	MG	2A	3310	1/1	0.91	0.09	25,25,25,25	0
56	MG	1A	8034	1/1	0.91	0.07	24,24,24,24	0
56	MG	2A	3058	1/1	0.91	0.11	42,42,42,42	0
56	MG	1A	8601	1/1	0.91	0.16	36,36,36,36	0
56	MG	2a	1652	1/1	0.91	0.14	28,28,28,28	0
56	MG	2a	1653	1/1	0.91	0.21	40,40,40,40	0
56	MG	2A	3319	1/1	0.91	0.10	68,68,68,68	0
56	MG	2A	3062	1/1	0.91	0.17	37,37,37,37	0
56	MG	2A	3604	1/1	0.91	0.10	43,43,43,43	0
56	MG	2A	3321	1/1	0.91	0.09	18,18,18,18	0
56	MG	2A	3323	1/1	0.91	0.11	47,47,47,47	0
56	MG	2A	3611	1/1	0.91	0.42	34,34,34,34	0
56	MG	1A	8485	1/1	0.91	0.07	30,30,30,30	0
56	MG	1a	1657	1/1	0.91	0.19	55,55,55,55	0
56	MG	1a	1658	1/1	0.91	0.17	29,29,29,29	0
56	MG	1B	3008	1/1	0.91	0.06	35,35,35,35	0
56	MG	2A	3897	1/1	0.91	0.12	59,59,59,59	0
56	MG	2A	3338	1/1	0.91	0.19	40,40,40,40	0
56	MG	2A	3901	1/1	0.91	0.08	29,29,29,29	0
56	MG	1A	8093	1/1	0.91	0.08	20,20,20,20	0
56	MG	2A	3341	1/1	0.91	0.09	43,43,43,43	0
56	MG	1A	8386	1/1	0.91	0.12	16,16,16,16	0
56	MG	2A	3344	1/1	0.91	0.09	41,41,41,41	0
56	MG	2A	3632	1/1	0.91	0.11	38,38,38,38	0
56	MG	2a	1684	1/1	0.91	0.20	41,41,41,41	0
56	MG	2A	3356	1/1	0.91	0.11	30,30,30,30	0
56	MG	2A	3081	1/1	0.91	0.08	27,27,27,27	0
56	MG	1A	8491	1/1	0.91	0.09	9,9,9,9	0
56	MG	2a	1693	1/1	0.91	0.09	47,47,47,47	0
56	MG	2a	1694	1/1	0.91	0.10	28,28,28,28	0
56	MG	2A	3639	1/1	0.91	0.19	41,41,41,41	0
56	MG	1A	8623	1/1	0.91	0.29	18,18,18,18	0
56	MG	1A	8261	1/1	0.91	0.21	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8497	1/1	0.91	0.08	20,20,20,20	0
56	MG	1D	307	1/1	0.91	0.19	20,20,20,20	0
56	MG	2A	3100	1/1	0.91	0.13	37,37,37,37	0
56	MG	1A	8104	1/1	0.91	0.09	44,44,44,44	0
56	MG	2A	3374	1/1	0.91	0.08	57,57,57,57	0
56	MG	1A	8504	1/1	0.91	0.07	30,30,30,30	0
56	MG	1A	8643	1/1	0.91	0.20	28,28,28,28	0
56	MG	2A	3382	1/1	0.91	0.10	38,38,38,38	0
56	MG	2A	3944	1/1	0.91	0.25	28,28,28,28	0
56	MG	2A	3384	1/1	0.91	0.09	40,40,40,40	0
56	MG	2A	3954	1/1	0.91	0.29	41,41,41,41	0
56	MG	1a	1793	1/1	0.91	0.08	45,45,45,45	0
56	MG	1a	1794	1/1	0.91	0.12	43,43,43,43	0
56	MG	2A	3391	1/1	0.91	0.10	20,20,20,20	0
56	MG	2A	3677	1/1	0.91	0.16	60,60,60,60	0
56	MG	1A	8105	1/1	0.91	0.16	12,12,12,12	0
56	MG	1A	8806	1/1	0.91	0.23	16,16,16,16	0
56	MG	2A	3971	1/1	0.91	0.17	41,41,41,41	0
56	MG	1a	1798	1/1	0.91	0.12	48,48,48,48	0
56	MG	1a	1799	1/1	0.91	0.06	35,35,35,35	0
56	MG	2A	3412	1/1	0.91	0.10	21,21,21,21	0
56	MG	1F	310	1/1	0.91	0.10	29,29,29,29	0
56	MG	2A	3419	1/1	0.91	0.08	48,48,48,48	0
56	MG	1A	8202	1/1	0.91	0.11	11,11,11,11	0
56	MG	2A	3143	1/1	0.91	0.08	33,33,33,33	0
56	MG	1a	1803	1/1	0.91	0.10	47,47,47,47	0
56	MG	2A	3149	1/1	0.91	0.14	32,32,32,32	0
56	MG	2B	3004	1/1	0.91	0.10	63,63,63,63	0
56	MG	1A	8327	1/1	0.91	0.07	32,32,32,32	0
56	MG	2A	3152	1/1	0.91	0.10	32,32,32,32	0
56	MG	2A	3442	1/1	0.91	0.08	23,23,23,23	0
56	MG	2A	3444	1/1	0.91	0.08	32,32,32,32	0
56	MG	1A	8818	1/1	0.91	0.30	33,33,33,33	0
56	MG	2a	1749	1/1	0.91	0.08	57,57,57,57	0
56	MG	2B	3010	1/1	0.91	0.12	38,38,38,38	0
56	MG	1a	1821	1/1	0.91	0.20	39,39,39,39	0
56	MG	1A	8654	1/1	0.91	0.24	32,32,32,32	0
56	MG	2A	3169	1/1	0.91	0.24	31,31,31,31	0
56	MG	1A	8662	1/1	0.91	0.13	29,29,29,29	0
56	MG	1A	8269	1/1	0.91	0.07	23,23,23,23	0
56	MG	2a	1764	1/1	0.91	0.14	55,55,55,55	0
56	MG	2A	3177	1/1	0.91	0.22	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8847	1/1	0.91	0.17	16,16,16,16	0
56	MG	1a	1710	1/1	0.91	0.08	47,47,47,47	0
56	MG	1a	1836	1/1	0.91	0.16	36,36,36,36	0
56	MG	2A	3195	1/1	0.91	0.14	31,31,31,31	0
56	MG	2A	3196	1/1	0.91	0.22	31,31,31,31	0
56	MG	2A	3197	1/1	0.91	0.14	37,37,37,37	0
56	MG	2D	303	1/1	0.91	0.09	25,25,25,25	0
56	MG	1A	8667	1/1	0.91	0.11	40,40,40,40	0
56	MG	1A	8119	1/1	0.91	0.14	29,29,29,29	0
56	MG	1A	8526	1/1	0.91	0.08	42,42,42,42	0
56	MG	1A	8336	1/1	0.91	0.10	32,32,32,32	0
56	MG	1A	8868	1/1	0.91	0.09	22,22,22,22	0
56	MG	1A	8686	1/1	0.91	0.09	38,38,38,38	0
56	MG	2a	1786	1/1	0.91	0.11	48,48,48,48	0
56	MG	2E	306	1/1	0.91	0.09	44,44,44,44	0
56	MG	2A	3207	1/1	0.91	0.36	44,44,44,44	0
56	MG	2A	3209	1/1	0.91	0.25	37,37,37,37	0
56	MG	2A	3743	1/1	0.91	0.18	47,47,47,47	0
56	MG	1A	8423	1/1	0.91	0.11	28,28,28,28	0
56	MG	1A	8879	1/1	0.91	0.13	25,25,25,25	0
56	MG	2A	3507	1/1	0.91	0.10	43,43,43,43	0
56	MG	2A	3508	1/1	0.91	0.14	44,44,44,44	0
56	MG	1l	201	1/1	0.91	0.11	42,42,42,42	0
56	MG	1a	1605	1/1	0.91	0.19	43,43,43,43	0
56	MG	2A	3511	1/1	0.91	0.15	39,39,39,39	0
56	MG	1a	1607	1/1	0.91	0.12	49,49,49,49	0
56	MG	1A	8538	1/1	0.91	0.09	14,14,14,14	0
56	MG	2A	3237	1/1	0.91	0.24	45,45,45,45	0
56	MG	2U	202	1/1	0.91	0.08	50,50,50,50	0
56	MG	1o	101	1/1	0.91	0.16	50,50,50,50	0
56	MG	1a	1736	1/1	0.91	0.10	40,40,40,40	0
56	MG	1a	1737	1/1	0.91	0.08	40,40,40,40	0
56	MG	2U	207	1/1	0.91	0.09	29,29,29,29	0
56	MG	2A	3779	1/1	0.91	0.10	34,34,34,34	0
56	MG	2A	3526	1/1	0.91	0.14	46,46,46,46	0
56	MG	20	101	1/1	0.91	0.16	46,46,46,46	0
56	MG	1A	8882	1/1	0.91	0.07	38,38,38,38	0
56	MG	1A	8274	1/1	0.91	0.06	23,23,23,23	0
56	MG	1A	8340	1/1	0.91	0.10	19,19,19,19	0
56	MG	2x	101	1/1	0.91	0.10	48,48,48,48	0
56	MG	2x	102	1/1	0.91	0.07	51,51,51,51	0
56	MG	23	102	1/1	0.91	0.15	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1743	1/1	0.91	0.16	41,41,41,41	0
56	MG	1A	8061	1/1	0.91	0.12	41,41,41,41	0
56	MG	1A	8902	1/1	0.91	0.21	51,51,51,51	0
56	MG	1A	8716	1/1	0.91	0.10	39,39,39,39	0
56	MG	2A	3802	1/1	0.91	0.13	54,54,54,54	0
56	MG	2A	3803	1/1	0.91	0.27	71,71,71,71	0
59	K	1x	3001	1/1	0.91	0.16	46,46,46,46	0
56	MG	1A	8050	1/1	0.91	0.08	23,23,23,23	0
56	MG	1A	8691	1/1	0.92	0.09	14,14,14,14	0
56	MG	2A	3862	1/1	0.92	0.11	32,32,32,32	0
56	MG	1A	8621	1/1	0.92	0.15	24,24,24,24	0
56	MG	1A	8331	1/1	0.92	0.10	19,19,19,19	0
56	MG	1d	503	1/1	0.92	0.15	38,38,38,38	0
56	MG	2A	3167	1/1	0.92	0.08	26,26,26,26	0
56	MG	2A	3393	1/1	0.92	0.10	27,27,27,27	0
56	MG	1d	504	1/1	0.92	0.08	45,45,45,45	0
56	MG	2a	1633	1/1	0.92	0.17	41,41,41,41	0
56	MG	1A	8706	1/1	0.92	0.07	39,39,39,39	0
56	MG	2A	3401	1/1	0.92	0.11	38,38,38,38	0
56	MG	1a	1620	1/1	0.92	0.10	46,46,46,46	0
56	MG	1B	3005	1/1	0.92	0.09	34,34,34,34	0
56	MG	2A	3408	1/1	0.92	0.09	38,38,38,38	0
56	MG	1g	3001	1/1	0.92	0.16	38,38,38,38	0
56	MG	2A	3643	1/1	0.92	0.12	27,27,27,27	0
56	MG	2A	3891	1/1	0.92	0.12	43,43,43,43	0
56	MG	2A	3181	1/1	0.92	0.10	31,31,31,31	0
56	MG	2a	1648	1/1	0.92	0.24	33,33,33,33	0
56	MG	2A	3416	1/1	0.92	0.09	28,28,28,28	0
56	MG	2A	3417	1/1	0.92	0.11	51,51,51,51	0
56	MG	1A	8171	1/1	0.92	0.10	28,28,28,28	0
56	MG	2A	3659	1/1	0.92	0.10	30,30,30,30	0
56	MG	2A	3185	1/1	0.92	0.13	45,45,45,45	0
56	MG	2A	3422	1/1	0.92	0.08	45,45,45,45	0
56	MG	2A	3424	1/1	0.92	0.22	50,50,50,50	0
56	MG	1B	3011	1/1	0.92	0.07	39,39,39,39	0
56	MG	2A	3909	1/1	0.92	0.30	29,29,29,29	0
56	MG	1A	8260	1/1	0.92	0.14	28,28,28,28	0
56	MG	1a	1631	1/1	0.92	0.14	34,34,34,34	0
56	MG	1A	8092	1/1	0.92	0.33	17,17,17,17	0
56	MG	2A	3672	1/1	0.92	0.12	46,46,46,46	0
56	MG	1A	8505	1/1	0.92	0.12	24,24,24,24	0
56	MG	1A	8001	1/1	0.92	0.08	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	3021	1/1	0.92	0.07	28,28,28,28	0
56	MG	1a	1747	1/1	0.92	0.10	65,65,65,65	0
56	MG	1A	8063	1/1	0.92	0.07	22,22,22,22	0
56	MG	1A	8863	1/1	0.92	0.14	24,24,24,24	0
56	MG	1D	303	1/1	0.92	0.07	17,17,17,17	0
56	MG	2A	3926	1/1	0.92	0.20	36,36,36,36	0
56	MG	1a	1644	1/1	0.92	0.20	38,38,38,38	0
56	MG	2A	3463	1/1	0.92	0.09	42,42,42,42	0
56	MG	1D	305	1/1	0.92	0.14	18,18,18,18	0
56	MG	2A	3469	1/1	0.92	0.13	31,31,31,31	0
56	MG	2A	3939	1/1	0.92	0.13	43,43,43,43	0
56	MG	1D	306	1/1	0.92	0.06	21,21,21,21	0
56	MG	2A	3950	1/1	0.92	0.12	41,41,41,41	0
56	MG	2A	3691	1/1	0.92	0.16	29,29,29,29	0
56	MG	1A	8736	1/1	0.92	0.30	38,38,38,38	0
56	MG	2A	3957	1/1	0.92	0.12	41,41,41,41	0
56	MG	1A	8649	1/1	0.92	0.19	18,18,18,18	0
56	MG	2A	3960	1/1	0.92	0.46	45,45,45,45	0
56	MG	2A	3961	1/1	0.92	0.27	35,35,35,35	0
56	MG	1A	8743	1/1	0.92	0.24	14,14,14,14	0
56	MG	2a	1704	1/1	0.92	0.17	38,38,38,38	0
56	MG	2A	3022	1/1	0.92	0.26	29,29,29,29	0
56	MG	2A	3025	1/1	0.92	0.15	33,33,33,33	0
56	MG	1A	8578	1/1	0.92	0.08	10,10,10,10	0
56	MG	2A	3240	1/1	0.92	0.11	57,57,57,57	0
56	MG	2A	3970	1/1	0.92	0.20	53,53,53,53	0
56	MG	2A	3241	1/1	0.92	0.07	49,49,49,49	0
56	MG	2A	3972	1/1	0.92	0.09	31,31,31,31	0
56	MG	2A	3487	1/1	0.92	0.21	26,26,26,26	0
56	MG	2A	3713	1/1	0.92	0.08	24,24,24,24	0
56	MG	1A	8583	1/1	0.92	0.13	8,8,8,8	0
56	MG	2A	3033	1/1	0.92	0.18	28,28,28,28	0
56	MG	2A	3984	1/1	0.92	0.21	37,37,37,37	0
56	MG	1A	8013	1/1	0.92	0.09	20,20,20,20	0
56	MG	2A	3986	1/1	0.92	0.10	37,37,37,37	0
56	MG	1A	8757	1/1	0.92	0.18	42,42,42,42	0
56	MG	1a	1770	1/1	0.92	0.14	47,47,47,47	0
56	MG	1A	8655	1/1	0.92	0.13	22,22,22,22	0
56	MG	2A	3258	1/1	0.92	0.07	36,36,36,36	0
56	MG	1a	1663	1/1	0.92	0.10	51,51,51,51	0
56	MG	1A	8885	1/1	0.92	0.08	31,31,31,31	0
56	MG	2A	3727	1/1	0.92	0.18	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1665	1/1	0.92	0.18	51,51,51,51	0
56	MG	1a	1666	1/1	0.92	0.17	31,31,31,31	0
56	MG	1A	8763	1/1	0.92	0.14	28,28,28,28	0
56	MG	2a	1733	1/1	0.92	0.09	69,69,69,69	0
56	MG	1A	8897	1/1	0.92	0.11	48,48,48,48	0
56	MG	1A	8043	1/1	0.92	0.06	24,24,24,24	0
56	MG	2B	3012	1/1	0.92	0.15	52,52,52,52	0
56	MG	2a	1742	1/1	0.92	0.09	62,62,62,62	0
56	MG	1A	8120	1/1	0.92	0.13	53,53,53,53	0
56	MG	2A	3275	1/1	0.92	0.07	42,42,42,42	0
56	MG	2a	1746	1/1	0.92	0.08	59,59,59,59	0
56	MG	1R	204	1/1	0.92	0.07	26,26,26,26	0
56	MG	1A	8242	1/1	0.92	0.07	44,44,44,44	0
56	MG	2a	1751	1/1	0.92	0.09	50,50,50,50	0
56	MG	1a	1678	1/1	0.92	0.08	43,43,43,43	0
56	MG	1a	1679	1/1	0.92	0.07	36,36,36,36	0
56	MG	2A	3747	1/1	0.92	0.12	39,39,39,39	0
56	MG	2a	1757	1/1	0.92	0.11	55,55,55,55	0
56	MG	1A	8669	1/1	0.92	0.09	27,27,27,27	0
56	MG	2a	1759	1/1	0.92	0.14	76,76,76,76	0
56	MG	1V	201	1/1	0.92	0.09	28,28,28,28	0
56	MG	2A	3754	1/1	0.92	0.17	36,36,36,36	0
56	MG	1A	8670	1/1	0.92	0.32	41,41,41,41	0
56	MG	1a	1683	1/1	0.92	0.14	39,39,39,39	0
56	MG	2A	3759	1/1	0.92	0.10	52,52,52,52	0
56	MG	2A	3760	1/1	0.92	0.10	47,47,47,47	0
56	MG	2A	3089	1/1	0.92	0.12	34,34,34,34	0
56	MG	2A	3301	1/1	0.92	0.13	52,52,52,52	0
56	MG	10	104	1/1	0.92	0.13	41,41,41,41	0
56	MG	2A	3767	1/1	0.92	0.10	52,52,52,52	0
56	MG	1A	8672	1/1	0.92	0.10	19,19,19,19	0
56	MG	2F	304	1/1	0.92	0.11	44,44,44,44	0
56	MG	2A	3772	1/1	0.92	0.10	43,43,43,43	0
56	MG	10	108	1/1	0.92	0.15	35,35,35,35	0
56	MG	2A	3094	1/1	0.92	0.16	38,38,38,38	0
56	MG	2A	3097	1/1	0.92	0.18	38,38,38,38	0
56	MG	1a	1689	1/1	0.92	0.14	41,41,41,41	0
56	MG	2A	3549	1/1	0.92	0.08	39,39,39,39	0
56	MG	2A	3780	1/1	0.92	0.13	44,44,44,44	0
56	MG	1A	8789	1/1	0.92	0.12	22,22,22,22	0
56	MG	2A	3101	1/1	0.92	0.16	48,48,48,48	0
56	MG	2A	3325	1/1	0.92	0.14	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1694	1/1	0.92	0.12	27,27,27,27	0
56	MG	2a	1798	1/1	0.92	0.10	49,49,49,49	0
56	MG	1a	1696	1/1	0.92	0.13	54,54,54,54	0
56	MG	2a	1801	1/1	0.92	0.15	61,61,61,61	0
56	MG	2A	3112	1/1	0.92	0.10	29,29,29,29	0
56	MG	2A	3796	1/1	0.92	0.09	29,29,29,29	0
56	MG	1A	8121	1/1	0.92	0.07	19,19,19,19	0
56	MG	1A	8532	1/1	0.92	0.20	15,15,15,15	0
56	MG	1a	1809	1/1	0.92	0.11	51,51,51,51	0
56	MG	2A	3122	1/1	0.92	0.10	55,55,55,55	0
56	MG	2V	201	1/1	0.92	0.07	32,32,32,32	0
56	MG	1A	8612	1/1	0.92	0.09	8,8,8,8	0
56	MG	2a	1814	1/1	0.92	0.09	40,40,40,40	0
56	MG	2X	101	1/1	0.92	0.08	33,33,33,33	0
56	MG	1a	1817	1/1	0.92	0.15	52,52,52,52	0
56	MG	2A	3577	1/1	0.92	0.11	25,25,25,25	0
56	MG	2a	1820	1/1	0.92	0.14	60,60,60,60	0
56	MG	20	102	1/1	0.92	0.13	43,43,43,43	0
56	MG	2A	3346	1/1	0.92	0.08	29,29,29,29	0
56	MG	2A	3582	1/1	0.92	0.07	27,27,27,27	0
56	MG	1A	8281	1/1	0.92	0.09	28,28,28,28	0
56	MG	2A	3128	1/1	0.92	0.11	48,48,48,48	0
56	MG	2A	3588	1/1	0.92	0.11	44,44,44,44	0
56	MG	27	101	1/1	0.92	0.28	39,39,39,39	0
56	MG	1A	8433	1/1	0.92	0.09	14,14,14,14	0
56	MG	2n	502	1/1	0.92	0.12	55,55,55,55	0
56	MG	2v	101	1/1	0.92	0.10	61,61,61,61	0
56	MG	2A	3133	1/1	0.92	0.22	39,39,39,39	0
56	MG	1A	8384	1/1	0.92	0.10	36,36,36,36	0
56	MG	1a	1714	1/1	0.92	0.08	42,42,42,42	0
56	MG	2A	3140	1/1	0.92	0.12	25,25,25,25	0
56	MG	2A	3142	1/1	0.92	0.11	36,36,36,36	0
56	MG	2x	107	1/1	0.92	0.09	52,52,52,52	0
56	MG	1a	1608	1/1	0.92	0.09	47,47,47,47	0
56	MG	1a	1610	1/1	0.92	0.14	36,36,36,36	0
56	MG	2a	1616	1/1	0.92	0.12	37,37,37,37	0
56	MG	2A	3375	1/1	0.92	0.11	24,24,24,24	0
56	MG	1A	8949	1/1	0.92	0.18	16,16,16,16	0
56	MG	1A	8970	1/1	0.92	0.12	29,29,29,29	0
56	MG	2a	1603	1/1	0.93	0.12	45,45,45,45	0
56	MG	2a	1606	1/1	0.93	0.21	35,35,35,35	0
56	MG	1A	8321	1/1	0.93	0.15	5,5,5,5	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3566	1/1	0.93	0.18	43,43,43,43	0
56	MG	2A	3086	1/1	0.93	0.28	40,40,40,40	0
56	MG	2A	3815	1/1	0.93	0.07	33,33,33,33	0
56	MG	2A	3568	1/1	0.93	0.11	22,22,22,22	0
56	MG	2a	1614	1/1	0.93	0.14	49,49,49,49	0
56	MG	1A	8517	1/1	0.93	0.10	32,32,32,32	0
56	MG	2A	3322	1/1	0.93	0.07	37,37,37,37	0
56	MG	2A	3828	1/1	0.93	0.18	58,58,58,58	0
56	MG	1A	8322	1/1	0.93	0.07	45,45,45,45	0
56	MG	2A	3324	1/1	0.93	0.09	33,33,33,33	0
56	MG	2A	3090	1/1	0.93	0.10	39,39,39,39	0
56	MG	2A	3580	1/1	0.93	0.18	49,49,49,49	0
56	MG	1A	8123	1/1	0.93	0.40	22,22,22,22	0
56	MG	1a	1784	1/1	0.93	0.12	54,54,54,54	0
56	MG	1A	8251	1/1	0.93	0.07	33,33,33,33	0
56	MG	2A	3585	1/1	0.93	0.22	33,33,33,33	0
56	MG	1A	8035	1/1	0.93	0.10	30,30,30,30	0
56	MG	2A	3850	1/1	0.93	0.10	39,39,39,39	0
56	MG	2a	1632	1/1	0.93	0.22	51,51,51,51	0
56	MG	2A	3852	1/1	0.93	0.10	40,40,40,40	0
56	MG	2a	1634	1/1	0.93	0.07	54,54,54,54	0
56	MG	1A	8829	1/1	0.93	0.21	42,42,42,42	0
56	MG	1A	8060	1/1	0.93	0.07	31,31,31,31	0
56	MG	1A	8040	1/1	0.93	0.15	32,32,32,32	0
56	MG	2A	3860	1/1	0.93	0.10	46,46,46,46	0
56	MG	1A	8329	1/1	0.93	0.07	24,24,24,24	0
56	MG	1G	3001	1/1	0.93	0.07	52,52,52,52	0
56	MG	2A	3599	1/1	0.93	0.06	48,48,48,48	0
56	MG	2a	1644	1/1	0.93	0.11	46,46,46,46	0
56	MG	1A	8003	1/1	0.93	0.09	29,29,29,29	0
56	MG	1A	8443	1/1	0.93	0.07	13,13,13,13	0
56	MG	1A	8147	1/1	0.93	0.19	18,18,18,18	0
56	MG	2A	3117	1/1	0.93	0.15	45,45,45,45	0
56	MG	2A	3871	1/1	0.93	0.08	56,56,56,56	0
56	MG	2A	3607	1/1	0.93	0.08	37,37,37,37	0
56	MG	2A	3118	1/1	0.93	0.25	48,48,48,48	0
56	MG	1A	8861	1/1	0.93	0.09	39,39,39,39	0
56	MG	2A	3613	1/1	0.93	0.09	62,62,62,62	0
56	MG	1P	201	1/1	0.93	0.10	18,18,18,18	0
56	MG	2A	3886	1/1	0.93	0.08	43,43,43,43	0
56	MG	2a	1657	1/1	0.93	0.18	38,38,38,38	0
56	MG	1A	8463	1/1	0.93	0.09	7,7,7,7	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8335	1/1	0.93	0.17	38,38,38,38	0
56	MG	1A	8110	1/1	0.93	0.17	14,14,14,14	0
56	MG	1A	8555	1/1	0.93	0.08	37,37,37,37	0
56	MG	1A	8064	1/1	0.93	0.07	23,23,23,23	0
56	MG	2A	3895	1/1	0.93	0.09	27,27,27,27	0
56	MG	2A	3627	1/1	0.93	0.06	55,55,55,55	0
56	MG	2a	1669	1/1	0.93	0.11	40,40,40,40	0
56	MG	2a	1670	1/1	0.93	0.11	53,53,53,53	0
56	MG	2a	1671	1/1	0.93	0.08	34,34,34,34	0
56	MG	1A	8206	1/1	0.93	0.15	18,18,18,18	0
56	MG	1V	203	1/1	0.93	0.07	40,40,40,40	0
56	MG	1A	8565	1/1	0.93	0.23	17,17,17,17	0
56	MG	1A	8697	1/1	0.93	0.08	32,32,32,32	0
56	MG	1a	1698	1/1	0.93	0.06	29,29,29,29	0
56	MG	1a	1827	1/1	0.93	0.12	62,62,62,62	0
56	MG	1A	8158	1/1	0.93	0.08	27,27,27,27	0
56	MG	1A	8029	1/1	0.93	0.09	15,15,15,15	0
56	MG	2A	3911	1/1	0.93	0.12	53,53,53,53	0
56	MG	2A	3147	1/1	0.93	0.20	36,36,36,36	0
56	MG	1a	1702	1/1	0.93	0.08	48,48,48,48	0
56	MG	2A	3648	1/1	0.93	0.09	34,34,34,34	0
56	MG	2A	3650	1/1	0.93	0.10	36,36,36,36	0
56	MG	2A	3653	1/1	0.93	0.11	41,41,41,41	0
56	MG	1a	1703	1/1	0.93	0.14	48,48,48,48	0
56	MG	1a	1837	1/1	0.93	0.14	39,39,39,39	0
56	MG	15	103	1/1	0.93	0.14	20,20,20,20	0
56	MG	2A	3407	1/1	0.93	0.12	29,29,29,29	0
56	MG	1A	8169	1/1	0.93	0.22	16,16,16,16	0
56	MG	2a	1701	1/1	0.93	0.14	82,82,82,82	0
56	MG	2A	3661	1/1	0.93	0.14	36,36,36,36	0
56	MG	1A	8479	1/1	0.93	0.11	38,38,38,38	0
56	MG	1A	8231	1/1	0.93	0.07	25,25,25,25	0
56	MG	19	104	1/1	0.93	0.10	34,34,34,34	0
56	MG	1A	8283	1/1	0.93	0.14	13,13,13,13	0
56	MG	1a	1719	1/1	0.93	0.10	35,35,35,35	0
56	MG	1a	1720	1/1	0.93	0.12	49,49,49,49	0
56	MG	2A	3946	1/1	0.93	0.48	29,29,29,29	0
56	MG	1A	8901	1/1	0.93	0.09	34,34,34,34	0
56	MG	1a	1724	1/1	0.93	0.11	50,50,50,50	0
56	MG	1A	8718	1/1	0.93	0.16	27,27,27,27	0
56	MG	2A	3955	1/1	0.93	0.25	35,35,35,35	0
56	MG	2A	3427	1/1	0.93	0.11	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3678	1/1	0.93	0.15	49,49,49,49	0
56	MG	2A	3959	1/1	0.93	0.30	38,38,38,38	0
56	MG	2A	3183	1/1	0.93	0.13	36,36,36,36	0
56	MG	1a	1606	1/1	0.93	0.18	36,36,36,36	0
56	MG	1A	8719	1/1	0.93	0.12	9,9,9,9	0
56	MG	2A	3192	1/1	0.93	0.11	29,29,29,29	0
56	MG	1A	8904	1/1	0.93	0.09	41,41,41,41	0
56	MG	1A	8594	1/1	0.93	0.09	36,36,36,36	0
56	MG	2A	3445	1/1	0.93	0.07	42,42,42,42	0
56	MG	2A	3687	1/1	0.93	0.07	30,30,30,30	0
56	MG	1A	8597	1/1	0.93	0.17	14,14,14,14	0
56	MG	1o	102	1/1	0.93	0.06	26,26,26,26	0
56	MG	1A	8233	1/1	0.93	0.12	21,21,21,21	0
56	MG	2A	3692	1/1	0.93	0.12	33,33,33,33	0
56	MG	1A	8486	1/1	0.93	0.10	26,26,26,26	0
56	MG	1x	3004	1/1	0.93	0.15	47,47,47,47	0
56	MG	2a	1736	1/1	0.93	0.11	68,68,68,68	0
56	MG	2a	1737	1/1	0.93	0.09	53,53,53,53	0
56	MG	1A	8378	1/1	0.93	0.12	24,24,24,24	0
56	MG	2A	3465	1/1	0.93	0.12	23,23,23,23	0
56	MG	1A	8604	1/1	0.93	0.10	29,29,29,29	0
56	MG	1A	8930	1/1	0.93	0.16	23,23,23,23	0
56	MG	2A	3471	1/1	0.93	0.07	35,35,35,35	0
56	MG	2A	3472	1/1	0.93	0.08	29,29,29,29	0
56	MG	2A	3208	1/1	0.93	0.09	31,31,31,31	0
56	MG	2A	3474	1/1	0.93	0.07	37,37,37,37	0
56	MG	1A	8605	1/1	0.93	0.21	41,41,41,41	0
56	MG	2A	3217	1/1	0.93	0.27	30,30,30,30	0
56	MG	1a	1741	1/1	0.93	0.09	47,47,47,47	0
56	MG	2A	3002	1/1	0.93	0.15	28,28,28,28	0
56	MG	1A	8608	1/1	0.93	0.14	29,29,29,29	0
56	MG	2A	3004	1/1	0.93	0.08	39,39,39,39	0
56	MG	2a	1760	1/1	0.93	0.08	56,56,56,56	0
56	MG	1a	1624	1/1	0.93	0.15	34,34,34,34	0
56	MG	2A	3723	1/1	0.93	0.13	45,45,45,45	0
56	MG	2A	3010	1/1	0.93	0.19	28,28,28,28	0
56	MG	2a	1765	1/1	0.93	0.25	47,47,47,47	0
56	MG	2A	3236	1/1	0.93	0.25	46,46,46,46	0
56	MG	2a	1767	1/1	0.93	0.21	65,65,65,65	0
56	MG	2A	3489	1/1	0.93	0.08	27,27,27,27	0
56	MG	1A	8610	1/1	0.93	0.15	41,41,41,41	0
56	MG	1A	8489	1/1	0.93	0.20	9,9,9,9	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3016	1/1	0.93	0.44	34,34,34,34	0
56	MG	2A	3496	1/1	0.93	0.08	36,36,36,36	0
56	MG	1a	1628	1/1	0.93	0.12	39,39,39,39	0
56	MG	2A	3020	1/1	0.93	0.18	26,26,26,26	0
56	MG	2A	3738	1/1	0.93	0.11	43,43,43,43	0
56	MG	2A	3021	1/1	0.93	0.18	30,30,30,30	0
56	MG	1A	8966	1/1	0.93	0.07	22,22,22,22	0
56	MG	2D	306	1/1	0.93	0.11	34,34,34,34	0
56	MG	2A	3249	1/1	0.93	0.18	31,31,31,31	0
56	MG	1A	8170	1/1	0.93	0.14	23,23,23,23	0
56	MG	2D	314	1/1	0.93	0.07	25,25,25,25	0
56	MG	2A	3029	1/1	0.93	0.76	31,31,31,31	0
56	MG	1a	1750	1/1	0.93	0.07	56,56,56,56	0
56	MG	2a	1793	1/1	0.93	0.10	52,52,52,52	0
56	MG	2E	301	1/1	0.93	0.12	37,37,37,37	0
56	MG	1A	8380	1/1	0.93	0.07	16,16,16,16	0
56	MG	1A	8026	1/1	0.93	0.17	10,10,10,10	0
56	MG	2A	3262	1/1	0.93	0.08	38,38,38,38	0
56	MG	2F	301	1/1	0.93	0.10	43,43,43,43	0
56	MG	2a	1800	1/1	0.93	0.09	39,39,39,39	0
56	MG	1A	8618	1/1	0.93	0.18	41,41,41,41	0
56	MG	2A	3756	1/1	0.93	0.12	28,28,28,28	0
56	MG	1A	8780	1/1	0.93	0.17	10,10,10,10	0
56	MG	2A	3521	1/1	0.93	0.14	34,34,34,34	0
56	MG	1B	3004	1/1	0.93	0.14	35,35,35,35	0
56	MG	2A	3039	1/1	0.93	0.12	38,38,38,38	0
56	MG	1A	8781	1/1	0.93	0.08	14,14,14,14	0
56	MG	1A	8307	1/1	0.93	0.06	18,18,18,18	0
56	MG	2A	3042	1/1	0.93	0.16	38,38,38,38	0
56	MG	2A	3043	1/1	0.93	0.09	42,42,42,42	0
56	MG	2P	201	1/1	0.93	0.10	38,38,38,38	0
56	MG	1B	3010	1/1	0.93	0.20	44,44,44,44	0
56	MG	1a	1645	1/1	0.93	0.22	34,34,34,34	0
56	MG	1a	1766	1/1	0.93	0.12	34,34,34,34	0
56	MG	1A	8314	1/1	0.93	0.08	12,12,12,12	0
56	MG	2A	3283	1/1	0.93	0.09	30,30,30,30	0
56	MG	2A	3537	1/1	0.93	0.07	33,33,33,33	0
56	MG	1A	8315	1/1	0.93	0.10	28,28,28,28	0
56	MG	1A	8122	1/1	0.93	0.07	18,18,18,18	0
56	MG	2A	3291	1/1	0.93	0.24	19,19,19,19	0
56	MG	2i	3001	1/1	0.93	0.10	36,36,36,36	0
56	MG	2j	201	1/1	0.93	0.12	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3783	1/1	0.93	0.14	55,55,55,55	0
56	MG	1a	1654	1/1	0.93	0.16	43,43,43,43	0
56	MG	1A	8246	1/1	0.93	0.24	45,45,45,45	0
56	MG	2o	3001	1/1	0.93	0.07	32,32,32,32	0
56	MG	1A	8632	1/1	0.93	0.10	55,55,55,55	0
56	MG	2A	3297	1/1	0.93	0.09	31,31,31,31	0
56	MG	2A	3795	1/1	0.93	0.08	28,28,28,28	0
56	MG	2x	103	1/1	0.93	0.17	49,49,49,49	0
56	MG	1A	8509	1/1	0.93	0.11	42,42,42,42	0
56	MG	1A	8641	1/1	0.93	0.10	20,20,20,20	0
56	MG	1A	8510	1/1	0.93	0.14	29,29,29,29	0
56	MG	2A	3800	1/1	0.93	0.10	34,34,34,34	0
56	MG	25	103	1/1	0.93	0.12	46,46,46,46	0
56	MG	2A	3077	1/1	0.93	0.19	30,30,30,30	0
56	MG	2A	3559	1/1	0.93	0.14	25,25,25,25	0
56	MG	2A	3561	1/1	0.93	0.21	32,32,32,32	0
56	MG	1a	1778	1/1	0.93	0.05	33,33,33,33	0
56	MG	2a	1602	1/1	0.93	0.20	48,48,48,48	0
56	MG	1A	8075	1/1	0.94	0.06	20,20,20,20	0
56	MG	1A	8193	1/1	0.94	0.09	28,28,28,28	0
56	MG	2Q	204	1/1	0.94	0.06	42,42,42,42	0
56	MG	2A	3740	1/1	0.94	0.27	39,39,39,39	0
56	MG	1A	8514	1/1	0.94	0.20	48,48,48,48	0
56	MG	2U	203	1/1	0.94	0.20	35,35,35,35	0
56	MG	1A	8631	1/1	0.94	0.07	53,53,53,53	0
56	MG	1h	8001	1/1	0.94	0.08	52,52,52,52	0
56	MG	1A	8794	1/1	0.94	0.08	24,24,24,24	0
56	MG	2A	3200	1/1	0.94	0.09	21,21,21,21	0
56	MG	1A	8154	1/1	0.94	0.10	22,22,22,22	0
56	MG	1A	8118	1/1	0.94	0.07	10,10,10,10	0
56	MG	1A	8157	1/1	0.94	0.08	23,23,23,23	0
56	MG	2A	3204	1/1	0.94	0.14	31,31,31,31	0
56	MG	1A	8801	1/1	0.94	0.08	25,25,25,25	0
56	MG	1A	8088	1/1	0.94	0.06	16,16,16,16	0
56	MG	2A	3488	1/1	0.94	0.08	30,30,30,30	0
56	MG	1A	8644	1/1	0.94	0.11	36,36,36,36	0
56	MG	1A	8016	1/1	0.94	0.06	18,18,18,18	0
56	MG	1A	8648	1/1	0.94	0.13	27,27,27,27	0
56	MG	2A	3492	1/1	0.94	0.08	35,35,35,35	0
56	MG	2A	3211	1/1	0.94	0.20	35,35,35,35	0
56	MG	2A	3213	1/1	0.94	0.14	32,32,32,32	0
56	MG	2A	3499	1/1	0.94	0.10	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	28	101	1/1	0.94	0.11	54,54,54,54	0
56	MG	1A	8525	1/1	0.94	0.06	10,10,10,10	0
56	MG	29	503	1/1	0.94	0.12	62,62,62,62	0
56	MG	2A	3219	1/1	0.94	0.10	29,29,29,29	0
56	MG	1a	1709	1/1	0.94	0.08	30,30,30,30	0
56	MG	1N	201	1/1	0.94	0.12	24,24,24,24	0
56	MG	1A	8205	1/1	0.94	0.09	25,25,25,25	0
56	MG	2a	1609	1/1	0.94	0.15	45,45,45,45	0
56	MG	1x	3008	1/1	0.94	0.16	36,36,36,36	0
56	MG	2A	3226	1/1	0.94	0.12	27,27,27,27	0
56	MG	2A	3227	1/1	0.94	0.13	34,34,34,34	0
56	MG	1x	3009	1/1	0.94	0.28	41,41,41,41	0
56	MG	2A	3230	1/1	0.94	0.21	33,33,33,33	0
56	MG	2A	3513	1/1	0.94	0.07	38,38,38,38	0
56	MG	1N	204	1/1	0.94	0.17	68,68,68,68	0
56	MG	2A	3235	1/1	0.94	0.06	43,43,43,43	0
56	MG	2A	3790	1/1	0.94	0.12	45,45,45,45	0
56	MG	2A	3794	1/1	0.94	0.07	63,63,63,63	0
56	MG	1A	8424	1/1	0.94	0.07	26,26,26,26	0
56	MG	1x	3013	1/1	0.94	0.13	53,53,53,53	0
56	MG	2A	3522	1/1	0.94	0.09	51,51,51,51	0
56	MG	1A	8824	1/1	0.94	0.08	37,37,37,37	0
56	MG	1A	8652	1/1	0.94	0.06	24,24,24,24	0
56	MG	1Q	205	1/1	0.94	0.07	26,26,26,26	0
56	MG	1A	8163	1/1	0.94	0.10	17,17,17,17	0
56	MG	2A	3243	1/1	0.94	0.24	31,31,31,31	0
56	MG	2A	3007	1/1	0.94	0.21	38,38,38,38	0
56	MG	2A	3808	1/1	0.94	0.08	31,31,31,31	0
56	MG	2A	3246	1/1	0.94	0.07	26,26,26,26	0
56	MG	1A	8836	1/1	0.94	0.07	17,17,17,17	0
56	MG	1A	8838	1/1	0.94	0.07	7,7,7,7	0
56	MG	2A	3250	1/1	0.94	0.33	40,40,40,40	0
56	MG	2A	3816	1/1	0.94	0.12	62,62,62,62	0
56	MG	1A	8270	1/1	0.94	0.08	20,20,20,20	0
56	MG	2A	3818	1/1	0.94	0.18	44,44,44,44	0
56	MG	1A	8657	1/1	0.94	0.14	19,19,19,19	0
56	MG	2A	3017	1/1	0.94	0.34	46,46,46,46	0
56	MG	1A	8659	1/1	0.94	0.09	23,23,23,23	0
56	MG	10	103	1/1	0.94	0.13	21,21,21,21	0
56	MG	2a	1647	1/1	0.94	0.19	48,48,48,48	0
56	MG	1A	8852	1/1	0.94	0.08	27,27,27,27	0
56	MG	1A	8210	1/1	0.94	0.10	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8663	1/1	0.94	0.10	21,21,21,21	0
56	MG	13	102	1/1	0.94	0.12	20,20,20,20	0
56	MG	1a	1738	1/1	0.94	0.09	43,43,43,43	0
56	MG	1A	8665	1/1	0.94	0.07	63,63,63,63	0
56	MG	2A	3845	1/1	0.94	0.24	51,51,51,51	0
56	MG	2A	3269	1/1	0.94	0.27	44,44,44,44	0
56	MG	1A	8539	1/1	0.94	0.10	26,26,26,26	0
56	MG	2A	3848	1/1	0.94	0.13	63,63,63,63	0
56	MG	2a	1659	1/1	0.94	0.14	46,46,46,46	0
56	MG	2A	3849	1/1	0.94	0.16	56,56,56,56	0
56	MG	2A	3555	1/1	0.94	0.09	35,35,35,35	0
56	MG	2A	3556	1/1	0.94	0.07	49,49,49,49	0
56	MG	2A	3557	1/1	0.94	0.33	33,33,33,33	0
56	MG	1A	8442	1/1	0.94	0.09	47,47,47,47	0
56	MG	1A	8865	1/1	0.94	0.10	28,28,28,28	0
56	MG	2A	3562	1/1	0.94	0.09	33,33,33,33	0
56	MG	2a	1668	1/1	0.94	0.10	46,46,46,46	0
56	MG	2A	3276	1/1	0.94	0.08	42,42,42,42	0
56	MG	2A	3277	1/1	0.94	0.18	59,59,59,59	0
56	MG	1A	8543	1/1	0.94	0.09	20,20,20,20	0
56	MG	2A	3038	1/1	0.94	0.16	30,30,30,30	0
56	MG	1A	8545	1/1	0.94	0.11	33,33,33,33	0
56	MG	2A	3868	1/1	0.94	0.09	48,48,48,48	0
56	MG	2a	1677	1/1	0.94	0.07	62,62,62,62	0
56	MG	2A	3569	1/1	0.94	0.09	43,43,43,43	0
56	MG	2A	3571	1/1	0.94	0.09	26,26,26,26	0
56	MG	1a	1602	1/1	0.94	0.18	54,54,54,54	0
56	MG	1A	8168	1/1	0.94	0.07	23,23,23,23	0
56	MG	1A	8445	1/1	0.94	0.07	18,18,18,18	0
56	MG	2A	3874	1/1	0.94	0.09	32,32,32,32	0
56	MG	2A	3876	1/1	0.94	0.30	30,30,30,30	0
56	MG	2a	1689	1/1	0.94	0.09	41,41,41,41	0
56	MG	1A	8876	1/1	0.94	0.12	10,10,10,10	0
56	MG	2A	3045	1/1	0.94	0.18	20,20,20,20	0
56	MG	2A	3884	1/1	0.94	0.09	37,37,37,37	0
56	MG	2A	3578	1/1	0.94	0.09	47,47,47,47	0
56	MG	2A	3048	1/1	0.94	0.06	40,40,40,40	0
56	MG	1A	8878	1/1	0.94	0.06	16,16,16,16	0
56	MG	1A	8449	1/1	0.94	0.06	61,61,61,61	0
56	MG	2A	3890	1/1	0.94	0.26	60,60,60,60	0
56	MG	2A	3051	1/1	0.94	0.13	29,29,29,29	0
56	MG	2A	3298	1/1	0.94	0.07	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1609	1/1	0.94	0.12	43,43,43,43	0
56	MG	2A	3302	1/1	0.94	0.14	48,48,48,48	0
56	MG	1A	8457	1/1	0.94	0.07	9,9,9,9	0
56	MG	2A	3312	1/1	0.94	0.06	25,25,25,25	0
56	MG	2A	3593	1/1	0.94	0.15	24,24,24,24	0
56	MG	1a	1755	1/1	0.94	0.12	60,60,60,60	0
56	MG	2A	3903	1/1	0.94	0.12	49,49,49,49	0
56	MG	2A	3904	1/1	0.94	0.21	47,47,47,47	0
56	MG	2A	3597	1/1	0.94	0.19	44,44,44,44	0
56	MG	1a	1611	1/1	0.94	0.13	38,38,38,38	0
56	MG	1A	8276	1/1	0.94	0.23	15,15,15,15	0
56	MG	2A	3318	1/1	0.94	0.12	30,30,30,30	0
56	MG	1A	8883	1/1	0.94	0.08	30,30,30,30	0
56	MG	1A	8133	1/1	0.94	0.07	15,15,15,15	0
56	MG	2A	3066	1/1	0.94	0.07	26,26,26,26	0
56	MG	1A	8688	1/1	0.94	0.07	20,20,20,20	0
56	MG	2A	3610	1/1	0.94	0.10	57,57,57,57	0
56	MG	1a	1617	1/1	0.94	0.12	53,53,53,53	0
56	MG	1A	8892	1/1	0.94	0.08	28,28,28,28	0
56	MG	1A	8222	1/1	0.94	0.14	18,18,18,18	0
56	MG	1A	8341	1/1	0.94	0.07	17,17,17,17	0
56	MG	1A	8346	1/1	0.94	0.12	14,14,14,14	0
56	MG	2A	3617	1/1	0.94	0.11	43,43,43,43	0
56	MG	2A	3082	1/1	0.94	0.17	35,35,35,35	0
56	MG	2A	3619	1/1	0.94	0.10	36,36,36,36	0
56	MG	2A	3330	1/1	0.94	0.07	23,23,23,23	0
56	MG	2A	3085	1/1	0.94	0.23	28,28,28,28	0
56	MG	2A	3931	1/1	0.94	0.09	47,47,47,47	0
56	MG	1A	8700	1/1	0.94	0.08	27,27,27,27	0
56	MG	1a	1772	1/1	0.94	0.09	53,53,53,53	0
56	MG	1A	8573	1/1	0.94	0.08	18,18,18,18	0
56	MG	1A	8348	1/1	0.94	0.06	7,7,7,7	0
56	MG	2a	1741	1/1	0.94	0.08	61,61,61,61	0
56	MG	1A	8579	1/1	0.94	0.14	27,27,27,27	0
56	MG	1A	8581	1/1	0.94	0.07	15,15,15,15	0
56	MG	2A	3951	1/1	0.94	0.19	30,30,30,30	0
56	MG	2A	3349	1/1	0.94	0.11	43,43,43,43	0
56	MG	1A	8714	1/1	0.94	0.08	9,9,9,9	0
56	MG	1A	8139	1/1	0.94	0.08	15,15,15,15	0
56	MG	2A	3096	1/1	0.94	0.19	21,21,21,21	0
56	MG	1A	8360	1/1	0.94	0.07	25,25,25,25	0
56	MG	1a	1637	1/1	0.94	0.23	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8914	1/1	0.94	0.12	46,46,46,46	0
56	MG	2A	3369	1/1	0.94	0.08	25,25,25,25	0
56	MG	1A	8474	1/1	0.94	0.09	13,13,13,13	0
56	MG	1A	8920	1/1	0.94	0.21	6,6,6,6	0
56	MG	2A	3655	1/1	0.94	0.07	25,25,25,25	0
56	MG	1A	8107	1/1	0.94	0.13	18,18,18,18	0
56	MG	1a	1786	1/1	0.94	0.08	56,56,56,56	0
56	MG	2A	3968	1/1	0.94	0.13	38,38,38,38	0
56	MG	1A	8922	1/1	0.94	0.08	16,16,16,16	0
56	MG	2A	3376	1/1	0.94	0.09	23,23,23,23	0
56	MG	2A	3377	1/1	0.94	0.10	32,32,32,32	0
56	MG	2A	3976	1/1	0.94	0.15	28,28,28,28	0
56	MG	1A	8925	1/1	0.94	0.11	32,32,32,32	0
56	MG	2A	3978	1/1	0.94	0.09	41,41,41,41	0
56	MG	1A	8725	1/1	0.94	0.12	18,18,18,18	0
56	MG	1a	1646	1/1	0.94	0.21	34,34,34,34	0
56	MG	1A	8364	1/1	0.94	0.10	26,26,26,26	0
56	MG	1A	8939	1/1	0.94	0.15	12,12,12,12	0
56	MG	2A	3389	1/1	0.94	0.07	45,45,45,45	0
56	MG	1A	8940	1/1	0.94	0.10	6,6,6,6	0
56	MG	1A	8480	1/1	0.94	0.09	34,34,34,34	0
56	MG	2A	3392	1/1	0.94	0.12	35,35,35,35	0
56	MG	1A	8144	1/1	0.94	0.18	35,35,35,35	0
56	MG	1A	8599	1/1	0.94	0.09	24,24,24,24	0
56	MG	1A	8960	1/1	0.94	0.06	20,20,20,20	0
56	MG	1A	8739	1/1	0.94	0.07	28,28,28,28	0
56	MG	1A	8741	1/1	0.94	0.16	25,25,25,25	0
56	MG	1A	8286	1/1	0.94	0.07	11,11,11,11	0
56	MG	1A	8371	1/1	0.94	0.10	11,11,11,11	0
56	MG	1a	1662	1/1	0.94	0.09	44,44,44,44	0
56	MG	2A	3411	1/1	0.94	0.09	36,36,36,36	0
56	MG	1A	8287	1/1	0.94	0.15	23,23,23,23	0
56	MG	2A	3688	1/1	0.94	0.08	47,47,47,47	0
56	MG	2A	3413	1/1	0.94	0.26	44,44,44,44	0
56	MG	1A	8751	1/1	0.94	0.10	44,44,44,44	0
56	MG	1A	8174	1/1	0.94	0.06	28,28,28,28	0
56	MG	2A	3148	1/1	0.94	0.12	50,50,50,50	0
56	MG	2A	3418	1/1	0.94	0.16	57,57,57,57	0
56	MG	1A	8376	1/1	0.94	0.06	14,14,14,14	0
56	MG	2A	3420	1/1	0.94	0.10	54,54,54,54	0
56	MG	2A	3150	1/1	0.94	0.18	35,35,35,35	0
56	MG	1B	3006	1/1	0.94	0.06	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	3007	1/1	0.94	0.19	37,37,37,37	0
56	MG	1A	8236	1/1	0.94	0.14	22,22,22,22	0
56	MG	2D	302	1/1	0.94	0.21	44,44,44,44	0
56	MG	1A	8175	1/1	0.94	0.06	25,25,25,25	0
56	MG	2a	1818	1/1	0.94	0.09	61,61,61,61	0
56	MG	2A	3159	1/1	0.94	0.12	36,36,36,36	0
56	MG	2A	3712	1/1	0.94	0.06	29,29,29,29	0
56	MG	2a	1821	1/1	0.94	0.07	71,71,71,71	0
56	MG	2D	309	1/1	0.94	0.06	37,37,37,37	0
56	MG	2D	312	1/1	0.94	0.08	39,39,39,39	0
56	MG	2A	3160	1/1	0.94	0.06	28,28,28,28	0
56	MG	2A	3162	1/1	0.94	0.10	39,39,39,39	0
56	MG	2A	3715	1/1	0.94	0.07	28,28,28,28	0
56	MG	1A	8308	1/1	0.94	0.06	41,41,41,41	0
56	MG	2A	3436	1/1	0.94	0.08	29,29,29,29	0
56	MG	2A	3718	1/1	0.94	0.05	30,30,30,30	0
56	MG	2A	3438	1/1	0.94	0.08	25,25,25,25	0
56	MG	1a	1835	1/1	0.94	0.13	43,43,43,43	0
56	MG	1a	1673	1/1	0.94	0.17	35,35,35,35	0
56	MG	2F	302	1/1	0.94	0.21	28,28,28,28	0
56	MG	2t	201	1/1	0.94	0.10	46,46,46,46	0
56	MG	1A	8765	1/1	0.94	0.07	23,23,23,23	0
56	MG	2F	305	1/1	0.94	0.13	26,26,26,26	0
56	MG	1A	8239	1/1	0.94	0.06	13,13,13,13	0
56	MG	2F	308	1/1	0.94	0.23	46,46,46,46	0
56	MG	2A	3448	1/1	0.94	0.08	65,65,65,65	0
56	MG	2A	3176	1/1	0.94	0.07	42,42,42,42	0
56	MG	1A	8108	1/1	0.94	0.18	18,18,18,18	0
56	MG	2A	3179	1/1	0.94	0.10	35,35,35,35	0
56	MG	1A	8777	1/1	0.94	0.09	31,31,31,31	0
56	MG	1b	3001	1/1	0.94	0.14	50,50,50,50	0
56	MG	1A	8150	1/1	0.94	0.10	36,36,36,36	0
56	MG	2A	3733	1/1	0.94	0.08	33,33,33,33	0
57	ZN	14	501	1/1	0.94	0.13	75,75,75,75	0
56	MG	1A	8319	1/1	0.94	0.06	27,27,27,27	0
56	MG	1A	8389	1/1	0.94	0.09	32,32,32,32	0
56	MG	1A	8833	1/1	0.95	0.09	12,12,12,12	0
56	MG	2A	3481	1/1	0.95	0.06	39,39,39,39	0
56	MG	1A	8187	1/1	0.95	0.11	20,20,20,20	0
56	MG	1a	1708	1/1	0.95	0.14	43,43,43,43	0
56	MG	1A	8437	1/1	0.95	0.08	6,6,6,6	0
56	MG	2A	3485	1/1	0.95	0.09	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3218	1/1	0.95	0.10	37,37,37,37	0
56	MG	2R	202	1/1	0.95	0.07	21,21,21,21	0
56	MG	2S	201	1/1	0.95	0.05	27,27,27,27	0
56	MG	2U	201	1/1	0.95	0.10	42,42,42,42	0
56	MG	1A	8438	1/1	0.95	0.08	34,34,34,34	0
56	MG	2A	3220	1/1	0.95	0.20	29,29,29,29	0
56	MG	1A	8344	1/1	0.95	0.07	26,26,26,26	0
56	MG	2A	3751	1/1	0.95	0.11	32,32,32,32	0
56	MG	1A	8671	1/1	0.95	0.08	17,17,17,17	0
56	MG	1A	8849	1/1	0.95	0.09	39,39,39,39	0
56	MG	2A	3009	1/1	0.95	0.17	42,42,42,42	0
56	MG	1a	1718	1/1	0.95	0.06	44,44,44,44	0
56	MG	2A	3495	1/1	0.95	0.19	57,57,57,57	0
56	MG	1A	8850	1/1	0.95	0.17	34,34,34,34	0
56	MG	2A	3498	1/1	0.95	0.09	45,45,45,45	0
56	MG	2A	3013	1/1	0.95	0.06	29,29,29,29	0
56	MG	20	103	1/1	0.95	0.11	62,62,62,62	0
56	MG	2A	3762	1/1	0.95	0.12	44,44,44,44	0
56	MG	1A	8054	1/1	0.95	0.09	9,9,9,9	0
56	MG	1A	8347	1/1	0.95	0.13	13,13,13,13	0
56	MG	2A	3233	1/1	0.95	0.18	28,28,28,28	0
56	MG	25	101	1/1	0.95	0.11	27,27,27,27	0
56	MG	2A	3234	1/1	0.95	0.07	42,42,42,42	0
56	MG	1A	8858	1/1	0.95	0.12	28,28,28,28	0
56	MG	1A	8675	1/1	0.95	0.06	17,17,17,17	0
56	MG	1A	8553	1/1	0.95	0.09	18,18,18,18	0
56	MG	1T	201	1/1	0.95	0.06	37,37,37,37	0
56	MG	1A	8447	1/1	0.95	0.08	13,13,13,13	0
56	MG	2A	3024	1/1	0.95	0.22	30,30,30,30	0
56	MG	2a	1601	1/1	0.95	0.09	47,47,47,47	0
56	MG	1A	8130	1/1	0.95	0.06	20,20,20,20	0
56	MG	1A	8451	1/1	0.95	0.09	19,19,19,19	0
56	MG	2a	1604	1/1	0.95	0.14	44,44,44,44	0
56	MG	2a	1605	1/1	0.95	0.11	40,40,40,40	0
56	MG	2A	3515	1/1	0.95	0.13	48,48,48,48	0
56	MG	2A	3244	1/1	0.95	0.30	30,30,30,30	0
56	MG	2A	3784	1/1	0.95	0.07	45,45,45,45	0
56	MG	2A	3518	1/1	0.95	0.08	24,24,24,24	0
56	MG	2A	3519	1/1	0.95	0.07	31,31,31,31	0
56	MG	1A	8349	1/1	0.95	0.06	13,13,13,13	0
56	MG	1a	1734	1/1	0.95	0.10	42,42,42,42	0
56	MG	1A	8351	1/1	0.95	0.06	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3792	1/1	0.95	0.09	44,44,44,44	0
56	MG	2A	3793	1/1	0.95	0.10	34,34,34,34	0
56	MG	1A	8568	1/1	0.95	0.07	11,11,11,11	0
56	MG	2a	1618	1/1	0.95	0.07	38,38,38,38	0
56	MG	2a	1619	1/1	0.95	0.15	50,50,50,50	0
56	MG	1A	8693	1/1	0.95	0.11	28,28,28,28	0
56	MG	2A	3251	1/1	0.95	0.08	43,43,43,43	0
56	MG	2A	3797	1/1	0.95	0.13	38,38,38,38	0
56	MG	2A	3036	1/1	0.95	0.10	34,34,34,34	0
56	MG	1A	8355	1/1	0.95	0.06	7,7,7,7	0
56	MG	2A	3255	1/1	0.95	0.07	45,45,45,45	0
56	MG	11	102	1/1	0.95	0.09	23,23,23,23	0
56	MG	2a	1627	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	8241	1/1	0.95	0.14	10,10,10,10	0
56	MG	2A	3531	1/1	0.95	0.26	36,36,36,36	0
56	MG	15	101	1/1	0.95	0.07	32,32,32,32	0
56	MG	2a	1631	1/1	0.95	0.22	42,42,42,42	0
56	MG	2A	3533	1/1	0.95	0.08	50,50,50,50	0
56	MG	1A	8577	1/1	0.95	0.09	21,21,21,21	0
56	MG	1A	8465	1/1	0.95	0.07	24,24,24,24	0
56	MG	1A	8881	1/1	0.95	0.13	53,53,53,53	0
56	MG	2a	1636	1/1	0.95	0.09	33,33,33,33	0
56	MG	2A	3538	1/1	0.95	0.10	32,32,32,32	0
56	MG	1A	8117	1/1	0.95	0.20	27,27,27,27	0
56	MG	2A	3540	1/1	0.95	0.08	48,48,48,48	0
56	MG	19	101	1/1	0.95	0.27	24,24,24,24	0
56	MG	2A	3542	1/1	0.95	0.07	23,23,23,23	0
56	MG	2A	3543	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3545	1/1	0.95	0.11	47,47,47,47	0
56	MG	19	103	1/1	0.95	0.08	23,23,23,23	0
56	MG	1A	8244	1/1	0.95	0.11	11,11,11,11	0
56	MG	2A	3271	1/1	0.95	0.28	42,42,42,42	0
56	MG	1A	8884	1/1	0.95	0.09	65,65,65,65	0
56	MG	1A	8301	1/1	0.95	0.07	27,27,27,27	0
56	MG	2A	3053	1/1	0.95	0.29	27,27,27,27	0
56	MG	1a	1603	1/1	0.95	0.09	39,39,39,39	0
56	MG	1A	8887	1/1	0.95	0.19	24,24,24,24	0
56	MG	1A	8305	1/1	0.95	0.13	29,29,29,29	0
56	MG	1A	8890	1/1	0.95	0.06	23,23,23,23	0
56	MG	1A	8368	1/1	0.95	0.17	14,14,14,14	0
56	MG	1A	8160	1/1	0.95	0.07	20,20,20,20	0
56	MG	2A	3065	1/1	0.95	0.21	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8135	1/1	0.95	0.10	26,26,26,26	0
56	MG	2A	3854	1/1	0.95	0.07	32,32,32,32	0
56	MG	2A	3068	1/1	0.95	0.14	34,34,34,34	0
56	MG	1a	1761	1/1	0.95	0.10	44,44,44,44	0
56	MG	2A	3292	1/1	0.95	0.08	51,51,51,51	0
56	MG	2A	3565	1/1	0.95	0.07	32,32,32,32	0
56	MG	2A	3070	1/1	0.95	0.18	39,39,39,39	0
56	MG	1a	1762	1/1	0.95	0.08	54,54,54,54	0
56	MG	2A	3074	1/1	0.95	0.15	33,33,33,33	0
56	MG	2A	3075	1/1	0.95	0.07	35,35,35,35	0
56	MG	1A	8722	1/1	0.95	0.13	22,22,22,22	0
56	MG	2A	3300	1/1	0.95	0.17	30,30,30,30	0
56	MG	1A	8595	1/1	0.95	0.05	35,35,35,35	0
56	MG	1A	8313	1/1	0.95	0.05	16,16,16,16	0
56	MG	2A	3303	1/1	0.95	0.07	30,30,30,30	0
56	MG	2A	3308	1/1	0.95	0.07	47,47,47,47	0
56	MG	2A	3309	1/1	0.95	0.07	38,38,38,38	0
56	MG	1A	8729	1/1	0.95	0.09	43,43,43,43	0
56	MG	1A	8731	1/1	0.95	0.16	40,40,40,40	0
56	MG	2A	3878	1/1	0.95	0.06	45,45,45,45	0
56	MG	1A	8905	1/1	0.95	0.08	42,42,42,42	0
56	MG	1A	8138	1/1	0.95	0.05	14,14,14,14	0
56	MG	2A	3881	1/1	0.95	0.17	56,56,56,56	0
56	MG	1A	8042	1/1	0.95	0.06	33,33,33,33	0
56	MG	2A	3586	1/1	0.95	0.07	33,33,33,33	0
56	MG	2A	3088	1/1	0.95	0.18	33,33,33,33	0
56	MG	1A	8735	1/1	0.95	0.06	15,15,15,15	0
56	MG	1A	8316	1/1	0.95	0.06	14,14,14,14	0
56	MG	1A	8257	1/1	0.95	0.14	11,11,11,11	0
56	MG	1A	8011	1/1	0.95	0.13	27,27,27,27	0
56	MG	2A	3594	1/1	0.95	0.06	44,44,44,44	0
56	MG	2A	3595	1/1	0.95	0.07	32,32,32,32	0
56	MG	1A	8917	1/1	0.95	0.18	21,21,21,21	0
56	MG	1A	8381	1/1	0.95	0.08	10,10,10,10	0
56	MG	2A	3095	1/1	0.95	0.10	29,29,29,29	0
56	MG	2A	3900	1/1	0.95	0.08	41,41,41,41	0
56	MG	1a	1627	1/1	0.95	0.10	37,37,37,37	0
56	MG	2A	3602	1/1	0.95	0.14	53,53,53,53	0
56	MG	1A	8142	1/1	0.95	0.28	11,11,11,11	0
56	MG	2A	3328	1/1	0.95	0.26	31,31,31,31	0
56	MG	1A	8212	1/1	0.95	0.13	33,33,33,33	0
56	MG	2A	3099	1/1	0.95	0.11	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8923	1/1	0.95	0.18	17,17,17,17	0
56	MG	2A	3608	1/1	0.95	0.10	21,21,21,21	0
56	MG	1a	1632	1/1	0.95	0.16	41,41,41,41	0
56	MG	2A	3102	1/1	0.95	0.20	29,29,29,29	0
56	MG	2A	3104	1/1	0.95	0.06	25,25,25,25	0
56	MG	2A	3913	1/1	0.95	0.20	34,34,34,34	0
56	MG	1A	8747	1/1	0.95	0.08	27,27,27,27	0
56	MG	1A	8045	1/1	0.95	0.36	11,11,11,11	0
56	MG	1A	8002	1/1	0.95	0.13	21,21,21,21	0
56	MG	1A	8932	1/1	0.95	0.08	21,21,21,21	0
56	MG	2A	3919	1/1	0.95	0.05	32,32,32,32	0
56	MG	2A	3115	1/1	0.95	0.06	41,41,41,41	0
56	MG	2A	3358	1/1	0.95	0.08	27,27,27,27	0
56	MG	1A	8049	1/1	0.95	0.20	12,12,12,12	0
56	MG	1A	8755	1/1	0.95	0.24	16,16,16,16	0
56	MG	1A	8941	1/1	0.95	0.16	45,45,45,45	0
56	MG	1A	8756	1/1	0.95	0.14	14,14,14,14	0
56	MG	1A	8226	1/1	0.95	0.12	17,17,17,17	0
56	MG	1A	8391	1/1	0.95	0.07	6,6,6,6	0
56	MG	2A	3930	1/1	0.95	0.20	48,48,48,48	0
56	MG	1A	8951	1/1	0.95	0.10	20,20,20,20	0
56	MG	2A	3933	1/1	0.95	0.05	51,51,51,51	0
56	MG	1A	8952	1/1	0.95	0.20	17,17,17,17	0
56	MG	1a	1649	1/1	0.95	0.22	32,32,32,32	0
56	MG	2A	3938	1/1	0.95	0.13	38,38,38,38	0
56	MG	1A	8394	1/1	0.95	0.07	37,37,37,37	0
56	MG	2A	3132	1/1	0.95	0.12	32,32,32,32	0
56	MG	1a	1651	1/1	0.95	0.05	26,26,26,26	0
56	MG	2A	3948	1/1	0.95	0.24	42,42,42,42	0
56	MG	2A	3641	1/1	0.95	0.24	35,35,35,35	0
56	MG	2a	1748	1/1	0.95	0.09	50,50,50,50	0
56	MG	1A	8964	1/1	0.95	0.11	12,12,12,12	0
56	MG	2A	3952	1/1	0.95	0.07	36,36,36,36	0
56	MG	1a	1806	1/1	0.95	0.13	49,49,49,49	0
56	MG	2A	3647	1/1	0.95	0.05	28,28,28,28	0
56	MG	2a	1754	1/1	0.95	0.07	42,42,42,42	0
56	MG	1a	1653	1/1	0.95	0.13	32,32,32,32	0
56	MG	1A	8622	1/1	0.95	0.07	26,26,26,26	0
56	MG	2A	3383	1/1	0.95	0.08	27,27,27,27	0
56	MG	1A	8506	1/1	0.95	0.14	30,30,30,30	0
56	MG	1a	1816	1/1	0.95	0.14	49,49,49,49	0
56	MG	2A	3145	1/1	0.95	0.09	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8774	1/1	0.95	0.07	25,25,25,25	0
56	MG	1A	8625	1/1	0.95	0.13	39,39,39,39	0
56	MG	1A	8507	1/1	0.95	0.07	33,33,33,33	0
56	MG	1A	8271	1/1	0.95	0.13	21,21,21,21	0
56	MG	2A	3662	1/1	0.95	0.07	43,43,43,43	0
56	MG	2A	3663	1/1	0.95	0.07	61,61,61,61	0
56	MG	1A	8401	1/1	0.95	0.11	28,28,28,28	0
56	MG	2a	1770	1/1	0.95	0.15	52,52,52,52	0
56	MG	2A	3665	1/1	0.95	0.10	29,29,29,29	0
56	MG	1A	8402	1/1	0.95	0.07	29,29,29,29	0
56	MG	2A	3974	1/1	0.95	0.14	27,27,27,27	0
56	MG	2A	3399	1/1	0.95	0.06	46,46,46,46	0
56	MG	2A	3400	1/1	0.95	0.08	41,41,41,41	0
56	MG	1A	8511	1/1	0.95	0.15	32,32,32,32	0
56	MG	2A	3154	1/1	0.95	0.09	31,31,31,31	0
56	MG	2A	3981	1/1	0.95	0.34	41,41,41,41	0
56	MG	2A	3405	1/1	0.95	0.11	28,28,28,28	0
56	MG	2A	3155	1/1	0.95	0.05	24,24,24,24	0
56	MG	1a	1833	1/1	0.95	0.20	39,39,39,39	0
56	MG	2A	3676	1/1	0.95	0.08	31,31,31,31	0
56	MG	2A	3157	1/1	0.95	0.14	40,40,40,40	0
56	MG	2A	3158	1/1	0.95	0.23	40,40,40,40	0
56	MG	1A	8785	1/1	0.95	0.10	23,23,23,23	0
56	MG	1A	8407	1/1	0.95	0.09	20,20,20,20	0
56	MG	2A	3414	1/1	0.95	0.07	46,46,46,46	0
56	MG	2A	3161	1/1	0.95	0.12	33,33,33,33	0
56	MG	1B	3009	1/1	0.95	0.11	37,37,37,37	0
56	MG	2A	3164	1/1	0.95	0.08	29,29,29,29	0
56	MG	1A	8515	1/1	0.95	0.08	28,28,28,28	0
56	MG	1A	8272	1/1	0.95	0.08	27,27,27,27	0
56	MG	1B	3012	1/1	0.95	0.12	25,25,25,25	0
56	MG	2A	3170	1/1	0.95	0.16	39,39,39,39	0
56	MG	2A	3171	1/1	0.95	0.09	33,33,33,33	0
56	MG	1A	8793	1/1	0.95	0.09	27,27,27,27	0
56	MG	2B	3013	1/1	0.95	0.07	51,51,51,51	0
56	MG	1A	8227	1/1	0.95	0.21	14,14,14,14	0
56	MG	2A	3175	1/1	0.95	0.08	35,35,35,35	0
56	MG	2A	3696	1/1	0.95	0.08	54,54,54,54	0
56	MG	2A	3697	1/1	0.95	0.18	35,35,35,35	0
56	MG	1A	8415	1/1	0.95	0.06	16,16,16,16	0
56	MG	2A	3430	1/1	0.95	0.10	30,30,30,30	0
56	MG	2a	1817	1/1	0.95	0.11	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	3018	1/1	0.95	0.07	41,41,41,41	0
56	MG	2A	3701	1/1	0.95	0.11	42,42,42,42	0
56	MG	2A	3178	1/1	0.95	0.08	31,31,31,31	0
56	MG	2A	3703	1/1	0.95	0.07	26,26,26,26	0
56	MG	1A	8033	1/1	0.95	0.09	27,27,27,27	0
56	MG	2A	3705	1/1	0.95	0.11	48,48,48,48	0
56	MG	2A	3435	1/1	0.95	0.07	33,33,33,33	0
56	MG	1A	8799	1/1	0.95	0.16	23,23,23,23	0
56	MG	1B	3024	1/1	0.95	0.06	18,18,18,18	0
56	MG	2g	3001	1/1	0.95	0.22	52,52,52,52	0
56	MG	2h	3001	1/1	0.95	0.12	30,30,30,30	0
56	MG	1A	8332	1/1	0.95	0.08	48,48,48,48	0
56	MG	1A	8230	1/1	0.95	0.17	13,13,13,13	0
56	MG	1A	8180	1/1	0.95	0.07	17,17,17,17	0
56	MG	1A	8279	1/1	0.95	0.06	30,30,30,30	0
56	MG	2A	3447	1/1	0.95	0.07	22,22,22,22	0
56	MG	1A	8653	1/1	0.95	0.13	47,47,47,47	0
56	MG	2A	3194	1/1	0.95	0.07	24,24,24,24	0
56	MG	1A	8530	1/1	0.95	0.10	27,27,27,27	0
56	MG	1A	8531	1/1	0.95	0.09	26,26,26,26	0
56	MG	1a	1687	1/1	0.95	0.17	39,39,39,39	0
56	MG	2A	3198	1/1	0.95	0.11	36,36,36,36	0
56	MG	1A	8076	1/1	0.95	0.26	22,22,22,22	0
56	MG	1E	303	1/1	0.95	0.08	11,11,11,11	0
56	MG	1E	304	1/1	0.95	0.04	27,27,27,27	0
56	MG	1A	8534	1/1	0.95	0.18	52,52,52,52	0
56	MG	1A	8427	1/1	0.95	0.07	7,7,7,7	0
56	MG	1a	1699	1/1	0.95	0.06	26,26,26,26	0
56	MG	1E	307	1/1	0.95	0.06	28,28,28,28	0
56	MG	1A	8428	1/1	0.95	0.11	14,14,14,14	0
56	MG	1F	303	1/1	0.95	0.24	19,19,19,19	0
56	MG	2A	3734	1/1	0.95	0.06	33,33,33,33	0
56	MG	2A	3735	1/1	0.95	0.09	46,46,46,46	0
56	MG	1A	8079	1/1	0.95	0.18	16,16,16,16	0
56	MG	2A	3044	1/1	0.96	0.17	39,39,39,39	0
56	MG	1A	8855	1/1	0.96	0.07	29,29,29,29	0
56	MG	1A	8044	1/1	0.96	0.11	7,7,7,7	0
56	MG	2A	3770	1/1	0.96	0.06	40,40,40,40	0
56	MG	2A	3771	1/1	0.96	0.15	41,41,41,41	0
56	MG	1U	202	1/1	0.96	0.10	17,17,17,17	0
56	MG	1A	8285	1/1	0.96	0.07	10,10,10,10	0
56	MG	2A	3516	1/1	0.96	0.10	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3259	1/1	0.96	0.12	33,33,33,33	0
56	MG	1A	8541	1/1	0.96	0.06	31,31,31,31	0
56	MG	1A	8353	1/1	0.96	0.08	7,7,7,7	0
56	MG	1A	8232	1/1	0.96	0.06	34,34,34,34	0
56	MG	2A	3054	1/1	0.96	0.08	22,22,22,22	0
56	MG	2A	3056	1/1	0.96	0.08	29,29,29,29	0
56	MG	1A	8062	1/1	0.96	0.08	13,13,13,13	0
56	MG	1A	8548	1/1	0.96	0.05	27,27,27,27	0
56	MG	10	107	1/1	0.96	0.07	36,36,36,36	0
56	MG	2A	3270	1/1	0.96	0.04	20,20,20,20	0
56	MG	1A	8679	1/1	0.96	0.19	34,34,34,34	0
56	MG	2A	3788	1/1	0.96	0.07	36,36,36,36	0
56	MG	2A	3272	1/1	0.96	0.17	30,30,30,30	0
56	MG	11	101	1/1	0.96	0.20	26,26,26,26	0
56	MG	2A	3791	1/1	0.96	0.06	52,52,52,52	0
56	MG	1A	8681	1/1	0.96	0.13	32,32,32,32	0
56	MG	1A	8137	1/1	0.96	0.17	11,11,11,11	0
56	MG	1A	8684	1/1	0.96	0.10	35,35,35,35	0
56	MG	1A	8361	1/1	0.96	0.08	26,26,26,26	0
56	MG	2A	3534	1/1	0.96	0.08	35,35,35,35	0
56	MG	2A	3278	1/1	0.96	0.08	30,30,30,30	0
56	MG	15	105	1/1	0.96	0.19	12,12,12,12	0
56	MG	1A	8448	1/1	0.96	0.07	8,8,8,8	0
56	MG	1A	8294	1/1	0.96	0.05	29,29,29,29	0
56	MG	2A	3801	1/1	0.96	0.09	41,41,41,41	0
56	MG	2A	3073	1/1	0.96	0.09	32,32,32,32	0
56	MG	2a	1608	1/1	0.96	0.11	36,36,36,36	0
56	MG	15	108	1/1	0.96	0.18	28,28,28,28	0
56	MG	2A	3284	1/1	0.96	0.08	41,41,41,41	0
56	MG	1A	8106	1/1	0.96	0.06	22,22,22,22	0
56	MG	2A	3286	1/1	0.96	0.09	21,21,21,21	0
56	MG	1A	8452	1/1	0.96	0.05	26,26,26,26	0
56	MG	2A	3812	1/1	0.96	0.06	22,22,22,22	0
56	MG	2A	3288	1/1	0.96	0.11	25,25,25,25	0
56	MG	2A	3290	1/1	0.96	0.07	31,31,31,31	0
56	MG	1A	8456	1/1	0.96	0.12	25,25,25,25	0
56	MG	1A	8558	1/1	0.96	0.06	42,42,42,42	0
56	MG	2A	3293	1/1	0.96	0.14	24,24,24,24	0
56	MG	2A	3080	1/1	0.96	0.13	31,31,31,31	0
56	MG	1A	8694	1/1	0.96	0.07	30,30,30,30	0
56	MG	1A	8886	1/1	0.96	0.07	24,24,24,24	0
56	MG	1A	8696	1/1	0.96	0.06	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3829	1/1	0.96	0.15	53,53,53,53	0
56	MG	1A	8296	1/1	0.96	0.07	21,21,21,21	0
56	MG	2A	3831	1/1	0.96	0.29	35,35,35,35	0
56	MG	1A	8299	1/1	0.96	0.07	28,28,28,28	0
56	MG	1A	8460	1/1	0.96	0.12	33,33,33,33	0
56	MG	2A	3834	1/1	0.96	0.12	55,55,55,55	0
56	MG	2A	3558	1/1	0.96	0.24	32,32,32,32	0
56	MG	1A	8893	1/1	0.96	0.05	21,21,21,21	0
56	MG	2A	3560	1/1	0.96	0.25	43,43,43,43	0
56	MG	1A	8703	1/1	0.96	0.06	28,28,28,28	0
56	MG	2A	3843	1/1	0.96	0.08	43,43,43,43	0
56	MG	2A	3305	1/1	0.96	0.07	41,41,41,41	0
56	MG	2A	3306	1/1	0.96	0.06	29,29,29,29	0
56	MG	2A	3307	1/1	0.96	0.12	43,43,43,43	0
56	MG	1A	8569	1/1	0.96	0.06	16,16,16,16	0
56	MG	1A	8570	1/1	0.96	0.05	34,34,34,34	0
56	MG	1A	8707	1/1	0.96	0.08	45,45,45,45	0
56	MG	1A	8571	1/1	0.96	0.09	34,34,34,34	0
56	MG	1A	8300	1/1	0.96	0.07	23,23,23,23	0
56	MG	1A	8178	1/1	0.96	0.17	14,14,14,14	0
56	MG	1A	8575	1/1	0.96	0.07	14,14,14,14	0
56	MG	1a	1616	1/1	0.96	0.14	45,45,45,45	0
56	MG	1A	8004	1/1	0.96	0.07	18,18,18,18	0
56	MG	1A	8373	1/1	0.96	0.07	13,13,13,13	0
56	MG	1A	8720	1/1	0.96	0.07	27,27,27,27	0
56	MG	1a	1782	1/1	0.96	0.07	38,38,38,38	0
56	MG	2A	3103	1/1	0.96	0.08	30,30,30,30	0
56	MG	1A	8036	1/1	0.96	0.04	17,17,17,17	0
56	MG	2A	3867	1/1	0.96	0.06	42,42,42,42	0
56	MG	1a	1621	1/1	0.96	0.12	26,26,26,26	0
56	MG	2A	3107	1/1	0.96	0.14	34,34,34,34	0
56	MG	1A	8723	1/1	0.96	0.05	20,20,20,20	0
56	MG	1A	8469	1/1	0.96	0.10	29,29,29,29	0
56	MG	2A	3113	1/1	0.96	0.06	29,29,29,29	0
56	MG	1A	8916	1/1	0.96	0.09	75,75,75,75	0
56	MG	2A	3331	1/1	0.96	0.14	48,48,48,48	0
56	MG	1A	8726	1/1	0.96	0.16	17,17,17,17	0
56	MG	2A	3592	1/1	0.96	0.06	42,42,42,42	0
56	MG	2A	3337	1/1	0.96	0.07	28,28,28,28	0
56	MG	2A	3116	1/1	0.96	0.22	36,36,36,36	0
56	MG	1A	8582	1/1	0.96	0.06	15,15,15,15	0
56	MG	2A	3883	1/1	0.96	0.09	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1790	1/1	0.96	0.07	46,46,46,46	0
56	MG	2A	3342	1/1	0.96	0.06	25,25,25,25	0
56	MG	1A	8728	1/1	0.96	0.10	24,24,24,24	0
56	MG	2A	3120	1/1	0.96	0.13	28,28,28,28	0
56	MG	2a	1673	1/1	0.96	0.07	33,33,33,33	0
56	MG	2a	1674	1/1	0.96	0.06	37,37,37,37	0
56	MG	2A	3600	1/1	0.96	0.11	40,40,40,40	0
56	MG	2A	3601	1/1	0.96	0.16	44,44,44,44	0
56	MG	1A	8069	1/1	0.96	0.11	18,18,18,18	0
56	MG	2A	3348	1/1	0.96	0.10	19,19,19,19	0
56	MG	1A	8377	1/1	0.96	0.09	20,20,20,20	0
56	MG	2A	3351	1/1	0.96	0.08	40,40,40,40	0
56	MG	1A	8589	1/1	0.96	0.27	13,13,13,13	0
56	MG	1a	1633	1/1	0.96	0.12	27,27,27,27	0
56	MG	2A	3360	1/1	0.96	0.10	33,33,33,33	0
56	MG	2A	3361	1/1	0.96	0.06	42,42,42,42	0
56	MG	1a	1634	1/1	0.96	0.13	22,22,22,22	0
56	MG	1A	8926	1/1	0.96	0.08	35,35,35,35	0
56	MG	2A	3130	1/1	0.96	0.06	27,27,27,27	0
56	MG	1A	8927	1/1	0.96	0.11	8,8,8,8	0
56	MG	2A	3615	1/1	0.96	0.27	36,36,36,36	0
56	MG	1A	8590	1/1	0.96	0.13	29,29,29,29	0
56	MG	1A	8111	1/1	0.96	0.12	12,12,12,12	0
56	MG	2A	3136	1/1	0.96	0.13	34,34,34,34	0
56	MG	2a	1698	1/1	0.96	0.09	40,40,40,40	0
56	MG	2A	3371	1/1	0.96	0.08	18,18,18,18	0
56	MG	1A	8115	1/1	0.96	0.10	13,13,13,13	0
56	MG	2A	3622	1/1	0.96	0.16	44,44,44,44	0
56	MG	1a	1804	1/1	0.96	0.10	46,46,46,46	0
56	MG	2a	1703	1/1	0.96	0.07	47,47,47,47	0
56	MG	1A	8938	1/1	0.96	0.10	12,12,12,12	0
56	MG	1A	8476	1/1	0.96	0.05	17,17,17,17	0
56	MG	1A	8248	1/1	0.96	0.11	17,17,17,17	0
56	MG	1A	8596	1/1	0.96	0.05	17,17,17,17	0
56	MG	1a	1815	1/1	0.96	0.12	57,57,57,57	0
56	MG	1A	8116	1/1	0.96	0.17	25,25,25,25	0
56	MG	1A	8946	1/1	0.96	0.09	11,11,11,11	0
56	MG	1A	8382	1/1	0.96	0.06	8,8,8,8	0
56	MG	1A	8383	1/1	0.96	0.10	10,10,10,10	0
56	MG	1A	8749	1/1	0.96	0.13	22,22,22,22	0
56	MG	2A	3386	1/1	0.96	0.16	29,29,29,29	0
56	MG	2A	3928	1/1	0.96	0.14	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8483	1/1	0.96	0.09	30,30,30,30	0
56	MG	2A	3645	1/1	0.96	0.15	29,29,29,29	0
56	MG	2a	1721	1/1	0.96	0.18	47,47,47,47	0
56	MG	1A	8953	1/1	0.96	0.19	13,13,13,13	0
56	MG	2A	3932	1/1	0.96	0.11	31,31,31,31	0
56	MG	1A	8958	1/1	0.96	0.08	28,28,28,28	0
56	MG	1a	1830	1/1	0.96	0.08	45,45,45,45	0
56	MG	2A	3936	1/1	0.96	0.12	20,20,20,20	0
56	MG	1a	1831	1/1	0.96	0.14	14,14,14,14	0
56	MG	1A	8038	1/1	0.96	0.11	40,40,40,40	0
56	MG	1A	8603	1/1	0.96	0.06	24,24,24,24	0
56	MG	2A	3940	1/1	0.96	0.22	8,8,8,8	0
56	MG	2A	3942	1/1	0.96	0.10	43,43,43,43	0
56	MG	2A	3943	1/1	0.96	0.08	40,40,40,40	0
56	MG	1A	8965	1/1	0.96	0.15	14,14,14,14	0
56	MG	1A	8318	1/1	0.96	0.05	6,6,6,6	0
56	MG	1A	8252	1/1	0.96	0.05	24,24,24,24	0
56	MG	1A	8198	1/1	0.96	0.08	8,8,8,8	0
56	MG	1A	8153	1/1	0.96	0.09	12,12,12,12	0
56	MG	1A	8258	1/1	0.96	0.15	24,24,24,24	0
56	MG	1B	3002	1/1	0.96	0.11	33,33,33,33	0
56	MG	1A	8039	1/1	0.96	0.05	12,12,12,12	0
56	MG	2A	3409	1/1	0.96	0.20	31,31,31,31	0
56	MG	2A	3956	1/1	0.96	0.33	35,35,35,35	0
56	MG	1A	8392	1/1	0.96	0.14	37,37,37,37	0
56	MG	1A	8052	1/1	0.96	0.13	12,12,12,12	0
56	MG	1d	505	1/1	0.96	0.05	56,56,56,56	0
56	MG	2A	3173	1/1	0.96	0.14	37,37,37,37	0
56	MG	2a	1750	1/1	0.96	0.07	67,67,67,67	0
56	MG	1A	8395	1/1	0.96	0.06	34,34,34,34	0
56	MG	1A	8619	1/1	0.96	0.18	20,20,20,20	0
56	MG	1A	8500	1/1	0.96	0.07	45,45,45,45	0
56	MG	1A	8156	1/1	0.96	0.18	25,25,25,25	0
56	MG	1A	8400	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	8020	1/1	0.96	0.16	8,8,8,8	0
56	MG	1a	1672	1/1	0.96	0.07	38,38,38,38	0
56	MG	1A	8208	1/1	0.96	0.15	11,11,11,11	0
56	MG	2A	3423	1/1	0.96	0.08	37,37,37,37	0
56	MG	1a	1675	1/1	0.96	0.06	19,19,19,19	0
56	MG	2a	1762	1/1	0.96	0.07	58,58,58,58	0
56	MG	1A	8265	1/1	0.96	0.20	18,18,18,18	0
56	MG	1A	8408	1/1	0.96	0.07	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3186	1/1	0.96	0.18	39,39,39,39	0
56	MG	2A	3190	1/1	0.96	0.24	32,32,32,32	0
56	MG	1A	8084	1/1	0.96	0.06	23,23,23,23	0
56	MG	2A	3432	1/1	0.96	0.07	45,45,45,45	0
56	MG	1A	8791	1/1	0.96	0.05	39,39,39,39	0
56	MG	1t	3001	1/1	0.96	0.11	37,37,37,37	0
56	MG	1A	8411	1/1	0.96	0.11	12,12,12,12	0
56	MG	1x	3003	1/1	0.96	0.21	31,31,31,31	0
56	MG	2A	3437	1/1	0.96	0.07	59,59,59,59	0
56	MG	1A	8634	1/1	0.96	0.13	39,39,39,39	0
56	MG	1B	3022	1/1	0.96	0.08	41,41,41,41	0
56	MG	1A	8512	1/1	0.96	0.06	28,28,28,28	0
56	MG	1A	8639	1/1	0.96	0.07	24,24,24,24	0
56	MG	1A	8640	1/1	0.96	0.04	40,40,40,40	0
56	MG	2a	1782	1/1	0.96	0.20	61,61,61,61	0
56	MG	1A	8412	1/1	0.96	0.07	6,6,6,6	0
56	MG	1x	3010	1/1	0.96	0.24	34,34,34,34	0
56	MG	2A	3451	1/1	0.96	0.09	46,46,46,46	0
56	MG	2A	3452	1/1	0.96	0.08	34,34,34,34	0
56	MG	2A	3453	1/1	0.96	0.09	44,44,44,44	0
56	MG	1A	8056	1/1	0.96	0.05	12,12,12,12	0
56	MG	2A	3458	1/1	0.96	0.06	37,37,37,37	0
56	MG	1a	1690	1/1	0.96	0.11	36,36,36,36	0
56	MG	1A	8213	1/1	0.96	0.06	14,14,14,14	0
56	MG	1x	3014	1/1	0.96	0.18	29,29,29,29	0
56	MG	2a	1797	1/1	0.96	0.09	47,47,47,47	0
56	MG	1a	1693	1/1	0.96	0.05	29,29,29,29	0
56	MG	2A	3464	1/1	0.96	0.14	40,40,40,40	0
56	MG	1A	8645	1/1	0.96	0.06	11,11,11,11	0
56	MG	1D	311	1/1	0.96	0.07	31,31,31,31	0
56	MG	2B	3019	1/1	0.96	0.06	62,62,62,62	0
56	MG	2A	3212	1/1	0.96	0.14	27,27,27,27	0
56	MG	2A	3470	1/1	0.96	0.10	24,24,24,24	0
56	MG	1A	8214	1/1	0.96	0.24	10,10,10,10	0
56	MG	2A	3216	1/1	0.96	0.18	28,28,28,28	0
56	MG	1D	313	1/1	0.96	0.09	33,33,33,33	0
56	MG	1A	8647	1/1	0.96	0.23	14,14,14,14	0
56	MG	2A	3476	1/1	0.96	0.16	34,34,34,34	0
56	MG	1A	8809	1/1	0.96	0.07	21,21,21,21	0
56	MG	1A	8014	1/1	0.96	0.07	5,5,5,5	0
56	MG	1A	8521	1/1	0.96	0.08	12,12,12,12	0
56	MG	1A	8161	1/1	0.96	0.23	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8819	1/1	0.96	0.19	20,20,20,20	0
56	MG	1A	8421	1/1	0.96	0.06	26,26,26,26	0
56	MG	1F	302	1/1	0.96	0.11	16,16,16,16	0
56	MG	2D	315	1/1	0.96	0.04	24,24,24,24	0
56	MG	1A	8524	1/1	0.96	0.09	31,31,31,31	0
56	MG	2d	503	1/1	0.96	0.06	54,54,54,54	0
56	MG	1a	1711	1/1	0.96	0.06	45,45,45,45	0
56	MG	1A	8089	1/1	0.96	0.08	20,20,20,20	0
56	MG	1A	8832	1/1	0.96	0.21	12,12,12,12	0
56	MG	1A	8224	1/1	0.96	0.12	15,15,15,15	0
56	MG	2A	3028	1/1	0.96	0.18	34,34,34,34	0
56	MG	1a	1717	1/1	0.96	0.15	32,32,32,32	0
56	MG	1A	8059	1/1	0.96	0.06	7,7,7,7	0
56	MG	2F	303	1/1	0.96	0.07	29,29,29,29	0
56	MG	2A	3031	1/1	0.96	0.20	27,27,27,27	0
56	MG	2A	3238	1/1	0.96	0.08	24,24,24,24	0
56	MG	1A	8528	1/1	0.96	0.10	18,18,18,18	0
56	MG	2F	307	1/1	0.96	0.27	37,37,37,37	0
56	MG	1A	8005	1/1	0.96	0.06	20,20,20,20	0
56	MG	2A	3497	1/1	0.96	0.09	28,28,28,28	0
56	MG	2A	3748	1/1	0.96	0.11	47,47,47,47	0
56	MG	1A	8660	1/1	0.96	0.05	16,16,16,16	0
56	MG	1A	8843	1/1	0.96	0.08	33,33,33,33	0
56	MG	1A	8846	1/1	0.96	0.14	37,37,37,37	0
56	MG	2A	3753	1/1	0.96	0.19	27,27,27,27	0
56	MG	2A	3501	1/1	0.96	0.08	41,41,41,41	0
56	MG	1A	8661	1/1	0.96	0.07	7,7,7,7	0
56	MG	1A	8098	1/1	0.96	0.27	19,19,19,19	0
56	MG	2P	202	1/1	0.96	0.27	37,37,37,37	0
56	MG	1A	8429	1/1	0.96	0.05	12,12,12,12	0
56	MG	1R	201	1/1	0.96	0.06	18,18,18,18	0
56	MG	2A	3506	1/1	0.96	0.05	33,33,33,33	0
56	MG	2x	112	1/1	0.96	0.21	39,39,39,39	0
56	MG	1A	8430	1/1	0.96	0.07	13,13,13,13	0
56	MG	1a	1732	1/1	0.96	0.06	38,38,38,38	0
56	MG	1A	8132	1/1	0.96	0.12	19,19,19,19	0
56	MG	1A	8773	1/1	0.97	0.07	29,29,29,29	0
56	MG	1A	8235	1/1	0.97	0.20	9,9,9,9	0
56	MG	2A	3215	1/1	0.97	0.05	26,26,26,26	0
56	MG	2A	3750	1/1	0.97	0.05	24,24,24,24	0
56	MG	2N	203	1/1	0.97	0.12	49,49,49,49	0
56	MG	1A	8626	1/1	0.97	0.05	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8173	1/1	0.97	0.17	15,15,15,15	0
56	MG	1A	8090	1/1	0.97	0.10	36,36,36,36	0
56	MG	1A	8091	1/1	0.97	0.17	16,16,16,16	0
56	MG	2Q	202	1/1	0.97	0.06	23,23,23,23	0
56	MG	1A	8513	1/1	0.97	0.07	27,27,27,27	0
56	MG	1A	8783	1/1	0.97	0.05	15,15,15,15	0
56	MG	1a	1674	1/1	0.97	0.14	40,40,40,40	0
56	MG	1A	8176	1/1	0.97	0.07	28,28,28,28	0
56	MG	1A	8633	1/1	0.97	0.08	10,10,10,10	0
56	MG	1A	8786	1/1	0.97	0.06	15,15,15,15	0
56	MG	1A	8037	1/1	0.97	0.04	14,14,14,14	0
56	MG	2A	3228	1/1	0.97	0.23	34,34,34,34	0
56	MG	2A	3765	1/1	0.97	0.07	48,48,48,48	0
56	MG	2A	3005	1/1	0.97	0.07	32,32,32,32	0
56	MG	1A	8019	1/1	0.97	0.22	12,12,12,12	0
56	MG	2A	3494	1/1	0.97	0.08	30,30,30,30	0
56	MG	2A	3231	1/1	0.97	0.22	32,32,32,32	0
56	MG	1A	8179	1/1	0.97	0.28	16,16,16,16	0
56	MG	2A	3008	1/1	0.97	0.07	27,27,27,27	0
56	MG	2X	102	1/1	0.97	0.07	40,40,40,40	0
56	MG	1B	3015	1/1	0.97	0.13	18,18,18,18	0
56	MG	1A	8790	1/1	0.97	0.10	20,20,20,20	0
56	MG	2A	3011	1/1	0.97	0.08	29,29,29,29	0
56	MG	1A	8518	1/1	0.97	0.08	35,35,35,35	0
56	MG	1A	8247	1/1	0.97	0.07	25,25,25,25	0
56	MG	1B	3019	1/1	0.97	0.05	23,23,23,23	0
56	MG	2A	3015	1/1	0.97	0.08	18,18,18,18	0
56	MG	1A	8520	1/1	0.97	0.07	9,9,9,9	0
56	MG	1a	1688	1/1	0.97	0.09	43,43,43,43	0
56	MG	1A	8097	1/1	0.97	0.08	18,18,18,18	0
56	MG	2A	3019	1/1	0.97	0.14	33,33,33,33	0
56	MG	1A	8797	1/1	0.97	0.04	20,20,20,20	0
56	MG	1a	1691	1/1	0.97	0.07	30,30,30,30	0
56	MG	2A	3247	1/1	0.97	0.14	25,25,25,25	0
56	MG	1A	8326	1/1	0.97	0.11	20,20,20,20	0
56	MG	1B	3025	1/1	0.97	0.10	26,26,26,26	0
56	MG	1A	8418	1/1	0.97	0.08	22,22,22,22	0
56	MG	2A	3026	1/1	0.97	0.15	28,28,28,28	0
56	MG	2A	3027	1/1	0.97	0.04	31,31,31,31	0
56	MG	2A	3253	1/1	0.97	0.10	39,39,39,39	0
56	MG	1A	8249	1/1	0.97	0.09	36,36,36,36	0
56	MG	1a	1697	1/1	0.97	0.05	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3256	1/1	0.97	0.13	33,33,33,33	0
56	MG	1A	8181	1/1	0.97	0.05	18,18,18,18	0
56	MG	1A	8066	1/1	0.97	0.08	25,25,25,25	0
56	MG	1A	8330	1/1	0.97	0.07	13,13,13,13	0
56	MG	2A	3260	1/1	0.97	0.05	26,26,26,26	0
56	MG	1A	8100	1/1	0.97	0.10	28,28,28,28	0
56	MG	1D	310	1/1	0.97	0.09	12,12,12,12	0
56	MG	1A	8529	1/1	0.97	0.13	21,21,21,21	0
56	MG	1A	8184	1/1	0.97	0.10	17,17,17,17	0
56	MG	2A	3807	1/1	0.97	0.06	29,29,29,29	0
56	MG	1A	8812	1/1	0.97	0.11	31,31,31,31	0
56	MG	2A	3266	1/1	0.97	0.08	25,25,25,25	0
56	MG	1A	8101	1/1	0.97	0.21	11,11,11,11	0
56	MG	1E	302	1/1	0.97	0.07	9,9,9,9	0
56	MG	1A	8188	1/1	0.97	0.28	16,16,16,16	0
56	MG	1A	8259	1/1	0.97	0.08	28,28,28,28	0
56	MG	1A	8431	1/1	0.97	0.05	17,17,17,17	0
56	MG	1A	8820	1/1	0.97	0.07	24,24,24,24	0
56	MG	1A	8537	1/1	0.97	0.03	21,21,21,21	0
56	MG	1A	8337	1/1	0.97	0.11	34,34,34,34	0
56	MG	2A	3046	1/1	0.97	0.13	26,26,26,26	0
56	MG	1A	8434	1/1	0.97	0.09	16,16,16,16	0
56	MG	1A	8540	1/1	0.97	0.05	21,21,21,21	0
56	MG	1F	306	1/1	0.97	0.08	7,7,7,7	0
56	MG	1A	8189	1/1	0.97	0.20	11,11,11,11	0
56	MG	1a	1723	1/1	0.97	0.05	40,40,40,40	0
56	MG	1A	8834	1/1	0.97	0.05	18,18,18,18	0
56	MG	1A	8191	1/1	0.97	0.13	17,17,17,17	0
56	MG	2A	3055	1/1	0.97	0.36	32,32,32,32	0
56	MG	1G	3003	1/1	0.97	0.15	31,31,31,31	0
56	MG	1A	8192	1/1	0.97	0.14	22,22,22,22	0
56	MG	1A	8668	1/1	0.97	0.13	32,32,32,32	0
56	MG	2A	3841	1/1	0.97	0.07	40,40,40,40	0
56	MG	2A	3059	1/1	0.97	0.05	21,21,21,21	0
56	MG	2A	3060	1/1	0.97	0.05	51,51,51,51	0
56	MG	1A	8544	1/1	0.97	0.12	27,27,27,27	0
56	MG	1A	8841	1/1	0.97	0.08	34,34,34,34	0
56	MG	1A	8441	1/1	0.97	0.05	16,16,16,16	0
56	MG	1A	8546	1/1	0.97	0.05	21,21,21,21	0
56	MG	1P	202	1/1	0.97	0.06	39,39,39,39	0
56	MG	2A	3851	1/1	0.97	0.07	37,37,37,37	0
56	MG	1A	8547	1/1	0.97	0.12	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8343	1/1	0.97	0.06	12,12,12,12	0
56	MG	2A	3855	1/1	0.97	0.05	32,32,32,32	0
56	MG	1Q	202	1/1	0.97	0.12	53,53,53,53	0
56	MG	1Q	203	1/1	0.97	0.05	19,19,19,19	0
56	MG	2A	3071	1/1	0.97	0.18	25,25,25,25	0
56	MG	1Q	204	1/1	0.97	0.05	20,20,20,20	0
56	MG	1A	8067	1/1	0.97	0.06	10,10,10,10	0
56	MG	1Q	206	1/1	0.97	0.04	17,17,17,17	0
56	MG	2a	1658	1/1	0.97	0.06	63,63,63,63	0
56	MG	1A	8851	1/1	0.97	0.08	33,33,33,33	0
56	MG	1R	203	1/1	0.97	0.04	16,16,16,16	0
56	MG	1A	8676	1/1	0.97	0.09	26,26,26,26	0
56	MG	1a	1745	1/1	0.97	0.06	41,41,41,41	0
56	MG	2A	3573	1/1	0.97	0.09	41,41,41,41	0
56	MG	1A	8677	1/1	0.97	0.06	24,24,24,24	0
56	MG	2a	1665	1/1	0.97	0.08	53,53,53,53	0
56	MG	1A	8444	1/1	0.97	0.07	12,12,12,12	0
56	MG	1A	8857	1/1	0.97	0.14	44,44,44,44	0
56	MG	2A	3083	1/1	0.97	0.11	25,25,25,25	0
56	MG	1A	8680	1/1	0.97	0.05	19,19,19,19	0
56	MG	1A	8068	1/1	0.97	0.10	16,16,16,16	0
56	MG	1V	202	1/1	0.97	0.14	26,26,26,26	0
56	MG	2A	3877	1/1	0.97	0.08	20,20,20,20	0
56	MG	1a	1752	1/1	0.97	0.05	45,45,45,45	0
56	MG	1A	8141	1/1	0.97	0.11	22,22,22,22	0
56	MG	1W	3001	1/1	0.97	0.09	21,21,21,21	0
56	MG	1W	3002	1/1	0.97	0.13	28,28,28,28	0
56	MG	2A	3882	1/1	0.97	0.05	46,46,46,46	0
56	MG	2a	1678	1/1	0.97	0.09	37,37,37,37	0
56	MG	1W	3003	1/1	0.97	0.10	12,12,12,12	0
56	MG	1A	8266	1/1	0.97	0.05	13,13,13,13	0
56	MG	2A	3589	1/1	0.97	0.30	30,30,30,30	0
56	MG	10	102	1/1	0.97	0.09	19,19,19,19	0
56	MG	2A	3887	1/1	0.97	0.05	41,41,41,41	0
56	MG	1A	8267	1/1	0.97	0.06	15,15,15,15	0
56	MG	1a	1760	1/1	0.97	0.05	56,56,56,56	0
56	MG	2a	1688	1/1	0.97	0.12	53,53,53,53	0
56	MG	1A	8028	1/1	0.97	0.07	11,11,11,11	0
56	MG	10	105	1/1	0.97	0.05	27,27,27,27	0
56	MG	2a	1691	1/1	0.97	0.07	52,52,52,52	0
56	MG	1a	1763	1/1	0.97	0.06	55,55,55,55	0
56	MG	1A	8557	1/1	0.97	0.20	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8867	1/1	0.97	0.08	55,55,55,55	0
56	MG	2A	3333	1/1	0.97	0.06	39,39,39,39	0
56	MG	2A	3336	1/1	0.97	0.06	44,44,44,44	0
56	MG	1A	8199	1/1	0.97	0.12	14,14,14,14	0
56	MG	1a	1767	1/1	0.97	0.16	55,55,55,55	0
56	MG	1A	8453	1/1	0.97	0.05	24,24,24,24	0
56	MG	2A	3340	1/1	0.97	0.06	32,32,32,32	0
56	MG	1A	8561	1/1	0.97	0.17	17,17,17,17	0
56	MG	2A	3106	1/1	0.97	0.10	31,31,31,31	0
56	MG	2A	3906	1/1	0.97	0.07	39,39,39,39	0
56	MG	13	101	1/1	0.97	0.06	17,17,17,17	0
56	MG	2A	3109	1/1	0.97	0.16	41,41,41,41	0
56	MG	2a	1706	1/1	0.97	0.06	55,55,55,55	0
56	MG	1A	8874	1/1	0.97	0.04	9,9,9,9	0
56	MG	2a	1709	1/1	0.97	0.06	33,33,33,33	0
56	MG	2A	3347	1/1	0.97	0.06	34,34,34,34	0
56	MG	1A	8563	1/1	0.97	0.13	11,11,11,11	0
56	MG	1A	8143	1/1	0.97	0.13	20,20,20,20	0
56	MG	1A	8695	1/1	0.97	0.05	11,11,11,11	0
56	MG	2A	3353	1/1	0.97	0.07	27,27,27,27	0
56	MG	2A	3355	1/1	0.97	0.04	20,20,20,20	0
56	MG	1A	8071	1/1	0.97	0.13	10,10,10,10	0
56	MG	1A	8073	1/1	0.97	0.15	17,17,17,17	0
56	MG	1A	8699	1/1	0.97	0.05	17,17,17,17	0
56	MG	17	101	1/1	0.97	0.07	21,21,21,21	0
56	MG	17	102	1/1	0.97	0.06	34,34,34,34	0
56	MG	2A	3363	1/1	0.97	0.07	26,26,26,26	0
56	MG	1A	8074	1/1	0.97	0.13	18,18,18,18	0
56	MG	1A	8461	1/1	0.97	0.05	10,10,10,10	0
56	MG	2A	3625	1/1	0.97	0.10	51,51,51,51	0
56	MG	1A	8275	1/1	0.97	0.18	10,10,10,10	0
56	MG	1A	8010	1/1	0.97	0.11	7,7,7,7	0
56	MG	1A	8365	1/1	0.97	0.13	24,24,24,24	0
56	MG	2A	3630	1/1	0.97	0.15	57,57,57,57	0
56	MG	1A	8207	1/1	0.97	0.07	11,11,11,11	0
56	MG	2A	3126	1/1	0.97	0.07	32,32,32,32	0
56	MG	2A	3635	1/1	0.97	0.08	36,36,36,36	0
56	MG	2A	3127	1/1	0.97	0.11	27,27,27,27	0
56	MG	2A	3935	1/1	0.97	0.11	68,68,68,68	0
56	MG	1A	8708	1/1	0.97	0.06	17,17,17,17	0
56	MG	2A	3638	1/1	0.97	0.06	32,32,32,32	0
56	MG	2A	3129	1/1	0.97	0.07	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8891	1/1	0.97	0.08	15,15,15,15	0
56	MG	1A	8112	1/1	0.97	0.17	13,13,13,13	0
56	MG	1A	8712	1/1	0.97	0.09	24,24,24,24	0
56	MG	1A	8896	1/1	0.97	0.08	35,35,35,35	0
56	MG	2A	3134	1/1	0.97	0.05	24,24,24,24	0
56	MG	2A	3380	1/1	0.97	0.07	25,25,25,25	0
56	MG	2A	3947	1/1	0.97	0.21	24,24,24,24	0
56	MG	2A	3135	1/1	0.97	0.04	24,24,24,24	0
56	MG	2A	3949	1/1	0.97	0.17	26,26,26,26	0
56	MG	1A	8280	1/1	0.97	0.06	18,18,18,18	0
56	MG	2A	3651	1/1	0.97	0.13	35,35,35,35	0
56	MG	1A	8209	1/1	0.97	0.07	15,15,15,15	0
56	MG	1A	8113	1/1	0.97	0.05	16,16,16,16	0
56	MG	1A	8472	1/1	0.97	0.07	11,11,11,11	0
56	MG	2A	3141	1/1	0.97	0.07	27,27,27,27	0
56	MG	1A	8114	1/1	0.97	0.22	20,20,20,20	0
56	MG	2a	1756	1/1	0.97	0.12	38,38,38,38	0
56	MG	1A	8586	1/1	0.97	0.11	27,27,27,27	0
56	MG	1A	8721	1/1	0.97	0.15	11,11,11,11	0
56	MG	1A	8587	1/1	0.97	0.08	21,21,21,21	0
56	MG	1A	8041	1/1	0.97	0.13	24,24,24,24	0
56	MG	2A	3395	1/1	0.97	0.12	38,38,38,38	0
56	MG	2A	3397	1/1	0.97	0.07	21,21,21,21	0
56	MG	1A	8475	1/1	0.97	0.06	28,28,28,28	0
56	MG	1a	1802	1/1	0.97	0.14	30,30,30,30	0
56	MG	1A	8910	1/1	0.97	0.11	19,19,19,19	0
56	MG	1A	8057	1/1	0.97	0.05	12,12,12,12	0
56	MG	2A	3669	1/1	0.97	0.05	34,34,34,34	0
56	MG	1a	1805	1/1	0.97	0.05	55,55,55,55	0
56	MG	2A	3403	1/1	0.97	0.05	40,40,40,40	0
56	MG	1A	8219	1/1	0.97	0.14	12,12,12,12	0
56	MG	2A	3973	1/1	0.97	0.05	35,35,35,35	0
56	MG	1A	8080	1/1	0.97	0.16	18,18,18,18	0
56	MG	2A	3975	1/1	0.97	0.10	22,22,22,22	0
56	MG	1a	1622	1/1	0.97	0.07	32,32,32,32	0
56	MG	2a	1776	1/1	0.97	0.06	51,51,51,51	0
56	MG	1A	8081	1/1	0.97	0.10	16,16,16,16	0
56	MG	1a	1813	1/1	0.97	0.07	49,49,49,49	0
56	MG	2A	3979	1/1	0.97	0.13	57,57,57,57	0
56	MG	2A	3410	1/1	0.97	0.05	45,45,45,45	0
56	MG	1a	1814	1/1	0.97	0.11	40,40,40,40	0
56	MG	1A	8031	1/1	0.97	0.09	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8083	1/1	0.97	0.10	15,15,15,15	0
56	MG	1A	8919	1/1	0.97	0.07	11,11,11,11	0
56	MG	1a	1818	1/1	0.97	0.09	41,41,41,41	0
56	MG	1a	1820	1/1	0.97	0.05	51,51,51,51	0
56	MG	1A	8225	1/1	0.97	0.14	10,10,10,10	0
56	MG	2a	1790	1/1	0.97	0.07	51,51,51,51	0
56	MG	1A	8298	1/1	0.97	0.04	12,12,12,12	0
56	MG	2A	3168	1/1	0.97	0.05	24,24,24,24	0
56	MG	1A	8600	1/1	0.97	0.07	26,26,26,26	0
56	MG	1a	1826	1/1	0.97	0.10	65,65,65,65	0
56	MG	1A	8737	1/1	0.97	0.06	24,24,24,24	0
56	MG	1A	8022	1/1	0.97	0.17	12,12,12,12	0
56	MG	1A	8165	1/1	0.97	0.06	10,10,10,10	0
56	MG	1A	8167	1/1	0.97	0.24	17,17,17,17	0
56	MG	2A	3426	1/1	0.97	0.05	55,55,55,55	0
56	MG	2a	1802	1/1	0.97	0.08	60,60,60,60	0
56	MG	1A	8304	1/1	0.97	0.04	17,17,17,17	0
56	MG	1A	8744	1/1	0.97	0.06	17,17,17,17	0
56	MG	2A	3429	1/1	0.97	0.06	37,37,37,37	0
56	MG	1A	8388	1/1	0.97	0.06	11,11,11,11	0
56	MG	1A	8933	1/1	0.97	0.11	20,20,20,20	0
56	MG	1A	8934	1/1	0.97	0.05	48,48,48,48	0
56	MG	2a	1811	1/1	0.97	0.05	59,59,59,59	0
56	MG	1A	8746	1/1	0.97	0.11	22,22,22,22	0
56	MG	1a	1641	1/1	0.97	0.14	33,33,33,33	0
56	MG	1A	8493	1/1	0.97	0.07	16,16,16,16	0
56	MG	1A	8748	1/1	0.97	0.11	18,18,18,18	0
56	MG	1A	8609	1/1	0.97	0.07	18,18,18,18	0
56	MG	1A	8942	1/1	0.97	0.04	11,11,11,11	0
56	MG	2B	3022	1/1	0.97	0.07	59,59,59,59	0
56	MG	2A	3441	1/1	0.97	0.06	38,38,38,38	0
56	MG	2A	3187	1/1	0.97	0.12	42,42,42,42	0
56	MG	2A	3188	1/1	0.97	0.25	33,33,33,33	0
56	MG	2A	3189	1/1	0.97	0.08	32,32,32,32	0
56	MG	1A	8229	1/1	0.97	0.07	21,21,21,21	0
56	MG	1A	8945	1/1	0.97	0.06	8,8,8,8	0
56	MG	2D	304	1/1	0.97	0.12	41,41,41,41	0
56	MG	1a	1648	1/1	0.97	0.20	38,38,38,38	0
56	MG	2A	3450	1/1	0.97	0.10	27,27,27,27	0
56	MG	2D	308	1/1	0.97	0.06	33,33,33,33	0
56	MG	2A	3193	1/1	0.97	0.07	27,27,27,27	0
56	MG	2D	310	1/1	0.97	0.13	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8306	1/1	0.97	0.06	14,14,14,14	0
56	MG	1A	8008	1/1	0.97	0.18	23,23,23,23	0
56	MG	2A	3456	1/1	0.97	0.05	23,23,23,23	0
56	MG	1A	8025	1/1	0.97	0.29	23,23,23,23	0
56	MG	1A	8502	1/1	0.97	0.19	18,18,18,18	0
56	MG	1A	8393	1/1	0.97	0.17	20,20,20,20	0
56	MG	1A	8311	1/1	0.97	0.04	11,11,11,11	0
56	MG	2E	302	1/1	0.97	0.06	26,26,26,26	0
56	MG	1A	8957	1/1	0.97	0.09	26,26,26,26	0
56	MG	1A	8762	1/1	0.97	0.05	34,34,34,34	0
56	MG	1A	8006	1/1	0.97	0.10	14,14,14,14	0
56	MG	1A	8963	1/1	0.97	0.19	14,14,14,14	0
56	MG	2A	3466	1/1	0.97	0.06	46,46,46,46	0
56	MG	2A	3467	1/1	0.97	0.11	52,52,52,52	0
56	MG	1A	8764	1/1	0.97	0.05	27,27,27,27	0
56	MG	1A	8125	1/1	0.97	0.11	30,30,30,30	0
56	MG	1A	8767	1/1	0.97	0.08	33,33,33,33	0
56	MG	1A	8968	1/1	0.97	0.06	34,34,34,34	0
56	MG	1A	8126	1/1	0.97	0.18	12,12,12,12	0
56	MG	1A	8971	1/1	0.97	0.14	9,9,9,9	0
56	MG	2A	3210	1/1	0.97	0.09	34,34,34,34	0
57	ZN	1n	102	1/1	0.97	0.04	55,55,55,55	0
57	ZN	2Y	202	1/1	0.97	0.04	66,66,66,66	0
57	ZN	24	501	1/1	0.97	0.13	99,99,99,99	0
58	SF4	2d	501	8/8	0.97	0.05	47,53,59,65	0
56	MG	1A	8769	1/1	0.97	0.09	20,20,20,20	0
56	MG	2A	3746	1/1	0.97	0.13	27,27,27,27	0
56	MG	1A	8875	1/1	0.98	0.15	10,10,10,10	0
56	MG	1A	8358	1/1	0.98	0.05	7,7,7,7	0
56	MG	1A	8877	1/1	0.98	0.05	38,38,38,38	0
56	MG	2A	3859	1/1	0.98	0.10	41,41,41,41	0
56	MG	1A	8611	1/1	0.98	0.06	17,17,17,17	0
56	MG	2A	3861	1/1	0.98	0.05	50,50,50,50	0
56	MG	2A	3214	1/1	0.98	0.05	32,32,32,32	0
56	MG	2A	3621	1/1	0.98	0.10	44,44,44,44	0
56	MG	1A	8724	1/1	0.98	0.13	17,17,17,17	0
56	MG	1A	8359	1/1	0.98	0.05	24,24,24,24	0
56	MG	1R	202	1/1	0.98	0.06	26,26,26,26	0
56	MG	1A	8613	1/1	0.98	0.07	36,36,36,36	0
56	MG	2A	3626	1/1	0.98	0.06	60,60,60,60	0
56	MG	1A	8240	1/1	0.98	0.15	13,13,13,13	0
56	MG	1A	8134	1/1	0.98	0.04	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8164	1/1	0.98	0.05	31,31,31,31	0
56	MG	1A	8363	1/1	0.98	0.09	15,15,15,15	0
56	MG	2A	3631	1/1	0.98	0.05	48,48,48,48	0
56	MG	1A	8439	1/1	0.98	0.07	6,6,6,6	0
56	MG	2A	3875	1/1	0.98	0.06	23,23,23,23	0
56	MG	1A	8733	1/1	0.98	0.08	54,54,54,54	0
56	MG	2A	3634	1/1	0.98	0.05	43,43,43,43	0
56	MG	2A	3225	1/1	0.98	0.09	42,42,42,42	0
56	MG	1A	8620	1/1	0.98	0.11	25,25,25,25	0
56	MG	1A	8297	1/1	0.98	0.07	13,13,13,13	0
56	MG	1A	8243	1/1	0.98	0.10	17,17,17,17	0
56	MG	2A	3047	1/1	0.98	0.07	18,18,18,18	0
56	MG	1A	8024	1/1	0.98	0.24	8,8,8,8	0
56	MG	1A	8738	1/1	0.98	0.07	38,38,38,38	0
56	MG	2A	3642	1/1	0.98	0.05	37,37,37,37	0
56	MG	1A	8894	1/1	0.98	0.07	8,8,8,8	0
56	MG	2a	1639	1/1	0.98	0.05	27,27,27,27	0
56	MG	2A	3644	1/1	0.98	0.05	40,40,40,40	0
56	MG	1A	8245	1/1	0.98	0.10	8,8,8,8	0
56	MG	1A	8740	1/1	0.98	0.06	27,27,27,27	0
56	MG	1A	8136	1/1	0.98	0.06	10,10,10,10	0
56	MG	1A	8446	1/1	0.98	0.04	26,26,26,26	0
56	MG	2A	3649	1/1	0.98	0.07	42,42,42,42	0
56	MG	1A	8303	1/1	0.98	0.04	11,11,11,11	0
56	MG	2A	3894	1/1	0.98	0.08	36,36,36,36	0
56	MG	1A	8053	1/1	0.98	0.06	11,11,11,11	0
56	MG	2A	3439	1/1	0.98	0.05	25,25,25,25	0
56	MG	2A	3898	1/1	0.98	0.05	46,46,46,46	0
56	MG	1A	8630	1/1	0.98	0.14	36,36,36,36	0
56	MG	1A	8203	1/1	0.98	0.04	15,15,15,15	0
56	MG	2A	3656	1/1	0.98	0.19	24,24,24,24	0
56	MG	1A	8533	1/1	0.98	0.12	28,28,28,28	0
56	MG	1A	8906	1/1	0.98	0.07	13,13,13,13	0
56	MG	1A	8450	1/1	0.98	0.05	14,14,14,14	0
56	MG	1A	8908	1/1	0.98	0.16	9,9,9,9	0
56	MG	1A	8017	1/1	0.98	0.10	13,13,13,13	0
56	MG	2A	3449	1/1	0.98	0.06	25,25,25,25	0
56	MG	15	104	1/1	0.98	0.17	16,16,16,16	0
56	MG	1A	8635	1/1	0.98	0.12	34,34,34,34	0
56	MG	1A	8752	1/1	0.98	0.06	12,12,12,12	0
56	MG	2A	3067	1/1	0.98	0.08	20,20,20,20	0
56	MG	2A	3454	1/1	0.98	0.04	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3455	1/1	0.98	0.04	40,40,40,40	0
56	MG	1A	8912	1/1	0.98	0.07	15,15,15,15	0
56	MG	1A	8055	1/1	0.98	0.20	10,10,10,10	0
56	MG	1A	8637	1/1	0.98	0.04	11,11,11,11	0
56	MG	1A	8638	1/1	0.98	0.06	18,18,18,18	0
56	MG	1A	8077	1/1	0.98	0.09	15,15,15,15	0
56	MG	2A	3674	1/1	0.98	0.05	32,32,32,32	0
56	MG	1A	8309	1/1	0.98	0.05	19,19,19,19	0
56	MG	1A	8918	1/1	0.98	0.05	16,16,16,16	0
56	MG	1A	8758	1/1	0.98	0.09	11,11,11,11	0
56	MG	1A	8094	1/1	0.98	0.07	12,12,12,12	0
56	MG	2A	3925	1/1	0.98	0.09	42,42,42,42	0
56	MG	1A	8761	1/1	0.98	0.05	7,7,7,7	0
56	MG	2A	3078	1/1	0.98	0.19	24,24,24,24	0
56	MG	1A	8312	1/1	0.98	0.06	7,7,7,7	0
56	MG	2A	3682	1/1	0.98	0.08	40,40,40,40	0
56	MG	1A	8459	1/1	0.98	0.07	24,24,24,24	0
56	MG	1A	8924	1/1	0.98	0.09	12,12,12,12	0
56	MG	1A	8253	1/1	0.98	0.17	23,23,23,23	0
56	MG	1A	8254	1/1	0.98	0.04	15,15,15,15	0
56	MG	2a	1685	1/1	0.98	0.05	41,41,41,41	0
56	MG	2a	1686	1/1	0.98	0.04	41,41,41,41	0
56	MG	2A	3084	1/1	0.98	0.18	21,21,21,21	0
56	MG	1A	8095	1/1	0.98	0.10	6,6,6,6	0
56	MG	1A	8928	1/1	0.98	0.24	16,16,16,16	0
56	MG	1A	8929	1/1	0.98	0.09	17,17,17,17	0
56	MG	1A	8096	1/1	0.98	0.07	10,10,10,10	0
56	MG	1A	8211	1/1	0.98	0.25	15,15,15,15	0
56	MG	1A	8770	1/1	0.98	0.04	21,21,21,21	0
56	MG	2A	3941	1/1	0.98	0.05	35,35,35,35	0
56	MG	2A	3695	1/1	0.98	0.04	33,33,33,33	0
56	MG	1A	8771	1/1	0.98	0.08	24,24,24,24	0
56	MG	1A	8772	1/1	0.98	0.06	27,27,27,27	0
56	MG	2A	3945	1/1	0.98	0.05	22,22,22,22	0
56	MG	1A	8935	1/1	0.98	0.20	5,5,5,5	0
56	MG	1A	8936	1/1	0.98	0.18	11,11,11,11	0
56	MG	1A	8937	1/1	0.98	0.04	11,11,11,11	0
56	MG	1A	8078	1/1	0.98	0.10	9,9,9,9	0
56	MG	1A	8145	1/1	0.98	0.12	15,15,15,15	0
56	MG	1A	8146	1/1	0.98	0.11	13,13,13,13	0
56	MG	1A	8551	1/1	0.98	0.07	32,32,32,32	0
56	MG	1A	8779	1/1	0.98	0.06	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8943	1/1	0.98	0.25	19,19,19,19	0
56	MG	2a	1708	1/1	0.98	0.06	29,29,29,29	0
56	MG	1A	8215	1/1	0.98	0.18	12,12,12,12	0
56	MG	1A	8216	1/1	0.98	0.24	15,15,15,15	0
56	MG	2A	3711	1/1	0.98	0.05	29,29,29,29	0
56	MG	1A	8656	1/1	0.98	0.12	22,22,22,22	0
56	MG	1A	8947	1/1	0.98	0.04	19,19,19,19	0
56	MG	1A	8217	1/1	0.98	0.13	11,11,11,11	0
56	MG	2A	3289	1/1	0.98	0.07	22,22,22,22	0
56	MG	1a	1630	1/1	0.98	0.15	17,17,17,17	0
56	MG	2A	3108	1/1	0.98	0.24	27,27,27,27	0
56	MG	1A	8658	1/1	0.98	0.28	9,9,9,9	0
56	MG	2A	3110	1/1	0.98	0.14	35,35,35,35	0
56	MG	1A	8950	1/1	0.98	0.06	26,26,26,26	0
56	MG	1A	8218	1/1	0.98	0.07	11,11,11,11	0
56	MG	1A	8065	1/1	0.98	0.04	11,11,11,11	0
56	MG	1A	8148	1/1	0.98	0.04	7,7,7,7	0
56	MG	1a	1808	1/1	0.98	0.04	35,35,35,35	0
56	MG	2A	3725	1/1	0.98	0.04	29,29,29,29	0
56	MG	2A	3299	1/1	0.98	0.03	41,41,41,41	0
56	MG	1A	8954	1/1	0.98	0.13	13,13,13,13	0
56	MG	1A	8955	1/1	0.98	0.27	11,11,11,11	0
56	MG	1A	8268	1/1	0.98	0.15	15,15,15,15	0
56	MG	1A	8396	1/1	0.98	0.04	14,14,14,14	0
56	MG	2A	3512	1/1	0.98	0.04	53,53,53,53	0
56	MG	2A	3304	1/1	0.98	0.05	47,47,47,47	0
56	MG	1A	8959	1/1	0.98	0.06	27,27,27,27	0
56	MG	1A	8664	1/1	0.98	0.04	26,26,26,26	0
56	MG	1A	8962	1/1	0.98	0.17	11,11,11,11	0
56	MG	1A	8560	1/1	0.98	0.07	18,18,18,18	0
56	MG	1a	1819	1/1	0.98	0.07	37,37,37,37	0
56	MG	2a	1738	1/1	0.98	0.04	43,43,43,43	0
56	MG	2a	1739	1/1	0.98	0.12	48,48,48,48	0
56	MG	1A	8397	1/1	0.98	0.06	18,18,18,18	0
56	MG	2A	3311	1/1	0.98	0.05	29,29,29,29	0
56	MG	1A	8562	1/1	0.98	0.12	9,9,9,9	0
56	MG	1A	8046	1/1	0.98	0.08	12,12,12,12	0
56	MG	1a	1824	1/1	0.98	0.07	54,54,54,54	0
56	MG	2a	1745	1/1	0.98	0.05	55,55,55,55	0
56	MG	1A	8796	1/1	0.98	0.07	35,35,35,35	0
56	MG	2A	3745	1/1	0.98	0.07	39,39,39,39	0
56	MG	1A	8969	1/1	0.98	0.13	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8564	1/1	0.98	0.23	11,11,11,11	0
56	MG	1A	8481	1/1	0.98	0.06	20,20,20,20	0
56	MG	1A	8567	1/1	0.98	0.05	31,31,31,31	0
56	MG	1A	8399	1/1	0.98	0.09	34,34,34,34	0
56	MG	1A	8673	1/1	0.98	0.17	32,32,32,32	0
56	MG	1a	1832	1/1	0.98	0.05	44,44,44,44	0
56	MG	1A	8151	1/1	0.98	0.07	10,10,10,10	0
56	MG	1A	8223	1/1	0.98	0.24	18,18,18,18	0
56	MG	1A	8047	1/1	0.98	0.18	6,6,6,6	0
56	MG	1A	8805	1/1	0.98	0.09	34,34,34,34	0
56	MG	1A	8405	1/1	0.98	0.04	16,16,16,16	0
56	MG	2A	3758	1/1	0.98	0.11	28,28,28,28	0
56	MG	1A	8808	1/1	0.98	0.12	17,17,17,17	0
56	MG	1A	8678	1/1	0.98	0.04	21,21,21,21	0
56	MG	1A	8487	1/1	0.98	0.10	31,31,31,31	0
56	MG	2A	3146	1/1	0.98	0.24	28,28,28,28	0
56	MG	2A	3334	1/1	0.98	0.04	23,23,23,23	0
56	MG	2A	3764	1/1	0.98	0.06	62,62,62,62	0
56	MG	1A	8406	1/1	0.98	0.13	42,42,42,42	0
56	MG	1A	8576	1/1	0.98	0.05	29,29,29,29	0
56	MG	2A	3544	1/1	0.98	0.04	38,38,38,38	0
56	MG	1A	8815	1/1	0.98	0.10	21,21,21,21	0
56	MG	1B	3013	1/1	0.98	0.04	24,24,24,24	0
56	MG	1A	8816	1/1	0.98	0.05	12,12,12,12	0
56	MG	2a	1773	1/1	0.98	0.07	52,52,52,52	0
56	MG	1A	8682	1/1	0.98	0.04	23,23,23,23	0
56	MG	1A	8102	1/1	0.98	0.14	16,16,16,16	0
56	MG	1A	8103	1/1	0.98	0.06	13,13,13,13	0
56	MG	2A	3776	1/1	0.98	0.06	51,51,51,51	0
56	MG	1A	8185	1/1	0.98	0.13	26,26,26,26	0
56	MG	2A	3345	1/1	0.98	0.05	39,39,39,39	0
56	MG	1A	8825	1/1	0.98	0.10	35,35,35,35	0
56	MG	2a	1781	1/1	0.98	0.05	61,61,61,61	0
56	MG	1A	8492	1/1	0.98	0.08	18,18,18,18	0
56	MG	1A	8186	1/1	0.98	0.07	26,26,26,26	0
56	MG	1A	8494	1/1	0.98	0.20	17,17,17,17	0
56	MG	2A	3350	1/1	0.98	0.12	28,28,28,28	0
56	MG	1B	3023	1/1	0.98	0.10	46,46,46,46	0
56	MG	2A	3352	1/1	0.98	0.08	60,60,60,60	0
56	MG	2E	304	1/1	0.98	0.10	21,21,21,21	0
56	MG	1A	8584	1/1	0.98	0.07	35,35,35,35	0
56	MG	2a	1791	1/1	0.98	0.04	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8690	1/1	0.98	0.04	20,20,20,20	0
56	MG	2A	3163	1/1	0.98	0.06	23,23,23,23	0
56	MG	1A	8835	1/1	0.98	0.08	36,36,36,36	0
56	MG	2A	3359	1/1	0.98	0.04	30,30,30,30	0
56	MG	1A	8030	1/1	0.98	0.19	20,20,20,20	0
56	MG	2A	3166	1/1	0.98	0.03	42,42,42,42	0
56	MG	1D	301	1/1	0.98	0.06	21,21,21,21	0
56	MG	1A	8837	1/1	0.98	0.04	18,18,18,18	0
56	MG	1D	304	1/1	0.98	0.04	14,14,14,14	0
56	MG	1A	8692	1/1	0.98	0.12	19,19,19,19	0
56	MG	1A	8496	1/1	0.98	0.06	21,21,21,21	0
56	MG	2a	1804	1/1	0.98	0.14	65,65,65,65	0
56	MG	1A	8018	1/1	0.98	0.12	10,10,10,10	0
56	MG	1D	309	1/1	0.98	0.10	26,26,26,26	0
56	MG	1A	8414	1/1	0.98	0.07	35,35,35,35	0
56	MG	2a	1808	1/1	0.98	0.07	53,53,53,53	0
56	MG	1A	8499	1/1	0.98	0.10	18,18,18,18	0
56	MG	1A	8844	1/1	0.98	0.18	15,15,15,15	0
56	MG	1A	8070	1/1	0.98	0.12	16,16,16,16	0
56	MG	2A	3579	1/1	0.98	0.12	25,25,25,25	0
56	MG	2A	3805	1/1	0.98	0.04	40,40,40,40	0
56	MG	1A	8698	1/1	0.98	0.06	30,30,30,30	0
56	MG	1E	301	1/1	0.98	0.09	22,22,22,22	0
56	MG	1A	8190	1/1	0.98	0.04	15,15,15,15	0
56	MG	2A	3583	1/1	0.98	0.04	25,25,25,25	0
56	MG	1a	1695	1/1	0.98	0.05	27,27,27,27	0
56	MG	1A	8503	1/1	0.98	0.06	23,23,23,23	0
56	MG	1A	8085	1/1	0.98	0.08	15,15,15,15	0
56	MG	1A	8702	1/1	0.98	0.04	30,30,30,30	0
56	MG	2A	3381	1/1	0.98	0.04	31,31,31,31	0
56	MG	1A	8012	1/1	0.98	0.03	18,18,18,18	0
56	MG	1A	8854	1/1	0.98	0.07	22,22,22,22	0
56	MG	2A	3819	1/1	0.98	0.05	32,32,32,32	0
56	MG	2A	3821	1/1	0.98	0.05	48,48,48,48	0
56	MG	1A	8345	1/1	0.98	0.04	30,30,30,30	0
56	MG	2A	3824	1/1	0.98	0.04	42,42,42,42	0
56	MG	1A	8856	1/1	0.98	0.06	18,18,18,18	0
56	MG	1A	8420	1/1	0.98	0.07	28,28,28,28	0
56	MG	2A	3387	1/1	0.98	0.07	47,47,47,47	0
56	MG	2A	3388	1/1	0.98	0.07	23,23,23,23	0
56	MG	1F	304	1/1	0.98	0.04	9,9,9,9	0
56	MG	1A	8109	1/1	0.98	0.04	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2Y	203	1/1	0.98	0.05	47,47,47,47	0
56	MG	1F	307	1/1	0.98	0.10	13,13,13,13	0
56	MG	1F	308	1/1	0.98	0.07	18,18,18,18	0
56	MG	1A	8422	1/1	0.98	0.04	33,33,33,33	0
56	MG	2A	3836	1/1	0.98	0.08	32,32,32,32	0
56	MG	1A	8195	1/1	0.98	0.26	8,8,8,8	0
56	MG	1A	8072	1/1	0.98	0.07	11,11,11,11	0
56	MG	2A	3839	1/1	0.98	0.06	27,27,27,27	0
56	MG	1A	8238	1/1	0.98	0.12	19,19,19,19	0
56	MG	1A	8715	1/1	0.98	0.05	17,17,17,17	0
56	MG	1A	8288	1/1	0.98	0.04	8,8,8,8	0
56	MG	2A	3844	1/1	0.98	0.06	46,46,46,46	0
56	MG	1A	8289	1/1	0.98	0.07	8,8,8,8	0
56	MG	1N	202	1/1	0.98	0.05	28,28,28,28	0
56	MG	2A	3023	1/1	0.98	0.08	43,43,43,43	0
56	MG	2A	3609	1/1	0.98	0.05	47,47,47,47	0
56	MG	1A	8606	1/1	0.98	0.12	26,26,26,26	0
56	MG	1A	8869	1/1	0.98	0.07	20,20,20,20	0
56	MG	1A	8607	1/1	0.98	0.07	18,18,18,18	0
56	MG	1A	8162	1/1	0.98	0.09	10,10,10,10	0
58	SF4	1d	501	8/8	0.98	0.05	48,49,54,54	0
56	MG	2A	3853	1/1	0.98	0.07	54,54,54,54	0
56	MG	1A	8873	1/1	0.98	0.05	10,10,10,10	0
56	MG	1A	8293	1/1	0.98	0.10	12,12,12,12	0
56	MG	1a	1715	1/1	0.99	0.03	32,32,32,32	0
56	MG	1A	8811	1/1	0.99	0.04	35,35,35,35	0
56	MG	1A	8166	1/1	0.99	0.03	14,14,14,14	0
56	MG	2A	3313	1/1	0.99	0.06	31,31,31,31	0
56	MG	1A	8614	1/1	0.99	0.19	41,41,41,41	0
56	MG	1A	8961	1/1	0.99	0.06	20,20,20,20	0
56	MG	2A	3316	1/1	0.99	0.21	34,34,34,34	0
56	MG	1A	8705	1/1	0.99	0.03	10,10,10,10	0
56	MG	1a	1811	1/1	0.99	0.04	58,58,58,58	0
56	MG	1a	1812	1/1	0.99	0.03	35,35,35,35	0
56	MG	1P	203	1/1	0.99	0.07	8,8,8,8	0
56	MG	1a	1722	1/1	0.99	0.03	32,32,32,32	0
56	MG	1A	8302	1/1	0.99	0.05	21,21,21,21	0
56	MG	1A	8366	1/1	0.99	0.04	14,14,14,14	0
56	MG	1a	1725	1/1	0.99	0.04	35,35,35,35	0
56	MG	1A	8889	1/1	0.99	0.10	17,17,17,17	0
56	MG	1A	8817	1/1	0.99	0.10	31,31,31,31	0
56	MG	1A	8967	1/1	0.99	0.21	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8007	1/1	0.99	0.06	8,8,8,8	0
56	MG	2A	3137	1/1	0.99	0.04	26,26,26,26	0
56	MG	1a	1822	1/1	0.99	0.05	25,25,25,25	0
56	MG	1A	8760	1/1	0.99	0.03	12,12,12,12	0
56	MG	1A	8709	1/1	0.99	0.03	23,23,23,23	0
56	MG	1A	8821	1/1	0.99	0.03	9,9,9,9	0
56	MG	1A	8822	1/1	0.99	0.07	44,44,44,44	0
56	MG	2A	3335	1/1	0.99	0.06	37,37,37,37	0
56	MG	1A	8535	1/1	0.99	0.05	31,31,31,31	0
56	MG	2A	3440	1/1	0.99	0.04	30,30,30,30	0
56	MG	2A	3652	1/1	0.99	0.05	43,43,43,43	0
56	MG	1A	8898	1/1	0.99	0.08	39,39,39,39	0
56	MG	1A	8342	1/1	0.99	0.05	9,9,9,9	0
56	MG	2A	3443	1/1	0.99	0.02	31,31,31,31	0
56	MG	1A	8826	1/1	0.99	0.03	14,14,14,14	0
56	MG	1A	8827	1/1	0.99	0.07	12,12,12,12	0
56	MG	2A	3769	1/1	0.99	0.04	31,31,31,31	0
56	MG	1U	203	1/1	0.99	0.08	13,13,13,13	0
56	MG	1A	8828	1/1	0.99	0.06	40,40,40,40	0
56	MG	1A	8713	1/1	0.99	0.04	9,9,9,9	0
56	MG	2A	3773	1/1	0.99	0.08	24,24,24,24	0
56	MG	1A	8830	1/1	0.99	0.05	27,27,27,27	0
56	MG	1A	8426	1/1	0.99	0.06	31,31,31,31	0
56	MG	1A	8766	1/1	0.99	0.03	37,37,37,37	0
56	MG	2D	305	1/1	0.99	0.04	33,33,33,33	0
56	MG	1A	8369	1/1	0.99	0.04	11,11,11,11	0
56	MG	2A	3896	1/1	0.99	0.03	28,28,28,28	0
56	MG	1X	101	1/1	0.99	0.03	20,20,20,20	0
56	MG	1A	8501	1/1	0.99	0.05	29,29,29,29	0
56	MG	1A	8580	1/1	0.99	0.03	27,27,27,27	0
56	MG	2D	311	1/1	0.99	0.03	29,29,29,29	0
56	MG	1A	8624	1/1	0.99	0.05	34,34,34,34	0
56	MG	1A	8149	1/1	0.99	0.10	11,11,11,11	0
56	MG	1A	8021	1/1	0.99	0.20	12,12,12,12	0
56	MG	2A	3354	1/1	0.99	0.04	27,27,27,27	0
56	MG	2A	3460	1/1	0.99	0.06	25,25,25,25	0
56	MG	1A	8466	1/1	0.99	0.08	25,25,25,25	0
56	MG	1A	8086	1/1	0.99	0.07	18,18,18,18	0
56	MG	2a	1789	1/1	0.99	0.04	63,63,63,63	0
56	MG	2A	3357	1/1	0.99	0.04	20,20,20,20	0
56	MG	1A	8775	1/1	0.99	0.03	9,9,9,9	0
56	MG	2a	1792	1/1	0.99	0.09	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3570	1/1	0.99	0.05	35,35,35,35	0
56	MG	1A	8842	1/1	0.99	0.08	11,11,11,11	0
56	MG	1A	8290	1/1	0.99	0.04	19,19,19,19	0
56	MG	1A	8432	1/1	0.99	0.02	26,26,26,26	0
56	MG	1A	8845	1/1	0.99	0.14	28,28,28,28	0
56	MG	1A	8778	1/1	0.99	0.03	21,21,21,21	0
56	MG	1A	8127	1/1	0.99	0.18	11,11,11,11	0
56	MG	1A	8848	1/1	0.99	0.10	13,13,13,13	0
56	MG	1A	8588	1/1	0.99	0.05	11,11,11,11	0
56	MG	2A	3918	1/1	0.99	0.04	43,43,43,43	0
56	MG	1A	8375	1/1	0.99	0.05	11,11,11,11	0
56	MG	1A	8435	1/1	0.99	0.04	16,16,16,16	0
56	MG	2A	3475	1/1	0.99	0.04	23,23,23,23	0
56	MG	1a	1676	1/1	0.99	0.12	30,30,30,30	0
56	MG	1D	302	1/1	0.99	0.04	11,11,11,11	0
56	MG	1A	8591	1/1	0.99	0.16	10,10,10,10	0
56	MG	1A	8730	1/1	0.99	0.04	62,62,62,62	0
56	MG	1A	8403	1/1	0.99	0.05	13,13,13,13	0
56	MG	1A	8292	1/1	0.99	0.03	26,26,26,26	0
56	MG	1A	8310	1/1	0.99	0.04	8,8,8,8	0
56	MG	2A	3809	1/1	0.99	0.04	20,20,20,20	0
56	MG	1A	8350	1/1	0.99	0.08	8,8,8,8	0
56	MG	2A	3811	1/1	0.99	0.05	47,47,47,47	0
56	MG	1A	8440	1/1	0.99	0.08	5,5,5,5	0
56	MG	1A	8032	1/1	0.99	0.08	6,6,6,6	0
56	MG	2A	3184	1/1	0.99	0.11	25,25,25,25	0
56	MG	1A	8860	1/1	0.99	0.09	22,22,22,22	0
56	MG	1A	8642	1/1	0.99	0.03	18,18,18,18	0
56	MG	1A	8862	1/1	0.99	0.07	42,42,42,42	0
56	MG	1A	8792	1/1	0.99	0.05	15,15,15,15	0
56	MG	2d	502	1/1	0.99	0.03	53,53,53,53	0
56	MG	1A	8278	1/1	0.99	0.03	8,8,8,8	0
56	MG	2A	3820	1/1	0.99	0.03	29,29,29,29	0
56	MG	1A	8410	1/1	0.99	0.05	35,35,35,35	0
56	MG	2A	3822	1/1	0.99	0.04	46,46,46,46	0
56	MG	2A	3707	1/1	0.99	0.04	31,31,31,31	0
56	MG	1A	8354	1/1	0.99	0.05	9,9,9,9	0
56	MG	2A	3825	1/1	0.99	0.04	27,27,27,27	0
56	MG	2A	3826	1/1	0.99	0.05	33,33,33,33	0
56	MG	1A	8204	1/1	0.99	0.28	20,20,20,20	0
56	MG	1A	8051	1/1	0.99	0.12	10,10,10,10	0
56	MG	1A	8357	1/1	0.99	0.03	6,6,6,6	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8870	1/1	0.99	0.09	20,20,20,20	0
56	MG	1A	8194	1/1	0.99	0.18	17,17,17,17	0
56	MG	1A	8334	1/1	0.99	0.04	13,13,13,13	0
56	MG	1A	8099	1/1	0.99	0.15	12,12,12,12	0
56	MG	1F	305	1/1	0.99	0.03	15,15,15,15	0
56	MG	1A	8256	1/1	0.99	0.17	14,14,14,14	0
56	MG	1A	8131	1/1	0.99	0.15	12,12,12,12	0
56	MG	1A	8566	1/1	0.99	0.04	22,22,22,22	0
56	MG	1F	309	1/1	0.99	0.12	14,14,14,14	0
56	MG	1a	1705	1/1	0.99	0.08	25,25,25,25	0
56	MG	1a	1795	1/1	0.99	0.08	52,52,52,52	0
56	MG	1a	1706	1/1	0.99	0.03	27,27,27,27	0
56	MG	2A	3842	1/1	0.99	0.08	48,48,48,48	0
56	MG	2A	3404	1/1	0.99	0.04	25,25,25,25	0
56	MG	1A	8750	1/1	0.99	0.04	31,31,31,31	0
56	MG	2A	3965	1/1	0.99	0.09	32,32,32,32	0
56	MG	1A	8338	1/1	0.99	0.06	13,13,13,13	0
57	ZN	1Y	501	1/1	0.99	0.02	47,47,47,47	0
56	MG	1A	8807	1/1	0.99	0.04	18,18,18,18	0
57	ZN	15	102	1/1	0.99	0.02	31,31,31,31	0
57	ZN	16	101	1/1	0.99	0.02	24,24,24,24	0
56	MG	1A	8454	1/1	0.99	0.04	16,16,16,16	0
56	MG	2A	3969	1/1	0.99	0.13	55,55,55,55	0
56	MG	1A	8455	1/1	0.99	0.04	22,22,22,22	0
57	ZN	25	102	1/1	0.99	0.04	53,53,53,53	0
57	ZN	26	101	1/1	0.99	0.02	42,42,42,42	0
57	ZN	29	501	1/1	0.99	0.02	52,52,52,52	0
57	ZN	2n	501	1/1	0.99	0.03	64,64,64,64	0
56	MG	1a	1712	1/1	0.99	0.04	39,39,39,39	0
56	MG	2A	3732	1/1	0.99	0.07	62,62,62,62	0
56	MG	1A	8956	1/1	0.99	0.16	11,11,11,11	0
56	MG	1A	8810	1/1	0.99	0.04	8,8,8,8	0
56	MG	2A	3366	1/1	1.00	0.04	29,29,29,29	0
56	MG	2A	3708	1/1	1.00	0.02	30,30,30,30	0
57	ZN	19	102	1/1	1.00	0.02	27,27,27,27	0
56	MG	1D	308	1/1	1.00	0.02	8,8,8,8	0
56	MG	1A	8710	1/1	1.00	0.03	16,16,16,16	0
56	MG	1A	8462	1/1	1.00	0.02	8,8,8,8	0
56	MG	1A	8404	1/1	1.00	0.03	8,8,8,8	0
56	MG	1A	8352	1/1	1.00	0.02	21,21,21,21	0
56	MG	1A	8477	1/1	1.00	0.05	14,14,14,14	0
56	MG	1A	8823	1/1	1.00	0.02	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	8574	1/1	1.00	0.03	15,15,15,15	0
56	MG	1A	8895	1/1	1.00	0.02	12,12,12,12	0
56	MG	2A	3396	1/1	1.00	0.02	25,25,25,25	0
56	MG	2A	3694	1/1	1.00	0.03	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.