Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 05:49 AM EDT

PDB ID	:	4Y4O / pdb_00004y4o
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome with rRNA modifications and bound to protein Y (YfiA) at 2.3A resolution
Authors	:	Polikanov, Y.S.; Melnikov, S.V.; Soll, D.; Steitz, T.A.
Deposited on	:	2015-02-10
Resolution	:	2.30 Å(reported)

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

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

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

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

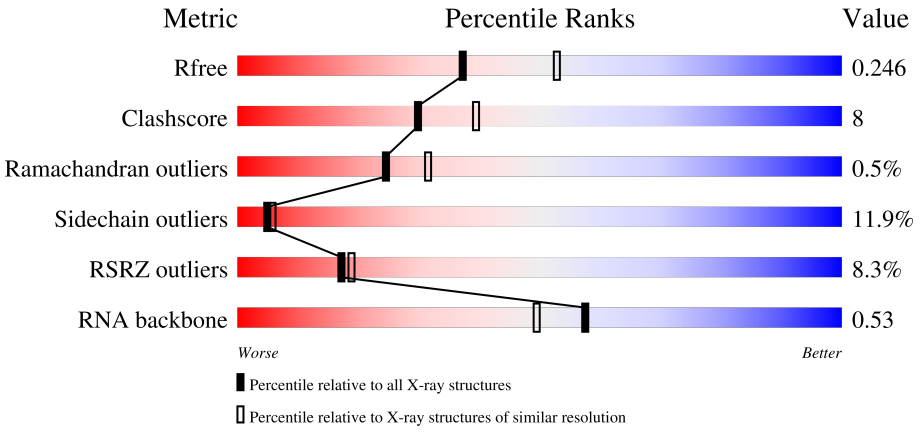
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)
RNA backbone	3983	1090 (2.60-2.00)

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

Mol	Chain	Length	Quality of chain
1	1A	2915	4% 69% 24% 6%
1	2A	2915	3% 60% 31% 8%
2	1B	121	% 72% 22% 5%
2	2B	121	% 60% 33% 7%

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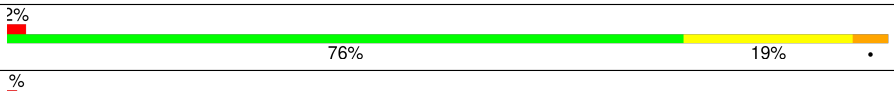
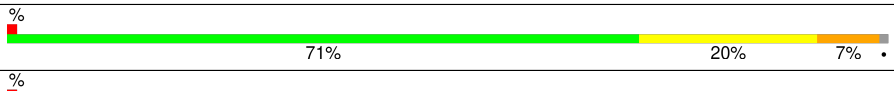
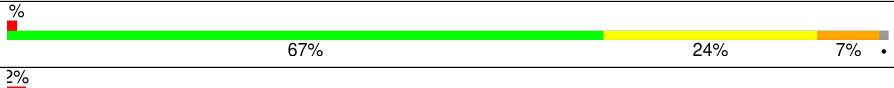
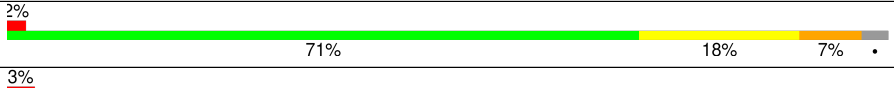
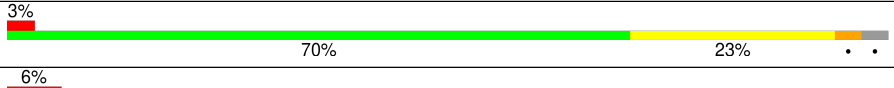
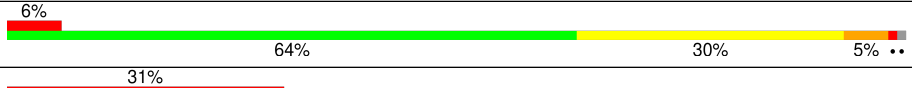
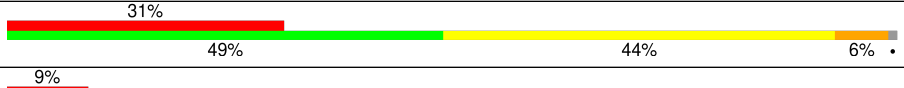
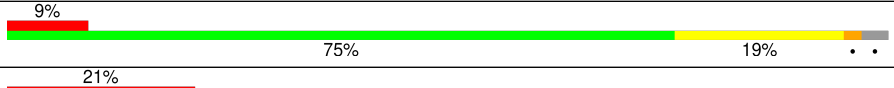
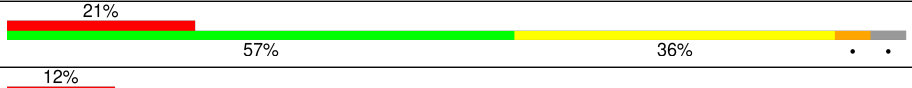
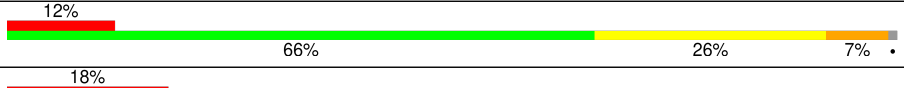
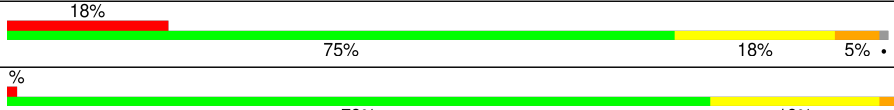
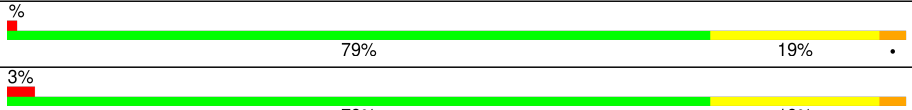
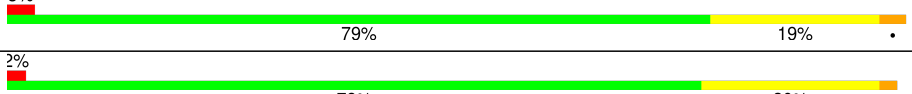
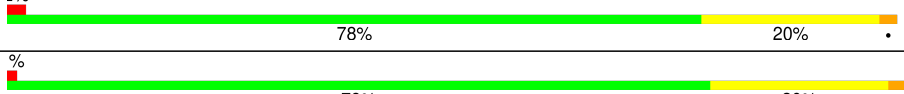
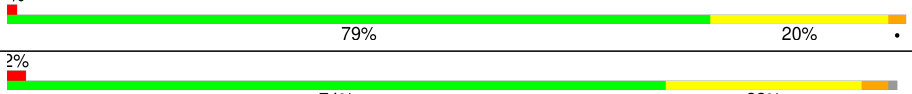
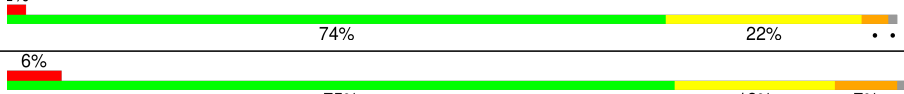
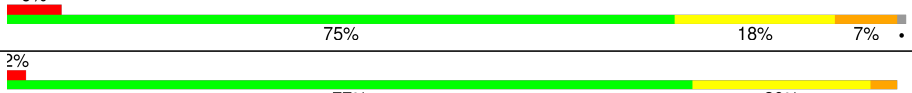
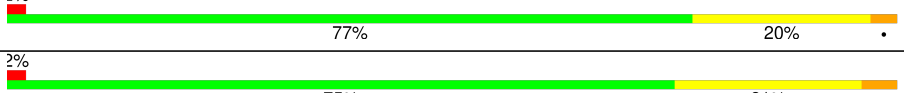
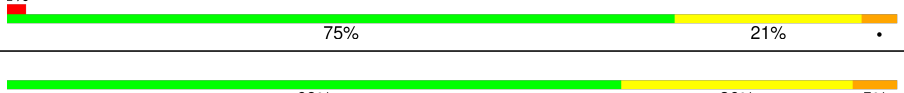
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
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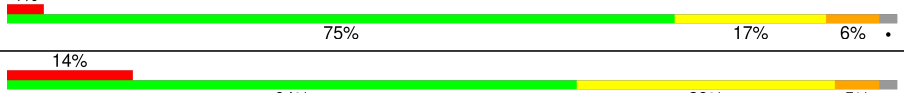
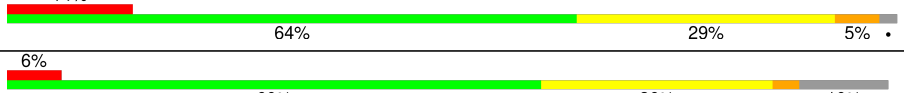
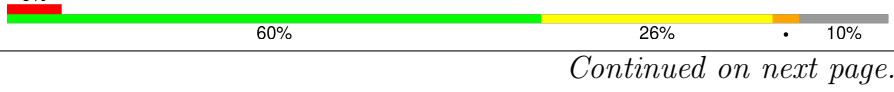
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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Mol	Chain	Length	Quality of chain
15	2T	146	3% 67% 19% 10%
16	1U	118	2% 72% 22%
16	2U	118	% 75% 19%
17	1V	101	2% 76% 19% 5%
17	2V	101	% 67% 21% 12%
18	1W	113	2% 77% 17% 5%
18	2W	113	3% 78% 18%
19	1X	96	7% 74% 22%
19	2X	96	5% 72% 24%
20	1Y	110	5% 75% 18%
20	2Y	110	13% 68% 26%
21	1Z	206	7% 74% 19% 5%
21	2Z	206	9% 67% 27%
22	10	85	2% 78% 9% 9%
22	20	85	4% 72% 15% 9%
23	11	98	% 76% 19%
23	21	98	3% 67% 26% 6%
24	12	72	7% 82% 15%
24	22	72	3% 69% 26%
25	13	60	5% 77% 18%
25	23	60	8% 78% 17%
26	14	71	18% 46% 38% 10%
26	24	71	52% 39% 46% 8%
27	15	60	2% 77% 18%
27	25	60	2% 80% 17%

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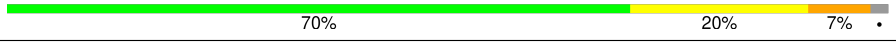
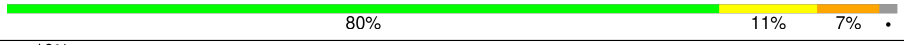
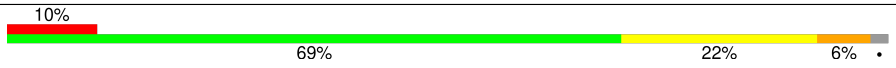
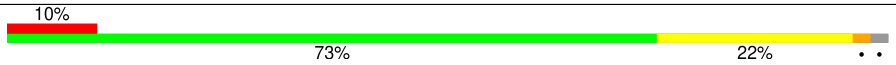
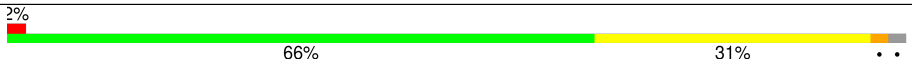
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
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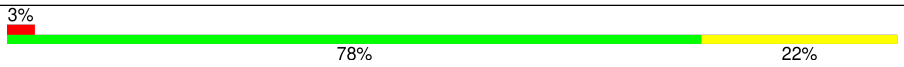
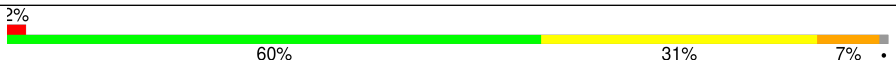
31	19	37	
31	29	37	
32	1a	1521	
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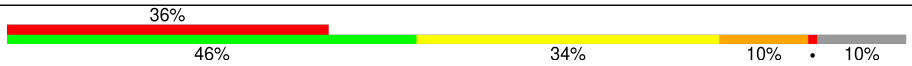
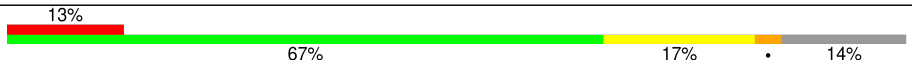
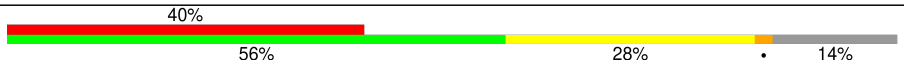
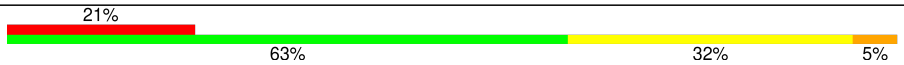
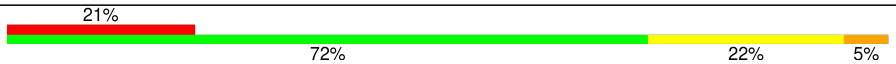
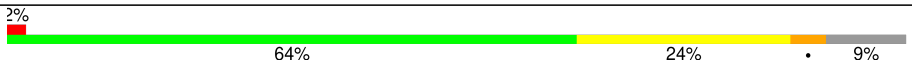
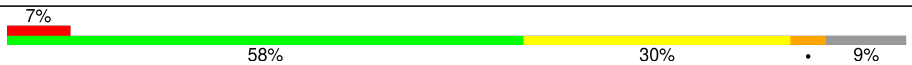
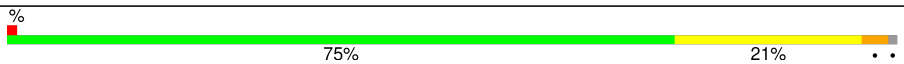
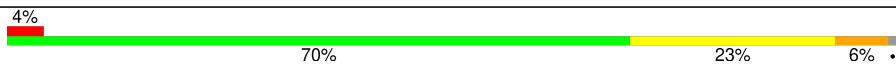
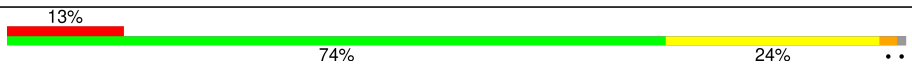
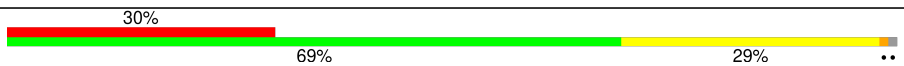
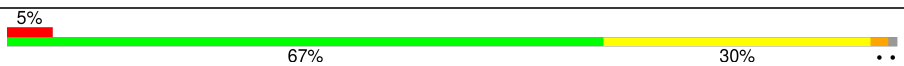
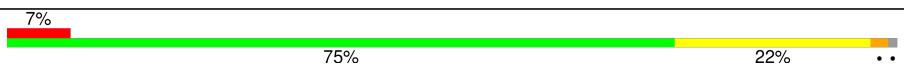
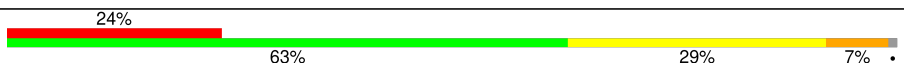
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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Mol	Chain	Length	Quality of chain
40	2i	128	57% 49% 45% 5%
41	1j	105	31% 56% 32% 8%
41	2j	105	55% 46% 37% 9% 9%
42	1k	129	9% 64% 22% 12%
42	2k	129	13% 68% 17% 12%
43	1l	132	8% 73% 17% 8%
43	2l	132	8% 70% 20% 8%
44	1m	126	8% 59% 28% 6% 8%
44	2m	126	40% 52% 35% 10%
45	1n	61	15% 66% 31%
45	2n	61	54% 57% 38%
46	1o	89	7% 63% 33%
46	2o	89	10% 75% 19%
47	1p	88	28% 65% 24% 5% 7%
47	2p	88	16% 60% 27% 6% 7%
48	1q	105	8% 71% 20% 6%
48	2q	105	4% 76% 15% 6%
49	1r	88	10% 50% 24% 23%
49	2r	88	7% 50% 24% 23%
50	1s	93	14% 57% 28% 11%
50	2s	93	60% 54% 31% 11%
51	1t	106	20% 57% 27% 6% 9%
51	2t	106	9% 60% 27% 8%
52	1u	27	22% 67% 19% 15%
52	2u	27	52% 41% 41% 15%

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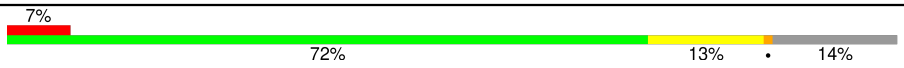
Mol	Chain	Length	Quality of chain
53	1y	113	
53	2y	113	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	MG	1A	3612	-	-	-	X
55	MPD	1a	1880	-	-	X	-

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 298502 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2872	Total	C	N	O	P	0	0	0
			61869	27540	11574	19884	2871			
1	2A	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			
21	2Z	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	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 protein called Ribosome-associated inhibitor A.

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

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1A	1075	Total 1075	Mg 1075	0	0
54	1B	30	Total 30	Mg 30	0	0
54	1D	14	Total 14	Mg 14	0	0
54	1E	6	Total 6	Mg 6	0	0
54	1F	10	Total 10	Mg 10	0	0
54	1G	4	Total 4	Mg 4	0	0
54	1H	2	Total 2	Mg 2	0	0
54	1N	3	Total 3	Mg 3	0	0
54	1O	1	Total 1	Mg 1	0	0
54	1P	2	Total 2	Mg 2	0	0
54	1Q	4	Total 4	Mg 4	0	0
54	1R	3	Total 3	Mg 3	0	0
54	1T	3	Total 3	Mg 3	0	0
54	1U	2	Total 2	Mg 2	0	0
54	1V	3	Total 3	Mg 3	0	0
54	1W	2	Total 2	Mg 2	0	0
54	1X	1	Total 1	Mg 1	0	0
54	1Z	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	10	5	Total Mg 5 5	0	0
54	11	4	Total Mg 4 4	0	0
54	13	2	Total Mg 2 2	0	0
54	14	1	Total Mg 1 1	0	0
54	15	2	Total Mg 2 2	0	0
54	17	2	Total Mg 2 2	0	0
54	18	1	Total Mg 1 1	0	0
54	19	2	Total Mg 2 2	0	0
54	1a	280	Total Mg 280 280	0	0
54	1b	1	Total Mg 1 1	0	0
54	1d	5	Total Mg 5 5	0	0
54	1e	4	Total Mg 4 4	0	0
54	1f	1	Total Mg 1 1	0	0
54	1g	3	Total Mg 3 3	0	0
54	1h	2	Total Mg 2 2	0	0
54	1i	1	Total Mg 1 1	0	0
54	1l	2	Total Mg 2 2	0	0
54	1n	2	Total Mg 2 2	0	0
54	1o	1	Total Mg 1 1	0	0
54	1q	2	Total Mg 2 2	0	0
54	1r	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	1t	1	Total Mg 1 1	0	0
54	1y	4	Total Mg 4 4	0	0
54	2A	761	Total Mg 761 761	0	0
54	2B	19	Total Mg 19 19	0	0
54	2D	9	Total Mg 9 9	0	0
54	2E	5	Total Mg 5 5	0	0
54	2F	3	Total Mg 3 3	0	0
54	2G	3	Total Mg 3 3	0	0
54	2I	1	Total Mg 1 1	0	0
54	2N	1	Total Mg 1 1	0	0
54	2O	2	Total Mg 2 2	0	0
54	2P	2	Total Mg 2 2	0	0
54	2Q	2	Total Mg 2 2	0	0
54	2R	1	Total Mg 1 1	0	0
54	2T	3	Total Mg 3 3	0	0
54	2V	1	Total Mg 1 1	0	0
54	2W	2	Total Mg 2 2	0	0
54	2X	1	Total Mg 1 1	0	0
54	20	2	Total Mg 2 2	0	0
54	21	1	Total Mg 1 1	0	0
54	26	1	Total Mg 1 1	0	0

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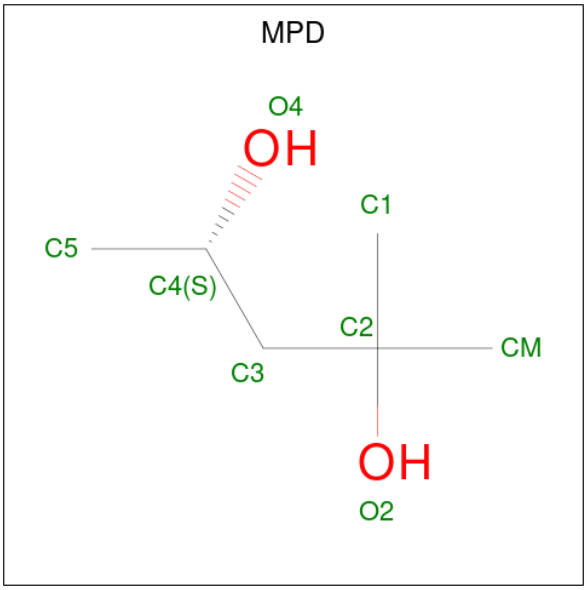
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	27	1	Total Mg 1 1	0	0
54	28	2	Total Mg 2 2	0	0
54	2a	193	Total Mg 193 193	0	0
54	2e	1	Total Mg 1 1	0	0
54	2f	1	Total Mg 1 1	0	0
54	2j	1	Total Mg 1 1	0	0
54	2l	1	Total Mg 1 1	0	0
54	2r	1	Total Mg 1 1	0	0
54	2t	1	Total Mg 1 1	0	0

- Molecule 55 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
55	1A	1	Total C O 8 6 2	0	0
55	1T	1	Total C O 8 6 2	0	0

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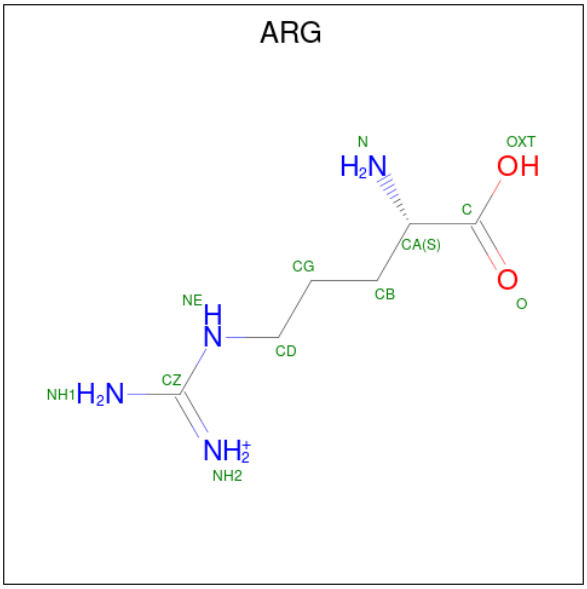
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
55	18	1	Total C O 8 6 2	0	0
55	1a	1	Total C O 8 6 2	0	0
55	2A	1	Total C O 8 6 2	0	0
55	2A	1	Total C O 8 6 2	0	0
55	2B	1	Total C O 8 6 2	0	0

- Molecule 56 is ARGININE (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1B	1	Total C N O 12 6 4 2	0	0
56	1F	1	Total C N O 12 6 4 2	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1Y	1	Total Zn 1 1	0	0
57	14	1	Total Zn 1 1	0	0

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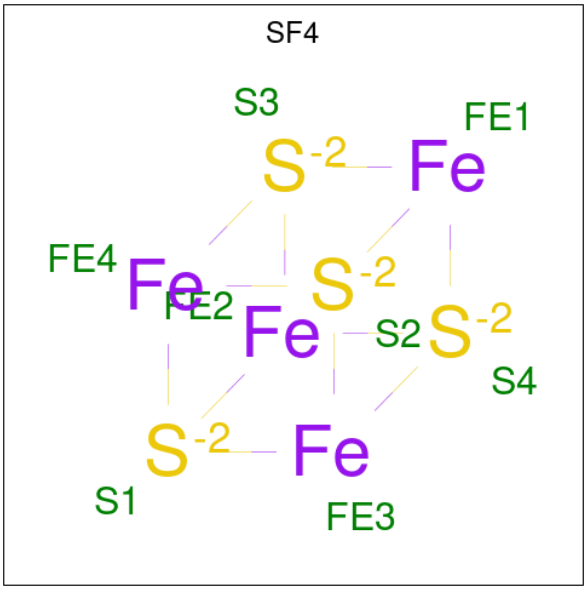
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	15	1	Total Zn 1 1	0	0
57	16	1	Total Zn 1 1	0	0
57	19	1	Total Zn 1 1	0	0
57	1n	1	Total Zn 1 1	0	0
57	2Y	1	Total Zn 1 1	0	0
57	24	1	Total Zn 1 1	0	0
57	25	1	Total Zn 1 1	0	0
57	26	1	Total Zn 1 1	0	0
57	29	1	Total Zn 1 1	0	0
57	2n	1	Total Zn 1 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

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

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1A	4154	Total	O	0	0
			4154	4154		
59	1B	109	Total	O	0	0
			109	109		
59	1D	119	Total	O	0	0
			119	119		
59	1E	81	Total	O	0	0
			81	81		
59	1F	66	Total	O	0	0
			66	66		
59	1G	20	Total	O	0	0
			20	20		
59	1H	16	Total	O	0	0
			16	16		
59	1I	9	Total	O	0	0
			9	9		
59	1N	55	Total	O	0	0
			55	55		
59	1O	29	Total	O	0	0
			29	29		
59	1P	56	Total	O	0	0
			56	56		
59	1Q	46	Total	O	0	0
			46	46		
59	1R	37	Total	O	0	0
			37	37		
59	1S	11	Total	O	0	0
			11	11		
59	1T	39	Total	O	0	0
			39	39		
59	1U	49	Total	O	0	0
			49	49		
59	1V	34	Total	O	0	0
			34	34		
59	1W	27	Total	O	0	0
			27	27		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1X	27	Total O 27 27	0	0
59	1Y	20	Total O 20 20	0	0
59	1Z	13	Total O 13 13	0	0
59	10	25	Total O 25 25	0	0
59	11	25	Total O 25 25	0	0
59	12	15	Total O 15 15	0	0
59	13	25	Total O 25 25	0	0
59	14	4	Total O 4 4	0	0
59	15	25	Total O 25 25	0	0
59	16	22	Total O 22 22	0	0
59	17	19	Total O 19 19	0	0
59	18	31	Total O 31 31	0	0
59	19	9	Total O 9 9	0	0
59	1a	599	Total O 599 599	0	0
59	1b	1	Total O 1 1	0	0
59	1c	1	Total O 1 1	0	0
59	1d	8	Total O 8 8	0	0
59	1e	5	Total O 5 5	0	0
59	1f	3	Total O 3 3	0	0
59	1h	1	Total O 1 1	0	0
59	1i	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1j	1	Total O 1 1	0	0
59	1k	1	Total O 1 1	0	0
59	1l	5	Total O 5 5	0	0
59	1m	2	Total O 2 2	0	0
59	1o	7	Total O 7 7	0	0
59	1p	3	Total O 3 3	0	0
59	1t	1	Total O 1 1	0	0
59	1y	7	Total O 7 7	0	0
59	2A	2665	Total O 2665 2665	0	0
59	2B	69	Total O 69 69	0	0
59	2D	59	Total O 59 59	0	0
59	2E	33	Total O 33 33	0	0
59	2F	26	Total O 26 26	0	0
59	2G	9	Total O 9 9	0	0
59	2H	4	Total O 4 4	0	0
59	2I	4	Total O 4 4	0	0
59	2N	6	Total O 6 6	0	0
59	2O	23	Total O 23 23	0	0
59	2P	30	Total O 30 30	0	0
59	2Q	28	Total O 28 28	0	0
59	2R	21	Total O 21 21	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	2S	7	Total O 7 7	0	0
59	2T	11	Total O 11 11	0	0
59	2U	20	Total O 20 20	0	0
59	2V	6	Total O 6 6	0	0
59	2W	20	Total O 20 20	0	0
59	2X	10	Total O 10 10	0	0
59	2Y	4	Total O 4 4	0	0
59	2Z	16	Total O 16 16	0	0
59	20	13	Total O 13 13	0	0
59	21	22	Total O 22 22	0	0
59	22	4	Total O 4 4	0	0
59	23	3	Total O 3 3	0	0
59	24	2	Total O 2 2	0	0
59	25	10	Total O 10 10	0	0
59	26	5	Total O 5 5	0	0
59	27	9	Total O 9 9	0	0
59	28	16	Total O 16 16	0	0
59	29	3	Total O 3 3	0	0
59	2a	459	Total O 459 459	0	0
59	2d	6	Total O 6 6	0	0
59	2e	2	Total O 2 2	0	0

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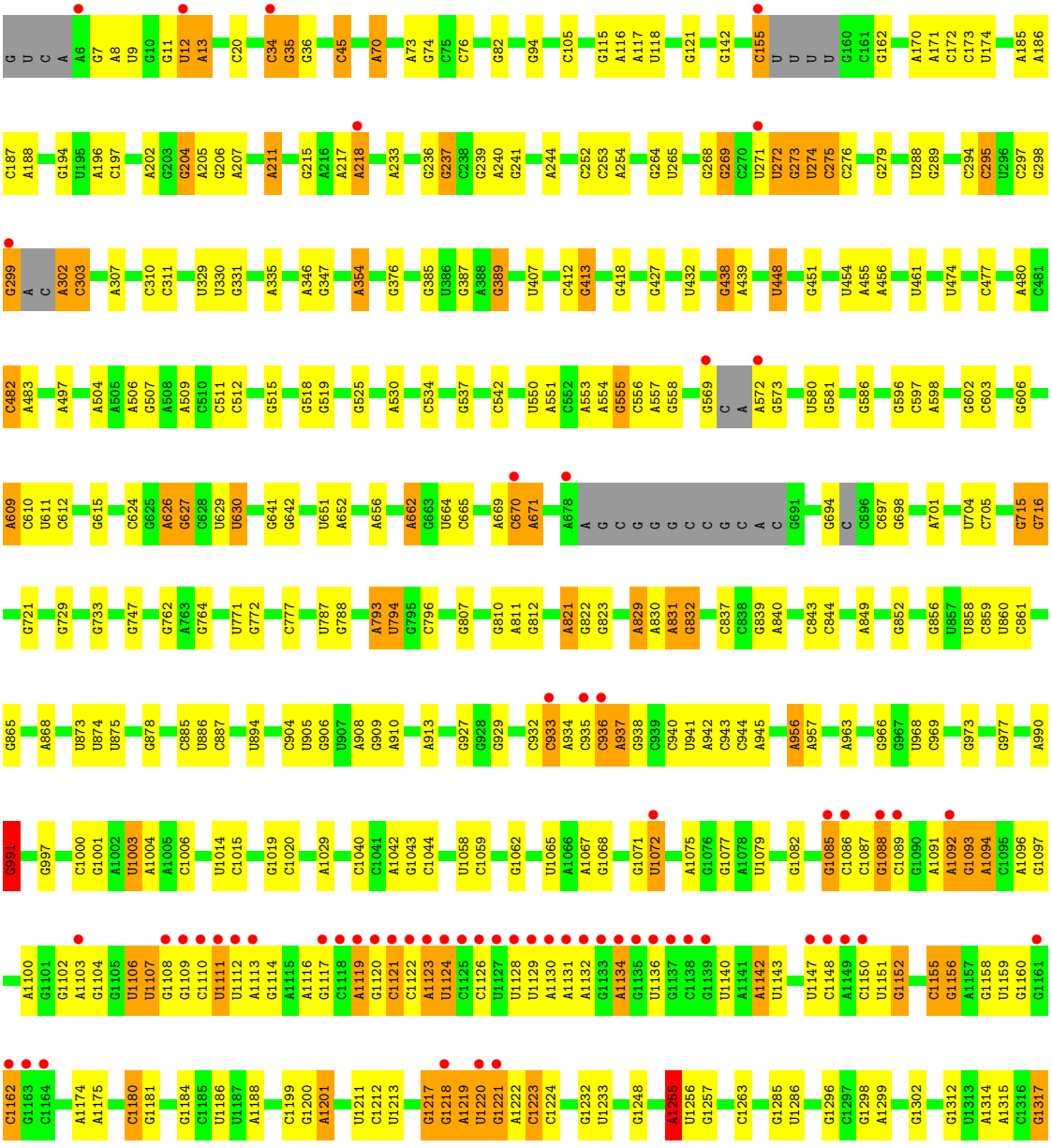
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	2f	1	Total O 1 1	0	0
59	2j	2	Total O 2 2	0	0
59	2l	5	Total O 5 5	0	0
59	2m	2	Total O 2 2	0	0
59	2o	2	Total O 2 2	0	0
59	2p	3	Total O 3 3	0	0
59	2q	1	Total O 1 1	0	0
59	2r	5	Total O 5 5	0	0
59	2t	2	Total O 2 2	0	0
59	2y	5	Total O 5 5	0	0

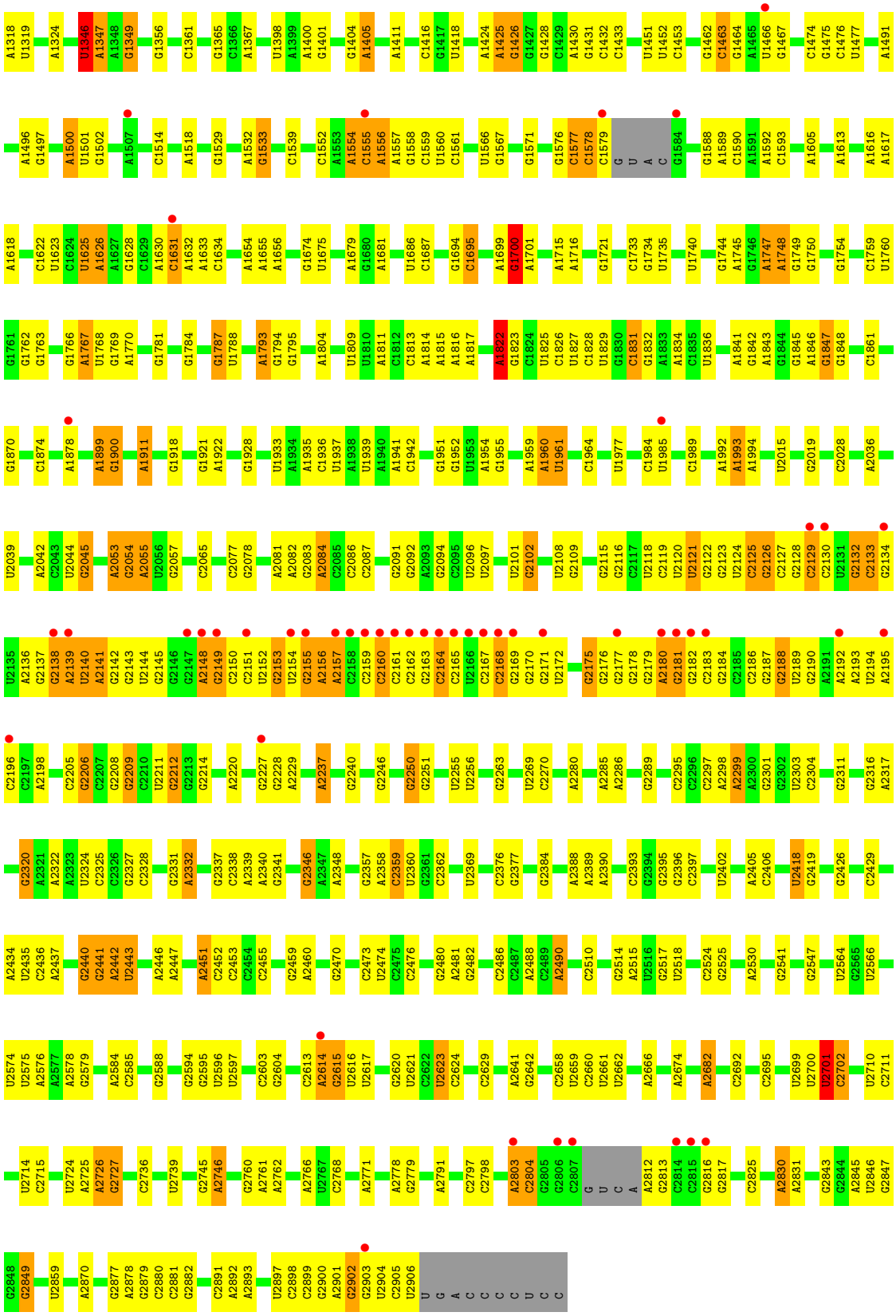
3 Residue-property plots (i)

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

- Molecule 1: 23S Ribosomal RNA

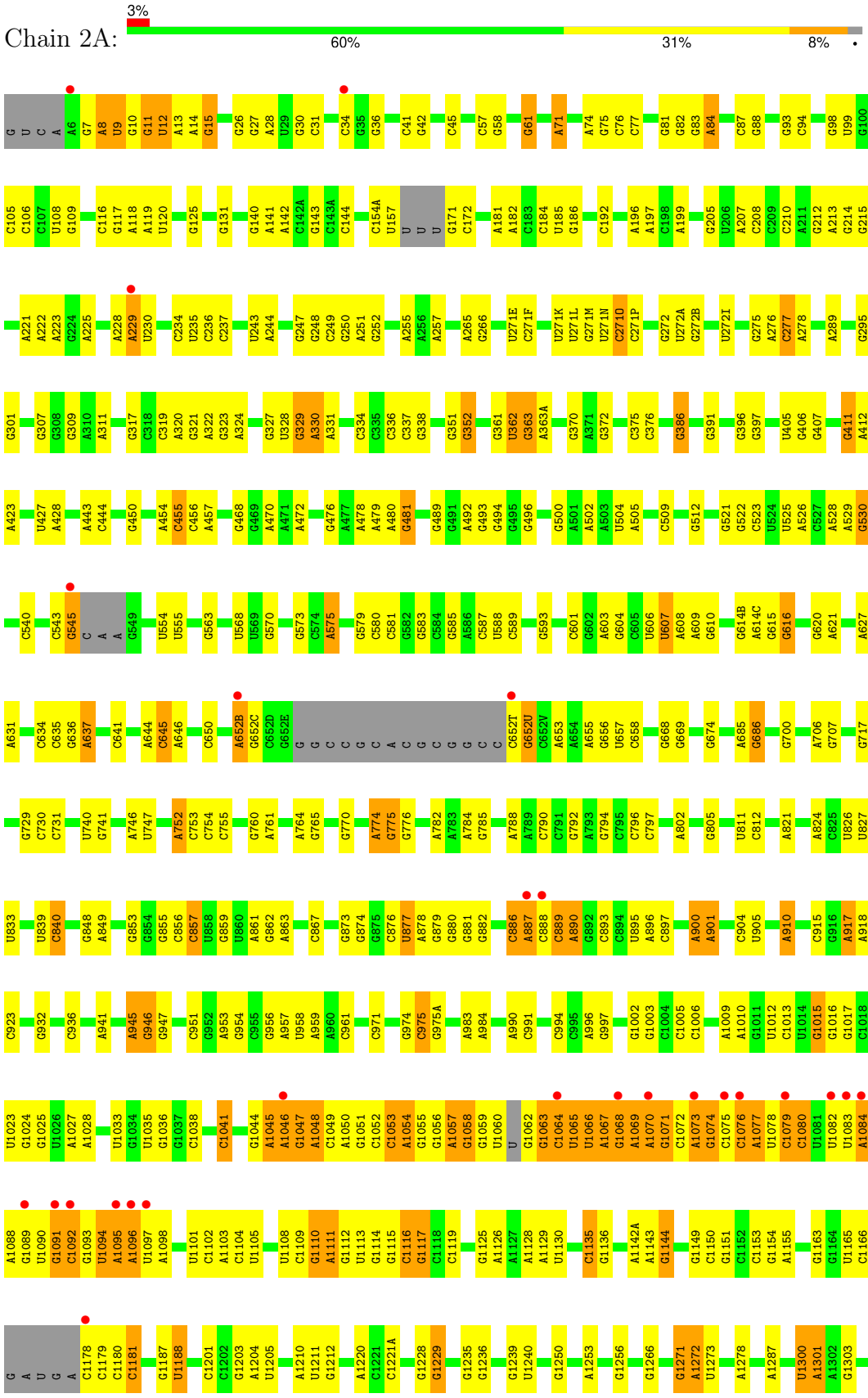
Chain 1A:

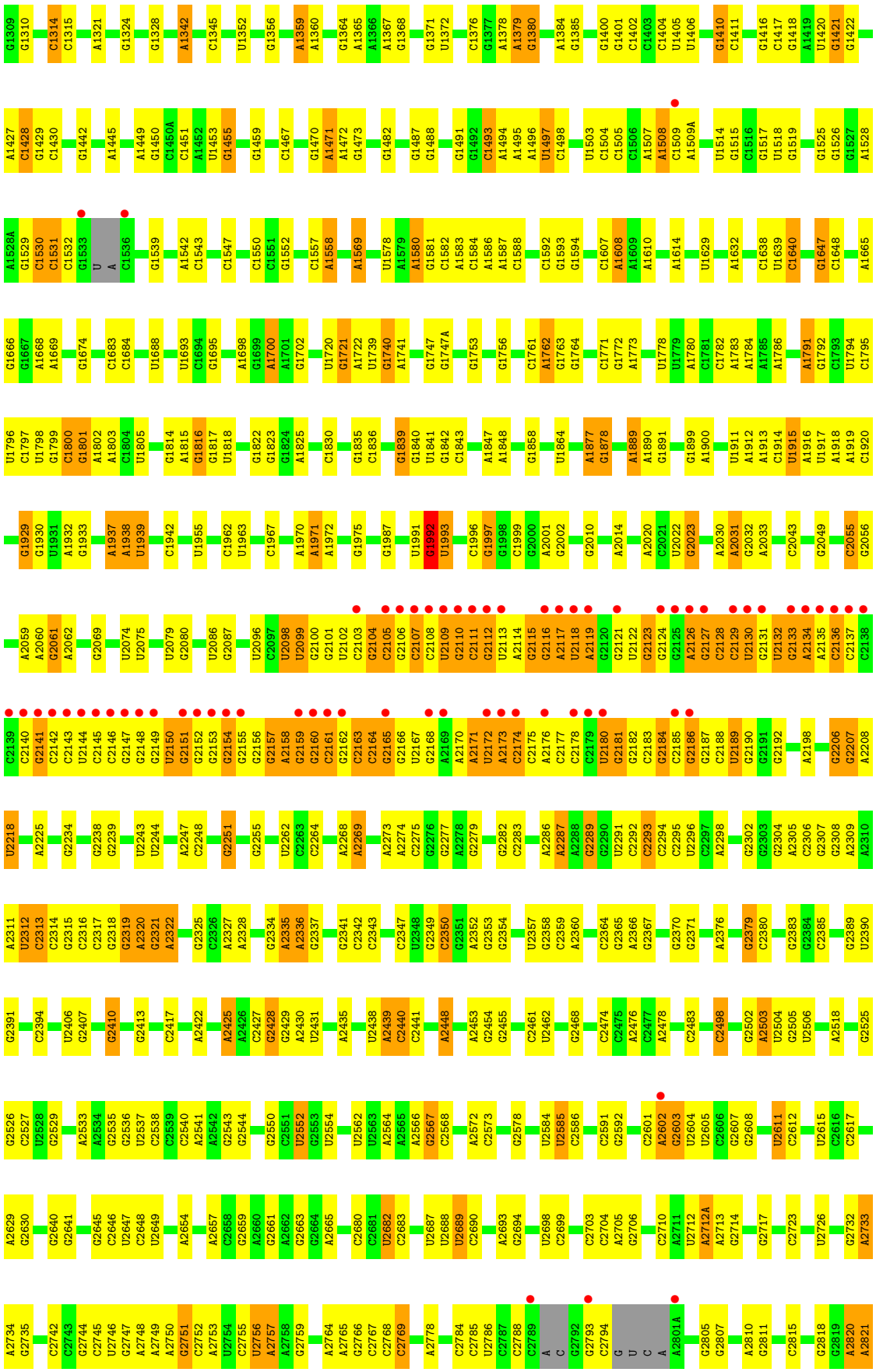


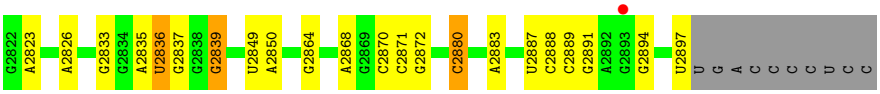


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

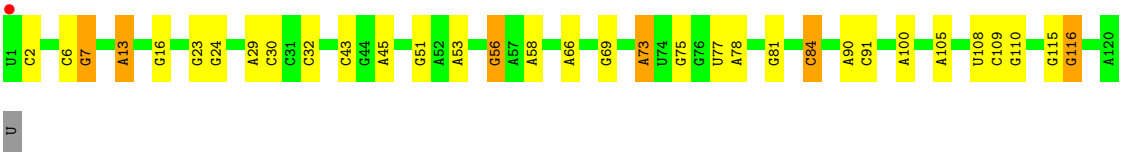






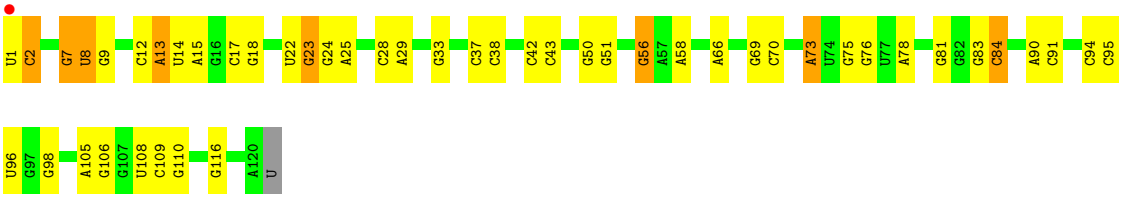
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



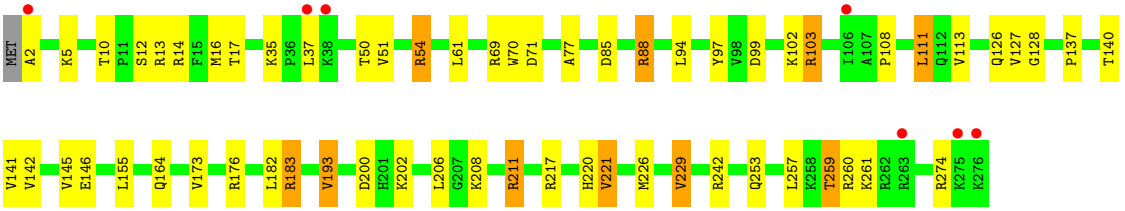
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



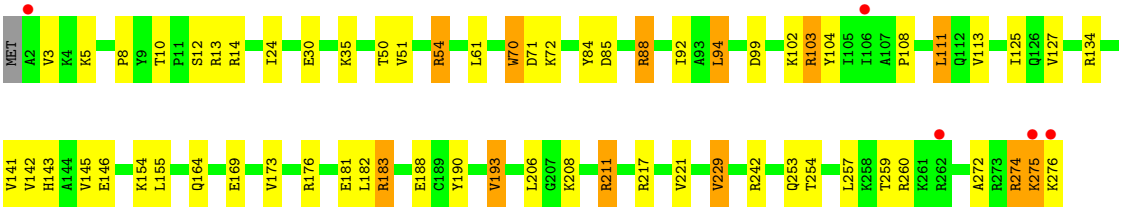
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



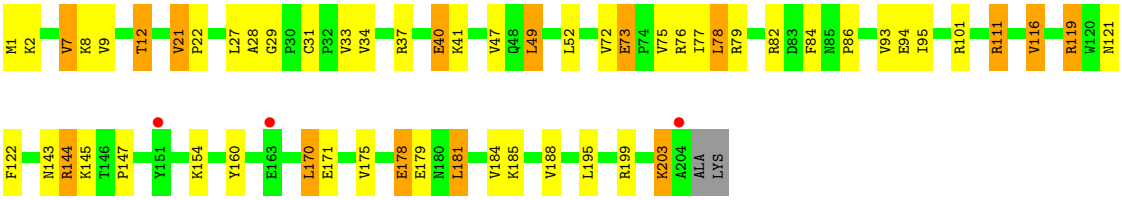
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



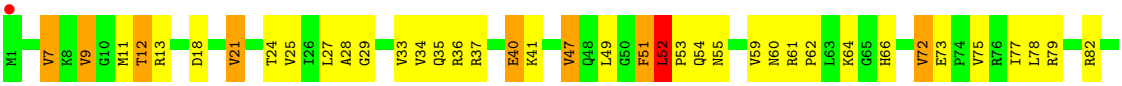
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



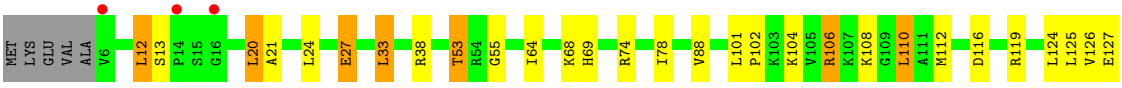
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



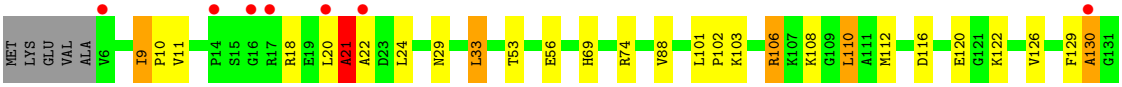
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



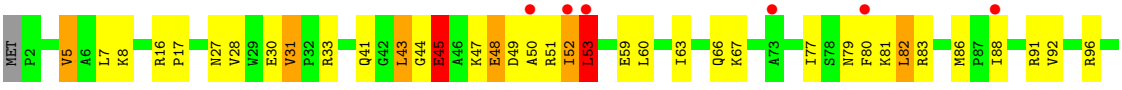
• Molecule 5: 50S ribosomal protein L4

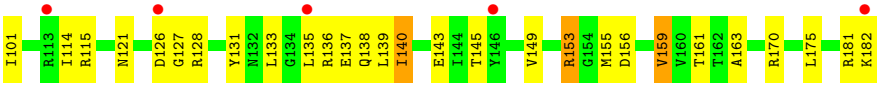
Chain 2F:



• Molecule 6: 50S ribosomal protein L5

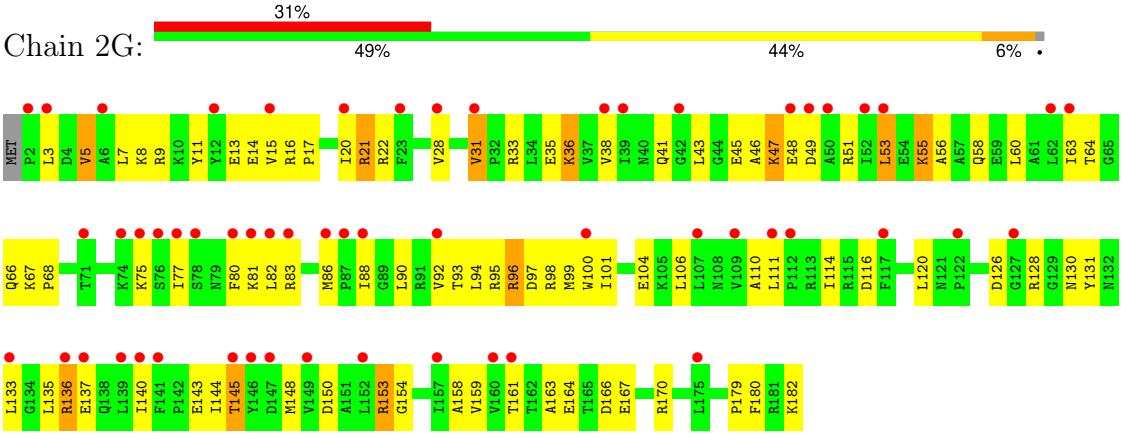
Chain 1G:





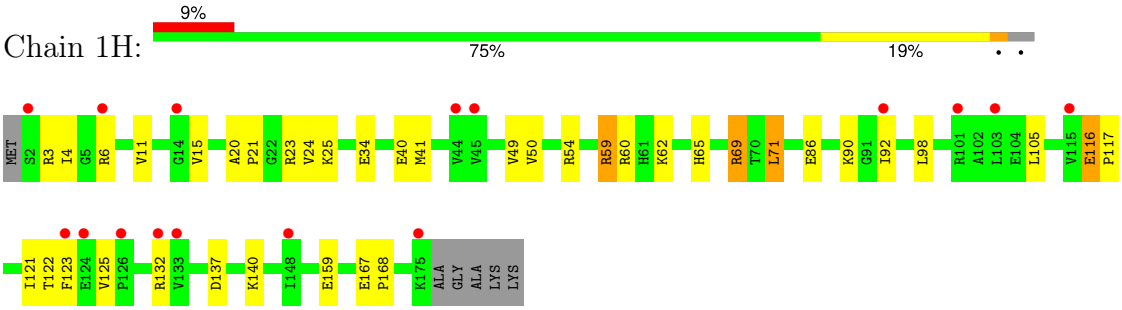
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



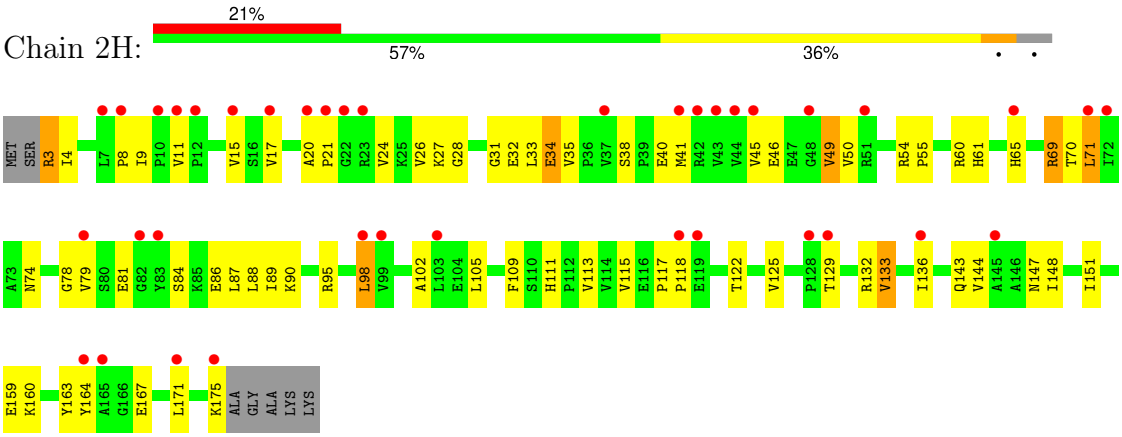
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



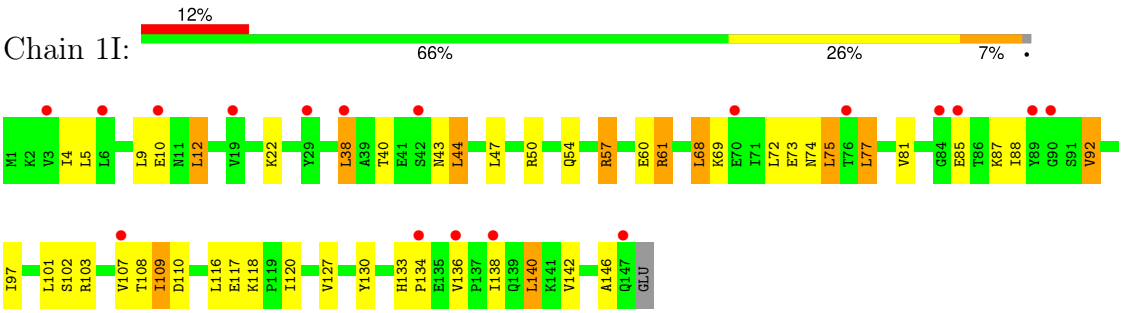
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



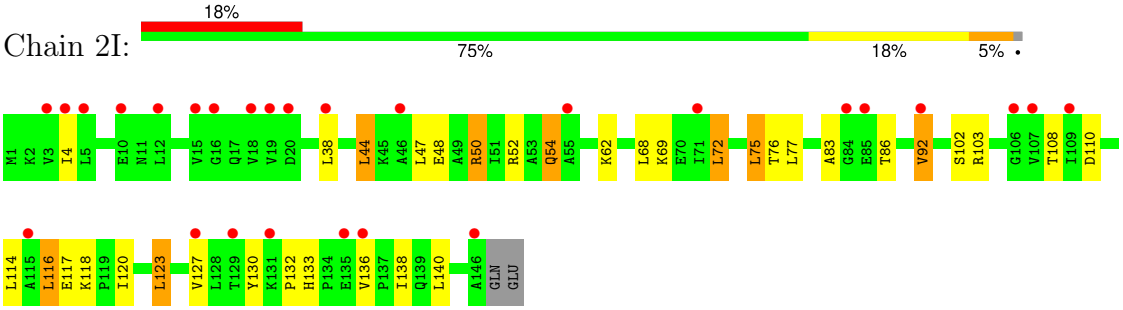
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



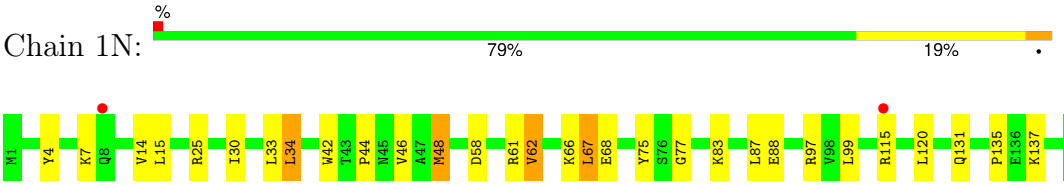
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



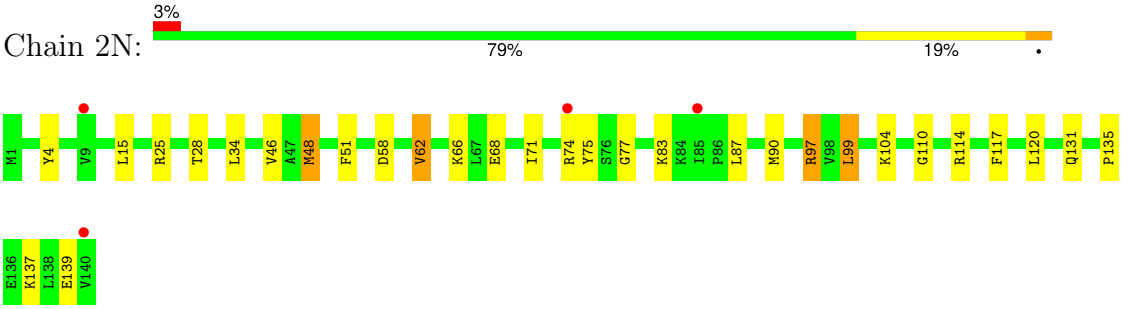
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



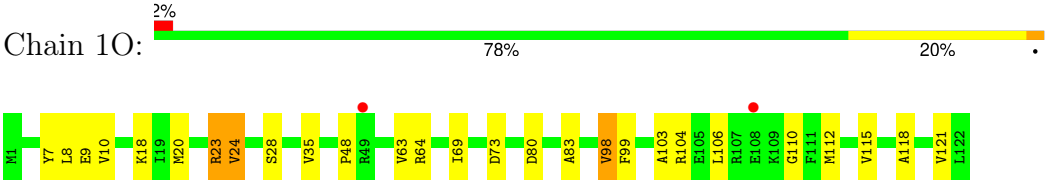
• Molecule 9: 50S ribosomal protein L13

Chain 2N:



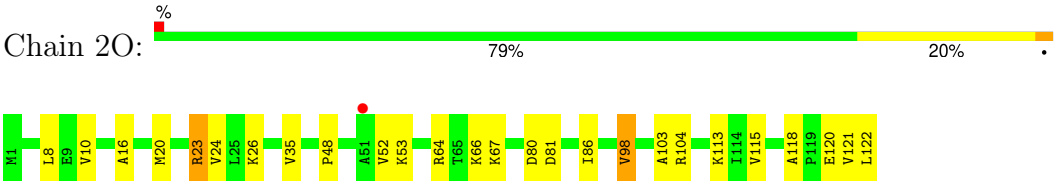
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



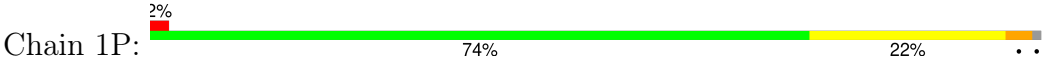
• Molecule 10: 50S ribosomal protein L14

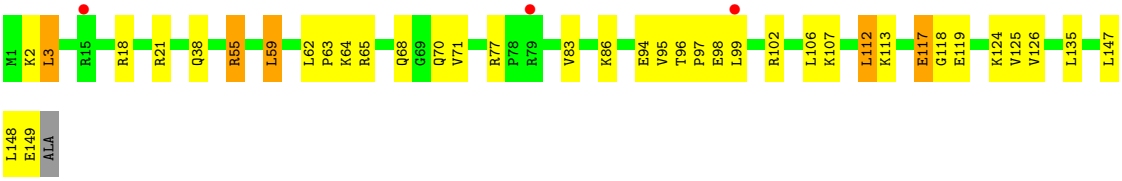
Chain 2O:



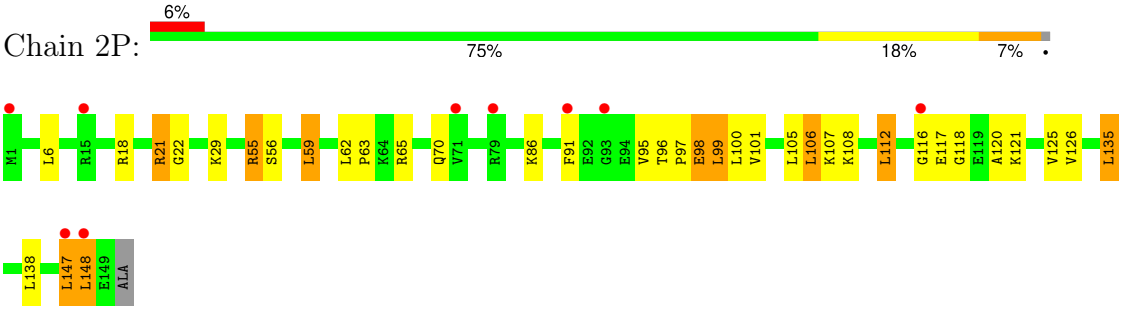
• Molecule 11: 50S ribosomal protein L15

Chain 1P:

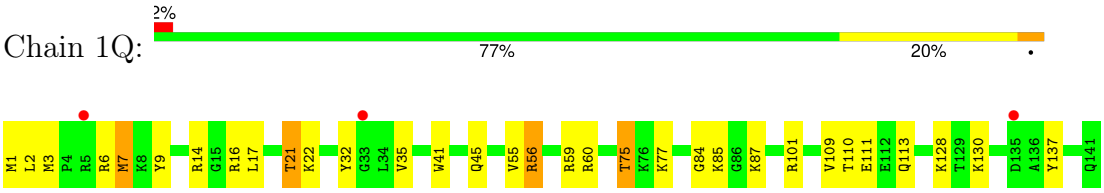




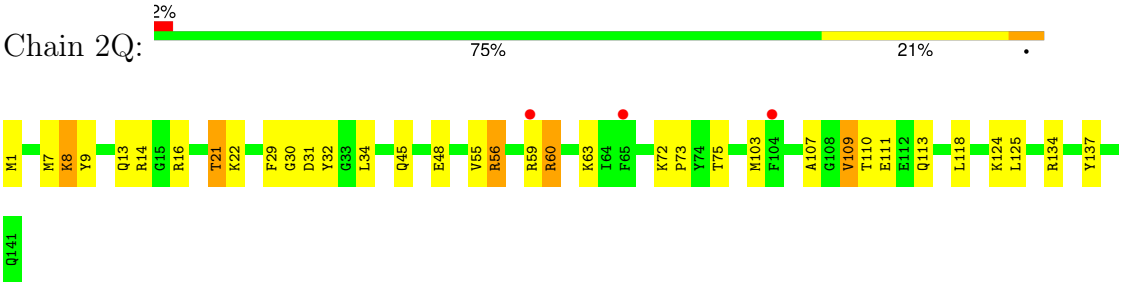
• Molecule 11: 50S ribosomal protein L15



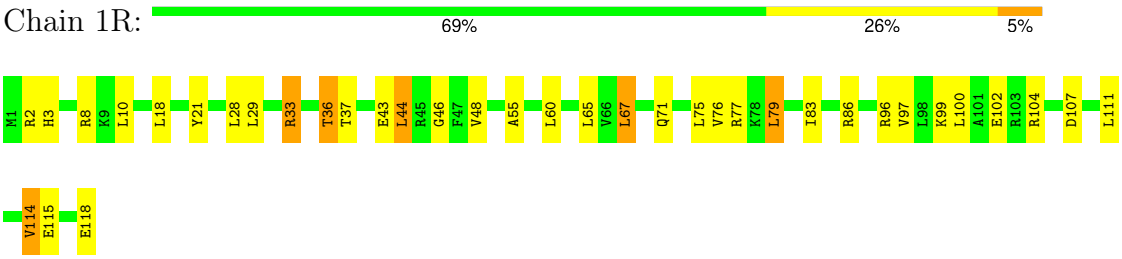
• Molecule 12: 50S ribosomal protein L16



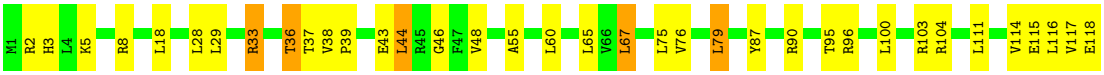
• Molecule 12: 50S ribosomal protein L16



• Molecule 13: 50S ribosomal protein L17

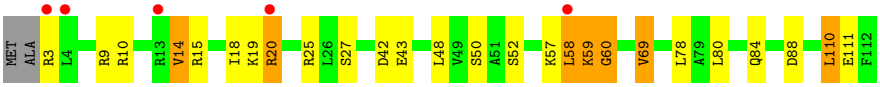


• Molecule 13: 50S ribosomal protein L17



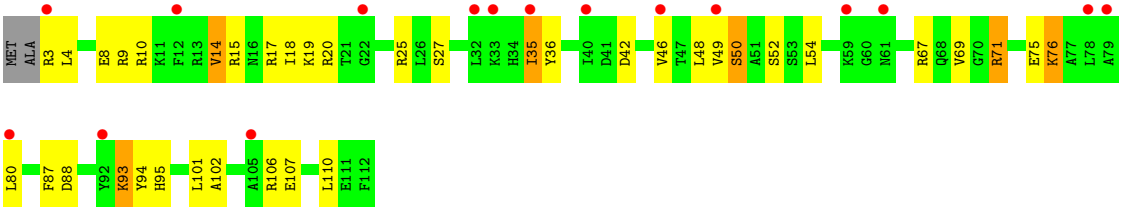
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



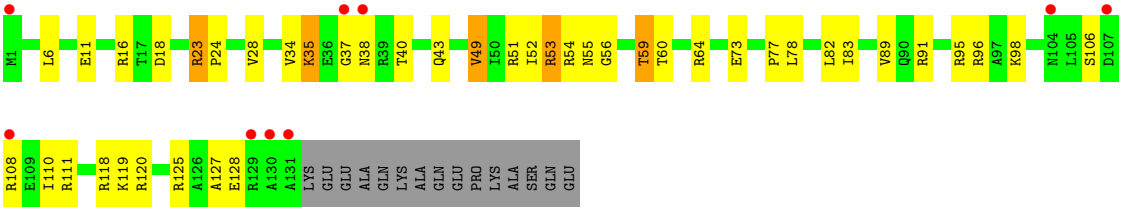
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



• Molecule 15: 50S ribosomal protein L19

Chain 1T:

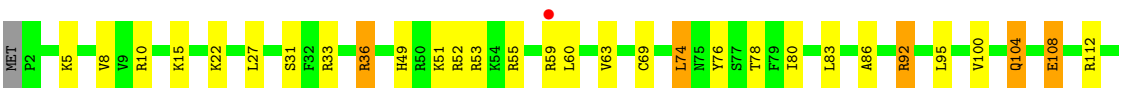


• Molecule 15: 50S ribosomal protein L19

Chain 2T:

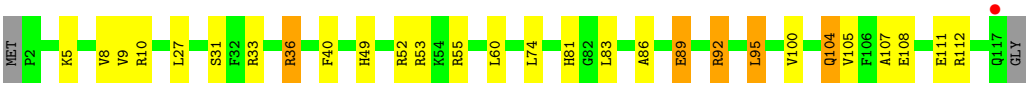
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



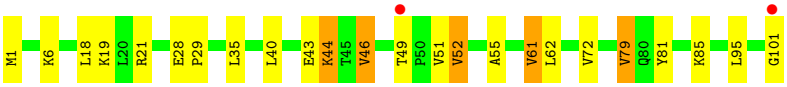
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



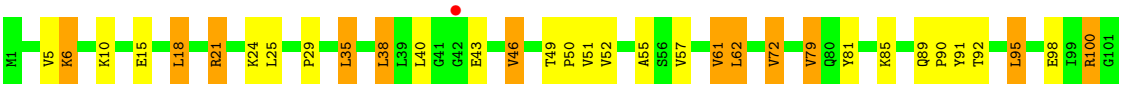
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



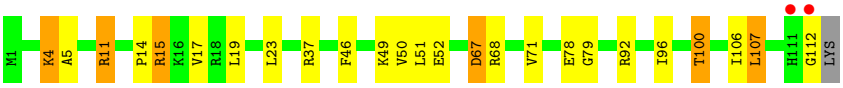
• Molecule 17: 50S ribosomal protein L21

Chain 2V:



• Molecule 18: 50S ribosomal protein L22

Chain 1W:



• Molecule 18: 50S ribosomal protein L22

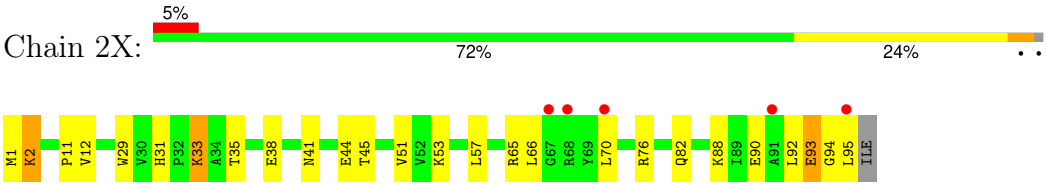
Chain 2W:

• Molecule 19: 50S ribosomal protein L23

Chain 1X:

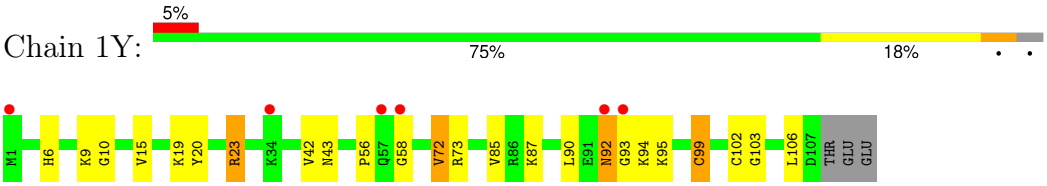
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



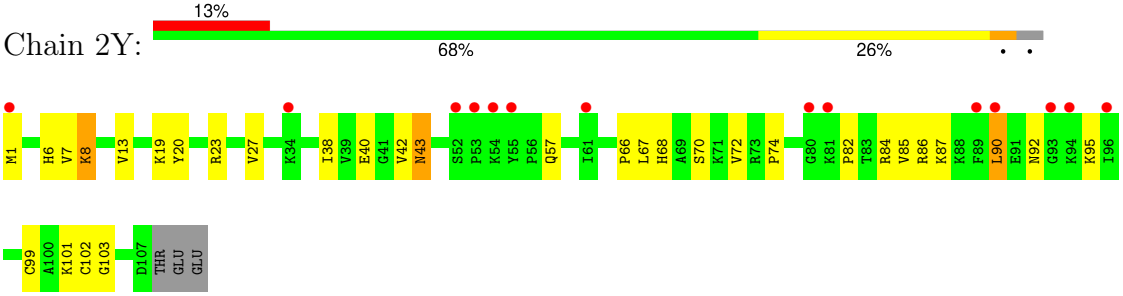
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



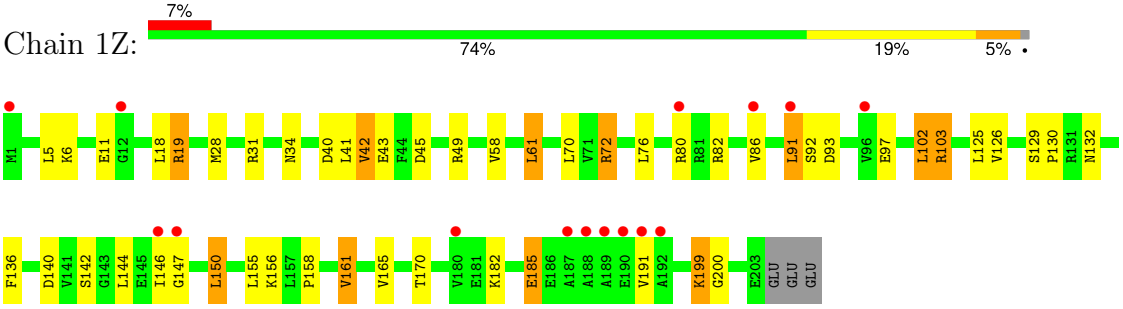
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



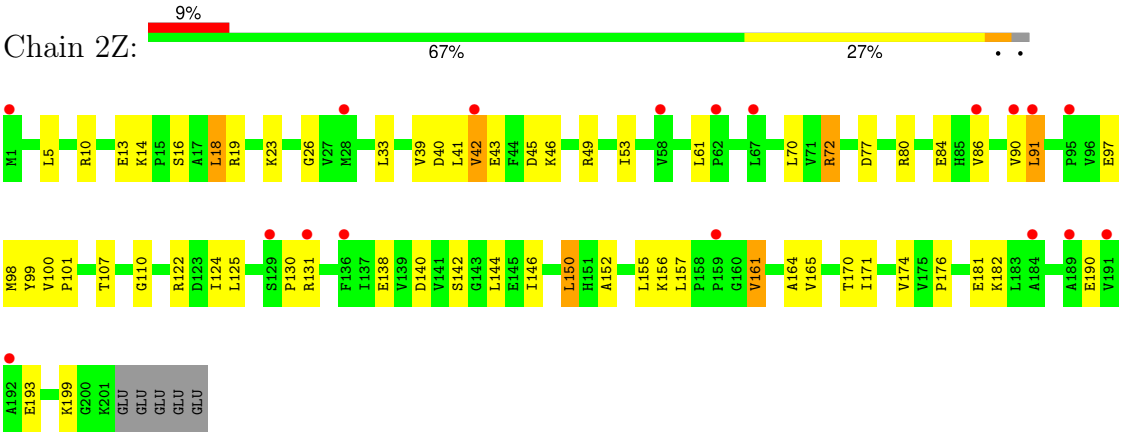
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



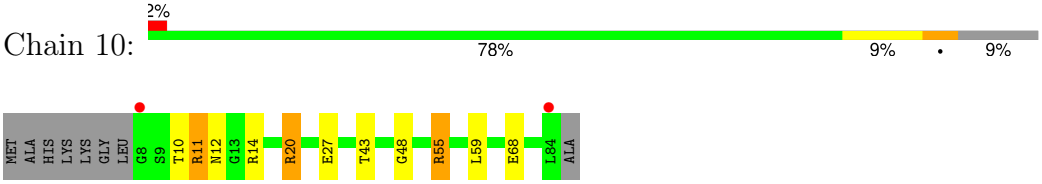
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



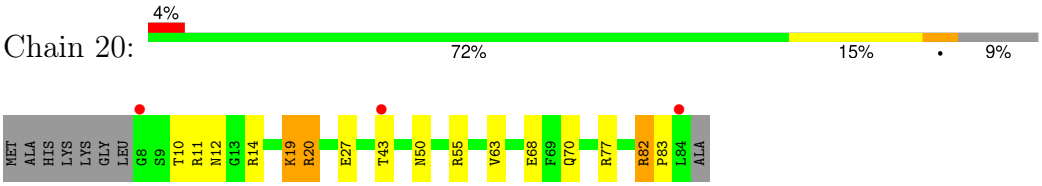
• Molecule 22: 50S ribosomal protein L27

Chain 10:



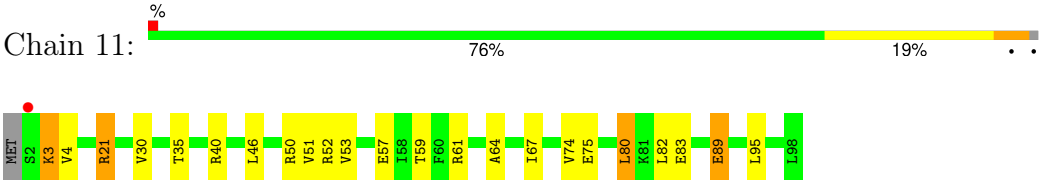
• Molecule 22: 50S ribosomal protein L27

Chain 20:



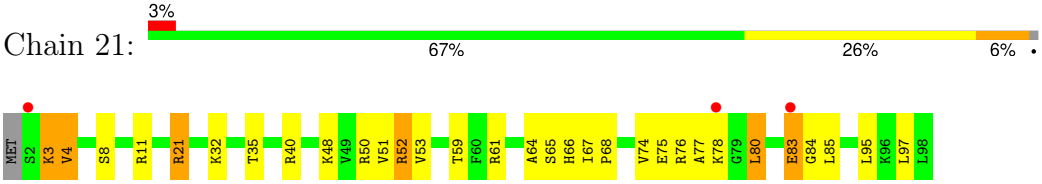
• Molecule 23: 50S ribosomal protein L28

Chain 11:



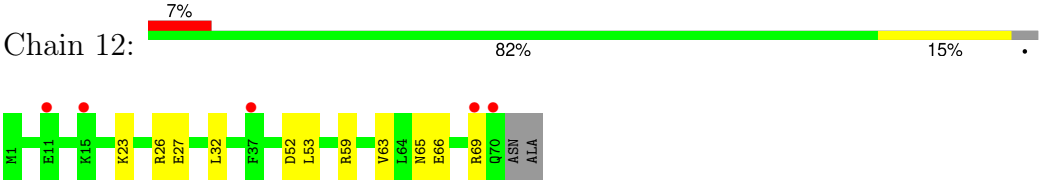
• Molecule 23: 50S ribosomal protein L28

Chain 21:



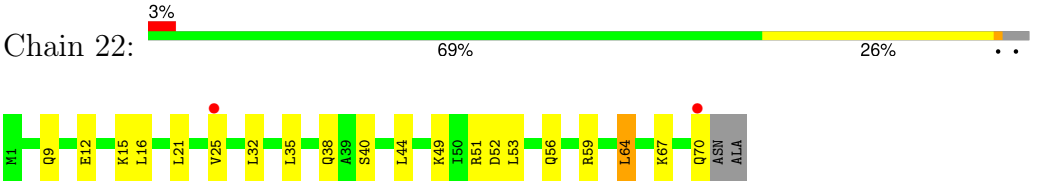
• Molecule 24: 50S ribosomal protein L29

Chain 12:



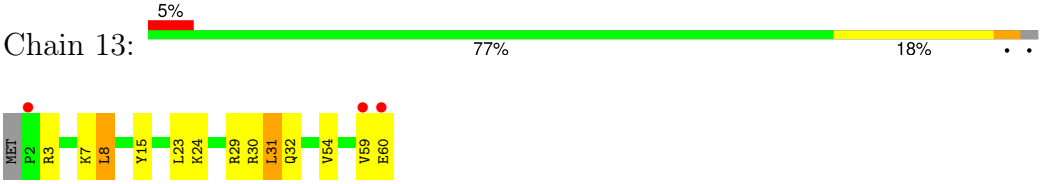
• Molecule 24: 50S ribosomal protein L29

Chain 22:



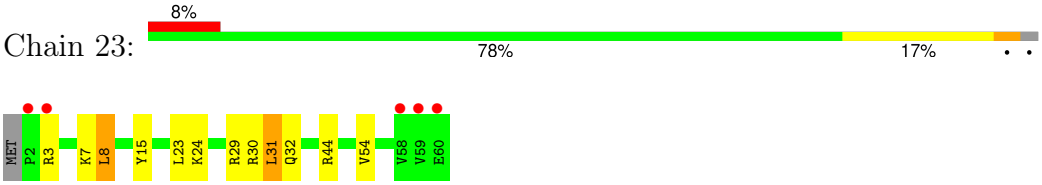
• Molecule 25: 50S ribosomal protein L30

Chain 13:



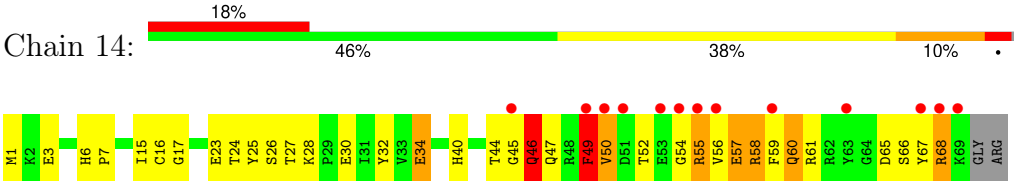
• Molecule 25: 50S ribosomal protein L30

Chain 23:



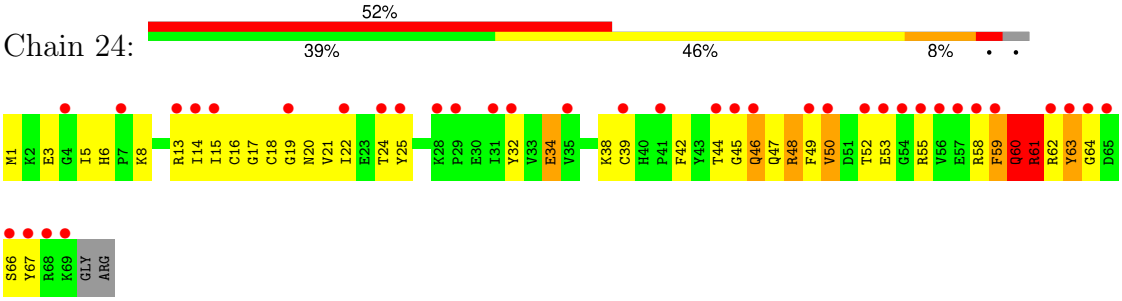
• Molecule 26: 50S ribosomal protein L31

Chain 14:



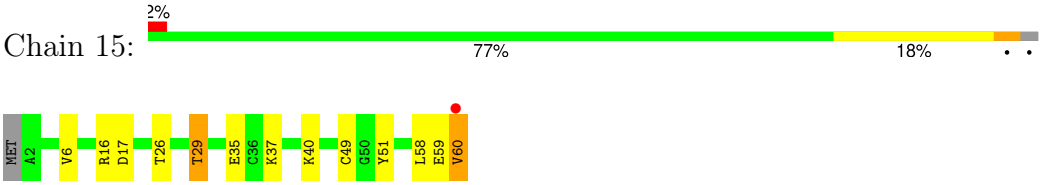
• Molecule 26: 50S ribosomal protein L31

Chain 24:



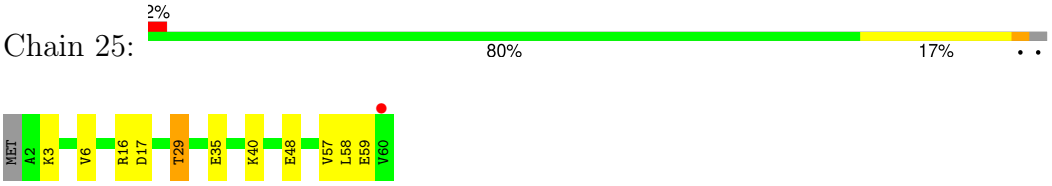
• Molecule 27: 50S ribosomal protein L32

Chain 15:



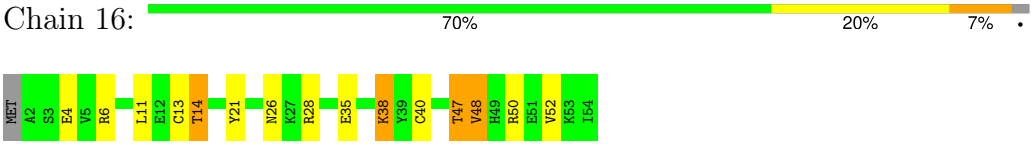
• Molecule 27: 50S ribosomal protein L32

Chain 25:



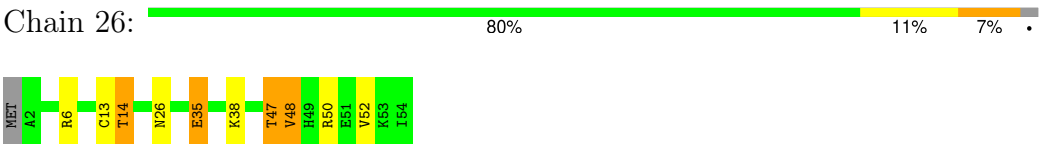
• Molecule 28: 50S ribosomal protein L33

Chain 16:



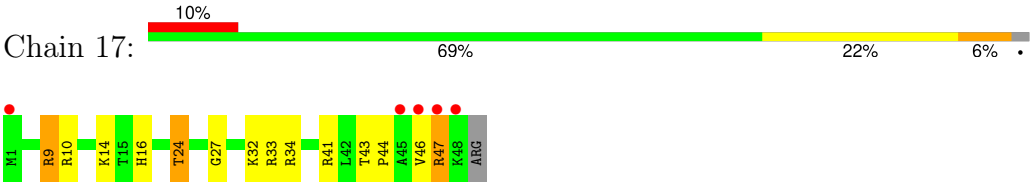
• Molecule 28: 50S ribosomal protein L33

Chain 26:



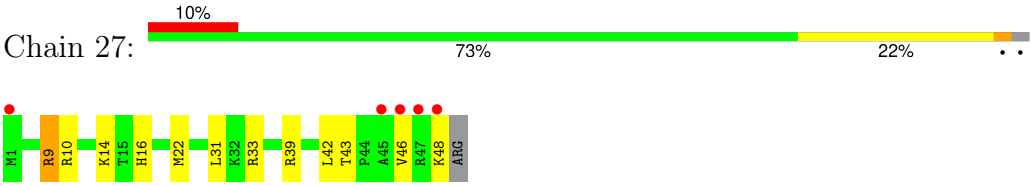
• Molecule 29: 50S ribosomal protein L34

Chain 17:



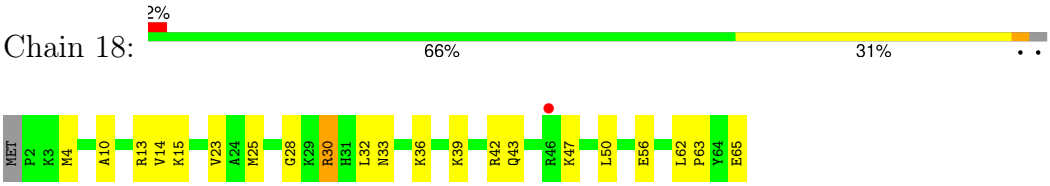
• Molecule 29: 50S ribosomal protein L34

Chain 27:



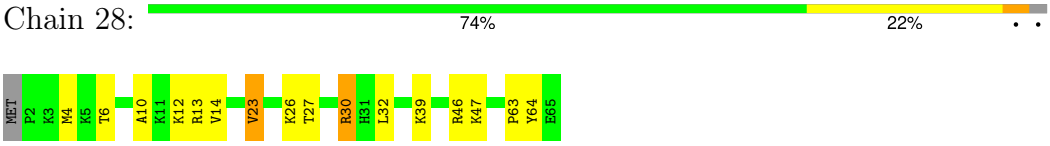
• Molecule 30: 50S ribosomal protein L35

Chain 18:



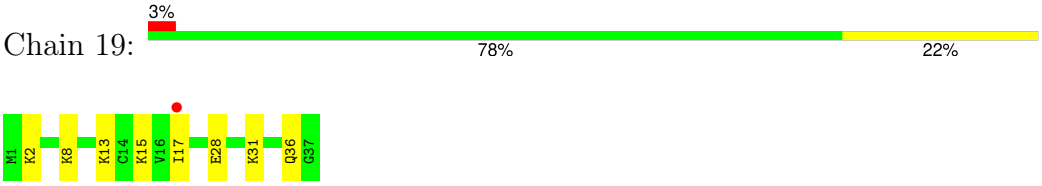
• Molecule 30: 50S ribosomal protein L35

Chain 28:



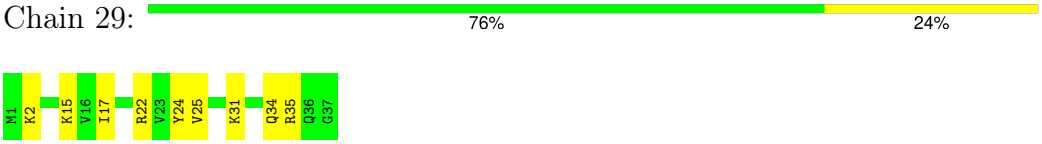
• Molecule 31: 50S ribosomal protein L36

Chain 19:



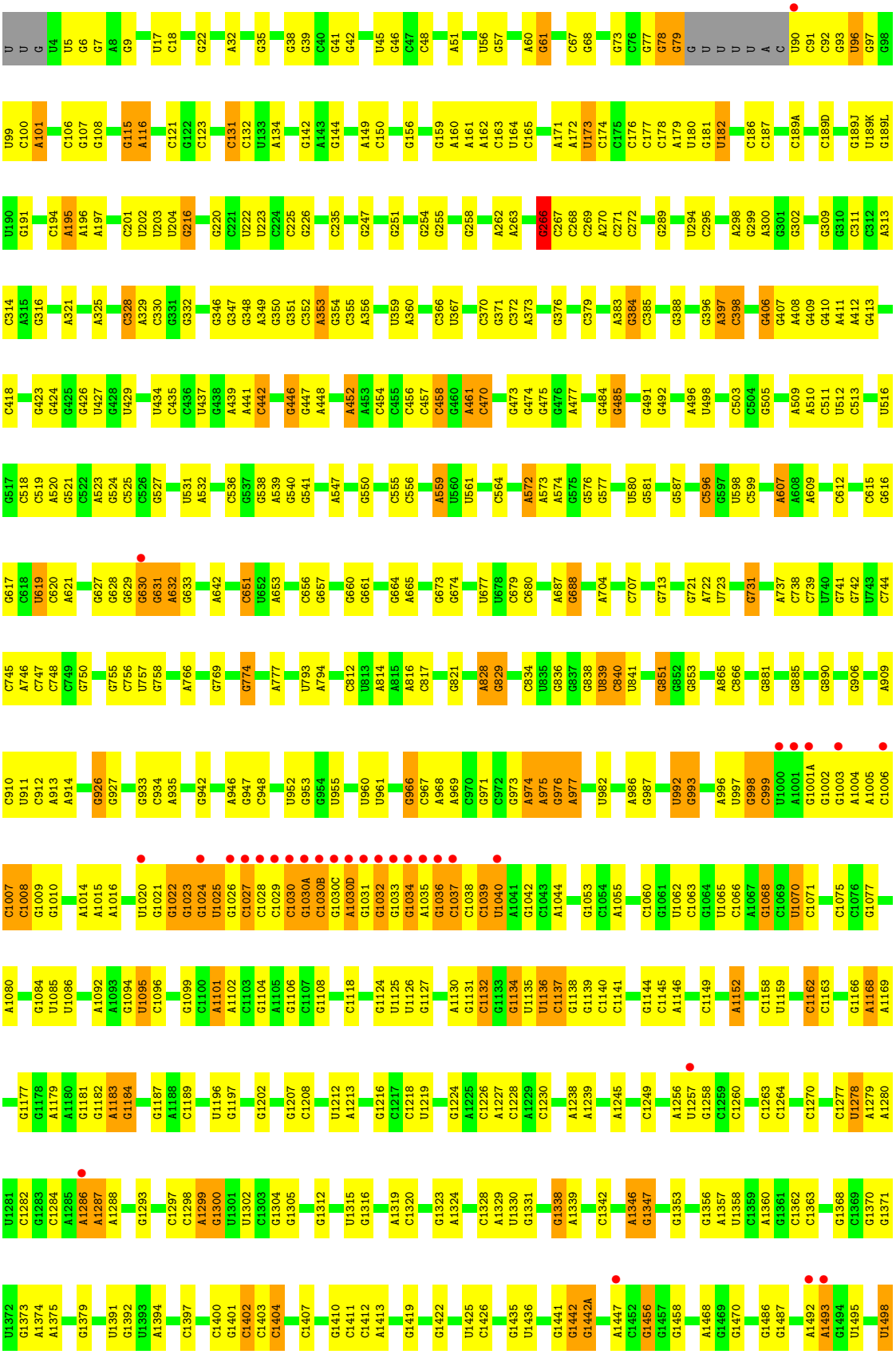
• Molecule 31: 50S ribosomal protein L36

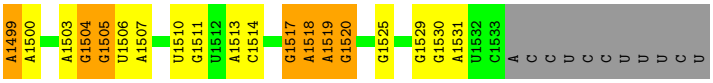
Chain 29:



• Molecule 32: 16S Ribosomal RNA

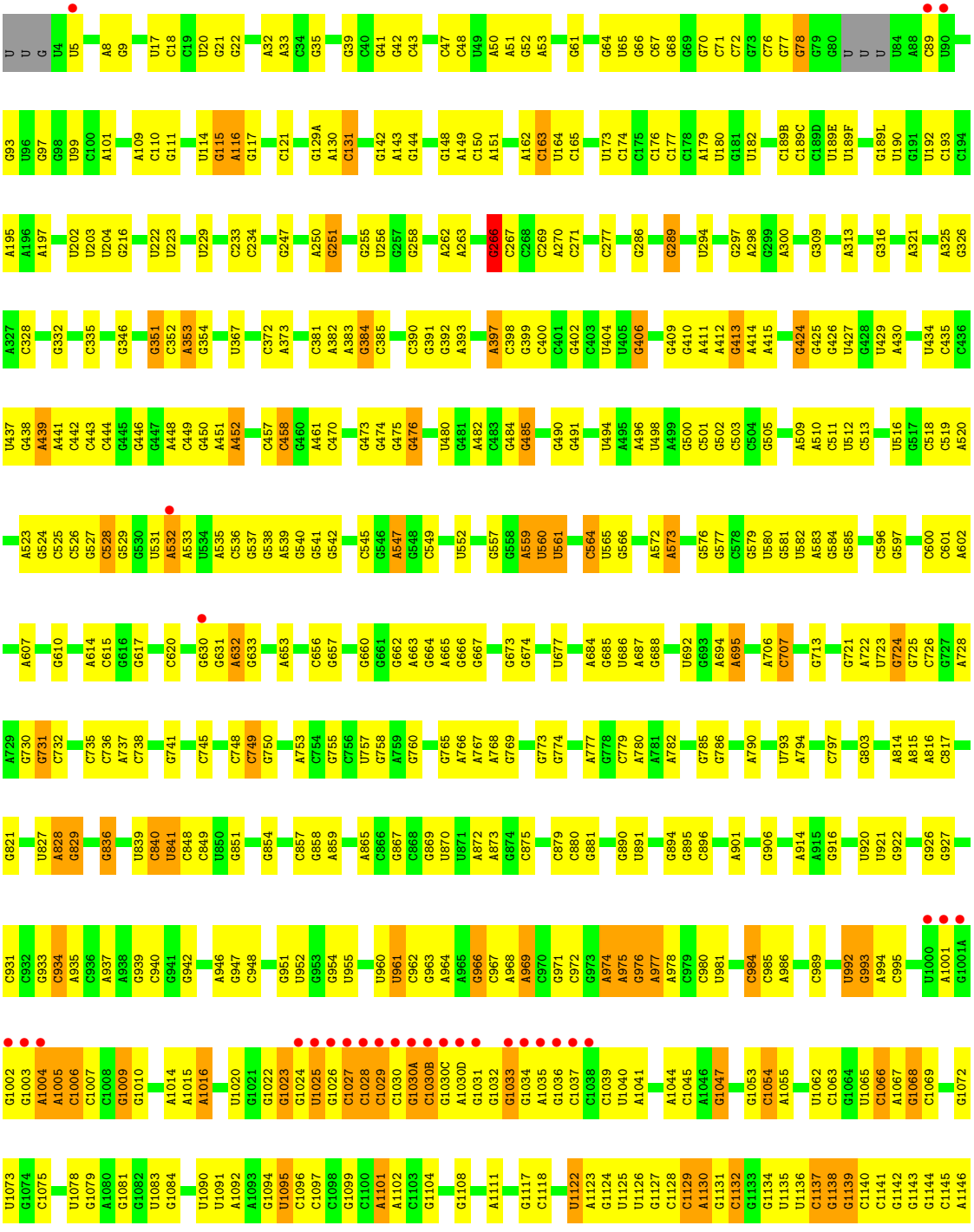
Chain 1a:

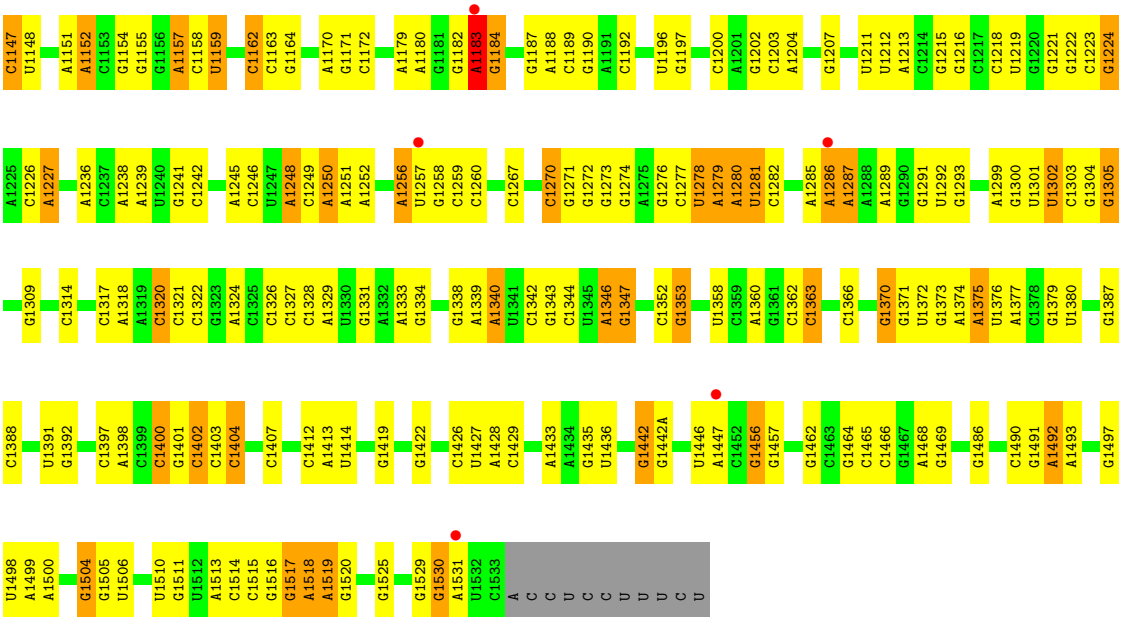




• Molecule 32: 16S Ribosomal RNA

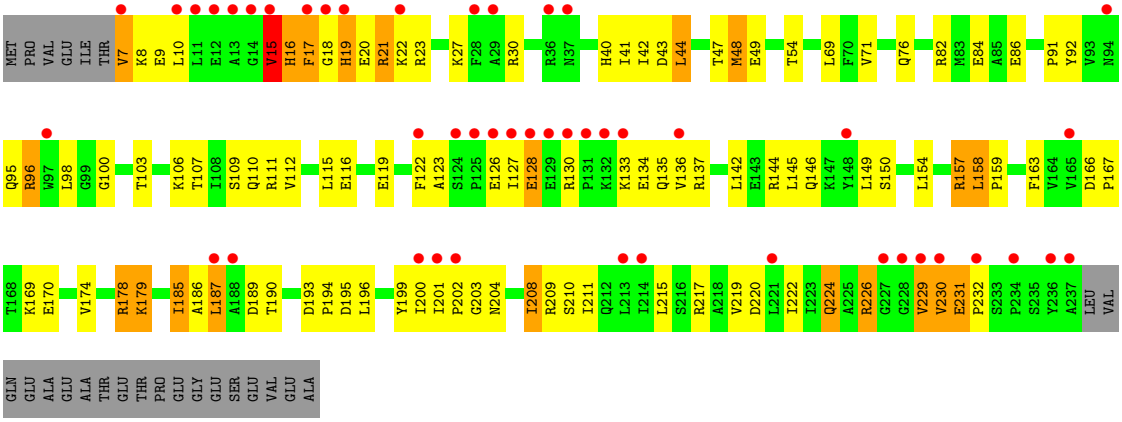
Chain 2a:





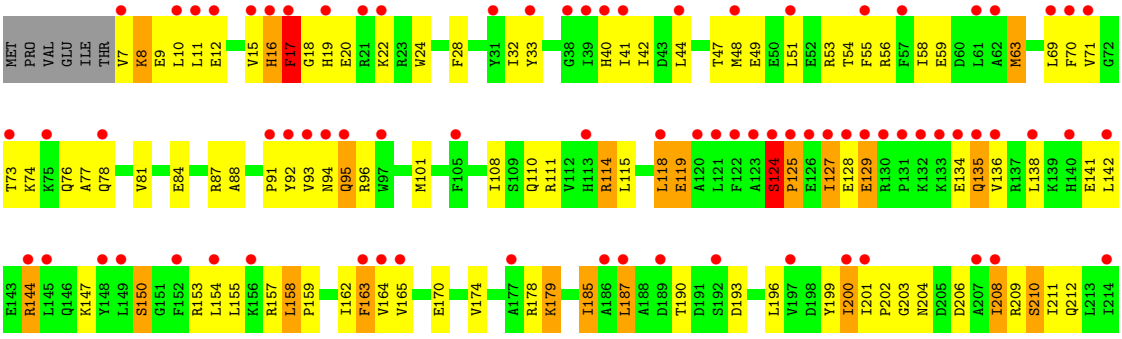
• Molecule 33: 30S ribosomal protein S2

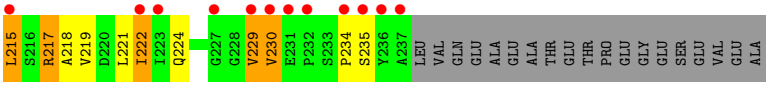
Chain 1b:



• Molecule 33: 30S ribosomal protein S2

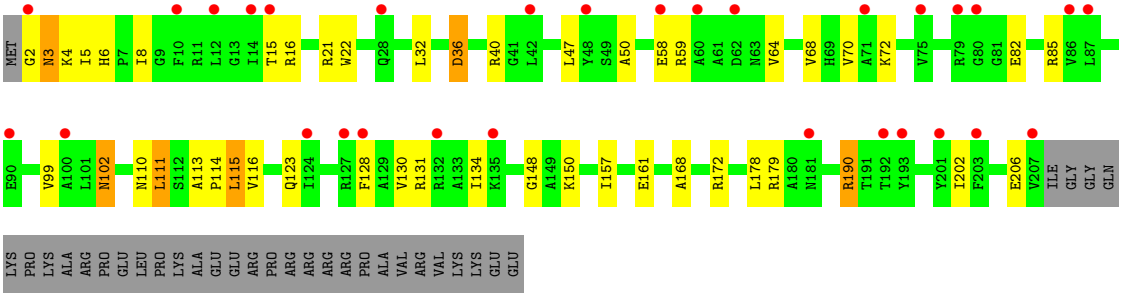
Chain 2b:





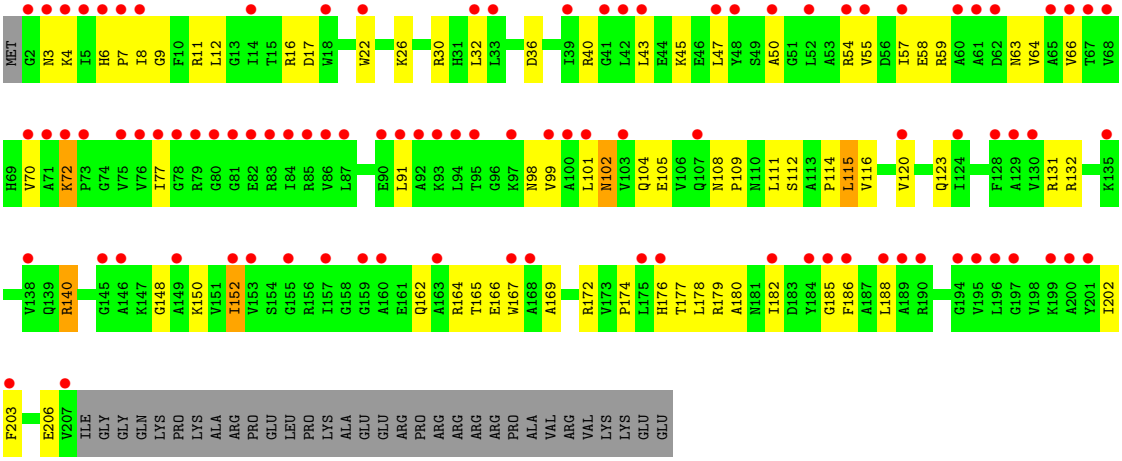
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



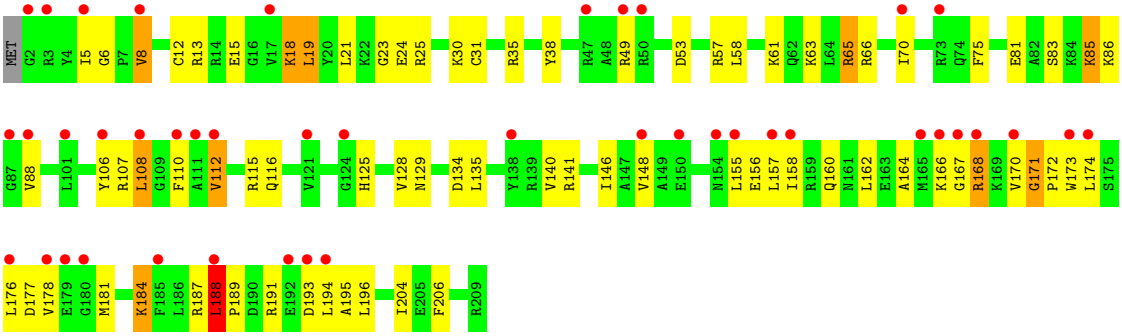
• Molecule 34: 30S ribosomal protein S3

Chain 2c:



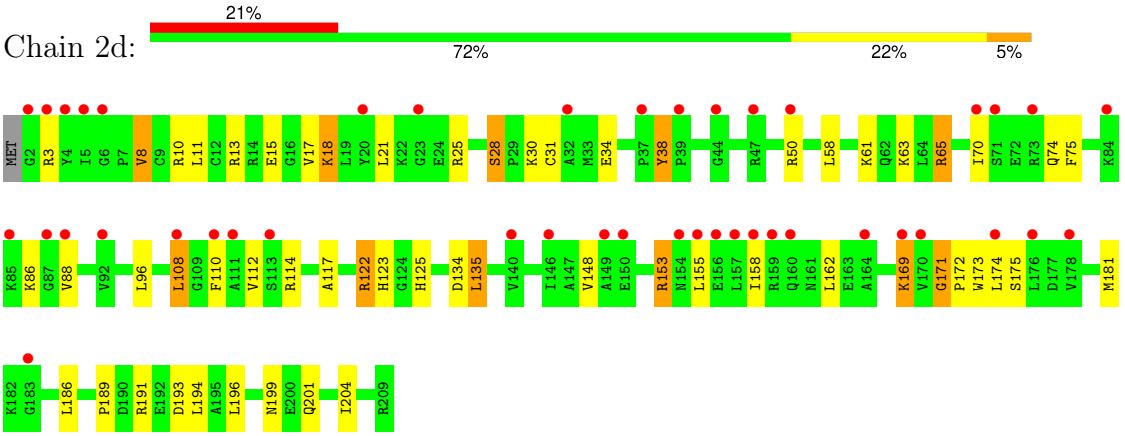
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



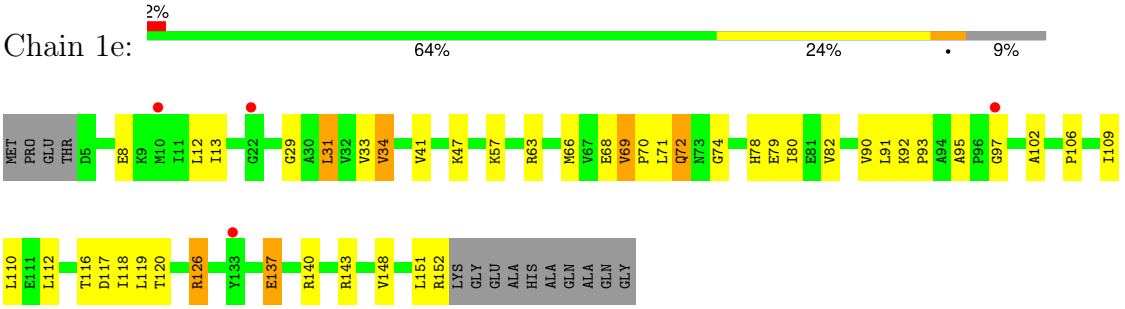
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



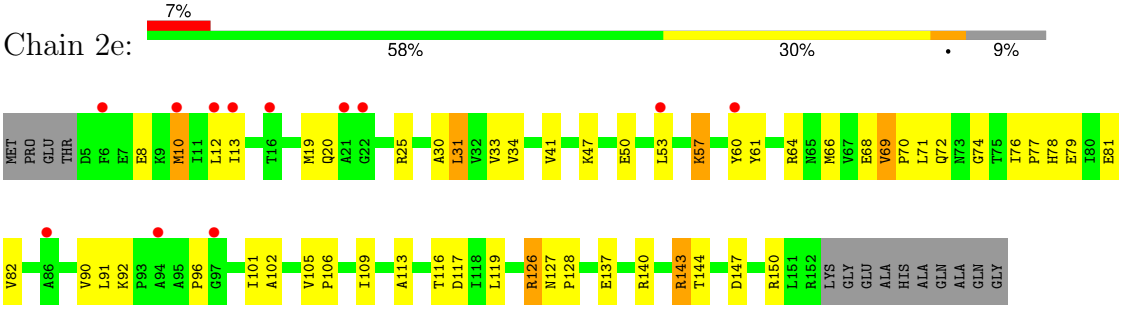
• Molecule 36: 30S ribosomal protein S5

Chain 1e:



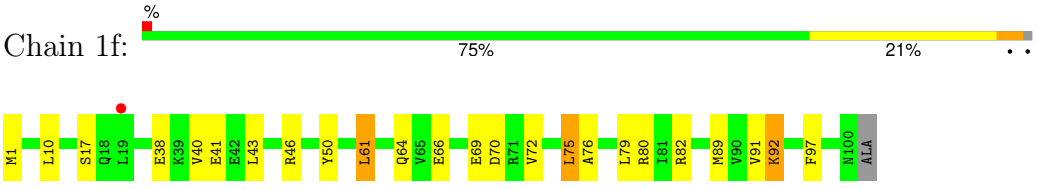
• Molecule 36: 30S ribosomal protein S5

Chain 2e:



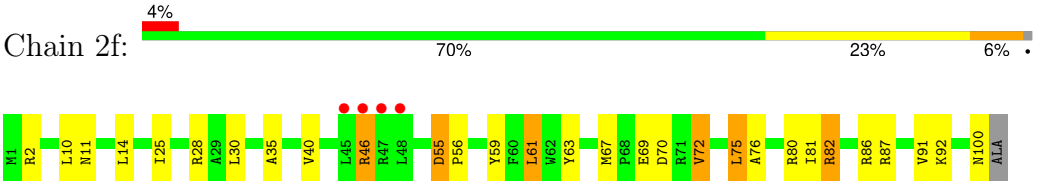
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



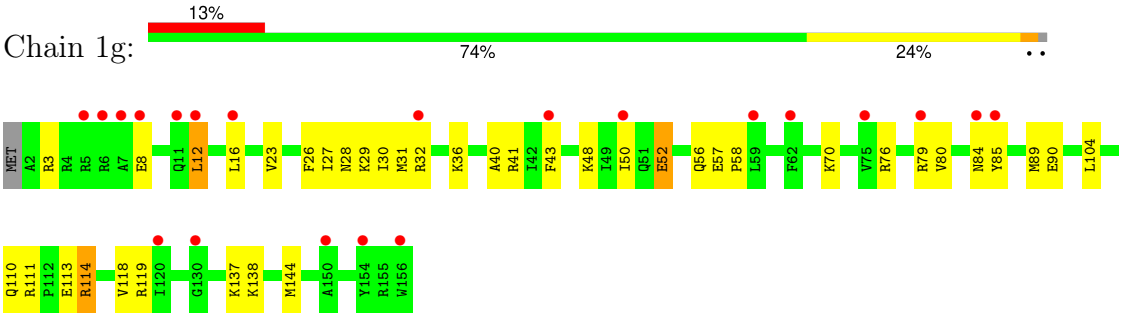
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



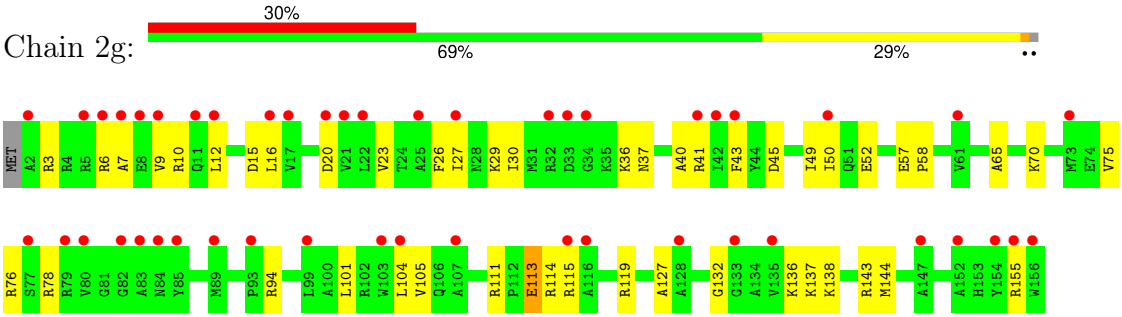
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



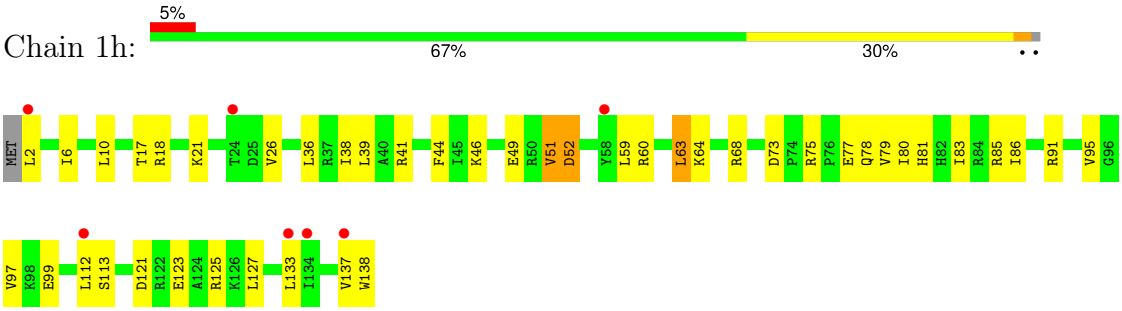
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



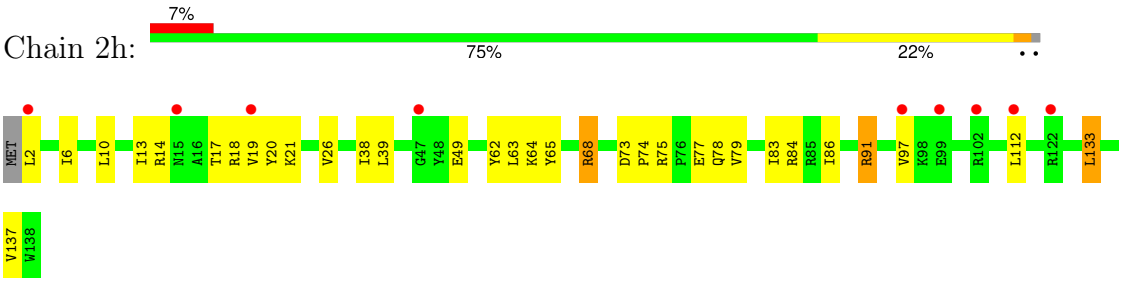
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



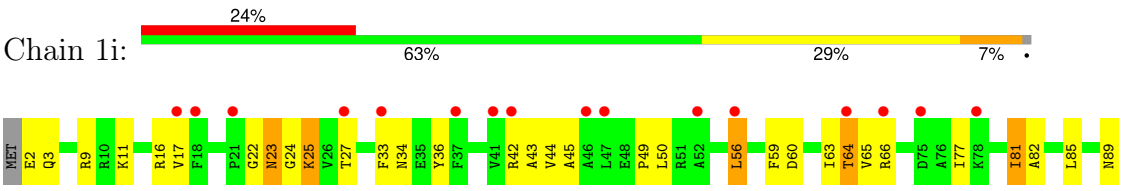
• Molecule 39: 30S ribosomal protein S8

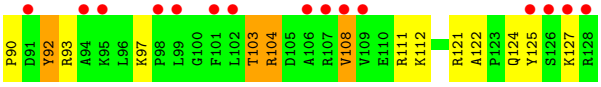
Chain 2h:



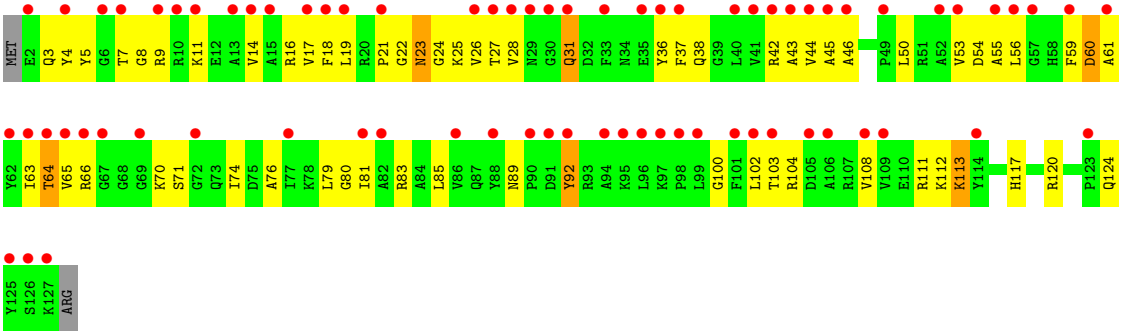
• Molecule 40: 30S ribosomal protein S9

Chain 1i:

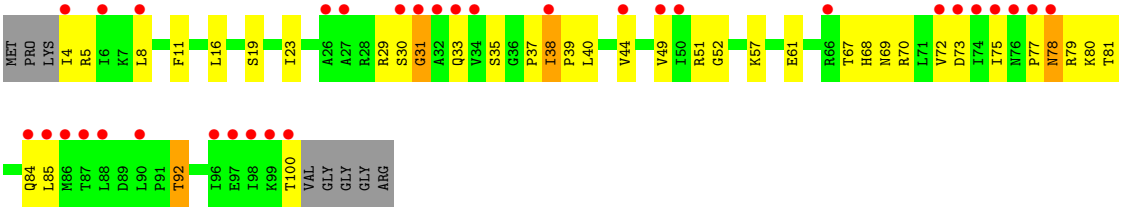




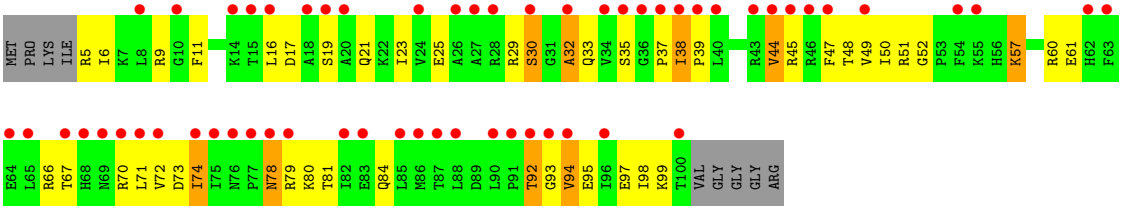
• Molecule 40: 30S ribosomal protein S9



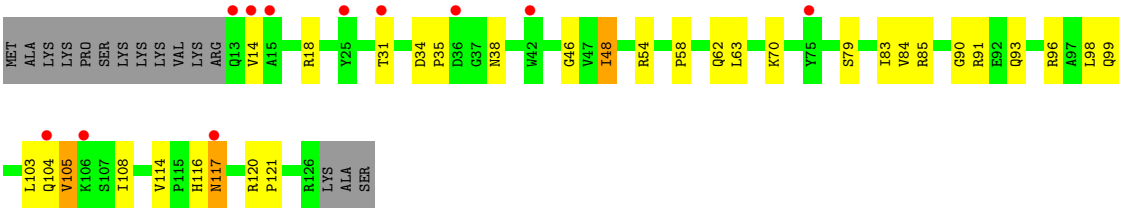
• Molecule 41: 30S ribosomal protein S10



• Molecule 41: 30S ribosomal protein S10

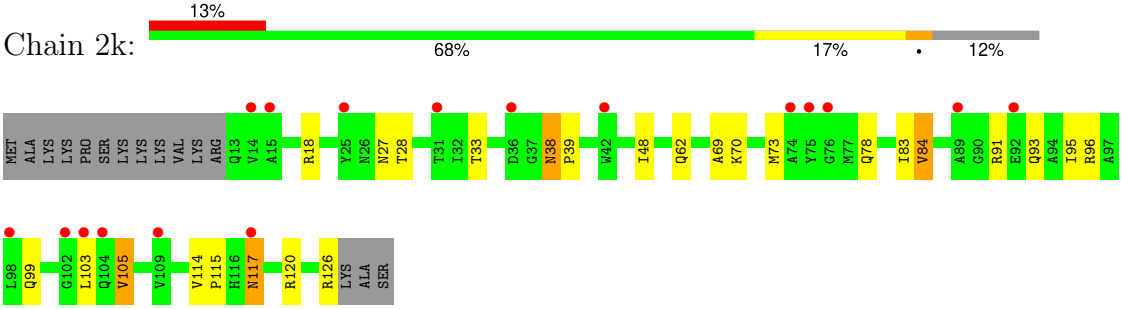


• Molecule 42: 30S ribosomal protein S11



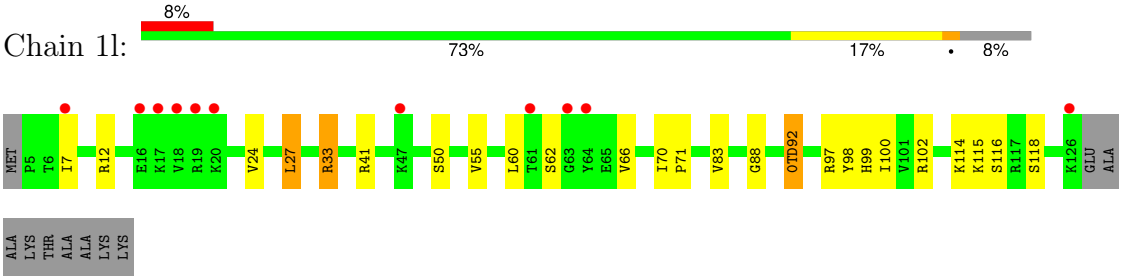
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



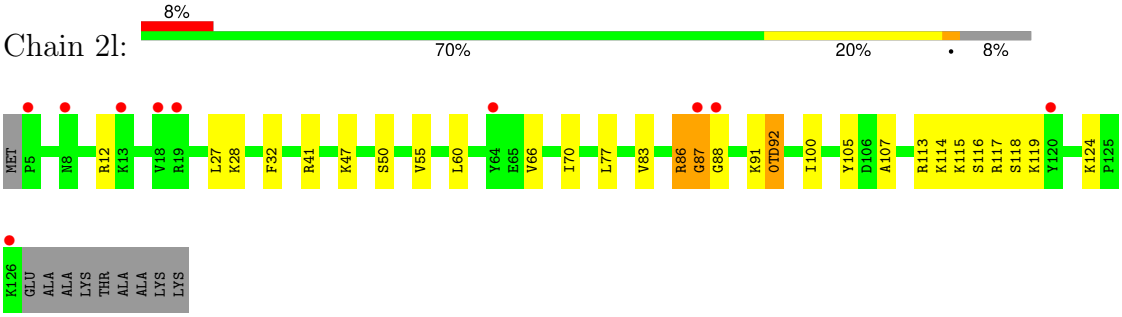
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



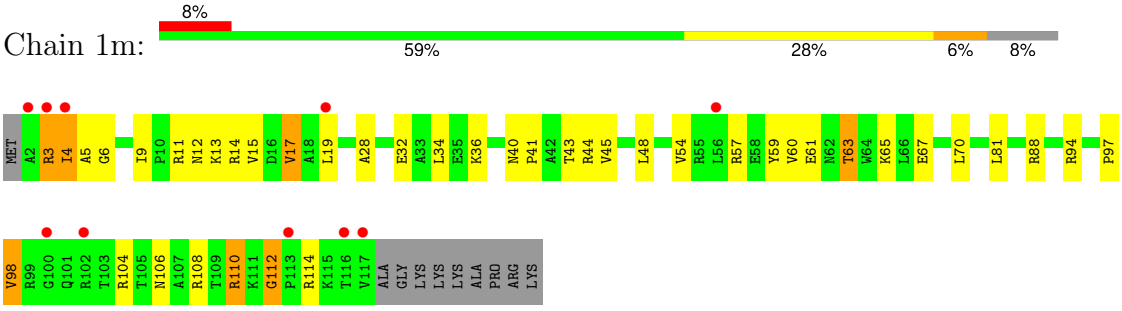
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



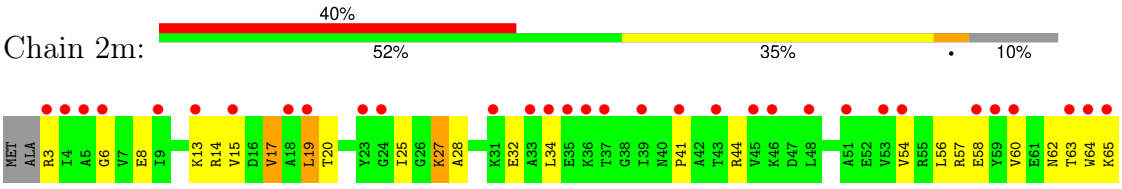
• Molecule 44: 30S ribosomal protein S13

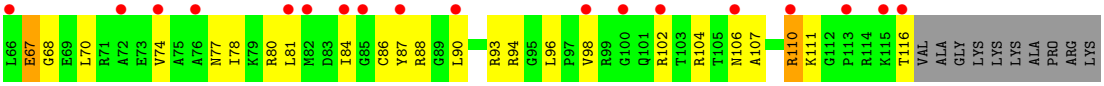
Chain 1m:



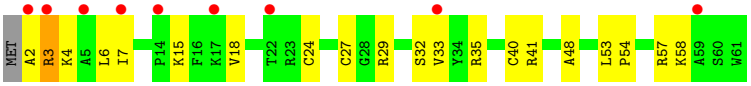
• Molecule 44: 30S ribosomal protein S13

Chain 2m:

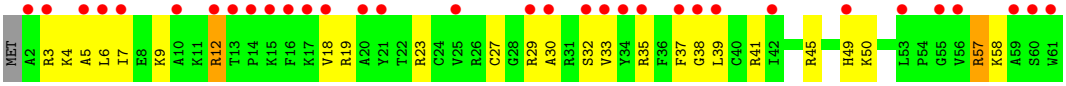




• Molecule 45: 30S ribosomal protein S14 type Z

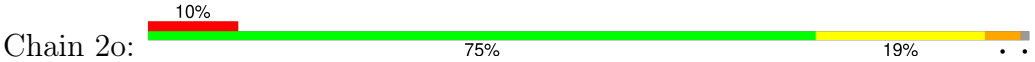


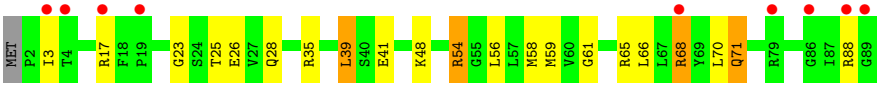
• Molecule 45: 30S ribosomal protein S14 type Z



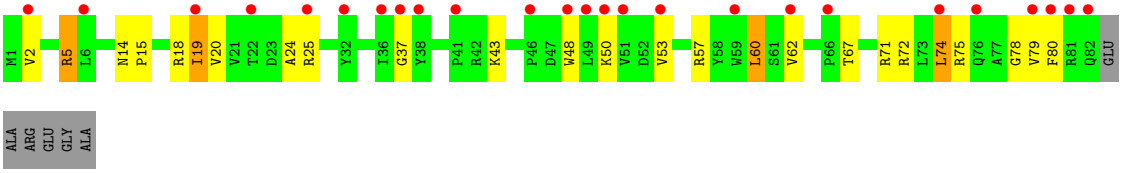
• Molecule 46: 30S ribosomal protein S15

• Molecule 46: 30S ribosomal protein S15

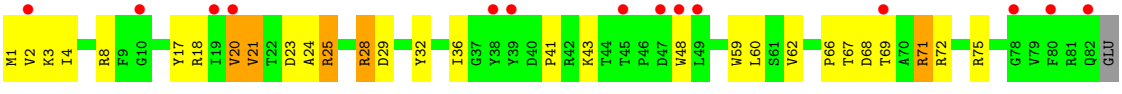




• Molecule 47: 30S ribosomal protein S16

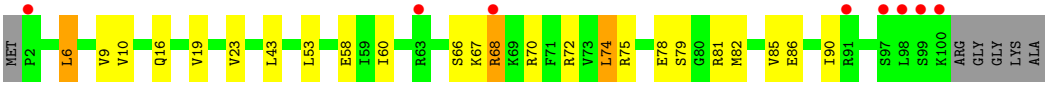


• Molecule 47: 30S ribosomal protein S16



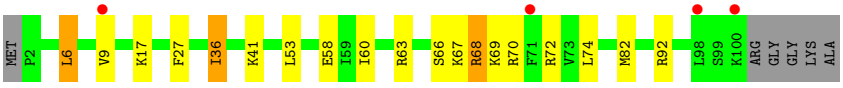
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



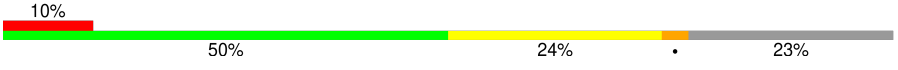
• Molecule 48: 30S ribosomal protein S17

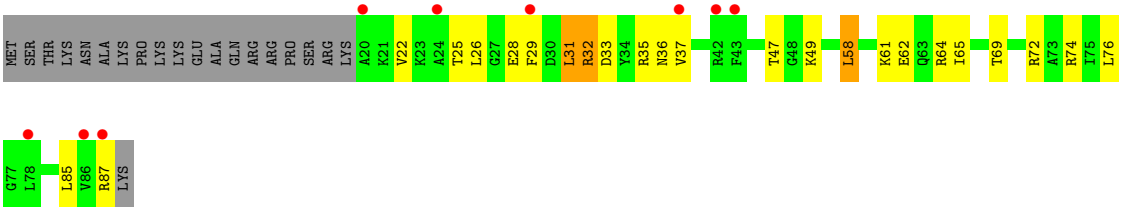
Chain 2q:



• Molecule 49: 30S ribosomal protein S18

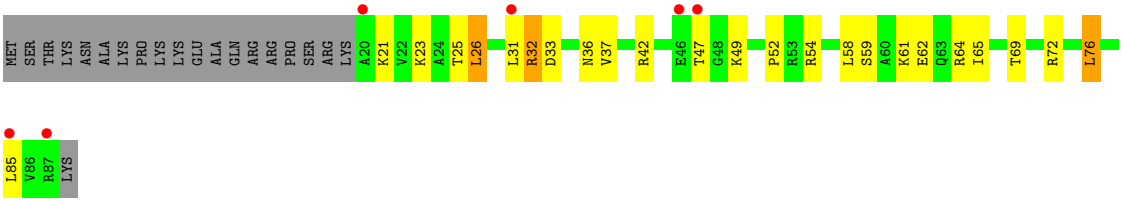
Chain 1r:





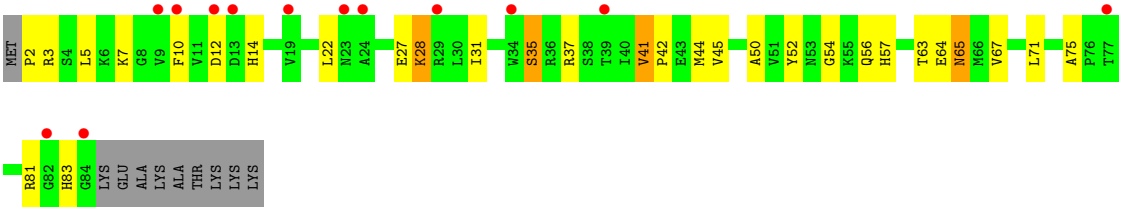
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



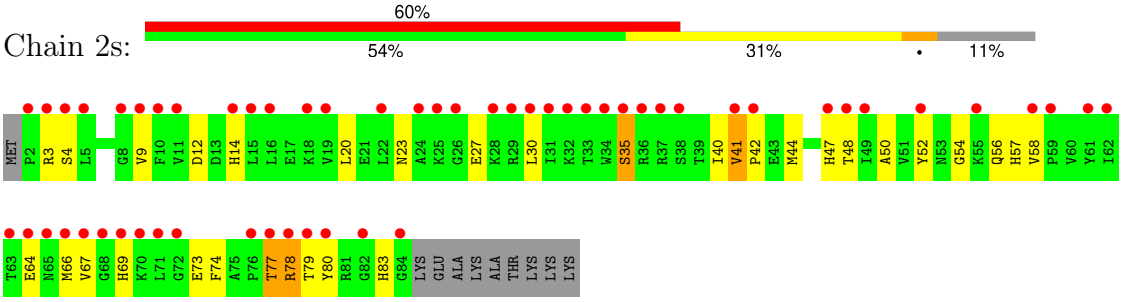
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



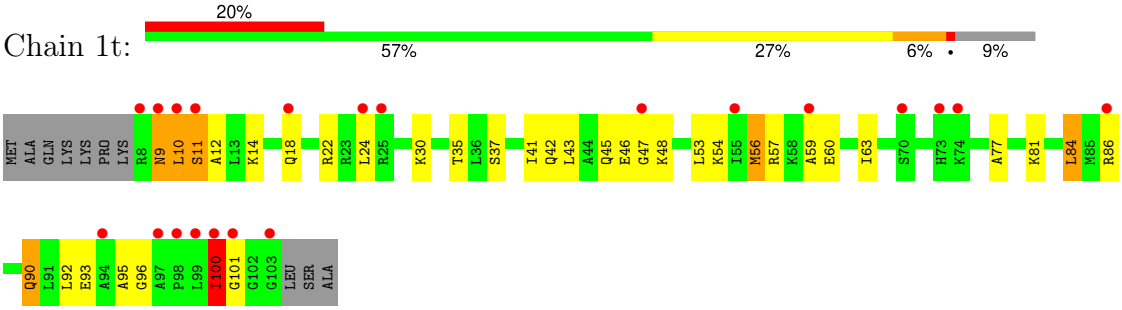
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



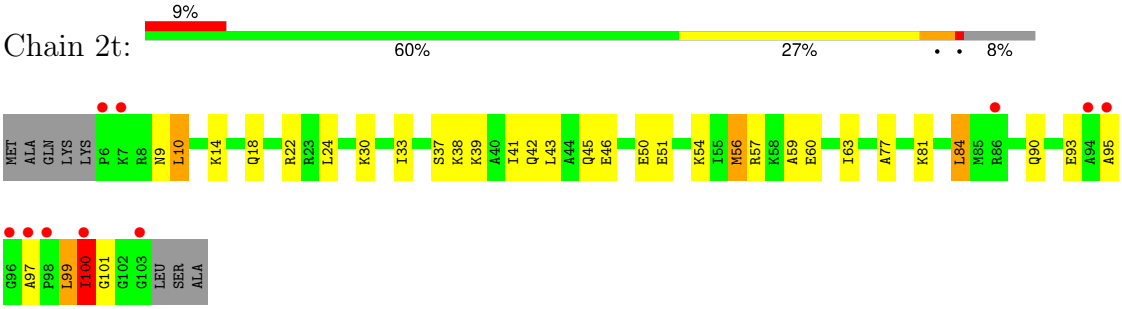
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



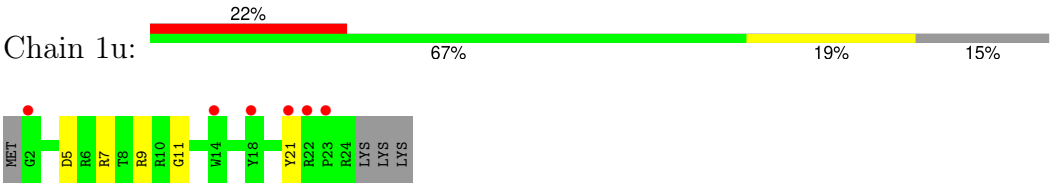
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



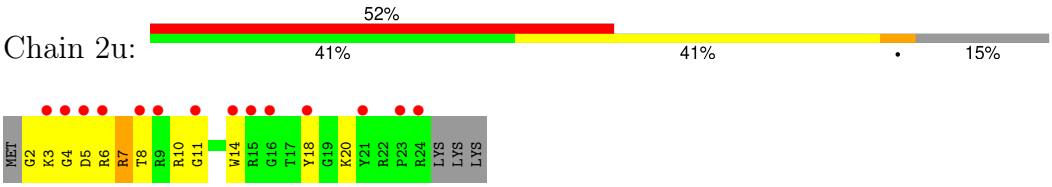
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



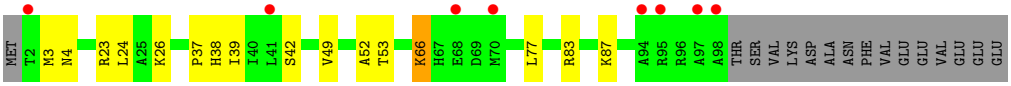
• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



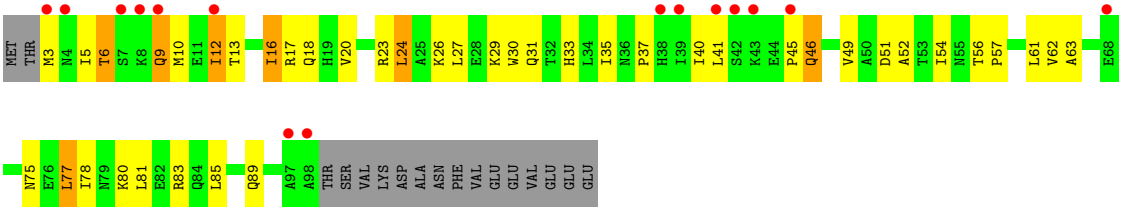
• Molecule 53: Ribosome-associated inhibitor A

Chain 1y:



• Molecule 53: Ribosome-associated inhibitor A

Chain 2y:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.16Å 448.37Å 618.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	173.22 – 2.30 173.22 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.5 (173.22-2.30) 97.5 (173.22-2.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.18 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.207 , 0.247 0.207 , 0.246	Depositor DCC
R_{free} test set	123763 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	48.4	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 54.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	298502	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.49% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, OMG, MA6, ZN, MPD, 7MG, M2G, PSU, 4OC, SF4, 5MC, 2MG, 0TD, MG, 5MU, UR3, 2MU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1A	0.39	0/69029	0.56	9/107746 (0.0%)
1	2A	0.32	0/68901	0.54	6/107544 (0.0%)
2	1B	0.31	0/2876	0.50	0/4486
2	2B	0.30	0/2878	0.49	0/4490
3	1D	0.62	0/2181	0.91	5/2940 (0.2%)
3	2D	0.51	0/2186	0.89	4/2944 (0.1%)
4	1E	0.62	0/1592	0.95	2/2149 (0.1%)
4	2E	0.52	0/1592	1.01	10/2149 (0.5%)
5	1F	0.61	1/1619 (0.1%)	0.86	1/2193 (0.0%)
5	2F	0.50	0/1615	0.93	3/2188 (0.1%)
6	1G	0.45	0/1451	0.94	7/1961 (0.4%)
6	2G	0.47	0/1449	0.94	3/1957 (0.2%)
7	1H	0.51	0/1356	0.88	1/1834 (0.1%)
7	2H	0.45	0/1350	0.97	5/1826 (0.3%)
8	1I	0.46	0/1109	0.94	3/1512 (0.2%)
8	2I	0.43	0/1091	0.89	1/1490 (0.1%)
9	1N	0.56	0/1148	0.88	0/1547
9	2N	0.42	0/1144	0.87	2/1543 (0.1%)
10	1O	0.59	0/943	0.93	2/1269 (0.2%)
10	2O	0.48	0/943	0.84	0/1269
11	1P	0.59	0/1152	0.92	0/1533
11	2P	0.44	0/1152	0.86	3/1533 (0.2%)
12	1Q	0.61	0/1143	0.86	0/1527
12	2Q	0.50	0/1143	0.87	0/1527
13	1R	0.62	0/982	0.91	0/1312
13	2R	0.52	0/982	0.87	0/1312
14	1S	0.51	0/887	0.87	0/1180
14	2S	0.47	0/880	0.90	0/1172
15	1T	0.57	0/1105	0.88	0/1477
15	2T	0.48	0/1097	0.86	2/1468 (0.1%)
16	1U	0.64	0/977	0.83	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.50	0/977	0.88	1/1301 (0.1%)
17	1V	0.54	0/786	0.88	0/1053
17	2V	0.49	0/782	0.88	0/1049
18	1W	0.62	0/897	0.84	0/1205
18	2W	0.56	0/897	0.82	0/1205
19	1X	0.59	0/764	0.90	0/1025
19	2X	0.51	0/764	0.86	0/1025
20	1Y	0.51	0/823	0.98	1/1099 (0.1%)
20	2Y	0.44	0/823	0.86	0/1100
21	1Z	0.46	0/1620	0.86	0/2200
21	2Z	0.45	0/1590	0.92	1/2162 (0.0%)
22	10	0.58	0/616	0.88	0/821
22	20	0.43	0/616	0.86	2/821 (0.2%)
23	11	0.56	0/761	0.83	0/1013
23	21	0.50	0/766	0.84	0/1018
24	12	0.51	0/590	0.78	0/781
24	22	0.42	0/594	0.77	0/785
25	13	0.59	0/474	0.92	0/635
25	23	0.48	0/469	0.88	0/630
26	14	0.49	0/559	1.16	7/754 (0.9%)
26	24	0.54	0/549	1.11	5/741 (0.7%)
27	15	0.61	0/473	0.89	0/639
27	25	0.53	0/469	0.80	0/635
28	16	0.58	0/460	0.81	2/613 (0.3%)
28	26	0.50	0/456	0.80	0/608
29	17	0.68	0/426	0.84	1/561 (0.2%)
29	27	0.54	0/426	0.83	0/561
30	18	0.61	0/525	0.81	0/691
30	28	0.49	0/525	0.86	0/691
31	19	0.60	0/310	0.87	0/407
31	29	0.44	0/310	0.86	0/407
32	1a	0.26	0/35795	0.46	1/55864 (0.0%)
32	2a	0.24	0/35890	0.44	3/56012 (0.0%)
33	1b	0.44	0/1876	0.98	5/2533 (0.2%)
33	2b	0.47	0/1860	0.96	5/2518 (0.2%)
34	1c	0.42	0/1582	0.86	2/2137 (0.1%)
34	2c	0.46	0/1566	0.93	5/2119 (0.2%)
35	1d	0.45	0/1695	0.93	5/2274 (0.2%)
35	2d	0.42	0/1698	0.90	4/2277 (0.2%)
36	1e	0.46	0/1149	0.88	2/1548 (0.1%)
36	2e	0.44	0/1149	0.91	6/1548 (0.4%)
37	1f	0.47	0/827	0.87	0/1120
37	2f	0.44	0/829	0.85	2/1123 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.40	0/1254	0.81	0/1683
38	2g	0.39	0/1248	0.83	0/1676
39	1h	0.41	0/1118	0.81	0/1506
39	2h	0.37	0/1108	0.85	0/1494
40	1i	0.41	0/1005	0.90	0/1351
40	2i	0.44	0/985	0.90	1/1329 (0.1%)
41	1j	0.43	0/732	0.94	0/993
41	2j	0.44	0/723	0.94	1/984 (0.1%)
42	1k	0.47	0/849	0.94	5/1150 (0.4%)
42	2k	0.45	0/848	0.91	2/1149 (0.2%)
43	1l	0.43	0/937	0.83	0/1260
43	2l	0.44	0/937	0.95	5/1260 (0.4%)
44	1m	0.42	0/924	0.92	5/1242 (0.4%)
44	2m	0.41	0/905	0.95	1/1217 (0.1%)
45	1n	0.43	0/501	0.74	0/664
45	2n	0.43	0/501	0.84	0/664
46	1o	0.43	0/739	0.88	1/985 (0.1%)
46	2o	0.41	0/739	0.85	0/985
47	1p	0.42	0/697	0.90	1/939 (0.1%)
47	2p	0.46	0/693	0.81	0/935
48	1q	0.41	0/836	0.81	0/1117
48	2q	0.39	0/836	0.81	0/1117
49	1r	0.42	0/560	0.91	1/746 (0.1%)
49	2r	0.40	0/560	0.80	0/746
50	1s	0.40	0/663	0.99	2/895 (0.2%)
50	2s	0.45	0/660	0.90	1/893 (0.1%)
51	1t	0.44	0/734	0.90	1/969 (0.1%)
51	2t	0.40	0/736	0.83	1/976 (0.1%)
52	1u	0.36	0/203	0.73	0/266
52	2u	0.42	0/203	0.80	0/266
53	1y	0.46	0/776	0.78	0/1048
53	2y	0.39	0/761	0.75	0/1030
All	All	0.38	1/309937 (0.0%)	0.64	157/463223 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
14	1S	0	1
19	1X	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	2X	0	1
33	1b	0	1
43	2l	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1F	132	VAL	CA-CB	5.65	1.60	1.53

All (157) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	1d	188	LEU	CA-C-N	10.70	131.39	119.83
35	1d	188	LEU	C-N-CA	10.70	131.39	119.83
43	2l	88	GLY	N-CA-C	8.59	123.75	112.25
1	2A	1992	G	C2'-C3'-O3'	8.21	121.81	109.50
33	1b	128	GLU	N-CA-C	-8.11	102.95	113.17
4	2E	190	GLY	CA-C-N	7.89	128.04	120.31
4	2E	190	GLY	C-N-CA	7.89	128.04	120.31
20	1Y	92	ASN	N-CA-C	7.79	120.76	111.33
43	2l	87	GLY	N-CA-C	7.53	126.00	112.22
44	2m	106	ASN	N-CA-C	7.17	121.29	111.54
26	24	61	ARG	N-CA-C	-7.09	102.09	111.24
44	1m	6	GLY	N-CA-C	-7.07	105.51	113.79
26	14	52	THR	N-CA-C	-7.07	104.66	112.72
43	2l	28	LYS	N-CA-C	7.05	120.97	111.24
35	2d	171	GLY	CA-C-N	6.93	127.51	119.47
35	2d	171	GLY	C-N-CA	6.93	127.51	119.47
6	1G	53	LEU	N-CA-C	-6.93	104.40	112.92
33	2b	193	ASP	CA-C-N	6.91	126.42	119.24
33	2b	193	ASP	C-N-CA	6.91	126.42	119.24
4	2E	72	VAL	N-CA-C	6.88	118.39	108.48
5	2F	9	ILE	N-CA-C	6.85	115.54	107.73
26	14	68	ARG	N-CA-C	6.84	120.22	109.96
3	1D	229	VAL	CB-CA-C	-6.77	102.16	112.05
34	2c	108	ASN	CA-C-N	6.75	126.70	119.28
34	2c	108	ASN	C-N-CA	6.75	126.70	119.28
28	16	40	CYS	CA-C-N	6.74	126.36	119.56
28	16	40	CYS	C-N-CA	6.74	126.36	119.56
1	1A	1700	G	C2'-C3'-O3'	6.70	119.56	109.50
4	2E	52	LEU	CA-C-N	-6.68	113.08	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	2E	52	LEU	C-N-CA	-6.68	113.08	119.76
26	24	19	GLY	N-CA-C	-6.66	106.13	115.32
35	1d	191	ARG	N-CA-C	-6.56	104.05	111.07
7	2H	38	SER	CA-C-N	6.40	126.09	119.56
7	2H	38	SER	C-N-CA	6.40	126.09	119.56
26	14	40	HIS	CA-C-N	6.39	127.83	119.84
26	14	40	HIS	C-N-CA	6.39	127.83	119.84
8	1I	110	ASP	CA-C-N	6.38	125.88	119.24
8	1I	110	ASP	C-N-CA	6.38	125.88	119.24
33	1b	193	ASP	CA-C-N	6.35	125.84	119.24
33	1b	193	ASP	C-N-CA	6.35	125.84	119.24
37	2f	55	ASP	CA-C-N	6.33	126.01	119.56
37	2f	55	ASP	C-N-CA	6.33	126.01	119.56
22	20	82	ARG	CA-C-N	6.32	126.29	119.78
22	20	82	ARG	C-N-CA	6.32	126.29	119.78
11	2P	22	GLY	CA-C-N	6.30	125.72	118.85
11	2P	22	GLY	C-N-CA	6.30	125.72	118.85
47	1p	5	ARG	N-CA-C	6.30	116.38	108.45
4	2E	51	PHE	CA-C-N	6.23	132.92	121.70
4	2E	51	PHE	C-N-CA	6.23	132.92	121.70
35	2d	38	TYR	CA-C-N	6.22	126.79	120.38
35	2d	38	TYR	C-N-CA	6.22	126.79	120.38
1	1A	537	G	O4'-C1'-N9	6.21	117.51	108.20
1	1A	1346	U	C4'-C3'-O3'	6.19	118.68	109.40
1	1A	1822	A	C5'-C4'-C3'	-6.19	106.72	116.00
8	1I	107	VAL	N-CA-C	6.18	117.00	108.84
3	1D	220	HIS	CA-C-N	-6.18	115.53	123.19
3	1D	220	HIS	C-N-CA	-6.18	115.53	123.19
50	1s	75	ALA	CA-C-N	6.14	126.17	119.90
50	1s	75	ALA	C-N-CA	6.14	126.17	119.90
3	2D	229	VAL	CB-CA-C	-6.14	104.00	112.04
6	1G	48	GLU	N-CA-C	-6.13	102.86	108.75
32	2a	266	G	C2'-C3'-O3'	6.07	118.61	109.50
26	14	66	SER	N-CA-C	6.07	120.41	113.19
36	2e	127	ASN	CA-C-N	6.02	125.50	119.24
36	2e	127	ASN	C-N-CA	6.02	125.50	119.24
3	1D	70	TRP	CA-C-N	6.02	128.62	120.38
3	1D	70	TRP	C-N-CA	6.02	128.62	120.38
34	2c	72	LYS	CA-C-N	6.01	125.72	119.05
34	2c	72	LYS	C-N-CA	6.01	125.72	119.05
50	2s	58	VAL	N-CA-C	6.01	113.03	107.56
4	1E	8	LYS	CA-C-N	-5.94	115.34	122.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	1E	8	LYS	C-N-CA	-5.94	115.34	122.35
46	1o	87	ILE	N-CA-C	5.92	116.69	111.90
3	2D	70	TRP	CA-C-N	5.89	128.18	120.28
3	2D	70	TRP	C-N-CA	5.89	128.18	120.28
1	2A	752	A	C2'-C3'-O3'	5.85	118.27	109.50
1	1A	2701	U	C4'-C3'-O3'	5.82	118.14	109.40
26	24	59	PHE	N-CA-C	5.80	117.43	107.28
42	2k	38	ASN	CA-C-N	5.78	126.11	119.93
42	2k	38	ASN	C-N-CA	5.78	126.11	119.93
44	1m	106	ASN	CB-CA-C	-5.77	108.28	115.89
40	2i	63	ILE	N-CA-C	5.72	116.52	108.17
1	1A	1255	A	C4'-C3'-O3'	5.72	117.98	109.40
42	1k	34	ASP	CA-C-N	-5.67	113.83	119.56
42	1k	34	ASP	C-N-CA	-5.67	113.83	119.56
42	1k	38	ASN	CA-C-N	5.64	125.97	119.93
42	1k	38	ASN	C-N-CA	5.64	125.97	119.93
43	2l	119	LYS	N-CA-C	-5.61	102.59	110.50
6	1G	96	ARG	CB-CA-C	-5.59	110.11	116.54
41	2j	32	ALA	N-CA-C	-5.59	102.19	110.46
16	2U	9	VAL	N-CA-C	5.59	115.78	110.53
5	2F	21	ALA	CA-C-N	5.58	131.74	121.70
5	2F	21	ALA	C-N-CA	5.58	131.74	121.70
6	2G	45	GLU	N-CA-C	-5.54	106.36	113.01
1	2A	2689	U	P-O3'-C3'	5.53	128.50	120.20
34	1c	99	VAL	N-CA-C	5.52	115.21	106.32
11	2P	116	GLY	N-CA-C	5.52	122.55	115.32
10	1O	9	GLU	CA-C-N	-5.51	115.85	122.90
10	1O	9	GLU	C-N-CA	-5.51	115.85	122.90
9	2N	110	GLY	CA-C-N	5.50	124.69	118.97
9	2N	110	GLY	C-N-CA	5.50	124.69	118.97
26	24	59	PHE	CA-C-N	5.50	131.60	121.70
26	24	59	PHE	C-N-CA	5.50	131.60	121.70
42	1k	116	HIS	N-CA-C	-5.50	104.77	112.25
1	1A	1346	U	P-O3'-C3'	5.48	128.43	120.20
49	1r	22	VAL	N-CA-C	5.46	116.84	110.62
7	2H	8	PRO	CA-C-N	-5.46	118.89	122.60
7	2H	8	PRO	C-N-CA	-5.46	118.89	122.60
26	14	55	ARG	CA-C-N	5.46	131.52	121.70
26	14	55	ARG	C-N-CA	5.46	131.52	121.70
35	1d	171	GLY	CA-C-N	5.41	125.74	119.47
35	1d	171	GLY	C-N-CA	5.41	125.74	119.47
51	1t	11	SER	N-CA-C	-5.39	106.47	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	266	G	P-O3'-C3'	5.39	128.29	120.20
7	1H	92	ILE	N-CA-C	5.35	115.55	110.42
3	2D	275	LYS	N-CA-C	-5.34	99.58	108.07
6	1G	127	GLY	N-CA-C	-5.33	108.74	115.08
1	2A	1791	A	C5'-C4'-C3'	-5.33	108.01	116.00
7	2H	45	VAL	N-CA-C	5.30	115.22	107.37
1	1A	991	G	O5'-P-OP1	-5.30	92.10	108.00
6	2G	96	ARG	CB-CA-C	-5.29	110.46	116.54
34	1c	4	LYS	N-CA-C	5.28	118.14	110.42
29	17	47	ARG	N-CA-C	5.28	118.88	112.23
6	1G	121	ASN	CA-C-N	5.27	125.08	119.28
6	1G	121	ASN	C-N-CA	5.27	125.08	119.28
33	1b	19	HIS	N-CA-C	5.27	114.79	107.73
33	1b	123	ALA	N-CA-C	-5.26	106.83	113.20
36	2e	105	VAL	CA-C-N	-5.25	113.62	119.19
36	2e	105	VAL	C-N-CA	-5.25	113.62	119.19
33	2b	19	HIS	N-CA-C	5.22	117.00	109.07
5	1F	24	LEU	N-CA-C	-5.21	103.10	110.29
1	2A	2689	U	C2'-C3'-O3'	5.20	117.30	109.50
6	1G	45	GLU	N-CA-C	-5.19	106.78	113.01
33	2b	124	SER	N-CA-C	5.19	121.28	109.81
8	2I	72	LEU	N-CA-C	5.18	116.74	111.14
43	2l	105	TYR	CB-CA-C	-5.18	110.18	117.23
21	2Z	176	PRO	O-C-N	5.16	123.58	121.15
32	2a	1183	A	P-O3'-C3'	5.16	127.94	120.20
4	2E	193	GLY	N-CA-C	-5.16	108.51	115.21
1	1A	1184	G	O5'-P-OP2	-5.13	92.60	108.00
51	2t	10	LEU	N-CA-C	5.13	117.54	111.33
1	2A	512	G	O4'-C1'-N9	5.11	115.87	108.20
44	1m	112	GLY	CA-C-N	5.10	125.09	119.89
44	1m	112	GLY	C-N-CA	5.10	125.09	119.89
33	2b	129	GLU	N-CA-C	-5.09	106.91	113.02
4	2E	21	VAL	CA-C-N	5.08	125.24	119.90
4	2E	21	VAL	C-N-CA	5.08	125.24	119.90
44	1m	114	ARG	N-CA-C	5.06	117.64	110.10
34	2c	4	LYS	N-CA-C	5.05	117.79	110.42
6	2G	144	ILE	N-CA-C	5.02	115.54	108.36
36	1e	95	ALA	CA-C-N	5.02	126.11	119.84
36	1e	95	ALA	C-N-CA	5.02	126.11	119.84
36	2e	68	GLU	CA-C-N	-5.01	118.44	123.04
36	2e	68	GLU	C-N-CA	-5.01	118.44	123.04
15	2T	19	LEU	CA-C-N	5.00	124.98	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	2T	19	LEU	C-N-CA	5.00	124.98	120.03
32	1a	266	G	C2'-C3'-O3'	5.00	117.00	109.50

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	1S	58	LEU	Peptide
19	1X	93	GLU	Peptide
33	1b	231	GLU	Peptide
19	2X	93	GLU	Peptide
43	2l	86	ARG	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61869	0	31203	523	0
1	2A	61758	0	31151	759	0
2	1B	2572	0	1305	26	0
2	2B	2573	0	1306	37	0
3	1D	2131	0	2207	42	0
3	2D	2136	0	2218	52	0
4	1E	1559	0	1618	41	0
4	2E	1559	0	1618	43	0
5	1F	1584	0	1625	42	0
5	2F	1580	0	1619	40	0
6	1G	1426	0	1445	44	0
6	2G	1424	0	1441	60	0
7	1H	1330	0	1407	20	0
7	2H	1324	0	1402	39	0
8	1I	1094	0	1127	27	0
8	2I	1076	0	1094	22	0
9	1N	1121	0	1195	14	0
9	2N	1117	0	1184	17	0
10	1O	933	0	996	19	0
10	2O	933	0	996	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	1P	1135	0	1212	29	0
11	2P	1135	0	1212	29	0
12	1Q	1122	0	1179	24	0
12	2Q	1122	0	1179	23	0
13	1R	968	0	1033	21	0
13	2R	968	0	1033	21	0
14	1S	877	0	938	18	0
14	2S	870	0	923	27	0
15	1T	1091	0	1151	36	0
15	2T	1083	0	1136	24	0
16	1U	959	0	1019	22	0
16	2U	959	0	1019	20	0
17	1V	775	0	841	14	0
17	2V	771	0	830	24	0
18	1W	886	0	940	14	0
18	2W	886	0	940	16	0
19	1X	750	0	814	17	0
19	2X	750	0	814	17	0
20	1Y	810	0	892	15	0
20	2Y	810	0	887	22	0
21	1Z	1587	0	1598	23	0
21	2Z	1557	0	1564	32	0
22	10	608	0	622	10	0
22	20	608	0	622	11	0
23	11	754	0	823	13	0
23	21	759	0	837	21	0
24	12	588	0	643	5	0
24	22	592	0	654	12	0
25	13	469	0	518	8	0
25	23	464	0	514	6	0
26	14	546	0	522	27	0
26	24	536	0	514	44	0
27	15	459	0	476	7	0
27	25	455	0	465	6	0
28	16	453	0	473	8	0
28	26	449	0	469	4	0
29	17	418	0	467	14	0
29	27	418	0	467	9	0
30	18	517	0	582	24	0
30	28	517	0	582	20	0
31	19	307	0	335	6	0
31	29	307	0	335	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	1a	32246	0	16296	380	0
32	2a	32331	0	16339	490	0
33	1b	1842	0	1862	56	0
33	2b	1825	0	1828	73	0
34	1c	1558	0	1557	31	0
34	2c	1542	0	1517	53	0
35	1d	1665	0	1687	60	0
35	2d	1668	0	1703	42	0
36	1e	1133	0	1191	25	0
36	2e	1133	0	1191	29	0
37	1f	814	0	808	14	0
37	2f	816	0	808	18	0
38	1g	1235	0	1249	24	0
38	2g	1229	0	1238	21	0
39	1h	1098	0	1143	22	0
39	2h	1088	0	1126	15	0
40	1i	986	0	990	33	0
40	2i	966	0	953	50	0
41	1j	719	0	672	27	0
41	2j	710	0	661	40	0
42	1k	834	0	838	16	0
42	2k	833	0	836	15	0
43	1l	932	0	981	18	0
43	2l	932	0	981	19	0
44	1m	914	0	954	29	0
44	2m	895	0	920	34	0
45	1n	492	0	529	14	0
45	2n	492	0	529	23	0
46	1o	728	0	760	19	0
46	2o	728	0	760	15	0
47	1p	681	0	697	18	0
47	2p	677	0	686	19	0
48	1q	823	0	891	16	0
48	2q	823	0	891	12	0
49	1r	555	0	618	13	0
49	2r	555	0	618	14	0
50	1s	648	0	658	25	0
50	2s	645	0	635	33	0
51	1t	732	0	809	22	0
51	2t	733	0	795	26	0
52	1u	199	0	208	2	0
52	2u	199	0	208	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	1y	764	0	786	10	0
53	2y	749	0	757	32	0
54	10	5	0	0	0	0
54	11	4	0	0	0	0
54	13	2	0	0	0	0
54	14	1	0	0	0	0
54	15	2	0	0	0	0
54	17	2	0	0	0	0
54	18	1	0	0	0	0
54	19	2	0	0	0	0
54	1A	1075	0	0	0	0
54	1B	30	0	0	0	0
54	1D	14	0	0	0	0
54	1E	6	0	0	0	0
54	1F	10	0	0	0	0
54	1G	4	0	0	0	0
54	1H	2	0	0	0	0
54	1N	3	0	0	0	0
54	1O	1	0	0	0	0
54	1P	2	0	0	0	0
54	1Q	4	0	0	0	0
54	1R	3	0	0	0	0
54	1T	3	0	0	0	0
54	1U	2	0	0	0	0
54	1V	3	0	0	0	0
54	1W	2	0	0	0	0
54	1X	1	0	0	0	0
54	1Z	1	0	0	0	0
54	1a	280	0	0	0	0
54	1b	1	0	0	0	0
54	1d	5	0	0	0	0
54	1e	4	0	0	0	0
54	1f	1	0	0	0	0
54	1g	3	0	0	0	0
54	1h	2	0	0	0	0
54	1i	1	0	0	0	0
54	1l	2	0	0	0	0
54	1n	2	0	0	0	0
54	1o	1	0	0	0	0
54	1q	2	0	0	0	0
54	1r	1	0	0	0	0
54	1t	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	1y	4	0	0	0	0
54	20	2	0	0	0	0
54	21	1	0	0	0	0
54	26	1	0	0	0	0
54	27	1	0	0	0	0
54	28	2	0	0	0	0
54	2A	761	0	0	0	0
54	2B	19	0	0	0	0
54	2D	9	0	0	0	0
54	2E	5	0	0	0	0
54	2F	3	0	0	0	0
54	2G	3	0	0	0	0
54	2I	1	0	0	0	0
54	2N	1	0	0	0	0
54	2O	2	0	0	0	0
54	2P	2	0	0	0	0
54	2Q	2	0	0	0	0
54	2R	1	0	0	0	0
54	2T	3	0	0	0	0
54	2V	1	0	0	0	0
54	2W	2	0	0	0	0
54	2X	1	0	0	0	0
54	2a	193	0	0	0	0
54	2e	1	0	0	0	0
54	2f	1	0	0	0	0
54	2j	1	0	0	0	0
54	2l	1	0	0	0	0
54	2r	1	0	0	0	0
54	2t	1	0	0	0	0
55	18	8	0	14	5	0
55	1A	8	0	14	1	0
55	1T	8	0	14	0	0
55	1a	8	0	14	8	0
55	2A	16	0	28	2	0
55	2B	8	0	14	0	0
56	1B	12	0	12	1	0
56	1F	12	0	12	3	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	10	25	0	0	0	0
59	11	25	0	0	0	0
59	12	15	0	0	0	0
59	13	25	0	0	0	0
59	14	4	0	0	0	0
59	15	25	0	0	0	0
59	16	22	0	0	0	0
59	17	19	0	0	2	0
59	18	31	0	0	2	0
59	19	9	0	0	1	0
59	1A	4154	0	0	66	0
59	1B	109	0	0	1	0
59	1D	119	0	0	2	0
59	1E	81	0	0	4	0
59	1F	66	0	0	3	0
59	1G	20	0	0	2	0
59	1H	16	0	0	0	0
59	1I	9	0	0	0	0
59	1N	55	0	0	0	0
59	1O	29	0	0	1	0
59	1P	56	0	0	2	0
59	1Q	46	0	0	2	0
59	1R	37	0	0	2	0
59	1S	11	0	0	0	0
59	1T	39	0	0	3	0
59	1U	49	0	0	6	0
59	1V	34	0	0	3	0
59	1W	27	0	0	0	0
59	1X	27	0	0	0	0
59	1Y	20	0	0	1	0
59	1Z	13	0	0	1	0
59	1a	599	0	0	20	0
59	1b	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	1c	1	0	0	0	0
59	1d	8	0	0	1	0
59	1e	5	0	0	1	0
59	1f	3	0	0	0	0
59	1h	1	0	0	0	0
59	1i	1	0	0	0	0
59	1j	1	0	0	0	0
59	1k	1	0	0	0	0
59	1l	5	0	0	0	0
59	1m	2	0	0	0	0
59	1o	7	0	0	2	0
59	1p	3	0	0	0	0
59	1t	1	0	0	0	0
59	1y	7	0	0	1	0
59	20	13	0	0	0	0
59	21	22	0	0	1	0
59	22	4	0	0	1	0
59	23	3	0	0	0	0
59	24	2	0	0	2	0
59	25	10	0	0	0	0
59	26	5	0	0	0	0
59	27	9	0	0	1	0
59	28	16	0	0	0	0
59	29	3	0	0	0	0
59	2A	2665	0	0	77	0
59	2B	69	0	0	8	0
59	2D	59	0	0	0	0
59	2E	33	0	0	2	0
59	2F	26	0	0	0	0
59	2G	9	0	0	0	0
59	2H	4	0	0	0	0
59	2I	4	0	0	1	0
59	2N	6	0	0	0	0
59	2O	23	0	0	3	0
59	2P	30	0	0	1	0
59	2Q	28	0	0	1	0
59	2R	21	0	0	1	0
59	2S	7	0	0	1	0
59	2T	11	0	0	0	0
59	2U	20	0	0	1	0
59	2V	6	0	0	0	0
59	2W	20	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	2X	10	0	0	0	0
59	2Y	4	0	0	0	0
59	2Z	16	0	0	2	0
59	2a	459	0	0	36	0
59	2d	6	0	0	0	0
59	2e	2	0	0	0	0
59	2f	1	0	0	0	0
59	2j	2	0	0	1	0
59	2l	5	0	0	0	0
59	2m	2	0	0	0	0
59	2o	2	0	0	0	0
59	2p	3	0	0	0	0
59	2q	1	0	0	0	0
59	2r	5	0	0	0	0
59	2t	2	0	0	0	0
59	2y	5	0	0	0	0
All	All	298502	0	194517	3979	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 8.

All (3979) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1128:U:H3	1:1A:1132:A:N6	1.32	1.27
1:2A:2128:C:N4	1:2A:2160:G:H1	1.46	1.11
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.32	1.10
32:1a:78:G:H1	32:1a:91:C:N4	1.49	1.09
1:2A:2602:A:H1'	1:2A:2603:G:H5"	1.36	1.08
1:1A:1128:U:O4	1:1A:1132:A:N1	1.98	0.96
26:24:59:PHE:HA	26:24:61:ARG:N	1.80	0.95
1:2A:1041:C:H42	1:2A:1114:G:H1	1.15	0.94
1:2A:2131:G:H5"	1:2A:2132:U:H5'	1.52	0.92
32:2a:758:G:N7	59:2a:3272:HOH:O	2.03	0.92
1:2A:1087:G:H1	1:2A:1102:C:H42	1.13	0.91
33:2b:15:VAL:HB	33:2b:209:ARG:HB3	1.53	0.91
2:1B:81:G:N7	56:1B:230:ARG:NH2	2.19	0.89
1:2A:1059:G:N1	1:2A:1079:C:N4	2.21	0.89
1:1A:2459:G:OP2	59:1A:4524:HOH:O	1.90	0.88
1:2A:2128:C:N3	1:2A:2160:G:N2	2.20	0.88
16:1U:33:ARG:NH1	59:1U:320:HOH:O	2.06	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:975:A:H4'	32:1a:976:G:H5"	1.53	0.88
29:17:34:ARG:NH1	29:17:41:ARG:O	2.07	0.87
1:2A:1647:G:OP1	59:2A:5241:HOH:O	1.92	0.87
32:2a:1030:C:H42	32:2a:1031:G:H1	1.14	0.87
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.23	0.87
32:1a:1441:G:H5"	32:1a:1442:G:H5'	1.56	0.86
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.57	0.86
1:1A:354:A:H2	1:1A:1255:A:HO2'	1.22	0.86
1:2A:1271:G:OP2	59:2A:5241:HOH:O	1.94	0.86
1:2A:2427:C:OP1	59:2A:4539:HOH:O	1.93	0.86
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.55	0.85
32:1a:587:G:N7	59:1a:2079:HOH:O	2.09	0.85
1:2A:1062:G:H5'	1:2A:1070:A:H5"	1.58	0.85
32:2a:1030:C:N3	32:2a:1031:G:N2	2.24	0.85
1:1A:239:G:OP2	30:18:13:ARG:NH2	2.09	0.85
1:1A:206:G:OP2	59:1A:4848:HOH:O	1.95	0.85
29:17:24:THR:HG22	29:17:27:GLY:H	1.41	0.84
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.59	0.84
32:1a:78:G:N2	32:1a:91:C:N3	2.24	0.84
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.10	0.84
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.60	0.84
32:1a:38:G:H22	32:1a:397:A:H5'	1.43	0.84
32:2a:617:G:N7	59:2a:3340:HOH:O	2.11	0.84
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.10	0.84
32:1a:664:G:H22	32:1a:741:G:H1	1.27	0.83
32:1a:1456:G:O6	51:1t:54:LYS:NZ	2.11	0.83
4:1E:121:ASN:ND2	59:1E:414:HOH:O	2.11	0.83
26:24:59:PHE:HA	26:24:61:ARG:H	1.40	0.83
32:2a:975:A:H4'	32:2a:976:G:H5"	1.61	0.83
1:1A:1186:U:OP1	9:1N:25:ARG:NH1	2.12	0.82
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.60	0.82
40:2i:53:VAL:O	40:2i:55:ALA:N	2.11	0.82
44:2m:107:ALA:HB3	44:2m:111:LYS:HD2	1.60	0.82
1:2A:1063:G:N2	1:2A:1075:C:N3	2.26	0.82
1:1A:1681:A:OP2	59:1A:4279:HOH:O	1.97	0.82
1:2A:1071:G:N2	1:2A:1089:G:O6	2.10	0.81
1:1A:2124:U:O2	1:1A:2209:G:O6	1.98	0.81
1:2A:1912:A:OP1	59:2A:4196:HOH:O	1.99	0.81
1:1A:1829:U:H5'	3:1D:259:THR:HG22	1.63	0.81
22:10:10:THR:HG22	22:10:12:ASN:H	1.45	0.81
32:2a:617:G:OP2	59:2a:3343:HOH:O	1.98	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:35:SER:HB3	41:2j:73:ASP:H	1.45	0.81
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.14	0.81
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.14	0.81
32:2a:1030:C:N4	32:2a:1031:G:H1	1.77	0.81
1:2A:250:G:OP2	30:28:13:ARG:NH2	2.13	0.81
1:2A:855:G:O6	59:2A:4407:HOH:O	1.99	0.81
1:2A:2102:U:O2	1:2A:2187:G:O6	1.98	0.81
11:2P:70:GLN:NE2	59:2P:326:HOH:O	2.11	0.81
32:2a:1164:G:H1	32:2a:1172:C:H42	1.28	0.81
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.63	0.81
33:2b:88:ALA:HB1	33:2b:222:ILE:HD11	1.63	0.81
32:1a:189(A):C:H42	32:1a:189(J):G:H1	1.29	0.80
32:1a:1025:U:O2	32:1a:1036:G:O6	1.99	0.80
1:1A:2476:C:O2'	59:1A:5028:HOH:O	1.99	0.80
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.63	0.80
32:1a:427:U:OP1	35:1d:13:ARG:NH2	2.15	0.80
32:1a:1025:U:C2	32:1a:1036:G:O6	2.34	0.80
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.62	0.80
1:1A:2859:U:OP2	15:1T:95:ARG:NH1	2.15	0.80
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.62	0.80
32:2a:1030:C:N4	32:2a:1031:G:N1	2.26	0.80
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.64	0.80
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.62	0.80
1:2A:587:C:OP2	11:2P:21:ARG:NH2	2.13	0.79
1:1A:1001:G:OP2	12:1Q:14:ARG:NH2	2.13	0.79
1:1A:1085:G:O6	1:1A:1162:C:N4	2.14	0.79
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.15	0.79
1:2A:1087:G:H1	1:2A:1102:C:N4	1.79	0.79
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.64	0.79
4:1E:47:VAL:HG21	4:1E:86:PRO:HD2	1.64	0.79
1:1A:1317:G:OP2	59:1A:5107:HOH:O	1.98	0.79
1:1A:1695:C:OP1	59:1A:5107:HOH:O	2.01	0.79
15:1T:95:ARG:HG2	15:1T:95:ARG:HH11	1.47	0.79
1:2A:1076:C:H1'	1:2A:1077:A:H5'	1.63	0.79
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.65	0.79
1:1A:1846:A:OP2	3:1D:54:ARG:NH2	2.15	0.79
32:1a:538:G:H5"	43:1l:114:LYS:HB2	1.62	0.79
32:1a:1401:G:N7	53:1y:83:ARG:NH1	2.31	0.78
50:2s:20:LEU:HD23	50:2s:23:ASN:HD22	1.46	0.78
1:2A:2640:G:O3'	9:2N:74:ARG:NH2	2.13	0.78
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:45:ASP:OD1	21:2Z:49:ARG:NH1	2.17	0.78
1:1A:2138:G:OP2	1:1A:2188:G:N2	2.16	0.78
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.48	0.78
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.66	0.78
1:2A:1629:U:O4	59:2A:4644:HOH:O	2.01	0.78
1:1A:1577:C:O2'	1:1A:1578:C:O5'	1.99	0.78
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.16	0.78
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.17	0.77
1:2A:2536:G:O6	59:2A:5224:HOH:O	1.99	0.77
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.65	0.77
1:2A:1059:G:C6	1:2A:1079:C:N4	2.52	0.77
33:2b:18:GLY:HA2	33:2b:42:ILE:HD12	1.66	0.77
32:1a:1003:G:N2	32:1a:1004:A:N3	2.33	0.77
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.50	0.77
1:1A:1296:G:N7	11:1P:18:ARG:NH2	2.33	0.77
8:1I:38:LEU:HD12	8:1I:38:LEU:H	1.49	0.77
32:1a:78:G:H1	32:1a:91:C:H42	0.82	0.77
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.02	0.76
32:2a:1292:U:OP2	38:2g:41:ARG:NH2	2.19	0.76
1:2A:2527:C:N4	59:2A:5224:HOH:O	2.15	0.76
1:1A:1106:U:H4'	1:1A:1107:U:H5'	1.68	0.76
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.68	0.76
22:20:10:THR:HG22	22:20:12:ASN:H	1.51	0.76
1:2A:585:G:OP2	59:2A:5237:HOH:O	2.04	0.76
1:1A:2159:C:C2	1:1A:2176:G:N2	2.51	0.75
32:2a:1047:G:H5"	45:2n:4:LYS:HD3	1.68	0.75
1:2A:83:G:H1	1:2A:102:G:HO2'	1.33	0.75
1:2A:1063:G:N1	1:2A:1075:C:N4	2.34	0.75
1:1A:1749:G:N7	59:1A:4825:HOH:O	2.18	0.75
1:2A:2122:U:H3	1:2A:2176:A:H61	1.34	0.75
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.20	0.75
1:2A:1059:G:N2	1:2A:1079:C:N3	2.33	0.75
1:2A:2140:C:H2'	1:2A:2141:G:H8	1.51	0.75
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HD13	1.68	0.75
1:2A:11:G:H2'	1:2A:12:U:H5'	1.67	0.75
1:2A:685:A:OP1	59:2A:6356:HOH:O	2.03	0.75
1:2A:1058:G:H1	1:2A:1080:C:H42	1.31	0.75
32:2a:1271:G:O2'	59:2a:3589:HOH:O	2.05	0.75
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.67	0.75
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.68	0.75
41:2j:38:ILE:HG12	41:2j:71:LEU:HB3	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:18:LYS:NZ	59:1O:8116:HOH:O	2.18	0.75
26:14:59:PHE:HZ	50:1s:45:VAL:HG21	1.52	0.75
32:2a:547:A:OP1	59:2a:3495:HOH:O	2.04	0.75
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.68	0.75
32:1a:1007:C:N3	32:1a:1022:G:O6	2.20	0.74
32:1a:1300:G:N7	59:1a:2115:HOH:O	2.19	0.74
23:21:75:GLU:HA	23:21:78:LYS:HE2	1.68	0.74
32:2a:977:A:N6	32:2a:1224:G:OP1	2.18	0.74
51:1t:86:ARG:O	51:1t:90:GLN:NE2	2.20	0.74
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.20	0.74
17:2V:6:LYS:HB2	17:2V:38:LEU:HD21	1.68	0.74
1:1A:2159:C:N4	1:1A:2176:G:H1	1.84	0.74
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.69	0.74
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.21	0.74
40:2i:23:ASN:H	40:2i:23:ASN:HD22	1.34	0.74
35:1d:148:VAL:HG11	35:1d:158:ILE:HD12	1.69	0.74
1:2A:1009:A:OP2	59:2A:4860:HOH:O	2.04	0.74
1:2A:1937:A:O2'	59:2A:5332:HOH:O	2.06	0.74
1:2A:2602:A:H1'	1:2A:2603:G:C5'	2.16	0.74
15:2T:16:ARG:NH2	15:2T:83:ILE:O	2.20	0.74
1:1A:1694:G:OP1	59:1A:5107:HOH:O	2.06	0.74
1:2A:397:G:N7	59:2A:4402:HOH:O	2.20	0.74
32:2a:673:G:H2'	32:2a:674:G:C8	2.22	0.74
2:1B:6:C:H2'	2:1B:7:G:H5"	1.70	0.74
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.52	0.74
32:2a:474:G:H2'	32:2a:475:G:H8	1.51	0.73
32:1a:992:U:H4'	32:1a:993:G:H5'	1.70	0.73
28:26:13:CYS:SG	28:26:47:THR:HG21	2.27	0.73
1:1A:610:C:OP2	11:1P:21:ARG:NH2	2.21	0.73
26:24:18:CYS:SG	26:24:39:CYS:HB3	2.28	0.73
32:1a:201:C:H42	32:1a:216:G:H1	1.35	0.73
14:2S:71:ARG:NH1	14:2S:107:GLU:OE1	2.21	0.73
20:2Y:23:ARG:HG2	20:2Y:42:VAL:HG22	1.67	0.73
20:2Y:90:LEU:HD12	20:2Y:92:ASN:HB3	1.70	0.73
32:1a:1086:U:H3	32:1a:1099:G:H22	1.37	0.73
1:2A:731:C:OP1	59:2A:4197:HOH:O	2.05	0.73
15:1T:54:ARG:HA	15:1T:59:THR:HB	1.71	0.73
1:2A:1798:U:OP2	3:2D:274:ARG:NH2	2.21	0.73
1:1A:1367:A:N1	59:1A:7945:HOH:O	2.21	0.73
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.53	0.73
6:1G:63:ILE:HA	6:1G:143:GLU:HG3	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.22	0.73
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.53	0.73
1:2A:1971:A:OP2	3:2D:242:ARG:NH2	2.21	0.73
21:2Z:10:ARG:NH2	21:2Z:26:GLY:O	2.21	0.72
1:2A:775:G:O3'	59:2A:4140:HOH:O	2.06	0.72
1:2A:1315:C:OP2	59:2A:4095:HOH:O	2.06	0.72
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.71	0.72
1:1A:796:C:OP2	59:1A:5392:HOH:O	2.06	0.72
32:2a:580:U:OP2	59:2a:3271:HOH:O	2.04	0.72
19:1X:88:LYS:NZ	19:1X:90:GLU:OE1	2.23	0.72
32:1a:346:G:H3'	55:1a:1880:MPD:H51	1.70	0.72
1:2A:775:G:OP1	59:2A:5539:HOH:O	2.07	0.72
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.23	0.72
1:2A:991:C:OP2	59:2A:4112:HOH:O	2.07	0.72
1:2A:1891:G:N7	59:2A:4587:HOH:O	2.22	0.72
1:2A:2584:U:H5"	1:2A:2602:A:C2	2.25	0.72
32:2a:353:A:OP1	59:2a:3289:HOH:O	2.06	0.72
1:1A:2164:C:C2	1:1A:2171:G:N1	2.58	0.72
1:2A:1314:C:OP1	59:2A:4095:HOH:O	2.07	0.72
2:2B:75:G:OP1	59:2B:3149:HOH:O	2.06	0.72
26:24:16:CYS:SG	26:24:17:GLY:N	2.63	0.72
1:1A:2039:U:OP1	59:1A:4218:HOH:O	2.08	0.72
41:2j:17:ASP:OD1	41:2j:70:ARG:NH1	2.22	0.72
14:2S:93:LYS:HD2	14:2S:95:HIS:HB2	1.71	0.72
1:1A:121:G:OP2	59:1A:4126:HOH:O	2.07	0.72
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.72	0.72
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.22	0.72
2:2B:58:A:OP2	59:2B:3126:HOH:O	2.08	0.71
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.23	0.71
1:2A:1076:C:H4'	1:2A:1077:A:OP1	1.88	0.71
32:2a:980:C:OP2	59:2a:3470:HOH:O	2.07	0.71
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.55	0.71
37:1f:89:MET:HE1	49:1r:72:ARG:HB3	1.73	0.71
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.54	0.71
51:1t:60:GLU:HG3	51:1t:81:LYS:HD2	1.72	0.71
1:1A:2162:C:H2'	1:1A:2163:G:H8	1.53	0.71
28:16:13:CYS:SG	28:16:47:THR:HG21	2.30	0.71
4:2E:11:MET:HG2	4:2E:24:THR:HG22	1.71	0.71
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.72	0.71
1:1A:1128:U:N3	1:1A:1132:A:N6	2.09	0.71
32:1a:316:G:OP2	32:1a:351:G:O2'	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:701:A:OP2	59:1A:4645:HOH:O	2.09	0.71
15:1T:56:GLY:O	15:1T:59:THR:HG23	1.91	0.71
1:2A:853:G:N7	59:2A:4879:HOH:O	2.24	0.71
1:2A:1038:C:H42	1:2A:1117:G:H1	1.39	0.71
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.23	0.71
1:1A:1424:A:OP1	29:17:10:ARG:NH2	2.23	0.71
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.26	0.71
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.21	0.70
32:1a:574:A:OP2	59:1a:1905:HOH:O	2.10	0.70
7:2H:98:LEU:HD22	7:2H:125:VAL:HG23	1.71	0.70
32:2a:538:G:H5"	43:2l:114:LYS:HB2	1.73	0.70
2:2B:50:G:OP2	59:2B:3163:HOH:O	2.08	0.70
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.71	0.70
1:2A:2391:G:OP1	59:2A:6372:HOH:O	2.09	0.70
1:1A:2614:A:N7	59:1A:5182:HOH:O	2.24	0.70
32:1a:73:G:H1	32:1a:96:U:H3	1.40	0.70
32:1a:1030(C):G:N7	32:1a:1031:G:N2	2.39	0.70
37:2f:10:LEU:HD21	37:2f:61:LEU:HD22	1.74	0.70
1:1A:2613:C:OP2	59:1A:7195:HOH:O	2.09	0.70
36:1e:143:ARG:NH1	39:1h:77:GLU:OE2	2.25	0.70
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.25	0.70
1:2A:951:C:OP1	59:2A:5274:HOH:O	2.08	0.70
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.25	0.70
1:2A:1839:G:O6	59:2A:5268:HOH:O	2.08	0.70
1:1A:1223:C:H2'	1:1A:1224:C:H6	1.57	0.70
1:1A:1834:A:O2'	3:1D:259:THR:HG21	1.92	0.70
1:1A:2584:A:C8	4:1E:144:ARG:HG2	2.26	0.70
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.54	0.70
1:1A:1223:C:H2'	1:1A:1224:C:C6	2.27	0.70
30:18:15:LYS:HB3	55:18:102:MPD:H53	1.74	0.70
1:2A:309:G:N3	1:2A:329:G:O2'	2.25	0.70
47:1p:53:VAL:HG13	47:1p:79:VAL:HG12	1.74	0.70
1:2A:2826:A:N7	59:2A:5995:HOH:O	2.25	0.70
32:2a:164:U:H2'	32:2a:165:C:C6	2.27	0.70
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.74	0.70
1:1A:1993:A:OP2	3:1D:242:ARG:NH2	2.25	0.69
34:2c:6:HIS:HD2	34:2c:9:GLY:H	1.38	0.69
32:2a:53:A:OP2	59:2a:3285:HOH:O	2.09	0.69
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.75	0.69
1:1A:1361:C:OP2	59:1A:4593:HOH:O	2.10	0.69
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:58:A:OP2	59:2B:3128:HOH:O	2.08	0.69
6:1G:115:ARG:HB3	6:1G:136:ARG:HH22	1.57	0.69
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.26	0.69
3:1D:88:ARG:NH1	59:1D:491:HOH:O	2.26	0.69
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.57	0.69
6:2G:63:ILE:HA	6:2G:143:GLU:HG3	1.73	0.69
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.57	0.69
1:1A:1151:U:H2'	1:1A:1152:G:C8	2.28	0.69
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.28	0.69
35:1d:18:LYS:NZ	35:1d:31:CYS:SG	2.65	0.69
35:1d:106:TYR:HE2	35:1d:107:ARG:HH11	1.38	0.69
24:22:35:LEU:HD21	24:22:49:LYS:HE2	1.74	0.69
34:2c:120:VAL:HA	34:2c:123:GLN:HE21	1.58	0.69
53:2y:52:ALA:HB2	53:2y:77:LEU:HD11	1.74	0.69
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.23	0.69
50:1s:41:VAL:HG12	50:1s:44:MET:HG3	1.75	0.69
32:2a:17:U:H2'	32:2a:18:C:C6	2.28	0.69
33:1b:21:ARG:O	33:1b:23:ARG:N	2.26	0.69
1:2A:1342:A:OP2	59:2A:3916:HOH:O	2.11	0.69
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.74	0.69
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.26	0.68
3:2D:134:ARG:NH1	3:2D:188:GLU:OE2	2.25	0.68
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.41	0.68
21:1Z:45:ASP:OD1	21:1Z:49:ARG:NH1	2.26	0.68
32:1a:1030:C:N3	32:1a:1031:G:N2	2.41	0.68
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.93	0.68
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.75	0.68
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.24	0.68
1:2A:331:A:N1	59:2A:5194:HOH:O	2.25	0.68
1:1A:497:A:OP1	59:1A:5956:HOH:O	2.11	0.68
1:1A:807:G:OP1	59:1A:5815:HOH:O	2.11	0.68
1:1A:1082:G:OP2	7:1H:59:ARG:NH1	2.27	0.68
1:1A:1556:A:H2'	1:1A:1557:A:O4'	1.94	0.68
1:1A:2849:G:H5'	13:1R:46:GLY:HA2	1.76	0.68
5:1F:164:ARG:HE	56:1F:311:ARG:HH22	1.41	0.68
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.74	0.68
1:1A:2084:A:OP1	59:1A:5709:HOH:O	2.10	0.68
4:1E:29:GLY:HA3	59:1E:430:HOH:O	1.92	0.68
35:1d:167:GLY:H	35:1d:168:ARG:NH2	1.91	0.68
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.27	0.68
32:2a:457:C:H2'	32:2a:458:C:H6	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:91:PRO:HG3	33:2b:155:LEU:HD23	1.73	0.68
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.59	0.68
32:1a:974:A:OP2	45:1n:29:ARG:NH2	2.26	0.68
1:1A:2798:C:OP1	4:1E:41:LYS:NZ	2.27	0.68
35:1d:85:LYS:HE3	35:1d:86:LYS:H	1.57	0.68
1:1A:894:U:OP2	59:1A:4429:HOH:O	2.12	0.68
1:1A:1405:A:H61	1:1A:1418:U:H3	1.41	0.68
6:1G:16:ARG:NH2	59:1G:3110:HOH:O	2.25	0.68
15:1T:35:LYS:HG2	15:1T:40:THR:HG22	1.74	0.68
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.27	0.68
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.76	0.68
6:1G:77:ILE:N	6:1G:82:LEU:O	2.25	0.67
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.75	0.67
1:2A:2156:G:N7	1:2A:2157:G:N2	2.43	0.67
1:2A:2255:G:OP2	59:2A:4439:HOH:O	2.11	0.67
1:2A:2413:G:O6	59:2A:5700:HOH:O	2.10	0.67
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	1.76	0.67
1:1A:1062:G:N7	59:1A:5460:HOH:O	2.26	0.67
3:2D:71:ASP:HB3	3:2D:103:ARG:HH22	1.60	0.67
18:2W:14:PRO:HG2	18:2W:78:GLU:HG2	1.76	0.67
36:2e:137:GLU:HG2	36:2e:140:ARG:HH11	1.59	0.67
44:2m:96:LEU:O	44:2m:110:ARG:NH1	2.26	0.67
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.75	0.67
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.59	0.67
35:2d:175:SER:HB3	35:2d:186:LEU:HD11	1.77	0.67
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.77	0.67
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.76	0.67
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.94	0.67
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.27	0.67
1:1A:2148:A:H4'	1:1A:2149:G:O5'	1.95	0.67
1:1A:2402:U:OP2	59:1A:8098:HOH:O	2.12	0.67
1:2A:1063:G:N1	1:2A:1075:C:C4	2.63	0.67
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.76	0.67
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5"	1.76	0.67
17:1V:29:PRO:HA	17:1V:61:VAL:HG22	1.75	0.67
32:1a:347:G:C8	55:1a:1880:MPD:H53	2.30	0.67
1:2A:1993:U:OP2	59:2A:6406:HOH:O	2.13	0.67
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.28	0.67
1:1A:2470:G:OP2	59:1A:5020:HOH:O	2.12	0.67
1:1A:2092:G:OP2	59:1A:7139:HOH:O	2.12	0.66
1:1A:2701:U:O2'	59:1A:7389:HOH:O	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.29	0.66
1:2A:833:U:O2	11:2P:55:ARG:NH2	2.28	0.66
1:2A:1153:C:OP2	59:2A:4098:HOH:O	2.13	0.66
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.77	0.66
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.59	0.66
4:1E:77:ILE:HD13	4:1E:195:LEU:HD13	1.77	0.66
32:1a:1230:C:OP2	59:1a:2096:HOH:O	2.13	0.66
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.76	0.66
33:2b:119:GLU:OE2	33:2b:153:ARG:NH1	2.27	0.66
1:1A:2596:U:H2'	1:1A:2597:U:H2'	1.77	0.66
50:1s:3:ARG:HH21	50:1s:7:LYS:HE2	1.60	0.66
32:2a:427:U:OP1	35:2d:13:ARG:NH2	2.26	0.66
1:1A:1312:G:O5'	18:1W:15:ARG:NH2	2.28	0.66
1:1A:2761:A:H5'	7:1H:4:ILE:HD12	1.76	0.66
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.75	0.66
26:24:48:ARG:HG2	26:24:52:THR:HA	1.76	0.66
32:2a:1500:A:OP1	59:2a:3390:HOH:O	2.13	0.66
12:1Q:22:LYS:NZ	59:1Q:309:HOH:O	2.29	0.66
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.76	0.66
16:1U:33:ARG:NH2	59:1U:322:HOH:O	2.29	0.66
44:1m:13:LYS:HA	44:1m:44:ARG:HH11	1.60	0.66
1:2A:1639:U:H2'	1:2A:1640:C:H5"	1.76	0.66
1:1A:239:G:P	30:18:13:ARG:HH22	2.17	0.66
1:1A:2045:G:H5'	1:1A:2629:C:H4'	1.78	0.66
17:1V:1:MET:HE1	17:1V:44:LYS:HD2	1.78	0.66
32:1a:1024:G:H2'	32:1a:1025:U:H5"	1.78	0.66
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.59	0.66
32:2a:1146:A:H3'	32:2a:1147:C:H5"	1.77	0.66
1:1A:721:G:N7	59:1A:7691:HOH:O	2.29	0.66
1:1A:721:G:H1'	5:1F:74:ARG:HD3	1.77	0.66
32:1a:1020:U:H2'	32:1a:1021:G:C8	2.30	0.66
32:1a:1297:C:O2'	38:1g:114:ARG:NH2	2.29	0.66
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.29	0.66
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.77	0.66
1:2A:1803:A:O2'	3:2D:259:THR:HG21	1.95	0.66
4:2E:111:ARG:HG3	4:2E:160:TYR:CD2	2.30	0.66
10:2O:66:LYS:NZ	59:2O:301:HOH:O	2.29	0.66
12:2Q:60:ARG:NH2	21:2Z:181:GLU:OE1	2.25	0.66
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.78	0.66
18:1W:14:PRO:HG2	18:1W:78:GLU:HG2	1.77	0.65
1:2A:1939:5MU:O5'	59:2A:5332:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.94	0.65
1:2A:2453:A:OP1	59:2A:5166:HOH:O	2.12	0.65
1:2A:2099:U:H3	1:2A:2190:G:H1	1.44	0.65
2:2B:22:U:H2'	2:2B:23:G:C8	2.31	0.65
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.61	0.65
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.78	0.65
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.79	0.65
32:1a:651:C:OP1	59:1a:2163:HOH:O	2.14	0.65
32:1a:1108:G:O6	59:1a:2035:HOH:O	2.13	0.65
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.77	0.65
10:2O:86:ILE:O	59:2O:310:HOH:O	2.13	0.65
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.79	0.65
1:1A:966:G:OP1	59:1A:8224:HOH:O	2.13	0.65
1:2A:957:A:OP2	59:2A:6108:HOH:O	2.14	0.65
1:2A:1068:G:H3'	1:2A:1096:A:OP2	1.96	0.65
1:2A:1250:G:N7	11:2P:18:ARG:NH2	2.44	0.65
23:21:76:ARG:HH22	23:21:97:LEU:HB3	1.61	0.65
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	1.78	0.65
1:2A:15:G:OP2	59:2A:4796:HOH:O	2.12	0.65
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.29	0.65
32:2a:266:G:N3	32:2a:266:G:H5"	2.11	0.65
1:1A:1121:C:N4	1:1A:1123:A:N1	2.45	0.65
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.79	0.65
1:2A:2152:G:H2'	1:2A:2153:G:C8	2.31	0.65
32:2a:964:A:OP1	59:2a:3424:HOH:O	2.14	0.65
32:1a:346:G:H5"	55:1a:1880:MPD:H4	1.79	0.65
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.78	0.65
23:21:3:LYS:HB2	23:21:61:ARG:NH1	2.12	0.65
1:1A:2156:A:N6	1:1A:2179:G:H4'	2.11	0.65
2:1B:75:G:H5"	2:1B:75:G:H8	1.62	0.65
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.79	0.65
37:1f:10:LEU:HD21	37:1f:61:LEU:HD22	1.78	0.65
53:1y:49:VAL:HG22	53:1y:66:LYS:HG3	1.78	0.65
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.32	0.65
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.79	0.65
23:11:3:LYS:HG3	23:11:4:VAL:H	1.61	0.65
35:1d:194:LEU:HD12	35:1d:195:ALA:H	1.62	0.65
1:1A:1405:A:N6	1:1A:1418:U:H3	1.94	0.64
21:2Z:157:LEU:HB3	21:2Z:161:VAL:HG12	1.78	0.64
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.78	0.64
1:1A:2151:C:N3	1:1A:2181:G:O6	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.80	0.64
6:2G:145:THR:HG23	6:2G:148:MET:HG2	1.78	0.64
32:2a:961:U:OP2	32:2a:1223:C:O2'	2.09	0.64
32:2a:1318:A:H5"	50:2s:3:ARG:HH22	1.62	0.64
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.69	0.64
40:2i:42:ARG:NH1	40:2i:71:SER:O	2.30	0.64
1:1A:2486:C:OP1	59:1A:5096:HOH:O	2.15	0.64
14:2S:50:SER:O	14:2S:76:LYS:NZ	2.29	0.64
17:2V:62:LEU:HD21	17:2V:95:LEU:HB2	1.79	0.64
17:2V:98:GLU:OE1	17:2V:100:ARG:NH1	2.30	0.64
1:1A:2623:U:H6	1:1A:2623:U:H5'	1.63	0.64
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.79	0.64
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.08	0.64
32:2a:444:C:H42	32:2a:490:G:H1	1.44	0.64
32:2a:1025:U:H3	32:2a:1036:G:H1	1.43	0.64
32:2a:1200:C:OP1	59:2a:3465:HOH:O	2.15	0.64
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.79	0.64
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.33	0.64
1:1A:1754:G:N7	59:1A:4852:HOH:O	2.29	0.64
1:1A:1788:U:OP1	59:1A:6708:HOH:O	2.15	0.64
1:1A:1861:C:OP2	59:1A:4793:HOH:O	2.15	0.64
1:2A:1495:A:OP2	59:2A:3891:HOH:O	2.15	0.64
16:2U:5:LYS:NZ	59:2U:306:HOH:O	2.28	0.64
32:2a:891:U:OP1	59:2a:3432:HOH:O	2.15	0.64
1:1A:615:G:O6	59:1A:4776:HOH:O	2.10	0.64
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.80	0.64
23:21:3:LYS:HB2	23:21:61:ARG:HH12	1.63	0.64
32:2a:1305:G:OP1	52:2u:2:GLY:N	2.31	0.64
1:1A:572:A:H61	17:1V:19:LYS:H	1.45	0.64
1:2A:1155:A:H5"	16:2U:55:ARG:HD3	1.80	0.64
1:2A:2723:C:OP1	13:2R:3:HIS:ND1	2.22	0.64
32:2a:289:G:OP2	59:2a:3290:HOH:O	2.14	0.64
1:1A:70:A:N7	19:1X:31:HIS:HE1	1.95	0.64
1:1A:1218:G:O2'	1:1A:1219:A:O5'	2.15	0.64
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.80	0.64
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.78	0.64
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.13	0.64
40:2i:53:VAL:C	40:2i:55:ALA:H	2.06	0.64
2:1B:116:G:H8	2:1B:116:G:H5"	1.62	0.64
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.30	0.64
32:1a:96:U:H2'	32:1a:97:G:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:13:ARG:NH1	35:1d:38:TYR:O	2.30	0.64
1:2A:2104:G:O6	1:2A:2185:C:N3	2.31	0.64
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.80	0.64
32:2a:1099:G:OP2	33:2b:144:ARG:NH2	2.31	0.64
1:1A:630:U:OP1	5:1F:102:PRO:HA	1.98	0.64
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.80	0.64
26:14:59:PHE:CZ	50:1s:45:VAL:HG21	2.32	0.64
6:2G:46:ALA:HB2	6:2G:53:LEU:HG	1.80	0.64
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.31	0.64
3:1D:113:VAL:HG12	59:1D:501:HOH:O	1.97	0.63
32:1a:176:C:H2'	32:1a:177:C:C6	2.33	0.63
32:1a:812:C:N3	59:1a:1935:HOH:O	2.29	0.63
20:2Y:82:PRO:O	20:2Y:101:LYS:NZ	2.27	0.63
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.16	0.63
1:1A:427:G:N7	59:1A:4813:HOH:O	2.30	0.63
32:1a:222:U:H2'	32:1a:223:U:C6	2.33	0.63
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.34	0.63
41:1j:33:GLN:O	41:1j:75:ILE:N	2.28	0.63
1:2A:1053:C:H2'	1:2A:1054:A:C8	2.33	0.63
32:2a:664:G:H22	32:2a:741:G:H1	1.47	0.63
1:1A:1151:U:H2'	1:1A:1152:G:H8	1.64	0.63
32:2a:335:C:O2'	32:2a:1433:A:N3	2.26	0.63
32:2a:503:C:OP2	43:2l:116:SER:HB3	1.99	0.63
2:1B:66:A:H61	2:1B:108:U:H2'	1.64	0.63
13:1R:99:LYS:NZ	59:1R:309:HOH:O	2.31	0.63
1:2A:588:U:H2'	1:2A:589:C:C6	2.32	0.63
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.32	0.63
8:2I:86:THR:HA	8:2I:123:LEU:HD23	1.80	0.63
30:18:56:GLU:HG2	59:18:222:HOH:O	1.99	0.63
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.31	0.63
1:2A:2602:A:H4'	1:2A:2603:G:OP1	1.99	0.63
32:2a:920:U:H2'	32:2a:921:U:C6	2.34	0.63
14:1S:59:LYS:HD2	14:1S:60:GLY:H	1.64	0.63
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.29	0.63
1:2A:84:A:N1	1:2A:98:G:O2'	2.31	0.63
1:2A:1530:C:H42	1:2A:1539:G:H1	1.45	0.63
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.32	0.63
33:1b:69:LEU:HD13	33:1b:91:PRO:HB2	1.81	0.63
1:1A:354:A:H2	1:1A:1255:A:O2'	1.80	0.62
32:1a:38:G:N2	32:1a:397:A:H5'	2.14	0.62
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1278:U:H5"	32:2a:1279:A:H5'	1.79	0.62
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.63	0.62
38:2g:15:ASP:OD1	38:2g:20:ASP:N	2.28	0.62
1:2A:2142:C:H2'	1:2A:2143:C:C6	2.34	0.62
21:2Z:5:LEU:HD11	21:2Z:39:VAL:HB	1.79	0.62
29:27:33:ARG:NH2	59:27:3107:HOH:O	2.31	0.62
43:2l:60:LEU:HD21	43:2l:66:VAL:HG22	1.82	0.62
1:1A:1501:U:OP1	13:1R:77:ARG:NH1	2.28	0.62
1:1A:2859:U:P	15:1T:95:ARG:HH12	2.22	0.62
51:1t:47:GLY:HA2	51:1t:48:LYS:HB2	1.81	0.62
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.82	0.62
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.81	0.62
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.33	0.62
1:1A:936:C:O2'	1:1A:937:A:O5'	2.14	0.62
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.14	0.62
32:2a:677:U:H3	32:2a:713:G:H22	1.47	0.62
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.12	0.62
42:2k:62:GLN:HB2	42:2k:93:GLN:HG3	1.80	0.62
1:1A:1040:C:OP1	16:1U:53:ARG:NH2	2.32	0.62
1:1A:2181:G:H2'	1:1A:2182:G:H8	1.63	0.62
6:1G:50:ALA:C	6:1G:52:ILE:H	2.07	0.62
37:1f:69:GLU:O	37:1f:72:VAL:HG12	1.99	0.62
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	1.80	0.62
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.82	0.62
1:2A:583:G:OP2	16:2U:10:ARG:HD2	1.99	0.62
32:2a:564:C:O2'	39:2h:91:ARG:NH2	2.33	0.62
1:1A:9:U:H3	1:1A:2641:A:H2	1.47	0.62
35:1d:167:GLY:H	35:1d:168:ARG:HH21	1.46	0.62
1:2A:528:A:OP2	9:2N:114:ARG:NH1	2.30	0.62
1:2A:2732:G:O6	59:2A:4787:HOH:O	2.13	0.62
33:2b:185:ILE:HG23	33:2b:199:TYR:HB2	1.81	0.62
10:1O:80:ASP:OD1	15:1T:64:ARG:NH2	2.32	0.62
24:12:23:LYS:O	24:12:27:GLU:HG3	2.00	0.62
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.80	0.62
1:2A:526:A:OP1	59:2A:4109:HOH:O	2.16	0.62
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.30	0.62
1:1A:2346:G:H5'	14:1S:9:ARG:HG2	1.82	0.62
33:1b:19:HIS:NE2	33:1b:189:ASP:OD2	2.33	0.62
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.35	0.62
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	1.81	0.62
1:1A:1112:U:H2'	1:1A:1113:A:C6	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2331:G:H22	14:1S:3:ARG:NE	1.98	0.61
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.82	0.61
13:1R:83:ILE:O	13:1R:86:ARG:HG2	1.99	0.61
1:2A:1075:C:H2'	1:2A:1076:C:H5'	1.80	0.61
34:2c:6:HIS:CD2	34:2c:9:GLY:H	2.17	0.61
1:1A:1186:U:P	9:1N:25:ARG:HH12	2.23	0.61
32:1a:673:G:H2'	32:1a:674:G:C8	2.35	0.61
32:1a:926:G:O6	59:1a:2023:HOH:O	2.16	0.61
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.35	0.61
1:2A:1067:A:O4'	1:2A:1068:G:N2	2.33	0.61
1:2A:1102:C:H2'	1:2A:1103:A:C8	2.35	0.61
1:2A:1250:G:H5"	59:2A:5238:HOH:O	1.99	0.61
1:2A:2206:G:H8	1:2A:2207:G:N7	1.98	0.61
6:2G:66:GLN:HG3	26:24:1:MET:HE3	1.80	0.61
6:2G:114:ILE:HG23	6:2G:136:ARG:NH2	2.15	0.61
59:2a:3655:HOH:O	35:2d:86:LYS:HD2	1.99	0.61
1:1A:1132:A:H3'	1:1A:1132:A:N3	2.14	0.61
1:1A:1232:G:H5"	17:1V:81:TYR:CE1	2.35	0.61
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.82	0.61
40:2i:50:LEU:HB2	40:2i:56:LEU:HD23	1.82	0.61
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.00	0.61
22:10:11:ARG:O	22:10:14:ARG:NH2	2.25	0.61
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.16	0.61
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.30	0.61
1:2A:1064:C:H3'	1:2A:1065:U:H5'	1.81	0.61
16:2U:36:ARG:HD2	16:2U:40:PHE:CZ	2.36	0.61
32:2a:1002:G:H2'	32:2a:1003:G:C8	2.35	0.61
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.82	0.61
1:1A:2614:A:H1'	1:1A:2615:G:H5"	1.81	0.61
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.82	0.61
15:1T:64:ARG:HB2	15:1T:73:GLU:HG2	1.81	0.61
26:24:59:PHE:CE1	50:2s:64:GLU:HB2	2.35	0.61
32:2a:101:A:H5'	51:2t:10:LEU:HD21	1.82	0.61
33:2b:78:GLN:O	33:2b:94:ASN:ND2	2.34	0.61
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.35	0.61
5:1F:101:LEU:O	5:1F:106:ARG:NH1	2.32	0.61
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.36	0.61
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.35	0.61
14:2S:93:LYS:NZ	59:2S:207:HOH:O	2.34	0.61
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.82	0.61
1:1A:2155:G:C2	1:1A:2179:G:H2'	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2443:U:OP1	59:1A:4321:HOH:O	2.16	0.61
5:1F:191:ARG:NH2	59:1F:463:HOH:O	2.32	0.61
6:1G:139:LEU:HD21	6:1G:149:VAL:HG11	1.81	0.61
1:2A:1065:U:H4'	1:2A:1066:U:H5'	1.82	0.61
1:2A:2525:G:O6	59:2A:5228:HOH:O	2.15	0.61
15:2T:95:ARG:HG2	15:2T:95:ARG:HH11	1.66	0.61
32:2a:955:U:O2'	50:2s:83:HIS:HD2	1.82	0.61
32:2a:1222:G:O6	59:2a:3470:HOH:O	2.15	0.61
34:2c:40:ARG:NH2	34:2c:55:VAL:O	2.34	0.61
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.36	0.61
1:1A:2348:A:H61	22:10:43:THR:HG22	1.66	0.61
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.32	0.61
1:1A:2153:G:N7	1:1A:2180:A:N6	2.49	0.61
11:1P:83:VAL:HG12	11:1P:112:LEU:HD21	1.82	0.61
1:2A:2128:C:H42	1:2A:2160:G:H1	0.71	0.61
1:2A:2274:A:OP2	59:2A:5693:HOH:O	2.16	0.60
32:2a:962:C:O2'	59:2a:3467:HOH:O	2.06	0.60
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.16	0.60
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.81	0.60
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.82	0.60
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.83	0.60
17:2V:40:LEU:HB2	17:2V:46:VAL:HG13	1.83	0.60
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.35	0.60
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.14	0.60
32:1a:173:U:OP1	59:1a:2410:HOH:O	2.16	0.60
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.81	0.60
1:2A:468:G:N7	29:27:39:ARG:NH2	2.46	0.60
1:2A:601:C:OP1	5:2F:108:LYS:HE3	2.01	0.60
4:2E:52:LEU:HB3	4:2E:53:PRO:HD2	1.83	0.60
4:2E:199:ARG:NH1	59:2E:423:HOH:O	2.33	0.60
24:22:16:LEU:O	24:22:67:LYS:NZ	2.34	0.60
25:23:8:LEU:HD13	25:23:31:LEU:HD22	1.82	0.60
26:24:20:ASN:HD21	26:24:38:LYS:HG3	1.64	0.60
32:2a:116:A:OP1	59:2a:3290:HOH:O	2.17	0.60
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	1.82	0.60
1:1A:849:A:OP1	59:1A:4444:HOH:O	2.16	0.60
5:1F:188:ARG:NH2	59:1F:417:HOH:O	2.33	0.60
1:2A:886:C:O2'	1:2A:889:C:N4	2.34	0.60
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.01	0.60
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.50	0.60
32:2a:978:A:O2'	32:2a:1322:C:N3	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1104:G:O5'	33:2b:111:ARG:HD2	2.02	0.60
32:1a:612:C:O2	32:1a:629:G:N2	2.34	0.60
32:2a:1035:A:H2'	32:2a:1036:G:C8	2.37	0.60
1:1A:1787:G:OP2	59:1A:5832:HOH:O	2.16	0.60
7:1H:25:LYS:HG3	7:1H:34:GLU:HG2	1.83	0.60
1:2A:1272:A:OP1	59:2A:4748:HOH:O	2.17	0.60
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.02	0.60
2:2B:14:U:OP2	2:2B:70:C:O2'	2.16	0.60
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.82	0.60
32:2a:662:G:H2'	32:2a:663:A:C8	2.36	0.60
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.37	0.60
46:2o:35:ARG:HH21	46:2o:59:MET:HE2	1.66	0.60
11:1P:68:GLN:HG3	59:1P:353:HOH:O	2.02	0.60
50:1s:52:TYR:HB2	50:1s:57:HIS:CE1	2.36	0.60
1:2A:2584:U:H2'	1:2A:2585:U:H2'	1.83	0.60
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.16	0.60
32:1a:77:G:H2'	32:1a:78:G:H5'	1.82	0.60
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.84	0.60
35:2d:108:LEU:HD13	35:2d:174:LEU:HD13	1.84	0.60
32:1a:596:C:OP2	59:1a:1957:HOH:O	2.16	0.60
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.84	0.60
1:2A:1041:C:N4	1:2A:1114:G:H1	1.96	0.60
22:20:11:ARG:O	22:20:14:ARG:NH2	2.30	0.60
34:2c:57:ILE:HG12	34:2c:66:VAL:HG22	1.83	0.60
1:1A:572:A:N6	17:1V:19:LYS:H	2.00	0.60
8:1I:4:ILE:HD11	8:1I:44:LEU:HD13	1.83	0.60
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.65	0.60
32:1a:17:U:H2'	32:1a:18:C:C6	2.37	0.60
32:1a:890:G:O2'	32:1a:906:G:O6	2.12	0.60
27:25:16:ARG:HG2	27:25:16:ARG:HH11	1.67	0.60
33:1b:40:HIS:HB3	33:1b:190:THR:HG21	1.83	0.59
38:1g:111:ARG:NH1	38:1g:113:GLU:OE1	2.35	0.59
51:1t:10:LEU:CD2	51:1t:11:SER:H	2.14	0.59
1:2A:144:C:H5'	19:2X:2:LYS:HE3	1.84	0.59
1:2A:1058:G:H1	1:2A:1080:C:N4	2.00	0.59
15:2T:24:PRO:HA	15:2T:49:VAL:HG22	1.84	0.59
1:1A:624:C:OP1	5:1F:108:LYS:HE3	2.02	0.59
1:1A:1094:A:OP2	1:1A:1155:C:N4	2.35	0.59
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.84	0.59
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.84	0.59
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:50:LEU:HD23	40:2i:85:LEU:HD11	1.83	0.59
59:1A:7611:HOH:O	4:1E:144:ARG:HD2	2.01	0.59
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.84	0.59
9:1N:15:LEU:HB2	9:1N:135:PRO:HB2	1.84	0.59
32:1a:376:G:H5"	47:1p:5:ARG:HD3	1.84	0.59
1:2A:82:G:N1	1:2A:103:A:OP2	2.29	0.59
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.17	0.59
1:1A:1588:G:O6	59:1A:5372:HOH:O	2.14	0.59
1:1A:2736:C:OP1	13:1R:3:HIS:ND1	2.29	0.59
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.85	0.59
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.65	0.59
41:2j:9:ARG:NH2	41:2j:95:GLU:OE1	2.35	0.59
28:16:14:THR:HB	28:16:48:VAL:O	2.03	0.59
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.31	0.59
32:2a:474:G:H2'	32:2a:475:G:C8	2.35	0.59
1:1A:2137:G:H2'	1:1A:2139:A:N6	2.17	0.59
1:1A:2584:A:N7	4:1E:144:ARG:HG2	2.18	0.59
19:1X:60:ARG:HH12	29:17:47:ARG:HH22	1.50	0.59
35:1d:196:LEU:HD12	35:1d:196:LEU:H	1.67	0.59
1:2A:2318:G:N2	14:2S:3:ARG:HH11	2.00	0.59
41:2j:61:GLU:OE1	45:2n:58:LYS:NZ	2.35	0.59
1:1A:2451:A:C8	1:1A:2451:A:H5'	2.38	0.59
15:1T:59:THR:HG21	59:1T:8121:HOH:O	2.02	0.59
32:1a:1470:G:N7	59:1a:2290:HOH:O	2.32	0.59
34:1c:82:GLU:OE1	34:1c:85:ARG:NH2	2.33	0.59
41:1j:52:GLY:O	45:1n:41:ARG:NH2	2.36	0.59
1:2A:1939:5MU:H2'	59:2A:5332:HOH:O	2.02	0.59
1:2A:2184:G:N1	1:2A:2185:C:O2	2.36	0.59
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.35	0.59
32:2a:434:U:H2'	32:2a:435:C:C6	2.37	0.59
32:2a:934:C:OP1	59:2a:3329:HOH:O	2.17	0.59
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.84	0.59
31:19:8:LYS:NZ	59:19:208:HOH:O	2.30	0.59
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.85	0.59
32:2a:890:G:O2'	32:2a:906:G:O6	2.16	0.59
35:2d:13:ARG:NH1	35:2d:38:TYR:O	2.34	0.59
1:1A:1899:A:H5'	1:1A:1900:G:OP2	2.03	0.59
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.38	0.59
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.02	0.59
35:1d:170:VAL:HG12	35:1d:174:LEU:HB2	1.85	0.59
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.85	0.59
32:2a:316:G:OP2	32:2a:351:G:O2'	2.19	0.59
1:1A:2320:G:O2'	1:1A:2322:A:N7	2.35	0.59
14:1S:15:ARG:O	14:1S:19:LYS:HG2	2.03	0.59
32:1a:266:G:H5"	32:1a:268:C:H41	1.67	0.59
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.36	0.59
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.01	0.59
48:1q:78:GLU:HG2	48:1q:79:SER:H	1.68	0.59
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.35	0.59
6:2G:114:ILE:HG23	6:2G:136:ARG:HH22	1.66	0.59
33:2b:212:GLN:NE2	33:2b:235:SER:OG	2.35	0.59
1:1A:1086:C:H2'	1:1A:1087:C:O4'	2.03	0.58
8:1I:72:LEU:HA	8:1I:75:LEU:HD11	1.83	0.58
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.48	0.58
7:2H:3:ARG:HB3	7:2H:3:ARG:HH11	1.68	0.58
32:2a:1137:C:H1'	32:2a:1138:G:C2	2.38	0.58
41:2j:52:GLY:O	45:2n:41:ARG:NH2	2.36	0.58
1:2A:2706:G:N7	59:2A:4725:HOH:O	2.32	0.58
2:2B:81:G:N7	59:2B:3116:HOH:O	2.31	0.58
7:2H:3:ARG:HB3	7:2H:3:ARG:NH1	2.18	0.58
25:13:8:LEU:HD13	25:13:31:LEU:HD22	1.85	0.58
32:1a:142:G:O2'	32:1a:196:A:N1	2.36	0.58
32:1a:406:G:H5'	35:1d:5:ILE:HD11	1.85	0.58
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.03	0.58
1:2A:1023:U:OP2	59:2A:4667:HOH:O	2.17	0.58
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.86	0.58
9:2N:90:MET:HE3	9:2N:97:ARG:HB3	1.83	0.58
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.36	0.58
1:1A:810:G:OP1	59:1A:5339:HOH:O	2.17	0.58
1:1A:2490:A:OP2	31:19:2:LYS:NZ	2.31	0.58
1:1A:2859:U:O4	15:1T:23:ARG:NH2	2.32	0.58
1:1A:2877:G:OP2	15:1T:119:LYS:NZ	2.23	0.58
11:1P:126:VAL:HG12	11:1P:148:LEU:HD21	1.85	0.58
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.18	0.58
1:2A:1153:C:OP1	16:2U:92:ARG:NH1	2.36	0.58
1:1A:302:A:O2'	1:1A:303:C:OP1	2.20	0.58
29:17:34:ARG:NH2	59:17:209:HOH:O	2.36	0.58
1:2A:652(B):A:H61	1:2A:655:A:H1'	1.67	0.58
6:2G:67:LYS:HD3	59:24:601:HOH:O	2.04	0.58
32:2a:942:G:H21	40:2i:124:GLN:NE2	2.01	0.58
1:1A:236:G:H4'	1:1A:413:G:C5	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2766:A:N3	31:19:15:LYS:NZ	2.49	0.58
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.86	0.58
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.37	0.58
46:2o:54:ARG:HD2	46:2o:58:MET:HE2	1.85	0.58
51:2t:9:ASN:HD22	51:2t:9:ASN:C	2.11	0.58
1:1A:1131:A:O2'	1:1A:1150:C:O2'	2.10	0.58
1:1A:1784:G:OP1	15:1T:95:ARG:HD3	2.03	0.58
1:1A:2658:C:H2'	1:1A:2659:U:O4'	2.03	0.58
1:2A:848:G:OP1	59:2A:5160:HOH:O	2.17	0.58
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.38	0.58
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.39	0.58
4:2E:24:THR:HG23	4:2E:186:GLY:O	2.04	0.58
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.85	0.58
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.37	0.58
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.36	0.58
1:1A:2164:C:O2	1:1A:2171:G:N1	2.37	0.58
32:1a:946:A:H2'	32:1a:947:G:C8	2.38	0.58
44:1m:4:ILE:HG12	44:1m:5:ALA:HB2	1.86	0.58
1:2A:644:A:H4'	1:2A:645:C:H5	1.68	0.58
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.19	0.58
1:1A:597:C:N3	4:1E:145:LYS:NZ	2.49	0.58
26:14:24:THR:OG1	26:14:25:TYR:N	2.35	0.58
32:1a:737:A:H2'	32:1a:738:C:C6	2.39	0.58
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.35	0.58
32:2a:1492:A:H2'	32:2a:1493:A:O4'	2.04	0.58
1:1A:2163:G:H2'	1:1A:2164:C:H5'	1.85	0.58
1:1A:2324:U:H5'	6:1G:88:ILE:HD11	1.86	0.58
27:15:16:ARG:HG2	27:15:16:ARG:HH11	1.68	0.58
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.84	0.58
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.18	0.58
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.85	0.58
41:1j:61:GLU:OE1	45:1n:58:LYS:NZ	2.36	0.58
1:2A:1087:G:N2	1:2A:1102:C:N3	2.45	0.58
32:2a:803:G:OP1	59:2a:3361:HOH:O	2.16	0.58
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.04	0.57
8:1I:54:GLN:HG3	8:1I:57:ARG:HH11	1.69	0.57
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.87	0.57
34:1c:70:VAL:HG22	34:1c:72:LYS:H	1.69	0.57
49:1r:47:THR:HG23	49:1r:49:LYS:HG3	1.85	0.57
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.03	0.57
19:2X:2:LYS:NZ	19:2X:38:GLU:OE2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:54:THR:HG21	33:2b:201:ILE:HD11	1.86	0.57
1:1A:1159:U:H2'	1:1A:1160:G:C8	2.38	0.57
34:1c:32:LEU:HD22	34:1c:59:ARG:NH1	2.20	0.57
35:1d:53:ASP:HB3	35:1d:57:ARG:HH12	1.69	0.57
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.85	0.57
44:1m:59:TYR:O	44:1m:63:THR:OG1	2.22	0.57
1:2A:1104:C:H2'	1:2A:1105:U:H6	1.69	0.57
1:2A:2152:G:H2'	1:2A:2153:G:H8	1.67	0.57
28:26:14:THR:HB	28:26:48:VAL:O	2.04	0.57
32:2a:937:A:OP2	59:2a:3278:HOH:O	2.17	0.57
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.87	0.57
1:1A:45:C:OP2	1:1A:204:G:H2'	2.04	0.57
59:1A:8241:HOH:O	29:17:32:LYS:HE2	2.05	0.57
1:2A:250:G:P	30:28:13:ARG:HH22	2.26	0.57
1:2A:1143:A:OP1	9:2N:25:ARG:NH2	2.37	0.57
6:2G:83:ARG:O	6:2G:86:MET:HB2	2.04	0.57
7:2H:11:VAL:HG21	7:2H:50:VAL:HG23	1.85	0.57
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.86	0.57
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.87	0.57
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.39	0.57
2:2B:66:A:H61	2:2B:109:C:H5'	1.69	0.57
25:23:7:LYS:HE3	25:23:32:GLN:HE21	1.68	0.57
32:2a:130:A:O2'	32:2a:131:C:O5'	2.21	0.57
42:2k:117:ASN:OD1	42:2k:117:ASN:N	2.36	0.57
46:1o:84:LYS:O	46:1o:84:LYS:HD3	2.05	0.57
1:2A:1059:G:N1	1:2A:1079:C:C4	2.72	0.57
1:2A:1062:G:O2'	1:2A:1063:G:H5'	2.04	0.57
1:2A:2218:U:O2	23:21:52:ARG:NH2	2.38	0.57
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.85	0.57
32:2a:1309:G:OP1	44:2m:88:ARG:HD2	2.04	0.57
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.85	0.57
1:1A:1451:U:H2'	1:1A:1452:U:C6	2.39	0.57
1:1A:1829:U:OP2	3:1D:274:ARG:NH2	2.33	0.57
1:1A:2825:C:H5'	27:15:29:THR:HG21	1.86	0.57
21:1Z:129:SER:HB3	21:1Z:132:ASN:HB2	1.87	0.57
32:1a:1158:C:H5	32:1a:1181:G:H1	1.52	0.57
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.20	0.57
32:2a:222:U:H2'	32:2a:223:U:C6	2.39	0.57
32:2a:1027:C:C5	32:2a:1034:G:O6	2.58	0.57
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.20	0.57
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.40	0.57
17:1V:85:LYS:NZ	59:1V:303:HOH:O	2.37	0.57
1:2A:8:A:H2'	1:2A:9:U:C6	2.39	0.57
1:2A:2122:U:H3	1:2A:2176:A:N6	2.00	0.57
32:2a:663:A:H5"	49:2r:61:LYS:HZ3	1.70	0.57
33:2b:33:TYR:N	33:2b:41:ILE:O	2.36	0.57
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.87	0.57
32:1a:262:A:H2'	32:1a:263:A:C8	2.39	0.57
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.86	0.57
1:2A:530:G:N1	1:2A:2023:G:OP1	2.35	0.57
1:2A:2137:C:C2	1:2A:2154:G:N1	2.73	0.57
1:2A:2849:U:P	15:2T:95:ARG:HH12	2.28	0.57
51:2t:33:ILE:O	51:2t:37:SER:OG	2.19	0.57
1:1A:461:U:OP2	59:1A:5857:HOH:O	2.17	0.57
32:1a:100:C:H2'	32:1a:101:A:C8	2.40	0.57
1:2A:1024:G:OP2	59:2A:4667:HOH:O	2.17	0.57
1:2A:1057:A:N7	1:2A:1086:A:H2'	2.19	0.57
1:2A:1772:G:O6	55:2A:3747:MPD:H32	2.05	0.57
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.84	0.57
1:2A:2080:G:OP1	23:21:35:THR:HG21	2.05	0.57
1:2A:2717:G:N7	59:2A:3899:HOH:O	2.33	0.57
3:2D:10:THR:OG1	3:2D:13:ARG:HG2	2.04	0.57
5:2F:122:LYS:NZ	5:2F:152:GLU:OE2	2.31	0.57
26:24:24:THR:OG1	26:24:25:TYR:N	2.34	0.57
36:2e:74:GLY:HA3	36:2e:116:THR:HG22	1.87	0.57
1:1A:1091:A:H5'	1:1A:1092:A:H5'	1.87	0.57
26:14:1:MET:HE2	26:14:6:HIS:CD2	2.40	0.57
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.87	0.57
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.87	0.57
33:2b:16:HIS:CD2	33:2b:210:SER:HB3	2.39	0.57
1:1A:973:G:N7	59:1A:4428:HOH:O	2.32	0.56
1:1A:2152:U:O2'	1:1A:2155:G:O2'	2.17	0.56
1:1A:2157:A:H61	1:1A:2177:G:H22	1.51	0.56
32:1a:1003:G:N2	32:1a:1004:A:H1'	2.19	0.56
1:2A:93:G:H2'	1:2A:94:C:C6	2.40	0.56
32:2a:986:A:N3	50:2s:52:TYR:OH	2.38	0.56
37:2f:46:ARG:HH11	37:2f:46:ARG:HB2	1.70	0.56
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.38	0.56
44:2m:54:VAL:HA	44:2m:57:ARG:HB3	1.87	0.56
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.86	0.56
39:1h:51:VAL:HG21	39:1h:60:ARG:HH11	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.05	0.56
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.40	0.56
2:2B:24:G:N7	2:2B:56:G:H2'	2.20	0.56
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.05	0.56
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.40	0.56
1:1A:1766:G:H5'	1:1A:1767:A:OP2	2.06	0.56
1:1A:2136:A:H3'	1:1A:2137:G:C8	2.41	0.56
5:1F:165:ARG:HA	5:1F:168:ARG:HD2	1.87	0.56
13:1R:36:THR:HG22	13:1R:37:THR:H	1.70	0.56
26:14:44:THR:O	26:14:46:GLN:N	2.38	0.56
32:1a:1030:C:H42	32:1a:1031:G:H1	1.53	0.56
39:1h:95:VAL:HB	39:1h:99:GLU:HB2	1.86	0.56
50:1s:41:VAL:HG22	50:1s:42:PRO:HD2	1.87	0.56
1:2A:997:G:OP1	16:2U:92:ARG:HG2	2.04	0.56
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.38	0.56
1:2A:2173:A:H2'	1:2A:2174:C:H5'	1.87	0.56
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.40	0.56
2:2B:13:A:N1	2:2B:69:G:O2'	2.32	0.56
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	1.87	0.56
23:21:64:ALA:HA	23:21:67:ILE:HG13	1.87	0.56
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.86	0.56
1:1A:1827:U:H2'	1:1A:1828:C:C6	2.39	0.56
1:1A:2205:C:H2'	1:1A:2206:G:C8	2.39	0.56
7:1H:3:ARG:HD3	7:1H:54:ARG:HH12	1.70	0.56
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.04	0.56
1:2A:1359:A:H61	1:2A:1372:U:H3	1.54	0.56
1:2A:2379:G:O2'	14:2S:17:ARG:NH2	2.27	0.56
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.88	0.56
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.06	0.56
41:2j:38:ILE:HD13	41:2j:71:LEU:HD22	1.87	0.56
1:1A:2164:C:N3	1:1A:2171:G:C6	2.73	0.56
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.40	0.56
32:1a:269:C:H2'	32:1a:270:A:C8	2.40	0.56
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.20	0.56
1:2A:2661:G:O6	7:2H:175:LYS:NZ	2.34	0.56
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	1.86	0.56
26:24:5:ILE:HB	59:24:601:HOH:O	2.05	0.56
26:24:20:ASN:ND2	26:24:38:LYS:HG3	2.21	0.56
32:2a:738:C:OP1	37:2f:2:ARG:NH1	2.38	0.56
51:2t:41:ILE:HD11	51:2t:84:LEU:HD23	1.88	0.56
1:1A:1356:G:OP2	29:17:9:ARG:HD2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:54:GLY:O	26:14:56:VAL:HA	2.06	0.56
1:2A:307:G:N7	59:2A:3802:HOH:O	2.33	0.56
1:2A:521:G:O6	59:2A:4792:HOH:O	2.16	0.56
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.40	0.56
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.24	0.56
3:2D:72:LYS:NZ	3:2D:99:ASP:OD2	2.33	0.56
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.38	0.56
32:2a:1164:G:H1	32:2a:1172:C:N4	1.99	0.56
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.06	0.56
1:1A:1748:A:OP2	59:1A:4826:HOH:O	2.18	0.56
32:1a:1004:A:O2'	32:1a:1038:C:O2	2.22	0.56
1:2A:876:C:H2'	1:2A:877:U:O4'	2.06	0.56
1:2A:2127:G:H2'	1:2A:2128:C:O4'	2.05	0.56
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.48	0.56
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.40	0.56
33:2b:118:LEU:HD13	33:2b:142:LEU:HB2	1.88	0.56
53:2y:12:ILE:HG23	53:2y:16:ILE:HG23	1.86	0.56
1:1A:868:A:H2'	1:1A:991:G:H5"	1.86	0.56
1:1A:1809:U:H2'	1:1A:1815:A:N6	2.21	0.56
1:1A:2745:G:OP1	4:1E:203:LYS:NZ	2.38	0.56
1:1A:2762:A:P	7:1H:3:ARG:HH21	2.29	0.56
51:1t:53:LEU:HD12	51:1t:100:ILE:HG13	1.86	0.56
1:2A:1418:G:N7	59:2A:4063:HOH:O	2.33	0.56
1:2A:1799:G:O2'	3:2D:181:GLU:OE2	2.21	0.56
32:2a:130:A:H5'	48:2q:63:ARG:HE	1.69	0.56
32:2a:660:G:H1	32:2a:745:C:H42	1.53	0.56
32:2a:1002:G:N3	32:2a:1003:G:H8	2.03	0.56
1:1A:105:C:OP1	59:1A:7981:HOH:O	2.17	0.56
12:1Q:21:THR:HG21	12:1Q:101:ARG:HB2	1.87	0.56
32:1a:524:G:H2'	32:1a:525:C:C6	2.41	0.56
32:1a:1375:A:H4'	38:1g:29:LYS:HE2	1.86	0.56
40:1i:16:ARG:HD3	40:1i:64:THR:HG21	1.88	0.56
1:2A:1063:G:H2'	1:2A:1065:U:H6	1.70	0.56
1:2A:2602:A:N7	59:2A:5099:HOH:O	2.33	0.56
36:2e:69:VAL:HG11	36:2e:113:ALA:HB1	1.88	0.56
1:1A:2596:U:OP1	59:1A:6773:HOH:O	2.17	0.56
13:1R:21:TYR:OH	13:1R:43:GLU:HG2	2.07	0.56
40:1i:16:ARG:H	40:1i:64:THR:HG22	1.71	0.56
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.70	0.56
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.41	0.56
32:2a:620:C:C2	35:2d:135:LEU:HG	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:666:G:H5'	32:2a:726:C:H1'	1.88	0.56
10:1O:118:ALA:O	55:1a:1880:MPD:H12	2.06	0.55
39:1h:17:THR:HG22	39:1h:63:LEU:HG	1.88	0.55
51:1t:56:MET:HG2	51:1t:84:LEU:HD13	1.88	0.55
1:2A:839:U:H2'	1:2A:840:C:C6	2.40	0.55
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.41	0.55
1:2A:2336:A:H61	22:20:43:THR:HG22	1.72	0.55
1:2A:2439:A:H5'	1:2A:2439:A:C8	2.41	0.55
26:24:61:ARG:HH22	50:2s:9:VAL:HG21	1.71	0.55
32:2a:975:A:N1	41:2j:48:THR:HB	2.21	0.55
40:2i:24:GLY:HA2	40:2i:59:PHE:O	2.05	0.55
45:2n:32:SER:OG	45:2n:41:ARG:HG2	2.06	0.55
1:1A:2102:G:OP1	23:11:35:THR:HG21	2.06	0.55
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.71	0.55
1:2A:2584:U:H5"	1:2A:2602:A:H2	1.66	0.55
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.88	0.55
32:2a:921:U:O2	36:2e:19:MET:HB2	2.06	0.55
35:2d:65:ARG:HG2	35:2d:75:PHE:CD1	2.40	0.55
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.06	0.55
16:1U:33:ARG:NH2	59:1U:307:HOH:O	2.08	0.55
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.39	0.55
1:2A:873:G:H1	1:2A:904:C:H42	1.53	0.55
33:2b:87:ARG:HD3	33:2b:234:PRO:HD2	1.88	0.55
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.40	0.55
1:1A:482:C:H4'	59:1A:6044:HOH:O	2.06	0.55
1:1A:1617:A:OP1	59:1A:7246:HOH:O	2.18	0.55
3:1D:71:ASP:HB3	3:1D:103:ARG:NH2	2.21	0.55
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.21	0.55
32:2a:67:C:H2'	32:2a:68:G:C8	2.41	0.55
32:2a:731:G:H5'	32:2a:766:A:H4'	1.88	0.55
34:2c:32:LEU:HD12	34:2c:59:ARG:NH1	2.22	0.55
36:2e:12:LEU:HD12	36:2e:128:PRO:HB2	1.89	0.55
49:2r:26:LEU:HD11	49:2r:42:ARG:NE	2.21	0.55
1:1A:2140:U:OP1	1:1A:2169:G:O2'	2.14	0.55
3:1D:85:ASP:OD2	3:1D:88:ARG:HD2	2.07	0.55
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.06	0.55
32:1a:396:G:O2'	32:1a:398:C:OP1	2.18	0.55
48:1q:86:GLU:O	48:1q:90:ILE:HG12	2.07	0.55
8:2I:4:ILE:HD11	8:2I:44:LEU:HD13	1.87	0.55
32:2a:1302:U:OP1	44:2m:13:LYS:NZ	2.38	0.55
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:346:A:OP1	5:1F:168:ARG:HD3	2.07	0.55
1:1A:762:G:C2	46:1o:56:LEU:HD21	2.42	0.55
1:2A:2104:G:N2	1:2A:2105:C:C4	2.72	0.55
1:2A:2115:G:H22	1:2A:2119:A:H5'	1.70	0.55
17:2V:43:GLU:N	17:2V:43:GLU:OE2	2.40	0.55
18:2W:60:ASN:HD22	18:2W:60:ASN:N	2.03	0.55
37:2f:25:ILE:HD13	37:2f:82:ARG:HE	1.72	0.55
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.41	0.55
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.42	0.55
1:1A:2658:C:OP2	1:1A:2745:G:O2'	2.23	0.55
6:1G:50:ALA:O	6:1G:52:ILE:N	2.40	0.55
1:2A:11:G:C2'	1:2A:12:U:H5'	2.37	0.55
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.42	0.55
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.23	0.55
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.71	0.55
21:2Z:125:LEU:HB3	21:2Z:165:VAL:HG13	1.89	0.55
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.89	0.55
1:1A:310:C:H2'	1:1A:311:C:C6	2.42	0.55
1:1A:2125:C:H2'	1:1A:2126:G:H5'	1.88	0.55
1:1A:2297:C:OP2	28:16:6:ARG:NH1	2.40	0.55
32:1a:176:C:H2'	32:1a:177:C:H6	1.72	0.55
32:1a:627:G:H2'	32:1a:628:G:H8	1.70	0.55
32:1a:881:G:P	43:1l:12:ARG:HH22	2.29	0.55
35:1d:8:VAL:HG22	35:1d:21:LEU:HD13	1.88	0.55
41:1j:78:ASN:O	41:1j:80:LYS:N	2.40	0.55
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.37	0.55
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	1.88	0.55
32:2a:35:G:O2'	43:2l:118:SER:O	2.23	0.55
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.22	0.55
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.89	0.55
12:1Q:21:THR:CG2	12:1Q:101:ARG:HB2	2.37	0.55
15:1T:51:ARG:NH1	59:1T:8135:HOH:O	2.34	0.55
1:2A:874:G:OP1	12:2Q:63:LYS:NZ	2.39	0.55
2:2B:105:A:OP1	21:2Z:72:ARG:NH1	2.40	0.55
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.72	0.55
32:2a:881:G:P	43:2l:12:ARG:HH22	2.30	0.55
33:2b:71:VAL:HG12	33:2b:93:VAL:HG22	1.89	0.55
38:2g:45:ASP:O	38:2g:49:ILE:HG13	2.07	0.55
1:1A:2156:A:H62	1:1A:2179:G:H4'	1.71	0.55
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.42	0.55
13:1R:33:ARG:NH1	13:1R:115:GLU:OE2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1045:A:H5'	1:2A:1047:G:O5'	2.07	0.55
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.07	0.55
10:2O:80:ASP:OD1	15:2T:64:ARG:NH2	2.40	0.55
32:2a:457:C:H2'	32:2a:458:C:C6	2.41	0.55
32:2a:992:U:H4'	32:2a:993:G:O5'	2.07	0.55
32:2a:1154:G:H2'	32:2a:1155:G:H8	1.72	0.55
32:1a:1020:U:H2'	32:1a:1021:G:H8	1.70	0.54
35:1d:15:GLU:HG3	35:1d:63:LYS:HD3	1.89	0.54
32:2a:402:G:O2'	32:2a:620:C:N3	2.38	0.54
32:2a:404:U:C5'	35:2d:122:ARG:HD3	2.37	0.54
32:2a:542:G:OP1	35:2d:10:ARG:NH1	2.32	0.54
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.89	0.54
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.88	0.54
1:1A:957:A:H2'	12:1Q:9:TYR:OH	2.07	0.54
1:1A:1941:A:N1	32:1a:1495:U:O2'	2.32	0.54
11:1P:126:VAL:CG1	11:1P:148:LEU:HD21	2.38	0.54
32:1a:629:G:H2'	32:1a:630:G:O4'	2.06	0.54
32:1a:973:G:H3'	32:1a:974:A:H5"	1.89	0.54
32:1a:986:A:N3	50:1s:52:TYR:OH	2.40	0.54
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.42	0.54
1:2A:2115:G:H21	1:2A:2171:A:H61	1.53	0.54
59:2A:6002:HOH:O	5:2F:74:ARG:HD2	2.06	0.54
32:2a:579:G:O3'	46:2o:54:ARG:NH1	2.41	0.54
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.38	0.54
41:2j:37:PRO:HA	41:2j:72:VAL:HG12	1.89	0.54
21:1Z:182:LYS:O	21:1Z:185:GLU:HG3	2.07	0.54
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.89	0.54
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.71	0.54
1:2A:1410:G:H2'	1:2A:1411:C:H6	1.73	0.54
1:2A:2118:U:H5	1:2A:2148:G:H1'	1.72	0.54
1:2A:2122:U:H2'	1:2A:2123:G:C8	2.43	0.54
1:2A:2431:U:OP1	59:2A:3938:HOH:O	2.18	0.54
6:2G:80:PHE:O	6:2G:82:LEU:N	2.40	0.54
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.36	0.54
32:2a:443:C:H2'	32:2a:444:C:C6	2.42	0.54
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.24	0.54
33:2b:7:VAL:O	33:2b:217:ARG:NE	2.40	0.54
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.42	0.54
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.89	0.54
2:2B:75:G:H5"	2:2B:75:G:H8	1.72	0.54
3:2D:164:GLN:NE2	3:2D:176:ARG:HH12	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:28:GLY:HA3	7:2H:79:VAL:HB	1.88	0.54
19:2X:88:LYS:HE2	19:2X:93:GLU:HG3	1.89	0.54
1:1A:331:G:H21	1:1A:354:A:H62	1.55	0.54
10:1O:104:ARG:HH22	15:1T:43:GLN:HE22	1.54	0.54
32:1a:1005:A:N3	32:1a:1036:G:N1	2.54	0.54
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.43	0.54
48:1q:78:GLU:HG2	48:1q:79:SER:N	2.23	0.54
59:2A:6415:HOH:O	5:2F:53:THR:HG21	2.07	0.54
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.88	0.54
17:2V:52:VAL:CG2	17:2V:55:ALA:HB3	2.38	0.54
51:2t:57:ARG:HH12	51:2t:100:ILE:HB	1.73	0.54
1:1A:1140:U:H2'	1:1A:1142:A:OP2	2.08	0.54
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.90	0.54
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.88	0.54
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.07	0.54
16:1U:104:GLN:CD	16:1U:104:GLN:H	2.13	0.54
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.31	0.54
1:2A:922:U:H2'	1:2A:923:C:C6	2.42	0.54
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.41	0.54
1:2A:2786:U:O2'	4:2E:62:PRO:O	2.22	0.54
32:2a:524:G:H2'	32:2a:525:C:C6	2.43	0.54
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.89	0.54
1:1A:11:G:H2'	1:1A:12:U:H5"	1.90	0.54
1:1A:1077:G:H21	31:19:36:GLN:HE22	1.56	0.54
1:1A:2155:G:H3'	1:1A:2179:G:H21	1.73	0.54
29:17:33:ARG:NH2	59:17:208:HOH:O	2.36	0.54
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.07	0.54
35:1d:83:SER:O	59:1d:608:HOH:O	2.17	0.54
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.43	0.54
4:2E:179:GLU:HB3	4:2E:181:LEU:HD22	1.88	0.54
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.07	0.54
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.35	0.54
1:1A:2164:C:N3	1:1A:2171:G:O6	2.41	0.54
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.90	0.54
30:18:47:LYS:NZ	55:18:102:MPD:H51	2.23	0.54
50:1s:63:THR:OG1	50:1s:65:ASN:ND2	2.41	0.54
32:2a:473:G:OP2	47:2p:75:ARG:HD3	2.07	0.54
32:2a:547:A:H5'	59:2a:3495:HOH:O	2.08	0.54
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.89	0.54
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.90	0.54
40:2i:23:ASN:ND2	40:2i:60:ASP:OD2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2289:G:OP2	22:10:10:THR:HG21	2.07	0.54
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.88	0.54
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.90	0.54
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.43	0.54
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.89	0.54
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.89	0.54
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.41	0.54
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.07	0.54
3:2D:92:ILE:HD12	3:2D:104:TYR:CD1	2.43	0.54
5:2F:11:VAL:HB	5:2F:18:ARG:HB3	1.90	0.54
32:2a:142:G:H2'	32:2a:143:A:H8	1.72	0.54
32:2a:1130:A:H5'	40:2i:18:PHE:CE2	2.42	0.54
34:2c:152:ILE:HB	34:2c:167:TRP:HB3	1.90	0.54
1:1A:1111:U:O2'	1:1A:1112:U:O4'	2.22	0.54
1:1A:2157:A:N6	1:1A:2177:G:H22	2.04	0.54
1:1A:2162:C:H2'	1:1A:2163:G:C8	2.40	0.54
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.43	0.54
13:1R:102:GLU:OE2	18:1W:37:ARG:NH2	2.36	0.54
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.38	0.54
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.07	0.54
1:2A:1472:A:H2'	1:2A:1473:G:O4'	2.08	0.54
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.90	0.54
34:2c:12:LEU:O	45:2n:57:ARG:NH2	2.40	0.54
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.89	0.54
50:2s:27:GLU:OE1	50:2s:47:HIS:NE2	2.36	0.54
53:2y:29:LYS:HG2	53:2y:30:TRP:CE3	2.42	0.54
1:1A:1766:G:H8	1:1A:1770:A:H62	1.54	0.53
1:1A:2164:C:O2	1:1A:2171:G:C2	2.61	0.53
1:1A:2179:G:H5"	1:1A:2180:A:OP1	2.07	0.53
5:1F:12:LEU:HD22	5:1F:124:LEU:HD21	1.91	0.53
18:1W:79:GLY:HA3	18:1W:100:THR:HG22	1.91	0.53
26:14:16:CYS:SG	26:14:17:GLY:N	2.81	0.53
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.08	0.53
1:2A:700:G:O2'	1:2A:1632:A:N3	2.30	0.53
1:2A:2142:C:N3	1:2A:2149:G:O6	2.41	0.53
3:2D:164:GLN:HE21	3:2D:176:ARG:HH12	1.55	0.53
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.89	0.53
26:24:50:VAL:HG21	44:2m:65:LYS:H	1.72	0.53
1:1A:1793:A:H2'	59:1A:4959:HOH:O	2.07	0.53
16:1U:51:LYS:NZ	59:1U:318:HOH:O	2.38	0.53
32:1a:96:U:H2'	32:1a:97:G:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:186:C:H2'	32:1a:187:C:C6	2.44	0.53
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.43	0.53
35:1d:53:ASP:HB3	35:1d:57:ARG:NH1	2.23	0.53
1:2A:2115:G:N1	1:2A:2117:A:N7	2.55	0.53
1:2A:2317:C:H2'	1:2A:2318:G:H5'	1.89	0.53
26:24:34:GLU:HB3	44:2m:57:ARG:CZ	2.38	0.53
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.07	0.53
1:1A:1346:U:H4'	1:1A:1347:A:C5'	2.38	0.53
18:1W:67:ASP:N	18:1W:67:ASP:OD1	2.40	0.53
32:1a:411:A:OP2	35:1d:25:ARG:NH2	2.41	0.53
32:1a:828:A:H2'	32:1a:829:G:O4'	2.07	0.53
1:2A:2115:G:H3'	1:2A:2116:G:C5'	2.39	0.53
11:2P:100:LEU:HD22	11:2P:105:LEU:HD12	1.89	0.53
53:2y:33:HIS:ND1	53:2y:35:ILE:HG12	2.23	0.53
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.43	0.53
15:1T:91:ARG:HD2	15:1T:120:ARG:NH1	2.23	0.53
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.26	0.53
1:2A:568:U:H5'	1:2A:945:A:N6	2.24	0.53
32:2a:952:U:H4'	32:2a:964:A:N1	2.23	0.53
53:2y:40:ILE:HB	53:2y:51:ASP:HB2	1.91	0.53
32:1a:330:C:OP2	59:1a:2062:HOH:O	2.18	0.53
50:1s:22:LEU:HD22	50:1s:28:LYS:HA	1.90	0.53
1:2A:634:C:H2'	1:2A:635:C:C6	2.44	0.53
1:2A:1036:G:H1	1:2A:1119:C:H42	1.54	0.53
1:2A:1171:G:N2	1:2A:1178:C:O2	2.42	0.53
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.43	0.53
6:2G:66:GLN:HB3	6:2G:92:VAL:HG21	1.90	0.53
13:2R:2:ARG:HD2	59:2R:8111:HOH:O	2.07	0.53
32:2a:552:U:O3'	43:2l:87:GLY:HA2	2.08	0.53
32:2a:560:U:H5'	32:2a:566:G:N2	2.24	0.53
32:2a:663:A:H5"	49:2r:61:LYS:NZ	2.22	0.53
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.42	0.53
38:2g:9:VAL:HG11	38:2g:94:ARG:HD3	1.91	0.53
44:2m:80:ARG:HH22	50:2s:69:HIS:CE1	2.14	0.53
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.90	0.53
1:1A:821:A:H2'	1:1A:821:A:N3	2.21	0.53
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.90	0.53
32:1a:1312:G:N7	50:1s:2:PRO:HD2	2.24	0.53
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.49	0.53
47:1p:74:LEU:O	47:1p:79:VAL:HG22	2.09	0.53
1:2A:1400:G:H2'	1:2A:1401:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1530:C:HO2'	1:2A:1531:C:P	2.28	0.53
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.07	0.53
33:2b:40:HIS:HB3	33:2b:190:THR:HG21	1.91	0.53
35:2d:15:GLU:HG3	35:2d:63:LYS:HD3	1.91	0.53
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.44	0.53
32:1a:77:G:C2'	32:1a:78:G:H5'	2.37	0.53
32:1a:966:M2G:H1'	53:1y:53:THR:HG21	1.89	0.53
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.90	0.53
40:1i:24:GLY:HA2	40:1i:59:PHE:O	2.09	0.53
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.43	0.53
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.08	0.53
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.26	0.53
7:2H:40:GLU:OE1	7:2H:60:ARG:NH1	2.42	0.53
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.91	0.53
13:2R:36:THR:HG22	13:2R:37:THR:H	1.73	0.53
14:2S:93:LYS:HD3	14:2S:94:TYR:N	2.23	0.53
32:2a:536:C:OP1	59:2a:3409:HOH:O	2.19	0.53
32:2a:539:A:H2'	32:2a:540:G:C8	2.44	0.53
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.72	0.53
32:2a:1505:G:OP2	59:2a:3386:HOH:O	2.19	0.53
1:1A:215:G:H21	1:1A:217:A:H62	1.55	0.53
1:1A:2175:G:H2'	1:1A:2176:G:C8	2.43	0.53
55:18:102:MPD:H12	55:18:102:MPD:H52	1.90	0.53
32:1a:366:C:N3	59:1a:2206:HOH:O	2.33	0.53
32:1a:1135:U:H4'	32:1a:1136:U:H5	1.73	0.53
35:1d:108:LEU:HB3	35:1d:110:PHE:CE1	2.43	0.53
37:1f:91:VAL:HG11	49:1r:72:ARG:NH1	2.24	0.53
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.90	0.53
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.90	0.53
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.27	0.53
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.43	0.53
1:2A:2641:G:P	9:2N:74:ARG:HH22	2.32	0.53
32:2a:64:G:H4'	32:2a:65:U:H3'	1.91	0.53
53:2y:10:MET:HE2	53:2y:12:ILE:HD11	1.89	0.53
1:1A:2132:G:H5"	1:1A:2133:C:H5	1.74	0.53
5:1F:33:LEU:HD13	5:1F:112:MET:HE2	1.91	0.53
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.43	0.53
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.26	0.53
29:17:24:THR:CG2	29:17:27:GLY:H	2.18	0.53
32:1a:189(K):U:H2'	32:1a:189(L):G:H8	1.74	0.53
43:1l:60:LEU:HD21	43:1l:66:VAL:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:637:A:H8	11:2P:117:GLU:HG3	1.74	0.53
1:2A:1065:U:H4'	1:2A:1066:U:C5'	2.38	0.53
1:2A:1110:G:H1'	1:2A:1111:A:C8	2.44	0.53
1:2A:1228:G:H2'	1:2A:1229:G:H5"	1.91	0.53
5:2F:165:ARG:HG2	5:2F:168:ARG:NH2	2.24	0.53
14:2S:93:LYS:HD2	14:2S:95:HIS:CB	2.38	0.53
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	1.91	0.53
39:2h:19:VAL:HG23	39:2h:21:LYS:HD3	1.91	0.53
40:2i:100:GLY:O	40:2i:103:THR:HG22	2.09	0.53
3:1D:102:LYS:C	3:1D:103:ARG:HG2	2.32	0.53
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.91	0.53
14:1S:59:LYS:CD	14:1S:60:GLY:H	2.22	0.53
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.90	0.53
33:1b:167:PRO:HG3	33:1b:186:ALA:HB1	1.92	0.53
40:1i:11:LYS:HA	40:1i:108:VAL:HG13	1.90	0.53
49:1r:33:ASP:OD2	49:1r:36:ASN:HB2	2.09	0.53
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	1.92	0.53
10:2O:64:ARG:NH1	10:2O:81:ASP:OD1	2.38	0.53
34:2c:109:PRO:HB3	34:2c:115:LEU:HD23	1.91	0.53
48:2q:41:LYS:HZ3	48:2q:92:ARG:HH21	1.56	0.53
1:1A:794:U:O2	1:1A:2036:A:H1'	2.08	0.52
4:1E:78:LEU:O	4:1E:79:ARG:NH1	2.38	0.52
6:1G:143:GLU:O	26:14:28:LYS:NZ	2.40	0.52
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.42	0.52
34:1c:102:ASN:HD22	34:1c:102:ASN:N	2.07	0.52
1:2A:2106:G:C4	1:2A:2107:C:H1'	2.45	0.52
1:2A:2168:G:H22	1:2A:2171:A:H2'	1.73	0.52
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.44	0.52
26:24:15:ILE:HD12	26:24:21:VAL:HG22	1.91	0.52
32:2a:1002:G:N3	32:2a:1003:G:C8	2.77	0.52
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.44	0.52
32:2a:1158:C:O2	32:2a:1158:C:H2'	2.09	0.52
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.42	0.52
1:1A:956:A:N1	1:1A:2289:G:H1'	2.24	0.52
1:1A:1001:G:H5"	12:1Q:77:LYS:HD2	1.92	0.52
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.91	0.52
32:1a:1030:C:N4	32:1a:1031:G:N1	2.47	0.52
32:1a:1518:MA6:N6	32:1a:1519:MA6:H103	2.23	0.52
41:1j:35:SER:N	41:1j:73:ASP:O	2.32	0.52
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.25	0.52
1:2A:1929:G:H5'	59:2A:5429:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2295:C:OP1	14:2S:10:ARG:NH1	2.43	0.52
2:2B:84:C:OP1	25:23:15:TYR:OH	2.21	0.52
4:2E:11:MET:CG	4:2E:24:THR:HG22	2.39	0.52
6:2G:16:ARG:NH2	6:2G:28:VAL:O	2.41	0.52
6:2G:77:ILE:HG21	6:2G:80:PHE:CD2	2.44	0.52
12:2Q:56:ARG:HH11	12:2Q:56:ARG:CG	2.22	0.52
1:1A:602:G:H2'	1:1A:603:C:C6	2.45	0.52
1:1A:2181:G:H2'	1:1A:2182:G:C8	2.44	0.52
1:1A:2614:A:N6	59:1A:5179:HOH:O	2.42	0.52
4:1E:73:GLU:H	4:1E:73:GLU:CD	2.17	0.52
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.25	0.52
32:1a:1030:C:N3	32:1a:1031:G:C2	2.78	0.52
1:2A:1110:G:H1'	1:2A:1111:A:H8	1.74	0.52
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.08	0.52
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.24	0.52
1:2A:2319:G:H22	14:2S:3:ARG:NE	2.08	0.52
17:2V:15:GLU:O	17:2V:18:LEU:HB2	2.09	0.52
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.10	0.52
44:2m:3:ARG:HG3	44:2m:8:GLU:HG3	1.91	0.52
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.10	0.52
4:1E:2:LYS:HB2	4:1E:95:ILE:HD12	1.92	0.52
6:1G:50:ALA:C	6:1G:52:ILE:N	2.67	0.52
33:1b:115:LEU:HD13	33:1b:145:LEU:HB3	1.90	0.52
34:1c:179:ARG:NH1	34:1c:206:GLU:OE1	2.42	0.52
1:2A:321:G:OP2	5:2F:135:LYS:HD3	2.09	0.52
1:2A:1079:C:N4	1:2A:1080:C:C2	2.75	0.52
1:2A:2335:A:C8	1:2A:2337:G:C5	2.97	0.52
1:2A:2349:G:H3'	1:2A:2350:C:H5"	1.91	0.52
25:23:29:ARG:HB2	25:23:30:ARG:HD3	1.92	0.52
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.44	0.52
1:1A:174:U:H4'	1:1A:207:A:H4'	1.91	0.52
1:1A:2159:C:H5	1:1A:2177:G:N1	2.08	0.52
8:1I:72:LEU:C	8:1I:74:ASN:H	2.18	0.52
32:1a:194:C:H2'	32:1a:195:A:H5"	1.90	0.52
32:1a:1177:G:OP2	40:1i:97:LYS:NZ	2.32	0.52
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.25	0.52
45:1n:4:LYS:O	45:1n:7:ILE:HG12	2.10	0.52
1:2A:747:U:O2	1:2A:2014:A:H1'	2.09	0.52
1:2A:918:A:H5"	2:2B:98:G:O2'	2.08	0.52
1:2A:1092:C:H2'	1:2A:1092:C:O2	2.07	0.52
1:2A:1721:G:H8	1:2A:1741:A:H62	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:85:ASP:OD2	3:2D:88:ARG:HD2	2.09	0.52
10:2O:104:ARG:NH1	59:2O:320:HOH:O	2.39	0.52
32:2a:1239:A:H62	32:2a:1299:A:H62	1.57	0.52
33:2b:16:HIS:O	33:2b:18:GLY:N	2.42	0.52
1:1A:515:G:N7	18:1W:49:LYS:NZ	2.58	0.52
1:1A:1220:U:O3'	1:1A:1221:G:H4'	2.09	0.52
1:1A:1617:A:H2'	1:1A:1618:A:C8	2.45	0.52
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.90	0.52
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.39	0.52
32:1a:975:A:H5'	32:1a:975:A:H8	1.75	0.52
32:1a:977:A:H1'	32:1a:982:U:O4	2.09	0.52
51:1t:10:LEU:HD23	51:1t:11:SER:H	1.73	0.52
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.07	0.52
1:2A:249:C:O2	30:28:12:LYS:NZ	2.31	0.52
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.57	0.52
1:2A:1045:A:H5"	1:2A:1046:A:OP1	2.09	0.52
1:2A:2304:G:H22	1:2A:2312:U:H3	1.57	0.52
35:2d:8:VAL:HG22	35:2d:21:LEU:HD13	1.91	0.52
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.91	0.52
1:1A:1000:C:OP1	12:1Q:87:LYS:HE2	2.09	0.52
1:1A:2396:G:OP2	22:10:55:ARG:NH1	2.43	0.52
2:1B:23:G:O6	59:1B:3129:HOH:O	2.18	0.52
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.40	0.52
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD3	1.90	0.52
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.90	0.52
35:1d:194:LEU:HD12	35:1d:195:ALA:N	2.25	0.52
1:2A:881:G:H2'	1:2A:882:G:C8	2.45	0.52
32:2a:76:C:H42	32:2a:93:G:H1	1.57	0.52
32:2a:632:A:H5'	32:2a:633:G:OP2	2.10	0.52
1:1A:1324:A:OP1	13:1R:36:THR:HG23	2.09	0.52
1:1A:1566:U:H2'	1:1A:1567:G:O4'	2.10	0.52
1:1A:1740:U:O2'	3:1D:14:ARG:NH2	2.43	0.52
1:1A:2804:C:H5'	1:1A:2902:G:N2	2.25	0.52
32:1a:1036:G:H5'	32:1a:1037:C:OP2	2.09	0.52
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.45	0.52
47:1p:43:LYS:HG2	47:1p:48:TRP:CE2	2.45	0.52
2:2B:7:G:H8	2:2B:7:G:H5"	1.74	0.52
3:2D:30:GLU:HG3	3:2D:94:LEU:HD21	1.91	0.52
44:2m:6:GLY:HA3	44:2m:67:GLU:HG3	1.90	0.52
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.92	0.52
1:1A:2116:G:OP1	8:1I:22:LYS:HD2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2136:A:H3'	1:1A:2137:G:H8	1.74	0.52
9:1N:15:LEU:HD12	9:1N:137:LYS:HG2	1.92	0.52
15:1T:23:ARG:HD3	59:1T:8123:HOH:O	2.09	0.52
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.24	0.52
32:1a:926:G:C6	53:1y:87:LYS:HG3	2.45	0.52
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.92	0.52
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.45	0.52
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.40	0.52
6:2G:28:VAL:O	6:2G:31:VAL:HG13	2.10	0.52
32:2a:1032:G:C2'	32:2a:1033:G:H5'	2.40	0.52
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.10	0.52
41:2j:32:ALA:HB1	41:2j:33:GLN:CD	2.34	0.52
1:1A:1072:U:O2	1:1A:1072:U:H2'	2.08	0.52
1:1A:1428:G:N7	59:1A:5198:HOH:O	2.34	0.52
1:1A:2164:C:H2'	1:1A:2165:C:C6	2.45	0.52
32:1a:45:U:H2'	32:1a:46:G:C8	2.44	0.52
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.09	0.52
1:2A:362:U:O2'	1:2A:363:G:H5'	2.10	0.52
1:2A:1101:U:H2'	1:2A:1102:C:H6	1.74	0.52
1:2A:2793:G:H2'	1:2A:2794:C:O4'	2.10	0.52
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.75	0.52
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.39	0.52
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.39	0.52
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.42	0.52
32:2a:1027:C:C4	32:2a:1034:G:O6	2.63	0.52
40:2i:53:VAL:HG11	40:2i:92:TYR:CE1	2.45	0.52
1:1A:1831:C:OP2	3:1D:183:ARG:NH2	2.43	0.51
4:1E:7:VAL:HG13	4:1E:27:LEU:HB3	1.92	0.51
20:1Y:73:ARG:HD3	59:1Y:5012:HOH:O	2.09	0.51
32:1a:955:U:O2'	50:1s:83:HIS:HD2	1.92	0.51
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.09	0.51
35:1d:65:ARG:HG2	35:1d:75:PHE:CD1	2.45	0.51
1:2A:706:A:H2'	1:2A:707:G:O4'	2.10	0.51
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.45	0.51
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.75	0.51
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.44	0.51
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.09	0.51
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.42	0.51
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD3	1.92	0.51
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.75	0.51
41:2j:78:ASN:O	41:2j:80:LYS:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:4:LYS:HG3	45:2n:7:ILE:HD11	1.92	0.51
50:2s:20:LEU:HD23	50:2s:23:ASN:ND2	2.22	0.51
1:1A:1124:U:C6	1:1A:1134:A:H5"	2.45	0.51
1:1A:2316:G:N2	6:1G:156:ASP:OD2	2.38	0.51
32:1a:1060:C:C4	34:1c:2:GLY:HA3	2.46	0.51
35:1d:164:ALA:O	35:1d:168:ARG:HD2	2.09	0.51
47:1p:79:VAL:HG23	47:1p:80:PHE:CD1	2.46	0.51
1:2A:1428:C:O2'	1:2A:1569:A:OP2	2.21	0.51
1:2A:2850:A:N7	1:2A:2868:A:O2'	2.35	0.51
32:2a:954:G:H21	32:2a:1227:A:H62	1.58	0.51
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.92	0.51
53:2y:5:ILE:HD12	53:2y:17:ARG:HG2	1.91	0.51
1:1A:1578:C:N4	1:1A:1579:C:H41	2.08	0.51
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	1.91	0.51
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.10	0.51
40:1i:33:PHE:HE1	40:1i:43:ALA:HB1	1.75	0.51
1:2A:212:G:H2'	1:2A:213:A:O4'	2.11	0.51
1:2A:1179:C:H2'	1:2A:1180:C:C6	2.45	0.51
6:2G:67:LYS:HE3	6:2G:68:PRO:O	2.10	0.51
26:24:13:ARG:NH2	26:24:21:VAL:HG11	2.25	0.51
32:2a:523:A:N1	43:2l:92:0TD:H6	2.26	0.51
1:1A:2692:C:OP2	4:1E:111:ARG:NH2	2.43	0.51
32:1a:1003:G:C2	32:1a:1004:A:H1'	2.45	0.51
40:1i:25:LYS:HA	40:1i:25:LYS:NZ	2.25	0.51
1:2A:2562:U:O2'	10:2O:23:ARG:HD3	2.09	0.51
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.11	0.51
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.93	0.51
18:2W:27:LYS:NZ	59:2W:8119:HOH:O	2.38	0.51
32:2a:115:G:OP1	59:2a:3481:HOH:O	2.19	0.51
32:2a:520:A:N1	32:2a:536:C:H1'	2.25	0.51
32:2a:1005:A:H5"	32:2a:1006:C:C5	2.45	0.51
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.44	0.51
41:2j:19:SER:O	41:2j:23:ILE:HG12	2.10	0.51
42:2k:84:VAL:HG11	42:2k:91:ARG:HH11	1.75	0.51
1:1A:1845:G:H4'	3:1D:51:VAL:HG21	1.92	0.51
2:1B:43:C:H5"	26:14:1:MET:HG2	1.91	0.51
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.92	0.51
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.10	0.51
29:17:24:THR:HG22	29:17:27:GLY:N	2.19	0.51
32:1a:346:G:N2	55:1a:1880:MPD:O4	2.44	0.51
32:1a:677:U:H3	32:1a:713:G:H22	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.45	0.51
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.45	0.51
44:1m:11:ARG:C	44:1m:13:LYS:H	2.19	0.51
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.46	0.51
1:2A:2319:G:H22	14:2S:3:ARG:CZ	2.23	0.51
33:2b:42:ILE:HD13	33:2b:203:GLY:HA2	1.93	0.51
34:2c:8:ILE:HG23	34:2c:16:ARG:HG2	1.91	0.51
1:1A:275:C:H2'	1:1A:276:C:C6	2.46	0.51
1:1A:1014:U:H2'	1:1A:1015:C:C6	2.45	0.51
1:1A:1822:A:H5"	1:1A:1822:A:H8	1.76	0.51
35:1d:81:GLU:O	35:1d:85:LYS:HB2	2.11	0.51
38:1g:16:LEU:HD11	40:1i:45:ALA:HB2	1.92	0.51
1:2A:1010:A:OP2	59:2A:4860:HOH:O	2.19	0.51
32:2a:70:G:H1	32:2a:99:U:H3	1.56	0.51
35:2d:70:ILE:HD11	35:2d:74:GLN:HB3	1.92	0.51
47:2p:23:ASP:OD1	47:2p:25:ARG:HD3	2.10	0.51
1:1A:2167:C:H5"	1:1A:2168:C:C5	2.46	0.51
1:1A:2880:C:H2'	1:1A:2881:C:O4'	2.11	0.51
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.32	0.51
32:1a:186:C:H2'	32:1a:187:C:H6	1.74	0.51
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.92	0.51
33:1b:9:GLU:CD	33:1b:217:ARG:HH22	2.18	0.51
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.25	0.51
1:2A:1049:C:O2	1:2A:1113:U:H4'	2.11	0.51
1:2A:2137:C:H1'	1:2A:2154:G:H22	1.75	0.51
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.93	0.51
13:2R:55:ALA:HB2	13:2R:79:LEU:HD13	1.93	0.51
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.10	0.51
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.10	0.51
32:2a:1457:G:OP1	51:2t:39:LYS:NZ	2.40	0.51
51:2t:56:MET:HE3	51:2t:84:LEU:HD22	1.93	0.51
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	1.93	0.51
17:1V:101:GLY:HA3	59:1V:332:HOH:O	2.11	0.51
32:1a:60:A:H4'	32:1a:61:G:H5'	1.92	0.51
32:1a:744:C:O2'	32:1a:851:G:N2	2.43	0.51
2:2B:7:G:H3'	2:2B:8:U:H5"	1.92	0.51
5:2F:130:ALA:HB3	5:2F:142:TRP:HD1	1.74	0.51
6:2G:11:TYR:HA	6:2G:15:VAL:HB	1.92	0.51
7:2H:89:ILE:O	7:2H:129:THR:HG23	2.11	0.51
16:2U:108:GLU:O	16:2U:112:ARG:HG2	2.11	0.51
32:2a:1118:C:P	40:2i:104:ARG:HH11	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.46	0.51
40:2i:111:ARG:O	40:2i:113:LYS:HD2	2.11	0.51
48:2q:27:PHE:CE2	48:2q:36:ILE:HD11	2.46	0.51
1:1A:943:C:H2'	1:1A:944:C:C6	2.46	0.51
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.46	0.51
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.46	0.51
13:1R:55:ALA:HB2	13:1R:79:LEU:HD13	1.92	0.51
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.93	0.51
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.93	0.51
32:1a:1003:G:C2	32:1a:1004:A:N3	2.79	0.51
33:1b:115:LEU:HD12	33:1b:142:LEU:HD12	1.93	0.51
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.15	0.51
38:1g:28:ASN:HA	38:1g:31:MET:HE2	1.93	0.51
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.46	0.51
1:2A:2105:C:N4	1:2A:2106:G:O6	2.43	0.51
26:24:50:VAL:HG21	44:2m:65:LYS:N	2.26	0.51
32:2a:706:A:H2'	32:2a:707:C:H5'	1.93	0.51
1:1A:662:A:H8	11:1P:117:GLU:HG3	1.74	0.51
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.11	0.51
32:1a:731:G:H5'	32:1a:766:A:H4'	1.93	0.51
32:1a:1007:C:C2'	32:1a:1008:C:H5'	2.41	0.51
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.25	0.51
32:1a:1525:G:OP1	42:1k:120:ARG:NH2	2.43	0.51
44:1m:3:ARG:HG3	44:1m:4:ILE:N	2.24	0.51
1:2A:740:U:H2'	1:2A:741:G:C8	2.46	0.51
1:2A:1753:G:OP1	15:2T:95:ARG:HD3	2.10	0.51
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	1.92	0.51
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.24	0.51
7:2H:90:LYS:HD2	7:2H:163:TYR:CD1	2.45	0.51
32:2a:765:G:H5"	32:2a:766:A:OP1	2.11	0.51
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.94	0.51
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.93	0.51
51:2t:42:GLN:O	51:2t:45:GLN:HB3	2.12	0.51
1:1A:555:G:N1	1:1A:2045:G:OP1	2.36	0.50
1:1A:1255:A:H5"	1:1A:1257:G:O4'	2.12	0.50
6:1G:143:GLU:OE2	26:14:26:SER:OG	2.29	0.50
27:15:16:ARG:NH1	27:15:17:ASP:OD1	2.44	0.50
32:1a:171:A:H2'	32:1a:172:A:C8	2.45	0.50
32:1a:457:C:H2'	32:1a:458:C:H6	1.76	0.50
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.93	0.50
1:2A:99:U:O4	20:2Y:8:LYS:NZ	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:265:A:N1	1:2A:427:U:O2'	2.44	0.50
1:2A:575:A:OP2	1:2A:2055:C:N4	2.44	0.50
1:2A:2061:G:H5"	1:2A:2503:2MA:C2	2.41	0.50
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.46	0.50
33:2b:53:ARG:HH22	33:2b:199:TYR:HE1	1.59	0.50
1:1A:1075:A:OP1	12:1Q:128:LYS:NZ	2.43	0.50
32:1a:7:G:H5'	32:1a:298:A:O4'	2.12	0.50
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.44	0.50
46:1o:74:ASP:OD2	46:1o:77:ARG:HG3	2.11	0.50
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.41	0.50
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.11	0.50
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.29	0.50
21:2Z:23:LYS:NZ	21:2Z:40:ASP:OD2	2.44	0.50
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.44	0.50
32:2a:942:G:H21	40:2i:124:GLN:HE22	1.58	0.50
32:2a:1036:G:H3'	32:2a:1037:C:C6	2.46	0.50
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.46	0.50
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	1.93	0.50
42:2k:115:PRO:C	42:2k:117:ASN:HA	2.36	0.50
51:2t:50:GLU:HB2	51:2t:99:LEU:HD23	1.93	0.50
1:1A:1848:G:OP1	3:1D:88:ARG:NH2	2.38	0.50
1:1A:2285:A:H2'	1:1A:2286:A:C8	2.46	0.50
2:1B:115:G:H2'	2:1B:116:G:H5"	1.93	0.50
4:1E:47:VAL:HG12	4:1E:49:LEU:HD13	1.93	0.50
32:1a:1492:A:H4'	32:1a:1493:A:N1	2.26	0.50
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.46	0.50
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.78	0.50
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.77	0.50
1:2A:523:C:H4'	1:2A:540:C:O2	2.11	0.50
1:2A:887:A:O2'	1:2A:889:C:OP2	2.19	0.50
1:2A:2115:G:H3'	1:2A:2116:G:H5'	1.93	0.50
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.46	0.50
6:2G:36:LYS:HE3	6:2G:95:ARG:NH1	2.26	0.50
6:2G:68:PRO:HB2	6:2G:90:LEU:HB3	1.93	0.50
30:28:46:ARG:HH21	30:28:46:ARG:HB2	1.76	0.50
32:2a:531:U:O3'	32:2a:532:A:H4'	2.10	0.50
33:2b:163:PHE:CD1	33:2b:185:ILE:HB	2.47	0.50
34:2c:174:PRO:HD2	34:2c:182:ILE:HD11	1.94	0.50
1:1A:551:A:H2'	59:1A:7499:HOH:O	2.11	0.50
2:1B:66:A:N6	2:1B:108:U:H2'	2.25	0.50
5:1F:197:ASP:OD1	5:1F:197:ASP:N	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:757:U:H2'	32:1a:758:G:O4'	2.11	0.50
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.26	0.50
36:1e:79:GLU:HG3	36:1e:93:PRO:HD2	1.93	0.50
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	1.93	0.50
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.11	0.50
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.45	0.50
32:2a:1066:C:O2'	32:2a:1067:A:H5'	2.11	0.50
33:2b:124:SER:HB2	33:2b:125:PRO:HD3	1.94	0.50
34:2c:70:VAL:HG22	34:2c:72:LYS:H	1.76	0.50
1:1A:1555:C:H3'	1:1A:1556:A:C5'	2.42	0.50
1:1A:1744:G:OP2	1:1A:1745:A:O2'	2.27	0.50
1:1A:2159:C:N3	1:1A:2176:G:N2	2.56	0.50
1:1A:2576:A:C2	1:1A:2659:U:H4'	2.46	0.50
8:1I:68:LEU:HD11	8:1I:109:ILE:HD11	1.93	0.50
41:1j:30:SER:OG	41:1j:81:THR:HG22	2.11	0.50
44:1m:57:ARG:O	44:1m:61:GLU:HG3	2.12	0.50
1:2A:1371:G:HO2'	1:2A:1372:U:H5	1.60	0.50
1:2A:2144:U:H1'	1:2A:2147:G:O6	2.12	0.50
6:2G:21:ARG:HG3	6:2G:22:ARG:N	2.25	0.50
6:2G:66:GLN:HG3	26:24:1:MET:CE	2.41	0.50
15:2T:108:ARG:NH1	32:2a:1464:G:OP1	2.45	0.50
21:2Z:40:ASP:HB3	21:2Z:43:GLU:HB2	1.92	0.50
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	1.92	0.50
1:1A:664:U:H2'	1:1A:665:C:C6	2.47	0.50
1:1A:1822:A:H5'	1:1A:1823:G:OP2	2.11	0.50
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.44	0.50
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.76	0.50
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.93	0.50
32:1a:616:G:O2'	32:1a:617:G:H5'	2.12	0.50
32:1a:1003:G:O2'	32:1a:1004:A:H4'	2.11	0.50
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.47	0.50
1:2A:796:C:H2'	1:2A:797:C:C6	2.46	0.50
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.12	0.50
5:2F:103:LYS:O	5:2F:106:ARG:HG2	2.12	0.50
26:24:61:ARG:NH2	50:2s:9:VAL:HG21	2.26	0.50
32:2a:117:G:OP2	59:2a:3290:HOH:O	2.19	0.50
32:2a:1030(A):G:H1'	32:2a:1030(C):G:C5	2.47	0.50
41:2j:25:GLU:O	41:2j:29:ARG:HG2	2.11	0.50
1:1A:704:U:H2'	1:1A:705:C:C6	2.47	0.50
1:1A:2150:C:H42	1:1A:2182:G:H1	1.59	0.50
32:1a:195:A:C6	32:1a:196:A:N1	2.80	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:473:G:H2'	32:1a:474:G:H8	1.77	0.50
32:1a:1124:G:N2	32:1a:1125:U:O4	2.45	0.50
39:1h:36:LEU:HD12	39:1h:59:LEU:HD13	1.93	0.50
53:1y:3:MET:HG3	53:1y:37:PRO:HG2	1.92	0.50
1:2A:1063:G:H1	1:2A:1075:C:N4	2.02	0.50
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.47	0.50
1:2A:2336:A:H61	22:20:43:THR:CG2	2.24	0.50
14:2S:10:ARG:O	14:2S:14:VAL:HG13	2.10	0.50
21:2Z:16:SER:HA	59:2Z:5002:HOH:O	2.10	0.50
32:2a:384:G:H2'	32:2a:385:C:C6	2.47	0.50
32:1a:1118:C:P	40:1i:104:ARG:HH11	2.34	0.50
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.94	0.50
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.94	0.50
1:2A:1074:G:C2	1:2A:1075:C:H1'	2.47	0.50
1:2A:2168:G:O2'	1:2A:2170:A:N7	2.28	0.50
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.47	0.50
59:2B:3159:HOH:O	6:2G:67:LYS:N	2.44	0.50
21:2Z:10:ARG:HH21	21:2Z:26:GLY:H	1.60	0.50
32:2a:406:G:O2'	35:2d:3:ARG:NH2	2.44	0.50
32:2a:438:G:O2'	32:2a:494:U:O4	2.28	0.50
1:1A:233:A:C2	1:1A:244:A:C4	3.00	0.50
6:1G:66:GLN:HB3	6:1G:92:VAL:HG21	1.93	0.50
32:1a:235:C:H5'	48:1q:70:ARG:HG2	1.93	0.50
32:1a:255:G:H1'	48:1q:16:GLN:NE2	2.27	0.50
39:1h:81:HIS:N	39:1h:138:TRP:O	2.45	0.50
1:2A:774:A:H2'	1:2A:774:A:N3	2.26	0.50
12:2Q:59:ARG:CZ	12:2Q:60:ARG:HH11	2.24	0.50
18:2W:23:LEU:O	18:2W:27:LYS:NZ	2.45	0.50
32:2a:535:A:H5"	59:2a:3353:HOH:O	2.12	0.50
1:1A:1346:U:H4'	1:1A:1347:A:H5"	1.93	0.49
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.35	0.49
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.94	0.49
38:1g:28:ASN:HD21	38:1g:36:LYS:NZ	2.09	0.49
44:1m:3:ARG:O	44:1m:57:ARG:NH2	2.38	0.49
1:2A:788:A:N6	59:2A:6356:HOH:O	2.45	0.49
1:2A:881:G:H2'	1:2A:882:G:H8	1.77	0.49
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.37	0.49
32:2a:270:A:H2'	32:2a:271:C:C6	2.46	0.49
32:2a:286:G:N7	59:2a:3207:HOH:O	2.35	0.49
33:2b:76:GLN:HE21	33:2b:206:ASP:HA	1.77	0.49
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1043:G:H5”	16:1U:92:ARG:HH21	1.77	0.49
1:1A:1087:C:H5’	1:1A:1088:G:OP2	2.12	0.49
32:1a:1002:G:C6	32:1a:1003:G:C2	3.00	0.49
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.35	0.49
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.12	0.49
1:2A:275:G:H2’	1:2A:276:A:O4’	2.12	0.49
1:2A:2136:C:C6	1:2A:2137:C:H5	2.31	0.49
32:2a:993:G:O6	32:2a:1045:C:N4	2.44	0.49
44:2m:96:LEU:C	44:2m:110:ARG:HG2	2.38	0.49
1:1A:211:A:H3’	1:1A:448:U:H5’	1.94	0.49
1:1A:2816:G:H2’	1:1A:2817:G:C8	2.47	0.49
32:1a:1030(C):G:H2’	32:1a:1030(D):A:C8	2.47	0.49
32:1a:1124:G:N7	32:1a:1145:C:O2’	2.45	0.49
32:1a:1525:G:P	42:1k:120:ARG:HH22	2.34	0.49
44:1m:88:ARG:HG3	44:1m:98:VAL:HG11	1.95	0.49
45:1n:32:SER:HB3	45:1n:41:ARG:HG2	1.94	0.49
49:1r:65:ILE:O	49:1r:69:THR:HG23	2.12	0.49
1:2A:652(T):C:H2’	1:2A:652(U):G:H8	1.71	0.49
1:2A:686:G:H5”	59:2A:6356:HOH:O	2.11	0.49
1:2A:861:A:C2	1:2A:917:A:C4	3.00	0.49
7:2H:9:ILE:N	7:2H:50:VAL:O	2.30	0.49
32:2a:1379:G:OP1	38:2g:6:ARG:NH1	2.46	0.49
33:2b:95:GLN:HG3	33:2b:147:LYS:O	2.11	0.49
37:2f:91:VAL:HG11	49:2r:72:ARG:HH12	1.75	0.49
47:2p:18:ARG:NH1	47:2p:32:TYR:OH	2.45	0.49
1:1A:217:A:H8	1:1A:218:A:H5’	1.77	0.49
1:1A:2151:C:O2	1:1A:2181:G:N1	2.37	0.49
1:1A:2250:G:N3	1:1A:2250:G:H2’	2.26	0.49
1:1A:2603:C:H2’	1:1A:2604:G:C8	2.47	0.49
16:1U:69:CYS:HB3	16:1U:74:LEU:HD13	1.94	0.49
26:14:50:VAL:HG11	44:1m:65:LYS:HA	1.95	0.49
32:1a:1498:UR3:H4’	32:1a:1519:MA6:H2	1.94	0.49
33:1b:231:GLU:HB3	33:1b:232:PRO:HD3	1.94	0.49
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.93	0.49
1:2A:616:G:H5’	5:2F:205:ARG:HD2	1.94	0.49
1:2A:1453:U:O2’	1:2A:1455:G:N7	2.43	0.49
1:2A:2315:G:H2’	1:2A:2316:C:C6	2.47	0.49
1:2A:2327:A:H2’	1:2A:2328:A:C8	2.47	0.49
1:2A:2849:U:H4’	1:2A:2868:A:C2	2.48	0.49
21:2Z:146:ILE:HA	21:2Z:174:VAL:HG12	1.95	0.49
32:2a:262:A:H2’	32:2a:263:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1504:G:OP1	59:2a:3391:HOH:O	2.20	0.49
34:2c:116:VAL:HG21	34:2c:202:ILE:HD11	1.93	0.49
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.78	0.49
26:14:59:PHE:CE1	50:1s:64:GLU:HG3	2.47	0.49
32:1a:452:A:H4'	47:1p:72:ARG:CZ	2.42	0.49
32:1a:540:G:H2'	32:1a:541:G:O4'	2.13	0.49
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.42	0.49
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.30	0.49
38:1g:70:LYS:O	38:1g:138:LYS:HE2	2.12	0.49
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.94	0.49
1:2A:336:C:H5"	20:2Y:6:HIS:ND1	2.27	0.49
1:2A:2114:A:O2'	1:2A:2168:G:OP1	2.31	0.49
1:2A:2357:U:OP1	22:20:20:ARG:HD3	2.12	0.49
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.48	0.49
32:2a:1227:A:OP1	50:2s:80:TYR:OH	2.25	0.49
35:2d:162:LEU:HD13	35:2d:181:MET:HG2	1.94	0.49
1:1A:1555:C:H3'	1:1A:1556:A:H5'	1.93	0.49
3:1D:77:ALA:HB2	3:1D:97:TYR:CD2	2.48	0.49
6:1G:33:ARG:HD3	59:1G:3110:HOH:O	2.13	0.49
10:1O:64:ARG:HB2	10:1O:83:ALA:HB3	1.95	0.49
12:1Q:3:MET:HE2	59:1Q:323:HOH:O	2.12	0.49
17:2V:25:LEU:H	17:2V:92:THR:HG1	1.57	0.49
18:2W:59:VAL:HG12	18:2W:60:ASN:HD22	1.78	0.49
26:24:1:MET:HE2	26:24:6:HIS:CD2	2.48	0.49
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.41	0.49
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.93	0.49
44:2m:81:LEU:HD13	44:2m:88:ARG:HG2	1.95	0.49
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.52	0.49
1:1A:2357:G:N3	1:1A:2393:C:H2'	2.27	0.49
1:1A:2406:C:OP2	30:18:30:ARG:HD2	2.13	0.49
3:1D:71:ASP:CB	3:1D:103:ARG:HH22	2.23	0.49
10:1O:104:ARG:HH22	15:1T:43:GLN:NE2	2.11	0.49
26:14:34:GLU:HB3	44:1m:57:ARG:CZ	2.42	0.49
32:1a:67:C:H2'	32:1a:68:G:C8	2.47	0.49
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.48	0.49
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.94	0.49
1:2A:829:A:N7	1:2A:2248:C:H5'	2.28	0.49
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.95	0.49
2:2B:17:C:H2'	2:2B:18:G:O4'	2.12	0.49
23:21:77:ALA:O	23:21:80:LEU:HB2	2.12	0.49
32:2a:939:G:H2'	32:2a:940:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1163:C:H2'	32:2a:1164:G:H8	1.78	0.49
32:2a:1221:G:OP1	32:2a:1320:C:N4	2.46	0.49
33:2b:55:PHE:CE1	33:2b:218:ALA:HA	2.46	0.49
33:2b:71:VAL:HG23	33:2b:164:VAL:HA	1.95	0.49
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.12	0.49
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.13	0.49
40:2i:17:VAL:HG11	40:2i:80:GLY:C	2.37	0.49
43:2l:77:LEU:HD21	43:2l:107:ALA:HA	1.95	0.49
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.94	0.49
1:1A:669:A:H4'	1:1A:670:C:H5	1.78	0.49
2:1B:13:A:N1	2:1B:69:G:O2'	2.37	0.49
5:1F:20:LEU:HD22	5:1F:21:ALA:H	1.78	0.49
32:1a:1338:G:H2'	32:1a:1339:A:C8	2.48	0.49
34:1c:8:ILE:HG23	34:1c:16:ARG:HG2	1.95	0.49
1:2A:108:U:H2'	1:2A:109:G:C8	2.48	0.49
1:2A:873:G:N2	1:2A:905:U:C2	2.81	0.49
1:2A:2128:C:H5'	1:2A:2129:C:OP2	2.12	0.49
1:2A:2391:G:O6	1:2A:2425:A:H8	1.96	0.49
27:25:16:ARG:NH1	27:25:16:ARG:HG2	2.27	0.49
31:29:2:LYS:HE2	31:29:31:LYS:O	2.12	0.49
32:2a:1291:G:OP1	38:2g:37:ASN:ND2	2.46	0.49
34:2c:114:PRO:HA	34:2c:185:GLY:HA3	1.95	0.49
1:1A:310:C:H2'	1:1A:311:C:H6	1.77	0.49
6:1G:77:ILE:HB	6:1G:82:LEU:HB3	1.94	0.49
13:1R:71:GLN:NE2	59:1R:337:HOH:O	2.46	0.49
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.34	0.49
32:1a:620:C:H2'	32:1a:621:A:O4'	2.13	0.49
32:1a:750:G:O2'	46:1o:22:THR:O	2.14	0.49
32:1a:1183:A:H3'	32:1a:1184:G:C5'	2.41	0.49
33:1b:174:VAL:O	33:1b:178:ARG:HB2	2.13	0.49
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	1.95	0.49
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	1.94	0.49
1:2A:272:G:N7	1:2A:421:U:H2'	2.27	0.49
1:2A:581:C:OP2	16:2U:33:ARG:HD3	2.11	0.49
1:2A:862:G:O2'	2:2B:78:A:N3	2.43	0.49
1:2A:2115:G:N2	1:2A:2171:A:H61	2.10	0.49
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.78	0.49
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.78	0.49
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.48	0.49
17:2V:29:PRO:HA	17:2V:61:VAL:HG22	1.94	0.49
19:2X:41:ASN:O	19:2X:45:THR:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:12:GLU:HA	24:22:15:LYS:HZ2	1.78	0.49
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.93	0.49
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.43	0.49
1:1A:82:G:OP1	20:1Y:95:LYS:NZ	2.45	0.49
1:1A:747:G:O2'	1:1A:1679:A:N3	2.44	0.49
3:1D:164:GLN:NE2	3:1D:176:ARG:HH12	2.11	0.49
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.77	0.49
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.78	0.49
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.13	0.49
32:1a:181:G:H4'	32:1a:182:U:H5'	1.95	0.49
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.48	0.49
33:1b:134:GLU:HG3	33:1b:137:ARG:NH2	2.28	0.49
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.45	0.49
51:1t:53:LEU:HD23	51:1t:56:MET:HE3	1.95	0.49
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.95	0.49
1:2A:910:A:N1	1:2A:2277:G:H1'	2.27	0.49
1:2A:1002:G:H2'	1:2A:1003:G:O4'	2.13	0.49
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.48	0.49
1:2A:1702:G:O6	59:2A:4755:HOH:O	2.20	0.49
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.48	0.49
32:2a:1279:A:OP1	41:2j:9:ARG:NH1	2.46	0.49
41:2j:5:ARG:N	59:2j:8101:HOH:O	2.45	0.49
1:1A:1921:G:N3	1:1A:1921:G:H2'	2.27	0.48
1:1A:2389:A:H2'	1:1A:2390:A:C8	2.48	0.48
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.27	0.48
27:15:49:CYS:C	27:15:60:VAL:HG11	2.38	0.48
32:1a:1298:C:H2'	38:1g:114:ARG:NH1	2.28	0.48
33:1b:15:VAL:O	33:1b:15:VAL:HG22	2.13	0.48
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.93	0.48
1:2A:8:A:H5"	9:2N:51:PHE:CZ	2.48	0.48
1:2A:606:U:H4'	1:2A:658:C:H4'	1.95	0.48
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.48	0.48
1:2A:2134:A:H8	1:2A:2156:G:H21	1.61	0.48
3:2D:71:ASP:HB3	3:2D:103:ARG:NH2	2.27	0.48
3:2D:275:LYS:HG3	3:2D:276:LYS:HA	1.94	0.48
11:2P:62:LEU:O	30:28:13:ARG:HD3	2.13	0.48
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.95	0.48
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.46	0.48
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.43	0.48
1:1A:933:C:H3'	1:1A:934:A:H5"	1.95	0.48
1:1A:1404:G:O2'	1:1A:1405:A:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2803:A:H2'	1:1A:2803:A:N3	2.27	0.48
26:14:7:PRO:HB2	26:14:27:THR:HG21	1.94	0.48
32:1a:314:C:OP2	59:1a:2063:HOH:O	2.20	0.48
32:1a:1158:C:H5	32:1a:1181:G:N1	2.11	0.48
36:1e:8:GLU:HG2	36:1e:34:VAL:CG2	2.43	0.48
37:1f:91:VAL:HG12	37:1f:92:LYS:O	2.14	0.48
1:2A:829:A:N7	1:2A:2247:A:O2'	2.44	0.48
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.28	0.48
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.47	0.48
1:2A:2141:G:O6	1:2A:2150:U:O2	2.31	0.48
32:2a:848:C:H2'	32:2a:849:C:H6	1.77	0.48
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.14	0.48
41:2j:16:LEU:HD23	41:2j:94:VAL:HG22	1.94	0.48
1:1A:298:G:H2'	1:1A:299:G:C8	2.48	0.48
1:1A:1686:U:O2'	1:1A:1687:C:H5'	2.12	0.48
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.13	0.48
32:1a:1505:G:O6	59:1a:2023:HOH:O	2.20	0.48
36:1e:137:GLU:HG2	36:1e:140:ARG:HH11	1.78	0.48
37:1f:91:VAL:HG11	49:1r:72:ARG:HH12	1.78	0.48
50:1s:12:ASP:OD2	50:1s:35:SER:HB3	2.13	0.48
1:2A:1063:G:H2'	1:2A:1065:U:C6	2.48	0.48
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.13	0.48
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.46	0.48
1:2A:2080:G:H5'	23:21:35:THR:HG23	1.94	0.48
1:2A:2118:U:O2'	1:2A:2119:A:H5"	2.13	0.48
2:2B:43:C:H5"	26:24:1:MET:HG2	1.95	0.48
7:2H:54:ARG:HD3	7:2H:65:HIS:ND1	2.27	0.48
32:2a:1291:G:O2'	40:2i:38:GLN:OE1	2.30	0.48
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.48	0.48
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.28	0.48
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.13	0.48
33:2b:76:GLN:HB2	33:2b:208:ILE:HG12	1.95	0.48
33:2b:114:ARG:NH1	33:2b:118:LEU:HG	2.28	0.48
41:2j:16:LEU:HD13	41:2j:70:ARG:HG2	1.94	0.48
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.46	0.48
6:1G:50:ALA:HB1	6:1G:52:ILE:HD12	1.93	0.48
7:1H:40:GLU:OE1	7:1H:60:ARG:NH1	2.47	0.48
19:1X:60:ARG:NH1	29:17:47:ARG:HH22	2.11	0.48
32:1a:201:C:H42	32:1a:216:G:H22	1.62	0.48
32:1a:309:G:O2'	32:1a:607:A:N1	2.45	0.48
32:1a:839:U:H1'	32:1a:840:C:OP1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1005:A:H8	32:1a:1005:A:O5'	1.96	0.48
32:1a:1179:A:O3'	40:1i:103:THR:HB	2.13	0.48
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.78	0.48
1:2A:300:A:H2'	1:2A:334:C:H1'	1.94	0.48
1:2A:878:A:H3'	1:2A:879:G:H8	1.77	0.48
1:2A:1587:A:H2'	1:2A:1588:C:C6	2.49	0.48
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.31	0.48
26:24:15:ILE:HB	26:24:32:TYR:CD1	2.48	0.48
32:2a:353:A:H5'	32:2a:353:A:H8	1.78	0.48
33:2b:128:GLU:OE1	33:2b:135:GLN:NE2	2.37	0.48
36:2e:116:THR:HG23	36:2e:117:ASP:OD2	2.14	0.48
1:1A:303:C:H42	1:1A:385:G:H1	1.60	0.48
1:1A:347:G:C8	5:1F:171:PRO:HG3	2.48	0.48
1:1A:518:G:H2'	1:1A:519:G:O4'	2.13	0.48
1:1A:2384:G:N3	59:1A:6578:HOH:O	2.35	0.48
1:1A:2812:A:H1'	1:1A:2904:U:H1'	1.95	0.48
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.43	0.48
12:1Q:56:ARG:HG3	12:1Q:56:ARG:HH11	1.78	0.48
21:1Z:28:MET:HE1	21:1Z:61:LEU:HD21	1.94	0.48
32:1a:437:U:O3'	35:1d:125:HIS:CE1	2.67	0.48
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.14	0.48
40:1i:43:ALA:O	40:1i:45:ALA:N	2.46	0.48
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.63	0.48
1:2A:154(A):C:H42	1:2A:171:G:H1	1.62	0.48
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.44	0.48
1:2A:1045:A:N3	1:2A:1045:A:H2'	2.29	0.48
1:2A:1050:A:H2	1:2A:2751:G:C2	2.31	0.48
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.13	0.48
1:2A:1639:U:C2'	1:2A:1640:C:H5"	2.41	0.48
1:2A:2142:C:O2	1:2A:2149:G:N1	2.46	0.48
1:1A:1400:A:H2'	1:1A:1401:G:O4'	2.14	0.48
1:1A:2118:U:H2'	1:1A:2119:C:C6	2.48	0.48
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.79	0.48
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.95	0.48
11:1P:62:LEU:O	30:18:13:ARG:HD3	2.14	0.48
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.60	0.48
32:1a:131:C:H2'	32:1a:132:C:C6	2.48	0.48
38:1g:12:LEU:HD12	38:1g:12:LEU:H	1.78	0.48
1:2A:247:G:H4'	1:2A:386:G:C5	2.49	0.48
1:2A:299:A:N1	1:2A:322:A:O2'	2.40	0.48
1:2A:1057:A:C2	1:2A:1058:G:C4	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2572:A:N7	4:2E:145:LYS:HB2	2.28	0.48
13:2R:118:GLU:CD	13:2R:118:GLU:H	2.21	0.48
32:2a:692:U:O2'	32:2a:694:A:N7	2.40	0.48
32:2a:1129:C:OP1	40:2i:16:ARG:NH1	2.46	0.48
1:1A:670:C:H5'	1:1A:671:A:OP2	2.14	0.48
1:1A:878:G:O2'	11:1P:38:GLN:NE2	2.47	0.48
1:1A:1841:A:H2'	1:1A:1842:G:O4'	2.13	0.48
1:1A:2096:U:H2'	1:1A:2097:U:C6	2.48	0.48
1:1A:2575:U:H4'	10:1O:28:SER:HA	1.96	0.48
5:1F:164:ARG:HE	56:1F:311:ARG:NH2	2.08	0.48
7:1H:90:LYS:HD3	7:1H:159:GLU:HG2	1.95	0.48
13:1R:118:GLU:H	13:1R:118:GLU:CD	2.22	0.48
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.25	0.48
1:2A:1084:A:C8	1:2A:1085:A:H4'	2.49	0.48
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.29	0.48
1:2A:1580:A:H8	1:2A:1580:A:OP2	1.96	0.48
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.13	0.48
1:2A:2104:G:N2	1:2A:2105:C:N3	2.61	0.48
1:2A:2353:G:N7	59:2A:5088:HOH:O	2.35	0.48
1:2A:2839:G:H5'	13:2R:46:GLY:CA	2.44	0.48
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.96	0.48
36:2e:60:TYR:CZ	36:2e:64:ARG:HD3	2.48	0.48
38:2g:70:LYS:O	38:2g:138:LYS:HE2	2.14	0.48
1:1A:729:G:OP1	59:1A:6522:HOH:O	2.19	0.48
1:1A:1630:A:H5'	1:1A:1631:C:OP1	2.14	0.48
4:1E:12:THR:HG21	15:1T:11:GLU:OE2	2.13	0.48
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.95	0.48
32:1a:909:A:H2'	32:1a:910:C:O4'	2.14	0.48
33:1b:82:ARG:HG3	33:1b:92:TYR:CZ	2.49	0.48
35:1d:6:GLY:O	35:1d:115:ARG:NH1	2.35	0.48
6:2G:170:ARG:NH2	6:2G:182:LYS:O	2.47	0.48
8:2I:114:LEU:HD12	8:2I:116:LEU:HB2	1.95	0.48
32:2a:1039:C:C4	32:2a:1040:U:C4	3.02	0.48
32:2a:1131:G:H2'	32:2a:1132:C:C6	2.49	0.48
32:2a:1516:G:H2'	32:2a:1518:MA6:OP2	2.14	0.48
33:2b:71:VAL:HG12	33:2b:93:VAL:CG2	2.43	0.48
34:2c:36:ASP:O	34:2c:40:ARG:HG3	2.14	0.48
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.14	0.48
1:1A:34:C:O2'	1:1A:35:G:H5'	2.14	0.48
1:1A:173:C:H2'	1:1A:174:U:C6	2.49	0.48
1:1A:1625:U:C2'	1:1A:1626:A:H5'	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2101:U:OP1	23:11:21:ARG:NH2	2.44	0.48
59:1A:7926:HOH:O	18:1W:92:ARG:HD2	2.13	0.48
32:1a:134:A:H1'	32:1a:325:A:C5	2.49	0.48
32:1a:1004:A:N7	32:1a:1036:G:N1	2.61	0.48
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.96	0.48
47:1p:19:ILE:HG22	47:1p:37:GLY:C	2.39	0.48
1:2A:30:G:H2'	1:2A:31:C:C6	2.48	0.48
1:2A:320:A:H4'	1:2A:322:A:N7	2.28	0.48
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.49	0.48
1:2A:1038:C:N4	1:2A:1117:G:H1	2.08	0.48
1:2A:1063:G:C6	1:2A:1075:C:N4	2.82	0.48
1:2A:1085:A:H5'	1:2A:1086:A:OP2	2.13	0.48
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.12	0.48
1:2A:1614:A:N1	18:2W:93:ALA:HB2	2.29	0.48
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.48	0.48
1:2A:2127:G:O6	1:2A:2161:C:N3	2.47	0.48
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.49	0.48
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.46	0.48
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.49	0.48
32:2a:404:U:H5'	35:2d:122:ARG:HD3	1.95	0.48
32:2a:1248:A:O2'	40:2i:70:LYS:NZ	2.32	0.48
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.49	0.48
44:2m:74:VAL:O	44:2m:78:ILE:HG13	2.14	0.48
1:1A:1221:G:N2	1:1A:1223:C:OP2	2.47	0.48
1:1A:1452:U:H2'	1:1A:1453:C:C6	2.49	0.48
1:1A:1500:A:H5"	59:1A:5538:HOH:O	2.12	0.48
1:1A:2123:G:H2'	1:1A:2124:U:C6	2.49	0.48
1:1A:2331:G:N2	14:1S:3:ARG:HA	2.29	0.48
5:1F:13:SER:OG	5:1F:127:GLU:OE2	2.29	0.48
12:1Q:35:VAL:CG1	12:1Q:130:LYS:HB3	2.44	0.48
1:2A:61:G:OP1	24:22:51:ARG:NH2	2.47	0.48
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.14	0.48
3:2D:102:LYS:C	3:2D:103:ARG:HG2	2.38	0.48
7:2H:87:LEU:HD23	7:2H:164:TYR:HA	1.95	0.48
20:2Y:20:TYR:CE1	20:2Y:43:ASN:HA	2.48	0.48
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.49	0.48
1:1A:1110:C:N4	1:1A:1111:U:C2	2.82	0.47
1:1A:2159:C:O2	1:1A:2159:C:H2'	2.13	0.47
4:1E:40:GLU:CD	4:1E:40:GLU:H	2.20	0.47
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.13	0.47
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:11:3:LYS:CG	23:11:4:VAL:H	2.23	0.47
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.49	0.47
38:1g:48:LYS:O	38:1g:52:GLU:HG2	2.14	0.47
50:1s:12:ASP:O	50:1s:14:HIS:N	2.45	0.47
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.49	0.47
1:2A:1557:C:H5"	1:2A:1558:A:OP2	2.14	0.47
1:2A:2756:U:H1'	1:2A:2757:A:H5"	1.96	0.47
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.47	0.47
32:2a:41:G:H2'	32:2a:42:G:C8	2.49	0.47
32:2a:1126:U:O4'	32:2a:1281:U:H1'	2.13	0.47
32:2a:1202:G:O4'	45:2n:29:ARG:NH1	2.47	0.47
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.94	0.47
40:2i:26:VAL:HA	40:2i:61:ALA:O	2.13	0.47
40:2i:31:GLN:HG3	40:2i:36:TYR:HB2	1.94	0.47
1:1A:626:A:H4'	1:1A:627:G:H5'	1.95	0.47
2:1B:78:A:C2	2:1B:100:A:C4	3.01	0.47
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	1.95	0.47
32:1a:384:G:H2'	32:1a:385:C:C6	2.49	0.47
35:1d:108:LEU:HB3	35:1d:110:PHE:CD1	2.48	0.47
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.14	0.47
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.13	0.47
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.49	0.47
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.47	0.47
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	1.96	0.47
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.96	0.47
11:2P:91:PHE:CE2	11:2P:99:LEU:HD21	2.50	0.47
19:2X:65:ARG:HB3	19:2X:70:LEU:HD23	1.97	0.47
32:2a:512:U:H2'	32:2a:513:C:C6	2.49	0.47
32:2a:767:A:H2'	32:2a:768:A:O4'	2.14	0.47
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.49	0.47
34:2c:164:ARG:HG2	34:2c:165:THR:N	2.29	0.47
38:2g:111:ARG:HD3	38:2g:113:GLU:OE2	2.14	0.47
44:2m:34:LEU:HD13	44:2m:41:PRO:HA	1.96	0.47
1:1A:1091:A:H1'	1:1A:1093:G:N3	2.29	0.47
6:1G:77:ILE:HG21	6:1G:80:PHE:CD2	2.49	0.47
15:1T:16:ARG:HD3	15:1T:18:ASP:OD1	2.14	0.47
28:16:35:GLU:HG3	28:16:50:ARG:HD3	1.95	0.47
32:1a:1084:G:C5	32:1a:1085:U:C4	3.02	0.47
33:1b:208:ILE:HA	33:1b:211:ILE:HD12	1.97	0.47
1:2A:455:C:N3	1:2A:472:A:H2'	2.29	0.47
1:2A:1027:A:C6	1:2A:1126:A:C4	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.29	0.47
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.29	0.47
4:2E:40:GLU:H	4:2E:40:GLU:CD	2.20	0.47
6:2G:116:ASP:OD1	44:2m:68:GLY:HA3	2.14	0.47
32:2a:920:U:H2'	32:2a:921:U:H6	1.79	0.47
32:2a:1276:G:H2'	32:2a:1277:C:C6	2.50	0.47
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.29	0.47
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	1.96	0.47
1:1A:1003:U:H4'	59:1A:6990:HOH:O	2.15	0.47
1:1A:1674:G:H2'	1:1A:1675:U:C6	2.49	0.47
18:1W:68:ARG:HH12	18:1W:112:GLY:H	1.62	0.47
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	1.96	0.47
21:1Z:103:ARG:HD2	21:1Z:136:PHE:CD2	2.50	0.47
30:18:47:LYS:CE	55:18:102:MPD:H51	2.44	0.47
32:1a:22:G:H4'	32:1a:885:G:C8	2.50	0.47
32:1a:79:G:C6	32:1a:90:U:N3	2.83	0.47
32:1a:457:C:H2'	32:1a:458:C:C6	2.49	0.47
32:1a:1162:C:H2'	32:1a:1163:C:H6	1.79	0.47
35:1d:173:TRP:CG	35:1d:189:PRO:HG3	2.50	0.47
1:2A:529:A:OP2	9:2N:114:ARG:NH2	2.48	0.47
1:2A:2131:G:N7	1:2A:2158:A:N6	2.55	0.47
1:2A:2133:G:N2	1:2A:2157:G:H2'	2.28	0.47
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.15	0.47
4:2E:119:ARG:HG2	4:2E:160:TYR:HB2	1.96	0.47
7:2H:69:ARG:HG3	7:2H:70:THR:N	2.28	0.47
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.96	0.47
32:2a:179:A:H2'	32:2a:180:U:H6	1.79	0.47
32:2a:266:G:O3'	48:2q:67:LYS:HB2	2.15	0.47
32:2a:757:U:H2'	32:2a:758:G:O4'	2.15	0.47
33:2b:134:GLU:O	33:2b:138:LEU:HG	2.15	0.47
34:2c:43:LEU:O	34:2c:47:LEU:HB2	2.14	0.47
32:1a:642:A:N3	39:1h:113:SER:OG	2.38	0.47
32:1a:1125:U:C4	41:1j:38:ILE:HD13	2.49	0.47
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.14	0.47
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.30	0.47
45:1n:4:LYS:HG3	45:1n:7:ILE:HD11	1.95	0.47
1:2A:228:A:H8	1:2A:229:A:H5'	1.79	0.47
1:2A:2111:C:H42	1:2A:2147:G:H22	1.63	0.47
59:2A:6198:HOH:O	18:2W:11:ARG:HD3	2.14	0.47
59:2A:6418:HOH:O	10:2O:26:LYS:HD2	2.14	0.47
5:2F:120:GLU:HB2	5:2F:122:LYS:HG2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:839:U:H5”	32:2a:840:C:H5	1.79	0.47
40:2i:50:LEU:HD11	40:2i:81:ILE:HD11	1.96	0.47
44:2m:15:VAL:O	44:2m:19:LEU:HD22	2.14	0.47
59:1A:7491:HOH:O	25:13:24:LYS:HD2	2.14	0.47
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	1.95	0.47
16:1U:15:LYS:NZ	59:1U:321:HOH:O	2.38	0.47
48:1q:74:LEU:HD13	48:1q:75:ARG:HG2	1.97	0.47
1:2A:493:G:OP2	59:2A:5413:HOH:O	2.20	0.47
1:2A:1665:A:H4’	10:2O:67:LYS:HB2	1.97	0.47
1:2A:2126:A:N6	1:2A:2162:G:O2’	2.47	0.47
1:2A:2134:A:C5	1:2A:2157:G:H5’	2.50	0.47
1:2A:2164:C:H3’	1:2A:2165:G:H8	1.79	0.47
4:2E:51:PHE:O	4:2E:77:ILE:N	2.42	0.47
7:2H:115:VAL:HG11	7:2H:148:ILE:HD11	1.95	0.47
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	1.96	0.47
1:1A:354:A:H2	1:1A:1255:A:C2’	2.28	0.47
1:1A:968:U:H2’	1:1A:969:C:C6	2.49	0.47
1:1A:1219:A:H1’	1:1A:1220:U:H5’	1.95	0.47
1:1A:1298:G:OP1	16:1U:36:ARG:NH2	2.47	0.47
10:1O:7:TYR:HE1	10:1O:20:MET:HE3	1.80	0.47
11:1P:94:GLU:HG3	11:1P:124:LYS:HD3	1.95	0.47
18:1W:4:LYS:HG2	18:1W:5:ALA:N	2.30	0.47
32:1a:519:C:OP2	43:1l:50:SER:OG	2.31	0.47
32:1a:632:A:H5’	32:1a:633:G:OP2	2.15	0.47
32:1a:1166:G:N2	32:1a:1169:A:H3’	2.30	0.47
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.97	0.47
1:2A:81:G:HO2’	1:2A:295:G:HO2’	1.61	0.47
1:2A:105:C:H2’	1:2A:106:C:C6	2.50	0.47
1:2A:236:C:H2’	1:2A:237:C:C6	2.50	0.47
1:2A:478:A:N1	1:2A:500:G:H4’	2.30	0.47
1:2A:824:A:H1’	1:2A:2358:G:N7	2.30	0.47
1:2A:1493:C:C5	1:2A:2206:G:H2’	2.49	0.47
1:2A:2811:G:OP1	4:2E:60:ASN:HB2	2.14	0.47
4:2E:29:GLY:HA3	59:2E:421:HOH:O	2.14	0.47
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	1.97	0.47
6:2G:11:TYR:OH	6:2G:33:ARG:HG3	2.13	0.47
8:2I:50:ARG:O	8:2I:54:GLN:NE2	2.48	0.47
10:2O:16:ALA:HB2	10:2O:52:VAL:HG21	1.96	0.47
26:24:46:GLN:HB3	26:24:48:ARG:HH21	1.79	0.47
32:2a:685:G:O2’	32:2a:686:U:H5’	2.15	0.47
32:2a:1127:G:H5’	32:2a:1280:A:O2’	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1305:G:H5'	52:2u:4:GLY:C	2.39	0.47
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.97	0.47
47:2p:43:LYS:HA	47:2p:48:TRP:HB3	1.96	0.47
47:2p:68:ASP:O	47:2p:71:ARG:HG2	2.14	0.47
50:2s:23:ASN:HA	50:2s:27:GLU:OE2	2.14	0.47
53:2y:23:ARG:NH1	53:2y:75:ASN:OD1	2.43	0.47
53:2y:29:LYS:HE3	53:2y:30:TRP:CZ3	2.50	0.47
1:1A:1201:A:OP1	16:1U:55:ARG:HD3	2.14	0.47
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.15	0.47
1:1A:2830:A:OP2	13:1R:2:ARG:NH2	2.47	0.47
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	1.97	0.47
11:1P:83:VAL:CG1	11:1P:112:LEU:HD21	2.45	0.47
32:1a:1075:C:OP1	33:1b:179:LYS:NZ	2.43	0.47
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.95	0.47
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.47	0.47
1:2A:185:U:H4'	1:2A:218:A:H4'	1.97	0.47
1:2A:422:A:H2'	1:2A:423:A:C8	2.50	0.47
1:2A:1063:G:N2	1:2A:1075:C:C2	2.72	0.47
1:2A:1525:G:H2'	1:2A:1526:G:C8	2.50	0.47
1:2A:2287:A:O2'	1:2A:2289:G:N7	2.38	0.47
10:2O:98:VAL:HG22	10:2O:118:ALA:HA	1.96	0.47
17:2V:40:LEU:HB2	17:2V:46:VAL:CG1	2.44	0.47
33:2b:44:LEU:HD22	33:2b:44:LEU:H	1.80	0.47
40:2i:16:ARG:HD3	40:2i:64:THR:HG21	1.97	0.47
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.15	0.47
51:2t:97:ALA:O	51:2t:99:LEU:HD13	2.14	0.47
1:1A:329:U:H2'	1:1A:330:U:C6	2.50	0.47
1:1A:1096:A:H2'	1:1A:1097:G:O4'	2.15	0.47
1:1A:1847:G:O6	3:1D:35:LYS:NZ	2.42	0.47
2:1B:90:A:N7	2:1B:91:C:H1'	2.30	0.47
6:1G:181:ARG:HG3	6:1G:182:LYS:N	2.30	0.47
11:1P:99:LEU:HD23	11:1P:102:ARG:HH21	1.80	0.47
30:18:42:ARG:HD2	59:18:213:HOH:O	2.15	0.47
32:1a:376:G:H5"	47:1p:5:ARG:CD	2.43	0.47
32:1a:747:C:H3'	32:1a:748:C:C6	2.49	0.47
38:1g:79:ARG:HA	38:1g:84:ASN:HA	1.96	0.47
51:1t:10:LEU:HD13	51:1t:12:ALA:HB2	1.96	0.47
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.15	0.47
1:2A:84:A:H5'	20:2Y:8:LYS:HB3	1.96	0.47
1:2A:479:A:H4'	1:2A:480:A:OP1	2.14	0.47
1:2A:947:G:N2	1:2A:971:C:C2	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1067:A:H5'	1:2A:1067:A:H8	1.79	0.47
1:2A:1747:G:H2'	1:2A:1747(A):G:H8	1.80	0.47
1:2A:2586:C:H6	1:2A:2586:C:O5'	1.98	0.47
3:2D:164:GLN:NE2	3:2D:176:ARG:HH22	2.13	0.47
4:2E:36:ARG:HH11	4:2E:85:ASN:ND2	2.13	0.47
6:2G:136:ARG:CD	6:2G:137:GLU:HG3	2.45	0.47
8:2I:102:SER:OG	8:2I:103:ARG:N	2.46	0.47
21:2Z:77:ASP:OD2	21:2Z:80:ARG:NH1	2.48	0.47
32:2a:501:C:H2'	32:2a:502:G:C8	2.49	0.47
32:2a:1053:G:N7	32:2a:1200:C:H5"	2.30	0.47
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.15	0.47
32:2a:1375:A:H4'	38:2g:29:LYS:HE2	1.95	0.47
34:2c:6:HIS:NE2	34:2c:8:ILE:HB	2.29	0.47
39:2h:73:ASP:OD1	39:2h:75:ARG:HD3	2.15	0.47
1:1A:9:U:N3	1:1A:2641:A:H2	2.12	0.47
1:1A:1834:A:H4'	3:1D:259:THR:HG23	1.97	0.47
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.14	0.47
32:1a:814:A:H2'	32:1a:816:A:H5"	1.96	0.47
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.50	0.47
47:1p:60:LEU:HD13	47:1p:60:LEU:HA	1.72	0.47
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.15	0.47
1:2A:644:A:H4'	1:2A:645:C:C5	2.49	0.47
1:2A:1084:A:N6	1:2A:1086:A:C8	2.83	0.47
1:2A:2113:U:H2'	1:2A:2114:A:O4'	2.13	0.47
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.15	0.47
55:2A:3747:MPD:HM2	59:2A:5941:HOH:O	2.15	0.47
18:2W:4:LYS:HE2	18:2W:6:ILE:HD11	1.97	0.47
36:2e:10:MET:HG2	36:2e:13:ILE:HD11	1.96	0.47
1:1A:1218:G:C2	1:1A:1220:U:H4'	2.49	0.46
1:1A:1532:A:H2'	1:1A:1533:G:C8	2.51	0.46
1:1A:2327:G:H2'	1:1A:2328:C:C6	2.50	0.46
4:1E:119:ARG:HG3	4:1E:160:TYR:HB2	1.97	0.46
33:1b:185:ILE:HG22	33:1b:199:TYR:CD2	2.49	0.46
36:1e:102:ALA:HB1	36:1e:106:PRO:HG2	1.97	0.46
1:2A:108:U:H2'	1:2A:109:G:H8	1.79	0.46
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.81	0.46
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.16	0.46
2:2B:42:C:O2	6:2G:93:THR:N	2.41	0.46
6:2G:55:LYS:HD3	6:2G:150:ASP:OD2	2.15	0.46
32:2a:814:A:N7	32:2a:816:A:C4	2.82	0.46
32:2a:1016:A:O5'	32:2a:1016:A:H8	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.15	0.46
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.15	0.46
1:1A:2086:C:H2'	1:1A:2087:C:C6	2.50	0.46
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.15	0.46
19:1X:60:ARG:HH12	29:17:47:ARG:NH2	2.11	0.46
21:1Z:199:LYS:HG3	21:1Z:200:GLY:N	2.30	0.46
26:14:49:PHE:HB3	26:14:50:VAL:H	1.54	0.46
26:14:68:ARG:HA	26:14:68:ARG:NH2	2.30	0.46
32:1a:92:C:H2'	32:1a:93:G:C8	2.51	0.46
32:1a:446:G:O6	59:1a:1955:HOH:O	2.20	0.46
32:1a:454:C:OP1	47:1p:75:ARG:NH2	2.48	0.46
32:1a:627:G:H2'	32:1a:628:G:C8	2.49	0.46
35:1d:108:LEU:HD12	35:1d:176:LEU:HB2	1.97	0.46
36:1e:31:LEU:HD23	36:1e:31:LEU:HA	1.76	0.46
39:1h:44:PHE:HB3	39:1h:80:ILE:HD11	1.96	0.46
1:2A:2104:G:O6	1:2A:2185:C:C4	2.68	0.46
6:2G:16:ARG:HH21	6:2G:31:VAL:HG22	1.80	0.46
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.97	0.46
32:2a:382:A:H2'	32:2a:383:A:C8	2.50	0.46
32:2a:448:A:P	32:2a:485:G:H22	2.38	0.46
32:2a:662:G:O2'	32:2a:836:G:OP1	2.33	0.46
32:2a:1183:A:H1'	32:2a:1184:G:OP1	2.15	0.46
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.79	0.46
40:2i:5:TYR:OH	40:2i:16:ARG:HG2	2.15	0.46
1:1A:611:U:H2'	1:1A:612:C:C6	2.50	0.46
1:1A:2682:A:H5"	1:1A:2682:A:H8	1.79	0.46
3:1D:137:PRO:O	3:1D:140:THR:HG23	2.15	0.46
32:1a:491:G:H2'	32:1a:492:G:O4'	2.16	0.46
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.16	0.46
33:1b:229:VAL:HG12	33:1b:230:VAL:H	1.80	0.46
38:1g:113:GLU:HG3	38:1g:118:VAL:HG12	1.96	0.46
39:1h:41:ARG:NH1	39:1h:123:GLU:OE2	2.48	0.46
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.79	0.46
51:1t:14:LYS:HE3	51:1t:18:GLN:NE2	2.30	0.46
1:2A:863:A:N7	59:2A:4927:HOH:O	2.35	0.46
1:2A:1082:U:O4	1:2A:1086:A:C6	2.69	0.46
1:2A:1086:A:OP1	1:2A:1104:C:O2'	2.33	0.46
1:2A:2122:U:H2'	1:2A:2123:G:H8	1.80	0.46
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.30	0.46
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.16	0.46
12:2Q:103:MET:HE1	12:2Q:125:LEU:HD13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:614:A:H2'	32:2a:615:C:C6	2.50	0.46
32:2a:1111:A:N1	34:2c:177:THR:OG1	2.40	0.46
39:2h:14:ARG:O	39:2h:18:ARG:HD3	2.15	0.46
1:1A:1405:A:N1	1:1A:1418:U:C4	2.84	0.46
1:1A:1476:C:H2'	1:1A:1477:U:C6	2.50	0.46
7:1H:4:ILE:O	7:1H:69:ARG:HG2	2.16	0.46
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	1.96	0.46
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.98	0.46
32:1a:745:C:H2'	32:1a:746:A:C8	2.50	0.46
1:2A:207:A:H2'	1:2A:208:C:O4'	2.16	0.46
1:2A:1151:G:H5"	16:2U:81:HIS:CD2	2.51	0.46
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.51	0.46
2:2B:73:A:C4	2:2B:105:A:C2	3.04	0.46
59:2B:3159:HOH:O	6:2G:66:GLN:HG2	2.13	0.46
30:28:6:THR:HG23	30:28:64:TYR:HD2	1.80	0.46
32:2a:294:U:OP1	32:2a:610:G:O2'	2.25	0.46
32:2a:585:G:N3	32:2a:879:C:H4'	2.30	0.46
32:2a:601:C:H2'	32:2a:602:A:C8	2.50	0.46
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.51	0.46
34:2c:140:ARG:NH1	34:2c:140:ARG:HB2	2.30	0.46
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.49	0.46
44:2m:20:THR:HA	44:2m:25:ILE:O	2.15	0.46
21:1Z:125:LEU:HB3	21:1Z:165:VAL:HG13	1.98	0.46
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.51	0.46
32:1a:270:A:H2'	32:1a:271:C:C6	2.50	0.46
34:1c:50:ALA:HB1	34:1c:70:VAL:HG21	1.98	0.46
40:1i:23:ASN:H	40:1i:23:ASN:HD22	1.64	0.46
41:1j:38:ILE:O	41:1j:38:ILE:HG13	2.15	0.46
1:2A:1528:A:OP2	59:2A:3987:HOH:O	2.21	0.46
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.30	0.46
1:2A:2107:C:H42	1:2A:2182:G:H1	1.63	0.46
1:2A:2544:G:H1'	1:2A:2646:C:H4'	1.97	0.46
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.15	0.46
6:2G:111:LEU:O	6:2G:114:ILE:HB	2.15	0.46
14:2S:101:LEU:C	14:2S:101:LEU:HD23	2.40	0.46
17:2V:35:LEU:HB2	17:2V:57:VAL:HG22	1.96	0.46
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.50	0.46
24:22:21:LEU:HB2	24:22:64:LEU:HD23	1.98	0.46
26:24:64:GLY:C	26:24:66:SER:N	2.74	0.46
32:2a:148:G:H2'	32:2a:149:A:H8	1.81	0.46
32:2a:404:U:H5"	35:2d:122:ARG:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.50	0.46
32:2a:1338:G:C6	32:2a:1339:A:C6	3.04	0.46
38:2g:16:LEU:HD11	40:2i:45:ALA:HB2	1.97	0.46
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.16	0.46
50:2s:14:HIS:HE1	50:2s:35:SER:OG	1.99	0.46
53:2y:23:ARG:O	53:2y:26:LYS:HB2	2.14	0.46
1:1A:1150:C:H2'	1:1A:1151:U:C6	2.50	0.46
1:1A:2122:G:H1	1:1A:2211:U:H3	1.63	0.46
1:1A:2163:G:C2'	1:1A:2164:C:H5'	2.45	0.46
1:1A:2455:C:OP1	5:1F:68:LYS:HD3	2.15	0.46
1:1A:2849:G:H5'	13:1R:46:GLY:CA	2.45	0.46
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	1.98	0.46
13:1R:10:LEU:HA	13:1R:10:LEU:HD23	1.74	0.46
32:1a:448:A:P	32:1a:485:G:H22	2.38	0.46
32:1a:572:A:OP2	59:1a:1905:HOH:O	2.21	0.46
34:1c:47:LEU:HD13	34:1c:68:VAL:HG11	1.98	0.46
44:1m:81:LEU:HD13	44:1m:88:ARG:HG2	1.98	0.46
46:1o:29:VAL:HG11	46:1o:67:LEU:HD21	1.97	0.46
1:2A:839:U:H2'	1:2A:840:C:H6	1.81	0.46
1:2A:1235:G:C6	1:2A:1236:G:N1	2.84	0.46
1:2A:2098:U:H2'	1:2A:2099:U:O4'	2.16	0.46
1:2A:2313:C:H2'	1:2A:2314:C:H6	1.80	0.46
1:2A:2820:A:P	13:2R:2:ARG:HH22	2.38	0.46
9:2N:75:TYR:CE2	9:2N:77:GLY:HA2	2.51	0.46
32:2a:662:G:H2'	32:2a:663:A:H8	1.78	0.46
32:2a:858:G:O6	32:2a:869:G:H3'	2.16	0.46
32:2a:1362:C:H2'	32:2a:1363:C:H5"	1.97	0.46
33:2b:9:GLU:C	33:2b:11:LEU:H	2.23	0.46
33:2b:229:VAL:HG12	33:2b:230:VAL:H	1.79	0.46
49:2r:59:SER:OG	49:2r:62:GLU:HG2	2.15	0.46
1:1A:609:A:N1	1:1A:856:G:O2'	2.46	0.46
1:1A:2124:U:C2	1:1A:2209:G:O6	2.69	0.46
1:1A:2724:U:H2'	1:1A:2727:G:H5"	1.98	0.46
3:1D:10:THR:OG1	3:1D:13:ARG:HG2	2.15	0.46
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE1	2.21	0.46
33:1b:15:VAL:HG23	33:1b:209:ARG:HB3	1.98	0.46
33:1b:220:ASP:O	33:1b:224:GLN:HB3	2.15	0.46
35:1d:108:LEU:HD22	35:1d:174:LEU:HD13	1.97	0.46
35:1d:166:LYS:HB2	35:1d:168:ARG:HH22	1.81	0.46
38:1g:90:GLU:OE2	38:1g:90:GLU:N	2.38	0.46
1:2A:1067:A:H4'	1:2A:1068:G:OP2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2747:G:O6	1:2A:2755:C:H5"	2.16	0.46
14:2S:25:ARG:HD3	14:2S:42:ASP:OD2	2.15	0.46
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.62	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.68	0.46
32:2a:581:G:OP1	46:2o:65:ARG:NH2	2.49	0.46
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.47	0.46
32:2a:977:A:O2'	32:2a:981:U:N3	2.48	0.46
1:1A:1044:C:P	16:1U:92:ARG:HH22	2.39	0.46
1:1A:2156:A:N3	1:1A:2181:G:H1'	2.31	0.46
4:1E:179:GLU:HB3	4:1E:181:LEU:HD22	1.97	0.46
6:1G:83:ARG:O	6:1G:86:MET:HB2	2.16	0.46
10:1O:98:VAL:HG22	10:1O:118:ALA:HA	1.98	0.46
32:1a:353:A:H5'	32:1a:353:A:H8	1.81	0.46
32:1a:756:C:H2'	32:1a:757:U:O4'	2.15	0.46
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.28	0.46
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.16	0.46
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.63	0.46
40:1i:125:TYR:OH	40:1i:127:LYS:HD3	2.14	0.46
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.97	0.46
1:2A:125:G:N3	29:27:48:LYS:HE2	2.31	0.46
1:2A:919:G:N2	1:2A:2269:A:OP2	2.48	0.46
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.31	0.46
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.60	0.46
1:2A:2788:C:P	4:2E:61:ARG:HH21	2.39	0.46
13:2R:8:ARG:NE	13:2R:43:GLU:OE2	2.42	0.46
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.97	0.46
32:2a:560:U:H4'	32:2a:561:U:O5'	2.16	0.46
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.50	0.46
41:2j:5:ARG:N	41:2j:99:LYS:O	2.48	0.46
44:2m:80:ARG:O	44:2m:84:ILE:HG23	2.16	0.46
1:1A:1110:C:H3'	1:1A:1111:U:H5"	1.98	0.46
1:1A:1296:G:H5"	59:1U:302:HOH:O	2.15	0.46
1:1A:1314:A:H2'	1:1A:1315:A:O4'	2.16	0.46
1:1A:1405:A:N1	1:1A:1418:U:O4	2.49	0.46
1:1A:2710:U:H2'	1:1A:2711:C:C6	2.51	0.46
2:1B:84:C:OP1	25:13:15:TYR:OH	2.23	0.46
16:1U:78:THR:HG23	16:1U:117:GLN:HE22	1.80	0.46
18:1W:4:LYS:HB2	18:1W:106:ILE:HG12	1.98	0.46
32:1a:587:G:H2'	59:1a:2374:HOH:O	2.15	0.46
32:1a:1124:G:H5'	41:1j:38:ILE:HG22	1.98	0.46
43:1l:27:LEU:HD12	43:1l:33:ARG:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:92:LEU:O	51:1t:96:GLY:N	2.45	0.46
1:2A:760:G:H2'	1:2A:761:A:O4'	2.15	0.46
1:2A:956:G:OP2	12:2Q:14:ARG:NH2	2.49	0.46
1:2A:1497:U:H5"	1:2A:1498:C:H5	1.80	0.46
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.69	0.46
1:2A:2742:C:OP1	31:29:35:ARG:HD3	2.16	0.46
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG11	1.98	0.46
32:2a:300:A:H1'	32:2a:565:U:O2	2.16	0.46
32:2a:947:G:H2'	32:2a:948:C:O4'	2.15	0.46
33:2b:114:ARG:NH1	33:2b:141:GLU:OE1	2.49	0.46
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	1.98	0.46
41:2j:30:SER:HG	41:2j:81:THR:HG22	1.81	0.46
1:1A:155:C:H3'	59:1A:8030:HOH:O	2.15	0.46
1:1A:2240:G:OP1	3:1D:261:LYS:NZ	2.33	0.46
1:1A:2359:C:H2'	1:1A:2360:U:C6	2.51	0.46
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.51	0.46
23:11:3:LYS:HG2	23:11:61:ARG:NH1	2.30	0.46
30:18:28:GLY:O	30:18:36:LYS:NZ	2.44	0.46
32:1a:437:U:O3'	35:1d:125:HIS:HE1	1.99	0.46
1:2A:2611:U:H3'	1:2A:2611:U:OP2	2.16	0.46
26:24:46:GLN:HB3	26:24:48:ARG:NH2	2.30	0.46
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.98	0.46
32:2a:192:U:H2'	32:2a:193:C:H6	1.81	0.46
32:2a:581:G:OP1	46:2o:61:GLY:HA3	2.16	0.46
32:2a:706:A:C2'	32:2a:707:C:H5'	2.46	0.46
32:2a:1456:G:O6	51:2t:54:LYS:NZ	2.46	0.46
33:2b:178:ARG:HH22	39:2h:68:ARG:HH22	1.63	0.46
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.97	0.46
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.81	0.46
1:1A:1218:G:O2'	1:1A:1219:A:O4'	2.34	0.45
1:1A:2899:C:H2'	1:1A:2900:G:O4'	2.16	0.45
4:1E:111:ARG:HG3	4:1E:160:TYR:CD2	2.51	0.45
7:1H:116:GLU:OE1	7:1H:116:GLU:HA	2.15	0.45
8:1I:81:VAL:HG21	8:1I:88:ILE:HD13	1.99	0.45
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.98	0.45
17:1V:6:LYS:HG2	59:1V:305:HOH:O	2.15	0.45
32:1a:447:G:H8	32:1a:447:G:O5'	2.00	0.45
32:1a:679:C:H2'	32:1a:680:C:C6	2.51	0.45
32:1a:1228:C:P	44:1m:108:ARG:HH22	2.38	0.45
35:1d:12:CYS:SG	35:1d:19:LEU:HB2	2.56	0.45
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:49:GLU:HG3	39:1h:51:VAL:HG22	1.97	0.45
44:1m:14:ARG:HB2	44:1m:17:VAL:HG23	1.99	0.45
1:2A:234:C:H2'	1:2A:235:U:C6	2.51	0.45
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.51	0.45
1:2A:1300:U:H4'	1:2A:1301:A:H5'	1.97	0.45
1:2A:2114:A:C2	1:2A:2115:G:H1'	2.51	0.45
1:2A:2163:C:H5"	1:2A:2164:C:OP2	2.16	0.45
1:2A:2174:C:H2'	1:2A:2175:C:C6	2.51	0.45
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.52	0.45
2:2B:66:A:N6	2:2B:109:C:H5'	2.31	0.45
3:2D:275:LYS:HA	3:2D:276:LYS:C	2.41	0.45
7:2H:98:LEU:HD12	7:2H:102:ALA:O	2.16	0.45
8:2I:50:ARG:HE	8:2I:50:ARG:HB3	1.32	0.45
21:2Z:140:ASP:OD1	21:2Z:142:SER:OG	2.32	0.45
23:21:3:LYS:HB3	23:21:4:VAL:H	1.56	0.45
26:24:50:VAL:HG11	44:2m:64:TRP:C	2.41	0.45
32:2a:43:C:OP1	59:2a:3301:HOH:O	2.21	0.45
32:2a:297:G:H4'	32:2a:557:G:H4'	1.97	0.45
32:2a:397:A:N7	32:2a:547:A:O2'	2.40	0.45
32:2a:399:G:H2'	32:2a:400:C:C6	2.51	0.45
32:2a:528:C:H5'	32:2a:529:G:OP2	2.17	0.45
32:2a:685:G:C2	32:2a:686:U:C4	3.04	0.45
32:2a:1004:A:H5"	32:2a:1025:U:C5	2.51	0.45
32:2a:1009:G:C2	32:2a:1010:G:C8	3.05	0.45
32:2a:1075:C:OP1	33:2b:179:LYS:NZ	2.41	0.45
32:2a:1270:C:O2'	32:2a:1314:C:H5'	2.16	0.45
33:2b:200:ILE:HB	33:2b:202:PRO:HD3	1.99	0.45
1:1A:2140:U:O2'	1:1A:2141:A:H5'	2.15	0.45
1:1A:2190:G:C2	1:1A:2193:A:C8	3.04	0.45
30:18:39:LYS:O	30:18:43:GLN:HG3	2.16	0.45
32:1a:539:A:OP2	43:1l:115:LYS:NZ	2.50	0.45
32:1a:1106:G:H5"	34:1c:172:ARG:HG2	1.99	0.45
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.16	0.45
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.16	0.45
1:2A:77:C:OP1	24:22:59:ARG:HD3	2.17	0.45
1:2A:289:A:N6	1:2A:351:G:O2'	2.48	0.45
1:2A:361:G:O2'	1:2A:362:U:H5'	2.15	0.45
1:2A:1530:C:N4	1:2A:1539:G:H1	2.13	0.45
1:2A:1792:G:O2'	1:2A:1830:C:OP1	2.32	0.45
13:2R:38:VAL:HB	13:2R:39:PRO:HD3	1.98	0.45
21:2Z:70:LEU:HD11	21:2Z:98:MET:SD	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:854:G:O6	59:2a:3437:HOH:O	2.21	0.45
32:2a:1039:C:N4	32:2a:1040:U:O4	2.49	0.45
32:2a:1372:U:OP1	40:2i:71:SER:HB3	2.17	0.45
34:2c:91:LEU:HD22	34:2c:101:LEU:HD22	1.98	0.45
41:2j:21:GLN:O	41:2j:25:GLU:HG2	2.17	0.45
51:2t:38:LYS:HE2	51:2t:38:LYS:HB3	1.71	0.45
1:1A:295:C:H42	1:1A:389:G:H1	1.64	0.45
1:1A:886:U:H2'	1:1A:887:C:C6	2.51	0.45
1:1A:1285:G:H2'	1:1A:1286:U:O4'	2.17	0.45
1:1A:2905:C:H2'	1:1A:2906:U:C6	2.50	0.45
4:1E:1:MET:HE1	4:1E:199:ARG:HG2	1.98	0.45
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.81	0.45
32:1a:191:G:O2'	51:1t:101:GLY:HA3	2.17	0.45
32:1a:1134:G:C2	32:1a:1141:C:C2	3.05	0.45
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	1.97	0.45
43:1l:24:VAL:HB	43:1l:27:LEU:HD22	1.98	0.45
45:1n:3:ARG:HA	45:1n:3:ARG:HD3	1.73	0.45
1:2A:1698:A:C8	1:2A:1700:A:O4'	2.70	0.45
3:2D:127:VAL:HA	3:2D:193:VAL:HG22	1.98	0.45
7:2H:17:VAL:HG22	7:2H:26:VAL:HG22	1.98	0.45
8:2I:48:GLU:HG3	8:2I:52:ARG:HH11	1.82	0.45
14:2S:36:TYR:OH	14:2S:54:LEU:HD22	2.16	0.45
24:22:59:ARG:NH2	59:22:5003:HOH:O	2.49	0.45
32:2a:828:A:H2'	32:2a:829:G:O4'	2.16	0.45
41:2j:57:LYS:HE2	41:2j:60:ARG:NH2	2.31	0.45
51:2t:59:ALA:O	51:2t:63:ILE:HG13	2.17	0.45
1:1A:2311:G:N7	59:1A:4989:HOH:O	2.36	0.45
4:1E:28:ALA:HB3	4:1E:93:VAL:CG1	2.46	0.45
6:1G:155:MET:HE2	6:1G:155:MET:HB3	1.88	0.45
32:1a:838:G:H2'	32:1a:839:U:H2'	1.98	0.45
32:1a:1183:A:H3'	32:1a:1184:G:H5"	1.98	0.45
40:1i:33:PHE:CE1	40:1i:43:ALA:HB1	2.51	0.45
44:1m:54:VAL:HA	44:1m:57:ARG:HB3	1.99	0.45
47:1p:75:ARG:HG3	47:1p:80:PHE:HD2	1.81	0.45
1:2A:1050:A:C2	1:2A:2751:G:C2	3.04	0.45
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.31	0.45
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.51	0.45
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.52	0.45
1:2A:1913:A:N1	32:2a:1492:A:N6	2.64	0.45
59:2A:6123:HOH:O	13:2R:103:ARG:NH1	2.48	0.45
21:2Z:14:LYS:HE2	21:2Z:14:LYS:HB3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:67:LYS:HA	24:22:70:GLN:OE1	2.16	0.45
26:24:47:GLN:C	26:24:49:PHE:H	2.24	0.45
32:2a:142:G:H2'	32:2a:143:A:C8	2.50	0.45
32:2a:149:A:H2'	32:2a:150:C:C6	2.51	0.45
32:2a:963:G:H5'	59:2a:3467:HOH:O	2.16	0.45
32:2a:1162:C:H2'	32:2a:1163:C:C6	2.52	0.45
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.81	0.45
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.52	0.45
1:1A:2081:A:O2'	5:1F:69:HIS:HD2	1.99	0.45
1:1A:2139:A:N6	1:1A:2193:A:C6	2.84	0.45
4:1E:185:LYS:NZ	59:1E:477:HOH:O	2.50	0.45
8:1I:117:GLU:HG3	8:1I:118:LYS:N	2.30	0.45
32:1a:996:A:H2'	32:1a:997:U:C6	2.51	0.45
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	1.98	0.45
45:1n:27:CYS:SG	45:1n:29:ARG:HB2	2.56	0.45
1:2A:1079:C:H5	1:2A:1080:C:C6	2.35	0.45
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.16	0.45
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	1.98	0.45
1:2A:2312:U:H5'	6:2G:88:ILE:HD11	1.98	0.45
6:2G:8:LYS:HD2	6:2G:100:TRP:CD1	2.51	0.45
25:23:7:LYS:HE3	25:23:32:GLN:NE2	2.32	0.45
26:24:13:ARG:CZ	26:24:21:VAL:HG11	2.47	0.45
26:24:44:THR:O	26:24:46:GLN:N	2.50	0.45
32:2a:229:U:O2'	47:2p:23:ASP:OD2	2.33	0.45
32:2a:444:C:N4	32:2a:490:G:H1	2.12	0.45
32:2a:490:G:H2'	32:2a:491:G:C8	2.52	0.45
32:2a:1054:C:H41	53:2y:46:GLN:CD	2.25	0.45
34:2c:50:ALA:O	34:2c:72:LYS:HB2	2.16	0.45
43:2l:32:PHE:CD2	43:2l:86:ARG:HB3	2.51	0.45
1:1A:1825:U:H2'	1:1A:1826:C:C6	2.51	0.45
1:1A:2128:G:C4	1:1A:2129:C:H1'	2.52	0.45
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.50	0.45
32:1a:555:C:H2'	32:1a:556:C:C6	2.52	0.45
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.99	0.45
1:2A:87:C:H5"	1:2A:88:G:H5'	1.98	0.45
1:2A:185:U:H2'	1:2A:186:G:C8	2.52	0.45
1:2A:848:G:H2'	1:2A:849:A:C8	2.52	0.45
1:2A:1050:A:H2'	1:2A:1051:G:H8	1.81	0.45
1:2A:1059:G:C2	1:2A:1079:C:N4	2.79	0.45
1:2A:1359:A:N1	1:2A:1372:U:O4	2.49	0.45
1:2A:1805:U:O2	3:2D:50:THR:HB	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2188:C:H2'	1:2A:2189:U:O4'	2.17	0.45
1:2A:2849:U:OP2	15:2T:95:ARG:NH1	2.50	0.45
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.99	0.45
6:2G:120:LEU:HB3	6:2G:131:TYR:OH	2.17	0.45
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	1.98	0.45
11:2P:59:LEU:HD21	30:28:10:ALA:HA	1.99	0.45
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.31	0.45
24:22:38:GLN:HB3	24:22:44:LEU:HB2	1.97	0.45
32:2a:1122:U:C4	32:2a:1123:A:N7	2.85	0.45
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	1.98	0.45
34:2c:115:LEU:HD12	34:2c:115:LEU:HA	1.77	0.45
1:1A:2108:U:H2'	1:1A:2109:G:C8	2.52	0.45
1:1A:2661:U:H2'	1:1A:2662:U:C6	2.52	0.45
12:1Q:137:TYR:HE2	21:1Z:49:ARG:NH1	2.15	0.45
26:14:59:PHE:HE1	50:1s:64:GLU:HG3	1.79	0.45
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.52	0.45
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.16	0.45
32:1a:1162:C:H2'	32:1a:1163:C:C6	2.52	0.45
33:1b:100:GLY:HA2	33:1b:103:THR:OG1	2.17	0.45
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.97	0.45
37:1f:97:PHE:HD2	49:1r:31:LEU:HD23	1.81	0.45
1:2A:244:A:C2	1:2A:255:A:C4	3.05	0.45
1:2A:300:A:H1'	1:2A:319:C:H1'	1.98	0.45
1:2A:863:A:P	12:2Q:22:LYS:HG3	2.57	0.45
1:2A:1695:G:H1'	3:2D:8:PRO:O	2.16	0.45
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.17	0.45
8:2I:69:LYS:HB2	8:2I:138:ILE:HG12	1.99	0.45
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.99	0.45
12:2Q:56:ARG:HH11	12:2Q:56:ARG:HG3	1.81	0.45
14:2S:4:LEU:HD22	14:2S:8:GLU:HB3	1.99	0.45
15:2T:23:ARG:HG3	15:2T:120:ARG:NH1	2.32	0.45
32:2a:519:C:OP2	43:2l:50:SER:OG	2.28	0.45
32:2a:657:G:H4'	46:2o:28:GLN:HG2	1.98	0.45
32:2a:737:A:H2'	32:2a:738:C:C6	2.52	0.45
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.52	0.45
32:2a:1374:A:OP1	38:2g:36:LYS:NZ	2.50	0.45
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.17	0.45
37:2f:55:ASP:HA	37:2f:56:PRO:HD2	1.84	0.45
41:2j:5:ARG:O	41:2j:98:ILE:HA	2.17	0.45
1:1A:1592:A:H2'	1:1A:1593:C:O4'	2.16	0.45
1:1A:1625:U:H2'	1:1A:1626:A:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2124:U:O2	1:1A:2209:G:C6	2.69	0.45
1:1A:2186:C:H5	1:1A:2187:G:C6	2.35	0.45
1:1A:2429:C:OP1	11:1P:65:ARG:NH2	2.50	0.45
21:1Z:34:ASN:HB2	59:1Z:8104:HOH:O	2.16	0.45
32:1a:225:C:H2'	32:1a:226:G:O4'	2.16	0.45
32:1a:598:U:H2'	32:1a:599:C:H6	1.81	0.45
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.17	0.45
38:1g:90:GLU:H	38:1g:90:GLU:CD	2.24	0.45
42:1k:18:ARG:NH2	42:1k:35:PRO:O	2.50	0.45
1:2A:218:A:C2	1:2A:235:U:H4'	2.51	0.45
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.50	0.45
5:2F:116:ASP:O	5:2F:120:GLU:HG3	2.17	0.45
32:2a:1003:G:H4'	59:2a:3590:HOH:O	2.15	0.45
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.17	0.45
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.81	0.45
37:2f:86:ARG:O	37:2f:87:ARG:HG2	2.16	0.45
42:2k:99:GLN:HG3	42:2k:105:VAL:HG11	1.98	0.45
1:1A:908:A:H2'	1:1A:909:G:O4'	2.17	0.45
1:1A:1001:G:P	12:1Q:14:ARG:HH22	2.34	0.45
1:1A:1715:A:H4'	1:1A:1716:A:O5'	2.17	0.45
1:1A:1749:G:H2'	1:1A:1750:G:O4'	2.16	0.45
1:1A:2028:C:O5'	1:1A:2028:C:H6	2.00	0.45
1:1A:2102:G:H8	1:1A:2102:G:H5"	1.81	0.45
2:1B:116:G:H5"	2:1B:116:G:C8	2.48	0.45
4:1E:76:ARG:NH1	59:1E:478:HOH:O	2.48	0.45
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.50	0.45
6:1G:137:GLU:HB2	6:1G:140:ILE:HD12	1.98	0.45
30:18:47:LYS:HE2	55:18:102:MPD:H51	1.99	0.45
32:1a:56:U:H2'	32:1a:57:G:C8	2.52	0.45
32:1a:721:G:H4'	32:1a:722:A:O4'	2.17	0.45
32:1a:1288:A:N1	32:1a:1371:G:H1'	2.32	0.45
33:1b:7:VAL:HG12	33:1b:217:ARG:HD2	1.99	0.45
53:1y:38:HIS:O	53:1y:52:ALA:HA	2.17	0.45
1:2A:861:A:H2'	1:2A:862:G:O4'	2.17	0.45
1:2A:1069:A:C5	1:2A:1095:A:H4'	2.52	0.45
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.52	0.45
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.43	0.45
1:2A:2648:C:H2'	1:2A:2649:U:H6	1.81	0.45
2:2B:42:C:O2'	59:2B:3159:HOH:O	2.09	0.45
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.33	0.45
32:2a:33:A:N3	43:2l:32:PHE:HE1	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:110:C:H2'	32:2a:111:G:O4'	2.16	0.45
32:2a:721:G:H4'	32:2a:722:A:O4'	2.17	0.45
40:2i:5:TYR:HH	40:2i:16:ARG:HG2	1.82	0.45
47:2p:21:VAL:HG11	47:2p:59:TRP:NE1	2.31	0.45
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.52	0.45
1:1A:418:G:H1'	1:1A:438:G:O4'	2.16	0.45
6:1G:43:LEU:C	6:1G:45:GLU:H	2.25	0.45
8:1I:54:GLN:HG3	8:1I:57:ARG:NH1	2.31	0.45
20:1Y:20:TYR:O	20:1Y:23:ARG:HB2	2.16	0.45
26:14:57:GLU:HB2	26:14:58:ARG:HA	2.00	0.45
32:1a:355:C:O2'	32:1a:388:G:N3	2.40	0.45
32:1a:1014:A:H4'	50:1s:14:HIS:CE1	2.52	0.45
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.99	0.45
35:1d:88:VAL:HG13	36:1e:97:GLY:HA2	1.99	0.45
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.98	0.45
1:2A:251:A:C5	1:2A:252:G:H1'	2.52	0.45
1:2A:543:C:H5"	1:2A:545:G:OP2	2.17	0.45
1:2A:954:G:H5"	12:2Q:13:GLN:HB3	1.99	0.45
1:2A:1047:G:O2'	1:2A:1048:A:O5'	2.31	0.45
2:2B:24:G:H4'	2:2B:25:A:C8	2.52	0.45
7:2H:74:ASN:O	7:2H:78:GLY:N	2.50	0.45
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	1.99	0.45
26:24:44:THR:C	26:24:46:GLN:H	2.25	0.45
32:2a:730:G:C5	32:2a:731:G:H1'	2.52	0.45
32:2a:758:G:H4'	32:2a:880:C:H4'	1.98	0.45
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.52	0.45
53:2y:20:VAL:O	53:2y:24:LEU:HB2	2.16	0.45
53:2y:52:ALA:HB1	53:2y:81:LEU:HD11	1.98	0.45
2:1B:66:A:H61	2:1B:109:C:H5'	1.82	0.44
3:1D:242:ARG:N	3:1D:242:ARG:HD3	2.32	0.44
8:1I:38:LEU:HD13	23:11:75:GLU:OE2	2.16	0.44
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.99	0.44
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.17	0.44
33:1b:166:ASP:OD2	33:1b:169:LYS:HB2	2.16	0.44
35:1d:155:LEU:O	35:1d:158:ILE:HG12	2.17	0.44
1:2A:271(O):C:H2'	1:2A:271(P):C:C6	2.52	0.44
1:2A:721:C:H2'	1:2A:722:A:C8	2.52	0.44
1:2A:2302:G:C6	1:2A:2315:G:C6	3.05	0.44
1:2A:2680:C:H5'	4:2E:189:PRO:HA	1.99	0.44
5:2F:184:TYR:CD2	5:2F:188:ARG:HD2	2.52	0.44
8:2I:72:LEU:O	8:2I:75:LEU:HD22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.99	0.44
32:2a:114:U:H2'	32:2a:115:G:C8	2.51	0.44
32:2a:143:A:O3'	32:2a:144:G:H8	2.00	0.44
32:2a:411:A:O2'	32:2a:413:G:H5'	2.17	0.44
32:2a:434:U:H2'	32:2a:435:C:H6	1.79	0.44
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.51	0.44
32:2a:857:C:H2'	32:2a:858:G:O4'	2.16	0.44
33:2b:218:ALA:O	33:2b:222:ILE:HG23	2.16	0.44
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.51	0.44
1:1A:1554:A:H4'	1:1A:1556:A:C5	2.52	0.44
1:1A:1961:5MU:OP1	1:1A:2616:U:O2'	2.32	0.44
1:1A:2116:G:P	8:1I:22:LYS:HD2	2.57	0.44
8:1I:38:LEU:HB2	8:1I:40:THR:HG23	1.98	0.44
32:1a:426:G:OP1	35:1d:38:TYR:OH	2.24	0.44
32:1a:434:U:H2'	32:1a:435:C:C6	2.52	0.44
32:1a:1152:A:OP1	41:1j:68:HIS:ND1	2.51	0.44
33:1b:178:ARG:HH11	33:1b:178:ARG:CG	2.30	0.44
36:1e:151:LEU:HD11	39:1h:77:GLU:CD	2.43	0.44
1:2A:26:G:C6	1:2A:27:G:N1	2.85	0.44
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.16	0.44
1:2A:1142(A):A:C2	1:2A:1144:G:C6	3.04	0.44
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.45	0.44
2:2B:15:A:OP2	2:2B:69:G:N2	2.49	0.44
2:2B:75:G:H5'	2:2B:76:G:OP2	2.17	0.44
7:2H:84:SER:HA	7:2H:133:VAL:O	2.17	0.44
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.52	0.44
16:2U:104:GLN:NE2	16:2U:105:VAL:H	2.16	0.44
32:2a:390:C:H2'	32:2a:391:G:C8	2.51	0.44
32:2a:500:G:H2'	32:2a:501:C:C6	2.52	0.44
32:2a:540:G:C6	32:2a:541:G:C5	3.06	0.44
32:2a:735:C:H2'	32:2a:736:C:H6	1.82	0.44
32:2a:895:G:H2'	32:2a:896:C:C6	2.53	0.44
34:2c:30:ARG:NH2	45:2n:38:GLY:HA2	2.32	0.44
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.32	0.44
4:1E:144:ARG:CG	4:1E:145:LYS:N	2.80	0.44
32:1a:359:U:H2'	32:1a:360:A:C8	2.52	0.44
32:1a:616:G:OP2	35:1d:141:ARG:NH2	2.50	0.44
32:1a:1023:G:H2'	32:1a:1024:G:C8	2.52	0.44
39:1h:73:ASP:OD1	39:1h:75:ARG:HD3	2.17	0.44
40:1i:22:GLY:HA3	40:1i:60:ASP:OD1	2.17	0.44
1:2A:330:A:HO2'	1:2A:331:A:H8	1.62	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:375:C:H2'	1:2A:376:C:C6	2.53	0.44
1:2A:1049:C:H2'	1:2A:1050:A:C8	2.52	0.44
1:2A:1364:G:P	23:21:3:LYS:HG3	2.58	0.44
1:2A:1404:C:H2'	1:2A:1405:U:H6	1.82	0.44
1:2A:2136:C:C2	1:2A:2155:G:N2	2.82	0.44
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.51	0.44
1:2A:2641:G:OP1	9:2N:74:ARG:NH1	2.51	0.44
1:2A:2659:G:O2'	7:2H:175:LYS:HE2	2.18	0.44
4:2E:54:GLN:OE1	4:2E:55:ASN:N	2.48	0.44
5:2F:132:VAL:CG2	5:2F:163:VAL:HG22	2.47	0.44
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.91	0.44
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.17	0.44
26:24:61:ARG:HD3	50:2s:42:PRO:HD3	2.00	0.44
32:2a:325:A:H2'	32:2a:326:G:O4'	2.17	0.44
32:2a:1329:A:P	44:2m:28:ALA:HB3	2.58	0.44
33:2b:92:TYR:CE1	33:2b:94:ASN:HB2	2.53	0.44
42:2k:78:GLN:O	42:2k:103:LEU:HA	2.18	0.44
1:1A:13:A:N1	1:1A:550:U:H2'	2.32	0.44
1:1A:1119:A:H2	1:1A:1120:G:C8	2.35	0.44
1:1A:2133:C:H42	1:1A:2169:G:N2	2.15	0.44
59:1A:6511:HOH:O	5:1F:74:ARG:HD2	2.17	0.44
2:1B:29:A:O2'	2:1B:58:A:N1	2.47	0.44
3:1D:202:LYS:NZ	32:1a:774:G:OP1	2.40	0.44
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.98	0.44
32:1a:1104:G:O5'	33:1b:111:ARG:HD2	2.17	0.44
34:1c:6:HIS:CD2	34:1c:8:ILE:HB	2.53	0.44
53:1y:24:LEU:HD11	53:1y:39:ILE:HD11	2.00	0.44
1:2A:493:G:H2'	1:2A:494:G:O4'	2.17	0.44
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.52	0.44
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.17	0.44
2:2B:17:C:N4	2:2B:109:C:N3	2.66	0.44
8:2I:102:SER:HB2	59:2I:5004:HOH:O	2.17	0.44
17:2V:21:ARG:HG2	17:2V:91:TYR:CD1	2.52	0.44
21:2Z:40:ASP:OD1	21:2Z:42:VAL:HG13	2.18	0.44
26:24:63:TYR:N	26:24:63:TYR:CD1	2.86	0.44
32:2a:176:C:H2'	32:2a:177:C:C6	2.52	0.44
32:2a:233:C:H2'	32:2a:234:C:H6	1.82	0.44
32:2a:867:G:O2'	32:2a:873:A:N1	2.47	0.44
32:2a:1400:5MC:N3	53:2y:63:ALA:HA	2.32	0.44
32:2a:1530:G:H2'	32:2a:1531:A:C8	2.52	0.44
51:2t:14:LYS:HE3	51:2t:18:GLN:NE2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1733:C:H2'	1:1A:1734:G:O4'	2.17	0.44
1:1A:2177:G:H2'	1:1A:2178:G:O4'	2.18	0.44
1:1A:2473:C:H2'	1:1A:2474:U:C6	2.53	0.44
14:1S:20:ARG:NH2	22:10:48:GLY:O	2.51	0.44
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.97	0.44
30:18:4:MET:HE3	30:18:63:PRO:CG	2.48	0.44
33:1b:44:LEU:HD12	33:1b:44:LEU:HA	1.73	0.44
1:2A:323:G:H1'	1:2A:1205:U:O2	2.17	0.44
1:2A:1097:U:O2	1:2A:1097:U:H2'	2.17	0.44
1:2A:1410:G:H1	1:2A:1592:C:H42	1.65	0.44
1:2A:1449:A:N3	1:2A:1529:G:H1'	2.33	0.44
1:2A:1842:G:O2'	3:2D:253:GLN:NE2	2.49	0.44
1:2A:2768:C:H2'	1:2A:2769:C:O4'	2.17	0.44
3:2D:5:LYS:HB3	3:2D:5:LYS:HE3	1.66	0.44
4:2E:170:LEU:HD23	4:2E:184:VAL:HG11	2.00	0.44
7:2H:117:PRO:HA	7:2H:118:PRO:HD3	1.85	0.44
10:2O:120:GLU:HG2	10:2O:122:LEU:HG	1.99	0.44
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.98	0.44
11:2P:106:LEU:HD13	11:2P:107:LYS:O	2.18	0.44
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.99	0.44
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.18	0.44
21:2Z:125:LEU:HG	21:2Z:164:ALA:HB3	1.98	0.44
26:24:59:PHE:HA	26:24:60:GLN:C	2.40	0.44
32:2a:116:A:H61	32:2a:313:A:H1'	1.81	0.44
32:2a:986:A:H1'	50:2s:54:GLY:O	2.17	0.44
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.33	0.44
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.32	0.44
35:2d:108:LEU:HB3	35:2d:110:PHE:CE1	2.53	0.44
53:2y:23:ARG:HB3	53:2y:78:ILE:HD11	1.99	0.44
53:2y:24:LEU:HD22	53:2y:24:LEU:HA	1.75	0.44
1:1A:843:C:H2'	1:1A:844:C:C6	2.52	0.44
1:1A:1199:C:H2'	1:1A:1200:G:O4'	2.18	0.44
1:1A:2171:G:H2'	1:1A:2172:U:O4'	2.17	0.44
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.18	0.44
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.99	0.44
15:1T:95:ARG:HH11	15:1T:95:ARG:CG	2.20	0.44
26:14:56:VAL:HB	26:14:60:GLN:HG2	1.97	0.44
26:14:59:PHE:C	26:14:61:ARG:H	2.25	0.44
32:1a:441:A:H3'	32:1a:442:C:H6	1.83	0.44
32:1a:609:A:OP1	47:1p:18:ARG:NH2	2.40	0.44
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1304:G:C6	32:1a:1305:G:N1	2.86	0.44
33:1b:222:ILE:O	33:1b:226:ARG:HG3	2.18	0.44
34:1c:123:GLN:O	34:1c:128:PHE:HB2	2.18	0.44
36:1e:69:VAL:HA	36:1e:70:PRO:HD3	1.66	0.44
37:1f:50:TYR:OH	49:1r:74:ARG:O	2.32	0.44
39:1h:46:LYS:HG3	39:1h:64:LYS:HB2	2.00	0.44
46:1o:17:ARG:NH2	59:1o:3105:HOH:O	2.44	0.44
46:1o:51:HIS:ND1	59:1o:3104:HOH:O	2.36	0.44
48:1q:67:LYS:O	48:1q:68:ARG:CB	2.65	0.44
30:28:63:PRO:HG2	30:28:64:TYR:CD2	2.52	0.44
32:2a:814:A:H2'	32:2a:816:A:H5"	1.99	0.44
34:2c:102:ASN:OD1	34:2c:102:ASN:N	2.50	0.44
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.32	0.44
51:2t:39:LYS:HE3	51:2t:39:LYS:HB2	1.83	0.44
1:1A:35:G:H2'	1:1A:36:G:O4'	2.18	0.44
1:1A:651:U:O4	11:1P:107:LYS:HE2	2.18	0.44
6:1G:47:LYS:O	6:1G:86:MET:HE2	2.17	0.44
21:1Z:80:ARG:O	21:1Z:82:ARG:HG3	2.17	0.44
32:1a:271:C:H2'	32:1a:272:C:H6	1.82	0.44
32:1a:411:A:OP2	35:1d:30:LYS:HD2	2.18	0.44
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.53	0.44
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	2.00	0.44
47:1p:57:ARG:NH2	47:1p:78:GLY:O	2.50	0.44
1:2A:13:A:N1	1:2A:525:U:H2'	2.33	0.44
1:2A:184:C:H2'	1:2A:185:U:C6	2.53	0.44
1:2A:770:G:OP2	59:2A:4150:HOH:O	2.21	0.44
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.18	0.44
1:2A:2101:G:N2	1:2A:2189:U:H1'	2.33	0.44
1:2A:2119:A:N6	1:2A:2168:G:H21	2.16	0.44
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.81	0.44
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.17	0.44
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.99	0.44
3:2D:164:GLN:HE21	3:2D:176:ARG:NH1	2.16	0.44
9:2N:99:LEU:HD23	9:2N:99:LEU:HA	1.87	0.44
21:2Z:91:LEU:HG	21:2Z:130:PRO:HG3	2.00	0.44
23:21:53:VAL:HG22	23:21:74:VAL:HG13	2.00	0.44
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.33	0.44
32:2a:256:U:OP1	48:2q:17:LYS:NZ	2.39	0.44
32:2a:1090:U:H2'	32:2a:1091:U:H6	1.83	0.44
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.18	0.44
32:2a:1490:C:H2'	32:2a:1491:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:18:ARG:HB2	42:2k:33:THR:OG1	2.17	0.44
47:2p:28:ARG:HG3	47:2p:29:ASP:N	2.31	0.44
47:2p:43:LYS:HA	47:2p:48:TRP:CB	2.48	0.44
48:2q:41:LYS:NZ	48:2q:92:ARG:HH21	2.15	0.44
53:2y:23:ARG:HB3	53:2y:78:ILE:CD1	2.47	0.44
1:1A:7:G:H2'	1:1A:8:A:O4'	2.18	0.44
1:1A:240:A:C5	1:1A:241:G:H1'	2.53	0.44
1:1A:1217:G:H3'	1:1A:1218:G:H5'	2.00	0.44
3:1D:5:LYS:HB3	3:1D:5:LYS:HE3	1.71	0.44
14:1S:58:LEU:HD12	14:1S:69:VAL:HG12	1.99	0.44
18:1W:46:PHE:O	18:1W:50:VAL:HG23	2.18	0.44
24:12:65:ASN:O	24:12:69:ARG:HB2	2.18	0.44
28:16:21:TYR:CE2	28:16:38:LYS:HG2	2.53	0.44
32:1a:664:G:N2	32:1a:741:G:H1	2.04	0.44
32:1a:1226:C:N4	44:1m:104:ARG:HD2	2.33	0.44
36:1e:116:THR:HG23	36:1e:117:ASP:OD2	2.17	0.44
51:1t:9:ASN:OD1	51:1t:9:ASN:N	2.51	0.44
1:2A:7:G:H2'	1:2A:8:A:C8	2.53	0.44
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.98	0.44
11:2P:55:ARG:HG2	11:2P:56:SER:O	2.17	0.44
12:2Q:7:MET:HG3	12:2Q:9:TYR:O	2.18	0.44
19:2X:1:MET:HE2	24:22:25:VAL:HG12	2.00	0.44
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.53	0.44
32:2a:437:U:O2'	35:2d:123:HIS:HD2	1.99	0.44
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.28	0.44
32:2a:632:A:H5"	32:2a:632:A:H8	1.83	0.44
32:2a:667:G:OP1	32:2a:732:C:O2'	2.29	0.44
32:2a:786:G:C2	32:2a:797:C:C2	3.06	0.44
33:2b:174:VAL:O	33:2b:178:ARG:HB2	2.17	0.44
36:2e:81:GLU:HG2	36:2e:90:VAL:HG13	1.99	0.44
53:2y:18:GLN:O	53:2y:18:GLN:NE2	2.51	0.44
53:2y:54:ILE:HB	53:2y:61:LEU:HD12	2.00	0.44
5:1F:38:ARG:NH2	59:1F:430:HOH:O	2.48	0.44
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.99	0.44
12:1Q:35:VAL:HG12	12:1Q:130:LYS:O	2.18	0.44
15:1T:95:ARG:NH1	15:1T:95:ARG:HG2	2.25	0.44
21:1Z:102:LEU:HD12	21:1Z:102:LEU:HA	1.85	0.44
32:1a:189(A):C:N4	32:1a:189(J):G:H1	2.07	0.44
32:1a:911:U:H2'	32:1a:912:C:C6	2.53	0.44
33:1b:96:ARG:HD2	33:1b:98:LEU:HD23	1.99	0.44
34:1c:22:TRP:CD1	34:1c:59:ARG:HD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.33	0.44
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.18	0.44
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.17	0.44
3:2D:164:GLN:HE21	3:2D:176:ARG:HH22	1.66	0.44
6:2G:5:VAL:HG23	6:2G:104:GLU:OE2	2.18	0.44
6:2G:41:GLN:NE2	6:2G:154:GLY:O	2.45	0.44
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.38	0.44
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	2.00	0.44
29:27:10:ARG:HG2	29:27:14:LYS:HD2	1.98	0.44
32:2a:384:G:H2'	32:2a:385:C:H6	1.82	0.44
32:2a:984:C:H2'	32:2a:985:C:H6	1.83	0.44
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.82	0.44
32:2a:1030(A):G:N2	32:2a:1030(D):A:OP2	2.51	0.44
34:2c:8:ILE:HD12	34:2c:16:ARG:HD3	2.00	0.44
36:2e:69:VAL:HG22	36:2e:71:LEU:HD22	1.98	0.44
1:1A:456:A:OP2	59:1A:4847:HOH:O	2.21	0.43
1:1A:721:G:C1'	5:1F:74:ARG:HD3	2.45	0.43
1:1A:858:U:H2'	11:1P:21:ARG:HA	2.00	0.43
6:1G:41:GLN:HE22	6:1G:153:ARG:HG2	1.82	0.43
10:1O:110:GLY:HA2	10:1O:112:MET:HE2	2.00	0.43
15:1T:106:SER:O	15:1T:110:ILE:HG13	2.18	0.43
25:13:59:VAL:O	25:13:60:GLU:HG2	2.18	0.43
26:14:15:ILE:HB	26:14:32:TYR:CD1	2.53	0.43
32:1a:178:C:H2'	32:1a:179:A:H8	1.83	0.43
32:1a:688:G:O2'	32:1a:704:A:N1	2.41	0.43
32:1a:1442:G:O2'	32:1a:1442(A):G:O5'	2.32	0.43
35:1d:164:ALA:O	35:1d:168:ARG:NH1	2.51	0.43
1:2A:406:G:N2	59:2A:6031:HOH:O	2.23	0.43
1:2A:826:U:OP1	1:2A:2428:G:H3'	2.18	0.43
1:2A:1683:C:H2'	1:2A:1684:C:C6	2.53	0.43
1:2A:2752:C:OP2	7:2H:4:ILE:HD11	2.17	0.43
2:2B:28:C:H2'	2:2B:29:A:O4'	2.18	0.43
26:24:14:ILE:HB	26:24:22:ILE:HD13	1.99	0.43
32:2a:452:A:N3	47:2p:72:ARG:NH1	2.66	0.43
32:2a:490:G:H2'	32:2a:491:G:H8	1.82	0.43
36:2e:69:VAL:HA	36:2e:70:PRO:HD3	1.64	0.43
45:2n:4:LYS:O	45:2n:7:ILE:HG12	2.17	0.43
1:1A:196:A:H2'	1:1A:197:C:O4'	2.17	0.43
1:1A:629:U:H4'	1:1A:705:C:H4'	1.99	0.43
1:1A:1836:U:O2	3:1D:50:THR:HB	2.17	0.43
7:1H:117:PRO:HG3	7:1H:123:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:28:GLU:HG3	17:1V:29:PRO:HD2	2.00	0.43
20:1Y:92:ASN:CB	20:1Y:94:LYS:H	2.30	0.43
24:12:63:VAL:O	24:12:66:GLU:HB2	2.18	0.43
32:1a:580:U:H2'	32:1a:581:G:O4'	2.19	0.43
32:1a:1328:C:OP1	52:1u:21:TYR:OH	2.30	0.43
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.22	0.43
46:1o:64:ARG:HH11	46:1o:68:ARG:HH21	1.65	0.43
48:1q:67:LYS:O	48:1q:68:ARG:HB3	2.17	0.43
51:1t:37:SER:O	51:1t:41:ILE:HG13	2.18	0.43
51:1t:43:LEU:HD22	51:1t:48:LYS:HD2	2.00	0.43
1:2A:27:G:O2'	1:2A:28:A:OP2	2.34	0.43
1:2A:570:G:O2'	1:2A:975:C:N4	2.49	0.43
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.54	0.43
1:2A:2104:G:O6	1:2A:2186:G:C4	2.71	0.43
1:2A:2134:A:O2'	1:2A:2159:G:H1'	2.18	0.43
5:2F:9:ILE:HA	5:2F:10:PRO:HD2	1.86	0.43
5:2F:53:THR:HG22	5:2F:56:GLU:OE2	2.18	0.43
6:2G:64:THR:HB	6:2G:94:LEU:HD21	2.00	0.43
7:2H:90:LYS:HD3	7:2H:159:GLU:HG2	2.00	0.43
15:2T:91:ARG:HD2	15:2T:120:ARG:NH1	2.32	0.43
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.53	0.43
32:2a:1030(A):G:H1'	32:2a:1030(C):G:N7	2.32	0.43
32:2a:1400:5MC:H1'	53:2y:80:LYS:HD2	1.99	0.43
35:2d:11:LEU:O	35:2d:15:GLU:HB2	2.17	0.43
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.19	0.43
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.83	0.43
44:2m:90:LEU:HD23	44:2m:93:ARG:HH21	1.83	0.43
1:1A:2133:C:H42	1:1A:2169:G:H22	1.66	0.43
1:1A:2724:U:O2'	1:1A:2726:A:H5'	2.18	0.43
6:1G:181:ARG:HG3	6:1G:182:LYS:H	1.83	0.43
32:1a:5:U:H1'	59:1a:2487:HOH:O	2.18	0.43
32:1a:106:C:O2'	32:1a:379:C:H5"	2.19	0.43
32:1a:986:A:H1'	50:1s:54:GLY:O	2.17	0.43
40:1i:49:PRO:HB3	40:1i:82:ALA:HB2	1.99	0.43
48:1q:58:GLU:OE2	48:1q:75:ARG:NH2	2.52	0.43
50:1s:22:LEU:HD12	50:1s:31:ILE:HD11	2.00	0.43
1:2A:656:G:H2'	1:2A:657:U:O4'	2.17	0.43
1:2A:910:A:H2	1:2A:2264:C:O2	2.02	0.43
1:2A:2154:G:H2'	1:2A:2155:G:C8	2.53	0.43
1:2A:2640:G:OP1	9:2N:97:ARG:NH2	2.51	0.43
2:2B:13:A:O2'	2:2B:14:U:H3'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:21:THR:HG22	59:2Q:3122:HOH:O	2.18	0.43
16:2U:49:HIS:HA	16:2U:52:ARG:HB3	1.99	0.43
32:2a:827:U:H2'	32:2a:870:U:O4	2.19	0.43
32:2a:901:A:O2'	32:2a:1513:A:OP1	2.33	0.43
32:2a:1002:G:C4	32:2a:1003:G:C8	3.06	0.43
32:2a:1128:C:H1'	32:2a:1147:C:N4	2.31	0.43
34:2c:22:TRP:CD1	34:2c:59:ARG:HD2	2.53	0.43
1:1A:237:G:OP1	59:1A:8219:HOH:O	2.21	0.43
1:1A:1560:U:H2'	1:1A:1561:C:C6	2.53	0.43
1:1A:1911:A:N1	1:1A:2246:G:H1'	2.34	0.43
1:1A:2053:A:C6	1:1A:2510:C:H1'	2.53	0.43
1:1A:2331:G:H22	14:1S:3:ARG:CZ	2.32	0.43
1:1A:2440:G:H5"	1:1A:2441:G:OP1	2.18	0.43
5:1F:27:GLU:HA	5:1F:27:GLU:OE2	2.18	0.43
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.75	0.43
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	2.01	0.43
26:14:57:GLU:CB	26:14:58:ARG:HA	2.49	0.43
32:1a:313:A:H2'	32:1a:314:C:C6	2.52	0.43
36:1e:71:LEU:C	36:1e:72:GLN:HG2	2.42	0.43
44:1m:11:ARG:O	44:1m:13:LYS:N	2.50	0.43
50:1s:71:LEU:HD23	50:1s:71:LEU:HA	1.83	0.43
1:2A:821:A:H2'	1:2A:946:G:H5"	2.01	0.43
1:2A:2162:G:H2'	1:2A:2163:C:C6	2.52	0.43
1:2A:2173:A:C2'	1:2A:2174:C:H5'	2.48	0.43
1:2A:2366:A:H2'	1:2A:2367:G:O4'	2.18	0.43
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.18	0.43
21:2Z:18:LEU:HD12	21:2Z:18:LEU:HA	1.72	0.43
30:28:23:VAL:CG1	30:28:47:LYS:HD3	2.48	0.43
32:2a:414:A:H2'	32:2a:415:A:H8	1.84	0.43
32:2a:1030:C:N3	32:2a:1031:G:C2	2.85	0.43
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.53	0.43
38:2g:101:LEU:O	38:2g:105:VAL:HG23	2.18	0.43
41:2j:45:ARG:HG2	41:2j:47:PHE:CZ	2.54	0.43
44:2m:87:TYR:HA	44:2m:90:LEU:HD12	1.99	0.43
53:2y:85:LEU:O	53:2y:89:GLN:HG2	2.19	0.43
1:1A:787:U:H2'	1:1A:788:G:C8	2.53	0.43
1:1A:1128:U:C4	1:1A:1132:A:N1	2.83	0.43
1:1A:2269:U:O2'	1:1A:2270:C:H5'	2.18	0.43
1:1A:2388:A:H2'	1:1A:2389:A:O4'	2.18	0.43
1:1A:2584:A:N7	4:1E:145:LYS:HB2	2.33	0.43
1:1A:2588:G:H1'	59:1A:4464:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2901:A:N6	1:1A:2902:G:N1	2.67	0.43
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.18	0.43
28:16:14:THR:HG21	28:16:48:VAL:HG13	2.01	0.43
32:1a:407:G:OP1	35:1d:115:ARG:HD3	2.18	0.43
32:1a:1368:G:OP2	40:1i:112:LYS:HG3	2.18	0.43
33:1b:41:ILE:HD13	33:1b:41:ILE:HA	1.84	0.43
36:1e:66:MET:HE3	36:1e:66:MET:HB3	1.95	0.43
37:1f:41:GLU:HG2	37:1f:43:LEU:HD12	2.00	0.43
1:2A:372:G:H8	23:21:65:SER:O	2.01	0.43
1:2A:608:A:H2'	1:2A:609:A:C8	2.53	0.43
1:2A:1049:C:H1'	1:2A:1113:U:O2'	2.19	0.43
1:2A:1324:G:C4	1:2A:1328:G:O6	2.71	0.43
5:2F:110:LEU:HD21	5:2F:181:LEU:HG	1.99	0.43
5:2F:129:PHE:O	5:2F:132:VAL:HG22	2.18	0.43
7:2H:35:VAL:HG13	7:2H:71:LEU:HD22	2.00	0.43
11:2P:135:LEU:HA	11:2P:135:LEU:HD23	1.73	0.43
16:2U:89:GLU:HB2	17:2V:50:PRO:CB	2.49	0.43
32:2a:109:A:C6	32:2a:326:G:C6	3.07	0.43
32:2a:539:A:C6	32:2a:540:G:C6	3.07	0.43
32:2a:790:A:H4'	53:2y:31:GLN:NE2	2.34	0.43
32:2a:964:A:N3	32:2a:969:A:O2'	2.47	0.43
32:2a:1400:5MC:N4	53:2y:62:VAL:HG23	2.33	0.43
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	2.01	0.43
40:2i:23:ASN:OD1	40:2i:25:LYS:HE3	2.18	0.43
50:2s:40:ILE:HB	50:2s:67:VAL:O	2.18	0.43
1:1A:771:U:H2'	1:1A:772:G:O4'	2.18	0.43
2:1B:24:G:N7	2:1B:56:G:H2'	2.34	0.43
17:1V:52:VAL:HG22	17:1V:55:ALA:HB3	2.01	0.43
32:1a:149:A:H2'	32:1a:150:C:C6	2.54	0.43
32:1a:254:G:OP1	48:1q:67:LYS:O	2.36	0.43
32:1a:1004:A:C5	32:1a:1037:C:C2	3.06	0.43
32:1a:1239:A:H62	32:1a:1299:A:N6	2.17	0.43
42:1k:79:SER:HA	42:1k:104:GLN:HB2	2.01	0.43
1:2A:674:G:H1'	5:2F:74:ARG:HD3	2.01	0.43
1:2A:975(A):G:C2	1:2A:990:A:C8	3.06	0.43
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.33	0.43
1:2A:1835:G:H5'	1:2A:1836:C:OP2	2.18	0.43
5:2F:29:ASN:H	5:2F:112:MET:CE	2.32	0.43
13:2R:33:ARG:NH1	13:2R:115:GLU:OE2	2.51	0.43
32:2a:437:U:O2'	35:2d:125:HIS:HE1	2.02	0.43
32:2a:1144:G:C6	32:2a:1145:C:C4	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:112:SER:O	34:2c:116:VAL:HG23	2.19	0.43
34:2c:186:PHE:HZ	34:2c:188:LEU:HD13	1.83	0.43
37:2f:69:GLU:O	37:2f:72:VAL:HG13	2.19	0.43
51:2t:43:LEU:HD13	51:2t:51:GLU:HB3	2.01	0.43
1:1A:904:C:N4	1:1A:905:U:O4	2.52	0.43
1:1A:997:G:OP1	12:1Q:16:ARG:NH2	2.52	0.43
1:1A:1781:G:O2'	1:1A:2870:A:N1	2.43	0.43
1:1A:1825:U:H2'	1:1A:1826:C:H6	1.84	0.43
2:1B:73:A:C4	2:1B:105:A:C2	3.07	0.43
11:1P:64:LYS:NZ	59:1P:353:HOH:O	2.18	0.43
12:1Q:1:MET:HE2	12:1Q:1:MET:HB3	1.86	0.43
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD21	1.99	0.43
32:1a:346:G:H21	55:1a:1880:MPD:H53	1.84	0.43
32:1a:512:U:H2'	32:1a:513:C:C6	2.54	0.43
33:1b:107:THR:O	33:1b:110:GLN:HB2	2.18	0.43
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.52	0.43
1:2A:1552:G:N7	59:2A:4534:HOH:O	2.37	0.43
1:2A:1668:A:H4'	1:2A:1669:A:O5'	2.18	0.43
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.34	0.43
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.40	0.43
32:2a:277:C:H5"	48:2q:68:ARG:NH2	2.33	0.43
32:2a:449:C:H2'	32:2a:450:G:O4'	2.18	0.43
32:2a:992:U:H5"	32:2a:993:G:C4	2.54	0.43
32:2a:1002:G:C2	32:2a:1003:G:C8	3.07	0.43
32:2a:1170:A:C5	32:2a:1171:G:H1'	2.53	0.43
33:2b:8:LYS:HG2	33:2b:9:GLU:H	1.84	0.43
35:2d:108:LEU:HA	35:2d:108:LEU:HD12	1.72	0.43
37:2f:10:LEU:HB2	37:2f:59:TYR:HB3	2.01	0.43
40:2i:112:LYS:HE2	40:2i:117:HIS:O	2.18	0.43
41:2j:6:ILE:HB	41:2j:72:VAL:HG22	2.01	0.43
1:1A:2055:A:O2'	1:1A:2057:G:OP2	2.33	0.43
1:1A:2141:A:H61	1:1A:2190:G:H21	1.66	0.43
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.73	0.43
20:1Y:92:ASN:HB3	20:1Y:94:LYS:HG2	2.00	0.43
27:15:35:GLU:HG3	27:15:51:TYR:CB	2.49	0.43
31:19:13:LYS:HG3	31:19:28:GLU:OE2	2.19	0.43
32:1a:160:A:H2'	32:1a:161:A:O4'	2.17	0.43
32:1a:164:U:H2'	32:1a:165:C:C6	2.53	0.43
32:1a:1030(B):C:O2	32:1a:1030(B):C:H2'	2.18	0.43
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.53	0.43
33:1b:157:ARG:HB3	33:1b:157:ARG:CZ	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:49:PRO:HD2	40:1i:81:ILE:HD11	2.01	0.43
42:1k:104:GLN:HE21	42:1k:104:GLN:HB3	1.62	0.43
51:1t:59:ALA:O	51:1t:63:ILE:HG13	2.19	0.43
1:2A:140:G:N3	1:2A:142:A:N6	2.56	0.43
1:2A:391:G:H1'	1:2A:411:G:O4'	2.19	0.43
1:2A:900:A:H2'	1:2A:901:A:O4'	2.18	0.43
1:2A:1082:U:O4	1:2A:1086:A:N1	2.52	0.43
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.19	0.43
1:2A:2031:A:N3	1:2A:2455:G:O2'	2.45	0.43
7:2H:70:THR:HG22	7:2H:74:ASN:HD21	1.83	0.43
8:2I:83:ALA:CB	8:2I:123:LEU:HD21	2.48	0.43
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.40	0.43
26:24:59:PHE:CZ	50:2s:64:GLU:HB2	2.54	0.43
32:2a:526:C:OP2	43:2l:91:LYS:HE3	2.19	0.43
32:2a:1036:G:H3'	32:2a:1037:C:H6	1.83	0.43
32:2a:1326:C:H5"	52:2u:18:TYR:O	2.19	0.43
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.31	0.43
33:2b:28:PHE:CD1	33:2b:190:THR:HA	2.54	0.43
34:2c:54:ARG:NH1	34:2c:54:ARG:HB3	2.34	0.43
40:2i:22:GLY:HA3	40:2i:60:ASP:OD1	2.19	0.43
44:2m:80:ARG:NH2	50:2s:69:HIS:HE1	2.04	0.43
45:2n:9:LYS:HG3	45:2n:12:ARG:NH1	2.33	0.43
1:1A:1102:G:H5"	1:1A:1103:A:O4'	2.19	0.43
1:1A:1233:U:H4'	17:1V:79:VAL:HG22	2.00	0.43
1:1A:1577:C:O2'	1:1A:1578:C:H6	2.02	0.43
1:1A:1735:U:O2	1:1A:1747:A:H5'	2.19	0.43
1:1A:2157:A:H4'	1:1A:2182:G:H4'	2.01	0.43
1:1A:2348:A:H61	22:10:43:THR:CG2	2.32	0.43
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.49	0.43
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.19	0.43
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.53	0.43
28:16:11:LEU:HB2	28:16:21:TYR:HB2	2.01	0.43
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.81	0.43
34:1c:5:ILE:HG13	34:1c:6:HIS:N	2.34	0.43
35:1d:31:CYS:O	35:1d:35:ARG:HG3	2.18	0.43
45:1n:24:CYS:HB2	45:1n:40:CYS:HB3	2.01	0.43
49:1r:29:PHE:HE1	49:1r:31:LEU:HD13	1.84	0.43
1:2A:579:G:H2'	1:2A:580:C:C6	2.53	0.43
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.52	0.43
1:2A:1971:A:P	3:2D:242:ARG:HH22	2.41	0.43
1:2A:1987:G:OP2	59:2A:5003:HOH:O	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2341:G:H2'	1:2A:2342:C:C6	2.53	0.43
1:2A:2370:G:C6	1:2A:2371:G:C6	3.07	0.43
2:2B:105:A:H2'	2:2B:106:G:O4'	2.19	0.43
4:2E:7:VAL:HG13	4:2E:27:LEU:HB3	2.00	0.43
6:2G:9:ARG:NH1	6:2G:13:GLU:OE1	2.50	0.43
6:2G:36:LYS:HE3	6:2G:95:ARG:HH12	1.83	0.43
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.33	0.43
32:2a:17:U:O2'	32:2a:1079:G:N3	2.47	0.43
32:2a:309:G:O2'	32:2a:607:A:N1	2.52	0.43
32:2a:1159:U:O4'	32:2a:1182:G:N2	2.52	0.43
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.50	0.43
34:2c:32:LEU:HD12	34:2c:59:ARG:HH12	1.82	0.43
1:1A:412:C:O2	11:1P:71:VAL:HG21	2.19	0.43
1:1A:2184:G:H4'	1:1A:2194:U:O2'	2.19	0.43
1:1A:2574:U:O2'	10:1O:23:ARG:HD3	2.19	0.43
1:1A:2702:C:OP2	1:1A:2702:C:H6	2.02	0.43
59:1A:8206:HOH:O	18:1W:11:ARG:HD3	2.19	0.43
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.84	0.43
11:1P:135:LEU:HD23	11:1P:135:LEU:HA	1.73	0.43
31:19:2:LYS:HE2	31:19:31:LYS:O	2.19	0.43
32:1a:35:G:O2'	43:1l:118:SER:O	2.29	0.43
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.49	0.43
44:1m:97:PRO:HA	44:1m:110:ARG:HD3	2.01	0.43
48:1q:10:VAL:HG13	48:1q:19:VAL:HB	2.01	0.43
53:1y:23:ARG:HH11	53:1y:26:LYS:HD2	1.84	0.43
1:2A:1115:G:H2'	1:2A:1116:C:C6	2.54	0.43
1:2A:1287:A:H8	13:2R:104:ARG:HD3	1.84	0.43
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.19	0.43
1:2A:2131:G:C5'	1:2A:2132:U:H5'	2.37	0.43
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.19	0.43
4:2E:119:ARG:CG	4:2E:160:TYR:HB2	2.49	0.43
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.52	0.43
32:2a:841:U:C5	32:2a:848:C:H1'	2.54	0.43
32:2a:869:G:H4'	32:2a:872:A:C8	2.54	0.43
32:2a:1164:G:N2	32:2a:1172:C:N3	2.64	0.43
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.54	0.43
33:2b:73:THR:OG1	33:2b:170:GLU:OE1	2.36	0.43
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.19	0.43
41:2j:49:VAL:HG22	41:2j:50:ILE:O	2.19	0.43
52:2u:6:ARG:C	52:2u:8:THR:H	2.27	0.43
1:1A:254:A:N1	1:1A:454:U:O2'	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:264:G:H2'	1:1A:265:U:O4'	2.19	0.42
1:1A:2211:U:C2'	1:1A:2212:G:H5'	2.49	0.42
12:1Q:7:MET:HE3	12:1Q:7:MET:HB2	1.46	0.42
29:17:16:HIS:HB2	29:17:44:PRO:HG2	2.00	0.42
32:1a:741:G:H2'	32:1a:742:G:O4'	2.19	0.42
32:1a:986:A:H2'	32:1a:987:G:O4'	2.19	0.42
32:1a:1010:G:H22	32:1a:1020:U:H1'	1.83	0.42
33:1b:10:LEU:HA	33:1b:48:MET:HE1	2.01	0.42
38:1g:110:GLN:HA	38:1g:110:GLN:HE21	1.83	0.42
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	2.01	0.42
1:2A:295:G:OP1	20:2Y:1:MET:HB2	2.19	0.42
1:2A:886:C:H1'	1:2A:890:A:N6	2.34	0.42
1:2A:1163:G:OP1	17:2V:24:LYS:NZ	2.44	0.42
1:2A:1638:C:H5"	1:2A:2710:C:O2'	2.19	0.42
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.54	0.42
2:2B:1:U:O2'	2:2B:2:C:O5'	2.33	0.42
2:2B:7:G:C3'	2:2B:8:U:H5"	2.49	0.42
8:2I:62:LYS:HG2	8:2I:133:HIS:NE2	2.33	0.42
9:2N:62:VAL:CG1	9:2N:66:LYS:HB2	2.49	0.42
32:2a:250:A:H4'	32:2a:251:G:O5'	2.17	0.42
32:2a:262:A:C6	32:2a:263:A:C6	3.07	0.42
32:2a:537:G:OP1	43:2l:113:ARG:NH2	2.45	0.42
32:2a:840:C:H4'	32:2a:841:U:OP2	2.17	0.42
32:2a:1029:C:N4	32:2a:1030:C:H41	2.17	0.42
32:2a:1267:C:O2	52:2u:20:LYS:HD2	2.19	0.42
32:2a:1352:C:H42	32:2a:1370:G:H1	1.65	0.42
35:2d:28:SER:HG	35:2d:30:LYS:H	1.65	0.42
36:2e:143:ARG:NH1	39:2h:77:GLU:OE2	2.43	0.42
41:2j:30:SER:OG	41:2j:84:GLN:NE2	2.52	0.42
52:2u:3:LYS:HB3	52:2u:14:TRP:CG	2.53	0.42
1:1A:273:G:O2'	1:1A:274:U:H5"	2.19	0.42
1:1A:1217:G:N3	1:1A:1217:G:H2'	2.34	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.49	0.42
7:1H:3:ARG:HB3	7:1H:6:ARG:HG2	2.01	0.42
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	2.00	0.42
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.51	0.42
32:1a:503:C:OP2	43:1l:116:SER:OG	2.24	0.42
32:1a:1039:C:H2'	32:1a:1040:U:H6	1.84	0.42
43:1l:7:ILE:HD13	43:1l:7:ILE:HA	1.91	0.42
46:1o:17:ARG:HH11	46:1o:17:ARG:HG3	1.84	0.42
1:2A:57:C:H2'	1:2A:58:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:116:C:H2'	1:2A:117:G:O4'	2.20	0.42
1:2A:1024:G:C6	1:2A:1025:G:C6	3.07	0.42
1:2A:1864:U:OP1	1:2A:2410:G:O2'	2.30	0.42
1:2A:2864:G:OP1	15:2T:119:LYS:HE3	2.19	0.42
4:2E:28:ALA:HB3	4:2E:93:VAL:CG1	2.49	0.42
5:2F:33:LEU:HB3	11:2P:6:LEU:HD21	2.01	0.42
7:2H:55:PRO:HG2	7:2H:61:HIS:ND1	2.34	0.42
25:23:24:LYS:HE2	25:23:24:LYS:HB2	1.83	0.42
26:24:53:GLU:H	26:24:53:GLU:CD	2.27	0.42
26:24:62:ARG:O	26:24:63:TYR:C	2.62	0.42
29:27:22:MET:SD	29:27:31:LEU:HD12	2.59	0.42
32:2a:1054:C:H41	53:2y:46:GLN:NE2	2.17	0.42
33:2b:48:MET:HA	33:2b:51:LEU:HD12	2.00	0.42
34:2c:54:ARG:HB3	34:2c:54:ARG:HH11	1.84	0.42
40:2i:53:VAL:HG21	40:2i:92:TYR:CZ	2.54	0.42
42:2k:84:VAL:HG21	42:2k:95:ILE:HD11	2.01	0.42
51:2t:37:SER:O	51:2t:41:ILE:HG12	2.19	0.42
53:2y:6:THR:HB	53:2y:40:ILE:HG12	2.01	0.42
1:1A:20:C:OP1	16:1U:22:LYS:NZ	2.50	0.42
1:1A:860:U:H2'	1:1A:861:C:C6	2.55	0.42
1:1A:1699:A:O2'	1:1A:1700:G:H5'	2.19	0.42
1:1A:1874:C:H5'	3:1D:253:GLN:NE2	2.34	0.42
1:1A:2177:G:C2	1:1A:2178:G:H1'	2.55	0.42
8:1I:77:LEU:HD12	8:1I:97:ILE:HG23	2.01	0.42
11:1P:96:THR:H	11:1P:99:LEU:HD12	1.82	0.42
17:1V:49:THR:HG22	17:1V:49:THR:O	2.19	0.42
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.92	0.42
32:1a:615:C:C2	32:1a:616:G:C8	3.08	0.42
32:1a:1131:G:H2'	32:1a:1132:C:C6	2.54	0.42
32:1a:1182:G:C4'	32:1a:1183:A:H5'	2.49	0.42
32:1a:1518:MA6:C6	32:1a:1519:MA6:H103	2.49	0.42
33:1b:47:THR:HA	33:1b:202:PRO:HG2	2.02	0.42
33:1b:128:GLU:C	33:1b:130:ARG:H	2.26	0.42
35:1d:188:LEU:HA	35:1d:189:PRO:HD3	1.63	0.42
40:1i:89:ASN:HA	40:1i:90:PRO:HD3	1.91	0.42
48:1q:6:LEU:HG	48:1q:23:VAL:HG11	2.01	0.42
1:2A:243:U:OP1	30:28:6:THR:OG1	2.29	0.42
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.19	0.42
12:2Q:137:TYR:HE2	21:2Z:49:ARG:NH1	2.16	0.42
13:2R:2:ARG:HG2	13:2R:5:LYS:HB2	2.02	0.42
14:2S:35:ILE:HD13	14:2S:36:TYR:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:6:LEU:HD12	15:2T:6:LEU:HA	1.83	0.42
20:2Y:19:LYS:HB3	20:2Y:19:LYS:HE2	1.89	0.42
26:24:64:GLY:C	26:24:66:SER:H	2.27	0.42
32:2a:724:G:C2	32:2a:725:G:C8	3.07	0.42
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.55	0.42
32:2a:1414:U:H3	32:2a:1486:G:H1	1.65	0.42
33:2b:32:ILE:HD13	33:2b:40:HIS:CD2	2.54	0.42
33:2b:63:MET:H	33:2b:63:MET:HG2	1.50	0.42
33:2b:74:LYS:HD3	33:2b:165:VAL:HG12	2.02	0.42
33:2b:127:ILE:C	33:2b:129:GLU:H	2.27	0.42
33:2b:178:ARG:HH22	39:2h:68:ARG:NH2	2.17	0.42
35:2d:171:GLY:HA2	35:2d:172:PRO:HD3	1.89	0.42
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.19	0.42
40:2i:89:ASN:O	40:2i:92:TYR:HB2	2.19	0.42
1:1A:236:G:H4'	1:1A:413:G:C6	2.54	0.42
1:1A:829:A:H5'	1:1A:830:A:N7	2.34	0.42
1:1A:1622:C:H2'	1:1A:1623:U:C6	2.54	0.42
6:1G:66:GLN:HG3	26:14:1:MET:CE	2.49	0.42
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.90	0.42
18:1W:68:ARG:NH1	18:1W:112:GLY:H	2.16	0.42
19:1X:66:LEU:HD22	19:1X:66:LEU:HA	1.90	0.42
32:1a:299:G:O5'	32:1a:299:G:H8	2.03	0.42
32:1a:346:G:H5"	55:1a:1880:MPD:C4	2.49	0.42
32:1a:1402:4OC:O5'	32:1a:1402:4OC:H6	2.19	0.42
1:2A:1401:G:H2'	1:2A:1402:C:O4'	2.19	0.42
1:2A:1761:C:H2'	1:2A:1762:A:H5"	2.01	0.42
1:2A:1802:A:N1	1:2A:1822:G:H1'	2.34	0.42
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.54	0.42
4:2E:59:VAL:HG12	4:2E:64:LYS:HG3	2.00	0.42
20:2Y:40:GLU:O	20:2Y:42:VAL:HG23	2.19	0.42
32:2a:277:C:H5"	48:2q:68:ARG:HH22	1.84	0.42
32:2a:1148:U:O2'	40:2i:66:ARG:NH1	2.45	0.42
32:2a:1250:A:H2	32:2a:1353:G:H21	1.67	0.42
32:2a:1277:C:O2'	32:2a:1279:A:C8	2.65	0.42
32:2a:1292:U:C2	32:2a:1293:G:C8	3.07	0.42
33:2b:24:TRP:HB3	33:2b:40:HIS:CE1	2.55	0.42
35:2d:148:VAL:HG11	35:2d:158:ILE:HG21	2.01	0.42
35:2d:153:ARG:NH1	35:2d:181:MET:SD	2.93	0.42
40:2i:50:LEU:HD21	40:2i:81:ILE:HG12	2.01	0.42
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.35	0.42
47:2p:66:PRO:HG2	47:2p:71:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1815:A:H4'	1:1A:1816:A:O5'	2.20	0.42
6:1G:5:VAL:HG13	6:1G:8:LYS:HE2	2.01	0.42
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.83	0.42
7:1H:71:LEU:HD12	7:1H:71:LEU:HA	1.86	0.42
32:1a:657:G:H4'	46:1o:28:GLN:HG2	2.00	0.42
32:1a:976:G:C8	32:1a:1362:C:N4	2.88	0.42
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.84	0.42
38:1g:111:ARG:HB3	38:1g:113:GLU:OE2	2.20	0.42
43:1l:97:ARG:HB2	43:1l:98:TYR:CE1	2.54	0.42
53:1y:23:ARG:NH1	53:1y:26:LYS:HD2	2.35	0.42
1:2A:210:C:H4'	1:2A:1367:A:H1'	2.02	0.42
1:2A:1094:U:H4'	1:2A:1096:A:N6	2.34	0.42
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.35	0.42
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.83	0.42
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	2.01	0.42
6:2G:56:ALA:HB2	6:2G:153:ARG:HH21	1.83	0.42
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.52	0.42
32:2a:409:G:H2'	32:2a:410:G:O4'	2.20	0.42
32:2a:583:A:H2'	32:2a:584:G:O4'	2.19	0.42
32:2a:692:U:H1'	32:2a:695:A:N7	2.34	0.42
32:2a:841:U:OP1	32:2a:841:U:H6	2.03	0.42
32:2a:894:G:C6	32:2a:895:G:C5	3.06	0.42
32:2a:1490:C:H2'	32:2a:1491:G:C8	2.55	0.42
33:2b:158:LEU:HA	33:2b:159:PRO:HD3	1.83	0.42
1:1A:504:A:N1	1:1A:525:G:H4'	2.35	0.42
1:1A:831:A:H5'	1:1A:832:G:OP1	2.20	0.42
1:1A:2159:C:C5	1:1A:2177:G:C2	3.07	0.42
1:1A:2614:A:H4'	1:1A:2615:G:OP1	2.19	0.42
59:1A:8186:HOH:O	11:1P:77:ARG:HD3	2.19	0.42
4:1E:47:VAL:HG23	4:1E:84:PHE:O	2.19	0.42
8:1I:38:LEU:H	8:1I:38:LEU:CD1	2.23	0.42
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	2.01	0.42
11:1P:112:LEU:HD22	11:1P:113:LYS:N	2.35	0.42
16:1U:112:ARG:HG2	16:1U:112:ARG:H	1.65	0.42
20:1Y:6:HIS:HE1	20:1Y:72:VAL:O	2.02	0.42
27:15:37:LYS:HA	27:15:37:LYS:HD3	1.82	0.42
32:1a:201:C:N4	32:1a:216:G:H22	2.17	0.42
32:1a:300:A:O2'	32:1a:564:C:N3	2.42	0.42
32:1a:1007:C:H2'	32:1a:1008:C:H5'	2.02	0.42
34:1c:190:ARG:HE	34:1c:190:ARG:HB2	1.73	0.42
41:1j:5:ARG:HE	41:1j:73:ASP:CG	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:945:A:C4	1:2A:2448:A:C2	3.08	0.42
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.55	0.42
1:2A:2359:C:H2'	1:2A:2360:A:O4'	2.19	0.42
1:2A:2657:A:O3'	7:2H:160:LYS:NZ	2.53	0.42
4:2E:79:ARG:HA	4:2E:79:ARG:HD3	1.83	0.42
8:2I:48:GLU:HG3	8:2I:52:ARG:NH1	2.35	0.42
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	2.00	0.42
22:20:19:LYS:HD2	22:20:19:LYS:N	2.34	0.42
30:28:23:VAL:HG13	30:28:47:LYS:HB3	2.02	0.42
32:2a:600:C:H2'	32:2a:601:C:H6	1.85	0.42
32:2a:779:C:H2'	32:2a:780:A:O4'	2.19	0.42
32:2a:1092:A:N3	32:2a:1183:A:N6	2.68	0.42
34:2c:180:ALA:HA	34:2c:206:GLU:HA	2.01	0.42
35:2d:17:VAL:HG12	35:2d:18:LYS:N	2.34	0.42
35:2d:169:LYS:NZ	35:2d:169:LYS:HB3	2.34	0.42
37:2f:30:LEU:HD23	37:2f:75:LEU:HD21	2.01	0.42
44:2m:20:THR:HG21	44:2m:27:LYS:HE2	2.02	0.42
49:2r:61:LYS:O	49:2r:65:ILE:HG12	2.20	0.42
49:2r:65:ILE:O	49:2r:69:THR:HG23	2.19	0.42
49:2r:76:LEU:HD12	49:2r:76:LEU:HA	1.73	0.42
50:2s:66:MET:HB2	50:2s:74:PHE:CZ	2.55	0.42
1:1A:909:G:H2'	1:1A:910:A:O4'	2.20	0.42
1:1A:1111:U:O2	1:1A:1112:U:N3	2.52	0.42
1:1A:2659:U:H2'	1:1A:2660:C:C6	2.54	0.42
10:1O:23:ARG:HG3	10:1O:24:VAL:N	2.34	0.42
32:1a:1030(C):G:C8	32:1a:1031:G:N2	2.87	0.42
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.35	0.42
35:1d:107:ARG:HG3	35:1d:173:TRP:HH2	1.84	0.42
36:1e:148:VAL:O	36:1e:152:ARG:HG2	2.19	0.42
40:1i:111:ARG:HG2	40:1i:112:LYS:N	2.33	0.42
42:1k:120:ARG:HA	42:1k:121:PRO:HD3	1.82	0.42
43:1l:33:ARG:HD2	43:1l:33:ARG:HA	1.65	0.42
1:2A:881:G:C2	1:2A:897:C:C4	3.08	0.42
1:2A:2142:C:N3	1:2A:2149:G:C6	2.88	0.42
1:2A:2157:G:C8	1:2A:2157:G:H3'	2.55	0.42
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.53	0.42
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.19	0.42
2:2B:95:C:H2'	2:2B:96:U:C6	2.54	0.42
7:2H:109:PHE:C	7:2H:111:HIS:H	2.27	0.42
16:2U:89:GLU:HB2	17:2V:50:PRO:HB3	2.00	0.42
26:24:18:CYS:HB2	26:24:20:ASN:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:59:PHE:HE1	50:2s:64:GLU:HB2	1.83	0.42
32:2a:1005:A:H1'	32:2a:1025:U:N3	2.35	0.42
32:2a:1072:G:H2'	32:2a:1073:U:C6	2.54	0.42
32:2a:1101:A:H4'	32:2a:1102:A:O5'	2.20	0.42
32:2a:1248:A:H2'	32:2a:1249:C:H6	1.84	0.42
33:2b:59:GLU:O	33:2b:63:MET:HG2	2.20	0.42
53:2y:3:MET:HB2	53:2y:37:PRO:HG2	2.01	0.42
1:1A:142:G:H4'	19:1X:35:THR:HG21	2.00	0.42
1:1A:1557:A:H2'	1:1A:1558:G:O4'	2.20	0.42
1:1A:2160:C:C4	1:1A:2161:C:N4	2.88	0.42
1:1A:2331:G:C2	14:1S:3:ARG:HA	2.55	0.42
1:1A:2369:U:OP1	22:10:20:ARG:HD3	2.19	0.42
1:1A:2797:C:H1'	4:1E:37:ARG:NH1	2.35	0.42
1:1A:2846:U:H2'	1:1A:2847:G:C8	2.54	0.42
2:1B:29:A:H2'	2:1B:30:C:O4'	2.19	0.42
8:1I:68:LEU:HD22	8:1I:68:LEU:HA	1.87	0.42
12:1Q:110:THR:HG23	12:1Q:113:GLN:OE1	2.19	0.42
32:1a:1060:C:N4	34:1c:2:GLY:HA3	2.35	0.42
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.54	0.42
33:1b:187:LEU:HA	33:1b:201:ILE:HB	2.02	0.42
1:2A:144:C:H5'	19:2X:2:LYS:CE	2.48	0.42
1:2A:192:C:O2'	1:2A:802:A:N3	2.48	0.42
1:2A:889:C:O2'	1:2A:890:A:O5'	2.31	0.42
1:2A:1058:G:N2	1:2A:1080:C:N3	2.57	0.42
1:2A:1071:G:C8	1:2A:1071:G:H3'	2.54	0.42
1:2A:1075:C:C2'	1:2A:1076:C:H5'	2.47	0.42
1:2A:1470:G:H5"	1:2A:1471:A:OP1	2.20	0.42
1:2A:2136:C:C6	1:2A:2136:C:OP2	2.73	0.42
4:2E:12:THR:HG22	4:2E:13:ARG:H	1.85	0.42
4:2E:18:ASP:HB3	15:2T:82:LEU:HD21	2.01	0.42
6:2G:136:ARG:HD2	6:2G:137:GLU:HG3	2.00	0.42
18:2W:79:GLY:HA3	18:2W:100:THR:HG22	2.02	0.42
20:2Y:23:ARG:NH1	20:2Y:23:ARG:HB2	2.35	0.42
32:2a:473:G:H2'	32:2a:474:G:H8	1.83	0.42
32:2a:942:G:C2	32:2a:1342:C:C2	3.07	0.42
32:2a:1321:C:H1'	50:2s:77:THR:HG21	2.02	0.42
33:2b:70:PHE:CE2	33:2b:163:PHE:HD2	2.38	0.42
42:2k:84:VAL:HG11	42:2k:91:ARG:HD2	2.02	0.42
45:2n:37:PHE:HB3	45:2n:39:LEU:HD12	2.02	0.42
1:1A:451:G:O6	55:1A:4028:MPD:H52	2.20	0.42
1:1A:2120:U:H2'	1:1A:2121:U:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:16:G:C6	2:1B:69:G:C2	3.08	0.42
5:1F:196:LEU:HD23	5:1F:196:LEU:HA	1.87	0.42
23:11:51:VAL:HG12	23:11:53:VAL:HG23	2.00	0.42
32:1a:461:A:O2'	32:1a:470:C:H5'	2.20	0.42
32:1a:947:G:H2'	32:1a:948:C:O4'	2.20	0.42
32:1a:998:G:H2'	32:1a:999:C:C6	2.55	0.42
32:1a:1035:A:O5'	32:1a:1035:A:H8	2.02	0.42
32:1a:1144:G:O2'	32:1a:1145:C:H5'	2.20	0.42
32:1a:1260:C:H4'	32:1a:1284:C:H5'	2.01	0.42
34:1c:134:ILE:HG22	34:1c:168:ALA:HB3	2.02	0.42
51:1t:77:ALA:O	51:1t:81:LYS:HG3	2.20	0.42
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.42	0.42
1:2A:352:G:N2	59:2A:5391:HOH:O	2.49	0.42
1:2A:1823:G:OP1	3:2D:54:ARG:NH1	2.52	0.42
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.55	0.42
1:2A:2836:U:C4	1:2A:2883:A:N6	2.87	0.42
4:2E:116:VAL:HG13	4:2E:122:PHE:CB	2.48	0.42
6:2G:126:ASP:HB2	6:2G:130:ASN:O	2.20	0.42
6:2G:166:ASP:O	6:2G:170:ARG:N	2.45	0.42
12:2Q:109:VAL:HG13	12:2Q:113:GLN:HB2	2.02	0.42
14:2S:19:LYS:HE3	14:2S:42:ASP:CG	2.44	0.42
14:2S:46:VAL:HG12	14:2S:48:LEU:HD22	2.01	0.42
15:2T:53:ARG:HB3	15:2T:53:ARG:HH11	1.84	0.42
22:20:82:ARG:HA	22:20:83:PRO:HD3	1.78	0.42
32:2a:77:G:H2'	32:2a:78:G:O4'	2.20	0.42
32:2a:1005:A:H5"	32:2a:1006:C:C6	2.55	0.42
40:2i:7:THR:O	40:2i:83:ARG:HD2	2.20	0.42
41:2j:80:LYS:O	41:2j:84:GLN:HB2	2.20	0.42
51:2t:50:GLU:HG3	51:2t:100:ILE:HD11	2.02	0.42
1:1A:1432:C:H2'	1:1A:1433:C:C6	2.55	0.42
2:1B:7:G:H5"	2:1B:7:G:H8	1.84	0.42
3:1D:182:LEU:HD23	3:1D:182:LEU:HA	1.84	0.42
4:1E:178:GLU:CD	4:1E:178:GLU:H	2.26	0.42
6:1G:101:ILE:HD13	26:14:25:TYR:HB2	2.02	0.42
32:1a:1007:C:N3	32:1a:1022:G:C6	2.87	0.42
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.35	0.42
33:1b:30:ARG:HH22	33:1b:194:PRO:HB2	1.85	0.42
33:1b:146:GLN:O	33:1b:150:SER:HB3	2.20	0.42
1:2A:276:A:H5"	1:2A:277:C:H5'	2.02	0.42
1:2A:1359:A:N6	1:2A:1372:U:H3	2.17	0.42
1:2A:1669:A:H5"	1:2A:2550:G:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.85	0.42
1:2A:1840:G:C6	1:2A:1841:U:C4	3.08	0.42
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	2.01	0.42
7:2H:27:LYS:HD3	7:2H:32:GLU:HB2	2.01	0.42
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.55	0.42
11:2P:120:ALA:HB1	11:2P:138:LEU:HD12	2.02	0.42
20:2Y:7:VAL:CG1	20:2Y:27:VAL:HG21	2.50	0.42
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.55	0.42
32:2a:1148:U:OP1	40:2i:7:THR:HG21	2.20	0.42
32:2a:1148:U:C2'	40:2i:66:ARG:HH12	2.32	0.42
32:2a:1215:G:C6	32:2a:1216:G:C5	3.08	0.42
37:2f:82:ARG:HA	37:2f:82:ARG:HD2	1.93	0.42
47:2p:3:LYS:O	47:2p:21:VAL:HA	2.19	0.42
51:2t:43:LEU:HD23	51:2t:43:LEU:HA	1.88	0.42
1:1A:840:A:OP2	1:1A:2094:G:H5'	2.20	0.41
1:1A:1131:A:O2'	1:1A:1132:A:O4'	2.38	0.41
5:1F:140:LEU:HD21	5:1F:170:LEU:HD11	2.01	0.41
21:1Z:40:ASP:OD1	21:1Z:42:VAL:HG13	2.20	0.41
26:14:1:MET:HE2	26:14:6:HIS:NE2	2.35	0.41
32:1a:107:G:H2'	32:1a:108:G:O4'	2.20	0.41
32:1a:159:G:N2	32:1a:162:A:OP2	2.28	0.41
32:1a:266:G:H2'	32:1a:266:G:N3	2.35	0.41
32:1a:598:U:O4	59:1a:1957:HOH:O	2.20	0.41
32:1a:738:C:H2'	32:1a:739:C:H6	1.85	0.41
32:1a:955:U:O2'	50:1s:83:HIS:CD2	2.71	0.41
47:1p:43:LYS:HG2	47:1p:48:TRP:NE1	2.35	0.41
1:2A:76:C:O3'	24:22:59:ARG:HG3	2.20	0.41
1:2A:171:G:H2'	1:2A:172:C:C6	2.55	0.41
1:2A:1919:A:O3'	32:2a:1517:G:H1'	2.20	0.41
2:2B:90:A:N7	2:2B:91:C:H1'	2.35	0.41
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.20	0.41
6:2G:170:ARG:HH21	6:2G:180:PHE:HB2	1.85	0.41
12:2Q:32:TYR:OH	12:2Q:111:GLU:OE1	2.24	0.41
31:29:22:ARG:HB2	31:29:24:TYR:CE1	2.54	0.41
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.20	0.41
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	2.02	0.41
33:2b:53:ARG:HG2	33:2b:56:ARG:HH21	1.85	0.41
33:2b:73:THR:HG22	33:2b:95:GLN:O	2.20	0.41
34:2c:64:VAL:O	34:2c:99:VAL:HA	2.20	0.41
39:2h:13:ILE:O	39:2h:17:THR:HG23	2.20	0.41
47:2p:1:MET:SD	47:2p:1:MET:N	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:865:G:H4'	1:1A:885:C:O3'	2.19	0.41
1:1A:1219:A:H4'	1:1A:1220:U:OP1	2.19	0.41
1:1A:1759:C:H2'	1:1A:1760:U:O4'	2.20	0.41
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.35	0.41
1:1A:2148:A:N3	1:1A:2184:G:N2	2.45	0.41
1:1A:2325:C:H4'	6:1G:91:ARG:HG3	2.00	0.41
4:1E:1:MET:O	4:1E:1:MET:HE3	2.19	0.41
8:1I:140:LEU:HD13	8:1I:142:VAL:HG22	2.03	0.41
9:1N:42:TRP:CE3	16:1U:63:VAL:HG11	2.55	0.41
15:1T:95:ARG:NH1	15:1T:95:ARG:CG	2.82	0.41
21:1Z:140:ASP:OD1	21:1Z:142:SER:OG	2.33	0.41
32:1a:349:A:O2'	32:1a:350:G:H5'	2.19	0.41
32:1a:1136:U:H5"	32:1a:1137:C:C2	2.55	0.41
35:1d:61:LYS:HD3	35:1d:206:PHE:CE2	2.55	0.41
42:1k:98:LEU:HD23	42:1k:98:LEU:HA	1.90	0.41
1:2A:223:A:N1	1:2A:407:G:O2'	2.46	0.41
1:2A:1045:A:H8	1:2A:1047:G:N3	2.17	0.41
1:2A:1517:G:C6	1:2A:1518:U:C4	3.08	0.41
1:2A:2032:G:OP2	1:2A:2454:G:O2'	2.29	0.41
1:2A:2752:C:H2'	1:2A:2753:A:O4'	2.20	0.41
5:2F:165:ARG:HG2	5:2F:168:ARG:HH21	1.83	0.41
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.85	0.41
32:2a:18:C:H4'	32:2a:1078:U:O2	2.19	0.41
32:2a:475:G:C2'	32:2a:476:G:H5'	2.49	0.41
32:2a:1047:G:H5"	45:2n:4:LYS:CD	2.46	0.41
32:2a:1083:U:C5	32:2a:1084:G:C6	3.08	0.41
32:2a:1096:C:H2'	32:2a:1097:C:H6	1.85	0.41
32:2a:1157:A:H5'	32:2a:1158:C:C6	2.55	0.41
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.55	0.41
32:2a:1426:C:H2'	32:2a:1427:U:C6	2.55	0.41
33:2b:15:VAL:O	33:2b:17:PHE:N	2.53	0.41
33:2b:22:LYS:HB2	33:2b:22:LYS:HE3	1.83	0.41
33:2b:92:TYR:OH	33:2b:150:SER:OG	2.37	0.41
34:2c:9:GLY:HA3	45:2n:49:HIS:HA	2.01	0.41
1:1A:504:A:C6	1:1A:506:A:C6	3.08	0.41
1:1A:2054:G:O2'	4:1E:145:LYS:HE3	2.20	0.41
1:1A:2159:C:C4	1:1A:2176:G:N1	2.78	0.41
1:1A:2331:G:C8	1:1A:2332:A:C2	3.08	0.41
1:1A:2377:G:O6	30:18:39:LYS:HE3	2.20	0.41
1:1A:2594:G:C2	1:1A:2595:G:C8	3.08	0.41
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.02	0.41
12:1Q:130:LYS:HB3	12:1Q:130:LYS:HE2	1.91	0.41
32:1a:660:G:C2	32:1a:746:A:C2	3.09	0.41
32:1a:1022:G:H5'	32:1a:1023:G:OP2	2.20	0.41
32:1a:1168:A:H2'	32:1a:1169:A:C8	2.55	0.41
33:1b:133:LYS:HA	33:1b:133:LYS:HD2	1.95	0.41
41:1j:29:ARG:C	41:1j:31:GLY:H	2.28	0.41
44:1m:13:LYS:HA	44:1m:44:ARG:NH1	2.30	0.41
53:1y:4:ASN:ND2	59:1y:305:HOH:O	2.53	0.41
1:2A:1371:G:O2'	1:2A:1372:U:H5	2.02	0.41
1:2A:1771:C:OP1	59:2A:4488:HOH:O	2.22	0.41
1:2A:1783:A:H5'	1:2A:2608:G:H4'	2.03	0.41
1:2A:2104:G:N1	1:2A:2185:C:O2	2.53	0.41
1:2A:2112:G:H2'	1:2A:2113:U:C6	2.55	0.41
1:2A:2394:C:OP2	30:28:30:ARG:HD2	2.20	0.41
1:2A:2504:U:OP2	59:2A:4092:HOH:O	2.22	0.41
3:2D:70:TRP:HB3	3:2D:190:TYR:CE1	2.54	0.41
26:24:44:THR:C	26:24:46:GLN:N	2.78	0.41
32:2a:382:A:H2'	32:2a:383:A:H8	1.83	0.41
32:2a:475:G:O2'	32:2a:476:G:H5'	2.21	0.41
32:2a:993:G:N3	32:2a:993:G:H2'	2.35	0.41
32:2a:1004:A:N6	32:2a:1037:C:C6	2.88	0.41
32:2a:1318:A:H5"	50:2s:3:ARG:NH2	2.32	0.41
32:2a:1340:A:OP1	53:2y:57:PRO:HB3	2.19	0.41
32:2a:1468:A:H2'	32:2a:1469:G:O4'	2.20	0.41
35:2d:173:TRP:CZ3	35:2d:193:ASP:HB3	2.54	0.41
37:2f:11:ASN:HB3	37:2f:14:LEU:HG	2.01	0.41
38:2g:23:VAL:O	38:2g:27:ILE:HG12	2.21	0.41
40:2i:28:VAL:N	40:2i:31:GLN:O	2.52	0.41
46:2o:39:LEU:HD23	46:2o:39:LEU:HA	1.90	0.41
1:1A:76:C:OP1	24:12:59:ARG:HD3	2.20	0.41
1:1A:172:C:N4	1:1A:202:A:H61	2.18	0.41
1:1A:1119:A:C2	1:1A:1120:G:C8	3.08	0.41
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.40	0.41
1:1A:2695:C:OP1	15:1T:53:ARG:NH2	2.52	0.41
5:1F:110:LEU:HD23	5:1F:110:LEU:HA	1.94	0.41
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.39	0.41
8:1I:102:SER:OG	8:1I:103:ARG:N	2.53	0.41
12:1Q:16:ARG:HG3	12:1Q:17:LEU:H	1.85	0.41
12:1Q:75:THR:HG21	12:1Q:87:LYS:NZ	2.35	0.41
32:1a:523:A:N1	43:1l:92:0TD:H6	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:952:U:O2'	32:1a:953:G:H5'	2.20	0.41
32:1a:1404:5MC:O2	32:1a:1519:MA6:O2'	2.32	0.41
33:1b:27:LYS:O	33:1b:30:ARG:NH1	2.54	0.41
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	2.03	0.41
40:1i:81:ILE:O	40:1i:85:LEU:HG	2.21	0.41
42:1k:108:ILE:HG22	49:1r:87:ARG:HG3	2.03	0.41
1:2A:272(I):U:H3	1:2A:363(A):A:H61	1.69	0.41
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.49	0.41
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.55	0.41
1:2A:1050:A:H2'	1:2A:1051:G:C8	2.54	0.41
1:2A:1427:A:H4'	1:2A:1428:C:O5'	2.20	0.41
1:2A:2319:G:C2	14:2S:3:ARG:HA	2.55	0.41
1:2A:2750:A:H8	1:2A:2750:A:OP1	2.03	0.41
2:2B:37:C:C5	2:2B:38:C:C5	3.08	0.41
6:2G:38:VAL:HB	6:2G:158:ALA:HB3	2.02	0.41
8:2I:83:ALA:HB3	8:2I:123:LEU:HD21	2.02	0.41
32:2a:148:G:H2'	32:2a:149:A:C8	2.55	0.41
32:2a:439:A:C5	32:2a:441:A:H1'	2.55	0.41
32:2a:1124:G:N7	32:2a:1145:C:O2'	2.52	0.41
35:2d:108:LEU:HB3	35:2d:110:PHE:CD1	2.55	0.41
35:2d:199:ASN:OD1	35:2d:201:GLN:HB2	2.21	0.41
36:2e:140:ARG:O	36:2e:143:ARG:NH2	2.53	0.41
1:1A:187:C:H5'	1:1A:2256:U:OP1	2.20	0.41
1:1A:252:C:H2'	1:1A:253:C:O4'	2.21	0.41
1:1A:873:U:OP1	1:1A:2440:G:H3'	2.19	0.41
1:1A:1217:G:C3'	1:1A:1218:G:H5'	2.50	0.41
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.55	0.41
6:1G:45:GLU:H	6:1G:45:GLU:HG2	1.49	0.41
6:1G:59:GLU:CD	6:1G:138:GLN:HE21	2.28	0.41
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.50	0.41
9:1N:67:LEU:C	9:1N:88:GLU:HG3	2.45	0.41
23:11:3:LYS:HG3	23:11:4:VAL:N	2.32	0.41
23:11:89:GLU:H	23:11:89:GLU:HG2	1.48	0.41
32:1a:1003:G:H8	32:1a:1003:G:O5'	2.03	0.41
49:1r:58:LEU:HG	49:1r:62:GLU:HB2	2.02	0.41
1:2A:637:A:H5"	11:2P:117:GLU:HG2	2.02	0.41
1:2A:994:C:O2	17:2V:10:LYS:HE3	2.21	0.41
1:2A:2158:A:H1'	1:2A:2159:G:C8	2.56	0.41
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.83	0.41
2:2B:9:G:OP1	14:2S:15:ARG:HD3	2.21	0.41
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:28:GLY:N	7:2H:31:GLY:O	2.53	0.41
17:2V:15:GLU:H	17:2V:18:LEU:HD12	1.86	0.41
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.56	0.41
32:2a:1492:A:H5"	43:2l:47:LYS:HD3	2.03	0.41
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.56	0.41
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	2.02	0.41
47:2p:4:ILE:HG23	47:2p:36:ILE:HD11	2.02	0.41
51:2t:57:ARG:NH1	51:2t:100:ILE:HB	2.33	0.41
1:1A:610:C:P	11:1P:21:ARG:HH22	2.41	0.41
1:1A:1496:A:N3	1:1A:1576:G:H1'	2.35	0.41
1:1A:1814:A:H5'	1:1A:2620:G:H4'	2.03	0.41
2:1B:32:C:C2	2:1B:51:G:N2	2.89	0.41
5:1F:164:ARG:O	5:1F:168:ARG:HB3	2.21	0.41
10:1O:80:ASP:CG	15:1T:64:ARG:HH22	2.28	0.41
14:1S:3:ARG:HA	14:1S:3:ARG:HE	1.85	0.41
14:1S:3:ARG:HE	14:1S:3:ARG:CA	2.34	0.41
14:1S:25:ARG:HD3	14:1S:42:ASP:OD2	2.19	0.41
15:1T:127:ALA:O	15:1T:128:GLU:HB3	2.21	0.41
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.86	0.41
20:1Y:19:LYS:HB3	20:1Y:19:LYS:HE2	1.84	0.41
25:13:29:ARG:HG3	25:13:30:ARG:HG3	2.03	0.41
32:1a:302:G:O2'	32:1a:556:C:H5"	2.21	0.41
32:1a:346:G:N2	55:1a:1880:MPD:HO4	2.18	0.41
32:1a:370:C:H2'	32:1a:371:G:C8	2.56	0.41
32:1a:707:C:OP1	42:1k:85:ARG:NH1	2.51	0.41
32:1a:1394:A:N1	32:1a:1500:A:O2'	2.48	0.41
37:1f:75:LEU:O	37:1f:79:LEU:HG	2.20	0.41
40:1i:34:ASN:HD22	40:1i:34:ASN:N	2.19	0.41
42:1k:48:ILE:HG13	42:1k:63:LEU:HB2	2.03	0.41
43:1l:33:ARG:NH1	43:1l:62:SER:HB3	2.36	0.41
44:1m:15:VAL:HG13	44:1m:43:THR:O	2.21	0.41
47:1p:14:ASN:N	47:1p:15:PRO:HD3	2.35	0.41
1:2A:522:G:H2'	1:2A:523:C:C6	2.55	0.41
1:2A:754:C:H2'	1:2A:755:C:C6	2.55	0.41
1:2A:1203:G:C6	1:2A:1204:A:N6	2.88	0.41
1:2A:1356:G:N2	1:2A:1376:C:C2	2.89	0.41
1:2A:1825:A:O4'	3:2D:254:THR:HG21	2.21	0.41
1:2A:2164:C:H5"	1:2A:2165:G:OP2	2.21	0.41
1:2A:2298:A:N6	1:2A:2318:G:H8	2.19	0.41
8:2I:75:LEU:HD23	8:2I:75:LEU:C	2.45	0.41
12:2Q:8:LYS:HB3	12:2Q:9:TYR:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.20	0.41
14:2S:87:PHE:CZ	14:2S:102:ALA:HB2	2.56	0.41
18:2W:19:LEU:HD12	18:2W:19:LEU:HA	1.90	0.41
21:2Z:100:VAL:HA	21:2Z:101:PRO:HD3	1.96	0.41
32:2a:189(L):G:H2'	32:2a:190:U:C6	2.54	0.41
32:2a:951:G:N7	44:2m:102:ARG:NH2	2.69	0.41
34:2c:50:ALA:HB1	34:2c:70:VAL:HG21	2.03	0.41
36:2e:66:MET:HE3	36:2e:66:MET:HB3	1.96	0.41
36:2e:76:ILE:HB	36:2e:77:PRO:HD2	2.03	0.41
42:2k:38:ASN:HA	42:2k:39:PRO:HD3	1.85	0.41
46:2o:71:GLN:HE21	46:2o:71:GLN:HB2	1.66	0.41
1:1A:1212:C:H2'	1:1A:1213:U:C6	2.55	0.41
1:1A:1633:A:H2'	1:1A:1634:C:C6	2.55	0.41
1:1A:2745:G:H3'	1:1A:2746:A:O4'	2.21	0.41
1:1A:2846:U:C4	1:1A:2893:A:N6	2.89	0.41
8:1I:134:PRO:C	8:1I:136:VAL:H	2.28	0.41
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.21	0.41
16:1U:49:HIS:HA	16:1U:52:ARG:HB3	2.02	0.41
34:1c:110:ASN:O	34:1c:111:LEU:HD23	2.21	0.41
35:1d:107:ARG:HA	35:1d:107:ARG:HD2	1.88	0.41
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.55	0.41
1:2A:1421:G:C2	1:2A:1422:G:C8	3.09	0.41
1:2A:1487:G:H2'	1:2A:1488:G:O4'	2.20	0.41
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.56	0.41
1:2A:2298:A:N6	1:2A:2318:G:C8	2.83	0.41
4:2E:35:GLN:OE1	4:2E:66:HIS:HE1	2.03	0.41
9:2N:104:LYS:HE3	9:2N:117:PHE:CZ	2.56	0.41
23:21:67:ILE:N	23:21:68:PRO:HD2	2.35	0.41
32:2a:397:A:H3'	32:2a:397:A:N3	2.36	0.41
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.56	0.41
40:2i:5:TYR:HE1	40:2i:16:ARG:HB3	1.86	0.41
41:2j:33:GLN:O	41:2j:74:ILE:HA	2.19	0.41
41:2j:44:VAL:HG13	41:2j:66:ARG:HG2	2.02	0.41
43:2l:92:0TD:H8	43:2l:92:0TD:H4	1.85	0.41
50:2s:12:ASP:OD2	50:2s:35:SER:HB3	2.20	0.41
1:1A:1766:G:H2'	1:1A:1769:G:O6	2.20	0.41
1:1A:2155:G:O2'	1:1A:2180:A:H2	2.04	0.41
1:1A:2376:C:H2'	1:1A:2377:G:O4'	2.21	0.41
1:1A:2879:G:H2'	1:1A:2880:C:O4'	2.20	0.41
3:1D:221:VAL:HG22	3:1D:226:MET:CE	2.50	0.41
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:12:VAL:HG21	19:1X:27:THR:HG22	2.02	0.41
21:1Z:40:ASP:HB3	21:1Z:43:GLU:HB2	2.01	0.41
32:1a:418:C:H1'	32:1a:540:G:O2'	2.20	0.41
32:1a:688:G:H5'	42:1k:46:GLY:C	2.45	0.41
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.21	0.41
32:1a:1095:U:H2'	32:1a:1096:C:O4'	2.19	0.41
32:1a:1249:C:H4'	40:1i:36:TYR:OH	2.21	0.41
36:1e:13:ILE:HA	36:1e:29:GLY:O	2.21	0.41
44:1m:108:ARG:NH1	44:1m:112:GLY:O	2.51	0.41
50:1s:27:GLU:CB	50:1s:28:LYS:HB3	2.50	0.41
1:2A:492:A:H2'	1:2A:493:G:O4'	2.21	0.41
1:2A:686:G:H1	29:27:16:HIS:CD2	2.38	0.41
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.35	0.41
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.49	0.41
12:2Q:30:GLY:HA2	12:2Q:107:ALA:HB2	2.02	0.41
16:2U:86:ALA:O	17:2V:49:THR:HG23	2.20	0.41
16:2U:112:ARG:HG2	16:2U:112:ARG:H	1.73	0.41
19:2X:31:HIS:CD2	19:2X:33:LYS:HB2	2.56	0.41
21:2Z:53:ILE:HA	59:2Z:5006:HOH:O	2.20	0.41
22:20:50:ASN:HB3	22:20:63:VAL:HG22	2.03	0.41
32:2a:1005:A:H3'	32:2a:1006:C:O4'	2.21	0.41
35:2d:191:ARG:HA	35:2d:191:ARG:HD2	1.79	0.41
41:2j:6:ILE:HA	41:2j:97:GLU:O	2.21	0.41
46:2o:17:ARG:HH11	46:2o:17:ARG:HG3	1.86	0.41
47:2p:20:VAL:HG21	47:2p:32:TYR:CD2	2.56	0.41
1:1A:215:G:N2	1:1A:217:A:H62	2.17	0.41
1:1A:721:G:H1'	5:1F:74:ARG:CD	2.49	0.41
1:1A:793:A:H8	59:1A:6064:HOH:O	2.04	0.41
1:1A:1111:U:O2	1:1A:1112:U:C4	2.73	0.41
1:1A:1463:C:H2'	1:1A:1464:G:O4'	2.21	0.41
1:1A:1576:G:C6	1:1A:1577:C:N4	2.89	0.41
1:1A:1954:A:H2'	1:1A:1955:G:O4'	2.21	0.41
1:1A:2164:C:C2	1:1A:2171:G:C6	3.08	0.41
1:1A:2357:G:H4'	1:1A:2358:A:H5"	2.03	0.41
1:1A:2377:G:N7	30:18:39:LYS:NZ	2.53	0.41
1:1A:2418:U:H2'	1:1A:2418:U:OP2	2.21	0.41
4:1E:170:LEU:HB3	4:1E:184:VAL:CG2	2.50	0.41
5:1F:157:VAL:HB	5:1F:194:MET:HG2	2.02	0.41
7:1H:121:ILE:HD13	7:1H:121:ILE:HA	1.94	0.41
8:1I:61:ARG:HD2	8:1I:61:ARG:N	2.36	0.41
15:1T:55:ASN:N	15:1T:59:THR:HG22	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:1:MET:HE1	24:12:26:ARG:NH2	2.36	0.41
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.29	0.41
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	2.03	0.41
30:18:4:MET:HE3	30:18:63:PRO:HG3	2.01	0.41
32:1a:179:A:H2'	32:1a:180:U:C6	2.56	0.41
32:1a:834:C:C2	32:1a:853:G:C2	3.08	0.41
32:1a:865:A:H2'	32:1a:866:C:C6	2.56	0.41
32:1a:942:G:C2	32:1a:1342:C:C2	3.09	0.41
32:1a:1055:A:O2'	34:1c:161:GLU:O	2.37	0.41
32:1a:1468:A:H8	32:1a:1468:A:O5'	2.03	0.41
32:1a:1499:A:H1'	32:1a:1520:G:H5'	2.03	0.41
33:1b:145:LEU:HD12	33:1b:149:LEU:HD12	2.03	0.41
33:1b:158:LEU:HA	33:1b:159:PRO:HD3	1.87	0.41
34:1c:113:ALA:HB3	34:1c:114:PRO:HD3	2.03	0.41
34:1c:115:LEU:HD12	34:1c:115:LEU:HA	1.82	0.41
35:1d:184:LYS:HB3	35:1d:184:LYS:NZ	2.35	0.41
36:1e:12:LEU:HD22	59:1e:303:HOH:O	2.21	0.41
42:1k:70:LYS:HE2	42:1k:70:LYS:HB2	1.82	0.41
47:1p:5:ARG:HH21	47:1p:24:ALA:HA	1.85	0.41
48:1q:81:ARG:HD2	48:1q:81:ARG:HA	1.79	0.41
51:1t:42:GLN:O	51:1t:45:GLN:HB3	2.20	0.41
1:2A:9:U:H3	1:2A:2629:A:H2	1.65	0.41
1:2A:593:G:H4'	30:28:4:MET:HE2	2.03	0.41
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.86	0.41
1:2A:1057:A:O2'	1:2A:1058:G:OP1	2.35	0.41
1:2A:1070:A:H2'	1:2A:1071:G:C8	2.56	0.41
1:2A:1110:G:OP2	1:2A:1110:G:H8	2.03	0.41
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.36	0.41
1:2A:2130:U:H3'	1:2A:2130:U:H6	1.85	0.41
1:2A:2186:G:C2	1:2A:2187:G:C5	3.08	0.41
59:2A:5977:HOH:O	4:2E:144:ARG:HD3	2.20	0.41
5:2F:53:THR:HG22	5:2F:56:GLU:CD	2.46	0.41
6:2G:47:LYS:HG2	6:2G:48:GLU:N	2.35	0.41
6:2G:126:ASP:HB3	6:2G:128:ARG:H	1.85	0.41
11:2P:96:THR:OG1	11:2P:98:GLU:HG2	2.21	0.41
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.50	0.41
23:21:11:ARG:HD2	59:21:208:HOH:O	2.20	0.41
29:27:42:LEU:HA	29:27:42:LEU:HD23	1.83	0.41
32:2a:71:C:H2'	32:2a:72:C:C6	2.56	0.41
32:2a:162:A:C5	32:2a:163:C:H1'	2.55	0.41
32:2a:392:G:H2'	32:2a:393:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:443:C:H2'	32:2a:444:C:H6	1.86	0.41
32:2a:451:A:N6	32:2a:480:U:H2'	2.36	0.41
32:2a:545:C:O2'	32:2a:549:C:OP1	2.33	0.41
32:2a:955:U:O2'	50:2s:83:HIS:CD2	2.70	0.41
32:2a:980:C:H1'	45:2n:19:ARG:HA	2.03	0.41
32:2a:1004:A:C5'	32:2a:1025:U:H5	2.34	0.41
32:2a:1054:C:H41	53:2y:46:GLN:CG	2.33	0.41
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.21	0.41
32:2a:1223:C:P	50:2s:78:ARG:HH22	2.43	0.41
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.56	0.41
38:2g:23:VAL:HG13	38:2g:43:PHE:CE2	2.56	0.41
44:2m:14:ARG:O	44:2m:17:VAL:HG23	2.21	0.41
51:2t:77:ALA:O	51:2t:81:LYS:HG3	2.20	0.41
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	2.03	0.41
3:1D:16:MET:HG2	3:1D:211:ARG:HH21	1.86	0.41
4:1E:21:VAL:HA	4:1E:22:PRO:HD3	1.88	0.41
4:1E:31:CYS:HB3	4:1E:49:LEU:HG	2.03	0.41
6:1G:43:LEU:HB3	6:1G:44:GLY:H	1.61	0.41
11:1P:86:LYS:HB3	11:1P:118:GLY:HA3	2.03	0.41
13:1R:44:LEU:HD23	13:1R:44:LEU:HA	1.82	0.41
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.79	0.41
30:18:50:LEU:HD23	30:18:50:LEU:HA	1.88	0.41
32:1a:161:A:H2'	32:1a:162:A:C8	2.56	0.41
32:1a:1517:G:N7	32:1a:1518:MA6:H103	2.36	0.41
42:1k:58:PRO:HA	42:1k:90:GLY:HA2	2.03	0.41
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.54	0.41
1:2A:185:U:H2'	1:2A:186:G:H8	1.85	0.41
1:2A:570:G:C6	1:2A:2030:A:C2	3.09	0.41
1:2A:635:C:H2'	1:2A:636:G:O4'	2.21	0.41
1:2A:1055:G:H2'	1:2A:1056:G:O4'	2.21	0.41
1:2A:2162:G:O3'	1:2A:2172:U:O2'	2.21	0.41
1:2A:2712:U:H1'	1:2A:2712(A):A:C8	2.56	0.41
6:2G:13:GLU:O	6:2G:17:PRO:HG2	2.20	0.41
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.53	0.41
32:2a:192:U:H5'	51:2t:101:GLY:HA3	2.02	0.41
32:2a:573:A:OP2	59:2a:3427:HOH:O	2.22	0.41
32:2a:748:C:H4'	32:2a:749:C:O5'	2.21	0.41
32:2a:865:A:H5'	32:2a:1078:U:O4	2.21	0.41
32:2a:946:A:H2'	32:2a:947:G:C8	2.56	0.41
32:2a:1140:C:H2'	32:2a:1141:C:H6	1.85	0.41
33:2b:114:ARG:O	33:2b:118:LEU:N	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:196:LEU:HD12	35:2d:196:LEU:H	1.86	0.41
37:2f:91:VAL:HG12	37:2f:92:LYS:O	2.20	0.41
41:2j:30:SER:OG	41:2j:81:THR:HG22	2.21	0.41
1:1A:606:G:OP2	16:1U:10:ARG:HD2	2.21	0.40
1:1A:1248:G:H5'	11:1P:3:LEU:HD23	2.04	0.40
1:1A:2118:U:H2'	1:1A:2119:C:H6	1.86	0.40
1:1A:2760:G:O6	1:1A:2768:C:H5"	2.22	0.40
5:1F:178:PRO:HB2	5:1F:201:VAL:CG2	2.51	0.40
7:1H:167:GLU:HA	7:1H:168:PRO:HD3	1.90	0.40
23:11:80:LEU:HB3	23:11:82:LEU:HG	2.02	0.40
32:1a:115:G:H4'	32:1a:116:A:O5'	2.21	0.40
32:1a:159:G:N2	32:1a:161:A:H3'	2.36	0.40
32:1a:520:A:N1	32:1a:536:C:H1'	2.35	0.40
32:1a:738:C:H2'	32:1a:739:C:C6	2.56	0.40
32:1a:1034:G:H3'	32:1a:1035:A:C8	2.55	0.40
41:1j:16:LEU:HD21	41:1j:70:ARG:HG2	2.03	0.40
44:1m:11:ARG:H	44:1m:11:ARG:HG3	1.68	0.40
46:1o:67:LEU:O	46:1o:71:GLN:HB3	2.21	0.40
1:2A:1075:C:N4	1:2A:1077:A:C5	2.89	0.40
1:2A:1310:G:OP2	29:27:9:ARG:HD2	2.21	0.40
1:2A:2109:U:H2'	1:2A:2110:G:C8	2.56	0.40
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.57	0.40
6:2G:35:GLU:HG3	6:2G:36:LYS:HD2	2.02	0.40
6:2G:46:ALA:O	6:2G:51:ARG:HA	2.21	0.40
8:2I:133:HIS:HD2	8:2I:136:VAL:HG23	1.86	0.40
17:2V:89:GLN:HA	17:2V:90:PRO:HD3	1.94	0.40
32:2a:684:A:C2	32:2a:685:G:C4	3.09	0.40
32:2a:1069:C:O2'	32:2a:1192:C:H1'	2.20	0.40
32:2a:1157:A:C5	32:2a:1180:A:C6	3.09	0.40
32:2a:1226:C:N4	44:2m:104:ARG:HD2	2.36	0.40
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.85	0.40
33:2b:58:ILE:CG2	33:2b:222:ILE:HG22	2.50	0.40
34:2c:6:HIS:HA	34:2c:7:PRO:HD3	1.80	0.40
36:2e:20:GLN:OE1	36:2e:25:ARG:HD2	2.21	0.40
47:2p:17:TYR:HE1	47:2p:41:PRO:HG3	1.85	0.40
1:1A:1147:U:H2'	1:1A:1148:C:H6	1.85	0.40
1:1A:1347:A:C8	1:1A:1349:G:C8	3.08	0.40
1:1A:2340:A:H2'	1:1A:2341:G:H8	1.84	0.40
1:1A:2524:C:H2'	1:1A:2525:G:O4'	2.21	0.40
5:1F:175:THR:O	56:1F:311:ARG:HD3	2.21	0.40
32:1a:41:G:H2'	32:1a:42:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:359:U:H2'	32:1a:360:A:H8	1.84	0.40
32:1a:408:A:H2'	32:1a:409:G:O4'	2.22	0.40
32:1a:630:G:O2'	32:1a:631:G:H5'	2.21	0.40
32:1a:1030:C:N4	32:1a:1032:G:O6	2.54	0.40
32:1a:1135:U:H4'	32:1a:1136:U:C5	2.54	0.40
35:1d:116:GLN:NE2	35:1d:157:LEU:HD11	2.36	0.40
35:1d:171:GLY:HA2	35:1d:172:PRO:HD3	1.98	0.40
38:1g:23:VAL:HG13	38:1g:43:PHE:CE2	2.57	0.40
38:1g:56:GLN:O	38:1g:58:PRO:HD3	2.21	0.40
43:1l:102:ARG:HA	43:1l:102:ARG:HD2	1.90	0.40
47:1p:25:ARG:HH11	47:1p:25:ARG:HG3	1.86	0.40
48:1q:43:LEU:HD12	48:1q:68:ARG:HG2	2.02	0.40
1:2A:225:A:O2'	1:2A:257:A:H4'	2.21	0.40
1:2A:554:U:C4	1:2A:555:U:C4	3.09	0.40
1:2A:629:G:H4'	1:2A:650:C:O2	2.22	0.40
1:2A:729:G:C8	3:2D:208:LYS:HD2	2.56	0.40
1:2A:1044:G:O2'	1:2A:1048:A:H1'	2.22	0.40
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.21	0.40
1:2A:2130:U:O2'	1:2A:2133:G:H4'	2.21	0.40
1:2A:2749:A:H3'	1:2A:2750:A:H2'	2.02	0.40
2:2B:83:G:H1	2:2B:94:C:H42	1.67	0.40
4:2E:178:GLU:H	4:2E:178:GLU:CD	2.29	0.40
6:2G:82:LEU:HA	6:2G:86:MET:SD	2.61	0.40
8:2I:62:LYS:HE2	8:2I:133:HIS:NE2	2.36	0.40
8:2I:117:GLU:HG3	8:2I:118:LYS:N	2.37	0.40
15:2T:29:ARG:HH11	15:2T:29:ARG:HD2	1.76	0.40
15:2T:114:LEU:HD23	15:2T:114:LEU:HA	1.81	0.40
18:2W:1:MET:HE2	18:2W:62:HIS:HB3	2.03	0.40
32:2a:189(B):C:H2'	32:2a:189(C):C:C6	2.56	0.40
32:2a:601:C:H2'	32:2a:602:A:H8	1.85	0.40
32:2a:1188:A:N6	59:2a:3499:HOH:O	2.54	0.40
38:2g:27:ILE:HD12	38:2g:40:ALA:HA	2.02	0.40
40:2i:37:PHE:HB3	40:2i:43:ALA:CB	2.51	0.40
47:2p:3:LYS:HD2	47:2p:24:ALA:HB2	2.03	0.40
1:1A:272:U:OP1	8:1I:50:ARG:NH2	2.52	0.40
1:1A:511:C:O2'	1:1A:512:C:H5'	2.22	0.40
1:1A:2115:G:C6	1:1A:2237:A:C8	3.09	0.40
1:1A:2143:G:O6	1:1A:2198:A:N6	2.54	0.40
1:1A:2316:G:H22	1:1A:2324:U:H3	1.70	0.40
1:1A:2451:A:C8	1:1A:2451:A:C5'	3.04	0.40
2:1B:66:A:N6	2:1B:109:C:H5'	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:164:GLN:HE21	3:1D:176:ARG:HH12	1.69	0.40
6:1G:53:LEU:H	6:1G:53:LEU:CD2	2.34	0.40
8:1I:133:HIS:ND1	8:1I:134:PRO:O	2.49	0.40
12:1Q:84:GLY:O	12:1Q:85:LYS:HB2	2.21	0.40
22:10:43:THR:HG23	22:10:43:THR:O	2.21	0.40
32:1a:123:C:OP1	32:1a:311:C:O2'	2.30	0.40
32:1a:407:G:H5"	35:1d:115:ARG:HB3	2.04	0.40
32:1a:1027:C:N3	32:1a:1034:G:C6	2.88	0.40
32:1a:1030:C:C4	32:1a:1030(A):G:H1'	2.56	0.40
32:1a:1187:G:H4'	40:1i:111:ARG:HH11	1.85	0.40
36:1e:78:HIS:HE1	36:1e:80:ILE:HD13	1.87	0.40
36:1e:90:VAL:O	36:1e:120:THR:HA	2.21	0.40
38:1g:80:VAL:HB	38:1g:85:TYR:CD2	2.56	0.40
41:1j:85:LEU:HD23	41:1j:85:LEU:HA	1.94	0.40
50:1s:63:THR:HG1	50:1s:65:ASN:HD21	1.68	0.40
1:2A:36:G:N3	1:2A:450:G:O2'	2.54	0.40
1:2A:41:C:H2'	1:2A:42:G:H8	1.86	0.40
1:2A:337:C:H2'	1:2A:338:G:O4'	2.21	0.40
1:2A:476:G:H4'	1:2A:502:A:N1	2.36	0.40
1:2A:904:C:H2'	1:2A:905:U:C6	2.56	0.40
1:2A:947:G:O2'	1:2A:984:A:N1	2.51	0.40
1:2A:1050:A:H2	1:2A:2751:G:N2	2.20	0.40
1:2A:1059:G:C2	1:2A:1079:C:N3	2.88	0.40
1:2A:1835:G:C8	1:2A:1835:G:H5"	2.57	0.40
1:2A:2282:G:H4'	1:2A:2389:G:O2'	2.20	0.40
1:2A:2293:C:H2'	1:2A:2294:C:C6	2.56	0.40
7:2H:34:GLU:H	7:2H:34:GLU:HG2	1.72	0.40
12:2Q:72:LYS:HA	12:2Q:73:PRO:HD2	1.97	0.40
19:2X:94:GLY:HA3	19:2X:95:LEU:O	2.21	0.40
32:2a:130:A:H1'	32:2a:263:A:O2'	2.22	0.40
32:2a:582:U:C2	32:2a:760:G:C6	3.10	0.40
32:2a:600:C:H2'	32:2a:601:C:C6	2.56	0.40
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.36	0.40
32:2a:1304:G:C6	32:2a:1305:G:N1	2.89	0.40
32:2a:1342:C:H2'	32:2a:1343:G:H8	1.86	0.40
32:2a:1428:A:H2'	32:2a:1429:C:O4'	2.22	0.40
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.21	0.40
46:2o:61:GLY:O	46:2o:65:ARG:HG3	2.21	0.40
1:1A:268:G:O2'	1:1A:269:G:H8	2.05	0.40
1:1A:580:U:H2'	1:1A:581:G:C8	2.56	0.40
1:1A:908:A:C2	1:1A:963:A:C4	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2159:C:H5	1:1A:2177:G:C2	2.40	0.40
2:1B:75:G:H5"	2:1B:75:G:C8	2.48	0.40
3:1D:71:ASP:OD2	3:1D:103:ARG:NH2	2.54	0.40
25:13:3:ARG:HH11	25:13:60:GLU:CD	2.23	0.40
32:1a:1038:C:H2'	32:1a:1039:C:C6	2.56	0.40
32:1a:1298:C:H4'	32:1a:1299:A:C4	2.56	0.40
32:1a:1330:U:O4	32:1a:1331:G:C6	2.74	0.40
34:1c:36:ASP:O	34:1c:40:ARG:HG3	2.20	0.40
35:1d:23:GLY:HA3	35:1d:112:VAL:HB	2.03	0.40
40:1i:43:ALA:C	40:1i:45:ALA:H	2.30	0.40
42:1k:62:GLN:HB2	42:1k:93:GLN:HG3	2.04	0.40
42:1k:84:VAL:HG11	42:1k:91:ARG:HD2	2.04	0.40
1:2A:479:A:N3	1:2A:481:G:H5"	2.37	0.40
1:2A:775:G:C4	1:2A:794:G:C8	3.10	0.40
1:2A:1056:G:H5"	1:2A:1057:A:H5'	2.04	0.40
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.09	0.40
1:2A:1889:A:C6	1:2A:1890:A:C6	3.10	0.40
1:2A:2306:C:C4	1:2A:2307:G:C6	3.08	0.40
1:2A:2390:U:O2'	1:2A:2391:G:H5'	2.20	0.40
1:2A:2572:A:N7	4:2E:144:ARG:HD2	2.36	0.40
1:2A:2607:G:H2'	1:2A:2608:G:O4'	2.21	0.40
1:2A:2646:C:H6	1:2A:2646:C:O5'	2.05	0.40
59:2A:6450:HOH:O	23:21:48:LYS:HE2	2.21	0.40
4:2E:111:ARG:H	4:2E:111:ARG:HG2	1.74	0.40
11:2P:147:LEU:O	11:2P:147:LEU:HD13	2.22	0.40
17:2V:5:VAL:HG11	17:2V:57:VAL:HG21	2.03	0.40
20:2Y:8:LYS:HB2	20:2Y:8:LYS:HE3	1.83	0.40
26:24:59:PHE:CA	26:24:61:ARG:H	2.20	0.40
32:2a:20:U:H2'	32:2a:21:G:O4'	2.21	0.40
32:2a:424:G:C2	32:2a:425:G:C8	3.09	0.40
32:2a:1525:G:P	42:2k:120:ARG:HH22	2.43	0.40
59:2a:3424:HOH:O	53:2y:9:GLN:NE2	2.51	0.40
34:2c:16:ARG:HG3	34:2c:17:ASP:N	2.36	0.40
37:2f:35:ALA:HA	37:2f:67:MET:HB3	2.03	0.40
1:1A:294:C:H2'	1:1A:295:C:O4'	2.21	0.40
1:1A:715:G:H5'	1:1A:716:G:OP2	2.22	0.40
1:1A:873:U:H4'	11:1P:55:ARG:HB2	2.04	0.40
1:1A:1093:G:H2'	1:1A:1156:G:N2	2.32	0.40
1:1A:1558:G:H2'	1:1A:1559:C:C6	2.56	0.40
1:1A:2891:C:H2'	1:1A:2892:A:O4'	2.21	0.40
5:1F:104:LYS:O	5:1F:108:LYS:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:64:ARG:NH2	10:1O:99:PHE:O	2.55	0.40
26:14:58:ARG:HG2	50:1s:67:VAL:HB	2.04	0.40
29:17:10:ARG:HG2	29:17:14:LYS:HD2	2.03	0.40
32:1a:294:U:H2'	32:1a:295:C:C6	2.56	0.40
32:1a:328:C:H4'	32:1a:329:A:H5'	2.04	0.40
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.37	0.40
41:1j:4:ILE:N	41:1j:100:THR:HG22	2.37	0.40
1:2A:83:G:N1	1:2A:102:G:O2'	2.42	0.40
1:2A:1057:A:C6	1:2A:1086:A:C2	3.10	0.40
1:2A:1899:G:N3	1:2A:1899:G:H2'	2.35	0.40
1:2A:2010:G:H5"	18:2W:42:ARG:HB2	2.03	0.40
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.38	0.40
1:2A:2189:U:N3	1:2A:2190:G:O6	2.55	0.40
1:2A:2365:G:O6	30:28:39:LYS:HE3	2.22	0.40
1:2A:2427:C:H5"	1:2A:2428:G:OP1	2.22	0.40
1:2A:2887:U:H2'	1:2A:2888:C:H6	1.86	0.40
6:2G:170:ARG:HH21	6:2G:180:PHE:CB	2.34	0.40
18:2W:60:ASN:N	18:2W:60:ASN:ND2	2.70	0.40
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.86	0.40
32:2a:848:C:H2'	32:2a:849:C:C6	2.55	0.40
32:2a:1014:A:H4'	50:2s:14:HIS:CE1	2.56	0.40
32:2a:1202:G:H1'	45:2n:29:ARG:HD2	2.04	0.40
32:2a:1256:A:OP2	34:2c:26:LYS:NZ	2.54	0.40
42:2k:69:ALA:O	42:2k:73:MET:HG3	2.21	0.40
44:2m:86:CYS:HA	50:2s:73:GLU:O	2.22	0.40
53:2y:24:LEU:HD13	53:2y:27:LEU:HD12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
3	2D	273/276 (99%)	260 (95%)	13 (5%)	0	100	100
4	1E	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	24	31
4	2E	202/206 (98%)	196 (97%)	6 (3%)	0	100	100
5	1F	201/210 (96%)	197 (98%)	4 (2%)	0	100	100
5	2F	201/210 (96%)	196 (98%)	3 (2%)	2 (1%)	12	15
6	1G	179/182 (98%)	167 (93%)	11 (6%)	1 (1%)	21	27
6	2G	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	21	27
7	1H	172/180 (96%)	167 (97%)	5 (3%)	0	100	100
7	2H	171/180 (95%)	165 (96%)	6 (4%)	0	100	100
8	1I	145/148 (98%)	133 (92%)	11 (8%)	1 (1%)	18	23
8	2I	144/148 (97%)	135 (94%)	9 (6%)	0	100	100
9	1N	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
9	2N	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	2O	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
11	1P	147/150 (98%)	141 (96%)	6 (4%)	0	100	100
11	2P	147/150 (98%)	141 (96%)	5 (3%)	1 (1%)	18	23
12	1Q	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
12	2Q	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
13	1R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
13	2R	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
14	1S	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	14	17
14	2S	108/112 (96%)	105 (97%)	3 (3%)	0	100	100
15	1T	129/146 (88%)	124 (96%)	5 (4%)	0	100	100
15	2T	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	114 (100%)	0	0	100	100
17	1V	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
17	2V	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
18	1W	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
18	2W	110/113 (97%)	110 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	1X	93/96 (97%)	92 (99%)	1 (1%)	0	100	100
19	2X	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
20	1Y	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
20	2Y	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
21	1Z	201/206 (98%)	196 (98%)	5 (2%)	0	100	100
21	2Z	199/206 (97%)	194 (98%)	5 (2%)	0	100	100
22	10	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
22	20	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
23	11	95/98 (97%)	94 (99%)	0	1 (1%)	11	13
23	21	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11	13
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
25	23	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	14	67/71 (94%)	56 (84%)	5 (8%)	6 (9%)	0	0
26	24	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	2	1
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	25	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
29	17	46/49 (94%)	46 (100%)	0	0	100	100
29	27	46/49 (94%)	46 (100%)	0	0	100	100
30	18	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	202 (88%)	20 (9%)	7 (3%)	3	2
33	2b	229/256 (90%)	205 (90%)	19 (8%)	5 (2%)	5	4
34	1c	204/239 (85%)	190 (93%)	14 (7%)	0	100	100
34	2c	204/239 (85%)	187 (92%)	17 (8%)	0	100	100
35	1d	206/209 (99%)	197 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	2d	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
36	1e	146/162 (90%)	144 (99%)	2 (1%)	0	100	100
36	2e	146/162 (90%)	145 (99%)	1 (1%)	0	100	100
37	1f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
37	2f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
38	1g	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
38	2g	153/156 (98%)	148 (97%)	4 (3%)	1 (1%)	18	23
39	1h	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
39	2h	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
40	1i	125/128 (98%)	115 (92%)	9 (7%)	1 (1%)	16	20
40	2i	124/128 (97%)	113 (91%)	8 (6%)	3 (2%)	4	4
41	1j	95/105 (90%)	83 (87%)	8 (8%)	4 (4%)	2	1
41	2j	94/105 (90%)	85 (90%)	7 (7%)	2 (2%)	5	4
42	1k	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	6	6
42	2k	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	14	17
43	1l	119/132 (90%)	117 (98%)	2 (2%)	0	100	100
43	2l	119/132 (90%)	116 (98%)	3 (2%)	0	100	100
44	1m	114/126 (90%)	105 (92%)	7 (6%)	2 (2%)	6	6
44	2m	112/126 (89%)	105 (94%)	6 (5%)	1 (1%)	14	17
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	2n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
46	1o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
46	2o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
47	1p	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
47	2p	80/88 (91%)	76 (95%)	4 (5%)	0	100	100
48	1q	97/105 (92%)	94 (97%)	2 (2%)	1 (1%)	12	15
48	2q	97/105 (92%)	95 (98%)	2 (2%)	0	100	100
49	1r	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
49	2r	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
50	1s	81/93 (87%)	78 (96%)	3 (4%)	0	100	100
50	2s	81/93 (87%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	1t	94/106 (89%)	86 (92%)	6 (6%)	2 (2%)	5 4
51	2t	96/106 (91%)	88 (92%)	6 (6%)	2 (2%)	5 4
52	1u	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
52	2u	21/27 (78%)	19 (90%)	1 (5%)	1 (5%)	2 1
53	1y	95/113 (84%)	94 (99%)	1 (1%)	0	100 100
53	2y	94/113 (83%)	89 (95%)	4 (4%)	1 (1%)	11 13
All	All	11629/12354 (94%)	11139 (96%)	435 (4%)	55 (0%)	24 31

All (55) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	14	49	PHE
33	1b	16	HIS
33	1b	17	PHE
33	1b	22	LYS
51	1t	95	ALA
23	21	3	LYS
33	2b	17	PHE
33	2b	20	GLU
33	2b	124	SER
40	2i	44	VAL
40	2i	54	ASP
6	1G	51	ARG
14	1S	60	GLY
26	14	45	GLY
26	14	47	GLN
40	1i	44	VAL
41	1j	31	GLY
41	1j	78	ASN
41	1j	79	ARG
6	2G	81	LYS
26	24	60	GLN
33	2b	10	LEU
41	2j	79	ARG
44	2m	67	GLU
51	2t	95	ALA
4	1E	52	LEU
44	1m	12	ASN
5	2F	21	ALA
26	24	45	GLY

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Mol	Chain	Res	Type
33	2b	125	PRO
41	2j	78	ASN
53	2y	45	PRO
26	14	46	GLN
26	14	55	ARG
33	1b	20	GLU
44	1m	67	GLU
38	2g	7	ALA
8	1I	73	GLU
23	11	3	LYS
26	14	60	GLN
33	1b	43	ASP
33	1b	127	ILE
42	1k	117	ASN
5	2F	130	ALA
26	24	55	ARG
51	2t	100	ILE
52	2u	7	ARG
48	1q	68	ARG
51	1t	100	ILE
11	2P	29	LYS
40	2i	11	LYS
42	1k	105	VAL
42	2k	105	VAL
33	1b	15	VAL
41	1j	77	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	1D	214/218 (98%)	192 (90%)	22 (10%)	7 8
3	2D	215/218 (99%)	193 (90%)	22 (10%)	7 8
4	1E	164/166 (99%)	139 (85%)	25 (15%)	3 3
4	2E	164/166 (99%)	138 (84%)	26 (16%)	2 2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	1F	160/166 (96%)	140 (88%)	20 (12%)	4 5
5	2F	159/166 (96%)	142 (89%)	17 (11%)	6 8
6	1G	144/156 (92%)	125 (87%)	19 (13%)	4 4
6	2G	142/156 (91%)	119 (84%)	23 (16%)	2 2
7	1H	144/148 (97%)	133 (92%)	11 (8%)	12 16
7	2H	143/148 (97%)	125 (87%)	18 (13%)	4 5
8	1I	111/124 (90%)	87 (78%)	24 (22%)	1 1
8	2I	108/124 (87%)	93 (86%)	15 (14%)	3 4
9	1N	119/119 (100%)	103 (87%)	16 (13%)	4 4
9	2N	118/119 (99%)	104 (88%)	14 (12%)	5 6
10	1O	100/100 (100%)	94 (94%)	6 (6%)	17 25
10	2O	100/100 (100%)	92 (92%)	8 (8%)	11 15
11	1P	115/116 (99%)	101 (88%)	14 (12%)	5 5
11	2P	115/116 (99%)	103 (90%)	12 (10%)	7 8
12	1Q	111/111 (100%)	100 (90%)	11 (10%)	7 9
12	2Q	111/111 (100%)	100 (90%)	11 (10%)	7 9
13	1R	101/101 (100%)	85 (84%)	16 (16%)	2 2
13	2R	101/101 (100%)	86 (85%)	15 (15%)	3 3
14	1S	87/88 (99%)	75 (86%)	12 (14%)	3 4
14	2S	85/88 (97%)	71 (84%)	14 (16%)	2 2
15	1T	115/127 (91%)	102 (89%)	13 (11%)	5 7
15	2T	113/127 (89%)	102 (90%)	11 (10%)	8 10
16	1U	93/94 (99%)	80 (86%)	13 (14%)	3 3
16	2U	93/94 (99%)	82 (88%)	11 (12%)	5 6
17	1V	81/82 (99%)	68 (84%)	13 (16%)	2 2
17	2V	80/82 (98%)	67 (84%)	13 (16%)	2 2
18	1W	90/92 (98%)	78 (87%)	12 (13%)	4 4
18	2W	90/92 (98%)	80 (89%)	10 (11%)	6 7
19	1X	77/78 (99%)	71 (92%)	6 (8%)	11 16
19	2X	77/78 (99%)	71 (92%)	6 (8%)	11 16
20	1Y	86/91 (94%)	80 (93%)	6 (7%)	14 19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
20	2Y	86/91 (94%)	77 (90%)	9 (10%)	6 8
21	1Z	169/179 (94%)	143 (85%)	26 (15%)	2 3
21	2Z	165/179 (92%)	144 (87%)	21 (13%)	4 5
22	10	61/67 (91%)	57 (93%)	4 (7%)	15 21
22	20	61/67 (91%)	58 (95%)	3 (5%)	22 34
23	11	79/83 (95%)	69 (87%)	10 (13%)	4 5
23	21	81/83 (98%)	71 (88%)	10 (12%)	4 5
24	12	65/67 (97%)	62 (95%)	3 (5%)	24 36
24	22	66/67 (98%)	61 (92%)	5 (8%)	12 16
25	13	51/52 (98%)	47 (92%)	4 (8%)	11 16
25	23	50/52 (96%)	44 (88%)	6 (12%)	5 5
26	14	58/63 (92%)	47 (81%)	11 (19%)	1 1
26	24	54/63 (86%)	43 (80%)	11 (20%)	1 1
27	15	51/52 (98%)	44 (86%)	7 (14%)	3 4
27	25	50/52 (96%)	43 (86%)	7 (14%)	3 3
28	16	51/52 (98%)	44 (86%)	7 (14%)	3 4
28	26	50/52 (96%)	44 (88%)	6 (12%)	5 5
29	17	41/42 (98%)	37 (90%)	4 (10%)	7 10
29	27	41/42 (98%)	38 (93%)	3 (7%)	13 18
30	18	54/55 (98%)	51 (94%)	3 (6%)	19 28
30	28	54/55 (98%)	49 (91%)	5 (9%)	8 11
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 55
31	29	34/34 (100%)	33 (97%)	1 (3%)	37 55
33	1b	191/220 (87%)	158 (83%)	33 (17%)	2 2
33	2b	187/220 (85%)	150 (80%)	37 (20%)	1 1
34	1c	144/188 (77%)	132 (92%)	12 (8%)	10 14
34	2c	140/188 (74%)	126 (90%)	14 (10%)	7 9
35	1d	171/181 (94%)	151 (88%)	20 (12%)	5 6
35	2d	172/181 (95%)	156 (91%)	16 (9%)	8 11
36	1e	114/123 (93%)	102 (90%)	12 (10%)	6 8
36	2e	114/123 (93%)	99 (87%)	15 (13%)	4 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
37	1f	85/90 (94%)	77 (91%)	8 (9%)	8 11
37	2f	85/90 (94%)	76 (89%)	9 (11%)	6 8
38	1g	120/127 (94%)	108 (90%)	12 (10%)	7 9
38	2g	119/127 (94%)	104 (87%)	15 (13%)	4 5
39	1h	116/119 (98%)	101 (87%)	15 (13%)	4 4
39	2h	114/119 (96%)	101 (89%)	13 (11%)	5 6
40	1i	91/99 (92%)	75 (82%)	16 (18%)	2 2
40	2i	88/99 (89%)	77 (88%)	11 (12%)	4 5
41	1j	68/92 (74%)	64 (94%)	4 (6%)	18 26
41	2j	68/92 (74%)	61 (90%)	7 (10%)	7 8
42	1k	83/99 (84%)	74 (89%)	9 (11%)	6 7
42	2k	83/99 (84%)	75 (90%)	8 (10%)	8 10
43	1l	96/108 (89%)	91 (95%)	5 (5%)	21 31
43	2l	96/108 (89%)	92 (96%)	4 (4%)	26 40
44	1m	90/101 (89%)	78 (87%)	12 (13%)	4 4
44	2m	87/101 (86%)	76 (87%)	11 (13%)	4 5
45	1n	49/50 (98%)	43 (88%)	6 (12%)	5 5
45	2n	49/50 (98%)	42 (86%)	7 (14%)	3 3
46	1o	78/80 (98%)	69 (88%)	9 (12%)	5 6
46	2o	78/80 (98%)	68 (87%)	10 (13%)	4 4
47	1p	69/74 (93%)	60 (87%)	9 (13%)	4 4
47	2p	68/74 (92%)	57 (84%)	11 (16%)	2 2
48	1q	94/97 (97%)	88 (94%)	6 (6%)	16 23
48	2q	94/97 (97%)	87 (93%)	7 (7%)	13 17
49	1r	59/77 (77%)	48 (81%)	11 (19%)	1 1
49	2r	59/77 (77%)	49 (83%)	10 (17%)	2 2
50	1s	68/80 (85%)	60 (88%)	8 (12%)	5 6
50	2s	67/80 (84%)	60 (90%)	7 (10%)	7 8
51	1t	71/82 (87%)	61 (86%)	10 (14%)	3 3
51	2t	70/82 (85%)	61 (87%)	9 (13%)	4 4
52	1u	18/22 (82%)	16 (89%)	2 (11%)	6 7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	2u	18/22 (82%)	16 (89%)	2 (11%)	6 7
53	1y	82/98 (84%)	79 (96%)	3 (4%)	30 45
53	2y	79/98 (81%)	68 (86%)	11 (14%)	3 4
All	All	9524/10260 (93%)	8396 (88%)	1128 (12%)	5 6

All (1128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	37	LEU
3	1D	54	ARG
3	1D	61	LEU
3	1D	88	ARG
3	1D	94	LEU
3	1D	99	ASP
3	1D	103	ARG
3	1D	111	LEU
3	1D	126	GLN
3	1D	141	VAL
3	1D	142	VAL
3	1D	155	LEU
3	1D	173	VAL
3	1D	183	ARG
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	257	LEU
3	1D	259	THR
3	1D	260	ARG
4	1E	7	VAL
4	1E	9	VAL
4	1E	12	THR
4	1E	21	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	40	GLU
4	1E	49	LEU
4	1E	72	VAL
4	1E	73	GLU
4	1E	75	VAL

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Mol	Chain	Res	Type
4	1E	78	LEU
4	1E	82	ARG
4	1E	94	GLU
4	1E	111	ARG
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG
4	1E	154	LYS
4	1E	170	LEU
4	1E	175	VAL
4	1E	178	GLU
4	1E	181	LEU
4	1E	188	VAL
4	1E	203	LYS
5	1F	12	LEU
5	1F	20	LEU
5	1F	27	GLU
5	1F	33	LEU
5	1F	53	THR
5	1F	88	VAL
5	1F	106	ARG
5	1F	110	LEU
5	1F	125	LEU
5	1F	126	VAL
5	1F	132	VAL
5	1F	140	LEU
5	1F	157	VAL
5	1F	162	LEU
5	1F	168	ARG
5	1F	170	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	197	ASP
5	1F	201	VAL
6	1G	5	VAL
6	1G	7	LEU
6	1G	31	VAL
6	1G	43	LEU
6	1G	45	GLU
6	1G	49	ASP
6	1G	52	ILE
6	1G	53	LEU

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Mol	Chain	Res	Type
6	1G	60	LEU
6	1G	81	LYS
6	1G	82	LEU
6	1G	133	LEU
6	1G	135	LEU
6	1G	140	ILE
6	1G	145	THR
6	1G	153	ARG
6	1G	159	VAL
6	1G	170	ARG
6	1G	175	LEU
7	1H	15	VAL
7	1H	23	ARG
7	1H	24	VAL
7	1H	49	VAL
7	1H	59	ARG
7	1H	62	LYS
7	1H	69	ARG
7	1H	71	LEU
7	1H	105	LEU
7	1H	116	GLU
7	1H	122	THR
8	1I	5	LEU
8	1I	9	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	38	LEU
8	1I	43	ASN
8	1I	44	LEU
8	1I	47	LEU
8	1I	57	ARG
8	1I	60	GLU
8	1I	61	ARG
8	1I	68	LEU
8	1I	69	LYS
8	1I	75	LEU
8	1I	77	LEU
8	1I	85	GLU
8	1I	87	LYS
8	1I	92	VAL
8	1I	101	LEU
8	1I	108	THR

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Mol	Chain	Res	Type
8	1I	109	ILE
8	1I	116	LEU
8	1I	127	VAL
8	1I	140	LEU
9	1N	7	LYS
9	1N	14	VAL
9	1N	33	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	61	ARG
9	1N	62	VAL
9	1N	67	LEU
9	1N	68	GLU
9	1N	83	LYS
9	1N	87	LEU
9	1N	97	ARG
9	1N	99	LEU
9	1N	115	ARG
9	1N	120	LEU
9	1N	131	GLN
10	1O	8	LEU
10	1O	10	VAL
10	1O	23	ARG
10	1O	24	VAL
10	1O	69	ILE
10	1O	98	VAL
11	1P	2	LYS
11	1P	3	LEU
11	1P	55	ARG
11	1P	59	LEU
11	1P	70	GLN
11	1P	95	VAL
11	1P	98	GLU
11	1P	106	LEU
11	1P	112	LEU
11	1P	117	GLU
11	1P	119	GLU
11	1P	125	VAL
11	1P	147	LEU
11	1P	149	GLU
12	1Q	2	LEU
12	1Q	6	ARG

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Mol	Chain	Res	Type
12	1Q	7	MET
12	1Q	21	THR
12	1Q	45	GLN
12	1Q	55	VAL
12	1Q	56	ARG
12	1Q	59	ARG
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	109	VAL
13	1R	8	ARG
13	1R	18	LEU
13	1R	28	LEU
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	60	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	75	LEU
13	1R	79	LEU
13	1R	96	ARG
13	1R	100	LEU
13	1R	111	LEU
13	1R	114	VAL
14	1S	14	VAL
14	1S	20	ARG
14	1S	43	GLU
14	1S	48	LEU
14	1S	50	SER
14	1S	52	SER
14	1S	57	LYS
14	1S	59	LYS
14	1S	69	VAL
14	1S	78	LEU
14	1S	80	LEU
14	1S	110	LEU
15	1T	6	LEU
15	1T	23	ARG
15	1T	28	VAL
15	1T	34	VAL
15	1T	35	LYS

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Mol	Chain	Res	Type
15	1T	49	VAL
15	1T	53	ARG
15	1T	59	THR
15	1T	78	LEU
15	1T	89	VAL
15	1T	96	ARG
15	1T	118	ARG
15	1T	125	ARG
16	1U	5	LYS
16	1U	8	VAL
16	1U	27	LEU
16	1U	31	SER
16	1U	36	ARG
16	1U	59	ARG
16	1U	60	LEU
16	1U	74	LEU
16	1U	83	LEU
16	1U	92	ARG
16	1U	95	LEU
16	1U	104	GLN
16	1U	108	GLU
17	1V	18	LEU
17	1V	21	ARG
17	1V	35	LEU
17	1V	43	GLU
17	1V	44	LYS
17	1V	46	VAL
17	1V	51	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	79	VAL
17	1V	95	LEU
18	1W	4	LYS
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	51	LEU
18	1W	52	GLU

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Mol	Chain	Res	Type
18	1W	67	ASP
18	1W	96	ILE
18	1W	100	THR
18	1W	107	LEU
19	1X	35	THR
19	1X	57	LEU
19	1X	66	LEU
19	1X	68	ARG
19	1X	76	ARG
19	1X	88	LYS
20	1Y	23	ARG
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	90	LEU
20	1Y	99	CYS
21	1Z	5	LEU
21	1Z	6	LYS
21	1Z	11	GLU
21	1Z	18	LEU
21	1Z	19	ARG
21	1Z	31	ARG
21	1Z	41	LEU
21	1Z	42	VAL
21	1Z	58	VAL
21	1Z	61	LEU
21	1Z	72	ARG
21	1Z	76	LEU
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	93	ASP
21	1Z	102	LEU
21	1Z	103	ARG
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	156	LYS
21	1Z	161	VAL
21	1Z	170	THR
21	1Z	185	GLU
21	1Z	191	VAL
21	1Z	199	LYS

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Mol	Chain	Res	Type
22	10	11	ARG
22	10	20	ARG
22	10	55	ARG
22	10	59	LEU
23	11	21	ARG
23	11	30	VAL
23	11	40	ARG
23	11	46	LEU
23	11	52	ARG
23	11	57	GLU
23	11	80	LEU
23	11	83	GLU
23	11	89	GLU
23	11	95	LEU
24	12	32	LEU
24	12	52	ASP
24	12	53	LEU
25	13	8	LEU
25	13	23	LEU
25	13	31	LEU
25	13	54	VAL
26	14	3	GLU
26	14	23	GLU
26	14	30	GLU
26	14	34	GLU
26	14	46	GLN
26	14	49	PHE
26	14	50	VAL
26	14	57	GLU
26	14	58	ARG
26	14	65	ASP
26	14	67	TYR
27	15	6	VAL
27	15	26	THR
27	15	29	THR
27	15	40	LYS
27	15	58	LEU
27	15	59	GLU
27	15	60	VAL
28	16	4	GLU
28	16	14	THR
28	16	28	ARG

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Mol	Chain	Res	Type
28	16	38	LYS
28	16	47	THR
28	16	48	VAL
28	16	52	VAL
29	17	9	ARG
29	17	24	THR
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	30	ARG
30	18	32	LEU
31	19	17	ILE
33	1b	7	VAL
33	1b	8	LYS
33	1b	15	VAL
33	1b	21	ARG
33	1b	44	LEU
33	1b	48	MET
33	1b	49	GLU
33	1b	71	VAL
33	1b	76	GLN
33	1b	95	GLN
33	1b	96	ARG
33	1b	106	LYS
33	1b	116	GLU
33	1b	122	PHE
33	1b	126	GLU
33	1b	135	GLN
33	1b	136	VAL
33	1b	144	ARG
33	1b	154	LEU
33	1b	157	ARG
33	1b	158	LEU
33	1b	170	GLU
33	1b	178	ARG
33	1b	179	LYS
33	1b	185	ILE
33	1b	187	LEU
33	1b	196	LEU
33	1b	200	ILE
33	1b	208	ILE
33	1b	224	GLN

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Mol	Chain	Res	Type
33	1b	226	ARG
33	1b	229	VAL
33	1b	230	VAL
34	1c	3	ASN
34	1c	15	THR
34	1c	21	ARG
34	1c	36	ASP
34	1c	64	VAL
34	1c	102	ASN
34	1c	111	LEU
34	1c	115	LEU
34	1c	131	ARG
34	1c	150	LYS
34	1c	178	LEU
34	1c	190	ARG
35	1d	8	VAL
35	1d	18	LYS
35	1d	19	LEU
35	1d	24	GLU
35	1d	49	ARG
35	1d	58	LEU
35	1d	65	ARG
35	1d	70	ILE
35	1d	85	LYS
35	1d	108	LEU
35	1d	112	VAL
35	1d	135	LEU
35	1d	168	ARG
35	1d	177	ASP
35	1d	178	VAL
35	1d	184	LYS
35	1d	187	ARG
35	1d	188	LEU
35	1d	193	ASP
35	1d	204	ILE
36	1e	31	LEU
36	1e	34	VAL
36	1e	41	VAL
36	1e	47	LYS
36	1e	57	LYS
36	1e	68	GLU
36	1e	69	VAL

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Mol	Chain	Res	Type
36	1e	72	GLN
36	1e	82	VAL
36	1e	91	LEU
36	1e	126	ARG
36	1e	137	GLU
37	1f	17	SER
37	1f	40	VAL
37	1f	46	ARG
37	1f	61	LEU
37	1f	70	ASP
37	1f	75	LEU
37	1f	82	ARG
37	1f	92	LYS
38	1g	8	GLU
38	1g	12	LEU
38	1g	32	ARG
38	1g	41	ARG
38	1g	52	GLU
38	1g	57	GLU
38	1g	76	ARG
38	1g	89	MET
38	1g	104	LEU
38	1g	114	ARG
38	1g	137	LYS
38	1g	144	MET
39	1h	2	LEU
39	1h	18	ARG
39	1h	21	LYS
39	1h	26	VAL
39	1h	38	ILE
39	1h	39	LEU
39	1h	51	VAL
39	1h	52	ASP
39	1h	63	LEU
39	1h	78	GLN
39	1h	91	ARG
39	1h	97	VAL
39	1h	112	LEU
39	1h	127	LEU
39	1h	137	VAL
40	1i	2	GLU
40	1i	3	GLN

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Mol	Chain	Res	Type
40	1i	23	ASN
40	1i	25	LYS
40	1i	27	THR
40	1i	42	ARG
40	1i	56	LEU
40	1i	64	THR
40	1i	65	VAL
40	1i	66	ARG
40	1i	81	ILE
40	1i	92	TYR
40	1i	93	ARG
40	1i	103	THR
40	1i	104	ARG
40	1i	108	VAL
41	1j	38	ILE
41	1j	44	VAL
41	1j	84	GLN
41	1j	92	THR
42	1k	14	VAL
42	1k	31	THR
42	1k	48	ILE
42	1k	54	ARG
42	1k	83	ILE
42	1k	96	ARG
42	1k	103	LEU
42	1k	114	VAL
42	1k	117	ASN
43	1l	27	LEU
43	1l	33	ARG
43	1l	41	ARG
43	1l	55	VAL
43	1l	83	VAL
44	1m	3	ARG
44	1m	4	ILE
44	1m	17	VAL
44	1m	19	LEU
44	1m	32	GLU
44	1m	36	LYS
44	1m	60	VAL
44	1m	63	THR
44	1m	70	LEU
44	1m	94	ARG

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Mol	Chain	Res	Type
44	1m	98	VAL
44	1m	110	ARG
45	1n	3	ARG
45	1n	6	LEU
45	1n	15	LYS
45	1n	18	VAL
45	1n	33	VAL
45	1n	57	ARG
46	1o	3	ILE
46	1o	26	GLU
46	1o	38	ARG
46	1o	39	LEU
46	1o	41	GLU
46	1o	48	LYS
46	1o	66	LEU
46	1o	71	GLN
46	1o	84	LYS
47	1p	2	VAL
47	1p	19	ILE
47	1p	20	VAL
47	1p	50	LYS
47	1p	60	LEU
47	1p	62	VAL
47	1p	67	THR
47	1p	71	ARG
47	1p	74	LEU
48	1q	6	LEU
48	1q	9	VAL
48	1q	60	ILE
48	1q	72	ARG
48	1q	74	LEU
48	1q	85	VAL
49	1r	25	THR
49	1r	26	LEU
49	1r	28	GLU
49	1r	31	LEU
49	1r	32	ARG
49	1r	35	ARG
49	1r	37	VAL
49	1r	58	LEU
49	1r	64	ARG
49	1r	76	LEU

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Mol	Chain	Res	Type
49	1r	85	LEU
50	1s	5	LEU
50	1s	28	LYS
50	1s	35	SER
50	1s	37	ARG
50	1s	41	VAL
50	1s	56	GLN
50	1s	65	ASN
50	1s	81	ARG
51	1t	9	ASN
51	1t	10	LEU
51	1t	24	LEU
51	1t	30	LYS
51	1t	46	GLU
51	1t	56	MET
51	1t	84	LEU
51	1t	90	GLN
51	1t	93	GLU
51	1t	100	ILE
52	1u	7	ARG
52	1u	9	ARG
53	1y	42	SER
53	1y	66	LYS
53	1y	77	LEU
3	2D	3	VAL
3	2D	54	ARG
3	2D	61	LEU
3	2D	88	ARG
3	2D	94	LEU
3	2D	103	ARG
3	2D	111	LEU
3	2D	113	VAL
3	2D	141	VAL
3	2D	142	VAL
3	2D	155	LEU
3	2D	169	GLU
3	2D	173	VAL
3	2D	183	ARG
3	2D	193	VAL
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL

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Mol	Chain	Res	Type
3	2D	229	VAL
3	2D	257	LEU
3	2D	260	ARG
3	2D	274	ARG
4	2E	7	VAL
4	2E	9	VAL
4	2E	12	THR
4	2E	21	VAL
4	2E	33	VAL
4	2E	34	VAL
4	2E	40	GLU
4	2E	47	VAL
4	2E	49	LEU
4	2E	52	LEU
4	2E	72	VAL
4	2E	73	GLU
4	2E	75	VAL
4	2E	78	LEU
4	2E	82	ARG
4	2E	111	ARG
4	2E	116	VAL
4	2E	119	ARG
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	188	VAL
5	2F	20	LEU
5	2F	24	LEU
5	2F	33	LEU
5	2F	88	VAL
5	2F	106	ARG
5	2F	110	LEU
5	2F	126	VAL
5	2F	140	LEU
5	2F	157	VAL
5	2F	162	LEU
5	2F	170	LEU
5	2F	175	THR

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Mol	Chain	Res	Type
5	2F	183	VAL
5	2F	192	LEU
5	2F	197	ASP
5	2F	200	GLU
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	7	LEU
6	2G	21	ARG
6	2G	31	VAL
6	2G	36	LYS
6	2G	43	LEU
6	2G	47	LYS
6	2G	49	ASP
6	2G	53	LEU
6	2G	55	LYS
6	2G	60	LEU
6	2G	75	LYS
6	2G	98	ARG
6	2G	133	LEU
6	2G	135	LEU
6	2G	136	ARG
6	2G	140	ILE
6	2G	145	THR
6	2G	153	ARG
6	2G	159	VAL
6	2G	164	GLU
6	2G	167	GLU
7	2H	3	ARG
7	2H	15	VAL
7	2H	24	VAL
7	2H	33	LEU
7	2H	34	GLU
7	2H	41	MET
7	2H	49	VAL
7	2H	69	ARG
7	2H	71	LEU
7	2H	81	GLU
7	2H	88	LEU
7	2H	95	ARG
7	2H	98	LEU
7	2H	105	LEU

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Mol	Chain	Res	Type
7	2H	122	THR
7	2H	133	VAL
7	2H	136	ILE
7	2H	171	LEU
8	2I	38	LEU
8	2I	44	LEU
8	2I	47	LEU
8	2I	50	ARG
8	2I	54	GLN
8	2I	68	LEU
8	2I	75	LEU
8	2I	76	THR
8	2I	77	LEU
8	2I	92	VAL
8	2I	108	THR
8	2I	116	LEU
8	2I	123	LEU
8	2I	127	VAL
8	2I	140	LEU
9	2N	28	THR
9	2N	34	LEU
9	2N	48	MET
9	2N	62	VAL
9	2N	68	GLU
9	2N	71	ILE
9	2N	83	LYS
9	2N	87	LEU
9	2N	97	ARG
9	2N	99	LEU
9	2N	120	LEU
9	2N	131	GLN
9	2N	137	LYS
9	2N	139	GLU
10	2O	8	LEU
10	2O	10	VAL
10	2O	20	MET
10	2O	23	ARG
10	2O	24	VAL
10	2O	53	LYS
10	2O	98	VAL
10	2O	113	LYS
11	2P	21	ARG

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Mol	Chain	Res	Type
11	2P	55	ARG
11	2P	59	LEU
11	2P	95	VAL
11	2P	98	GLU
11	2P	99	LEU
11	2P	106	LEU
11	2P	112	LEU
11	2P	125	VAL
11	2P	135	LEU
11	2P	147	LEU
11	2P	148	LEU
12	2Q	1	MET
12	2Q	8	LYS
12	2Q	16	ARG
12	2Q	21	THR
12	2Q	45	GLN
12	2Q	48	GLU
12	2Q	55	VAL
12	2Q	56	ARG
12	2Q	60	ARG
12	2Q	75	THR
12	2Q	109	VAL
13	2R	18	LEU
13	2R	28	LEU
13	2R	29	LEU
13	2R	33	ARG
13	2R	36	THR
13	2R	44	LEU
13	2R	60	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
13	2R	114	VAL
14	2S	14	VAL
14	2S	20	ARG
14	2S	35	ILE
14	2S	49	VAL
14	2S	50	SER

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Mol	Chain	Res	Type
14	2S	52	SER
14	2S	67	ARG
14	2S	69	VAL
14	2S	71	ARG
14	2S	75	GLU
14	2S	76	LYS
14	2S	80	LEU
14	2S	93	LYS
14	2S	110	LEU
15	2T	6	LEU
15	2T	13	ARG
15	2T	23	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	49	VAL
15	2T	53	ARG
15	2T	78	LEU
15	2T	89	VAL
15	2T	96	ARG
15	2T	118	ARG
16	2U	8	VAL
16	2U	27	LEU
16	2U	31	SER
16	2U	36	ARG
16	2U	60	LEU
16	2U	74	LEU
16	2U	83	LEU
16	2U	89	GLU
16	2U	92	ARG
16	2U	95	LEU
16	2U	104	GLN
17	2V	6	LYS
17	2V	18	LEU
17	2V	21	ARG
17	2V	35	LEU
17	2V	38	LEU
17	2V	46	VAL
17	2V	51	VAL
17	2V	61	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL

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Mol	Chain	Res	Type
17	2V	95	LEU
17	2V	100	ARG
18	2W	11	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	51	LEU
18	2W	52	GLU
18	2W	67	ASP
18	2W	96	ILE
18	2W	100	THR
18	2W	107	LEU
19	2X	2	LYS
19	2X	33	LYS
19	2X	57	LEU
19	2X	66	LEU
19	2X	76	ARG
19	2X	90	GLU
20	2Y	8	LYS
20	2Y	43	ASN
20	2Y	57	GLN
20	2Y	67	LEU
20	2Y	70	SER
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	90	LEU
20	2Y	99	CYS
21	2Z	13	GLU
21	2Z	18	LEU
21	2Z	41	LEU
21	2Z	42	VAL
21	2Z	46	LYS
21	2Z	61	LEU
21	2Z	72	ARG
21	2Z	86	VAL
21	2Z	91	LEU
21	2Z	107	THR
21	2Z	131	ARG
21	2Z	138	GLU
21	2Z	150	LEU
21	2Z	156	LYS
21	2Z	161	VAL

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Mol	Chain	Res	Type
21	2Z	170	THR
21	2Z	171	ILE
21	2Z	182	LYS
21	2Z	190	GLU
21	2Z	193	GLU
21	2Z	199	LYS
22	20	19	LYS
22	20	20	ARG
22	20	70	GLN
23	21	4	VAL
23	21	21	ARG
23	21	32	LYS
23	21	40	ARG
23	21	51	VAL
23	21	52	ARG
23	21	80	LEU
23	21	83	GLU
23	21	85	LEU
23	21	95	LEU
24	22	32	LEU
24	22	40	SER
24	22	52	ASP
24	22	53	LEU
24	22	64	LEU
25	23	3	ARG
25	23	8	LEU
25	23	23	LEU
25	23	31	LEU
25	23	44	ARG
25	23	54	VAL
26	24	3	GLU
26	24	8	LYS
26	24	34	GLU
26	24	46	GLN
26	24	48	ARG
26	24	50	VAL
26	24	58	ARG
26	24	60	GLN
26	24	61	ARG
26	24	63	TYR
26	24	67	TYR
27	25	6	VAL

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Mol	Chain	Res	Type
27	25	29	THR
27	25	35	GLU
27	25	40	LYS
27	25	48	GLU
27	25	58	LEU
27	25	59	GLU
28	26	14	THR
28	26	35	GLU
28	26	38	LYS
28	26	47	THR
28	26	48	VAL
28	26	52	VAL
29	27	9	ARG
29	27	43	THR
29	27	46	VAL
30	28	14	VAL
30	28	23	VAL
30	28	26	LYS
30	28	30	ARG
30	28	32	LEU
31	29	17	ILE
33	2b	8	LYS
33	2b	12	GLU
33	2b	16	HIS
33	2b	17	PHE
33	2b	49	GLU
33	2b	63	MET
33	2b	81	VAL
33	2b	95	GLN
33	2b	96	ARG
33	2b	110	GLN
33	2b	114	ARG
33	2b	115	LEU
33	2b	118	LEU
33	2b	119	GLU
33	2b	127	ILE
33	2b	135	GLN
33	2b	136	VAL
33	2b	144	ARG
33	2b	150	SER
33	2b	154	LEU
33	2b	157	ARG

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Mol	Chain	Res	Type
33	2b	158	LEU
33	2b	163	PHE
33	2b	179	LYS
33	2b	185	ILE
33	2b	187	LEU
33	2b	196	LEU
33	2b	200	ILE
33	2b	208	ILE
33	2b	210	SER
33	2b	215	LEU
33	2b	217	ARG
33	2b	221	LEU
33	2b	222	ILE
33	2b	224	GLN
33	2b	229	VAL
33	2b	230	VAL
34	2c	3	ASN
34	2c	45	LYS
34	2c	77	ILE
34	2c	102	ASN
34	2c	104	GLN
34	2c	105	GLU
34	2c	111	LEU
34	2c	115	LEU
34	2c	131	ARG
34	2c	132	ARG
34	2c	140	ARG
34	2c	152	ILE
34	2c	162	GLN
34	2c	178	LEU
35	2d	8	VAL
35	2d	18	LYS
35	2d	28	SER
35	2d	34	GLU
35	2d	50	ARG
35	2d	58	LEU
35	2d	65	ARG
35	2d	96	LEU
35	2d	108	LEU
35	2d	112	VAL
35	2d	122	ARG
35	2d	135	LEU

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Mol	Chain	Res	Type
35	2d	153	ARG
35	2d	169	LYS
35	2d	194	LEU
35	2d	204	ILE
36	2e	8	GLU
36	2e	10	MET
36	2e	31	LEU
36	2e	34	VAL
36	2e	41	VAL
36	2e	47	LYS
36	2e	57	LYS
36	2e	69	VAL
36	2e	72	GLN
36	2e	79	GLU
36	2e	82	VAL
36	2e	91	LEU
36	2e	126	ARG
36	2e	143	ARG
36	2e	150	ARG
37	2f	28	ARG
37	2f	40	VAL
37	2f	46	ARG
37	2f	61	LEU
37	2f	63	TYR
37	2f	70	ASP
37	2f	72	VAL
37	2f	75	LEU
37	2f	82	ARG
38	2g	10	ARG
38	2g	12	LEU
38	2g	52	GLU
38	2g	57	GLU
38	2g	75	VAL
38	2g	76	ARG
38	2g	78	ARG
38	2g	104	LEU
38	2g	113	GLU
38	2g	114	ARG
38	2g	115	ARG
38	2g	137	LYS
38	2g	143	ARG
38	2g	144	MET

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Mol	Chain	Res	Type
38	2g	155	ARG
39	2h	2	LEU
39	2h	26	VAL
39	2h	38	ILE
39	2h	39	LEU
39	2h	63	LEU
39	2h	68	ARG
39	2h	78	GLN
39	2h	84	ARG
39	2h	91	ARG
39	2h	97	VAL
39	2h	112	LEU
39	2h	133	LEU
39	2h	137	VAL
40	2i	3	GLN
40	2i	23	ASN
40	2i	27	THR
40	2i	31	GLN
40	2i	60	ASP
40	2i	64	THR
40	2i	65	VAL
40	2i	92	TYR
40	2i	102	LEU
40	2i	108	VAL
40	2i	113	LYS
41	2j	30	SER
41	2j	38	ILE
41	2j	44	VAL
41	2j	57	LYS
41	2j	74	ILE
41	2j	92	THR
41	2j	94	VAL
42	2k	48	ILE
42	2k	70	LYS
42	2k	83	ILE
42	2k	84	VAL
42	2k	96	ARG
42	2k	114	VAL
42	2k	117	ASN
42	2k	126	ARG
43	2l	27	LEU
43	2l	41	ARG

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Mol	Chain	Res	Type
43	2l	55	VAL
43	2l	83	VAL
44	2m	17	VAL
44	2m	19	LEU
44	2m	27	LYS
44	2m	32	GLU
44	2m	60	VAL
44	2m	63	THR
44	2m	70	LEU
44	2m	94	ARG
44	2m	98	VAL
44	2m	110	ARG
44	2m	116	THR
45	2n	3	ARG
45	2n	6	LEU
45	2n	12	ARG
45	2n	18	VAL
45	2n	33	VAL
45	2n	50	LYS
45	2n	57	ARG
46	2o	3	ILE
46	2o	26	GLU
46	2o	39	LEU
46	2o	41	GLU
46	2o	48	LYS
46	2o	54	ARG
46	2o	66	LEU
46	2o	68	ARG
46	2o	71	GLN
46	2o	88	ARG
47	2p	2	VAL
47	2p	8	ARG
47	2p	20	VAL
47	2p	21	VAL
47	2p	25	ARG
47	2p	28	ARG
47	2p	60	LEU
47	2p	62	VAL
47	2p	67	THR
47	2p	69	THR
47	2p	71	ARG
48	2q	6	LEU

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Mol	Chain	Res	Type
48	2q	9	VAL
48	2q	36	ILE
48	2q	60	ILE
48	2q	68	ARG
48	2q	72	ARG
48	2q	74	LEU
49	2r	21	LYS
49	2r	25	THR
49	2r	26	LEU
49	2r	31	LEU
49	2r	32	ARG
49	2r	37	VAL
49	2r	58	LEU
49	2r	64	ARG
49	2r	76	LEU
49	2r	85	LEU
50	2s	35	SER
50	2s	41	VAL
50	2s	48	THR
50	2s	56	GLN
50	2s	77	THR
50	2s	78	ARG
50	2s	79	THR
51	2t	24	LEU
51	2t	30	LYS
51	2t	46	GLU
51	2t	56	MET
51	2t	84	LEU
51	2t	90	GLN
51	2t	93	GLU
51	2t	99	LEU
51	2t	100	ILE
52	2u	7	ARG
52	2u	10	ARG
53	2y	6	THR
53	2y	9	GLN
53	2y	12	ILE
53	2y	13	THR
53	2y	16	ILE
53	2y	24	LEU
53	2y	41	LEU
53	2y	46	GLN

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Mol	Chain	Res	Type
53	2y	49	VAL
53	2y	56	THR
53	2y	77	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (172) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	164	GLN
3	1D	253	GLN
4	1E	85	ASN
4	1E	143	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	169	ASN
5	1F	203	GLN
6	1G	26	GLN
6	1G	108	ASN
6	1G	132	ASN
8	1I	43	ASN
8	1I	54	GLN
9	1N	94	HIS
11	1P	38	GLN
12	1Q	45	GLN
13	1R	71	GLN
15	1T	43	GLN
15	1T	58	ASN
15	1T	84	GLN
15	1T	123	GLN
16	1U	81	HIS
16	1U	94	ASN
16	1U	117	GLN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	43	ASN
20	1Y	92	ASN
21	1Z	118	GLN
22	10	35	ASN
25	13	32	GLN
26	14	47	GLN
28	16	20	ASN
31	19	36	GLN

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Mol	Chain	Res	Type
33	1b	95	GLN
33	1b	224	GLN
34	1c	6	HIS
34	1c	28	GLN
34	1c	102	ASN
34	1c	123	GLN
34	1c	136	GLN
35	1d	77	ASN
35	1d	123	HIS
35	1d	129	ASN
35	1d	160	GLN
36	1e	20	GLN
36	1e	38	GLN
36	1e	56	GLN
36	1e	141	GLN
37	1f	73	ASN
37	1f	100	ASN
38	1g	13	GLN
38	1g	28	ASN
38	1g	56	GLN
38	1g	86	GLN
38	1g	106	GLN
38	1g	110	GLN
40	1i	23	ASN
40	1i	34	ASN
40	1i	124	GLN
41	1j	56	HIS
42	1k	93	GLN
42	1k	104	GLN
43	1l	8	ASN
43	1l	99	HIS
44	1m	77	ASN
44	1m	92	HIS
46	1o	28	GLN
47	1p	13	HIS
47	1p	16	HIS
47	1p	76	GLN
48	1q	16	GLN
50	1s	56	GLN
50	1s	57	HIS
50	1s	65	ASN
50	1s	69	HIS

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Mol	Chain	Res	Type
50	1s	83	HIS
51	1t	42	GLN
51	1t	75	ASN
53	1y	38	HIS
53	1y	89	GLN
3	2D	126	GLN
3	2D	164	GLN
3	2D	253	GLN
4	2E	85	ASN
5	2F	69	HIS
5	2F	169	ASN
5	2F	203	GLN
6	2G	26	GLN
6	2G	132	ASN
7	2H	74	ASN
8	2I	43	ASN
8	2I	54	GLN
9	2N	56	ASN
11	2P	27	HIS
11	2P	38	GLN
11	2P	70	GLN
12	2Q	141	GLN
13	2R	91	GLN
15	2T	58	ASN
15	2T	123	GLN
16	2U	94	ASN
16	2U	104	GLN
17	2V	64	HIS
17	2V	80	GLN
18	2W	60	ASN
19	2X	31	HIS
19	2X	41	ASN
19	2X	82	GLN
20	2Y	6	HIS
21	2Z	50	GLN
21	2Z	75	ASN
21	2Z	151	HIS
24	22	9	GLN
24	22	56	GLN
25	23	32	GLN
26	24	40	HIS
28	26	20	ASN

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Mol	Chain	Res	Type
31	29	36	GLN
33	2b	19	HIS
33	2b	76	GLN
33	2b	95	GLN
33	2b	212	GLN
34	2c	6	HIS
34	2c	28	GLN
34	2c	37	GLN
34	2c	123	GLN
34	2c	136	GLN
34	2c	176	HIS
34	2c	181	ASN
35	2d	77	ASN
35	2d	123	HIS
35	2d	125	HIS
35	2d	161	ASN
36	2e	56	GLN
36	2e	78	HIS
36	2e	141	GLN
37	2f	100	ASN
38	2g	28	ASN
38	2g	56	GLN
38	2g	64	GLN
38	2g	148	ASN
39	2h	78	GLN
40	2i	23	ASN
40	2i	31	GLN
40	2i	73	GLN
40	2i	89	ASN
40	2i	124	GLN
41	2j	68	HIS
41	2j	84	GLN
42	2k	93	GLN
42	2k	104	GLN
43	2l	99	HIS
44	2m	12	ASN
44	2m	77	ASN
46	2o	28	GLN
46	2o	62	GLN
46	2o	71	GLN
47	2p	16	HIS
48	2q	16	GLN

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Mol	Chain	Res	Type
50	2s	14	HIS
50	2s	23	ASN
50	2s	56	GLN
50	2s	69	HIS
50	2s	83	HIS
51	2t	9	ASN
51	2t	18	GLN
53	2y	18	GLN
53	2y	31	GLN
53	2y	36	ASN
53	2y	46	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	410 (14%)	41 (1%)
1	2A	2858/2915 (98%)	485 (16%)	41 (1%)
2	1B	119/121 (98%)	10 (8%)	0
2	2B	119/121 (98%)	14 (11%)	0
32	1a	1497/1521 (98%)	231 (15%)	0
32	2a	1501/1521 (98%)	252 (16%)	0
All	All	8959/9114 (98%)	1402 (15%)	82 (0%)

All (1402) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	13	A
1	1A	34	C
1	1A	35	G
1	1A	45	C
1	1A	70	A
1	1A	73	A
1	1A	74	G
1	1A	94	G
1	1A	116	A
1	1A	117	A
1	1A	118	U
1	1A	155	C
1	1A	162	G
1	1A	170	A

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Mol	Chain	Res	Type
1	1A	171	A
1	1A	185	A
1	1A	186	A
1	1A	194	G
1	1A	204	G
1	1A	205	A
1	1A	211	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	275	C
1	1A	279	G
1	1A	288	U
1	1A	289	G
1	1A	295	C
1	1A	297	C
1	1A	299	G
1	1A	303	C
1	1A	307	A
1	1A	335	A
1	1A	354	A
1	1A	376	G
1	1A	387	G
1	1A	389	G
1	1A	407	U
1	1A	413	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	477	C
1	1A	480	A
1	1A	482	C
1	1A	483	A
1	1A	507	G
1	1A	530	A

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Mol	Chain	Res	Type
1	1A	534	C
1	1A	553	A
1	1A	554	A
1	1A	555	G
1	1A	556	C
1	1A	557	A
1	1A	558	G
1	1A	569	G
1	1A	573	G
1	1A	586	G
1	1A	596	G
1	1A	598	A
1	1A	609	A
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	641	G
1	1A	642	G
1	1A	652	A
1	1A	662	A
1	1A	670	C
1	1A	671	A
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	764	G
1	1A	777	C
1	1A	793	A
1	1A	794	U
1	1A	811	A
1	1A	812	G
1	1A	821	A
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	831	A
1	1A	832	G
1	1A	837	C
1	1A	839	G

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Mol	Chain	Res	Type
1	1A	852	G
1	1A	859	C
1	1A	874	U
1	1A	875	U
1	1A	906	G
1	1A	913	A
1	1A	927	G
1	1A	929	G
1	1A	932	C
1	1A	933	C
1	1A	935	C
1	1A	936	C
1	1A	937	A
1	1A	938	G
1	1A	940	C
1	1A	942	A
1	1A	945	A
1	1A	956	A
1	1A	977	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	1029	A
1	1A	1042	A
1	1A	1058	U
1	1A	1059	C
1	1A	1068	G
1	1A	1072	U
1	1A	1079	U
1	1A	1085	G
1	1A	1088	G
1	1A	1089	C
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A
1	1A	1100	A
1	1A	1104	G
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	1111	U
1	1A	1114	G
1	1A	1116	A
1	1A	1117	G
1	1A	1119	A
1	1A	1121	C
1	1A	1122	C
1	1A	1123	A
1	1A	1124	U
1	1A	1126	C
1	1A	1129	U
1	1A	1130	A
1	1A	1134	A
1	1A	1136	U
1	1A	1142	A
1	1A	1143	U
1	1A	1152	G
1	1A	1155	C
1	1A	1156	G
1	1A	1158	G
1	1A	1162	C
1	1A	1174	A
1	1A	1175	A
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	1255	A
1	1A	1256	U
1	1A	1263	C
1	1A	1299	A
1	1A	1302	G
1	1A	1317	G
1	1A	1318	A

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Mol	Chain	Res	Type
1	1A	1319	U
1	1A	1346	U
1	1A	1347	A
1	1A	1349	G
1	1A	1365	G
1	1A	1398	U
1	1A	1405	A
1	1A	1411	A
1	1A	1416	C
1	1A	1426	G
1	1A	1430	A
1	1A	1431	G
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	1502	G
1	1A	1514	C
1	1A	1518	A
1	1A	1529	G
1	1A	1533	G
1	1A	1539	C
1	1A	1552	C
1	1A	1554	A
1	1A	1555	C
1	1A	1556	A
1	1A	1571	G
1	1A	1578	C
1	1A	1589	A
1	1A	1590	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
1	1A	1631	C
1	1A	1632	A

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Mol	Chain	Res	Type
1	1A	1654	A
1	1A	1655	A
1	1A	1656	A
1	1A	1695	C
1	1A	1700	G
1	1A	1701	A
1	1A	1721	G
1	1A	1747	A
1	1A	1748	A
1	1A	1762	G
1	1A	1763	G
1	1A	1767	A
1	1A	1768	U
1	1A	1787	G
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1811	A
1	1A	1813	C
1	1A	1822	A
1	1A	1831	C
1	1A	1832	G
1	1A	1843	A
1	1A	1847	G
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	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	2054	G
1	1A	2055	A
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	2102	G
1	1A	2121	U
1	1A	2125	C
1	1A	2126	G
1	1A	2127	C
1	1A	2129	C
1	1A	2130	C
1	1A	2132	G
1	1A	2134	G
1	1A	2138	G
1	1A	2139	A
1	1A	2140	U
1	1A	2141	A
1	1A	2142	G
1	1A	2144	U
1	1A	2145	G
1	1A	2148	A
1	1A	2149	G
1	1A	2153	G
1	1A	2154	U
1	1A	2155	G
1	1A	2156	A
1	1A	2157	A
1	1A	2160	C
1	1A	2164	C
1	1A	2168	C

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Mol	Chain	Res	Type
1	1A	2170	G
1	1A	2175	G
1	1A	2180	A
1	1A	2181	G
1	1A	2183	C
1	1A	2188	G
1	1A	2192	A
1	1A	2195	A
1	1A	2196	C
1	1A	2206	G
1	1A	2208	G
1	1A	2209	G
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	2295	C
1	1A	2299	A
1	1A	2301	G
1	1A	2317	A
1	1A	2320	G
1	1A	2332	A
1	1A	2337	G
1	1A	2338	C
1	1A	2346	G
1	1A	2359	C
1	1A	2362	C
1	1A	2395	G
1	1A	2397	C
1	1A	2405	A
1	1A	2418	U
1	1A	2419	G
1	1A	2426	G
1	1A	2434	A
1	1A	2435	U
1	1A	2436	C

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Mol	Chain	Res	Type
1	1A	2437	A
1	1A	2440	G
1	1A	2441	G
1	1A	2442	A
1	1A	2443	U
1	1A	2446	A
1	1A	2447	A
1	1A	2451	A
1	1A	2452	C
1	1A	2453	C
1	1A	2460	A
1	1A	2480	G
1	1A	2481	A
1	1A	2482	G
1	1A	2488	A
1	1A	2490	A
1	1A	2514	G
1	1A	2517	G
1	1A	2518	U
1	1A	2530	A
1	1A	2541	G
1	1A	2547	G
1	1A	2566	U
1	1A	2578	A
1	1A	2579	G
1	1A	2585	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	2682	A
1	1A	2701	U
1	1A	2702	C
1	1A	2714	U
1	1A	2715	C
1	1A	2725	A
1	1A	2726	A
1	1A	2727	G

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Mol	Chain	Res	Type
1	1A	2739	U
1	1A	2746	A
1	1A	2771	A
1	1A	2778	A
1	1A	2779	G
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	2849	G
1	1A	2882	G
1	1A	2902	G
1	1A	2903	G
2	1B	2	C
2	1B	7	G
2	1B	13	A
2	1B	45	A
2	1B	53	A
2	1B	56	G
2	1B	73	A
2	1B	84	C
2	1B	110	G
2	1B	116	G
32	1a	6	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	78	G
32	1a	79	G
32	1a	96	U
32	1a	99	U
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C

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Mol	Chain	Res	Type
32	1a	131	C
32	1a	144	G
32	1a	156	G
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(D)	C
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	220	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	352	C
32	1a	353	A
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	383	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	423	G
32	1a	424	G
32	1a	429	U

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Mol	Chain	Res	Type
32	1a	439	A
32	1a	442	C
32	1a	446	G
32	1a	452	A
32	1a	456	C
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	475	G
32	1a	477	A
32	1a	484	G
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	550	G
32	1a	559	A
32	1a	561	U
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	607	A
32	1a	619	U
32	1a	630	G
32	1a	631	G
32	1a	632	A
32	1a	651	C
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	687	A
32	1a	688	G

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Mol	Chain	Res	Type
32	1a	723	U
32	1a	731	G
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	839	U
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	913	A
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	968	A
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	998	G
32	1a	999	C
32	1a	1001(A)	G
32	1a	1006	C
32	1a	1007	C
32	1a	1008	C
32	1a	1009	G
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G

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Mol	Chain	Res	Type
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	1030(B)	C
32	1a	1030(D)	A
32	1a	1032	G
32	1a	1034	G
32	1a	1036	G
32	1a	1037	C
32	1a	1039	C
32	1a	1040	U
32	1a	1042	G
32	1a	1044	A
32	1a	1053	G
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1070	U
32	1a	1092	A
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1126	U
32	1a	1127	G
32	1a	1130	A
32	1a	1132	C
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1140	C
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1162	C
32	1a	1168	A
32	1a	1183	A

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Mol	Chain	Res	Type
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1212	U
32	1a	1213	A
32	1a	1224	G
32	1a	1227	A
32	1a	1238	A
32	1a	1245	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	1293	G
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
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	1379	G
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1456	G
32	1a	1493	A
32	1a	1499	A
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G

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Mol	Chain	Res	Type
32	1a	1506	U
32	1a	1517	G
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	8	A
1	2A	10	G
1	2A	11	G
1	2A	12	U
1	2A	14	A
1	2A	15	G
1	2A	34	C
1	2A	45	C
1	2A	61	G
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	157	U
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	271(K)	U
1	2A	271(L)	U

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Mol	Chain	Res	Type
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(A)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	311	A
1	2A	317	G
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	370	G
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	428	A
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	496	G
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	573	G
1	2A	575	A

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Mol	Chain	Res	Type
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	610	G
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	620	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(U)	G
1	2A	653	A
1	2A	668	G
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	765	G
1	2A	774	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	790	C
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	867	C
1	2A	877	U

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Mol	Chain	Res	Type
1	2A	880	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	895	U
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	915	C
1	2A	917	A
1	2A	932	G
1	2A	936	C
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	1012	U
1	2A	1013	C
1	2A	1015	G
1	2A	1017	G
1	2A	1033	U
1	2A	1035	U
1	2A	1041	C
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1048	A
1	2A	1052	C
1	2A	1053	C
1	2A	1054	A
1	2A	1058	G
1	2A	1060	U

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Mol	Chain	Res	Type
1	2A	1063	G
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1069	A
1	2A	1070	A
1	2A	1071	G
1	2A	1072	C
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1080	C
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	1094	U
1	2A	1095	A
1	2A	1096	A
1	2A	1098	A
1	2A	1108	U
1	2A	1109	C
1	2A	1110	G
1	2A	1112	G
1	2A	1116	C
1	2A	1117	G
1	2A	1128	A
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1144	G

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Mol	Chain	Res	Type
1	2A	1171	G
1	2A	1181	C
1	2A	1188	U
1	2A	1210	A
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1229	G
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	1303	G
1	2A	1306	C
1	2A	1308	A
1	2A	1314	C
1	2A	1321	A
1	2A	1342	A
1	2A	1345	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1410	G
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	1451	C
1	2A	1455	G
1	2A	1459	G
1	2A	1467	C

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Mol	Chain	Res	Type
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
1	2A	1494	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1532	C
1	2A	1542	A
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1610	A
1	2A	1640	C
1	2A	1647	G
1	2A	1648	C
1	2A	1674	G
1	2A	1700	A
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
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	1817	G

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Mol	Chain	Res	Type
1	2A	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1858	G
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1914	C
1	2A	1918	A
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	1975	G
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2049	G
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	2098	U
1	2A	2099	U
1	2A	2100	G
1	2A	2103	C
1	2A	2104	G

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Mol	Chain	Res	Type
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2115	G
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2121	G
1	2A	2123	G
1	2A	2124	G
1	2A	2126	A
1	2A	2127	G
1	2A	2128	C
1	2A	2129	C
1	2A	2130	U
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2141	G
1	2A	2145	C
1	2A	2146	C
1	2A	2150	U
1	2A	2151	G
1	2A	2154	G
1	2A	2157	G
1	2A	2158	A
1	2A	2159	G
1	2A	2160	G
1	2A	2161	C
1	2A	2163	C
1	2A	2164	C
1	2A	2165	G
1	2A	2167	U
1	2A	2172	U
1	2A	2173	A

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Mol	Chain	Res	Type
1	2A	2174	C
1	2A	2177	C
1	2A	2178	C
1	2A	2180	U
1	2A	2181	G
1	2A	2183	C
1	2A	2184	G
1	2A	2186	G
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
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	2287	A
1	2A	2289	G
1	2A	2293	C
1	2A	2305	A
1	2A	2308	G
1	2A	2309	A
1	2A	2311	A
1	2A	2312	U
1	2A	2313	C
1	2A	2319	G
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	2343	C
1	2A	2347	C
1	2A	2350	C

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Mol	Chain	Res	Type
1	2A	2354	G
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U
1	2A	2407	G
1	2A	2410	G
1	2A	2422	A
1	2A	2425	A
1	2A	2428	G
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2440	C
1	2A	2441	C
1	2A	2448	A
1	2A	2468	G
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2498	C
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2529	G
1	2A	2535	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2585	U
1	2A	2602	A
1	2A	2603	G
1	2A	2611	U
1	2A	2612	C
1	2A	2615	U
1	2A	2630	G
1	2A	2654	A
1	2A	2663	G

Continued on next page...

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Mol	Chain	Res	Type
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2744	G
1	2A	2751	G
1	2A	2757	A
1	2A	2759	G
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2769	C
1	2A	2778	A
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2836	U
1	2A	2839	G
1	2A	2872	G
1	2A	2880	C
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	7	G
2	2B	8	U
2	2B	12	C
2	2B	13	A
2	2B	23	G
2	2B	33	G
2	2B	51	G
2	2B	56	G
2	2B	73	A
2	2B	84	C
2	2B	108	U
2	2B	110	G

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Mol	Chain	Res	Type
2	2B	116	G
32	2a	5	U
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	50	A
32	2a	51	A
32	2a	52	G
32	2a	61	G
32	2a	66	G
32	2a	78	G
32	2a	89	C
32	2a	97	G
32	2a	115	G
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	151	A
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	269	C
32	2a	289	G
32	2a	298	A
32	2a	321	A
32	2a	328	C

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Mol	Chain	Res	Type
32	2a	332	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	381	C
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	446	G
32	2a	452	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	476	G
32	2a	482	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	528	C
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	560	U

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Mol	Chain	Res	Type
32	2a	561	U
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	597	G
32	2a	630	G
32	2a	631	G
32	2a	632	A
32	2a	653	A
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	707	C
32	2a	723	U
32	2a	724	G
32	2a	728	A
32	2a	731	G
32	2a	749	C
32	2a	753	A
32	2a	755	G
32	2a	773	G
32	2a	774	G
32	2a	777	A
32	2a	785	G
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	836	G
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	859	A
32	2a	875	C
32	2a	914	A

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Mol	Chain	Res	Type
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	935	A
32	2a	960	U
32	2a	961	U
32	2a	966	M2G
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	984	C
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	995	C
32	2a	1001	A
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1016	A
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	1033	G
32	2a	1041	A
32	2a	1044	A

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Mol	Chain	Res	Type
32	2a	1047	G
32	2a	1054	C
32	2a	1055	A
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	1122	U
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	1138	G
32	2a	1139	G
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1162	C
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
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	1248	A
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G

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Mol	Chain	Res	Type
32	2a	1259	C
32	2a	1260	C
32	2a	1270	C
32	2a	1272	G
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1281	U
32	2a	1282	C
32	2a	1286	A
32	2a	1287	A
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1317	C
32	2a	1320	C
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1370	G
32	2a	1375	A
32	2a	1380	U
32	2a	1397	C
32	2a	1398	A
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1456	G
32	2a	1462	G
32	2a	1492	A
32	2a	1497	G
32	2a	1499	A
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G

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Mol	Chain	Res	Type
32	2a	1530	G

All (82) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	34	C
1	1A	115	G
1	1A	185	A
1	1A	188	A
1	1A	302	A
1	1A	509	A
1	1A	596	G
1	1A	793	A
1	1A	811	A
1	1A	821	A
1	1A	874	U
1	1A	913	A
1	1A	935	C
1	1A	941	U
1	1A	1003	U
1	1A	1019	G
1	1A	1065	U
1	1A	1067	A
1	1A	1093	G
1	1A	1188	A
1	1A	1201	A
1	1A	1220	U
1	1A	1221	G
1	1A	1255	A
1	1A	1346	U
1	1A	1425	A
1	1A	1577	C
1	1A	1654	A
1	1A	1700	G
1	1A	1793	A
1	1A	2019	G
1	1A	2133	C
1	1A	2148	A
1	1A	2418	U
1	1A	2434	A
1	1A	2442	A
1	1A	2451	A

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Mol	Chain	Res	Type
1	1A	2614	A
1	1A	2623	U
1	1A	2701	U
1	1A	2902	G
1	2A	9	U
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	774	A
1	2A	827	U
1	2A	840	C
1	2A	856	C
1	2A	900	A
1	2A	974	G
1	2A	1047	G
1	2A	1053	C
1	2A	1057	A
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1076	C
1	2A	1111	A
1	2A	1210	A
1	2A	1379	A
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G
1	2A	1530	C
1	2A	1608	A
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2321	G
1	2A	2406	U
1	2A	2439	A
1	2A	2601	C
1	2A	2602	A

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Mol	Chain	Res	Type
1	2A	2689	U
1	2A	2726	U
1	2A	2756	U

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

48 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	PSU	1a	516	54,32	18,21,22	1.40	2 (11%)	21,30,33	2.01	5 (23%)
32	UR3	1a	1498	32	19,22,23	0.97	0	26,32,35	1.82	3 (11%)
32	5MC	1a	967	32	19,22,23	1.67	3 (15%)	26,32,35	1.16	3 (11%)
1	PSU	2A	1917	1	18,21,22	1.35	2 (11%)	21,30,33	2.12	3 (14%)
32	MA6	1a	1519	32	23,26,27	1.56	4 (17%)	33,38,41	2.30	10 (30%)
32	2MG	2a	1207	32	23,26,27	1.22	3 (13%)	33,38,41	2.17	8 (24%)
1	2MA	2A	2503	54,1	22,25,26	1.49	5 (22%)	32,37,40	2.37	9 (28%)
32	2MG	1a	1207	54,32	23,26,27	1.24	2 (8%)	33,38,41	2.52	12 (36%)
1	4OC	1A	1942	54,1	19,22,24	0.82	0	25,31,35	0.94	1 (4%)
1	5MU	2A	1915	1	19,22,23	1.51	4 (21%)	27,32,35	2.16	8 (29%)
32	5MC	2a	1404	32	19,22,23	1.86	3 (15%)	26,32,35	1.31	4 (15%)
1	5MC	2A	1962	54,1	19,22,23	1.56	3 (15%)	26,32,35	1.28	3 (11%)
32	M2G	1a	966	32	24,27,28	1.32	4 (16%)	33,40,43	1.85	5 (15%)
32	5MC	1a	1407	32	19,22,23	1.86	3 (15%)	26,32,35	1.27	3 (11%)
1	PSU	1A	2617	1	18,21,22	1.44	3 (16%)	21,30,33	1.96	4 (19%)
32	MA6	2a	1519	32	23,26,27	1.61	5 (21%)	33,38,41	2.38	13 (39%)
1	5MC	1A	1984	54,1	19,22,23	1.57	2 (10%)	26,32,35	1.46	4 (15%)
1	OMG	2A	2251	54,1	23,26,27	1.14	2 (8%)	32,38,41	2.00	6 (18%)
32	M2G	2a	966	54,32	24,27,28	1.24	3 (12%)	33,40,43	1.88	6 (18%)
32	4OC	1a	1402	32	20,23,24	0.74	1 (5%)	25,32,35	0.96	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MU	2A	1939	54,1	19,22,23	1.35	5 (26%)	27,32,35	2.51	7 (25%)
43	0TD	2l	92	43	8,9,10	4.87	2 (25%)	6,11,13	2.22	2 (33%)
1	5MU	1A	1937	54,1	19,22,23	1.46	5 (26%)	27,32,35	2.28	8 (29%)
1	PSU	1A	1939	1	18,21,22	1.36	3 (16%)	21,30,33	1.88	4 (19%)
32	PSU	2a	516	54,32	18,21,22	1.30	2 (11%)	21,30,33	2.19	5 (23%)
32	5MC	2a	967	32	19,22,23	1.88	3 (15%)	26,32,35	1.15	3 (11%)
32	UR3	2a	1498	54,32	19,22,23	0.96	1 (5%)	26,32,35	1.72	3 (11%)
1	5MC	2A	1942	1	19,22,23	1.75	3 (15%)	26,32,35	1.27	2 (7%)
32	5MC	1a	1400	32	19,22,23	1.80	3 (15%)	26,32,35	1.29	2 (7%)
32	MA6	2a	1518	32	23,26,27	1.57	4 (17%)	33,38,41	2.27	12 (36%)
1	2MA	1A	2515	54,1	22,25,26	1.48	5 (22%)	32,37,40	2.48	9 (28%)
32	MA6	1a	1518	32	23,26,27	1.59	5 (21%)	33,38,41	2.25	13 (39%)
43	0TD	1l	92	43	8,9,10	8.01	6 (75%)	6,11,13	4.26	2 (33%)
1	PSU	2A	2605	1	18,21,22	1.35	3 (16%)	21,30,33	1.97	5 (23%)
1	5MC	1A	1964	54,1	19,22,23	1.55	3 (15%)	26,32,35	1.10	2 (7%)
32	5MC	2a	1407	32	19,22,23	1.58	3 (15%)	26,32,35	1.20	3 (11%)
1	OMG	1A	2263	54,1	23,26,27	1.27	3 (13%)	32,38,41	2.03	6 (18%)
32	7MG	2a	527	32	23,26,27	1.43	4 (17%)	27,39,42	2.56	5 (18%)
32	7MG	1a	527	54,32	23,26,27	1.31	3 (13%)	27,39,42	2.52	6 (22%)
32	4OC	2a	1402	32	20,23,24	0.74	0	25,32,35	0.95	1 (4%)
1	4OC	2A	1920	1	19,22,24	0.82	0	25,31,35	0.99	1 (4%)
1	PSU	1A	1933	1	18,21,22	1.35	2 (11%)	21,30,33	1.97	4 (19%)
32	5MC	2a	1400	32	19,22,23	1.79	3 (15%)	26,32,35	1.15	3 (11%)
1	PSU	2A	1911	1	18,21,22	1.44	2 (11%)	21,30,33	2.00	4 (19%)
1	5MU	1A	1961	1	19,22,23	1.33	4 (21%)	27,32,35	2.30	7 (25%)
32	5MC	1a	1404	32	19,22,23	1.66	3 (15%)	26,32,35	1.20	3 (11%)
1	2MU	1A	2564	54,1	19,22,24	1.32	3 (15%)	25,31,36	1.87	6 (24%)
1	2MU	2A	2552	54,1	19,22,24	1.32	3 (15%)	25,31,36	1.95	5 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	PSU	1a	516	54,32	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
1	2MA	2A	2503	54,1	-	0/7/25/26	0/3/3/3
32	2MG	1a	1207	54,32	-	0/9/27/28	0/3/3/3
1	4OC	1A	1942	54,1	-	1/9/27/30	0/2/2/2
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	54,1	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	2617	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	5/11/29/30	0/3/3/3
1	5MC	1A	1984	54,1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	54,1	-	1/9/27/28	0/3/3/3
32	M2G	2a	966	54,32	-	0/11/29/30	0/3/3/3
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
1	5MU	2A	1939	54,1	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	3/7/12/14	-
1	5MU	1A	1937	54,1	-	2/7/25/26	0/2/2/2
1	PSU	1A	1939	1	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	54,32	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	54,32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	1/11/29/30	0/3/3/3
1	2MA	1A	2515	54,1	-	1/7/25/26	0/3/3/3
32	MA6	1a	1518	32	-	3/11/29/30	0/3/3/3
43	0TD	1l	92	43	-	2/7/12/14	-
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1964	54,1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	OMG	1A	2263	54,1	-	1/9/27/28	0/3/3/3
32	7MG	2a	527	32	-	0/7/37/38	0/3/3/3
32	7MG	1a	527	54,32	-	2/7/37/38	0/3/3/3
32	4OC	2a	1402	32	-	1/9/29/30	0/2/2/2
1	4OC	2A	1920	1	-	0/9/27/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1961	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	2MU	1A	2564	54,1	-	0/9/27/28	0/2/2/2
1	2MU	2A	2552	54,1	-	0/9/27/28	0/2/2/2

All (140) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-17.14	1.65	1.82
43	1l	92	0TD	CB-CA	-13.64	1.50	1.54
43	2l	92	0TD	CB-SB	-12.72	1.69	1.82
32	2a	967	5MC	C5-C4	7.09	1.49	1.44
32	2a	1404	5MC	C5-C4	6.91	1.49	1.44
32	1a	1407	5MC	C5-C4	6.87	1.49	1.44
32	2a	1400	5MC	C5-C4	6.64	1.49	1.44
1	2A	1942	5MC	C5-C4	6.44	1.49	1.44
32	1a	1400	5MC	C5-C4	6.43	1.49	1.44
32	1a	967	5MC	C5-C4	6.01	1.48	1.44
32	1a	1404	5MC	C5-C4	5.97	1.48	1.44
32	2a	1407	5MC	C5-C4	5.61	1.48	1.44
1	1A	1984	5MC	C5-C4	5.52	1.48	1.44
1	2A	1962	5MC	C5-C4	5.47	1.48	1.44
1	1A	1964	5MC	C5-C4	5.19	1.48	1.44
32	2a	1518	MA6	C5-C4	5.02	1.48	1.39
32	2a	1519	MA6	C5-C4	4.93	1.47	1.39
32	1a	1518	MA6	C5-C4	4.80	1.47	1.39
32	1a	1519	MA6	C5-C4	4.72	1.47	1.39
1	2A	2503	2MA	C5-C4	4.37	1.46	1.39
43	2l	92	0TD	CB-CA	-4.25	1.53	1.54
1	2A	1911	PSU	C6-C5	3.86	1.39	1.35
32	1a	516	PSU	C6-C5	3.70	1.39	1.35
1	1A	2515	2MA	C5-C4	3.68	1.45	1.39
1	1A	2515	2MA	C5-N7	-3.67	1.32	1.39
1	1A	2617	PSU	C6-C5	3.54	1.39	1.35
43	1l	92	0TD	CA-N	-3.41	1.37	1.47
32	1a	527	7MG	C4-N9	-3.39	1.33	1.37
1	1A	1939	PSU	C6-C5	3.33	1.39	1.35
32	2a	527	7MG	C5-C4	3.33	1.47	1.37
1	1A	1933	PSU	C6-C5	3.25	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1519	MA6	C5-C6	3.23	1.49	1.41
32	1a	527	7MG	C5-C4	3.20	1.47	1.37
1	1A	2617	PSU	C4-N3	-3.19	1.32	1.38
32	2a	1207	2MG	C5-C4	3.17	1.47	1.38
1	2A	1917	PSU	C6-C5	3.17	1.38	1.35
32	1a	966	M2G	C5-C4	3.14	1.47	1.38
32	1a	1407	5MC	C6-C5	3.12	1.39	1.34
32	1a	1400	5MC	C6-C5	3.12	1.39	1.34
1	2A	1915	5MU	C6-C5	3.11	1.39	1.34
1	1A	2263	OMG	C5-C4	3.10	1.47	1.38
32	2a	966	M2G	C5-C4	3.07	1.47	1.38
32	1a	1518	MA6	C5-C6	3.05	1.49	1.41
1	1A	1984	5MC	C6-N1	-3.04	1.32	1.38
32	2a	516	PSU	C6-C5	3.03	1.38	1.35
32	2a	1518	MA6	C5-C6	3.03	1.49	1.41
1	2A	1915	5MU	C2-N1	3.02	1.43	1.38
32	2a	527	7MG	C4-N9	-3.02	1.34	1.37
1	2A	2251	OMG	C5-C4	2.99	1.46	1.38
1	1A	1937	5MU	C2-N1	2.98	1.43	1.38
1	2A	2605	PSU	C4-N3	-2.96	1.33	1.38
1	1A	1964	5MC	C6-C5	2.93	1.39	1.34
32	1a	1404	5MC	C6-C5	2.92	1.39	1.34
32	2a	1404	5MC	C6-C5	2.92	1.39	1.34
1	1A	2564	2MU	C4-N3	-2.91	1.33	1.38
1	2A	1939	5MU	C4-N3	-2.91	1.33	1.38
32	1a	1519	MA6	C5-C6	2.91	1.48	1.41
1	1A	2263	OMG	C6-N1	-2.89	1.33	1.38
1	1A	1937	5MU	C4-N3	-2.88	1.33	1.38
32	1a	1207	2MG	C5-C4	2.86	1.46	1.38
1	1A	1937	5MU	C6-C5	2.83	1.39	1.34
43	1l	92	0TD	OD2-CG	-2.81	1.21	1.30
32	2a	1407	5MC	C6-C5	2.77	1.39	1.34
32	2a	527	7MG	C8-N9	2.74	1.47	1.45
1	2A	2605	PSU	C6-C5	2.74	1.38	1.35
1	2A	1915	5MU	C4-N3	-2.72	1.33	1.38
32	2a	967	5MC	C6-C5	2.72	1.39	1.34
1	2A	1942	5MC	C6-C5	2.72	1.39	1.34
1	1A	1961	5MU	C6-C5	2.71	1.39	1.34
1	2A	1939	5MU	C6-C5	2.70	1.39	1.34
32	2a	1400	5MC	C6-C5	2.70	1.39	1.34
32	1a	966	M2G	C2-N2	2.69	1.40	1.35
32	2a	966	M2G	C2-N2	2.69	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2564	2MU	C5-C4	2.67	1.49	1.43
43	1l	92	0TD	CB-CG	-2.67	1.47	1.52
1	1A	1964	5MC	C6-N1	-2.66	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.64	1.33	1.38
1	2A	1962	5MC	C6-C5	2.64	1.38	1.34
32	1a	967	5MC	C6-C5	2.63	1.38	1.34
32	1a	1519	MA6	C5-N7	-2.61	1.34	1.39
32	1a	966	M2G	C6-N1	-2.61	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.60	1.34	1.38
43	1l	92	0TD	CSB-SB	-2.58	1.74	1.79
32	2a	1519	MA6	C8-N7	2.58	1.36	1.31
1	2A	2552	2MU	C5-C4	2.58	1.49	1.43
1	1A	1933	PSU	C4-N3	-2.58	1.34	1.38
1	2A	2552	2MU	C4-N3	-2.58	1.34	1.38
32	2a	527	7MG	C6-N1	-2.52	1.34	1.38
1	1A	2515	2MA	C8-N9	-2.50	1.33	1.37
32	1a	1400	5MC	C6-N1	-2.48	1.33	1.38
1	1A	1961	5MU	C6-N1	-2.46	1.33	1.38
1	1A	1939	PSU	C4-N3	-2.46	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.44	1.34	1.38
1	2A	1915	5MU	C4-C5	2.43	1.48	1.44
1	2A	2552	2MU	C2-N1	2.42	1.42	1.38
1	2A	2251	OMG	C6-N1	-2.41	1.34	1.38
32	1a	1519	MA6	C8-N7	2.40	1.36	1.31
32	1a	1518	MA6	C8-N7	2.39	1.36	1.31
1	2A	2503	2MA	C4-N9	-2.39	1.32	1.37
1	2A	2503	2MA	C5-N7	-2.38	1.34	1.39
32	1a	1404	5MC	C6-N1	-2.38	1.34	1.38
32	1a	1518	MA6	C5-N7	-2.36	1.34	1.39
32	1a	1518	MA6	C4-N9	-2.36	1.32	1.37
1	2A	1939	5MU	C4-C5	2.34	1.48	1.44
32	2a	1400	5MC	C6-N1	-2.32	1.34	1.38
32	2a	516	PSU	C4-N3	-2.31	1.34	1.38
32	2a	967	5MC	C6-N1	-2.30	1.34	1.38
1	2A	1942	5MC	C6-N1	-2.28	1.34	1.38
32	2a	1404	5MC	C6-N1	-2.27	1.34	1.38
1	2A	2605	PSU	C2-N3	-2.27	1.33	1.37
1	1A	1961	5MU	C4-C5	2.25	1.48	1.44
32	1a	516	PSU	C4-N3	-2.24	1.34	1.38
32	2a	1518	MA6	C5-N7	-2.23	1.35	1.39
32	1a	527	7MG	C6-N1	-2.22	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.21	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2503	2MA	C8-N7	2.21	1.35	1.31
1	1A	2564	2MU	C2-N3	-2.19	1.34	1.38
32	2a	1407	5MC	C6-N1	-2.18	1.34	1.38
32	2a	1518	MA6	C8-N7	2.16	1.35	1.31
1	2A	1939	5MU	C6-N1	-2.16	1.34	1.38
1	1A	1937	5MU	C2-N3	-2.15	1.34	1.38
32	1a	967	5MC	C6-N1	-2.13	1.34	1.38
1	1A	2515	2MA	C4-N9	-2.12	1.33	1.37
32	2a	1498	UR3	C6-C5	2.11	1.40	1.35
1	1A	2263	OMG	C5-N7	-2.09	1.34	1.39
32	2a	966	M2G	C4-N9	-2.09	1.32	1.38
32	2a	1519	MA6	C4-N9	-2.09	1.33	1.37
32	2a	1207	2MG	C6-N1	-2.08	1.35	1.38
1	1A	2515	2MA	C8-N7	2.07	1.35	1.31
32	2a	1207	2MG	C5-N7	-2.07	1.34	1.39
1	1A	2617	PSU	C2-N3	-2.04	1.34	1.37
1	1A	1939	PSU	C2-N3	-2.04	1.34	1.37
1	2A	1939	5MU	C2-N3	-2.04	1.34	1.38
32	1a	966	M2G	C4-N9	-2.03	1.32	1.38
32	2a	1519	MA6	C5-N7	-2.02	1.35	1.39
32	1a	1407	5MC	C6-N1	-2.01	1.34	1.38
1	1A	1937	5MU	C4-C5	2.01	1.48	1.44
1	1A	1961	5MU	C4-N3	-2.01	1.35	1.38
32	1a	1402	4OC	C6-C5	2.00	1.39	1.35
1	2A	2503	2MA	C5-C6	2.00	1.46	1.41

All (244) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	527	7MG	N9-C4-N3	8.67	138.17	125.46
32	1a	527	7MG	N9-C4-N3	8.43	137.81	125.46
1	1A	2515	2MA	C5-C4-N3	-8.39	118.34	127.18
43	1l	92	0TD	CB-CA-N	-7.92	93.06	109.10
32	1a	1498	UR3	C4-N3-C2	-7.34	118.67	124.58
32	1a	1207	2MG	C2-N3-C4	7.29	121.12	112.00
32	2a	1498	UR3	C4-N3-C2	-7.04	118.92	124.58
1	1A	2515	2MA	N3-C4-N9	6.81	135.63	126.99
32	2a	1207	2MG	C2-N3-C4	6.71	120.40	112.00
1	2A	2503	2MA	C5-C4-N3	-6.69	120.13	127.18
1	2A	1911	PSU	N1-C2-N3	6.52	122.05	115.17
32	2a	516	PSU	N1-C2-N3	6.47	122.00	115.17
1	2A	1939	5MU	C4-N3-C2	-6.41	118.94	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2503	2MA	N3-C4-N9	6.35	135.04	126.99
43	1l	92	0TD	CSB-SB-CB	6.28	113.66	102.36
1	1A	2617	PSU	N1-C2-N3	6.26	121.77	115.17
1	2A	1917	PSU	N1-C2-N3	6.24	121.75	115.17
32	1a	1519	MA6	C5-C4-N3	-6.21	118.17	126.72
1	1A	2263	OMG	C5-C4-N3	-6.06	118.74	128.39
32	1a	966	M2G	C5-C4-N3	-5.97	118.89	128.39
1	2A	1939	5MU	C5-C4-N3	5.96	120.50	115.32
32	1a	1207	2MG	C5-C4-N3	-5.86	119.06	128.39
1	2A	1939	5MU	N3-C2-N1	5.86	122.52	114.89
1	1A	1933	PSU	N1-C2-N3	5.82	121.31	115.17
1	2A	2251	OMG	C5-C4-N3	-5.81	119.14	128.39
32	1a	516	PSU	N1-C2-N3	5.70	121.18	115.17
1	2A	2605	PSU	N1-C2-N3	5.69	121.17	115.17
1	1A	1961	5MU	C4-N3-C2	-5.64	119.95	127.34
32	2a	1207	2MG	C5-C4-N3	-5.62	119.45	128.39
32	2a	1518	MA6	C5-C4-N3	-5.61	118.99	126.72
1	1A	1939	PSU	N1-C2-N3	5.61	121.08	115.17
32	2a	966	M2G	C5-C4-N3	-5.61	119.47	128.39
1	2A	2552	2MU	N3-C2-N1	5.42	121.94	114.89
32	2a	527	7MG	C5-C4-N3	-5.40	118.00	128.13
32	2a	1519	MA6	C5-C4-N3	-5.39	119.29	126.72
32	1a	527	7MG	C5-C4-N3	-5.29	118.20	128.13
32	2a	527	7MG	N9-C8-N7	-5.28	95.90	103.37
1	1A	2263	OMG	C2-N3-C4	5.24	121.33	112.30
1	2A	2251	OMG	C2-N3-C4	5.24	121.33	112.30
1	2A	2552	2MU	C4-N3-C2	-5.22	120.14	126.61
1	2A	1915	5MU	N3-C2-N1	5.21	121.67	114.89
32	1a	1518	MA6	C5-C4-N3	-5.17	119.60	126.72
1	1A	2564	2MU	N3-C2-N1	5.12	121.56	114.89
32	2a	1519	MA6	C10-N6-C6	-5.10	107.54	120.52
1	1A	1937	5MU	N3-C2-N1	5.03	121.44	114.89
1	1A	1961	5MU	C5-C4-N3	5.03	119.70	115.32
1	1A	1961	5MU	O4-C4-C5	-4.93	119.27	124.92
1	1A	2515	2MA	N6-C6-N1	4.91	123.65	117.03
1	1A	1961	5MU	N3-C2-N1	4.91	121.28	114.89
32	1a	527	7MG	N9-C8-N7	-4.84	96.53	103.37
1	2A	1917	PSU	O2-C2-N1	-4.77	117.87	122.79
1	1A	1937	5MU	C5-C4-N3	4.75	119.45	115.32
1	1A	1937	5MU	C4-N3-C2	-4.73	121.14	127.34
32	2a	1519	MA6	C4-C5-N7	-4.72	105.18	110.58
1	2A	1915	5MU	C4-N3-C2	-4.70	121.17	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1400	5MC	C5-C6-N1	-4.70	118.21	123.31
1	2A	2503	2MA	C4-N9-C8	4.62	110.59	105.74
32	2a	966	M2G	C2-N3-C4	4.56	120.94	112.51
32	2a	516	PSU	C4-N3-C2	-4.55	120.11	126.37
32	1a	1518	MA6	C2-N1-C6	4.52	122.87	111.83
32	1a	1518	MA6	C4-C5-N7	-4.49	105.45	110.58
1	1A	2564	2MU	C4-N3-C2	-4.46	121.07	126.61
1	1A	2263	OMG	N9-C4-N3	4.40	134.76	125.95
32	2a	516	PSU	O2-C2-N1	-4.37	118.28	122.79
32	2a	527	7MG	C2-N3-C4	4.35	119.80	112.30
32	1a	966	M2G	N9-C4-N3	4.35	134.65	125.95
32	1a	966	M2G	C2-N3-C4	4.34	120.53	112.51
32	2a	1519	MA6	C2-N1-C6	4.32	122.39	111.83
32	1a	527	7MG	C2-N3-C4	4.30	119.70	112.30
32	2a	1518	MA6	C2-N1-C6	4.29	122.31	111.83
32	1a	1519	MA6	N3-C4-N9	4.29	134.46	127.17
32	2a	1518	MA6	N3-C4-N9	4.28	134.45	127.17
32	1a	1519	MA6	C4-C5-N7	-4.27	105.70	110.58
43	2l	92	0TD	CSB-SB-CB	4.25	110.00	102.36
1	1A	1984	5MC	C1'-N1-C6	-4.24	114.16	121.15
1	1A	1937	5MU	O4-C4-C5	-4.23	120.08	124.92
1	2A	2503	2MA	N6-C6-N1	4.21	122.71	117.03
1	2A	2605	PSU	C4-N3-C2	-4.21	120.57	126.37
1	2A	2251	OMG	N9-C4-N3	4.16	134.28	125.95
1	1A	1937	5MU	C1'-N1-C2	4.13	125.00	117.59
32	2a	1518	MA6	C9-N6-C6	-4.10	110.08	120.52
32	1a	1519	MA6	C9-N6-C6	-4.09	110.11	120.52
32	1a	1518	MA6	C9-N6-C6	-4.09	110.12	120.52
1	2A	1917	PSU	C4-N3-C2	-4.09	120.74	126.37
32	1a	1207	2MG	C6-C5-N7	4.07	137.69	130.29
1	2A	1915	5MU	C5-C4-N3	4.04	118.83	115.32
1	1A	1933	PSU	C4-N3-C2	-4.02	120.84	126.37
32	1a	1207	2MG	N1-C2-N2	4.01	120.65	116.56
32	1a	1519	MA6	C2-N1-C6	4.01	121.61	111.83
32	1a	516	PSU	C4-N3-C2	-3.99	120.88	126.37
1	2A	1942	5MC	C5-C6-N1	-3.98	118.99	123.31
1	2A	1939	5MU	C5-C6-N1	-3.93	119.05	123.31
32	2a	1207	2MG	N9-C4-N3	3.91	133.76	125.95
32	2a	1518	MA6	C4-C5-N7	-3.90	106.12	110.58
1	2A	1939	5MU	O2-C2-N1	-3.85	117.78	122.80
1	1A	2564	2MU	O2-C2-N1	-3.83	117.81	122.80
32	1a	1404	5MC	C5-C6-N1	-3.83	119.16	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1407	5MC	C5-C6-N1	-3.82	119.16	123.31
32	2a	1404	5MC	C5-C4-N3	-3.81	117.85	121.75
32	2a	966	M2G	N9-C4-N3	3.81	133.57	125.95
1	2A	1939	5MU	O4-C4-C5	-3.80	120.57	124.92
32	2a	966	M2G	C6-C5-N7	3.78	137.18	130.29
1	1A	1939	PSU	C4-N3-C2	-3.78	121.16	126.37
1	2A	1911	PSU	C4-N3-C2	-3.77	121.18	126.37
1	1A	2617	PSU	C4-N3-C2	-3.77	121.18	126.37
32	2a	967	5MC	C5-C6-N1	-3.76	119.23	123.31
32	1a	516	PSU	O2-C2-N1	-3.76	118.92	122.79
1	1A	1933	PSU	O2-C2-N1	-3.73	118.94	122.79
1	1A	2263	OMG	C6-C5-N7	3.72	137.05	130.29
32	2a	1519	MA6	C2-N3-C4	3.70	120.87	111.83
1	2A	1962	5MC	C5-C6-N1	-3.66	119.33	123.31
32	1a	1207	2MG	N9-C4-N3	3.63	133.22	125.95
32	2a	1519	MA6	N3-C4-N9	3.60	133.28	127.17
32	1a	1519	MA6	C2-N3-C4	3.59	120.59	111.83
1	1A	1961	5MU	O2-C2-N1	-3.57	118.16	122.80
1	2A	1915	5MU	C1'-N1-C2	3.54	123.95	117.59
1	2A	2251	OMG	C6-C5-N7	3.53	136.71	130.29
32	1a	1518	MA6	N3-C4-N9	3.52	133.15	127.17
32	1a	1518	MA6	C2-N3-C4	3.46	120.29	111.83
32	2a	1207	2MG	C6-C5-N7	3.46	136.58	130.29
32	2a	1518	MA6	C2-N3-C4	3.42	120.19	111.83
32	1a	967	5MC	C5-C6-N1	-3.39	119.63	123.31
32	1a	1498	UR3	C5-C4-N3	3.38	119.50	115.04
1	1A	1961	5MU	C5-C6-N1	-3.38	119.64	123.31
32	2a	1519	MA6	N1-C2-N3	-3.35	123.50	128.58
32	2a	1207	2MG	N1-C2-N2	3.35	119.98	116.56
32	1a	966	M2G	C6-C5-N7	3.32	136.34	130.29
1	1A	1937	5MU	C1'-N1-C6	-3.32	115.68	121.15
32	2a	1400	5MC	C5-C6-N1	-3.29	119.74	123.31
32	1a	1207	2MG	N2-C2-N3	-3.27	116.35	120.51
32	2a	1498	UR3	C5-C4-N3	3.24	119.31	115.04
1	2A	1915	5MU	O4-C4-C5	-3.24	121.21	124.92
1	2A	2503	2MA	C2-N1-C6	3.23	123.07	118.10
32	1a	1207	2MG	C4-C5-N7	-3.23	105.56	110.67
32	1a	1518	MA6	N1-C2-N3	-3.22	123.71	128.58
1	1A	2515	2MA	C4-C5-N7	-3.20	106.92	110.58
32	2a	1404	5MC	C5-C6-N1	-3.20	119.84	123.31
32	2a	1518	MA6	C10-N6-C6	-3.19	112.41	120.52
1	1A	1964	5MC	C5-C6-N1	-3.18	119.86	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2552	2MU	O2-C2-N1	-3.16	118.68	122.80
32	2a	1407	5MC	C5-C6-N1	-3.14	119.90	123.31
32	2a	1519	MA6	C5-N7-C8	3.13	108.36	103.45
1	2A	2503	2MA	N9-C8-N7	-3.06	109.60	113.94
1	1A	1939	PSU	O2-C2-N1	-3.04	119.65	122.79
32	2a	1519	MA6	C6-C5-N7	2.97	138.18	133.43
1	2A	2552	2MU	C5-C4-N3	2.96	118.94	114.80
32	1a	1518	MA6	C5-N7-C8	2.92	108.04	103.45
1	1A	1964	5MC	C5-C4-N3	-2.91	118.77	121.75
32	2a	1518	MA6	N1-C2-N3	-2.90	124.19	128.58
32	1a	1404	5MC	C5-C4-N3	-2.87	118.81	121.75
32	1a	516	PSU	C6-C5-C4	-2.87	116.24	118.17
32	1a	1519	MA6	C5-N7-C8	2.85	107.93	103.45
1	1A	1984	5MC	C5-C6-N1	-2.85	120.22	123.31
1	2A	1911	PSU	O2-C2-N1	-2.83	119.86	122.79
1	1A	2263	OMG	C4-C5-N7	-2.82	106.21	110.67
1	2A	1920	4OC	O2-C2-N3	-2.82	117.89	122.33
32	2a	966	M2G	C4-C5-N7	-2.81	106.22	110.67
32	2a	527	7MG	C5-C6-N1	2.80	115.87	110.94
32	2a	1207	2MG	C4-C5-N7	-2.80	106.23	110.67
32	2a	1407	5MC	C5-C4-N3	-2.80	118.89	121.75
1	1A	2515	2MA	C4-N9-C8	2.79	108.67	105.74
1	1A	2515	2MA	C5-N7-C8	2.79	107.83	103.45
32	2a	1207	2MG	N2-C2-N3	-2.79	116.96	120.51
1	1A	2564	2MU	C2'-C1'-N1	-2.76	109.00	114.24
1	2A	1942	5MC	C5-C4-N3	-2.76	118.92	121.75
1	2A	1915	5MU	C5-C6-N1	-2.75	120.32	123.31
32	1a	1518	MA6	C10-N6-C6	-2.75	113.53	120.52
1	2A	1915	5MU	C1'-N1-C6	-2.75	116.62	121.15
1	2A	2503	2MA	C4-C5-N7	-2.72	107.47	110.58
32	1a	966	M2G	C4-C5-N7	-2.72	106.36	110.67
1	1A	1937	5MU	O2-C2-N3	-2.70	116.50	121.49
32	1a	1407	5MC	C5-C4-N3	-2.70	118.98	121.75
32	1a	1519	MA6	C10-N6-C6	-2.70	113.65	120.52
32	1a	1518	MA6	C6-C5-N7	2.70	137.74	133.43
32	1a	1519	MA6	N1-C2-N3	-2.70	124.50	128.58
32	2a	1518	MA6	C5-N7-C8	2.68	107.67	103.45
32	1a	527	7MG	C5-C6-N1	2.68	115.66	110.94
32	1a	1407	5MC	O2-C2-N3	-2.68	118.10	122.33
32	2a	1407	5MC	O2-C2-N3	-2.68	118.11	122.33
1	1A	2564	2MU	C5-C4-N3	2.66	118.53	114.80
32	2a	1519	MA6	C10-N6-C9	-2.64	107.70	116.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1984	5MC	CM5-C5-C6	-2.61	119.32	122.85
1	2A	2503	2MA	C5-N7-C8	2.59	107.52	103.45
32	1a	1400	5MC	C5-C4-N3	-2.58	119.11	121.75
32	2a	1404	5MC	O2-C2-N3	-2.57	118.29	122.33
1	2A	1915	5MU	O2-C2-N3	-2.55	116.78	121.49
1	2A	2251	OMG	C4-C5-N7	-2.55	106.63	110.67
32	2a	516	PSU	C5-C6-N1	-2.55	118.60	122.14
32	2a	1518	MA6	N1-C6-N6	2.54	119.95	116.86
32	2a	1519	MA6	C9-N6-C6	-2.54	114.06	120.52
32	2a	1402	4OC	C6-C5-C4	2.52	120.04	117.00
32	2a	1519	MA6	C4-N9-C8	2.52	108.39	105.74
32	1a	1402	4OC	C6-C5-C4	2.52	120.04	117.00
32	2a	1400	5MC	C5-C4-N3	-2.52	119.17	121.75
1	2A	2552	2MU	O4-C4-C5	-2.51	120.83	125.16
32	1a	1518	MA6	C4-N9-C8	2.50	108.36	105.74
1	1A	1937	5MU	C5-C6-N1	-2.48	120.61	123.31
32	1a	1207	2MG	CM2-N2-C2	-2.47	118.34	123.65
32	2a	1518	MA6	C4-N9-C8	2.47	108.33	105.74
32	1a	1518	MA6	C10-N6-C9	-2.43	108.38	116.18
43	2l	92	0TD	OD2-CG-CB	2.41	118.35	113.15
32	1a	967	5MC	C5-C4-N3	-2.40	119.30	121.75
1	2A	1962	5MC	C1'-N1-C6	-2.40	117.20	121.15
1	1A	1942	4OC	O2-C2-N3	-2.40	118.55	122.33
32	1a	1207	2MG	O3'-C3'-C2'	2.39	119.48	111.82
1	1A	2515	2MA	N9-C8-N7	-2.39	110.55	113.94
1	1A	2617	PSU	O2-C2-N3	-2.39	117.62	121.86
32	2a	516	PSU	O4'-C1'-C2'	2.34	108.39	105.15
32	1a	527	7MG	O6-C6-C5	-2.34	121.88	127.62
1	1A	1939	PSU	C6-C5-C4	-2.33	116.60	118.17
32	2a	1519	MA6	N9-C8-N7	-2.32	110.64	113.94
1	2A	2605	PSU	C6-C5-C4	-2.31	116.62	118.17
1	1A	1961	5MU	C5M-C5-C4	2.31	121.25	118.78
32	2a	967	5MC	CM5-C5-C6	-2.31	119.73	122.85
1	2A	2605	PSU	O2-C2-N1	-2.27	120.45	122.79
32	1a	1404	5MC	CM5-C5-C6	-2.24	119.82	122.85
32	1a	1519	MA6	N1-C6-N6	2.23	119.57	116.86
1	1A	2564	2MU	O4-C4-C5	-2.22	121.34	125.16
32	2a	1400	5MC	CM5-C5-C6	-2.22	119.85	122.85
1	2A	1939	5MU	C5M-C5-C4	2.22	121.15	118.78
32	2a	1404	5MC	CM5-C5-C6	-2.20	119.87	122.85
32	1a	1498	UR3	C3U-N3-C2	2.18	121.14	117.33
1	2A	2251	OMG	O6-C6-C5	-2.18	120.77	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	966	M2G	O6-C6-C5	-2.17	120.79	126.53
32	1a	1207	2MG	C8-N7-C5	2.17	108.12	104.26
1	1A	1984	5MC	C1'-N1-C2	2.16	123.21	118.44
1	2A	1962	5MC	C5-C4-N4	-2.15	118.36	121.39
32	2a	967	5MC	C5-C4-N3	-2.15	119.56	121.75
32	1a	1518	MA6	N9-C8-N7	-2.14	110.89	113.94
1	1A	2515	2MA	C2-N1-C6	2.14	121.39	118.10
1	1A	2263	OMG	C8-N7-C5	2.14	108.07	104.26
1	2A	2503	2MA	C4-N9-C1'	-2.13	121.66	126.63
1	2A	1911	PSU	O2-C2-N3	-2.12	118.09	121.86
32	2a	1498	UR3	C3U-N3-C4	2.12	120.81	117.87
1	1A	2617	PSU	O2-C2-N1	-2.11	120.61	122.79
32	1a	967	5MC	O2-C2-N3	-2.10	119.02	122.33
1	2A	2605	PSU	C5-C6-N1	-2.07	119.26	122.14
32	1a	1207	2MG	C2-N1-C6	-2.06	122.06	124.55
1	1A	2515	2MA	C5-C6-N6	-2.05	118.22	123.29
32	2a	1518	MA6	C10-N6-C9	-2.03	109.65	116.18
1	1A	1933	PSU	O4'-C1'-C2'	2.03	107.96	105.15
32	2a	1207	2MG	O6-C6-C5	-2.02	121.19	126.53
32	1a	516	PSU	O4'-C1'-C2'	2.02	107.95	105.15
32	1a	1207	2MG	O3'-C3'-C4'	2.02	116.88	111.08

There are no chirality outliers.

All (29) 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	1518	MA6	C5-C6-N6-C9
43	1l	92	0TD	SB-CB-CG-OD2
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
32	2a	1519	MA6	C5-C6-N6-C10
43	2l	92	0TD	O-C-CA-CB
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1518	MA6	N1-C6-N6-C9
32	2a	1519	MA6	N1-C6-N6-C10
32	1a	1519	MA6	C5-C6-N6-C10
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	527	7MG	C3'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB

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Mol	Chain	Res	Type	Atoms
43	2l	92	0TD	CG-CB-SB-CSB
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	2a	1518	MA6	C5-C6-N6-C10
32	2a	1519	MA6	C5-C6-N6-C9
1	1A	2515	2MA	C4'-C5'-O5'-P
43	2l	92	0TD	CA-CB-SB-CSB
1	2A	2251	OMG	C1'-C2'-O2'-CM2
32	1a	1518	MA6	C5-C6-N6-C10
32	1a	1402	4OC	C3'-C4'-C5'-O5'
32	1a	527	7MG	C4'-C5'-O5'-P
1	1A	1942	4OC	C2'-C1'-N1-C2

There are no ring outliers.

19 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1498	UR3	1	0
32	1a	1519	MA6	4	0
1	2A	2503	2MA	1	0
1	2A	1915	5MU	1	0
32	2a	1404	5MC	1	0
32	1a	966	M2G	1	0
32	2a	1519	MA6	1	0
1	2A	2251	OMG	1	0
32	1a	1402	4OC	2	0
1	2A	1939	5MU	3	0
43	2l	92	0TD	2	0
32	2a	1518	MA6	1	0
32	1a	1518	MA6	3	0
43	1l	92	0TD	1	0
32	2a	1402	4OC	1	0
32	2a	1400	5MC	4	0
1	1A	1961	5MU	1	0
32	1a	1404	5MC	1	0
1	2A	2552	2MU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2540 ligands modelled in this entry, 2529 are monoatomic - leaving 11 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
55	MPD	1a	1880	-	7,7,7	0.62	0	9,10,10	0.69	0
55	MPD	2A	3748	-	7,7,7	0.33	0	9,10,10	0.26	0
55	MPD	18	102	-	7,7,7	0.23	0	9,10,10	0.58	0
55	MPD	2A	3747	-	7,7,7	0.39	0	9,10,10	0.51	0
56	ARG	1B	230	54	10,11,11	0.82	1 (10%)	9,13,13	1.27	1 (11%)
58	SF4	1d	501	35	0,12,12	-	-	-		
58	SF4	2d	501	35	0,12,12	-	-	-		
55	MPD	2B	3020	-	7,7,7	0.33	0	9,10,10	0.37	0
55	MPD	1A	4028	-	7,7,7	0.32	0	9,10,10	0.16	0
55	MPD	1T	8004	-	7,7,7	0.33	0	9,10,10	0.32	0
56	ARG	1F	311	-	10,11,11	0.73	1 (10%)	9,13,13	1.08	1 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	MPD	1a	1880	-	-	1/5/5/5	-
55	MPD	2A	3748	-	-	5/5/5/5	-
55	MPD	18	102	-	-	2/5/5/5	-
55	MPD	2A	3747	-	-	0/5/5/5	-
56	ARG	1B	230	54	-	2/11/11/11	-
58	SF4	1d	501	35	-	-	0/6/5/5
58	SF4	2d	501	35	-	-	0/6/5/5
55	MPD	2B	3020	-	-	1/5/5/5	-
55	MPD	1A	4028	-	-	1/5/5/5	-
55	MPD	1T	8004	-	-	2/5/5/5	-
56	ARG	1F	311	-	-	3/11/11/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	1B	230	ARG	OXT-C	-2.47	1.22	1.30
56	1F	311	ARG	OXT-C	-2.04	1.24	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	1F	311	ARG	OXT-C-O	-3.05	117.16	124.08
56	1B	230	ARG	OXT-C-O	-2.82	117.69	124.08

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	18	102	MPD	C2-C3-C4-C5
55	2A	3748	MPD	C2-C3-C4-O4
55	2A	3748	MPD	C2-C3-C4-C5
56	1F	311	ARG	C-CA-CB-CG
56	1B	230	ARG	NE-CD-CG-CB
56	1B	230	ARG	CA-CB-CG-CD
55	1A	4028	MPD	O2-C2-C3-C4
55	1T	8004	MPD	O2-C2-C3-C4
55	2A	3748	MPD	O2-C2-C3-C4
55	18	102	MPD	C2-C3-C4-O4
55	2A	3748	MPD	C1-C2-C3-C4
55	2A	3748	MPD	CM-C2-C3-C4
55	1a	1880	MPD	C2-C3-C4-C5
56	1F	311	ARG	CA-CB-CG-CD
55	1T	8004	MPD	C2-C3-C4-O4
55	2B	3020	MPD	C2-C3-C4-O4
56	1F	311	ARG	O-C-CA-N

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	1a	1880	MPD	8	0
55	18	102	MPD	5	0
55	2A	3747	MPD	2	0
56	1B	230	ARG	1	0
55	1A	4028	MPD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	1F	311	ARG	3	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	1A	2861/2915 (98%)	-0.46	111 (3%) 43 45	23, 40, 90, 100	0
1	2A	2856/2915 (97%)	-0.35	98 (3%) 48 50	26, 44, 91, 104	0
2	1B	120/121 (99%)	-0.15	1 (0%) 82 83	34, 56, 71, 86	0
2	2B	120/121 (99%)	0.21	1 (0%) 82 83	41, 61, 74, 87	0
3	1D	275/276 (99%)	0.03	7 (2%) 58 60	23, 37, 53, 78	0
3	2D	275/276 (99%)	0.02	5 (1%) 67 69	25, 41, 55, 77	0
4	1E	204/206 (99%)	0.20	3 (1%) 72 73	22, 43, 63, 72	0
4	2E	204/206 (99%)	0.20	2 (0%) 79 80	26, 47, 65, 74	0
5	1F	203/210 (96%)	0.33	5 (2%) 58 60	20, 46, 72, 84	0
5	2F	203/210 (96%)	0.50	7 (3%) 48 50	25, 52, 73, 85	0
6	1G	181/182 (99%)	0.81	11 (6%) 27 29	54, 70, 81, 90	0
6	2G	181/182 (99%)	1.64	56 (30%) 1 1	58, 73, 83, 91	0
7	1H	174/180 (96%)	1.06	16 (9%) 14 16	45, 62, 73, 78	0
7	2H	173/180 (96%)	1.47	38 (21%) 2 2	54, 67, 76, 80	0
8	1I	147/148 (99%)	1.22	18 (12%) 8 9	43, 71, 80, 84	0
8	2I	146/148 (98%)	1.39	27 (18%) 3 4	47, 71, 81, 84	0
9	1N	140/140 (100%)	-0.03	2 (1%) 73 75	25, 36, 60, 81	0
9	2N	140/140 (100%)	0.78	4 (2%) 53 56	39, 58, 74, 81	0
10	1O	122/122 (100%)	-0.10	2 (1%) 70 72	25, 37, 57, 64	0
10	2O	122/122 (100%)	0.39	1 (0%) 82 83	38, 52, 66, 74	0
11	1P	149/150 (99%)	0.18	3 (2%) 65 66	19, 43, 67, 78	0
11	2P	149/150 (99%)	0.66	9 (6%) 27 29	32, 62, 79, 85	0
12	1Q	141/141 (100%)	0.25	3 (2%) 63 65	28, 44, 58, 72	0
12	2Q	141/141 (100%)	0.37	3 (2%) 63 65	33, 49, 61, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.13	0 100 100	27, 38, 54, 63	0
13	2R	118/118 (100%)	-0.01	0 100 100	32, 42, 56, 64	0
14	1S	110/112 (98%)	0.67	5 (4%) 38 40	42, 56, 67, 71	0
14	2S	110/112 (98%)	1.29	16 (14%) 6 7	48, 60, 70, 74	0
15	1T	131/146 (89%)	0.55	9 (6%) 23 25	34, 47, 72, 82	0
15	2T	131/146 (89%)	0.36	5 (3%) 44 46	39, 49, 74, 83	0
16	1U	116/118 (98%)	0.11	2 (1%) 69 70	25, 36, 53, 68	0
16	2U	116/118 (98%)	0.33	1 (0%) 81 82	30, 43, 57, 70	0
17	1V	101/101 (100%)	0.48	2 (1%) 65 66	26, 48, 63, 73	0
17	2V	101/101 (100%)	0.64	1 (0%) 79 80	30, 54, 67, 74	0
18	1W	112/113 (99%)	-0.05	2 (1%) 67 69	28, 34, 55, 87	0
18	2W	112/113 (99%)	0.07	3 (2%) 56 58	32, 38, 58, 87	0
19	1X	95/96 (98%)	0.40	7 (7%) 20 22	32, 42, 63, 74	0
19	2X	95/96 (98%)	0.67	5 (5%) 32 34	37, 47, 67, 76	0
20	1Y	107/110 (97%)	0.83	6 (5%) 30 32	39, 54, 69, 78	0
20	2Y	107/110 (97%)	1.18	14 (13%) 7 8	43, 58, 72, 80	0
21	1Z	203/206 (98%)	1.03	15 (7%) 20 22	45, 63, 78, 83	0
21	2Z	201/206 (97%)	1.16	18 (8%) 15 16	50, 66, 78, 82	0
22	10	77/85 (90%)	-0.15	2 (2%) 57 59	26, 35, 52, 63	0
22	20	77/85 (90%)	0.93	3 (3%) 43 45	41, 57, 68, 81	0
23	11	97/98 (98%)	0.16	1 (1%) 79 80	26, 41, 68, 76	0
23	21	97/98 (98%)	0.43	3 (3%) 51 53	35, 51, 72, 75	0
24	12	70/72 (97%)	0.69	5 (7%) 22 24	40, 53, 65, 82	0
24	22	70/72 (97%)	0.73	2 (2%) 53 56	45, 59, 68, 81	0
25	13	59/60 (98%)	0.23	3 (5%) 33 35	28, 40, 67, 80	0
25	23	59/60 (98%)	0.72	5 (8%) 16 18	34, 45, 70, 80	0
26	14	69/71 (97%)	1.32	13 (18%) 3 4	67, 81, 90, 94	0
26	24	69/71 (97%)	2.36	37 (53%) 0 0	70, 82, 90, 94	0
27	15	59/60 (98%)	-0.11	1 (1%) 69 70	22, 37, 59, 69	0
27	25	59/60 (98%)	-0.09	1 (1%) 69 70	25, 40, 61, 70	0
28	16	53/54 (98%)	0.24	0 100 100	34, 45, 61, 64	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.29	0 100 100	39, 49, 61, 66	0
29	17	48/49 (97%)	0.08	5 (10%) 11 13	22, 30, 58, 68	0
29	27	48/49 (97%)	0.04	5 (10%) 11 13	26, 33, 60, 68	0
30	18	64/65 (98%)	0.09	1 (1%) 70 72	30, 38, 45, 61	0
30	28	64/65 (98%)	0.15	0 100 100	33, 42, 49, 64	0
31	19	37/37 (100%)	-0.08	1 (2%) 56 58	29, 39, 55, 56	0
31	29	37/37 (100%)	0.67	0 100 100	45, 60, 72, 75	0
32	1a	1488/1521 (97%)	0.05	31 (2%) 63 65	34, 63, 89, 102	0
32	2a	1492/1521 (98%)	0.27	34 (2%) 61 63	44, 73, 92, 103	0
33	1b	231/256 (90%)	1.38	47 (20%) 3 3	65, 78, 86, 91	0
33	2b	231/256 (90%)	1.91	91 (39%) 1 0	67, 79, 87, 93	0
34	1c	206/239 (86%)	1.30	30 (14%) 6 6	63, 74, 83, 89	0
34	2c	206/239 (86%)	2.05	96 (46%) 0 0	65, 76, 84, 90	0
35	1d	208/209 (99%)	1.45	43 (20%) 2 3	55, 69, 79, 84	0
35	2d	208/209 (99%)	1.42	43 (20%) 2 3	57, 69, 78, 84	0
36	1e	148/162 (91%)	0.71	4 (2%) 56 58	46, 61, 72, 87	0
36	2e	148/162 (91%)	1.16	12 (8%) 18 19	56, 70, 79, 87	0
37	1f	100/101 (99%)	0.84	1 (1%) 79 80	53, 64, 74, 79	0
37	2f	100/101 (99%)	0.97	4 (4%) 42 44	53, 64, 74, 79	0
38	1g	155/156 (99%)	1.18	21 (13%) 7 8	62, 72, 81, 84	0
38	2g	155/156 (99%)	1.69	47 (30%) 1 1	66, 74, 81, 84	0
39	1h	137/138 (99%)	0.90	7 (5%) 33 35	54, 67, 74, 77	0
39	2h	137/138 (99%)	1.03	9 (6%) 24 26	56, 68, 75, 78	0
40	1i	127/128 (99%)	1.51	31 (24%) 2 2	60, 78, 85, 88	0
40	2i	126/128 (98%)	2.26	73 (57%) 0 0	64, 79, 86, 89	0
41	1j	97/105 (92%)	1.71	33 (34%) 1 1	59, 79, 88, 91	0
41	2j	96/105 (91%)	2.34	58 (60%) 0 0	65, 80, 88, 91	0
42	1k	114/129 (88%)	1.02	11 (9%) 13 15	46, 63, 77, 79	0
42	2k	114/129 (88%)	1.21	17 (14%) 5 6	48, 65, 77, 80	0
43	1l	121/132 (91%)	0.90	11 (9%) 15 16	48, 58, 70, 75	0
43	2l	121/132 (91%)	0.88	10 (8%) 17 19	51, 60, 70, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	116/126 (92%)	0.90	10 (8%) 16 17	54, 71, 79, 84	0
44	2m	114/126 (90%)	2.01	50 (43%) 0 0	73, 82, 87, 91	0
45	1n	60/61 (98%)	1.28	9 (15%) 5 6	64, 71, 78, 79	0
45	2n	60/61 (98%)	2.12	33 (55%) 0 0	67, 74, 80, 87	0
46	1o	88/89 (98%)	0.83	6 (6%) 23 25	46, 64, 77, 79	0
46	2o	88/89 (98%)	1.02	9 (10%) 12 13	50, 65, 78, 80	0
47	1p	82/88 (93%)	1.69	25 (30%) 1 1	58, 68, 78, 81	0
47	2p	82/88 (93%)	1.59	14 (17%) 4 5	59, 68, 77, 83	0
48	1q	99/105 (94%)	1.09	8 (8%) 18 19	53, 66, 75, 79	0
48	2q	99/105 (94%)	0.93	4 (4%) 42 44	53, 66, 76, 80	0
49	1r	68/88 (77%)	0.92	9 (13%) 7 8	55, 65, 77, 79	0
49	2r	68/88 (77%)	0.95	6 (8%) 15 17	55, 66, 77, 79	0
50	1s	83/93 (89%)	1.45	13 (15%) 5 6	67, 77, 83, 85	0
50	2s	83/93 (89%)	2.34	56 (67%) 0 0	70, 79, 84, 86	0
51	1t	96/106 (90%)	1.40	21 (21%) 2 2	57, 68, 79, 83	0
51	2t	98/106 (92%)	1.05	10 (10%) 12 13	57, 69, 81, 83	0
52	1u	23/27 (85%)	1.53	6 (26%) 1 2	69, 72, 76, 78	0
52	2u	23/27 (85%)	2.18	14 (60%) 0 0	71, 74, 77, 80	0
53	1y	97/113 (85%)	0.69	8 (8%) 17 19	44, 56, 70, 74	0
53	2y	96/113 (84%)	1.19	15 (15%) 5 6	57, 71, 79, 83	0
All	All	20766/21468 (96%)	0.41	1722 (8%) 17 19	19, 58, 85, 104	0

All (1722) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	8.7
26	24	56	VAL	7.9
1	1A	1122	C	7.8
40	2i	102	LEU	6.8
15	1T	131	ALA	6.6
53	1y	98	ALA	6.6
45	1n	2	ALA	6.4
53	2y	98	ALA	6.1
23	21	2	SER	5.9
33	1b	237	ALA	5.8

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Mol	Chain	Res	Type	RSRZ
1	1A	2614	A	5.7
1	1A	1110	C	5.7
8	2I	146	ALA	5.7
15	1T	37	GLY	5.6
1	1A	1133	G	5.6
43	2l	18	VAL	5.5
33	2b	237	ALA	5.5
26	24	49	PHE	5.5
34	2c	86	VAL	5.4
1	2A	2602	A	5.4
35	1d	179	GLU	5.4
22	20	84	LEU	5.4
23	11	2	SER	5.3
44	2m	116	THR	5.3
33	2b	236	TYR	5.3
40	2i	7	THR	5.2
35	1d	2	GLY	5.1
44	2m	102	ARG	5.1
40	2i	126	SER	5.1
26	14	59	PHE	5.1
50	2s	35	SER	5.1
15	1T	130	ALA	5.1
27	15	60	VAL	5.1
50	2s	9	VAL	5.0
33	2b	127	ILE	5.0
41	2j	37	PRO	4.9
24	12	70	GLN	4.9
34	2c	94	LEU	4.9
15	2T	130	ALA	4.9
51	2t	6	PRO	4.9
26	24	63	TYR	4.9
26	14	50	VAL	4.9
47	2p	82	GLN	4.8
20	2Y	1	MET	4.8
40	2i	125	TYR	4.8
25	23	2	PRO	4.7
26	14	56	VAL	4.7
26	14	49	PHE	4.7
7	1H	2	SER	4.7
48	1q	99	SER	4.6
8	2I	3	VAL	4.6
33	2b	122	PHE	4.6

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Mol	Chain	Res	Type	RSRZ
17	1V	101	GLY	4.6
1	1A	1121	C	4.6
1	1A	1123	A	4.5
44	1m	117	VAL	4.5
26	24	50	VAL	4.5
29	17	45	ALA	4.5
33	2b	133	LYS	4.5
41	2j	75	ILE	4.5
1	1A	1555	C	4.5
33	2b	7	VAL	4.4
19	1X	95	LEU	4.4
9	2N	140	VAL	4.4
33	1b	7	VAL	4.4
3	1D	276	LYS	4.4
1	2A	1536	C	4.4
33	1b	11	LEU	4.4
41	2j	90	LEU	4.4
1	2A	2140	C	4.4
43	1l	63	GLY	4.4
40	2i	2	GLU	4.3
33	2b	121	LEU	4.3
38	2g	16	LEU	4.3
1	1A	1134	A	4.3
38	2g	5	ARG	4.3
19	2X	95	LEU	4.3
33	2b	123	ALA	4.3
33	2b	97	TRP	4.3
22	10	84	LEU	4.3
33	1b	127	ILE	4.3
26	24	55	ARG	4.2
38	2g	7	ALA	4.2
50	2s	2	PRO	4.2
1	2A	2138	C	4.2
45	2n	18	VAL	4.2
41	2j	63	PHE	4.2
50	2s	10	PHE	4.2
3	2D	276	LYS	4.2
38	1g	16	LEU	4.2
44	2m	9	ILE	4.2
1	1A	1109	G	4.2
33	2b	131	PRO	4.2
39	2h	2	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
41	1j	74	ILE	4.1
1	2A	1064	C	4.1
40	1i	128	ARG	4.1
40	2i	88	TYR	4.1
42	1k	25	TYR	4.1
35	1d	167	GLY	4.1
41	2j	38	ILE	4.1
1	2A	2146	C	4.1
33	1b	129	GLU	4.1
36	2e	13	ILE	4.1
34	2c	207	VAL	4.1
38	2g	32	ARG	4.1
49	2r	87	ARG	4.1
1	2A	2147	G	4.1
20	1Y	1	MET	4.1
6	2G	50	ALA	4.0
15	2T	131	ALA	4.0
32	1a	1001	A	4.0
3	1D	275	LYS	4.0
26	24	66	SER	4.0
1	2A	2139	C	4.0
26	24	52	THR	4.0
34	1c	2	GLY	4.0
33	1b	236	TYR	4.0
34	2c	90	GLU	4.0
41	1j	75	ILE	4.0
34	2c	80	GLY	4.0
34	2c	81	GLY	4.0
34	2c	128	PHE	4.0
41	2j	47	PHE	4.0
43	1l	64	TYR	4.0
7	2H	45	VAL	4.0
33	1b	10	LEU	4.0
1	1A	1132	A	4.0
33	2b	10	LEU	3.9
40	1i	102	LEU	3.9
44	2m	6	GLY	3.9
1	1A	1137	G	3.9
33	2b	165	VAL	3.9
34	2c	196	LEU	3.9
50	2s	15	LEU	3.9
50	1s	9	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
44	1m	100	GLY	3.9
51	2t	103	GLY	3.9
34	2c	65	ALA	3.9
26	24	65	ASP	3.9
1	2A	1171	G	3.9
1	1A	1136	U	3.9
8	1I	147	GLN	3.9
39	1h	112	LEU	3.9
1	2A	2142	C	3.9
1	2A	2145	C	3.9
26	14	63	TYR	3.8
42	2k	75	TYR	3.8
33	2b	15	VAL	3.8
44	2m	98	VAL	3.8
35	1d	194	LEU	3.8
15	1T	38	ASN	3.8
40	2i	101	PHE	3.8
41	2j	91	PRO	3.8
35	2d	5	ILE	3.8
1	1A	2816	G	3.8
6	2G	146	TYR	3.8
34	2c	48	TYR	3.8
34	2c	188	LEU	3.8
18	1W	111	HIS	3.8
1	1A	1150	C	3.8
34	2c	77	ILE	3.8
46	1o	89	GLY	3.8
44	1m	2	ALA	3.8
1	1A	2815	C	3.8
5	2F	6	VAL	3.8
33	2b	136	VAL	3.8
33	2b	230	VAL	3.8
41	2j	34	VAL	3.8
43	1l	18	VAL	3.8
41	1j	32	ALA	3.7
1	1A	1148	C	3.7
1	2A	34	C	3.7
32	1a	1030(B)	C	3.7
33	2b	208	ILE	3.7
51	1t	103	GLY	3.7
8	2I	18	VAL	3.7
4	1E	204	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
5	2F	14	PRO	3.7
51	1t	10	LEU	3.7
46	2o	3	ILE	3.7
8	2I	16	GLY	3.7
41	2j	76	ASN	3.7
34	2c	79	ARG	3.7
45	2n	3	ARG	3.7
1	1A	1124	U	3.7
1	2A	229	A	3.7
52	2u	14	TRP	3.6
42	1k	14	VAL	3.6
53	1y	94	ALA	3.6
1	2A	1076	C	3.6
33	2b	11	LEU	3.6
33	1b	229	VAL	3.6
33	2b	232	PRO	3.6
35	2d	149	ALA	3.6
45	2n	59	ALA	3.6
47	1p	46	PRO	3.6
6	2G	52	ILE	3.6
7	1H	92	ILE	3.6
33	2b	57	PHE	3.6
35	1d	70	ILE	3.6
40	2i	99	LEU	3.6
42	2k	36	ASP	3.6
50	2s	11	VAL	3.6
6	2G	76	SER	3.6
1	1A	1221	G	3.6
1	2A	2143	C	3.6
3	2D	262	ARG	3.6
41	1j	98	ILE	3.6
50	2s	31	ILE	3.6
46	2o	86	GLY	3.6
29	27	48	LYS	3.6
38	2g	33	ASP	3.6
8	1I	10	GLU	3.6
50	2s	24	ALA	3.6
51	2t	97	ALA	3.6
48	1q	97	SER	3.5
1	2A	652(B)	A	3.5
1	1A	1120	G	3.5
14	2S	61	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
40	2i	91	ASP	3.5
26	24	57	GLU	3.5
40	2i	14	VAL	3.5
44	2m	54	VAL	3.5
45	2n	14	PRO	3.5
38	1g	156	TRP	3.5
1	1A	1118	C	3.5
44	2m	59	TYR	3.5
1	2A	2148	G	3.5
29	17	48	LYS	3.5
18	2W	112	GLY	3.5
47	1p	19	ILE	3.5
50	2s	30	LEU	3.5
14	1S	3	ARG	3.5
41	2j	46	ARG	3.5
1	1A	2165	C	3.5
1	2A	2141	G	3.5
18	2W	111	HIS	3.5
32	2a	1030(A)	G	3.5
8	2I	20	ASP	3.5
35	1d	150	GLU	3.5
26	24	44	THR	3.5
35	1d	49	ARG	3.5
41	2j	72	VAL	3.5
4	2E	204	ALA	3.5
33	2b	38	GLY	3.5
6	2G	82	LEU	3.5
33	2b	21	ARG	3.5
51	1t	8	ARG	3.5
1	1A	1127	U	3.5
41	1j	87	THR	3.4
33	1b	187	LEU	3.4
1	1A	2806	G	3.4
1	2A	2154	G	3.4
2	2B	1	U	3.4
41	2j	86	MET	3.4
7	2H	136	ILE	3.4
40	1i	56	LEU	3.4
6	1G	182	LYS	3.4
40	2i	90	PRO	3.4
44	1m	116	THR	3.4
41	1j	34	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
38	1g	8	GLU	3.4
53	1y	95	ARG	3.4
40	2i	30	GLY	3.4
16	1U	117	GLN	3.4
41	2j	96	ILE	3.4
32	1a	1257	U	3.4
33	1b	97	TRP	3.4
47	2p	48	TRP	3.4
41	2j	77	PRO	3.4
42	2k	25	TYR	3.4
8	1I	136	VAL	3.4
9	2N	9	VAL	3.4
34	2c	66	VAL	3.4
41	2j	24	VAL	3.4
36	1e	22	GLY	3.4
6	2G	147	ASP	3.4
6	2G	53	LEU	3.3
41	1j	90	LEU	3.3
33	1b	131	PRO	3.3
33	1b	232	PRO	3.3
38	1g	85	TYR	3.3
40	2i	18	PHE	3.3
44	2m	31	LYS	3.3
1	2A	1046	A	3.3
41	1j	88	LEU	3.3
34	2c	124	ILE	3.3
32	1a	1030	C	3.3
52	2u	23	PRO	3.3
53	1y	2	THR	3.3
20	2Y	55	TYR	3.3
1	2A	2155	G	3.3
33	1b	188	ALA	3.3
38	2g	80	VAL	3.3
41	2j	44	VAL	3.3
34	2c	2	GLY	3.3
38	1g	84	ASN	3.3
44	2m	106	ASN	3.3
41	2j	88	LEU	3.3
44	2m	66	LEU	3.3
1	1A	1126	C	3.3
33	2b	163	PHE	3.3
40	2i	92	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
47	2p	38	TYR	3.3
21	2Z	191	VAL	3.3
40	2i	109	VAL	3.3
18	1W	112	GLY	3.3
38	2g	34	GLY	3.3
33	1b	130	ARG	3.3
35	1d	168	ARG	3.3
38	2g	42	ILE	3.3
41	2j	74	ILE	3.3
17	1V	49	THR	3.3
50	2s	34	TRP	3.3
33	2b	207	ALA	3.2
50	2s	71	LEU	3.2
32	2a	1030(B)	C	3.2
33	2b	17	PHE	3.2
26	24	67	TYR	3.2
40	2i	4	TYR	3.2
29	17	46	VAL	3.2
20	2Y	93	GLY	3.2
41	2j	10	GLY	3.2
1	1A	1135	G	3.2
42	1k	36	ASP	3.2
40	2i	56	LEU	3.2
21	1Z	146	ILE	3.2
1	1A	1125	C	3.2
33	1b	17	PHE	3.2
52	2u	24	ARG	3.2
34	1c	207	VAL	3.2
34	2c	163	ALA	3.2
6	2G	42	GLY	3.2
26	24	54	GLY	3.2
40	2i	41	VAL	3.2
2	1B	1	U	3.2
6	2G	81	LYS	3.2
40	1i	91	ASP	3.2
7	2H	71	LEU	3.2
34	2c	33	LEU	3.2
7	2H	12	PRO	3.2
1	2A	2801(A)	A	3.2
6	1G	88	ILE	3.2
41	1j	4	ILE	3.2
45	2n	7	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
40	2i	27	THR	3.2
1	1A	2164	C	3.2
29	17	1	MET	3.2
45	1n	3	ARG	3.2
6	2G	74	LYS	3.2
8	2I	136	VAL	3.2
14	2S	79	ALA	3.2
25	23	60	GLU	3.2
35	1d	170	VAL	3.2
40	2i	43	ALA	3.2
46	2o	89	GLY	3.2
1	1A	2138	G	3.2
6	2G	2	PRO	3.2
32	2a	1036	G	3.2
33	1b	234	PRO	3.2
35	1d	188	LEU	3.2
34	2c	152	ILE	3.2
44	2m	4	ILE	3.2
41	2j	67	THR	3.2
29	17	47	ARG	3.1
1	1A	34	C	3.1
1	1A	935	C	3.1
1	2A	2179	C	3.1
32	2a	1030	C	3.1
33	1b	29	ALA	3.1
33	2b	177	ALA	3.1
35	2d	183	GLY	3.1
36	2e	22	GLY	3.1
45	2n	55	GLY	3.1
34	2c	138	VAL	3.1
6	2G	3	LEU	3.1
53	2y	45	PRO	3.1
47	1p	59	TRP	3.1
50	2s	25	LYS	3.1
1	1A	2814	C	3.1
1	2A	2136	C	3.1
8	2I	10	GLU	3.1
8	1I	84	GLY	3.1
21	1Z	12	GLY	3.1
40	1i	75	ASP	3.1
50	2s	82	GLY	3.1
49	1r	24	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
33	1b	165	VAL	3.1
42	1k	13	GLN	3.1
47	1p	82	GLN	3.1
38	2g	85	TYR	3.1
40	2i	66	ARG	3.1
1	2A	2152	G	3.1
3	1D	38	LYS	3.1
33	2b	22	LYS	3.1
42	2k	31	THR	3.1
50	2s	79	THR	3.1
1	2A	2144	U	3.1
26	14	45	GLY	3.1
40	2i	108	VAL	3.1
50	1s	19	VAL	3.1
33	2b	138	LEU	3.1
19	1X	69	TYR	3.1
33	2b	148	TYR	3.1
35	1d	50	ARG	3.1
34	2c	135	LYS	3.1
35	1d	138	TYR	3.1
38	2g	154	TYR	3.1
41	2j	55	LYS	3.1
35	1d	173	TRP	3.1
1	1A	2129	C	3.1
26	24	59	PHE	3.1
41	1j	76	ASN	3.1
42	2k	15	ALA	3.1
25	13	2	PRO	3.1
33	2b	93	VAL	3.1
34	1c	87	LEU	3.1
49	2r	85	LEU	3.1
51	1t	24	LEU	3.1
4	1E	163	GLU	3.0
1	1A	1149	A	3.0
41	2j	87	THR	3.0
34	2c	159	GLY	3.0
50	2s	26	GLY	3.0
7	2H	21	PRO	3.0
34	2c	68	VAL	3.0
35	2d	155	LEU	3.0
39	1h	133	LEU	3.0
40	2i	96	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
41	2j	8	LEU	3.0
50	2s	19	VAL	3.0
51	2t	100	ILE	3.0
1	1A	1113	A	3.0
50	1s	77	THR	3.0
1	2A	1091	G	3.0
32	2a	630	G	3.0
41	1j	33	GLN	3.0
1	1A	1072	U	3.0
1	1A	2166	U	3.0
32	2a	1257	U	3.0
19	2X	68	ARG	3.0
35	1d	166	LYS	3.0
1	2A	2111	C	3.0
6	1G	80	PHE	3.0
32	2a	1027	C	3.0
21	2Z	1	MET	3.0
41	1j	26	ALA	3.0
50	1s	24	ALA	3.0
33	2b	44	LEU	3.0
34	2c	99	VAL	3.0
41	2j	85	LEU	3.0
14	2S	35	ILE	3.0
34	1c	193	TYR	3.0
41	2j	82	ILE	3.0
47	1p	32	TYR	3.0
35	1d	47	ARG	3.0
1	1A	1112	U	3.0
1	1A	2181	G	3.0
1	2A	2153	G	3.0
52	2u	16	GLY	3.0
33	1b	125	PRO	3.0
7	2H	20	ALA	3.0
34	2c	149	ALA	3.0
41	2j	83	GLU	3.0
8	2I	19	VAL	3.0
34	2c	47	LEU	3.0
45	2n	6	LEU	3.0
33	1b	19	HIS	3.0
50	2s	14	HIS	3.0
15	1T	129	ARG	3.0
26	14	69	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
45	2n	17	LYS	3.0
50	2s	63	THR	3.0
40	2i	59	PHE	2.9
45	2n	16	PHE	2.9
50	2s	76	PRO	3.0
34	2c	100	ALA	2.9
34	2c	87	LEU	2.9
34	2c	175	LEU	2.9
8	2I	109	ILE	2.9
1	1A	6	A	2.9
1	2A	2169	A	2.9
40	1i	125	TYR	2.9
7	2H	82	GLY	2.9
33	2b	129	GLU	2.9
34	2c	62	ASP	2.9
40	2i	105	ASP	2.9
41	1j	78	ASN	2.9
1	1A	2163	G	2.9
32	1a	1036	G	2.9
40	2i	98	PRO	2.9
32	2a	1028	C	2.9
33	2b	215	LEU	2.9
40	1i	106	ALA	2.9
40	2i	94	ALA	2.9
41	1j	27	ALA	2.9
7	2H	15	VAL	2.9
40	2i	11	LYS	2.9
51	1t	74	LYS	2.9
37	2f	46	ARG	2.9
48	1q	63	ARG	2.9
38	1g	50	ILE	2.9
41	1j	100	THR	2.9
34	1c	201	TYR	2.9
41	2j	35	SER	2.9
44	2m	87	TYR	2.9
45	2n	34	TYR	2.9
50	2s	52	TYR	2.9
33	1b	228	GLY	2.9
40	2i	6	GLY	2.9
51	2t	96	GLY	2.9
20	2Y	53	PRO	2.9
1	2A	2112	G	2.9

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Mol	Chain	Res	Type	RSRZ
40	1i	127	LYS	2.9
43	1l	47	LYS	2.9
12	2Q	59	ARG	2.9
33	2b	118	LEU	2.9
34	2c	42	LEU	2.9
40	1i	46	ALA	2.9
45	2n	5	ALA	2.9
49	1r	20	ALA	2.9
6	2G	92	VAL	2.9
7	2H	44	VAL	2.9
26	24	14	ILE	2.9
26	24	31	ILE	2.9
33	2b	214	ILE	2.9
44	1m	4	ILE	2.9
44	2m	39	ILE	2.9
34	2c	95	THR	2.9
41	2j	15	THR	2.9
1	2A	2117	A	2.9
26	14	67	TYR	2.9
40	2i	62	TYR	2.9
40	2i	67	GLY	2.9
50	1s	84	GLY	2.9
26	24	29	PRO	2.9
35	2d	85	LYS	2.9
50	2s	59	PRO	2.9
51	1t	73	HIS	2.9
6	2G	133	LEU	2.9
20	2Y	90	LEU	2.9
34	2c	160	ALA	2.9
35	1d	108	LEU	2.9
35	2d	108	LEU	2.9
36	2e	6	PHE	2.9
40	2i	106	ALA	2.9
44	2m	90	LEU	2.9
48	2q	98	LEU	2.9
1	1A	1161	G	2.9
32	1a	1003	G	2.9
32	1a	1032	G	2.9
32	1a	1033	G	2.9
41	1j	49	VAL	2.9
6	2G	88	ILE	2.9
50	2s	77	THR	2.9

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Mol	Chain	Res	Type	RSRZ
32	1a	1286	A	2.8
38	2g	84	ASN	2.9
44	2m	24	GLY	2.8
9	1N	115	ARG	2.8
21	1Z	189	ALA	2.8
33	1b	122	PHE	2.8
34	1c	10	PHE	2.8
40	2i	13	ALA	2.8
41	2j	32	ALA	2.8
1	2A	2116	G	2.8
32	1a	1030(A)	G	2.8
34	2c	195	VAL	2.8
44	2m	15	VAL	2.8
44	2m	45	VAL	2.8
33	1b	201	ILE	2.8
46	1o	3	ILE	2.8
34	1c	62	ASP	2.8
11	2P	116	GLY	2.8
17	2V	42	GLY	2.8
36	2e	97	GLY	2.8
51	1t	47	GLY	2.8
53	2y	42	SER	2.8
41	2j	62	HIS	2.8
51	1t	18	GLN	2.8
33	2b	187	LEU	2.8
40	1i	99	LEU	2.8
44	1m	56	LEU	2.8
34	2c	50	ALA	2.8
34	2c	186	PHE	2.8
38	2g	116	ALA	2.8
41	2j	27	ALA	2.8
24	22	25	VAL	2.8
25	23	59	VAL	2.8
32	1a	1001(A)	G	2.8
32	2a	1001(A)	G	2.8
45	2n	33	VAL	2.8
47	1p	53	VAL	2.8
33	2b	132	LYS	2.8
40	2i	95	LYS	2.8
14	1S	13	ARG	2.8
33	2b	130	ARG	2.8
34	2c	67	THR	2.8

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Mol	Chain	Res	Type	RSRZ
38	1g	32	ARG	2.8
26	24	45	GLY	2.8
40	1i	126	SER	2.8
9	1N	8	GLN	2.8
21	2Z	95	PRO	2.8
38	2g	93	PRO	2.8
8	1I	38	LEU	2.8
49	2r	20	ALA	2.8
51	2t	95	ALA	2.8
1	1A	2167	C	2.8
20	2Y	54	LYS	2.8
7	2H	11	VAL	2.8
38	2g	21	VAL	2.8
33	2b	16	HIS	2.8
33	2b	200	ILE	2.8
33	2b	201	ILE	2.8
24	22	70	GLN	2.8
41	1j	31	GLY	2.8
41	2j	93	GLY	2.8
47	2p	10	GLY	2.8
1	1A	2139	A	2.8
1	2A	6	A	2.8
32	2a	1035	A	2.8
34	1c	90	GLU	2.8
38	1g	12	LEU	2.8
47	2p	39	TYR	2.8
45	2n	15	LYS	2.8
21	2Z	189	ALA	2.8
15	2T	111	ARG	2.8
1	1A	1111	U	2.8
1	1A	1128	U	2.8
1	2A	2137	C	2.8
26	24	35	VAL	2.8
40	2i	28	VAL	2.8
41	1j	72	VAL	2.8
47	2p	2	VAL	2.8
31	19	17	ILE	2.7
35	2d	146	ILE	2.7
41	2j	78	ASN	2.7
51	1t	55	ILE	2.7
12	1Q	33	GLY	2.7
26	14	54	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	1A	218	A	2.7
26	24	69	LYS	2.7
47	1p	50	LYS	2.7
7	2H	171	LEU	2.7
45	2n	39	LEU	2.7
35	2d	4	TYR	2.7
38	2g	128	ALA	2.7
21	2Z	136	PHE	2.7
38	1g	62	PHE	2.7
1	1A	1138	C	2.7
1	2A	1509	C	2.7
21	2Z	58	VAL	2.7
50	2s	41	VAL	2.7
34	1c	15	THR	2.7
1	2A	2133	G	2.7
32	2a	1003	G	2.7
34	2c	57	ILE	2.7
42	2k	102	GLY	2.7
41	2j	30	SER	2.7
41	1j	77	PRO	2.7
41	2j	39	PRO	2.7
35	1d	192	GLU	2.7
1	2A	2135	A	2.7
3	2D	275	LYS	2.7
14	2S	33	LYS	2.7
38	2g	156	TRP	2.7
43	1l	20	LYS	2.7
36	2e	10	MET	2.7
3	1D	37	LEU	2.7
35	1d	3	ARG	2.7
42	2k	98	LEU	2.7
44	1m	19	LEU	2.7
44	2m	81	LEU	2.7
33	2b	92	TYR	2.7
36	1e	133	TYR	2.7
45	2n	21	TYR	2.7
51	2t	94	ALA	2.7
33	2b	70	PHE	2.7
34	1c	86	VAL	2.7
35	1d	112	VAL	2.7
40	2i	53	VAL	2.7
20	1Y	92	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
41	2j	100	THR	2.7
45	2n	13	THR	2.7
33	2b	227	GLY	2.7
34	2c	155	GLY	2.7
32	2a	1033	G	2.7
44	2m	113	PRO	2.7
51	1t	98	PRO	2.7
7	2H	42	ARG	2.7
34	2c	190	ARG	2.7
46	2o	68	ARG	2.7
52	2u	6	ARG	2.7
53	1y	70	MET	2.7
6	2G	62	LEU	2.7
33	2b	51	LEU	2.7
33	2b	149	LEU	2.7
35	1d	155	LEU	2.7
32	1a	1000	U	2.7
33	2b	120	ALA	2.7
34	2c	92	ALA	2.7
34	2c	189	ALA	2.7
38	2g	2	ALA	2.7
45	2n	20	ALA	2.7
6	2G	12	TYR	2.7
7	1H	44	VAL	2.7
7	2H	17	VAL	2.7
8	2I	15	VAL	2.7
33	2b	164	VAL	2.7
34	2c	70	VAL	2.7
40	2i	17	VAL	2.7
6	2G	75	LYS	2.7
7	1H	175	LYS	2.7
21	1Z	190	GLU	2.7
6	2G	77	ILE	2.7
34	2c	39	ILE	2.7
34	2c	197	GLY	2.7
50	2s	8	GLY	2.7
44	1m	113	PRO	2.7
19	1X	65	ARG	2.7
26	24	58	ARG	2.7
38	2g	41	ARG	2.7
1	1A	2169	G	2.7
1	1A	2177	G	2.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2110	G	2.7
1	2A	2168	G	2.7
32	2a	1286	A	2.7
19	2X	70	LEU	2.7
37	2f	45	LEU	2.7
47	1p	48	TRP	2.7
51	1t	99	LEU	2.7
1	1A	2154	U	2.6
40	1i	33	PHE	2.6
38	2g	9	VAL	2.6
44	2m	53	VAL	2.6
50	1s	13	ASP	2.6
5	2F	16	GLY	2.6
41	2j	36	GLY	2.6
43	2l	87	GLY	2.6
6	2G	136	ARG	2.6
46	2o	88	ARG	2.6
50	2s	38	SER	2.6
32	1a	630	G	2.6
32	2a	1034	G	2.6
1	2A	1086	A	2.6
1	2A	1095	A	2.6
34	2c	91	LEU	2.6
35	2d	157	LEU	2.6
50	2s	69	HIS	2.6
40	2i	97	LYS	2.6
43	1l	126	LYS	2.6
21	1Z	192	ALA	2.6
34	2c	60	ALA	2.6
34	2c	71	ALA	2.6
45	1n	59	ALA	2.6
41	2j	64	GLU	2.6
35	2d	20	TYR	2.6
42	1k	117	ASN	2.6
15	1T	108	ARG	2.6
50	2s	29	ARG	2.6
52	2u	9	ARG	2.6
6	2G	161	THR	2.6
7	2H	79	VAL	2.6
21	1Z	191	VAL	2.6
33	1b	136	VAL	2.6
35	1d	178	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
15	2T	37	GLY	2.6
36	1e	97	GLY	2.6
40	2i	72	GLY	2.6
44	2m	85	GLY	2.6
50	2s	48	THR	2.6
1	1A	2807	C	2.6
26	24	22	ILE	2.6
1	2A	2160	G	2.6
33	2b	145	LEU	2.6
35	1d	101	LEU	2.6
44	2m	48	LEU	2.6
48	1q	98	LEU	2.6
53	1y	41	LEU	2.6
39	2h	99	GLU	2.6
44	2m	64	TRP	2.6
49	2r	46	GLU	2.6
38	1g	7	ALA	2.6
38	2g	83	ALA	2.6
40	2i	52	ALA	2.6
39	2h	122	ARG	2.6
34	2c	3	ASN	2.6
35	1d	193	ASP	2.6
42	2k	117	ASN	2.6
12	2Q	104	PHE	2.6
41	2j	54	PHE	2.6
6	2G	87	PRO	2.6
27	25	60	VAL	2.6
34	2c	76	VAL	2.6
34	2c	145	GLY	2.6
35	1d	87	GLY	2.6
35	2d	6	GLY	2.6
40	2i	86	VAL	2.6
44	2m	41	PRO	2.6
50	2s	58	VAL	2.6
52	2u	18	TYR	2.6
1	1A	936	C	2.6
1	1A	1162	C	2.6
1	1A	2161	C	2.6
1	1A	2162	C	2.6
3	1D	106	ILE	2.6
35	1d	5	ILE	2.6
14	2S	59	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
38	1g	11	GLN	2.6
40	1i	78	LYS	2.6
40	2i	127	LYS	2.6
48	1q	100	LYS	2.6
1	1A	572	A	2.6
1	1A	2180	A	2.6
8	2I	5	LEU	2.6
34	2c	52	LEU	2.6
44	2m	34	LEU	2.6
1	2A	1083	U	2.6
1	2A	2125	G	2.6
1	2A	2151	G	2.6
25	13	60	GLU	2.6
50	2s	64	GLU	2.6
14	2S	3	ARG	2.6
40	2i	10	ARG	2.6
41	2j	26	ALA	2.6
7	2H	41	MET	2.6
7	2H	129	THR	2.6
26	24	19	GLY	2.6
43	2l	88	GLY	2.6
7	1H	45	VAL	2.6
8	1I	3	VAL	2.6
21	2Z	42	VAL	2.6
33	1b	15	VAL	2.6
33	1b	230	VAL	2.6
34	2c	55	VAL	2.6
34	2c	75	VAL	2.6
45	1n	33	VAL	2.6
49	1r	86	VAL	2.6
6	2G	39	ILE	2.6
34	1c	14	ILE	2.6
34	1c	124	ILE	2.6
34	2c	182	ILE	2.6
1	1A	2168	C	2.6
8	2I	12	LEU	2.5
33	1b	12	GLU	2.5
33	2b	154	LEU	2.5
41	2j	65	LEU	2.5
47	1p	6	LEU	2.5
1	2A	1070	A	2.5
26	24	13	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
21	2Z	192	ALA	2.5
38	2g	107	ALA	2.5
34	1c	80	GLY	2.5
40	2i	103	THR	2.5
6	2G	78	SER	2.5
6	2G	109	VAL	2.5
40	2i	63	ILE	2.5
1	1A	2130	C	2.5
32	1a	1006	C	2.5
50	2s	80	TYR	2.5
33	1b	126	GLU	2.5
33	2b	231	GLU	2.5
41	1j	97	GLU	2.5
1	1A	1985	U	2.5
1	2A	2130	U	2.5
33	1b	221	LEU	2.5
34	2c	101	LEU	2.5
38	2g	22	LEU	2.5
42	2k	103	LEU	2.5
1	1A	2195	A	2.5
32	1a	1030(D)	A	2.5
36	1e	10	MET	2.5
21	1Z	187	ALA	2.5
33	1b	37	ASN	2.5
41	2j	18	ALA	2.5
8	2I	131	LYS	2.5
22	20	8	GLY	2.5
26	24	28	LYS	2.5
44	2m	43	THR	2.5
47	1p	22	THR	2.5
34	2c	22	TRP	2.5
33	1b	124	SER	2.5
33	2b	229	VAL	2.5
34	1c	75	VAL	2.5
34	2c	107	GLN	2.5
34	2c	120	VAL	2.5
50	2s	4	SER	2.5
35	2d	158	ILE	2.5
47	2p	19	ILE	2.5
1	1A	1089	C	2.5
1	2A	1092	C	2.5
26	24	32	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
33	2b	126	GLU	2.5
44	2m	35	GLU	2.5
35	2d	73	ARG	2.5
37	2f	47	ARG	2.5
50	2s	36	ARG	2.5
7	1H	103	LEU	2.5
14	1S	58	LEU	2.5
21	2Z	91	LEU	2.5
38	2g	12	LEU	2.5
41	1j	85	LEU	2.5
1	1A	2148	A	2.5
1	1A	2803	A	2.5
1	2A	1085	A	2.5
15	1T	104	ASN	2.5
20	2Y	94	LYS	2.5
32	1a	1024	G	2.5
32	1a	1031	G	2.5
34	2c	61	ALA	2.5
34	2c	93	LYS	2.5
40	2i	61	ALA	2.5
44	2m	5	ALA	2.5
50	2s	32	LYS	2.5
34	2c	73	PRO	2.5
52	2u	11	GLY	2.5
20	1Y	57	GLN	2.5
6	2G	80	PHE	2.5
8	1I	70	GLU	2.5
35	1d	110	PHE	2.5
21	1Z	96	VAL	2.5
34	2c	54	ARG	2.5
34	2c	84	ILE	2.5
40	2i	9	ARG	2.5
42	2k	42	TRP	2.5
1	1A	2151	C	2.5
1	1A	1220	U	2.5
1	2A	2172	U	2.5
32	2a	1025	U	2.5
1	1A	1507	A	2.5
1	2A	1096	A	2.5
35	1d	165	MET	2.5
34	2c	97	LYS	2.5
44	2m	115	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
35	2d	154	ASN	2.5
40	2i	29	ASN	2.5
33	2b	140	HIS	2.5
44	2m	51	ALA	2.5
1	1A	1218	G	2.5
1	1A	2903	G	2.5
1	2A	2124	G	2.5
1	2A	2149	G	2.5
5	1F	14	PRO	2.5
22	10	8	GLY	2.5
26	24	7	PRO	2.5
26	24	41	PRO	2.5
32	2a	1031	G	2.5
40	2i	49	PRO	2.5
45	1n	14	PRO	2.5
47	1p	76	GLN	2.5
52	2u	4	GLY	2.5
7	2H	119	GLU	2.4
35	2d	50	ARG	2.4
14	2S	49	VAL	2.4
33	1b	28	PHE	2.4
35	2d	113	SER	2.4
38	1g	43	PHE	2.4
51	1t	11	SER	2.4
1	1A	1129	U	2.4
1	2A	1082	U	2.4
32	2a	1000	U	2.4
1	1A	2158	C	2.4
1	2A	1075	C	2.4
14	2S	92	TYR	2.4
37	1f	19	LEU	2.4
41	2j	40	LEU	2.4
44	2m	82	MET	2.4
50	2s	28	LYS	2.4
5	1F	133	ASN	2.4
33	2b	135	GLN	2.4
53	2y	9	GLN	2.4
3	2D	2	ALA	2.4
6	2G	122	PRO	2.4
7	1H	101	ARG	2.4
10	2O	51	ALA	2.4
19	1X	60	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
19	1X	68	ARG	2.4
21	1Z	188	ALA	2.4
20	2Y	80	GLY	2.4
24	12	69	ARG	2.4
34	2c	85	ARG	2.4
40	2i	55	ALA	2.4
45	1n	5	ALA	2.4
35	2d	156	GLU	2.4
47	1p	37	GLY	2.4
50	1s	29	ARG	2.4
50	2s	37	ARG	2.4
1	2A	2106	G	2.4
1	2A	2793	G	2.4
6	2G	63	ILE	2.4
8	2I	107	VAL	2.4
33	1b	214	ILE	2.4
33	2b	152	PHE	2.4
34	2c	8	ILE	2.4
38	1g	120	ILE	2.4
48	2q	9	VAL	2.4
1	2A	1097	U	2.4
1	2A	2113	U	2.4
1	2A	2118	U	2.4
50	2s	55	LYS	2.4
1	2A	1178	C	2.4
6	2G	139	LEU	2.4
32	1a	1028	C	2.4
32	1a	1037	C	2.4
32	2a	89	C	2.4
35	1d	157	LEU	2.4
36	2e	12	LEU	2.4
1	1A	1119	A	2.4
1	2A	1084	A	2.4
32	1a	1035	A	2.4
32	1a	1492	A	2.4
32	1a	1493	A	2.4
32	2a	532	A	2.4
32	2a	1001	A	2.4
33	2b	40	HIS	2.4
7	1H	132	ARG	2.4
33	1b	36	ARG	2.4
35	2d	160	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
38	2g	115	ARG	2.4
43	1l	19	ARG	2.4
44	2m	110	ARG	2.4
50	1s	23	ASN	2.4
21	2Z	159	PRO	2.4
29	27	45	ALA	2.4
34	2c	78	GLY	2.4
40	1i	94	ALA	2.4
42	1k	15	ALA	2.4
50	2s	68	GLY	2.4
33	2b	124	SER	2.4
34	2c	5	ILE	2.4
34	2c	72	LYS	2.4
6	2G	31	VAL	2.4
8	1I	19	VAL	2.4
34	2c	203	PHE	2.4
38	1g	75	VAL	2.4
44	2m	60	VAL	2.4
50	2s	49	ILE	2.4
41	1j	86	MET	2.4
1	1A	1164	C	2.4
1	1A	1579	C	2.4
1	1A	2196	C	2.4
8	2I	38	LEU	2.4
33	2b	19	HIS	2.4
40	2i	36	TYR	2.4
41	2j	68	HIS	2.4
47	1p	38	TYR	2.4
50	2s	3	ARG	2.4
1	1A	1092	A	2.4
10	1O	108	GLU	2.4
44	2m	58	GLU	2.4
21	2Z	62	PRO	2.4
34	2c	7	PRO	2.4
8	1I	90	GLY	2.4
14	2S	22	GLY	2.4
14	2S	105	ALA	2.4
26	24	64	GLY	2.4
36	2e	21	ALA	2.4
38	1g	130	GLY	2.4
40	2i	69	GLY	2.4
42	2k	74	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
44	2m	33	ALA	2.4
53	1y	97	ALA	2.4
43	1l	61	THR	2.4
1	1A	1139	G	2.4
32	1a	1026	G	2.4
32	1a	1030(C)	G	2.4
6	2G	141	PHE	2.4
33	1b	200	ILE	2.4
34	2c	103	VAL	2.4
38	2g	43	PHE	2.4
38	2g	73	MET	2.4
41	1j	38	ILE	2.4
45	2n	25	VAL	2.4
50	2s	62	ILE	2.4
7	2H	7	LEU	2.4
35	1d	176	LEU	2.4
37	2f	48	LEU	2.4
41	2j	71	LEU	2.4
11	1P	15	ARG	2.4
25	23	3	ARG	2.4
42	1k	104	GLN	2.4
7	2H	164	TYR	2.3
15	1T	107	ASP	2.3
36	2e	60	TYR	2.3
43	2l	64	TYR	2.3
52	1u	18	TYR	2.3
52	1u	21	TYR	2.3
53	2y	4	ASN	2.3
1	2A	2134	A	2.3
11	2P	93	GLY	2.3
6	2G	6	ALA	2.3
33	1b	132	LYS	2.3
35	1d	124	GLY	2.3
35	2d	111	ALA	2.3
35	2d	169	LYS	2.3
44	2m	100	GLY	2.3
50	2s	84	GLY	2.3
38	2g	25	ALA	2.3
40	2i	82	ALA	2.3
6	2G	71	THR	2.3
26	24	24	THR	2.3
44	2m	63	THR	2.3

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Mol	Chain	Res	Type	RSRZ
8	1I	42	SER	2.3
41	2j	19	SER	2.3
1	2A	2109	U	2.3
1	1A	2182	G	2.3
1	1A	2227	G	2.3
1	2A	2186	G	2.3
7	1H	115	VAL	2.3
7	2H	99	VAL	2.3
25	13	59	VAL	2.3
33	2b	71	VAL	2.3
33	2b	222	ILE	2.3
35	1d	8	VAL	2.3
39	1h	137	VAL	2.3
40	1i	41	VAL	2.3
40	2i	44	VAL	2.3
49	1r	37	VAL	2.3
12	1Q	5	ARG	2.3
41	2j	79	ARG	2.3
45	2n	35	ARG	2.3
47	2p	49	LEU	2.3
50	2s	16	LEU	2.3
8	2I	85	GLU	2.3
35	2d	150	GLU	2.3
1	1A	1631	C	2.3
1	1A	2183	C	2.3
1	2A	2103	C	2.3
6	1G	146	TYR	2.3
32	2a	1447	A	2.3
40	2i	114	TYR	2.3
52	1u	14	TRP	2.3
33	2b	125	PRO	2.3
5	2F	130	ALA	2.3
34	2c	129	ALA	2.3
34	2c	200	ALA	2.3
36	2e	16	THR	2.3
11	2P	15	ARG	2.3
38	2g	155	ARG	2.3
26	24	15	ILE	2.3
35	2d	70	ILE	2.3
38	2g	50	ILE	2.3
41	1j	6	ILE	2.3
43	1l	7	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
8	2I	127	VAL	2.3
1	1A	1163	G	2.3
32	2a	1024	G	2.3
33	1b	128	GLU	2.3
33	2b	128	GLU	2.3
40	1i	37	PHE	2.3
40	1i	108	VAL	2.3
47	2p	80	PHE	2.3
35	2d	176	LEU	2.3
36	2e	53	LEU	2.3
38	2g	104	LEU	2.3
40	2i	40	LEU	2.3
50	2s	5	LEU	2.3
43	2l	5	PRO	2.3
47	1p	41	PRO	2.3
1	2A	1073	A	2.3
1	2A	2119	A	2.3
6	2G	100	TRP	2.3
7	1H	14	GLY	2.3
26	24	25	TYR	2.3
33	1b	227	GLY	2.3
42	1k	42	TRP	2.3
50	2s	61	TYR	2.3
3	1D	2	ALA	2.3
6	2G	86	MET	2.3
50	2s	33	THR	2.3
5	2F	17	ARG	2.3
32	1a	1020	U	2.3
34	1c	127	ARG	2.3
35	2d	47	ARG	2.3
44	1m	102	ARG	2.3
45	2n	12	ARG	2.3
45	2n	49	HIS	2.3
6	2G	48	GLU	2.3
33	2b	78	GLN	2.3
34	2c	82	GLU	2.3
44	2m	84	ILE	2.3
51	1t	100	ILE	2.3
53	2y	39	ILE	2.3
7	2H	43	VAL	2.3
11	2P	71	VAL	2.3
21	1Z	86	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
29	27	46	VAL	2.3
35	1d	88	VAL	2.3
40	2i	26	VAL	2.3
47	1p	51	VAL	2.3
47	2p	20	VAL	2.3
6	1G	53	LEU	2.3
11	2P	148	LEU	2.3
1	2A	545	G	2.3
1	2A	1533	G	2.3
1	2A	2162	G	2.3
20	1Y	34	LYS	2.3
38	1g	59	LEU	2.3
39	1h	2	LEU	2.3
40	2i	19	LEU	2.3
43	2l	126	LYS	2.3
44	2m	13	LYS	2.3
47	1p	74	LEU	2.3
32	2a	1026	G	2.3
51	1t	9	ASN	2.3
1	1A	2160	C	2.3
1	2A	2174	C	2.3
48	1q	2	PRO	2.3
1	1A	1131	A	2.3
20	1Y	58	GLY	2.3
32	2a	1030(D)	A	2.3
35	1d	180	GLY	2.3
38	2g	133	GLY	2.3
21	2Z	28	MET	2.3
33	2b	48	MET	2.3
8	1I	89	TYR	2.3
6	1G	50	ALA	2.3
7	2H	165	ALA	2.3
21	1Z	80	ARG	2.3
29	27	47	ARG	2.3
30	18	46	ARG	2.3
34	2c	201	TYR	2.3
33	2b	186	ALA	2.3
34	2c	168	ALA	2.3
35	1d	73	ARG	2.3
38	2g	152	ALA	2.3
40	2i	42	ARG	2.3
8	1I	76	THR	2.3

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Mol	Chain	Res	Type	RSRZ
50	1s	39	THR	2.3
38	2g	77	SER	2.3
7	1H	124	GLU	2.3
6	1G	52	ILE	2.3
20	2Y	34	LYS	2.3
34	2c	14	ILE	2.3
35	1d	158	ILE	2.3
35	2d	84	LYS	2.3
41	1j	99	LYS	2.3
45	1n	7	ILE	2.3
46	1o	87	ILE	2.3
53	2y	12	ILE	2.3
8	1I	107	VAL	2.3
11	1P	99	LEU	2.2
34	2c	43	LEU	2.2
35	2d	174	LEU	2.2
38	2g	135	VAL	2.3
41	2j	16	LEU	2.2
42	2k	109	VAL	2.3
45	2n	53	LEU	2.2
47	1p	2	VAL	2.3
48	2q	71	PHE	2.2
1	1A	1108	G	2.2
1	1A	1117	G	2.2
1	2A	1087	G	2.2
1	2A	2121	G	2.2
26	14	51	ASP	2.2
35	1d	154	ASN	2.2
39	2h	15	ASN	2.2
1	1A	155	C	2.2
1	2A	2129	C	2.2
35	2d	39	PRO	2.2
6	1G	113	ARG	2.2
11	1P	79	ARG	2.2
26	24	62	ARG	2.2
35	2d	87	GLY	2.2
35	2d	159	ARG	2.2
38	2g	6	ARG	2.2
47	1p	81	ARG	2.2
51	1t	101	GLY	2.2
52	1u	22	ARG	2.2
1	1A	2157	A	2.2

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Mol	Chain	Res	Type	RSRZ
8	2I	135	GLU	2.2
35	2d	32	ALA	2.2
35	2d	164	ALA	2.2
38	1g	150	ALA	2.2
43	2l	120	TYR	2.2
53	2y	38	HIS	2.2
16	2U	117	GLN	2.2
44	2m	36	LYS	2.2
44	2m	46	LYS	2.2
53	2y	43	LYS	2.2
9	2N	85	ILE	2.2
20	2Y	96	ILE	2.2
39	1h	134	ILE	2.2
21	2Z	86	VAL	2.2
35	1d	174	LEU	2.2
39	2h	97	VAL	2.2
49	2r	31	LEU	2.2
50	2s	22	LEU	2.2
24	12	37	PHE	2.2
34	1c	128	PHE	2.2
50	1s	10	PHE	2.2
33	1b	94	ASN	2.2
33	2b	94	ASN	2.2
52	2u	5	ASP	2.2
1	1A	2155	G	2.2
7	2H	10	PRO	2.2
7	2H	118	PRO	2.2
32	2a	1002	G	2.2
40	1i	42	ARG	2.2
40	1i	98	PRO	2.2
48	1q	91	ARG	2.2
50	2s	78	ARG	2.2
51	1t	25	ARG	2.2
1	2A	2108	C	2.2
1	2A	2161	C	2.2
5	1F	134	GLY	2.2
26	24	53	GLU	2.2
32	2a	1183	A	2.2
43	1l	16	GLU	2.2
33	1b	22	LYS	2.2
33	2b	75	LYS	2.2
34	1c	135	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
38	2g	147	ALA	2.2
51	2t	7	LYS	2.2
40	1i	27	THR	2.2
44	2m	37	THR	2.2
35	2d	71	SER	2.2
38	1g	154	TYR	2.2
39	1h	58	TYR	2.2
41	1j	30	SER	2.2
6	2G	20	ILE	2.2
40	2i	77	ILE	2.2
5	2F	20	LEU	2.2
21	2Z	67	LEU	2.2
40	1i	47	LEU	2.2
6	2G	15	VAL	2.2
7	1H	133	VAL	2.2
21	2Z	90	VAL	2.2
35	2d	92	VAL	2.2
40	1i	17	VAL	2.2
47	1p	80	PHE	2.2
33	2b	144	ARG	2.2
35	2d	3	ARG	2.2
41	2j	70	ARG	2.2
50	1s	12	ASP	2.2
50	2s	65	ASN	2.2
51	2t	86	ARG	2.2
40	2i	21	PRO	2.2
46	2o	19	PRO	2.2
1	1A	2134	G	2.2
1	2A	1089	G	2.2
1	2A	2893	G	2.2
8	2I	84	GLY	2.2
32	1a	1034	G	2.2
32	2a	1030(C)	G	2.2
34	2c	41	GLY	2.2
35	2d	2	GLY	2.2
47	2p	78	GLY	2.2
1	2A	2107	C	2.2
7	2H	175	LYS	2.2
32	1a	1029	C	2.2
32	2a	1038	C	2.2
33	2b	134	GLU	2.2
53	2y	68	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
34	2c	4	LYS	2.2
34	2c	199	LYS	2.2
1	1A	1147	U	2.2
1	1A	1878	A	2.2
1	2A	2176	A	2.2
32	1a	90	U	2.2
8	2I	46	ALA	2.2
34	1c	71	ALA	2.2
40	1i	64	THR	2.2
40	2i	45	ALA	2.2
42	1k	31	THR	2.2
45	1n	22	THR	2.2
45	2n	10	ALA	2.2
45	2n	30	ALA	2.2
45	2n	60	SER	2.2
51	1t	70	SER	2.2
4	1E	151	TYR	2.2
33	2b	31	TYR	2.2
33	2b	33	TYR	2.2
42	1k	75	TYR	2.2
52	2u	21	TYR	2.2
34	2c	18	TRP	2.2
34	2c	167	TRP	2.2
45	2n	61	TRP	2.2
3	2D	106	ILE	2.2
6	2G	140	ILE	2.2
14	2S	40	ILE	2.2
6	2G	83	ARG	2.2
6	2G	175	LEU	2.2
7	1H	6	ARG	2.2
14	1S	20	ARG	2.2
18	2W	92	ARG	2.2
33	1b	213	LEU	2.2
33	2b	41	ILE	2.2
33	2b	69	LEU	2.2
41	1j	50	ILE	2.2
44	1m	3	ARG	2.2
11	2P	1	MET	2.2
33	2b	189	ASP	2.2
40	2i	65	VAL	2.2
41	1j	44	VAL	2.2
47	1p	79	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
40	1i	101	PHE	2.2
40	2i	37	PHE	2.2
50	2s	66	MET	2.2
33	1b	202	PRO	2.2
33	2b	91	PRO	2.2
33	2b	234	PRO	2.2
40	2i	123	PRO	2.2
19	1X	15	GLU	2.2
26	14	53	GLU	2.2
38	2g	8	GLU	2.2
21	1Z	147	GLY	2.2
26	24	4	GLY	2.2
26	24	46	GLN	2.2
33	1b	14	GLY	2.2
33	2b	95	GLN	2.2
35	2d	23	GLY	2.2
38	2g	82	GLY	2.2
42	2k	104	GLN	2.2
1	1A	1584	G	2.2
1	2A	2105	C	2.2
1	2A	2185	C	2.2
32	2a	5	U	2.2
6	1G	73	ALA	2.2
7	2H	145	ALA	2.2
8	2I	55	ALA	2.2
8	2I	115	ALA	2.2
33	1b	13	ALA	2.2
33	2b	62	ALA	2.2
33	2b	73	THR	2.2
34	2c	146	ALA	2.2
35	1d	111	ALA	2.2
39	1h	24	THR	2.2
40	2i	15	ALA	2.2
47	2p	45	THR	2.2
52	2u	8	THR	2.2
53	2y	97	ALA	2.2
34	1c	132	ARG	2.1
38	1g	5	ARG	2.1
38	1g	79	ARG	2.1
48	1q	68	ARG	2.1
49	1r	42	ARG	2.1
49	1r	87	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	107	LEU	2.1
6	2G	157	ILE	2.1
7	1H	148	ILE	2.1
7	2H	98	LEU	2.1
7	2H	103	LEU	2.1
14	2S	80	LEU	2.1
20	2Y	61	ILE	2.1
33	2b	39	ILE	2.1
34	2c	32	LEU	2.1
41	1j	96	ILE	2.1
38	2g	103	TRP	2.1
49	1r	78	LEU	2.1
6	2G	49	ASP	2.1
29	27	1	MET	2.1
40	1i	109	VAL	2.1
41	1j	73	ASP	2.1
53	2y	3	MET	2.1
6	2G	160	VAL	2.1
33	2b	197	VAL	2.1
42	2k	14	VAL	2.1
47	1p	62	VAL	2.1
6	2G	117	PHE	2.1
20	2Y	89	PHE	2.1
33	2b	55	PHE	2.1
34	1c	203	PHE	2.1
35	2d	110	PHE	2.1
50	2s	18	LYS	2.1
19	2X	67	GLY	2.1
50	1s	82	GLY	2.1
1	1A	670	C	2.1
1	2A	2165	G	2.1
1	2A	2126	A	2.1
19	2X	91	ALA	2.1
34	1c	60	ALA	2.1
34	1c	100	ALA	2.1
34	1c	192	THR	2.1
49	2r	47	THR	2.1
7	2H	23	ARG	2.1
7	2H	51	ARG	2.1
9	2N	74	ARG	2.1
16	1U	59	ARG	2.1
26	14	68	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
34	2c	83	ARG	2.1
41	1j	66	ARG	2.1
41	2j	43	ARG	2.1
44	2m	3	ARG	2.1
4	2E	1	MET	2.1
34	1c	48	TYR	2.1
34	2c	184	TYR	2.1
8	1I	6	LEU	2.1
8	2I	4	ILE	2.1
23	21	78	LYS	2.1
33	2b	61	LEU	2.1
33	2b	142	LEU	2.1
38	2g	27	ILE	2.1
40	1i	95	LYS	2.1
42	1k	106	LYS	2.1
44	2m	65	LYS	2.1
47	1p	49	LEU	2.1
33	2b	12	GLU	2.1
47	2p	47	ASP	2.1
5	1F	6	VAL	2.1
6	2G	38	VAL	2.1
6	2G	149	VAL	2.1
35	1d	121	VAL	2.1
35	2d	88	VAL	2.1
35	2d	178	VAL	2.1
41	2j	49	VAL	2.1
11	2P	91	PHE	2.1
40	2i	31	GLN	2.1
7	2H	22	GLY	2.1
39	2h	47	GLY	2.1
1	1A	271	U	2.1
1	1A	933	C	2.1
1	1A	1086	C	2.1
1	1A	2159	C	2.1
1	1A	299	G	2.1
1	1A	678	A	2.1
1	1A	1085	G	2.1
1	1A	1103	A	2.1
1	1A	1130	A	2.1
1	2A	887	A	2.1
1	2A	2127	G	2.1
10	1O	49	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
11	2P	79	ARG	2.1
21	2Z	131	ARG	2.1
26	24	68	ARG	2.1
34	1c	79	ARG	2.1
46	2o	79	ARG	2.1
47	1p	25	ARG	2.1
21	2Z	129	SER	2.1
40	2i	46	ALA	2.1
42	2k	89	ALA	2.1
44	2m	72	ALA	2.1
51	1t	59	ALA	2.1
41	2j	14	LYS	2.1
43	2l	13	LYS	2.1
6	1G	135	LEU	2.1
6	2G	137	GLU	2.1
6	2G	152	LEU	2.1
14	1S	4	LEU	2.1
34	1c	42	LEU	2.1
8	1I	29	TYR	2.1
8	1I	138	ILE	2.1
8	2I	71	ILE	2.1
11	2P	147	LEU	2.1
41	1j	8	LEU	2.1
53	2y	41	LEU	2.1
6	1G	126	ASP	2.1
41	2j	69	ASN	2.1
43	2l	8	ASN	2.1
33	2b	113	HIS	2.1
8	1I	134	PRO	2.1
14	2S	46	VAL	2.1
21	1Z	180	VAL	2.1
25	23	58	VAL	2.1
34	2c	153	VAL	2.1
35	1d	148	VAL	2.1
35	2d	140	VAL	2.1
40	1i	21	PRO	2.1
47	1p	66	PRO	2.1
50	2s	67	VAL	2.1
51	2t	98	PRO	2.1
52	1u	23	PRO	2.1
12	2Q	65	PHE	2.1
40	2i	33	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
50	1s	34	TRP	2.1
5	1F	16	GLY	2.1
19	1X	94	GLY	2.1
20	1Y	93	GLY	2.1
40	2i	57	GLY	2.1
45	2n	38	GLY	2.1
1	1A	1466	U	2.1
1	2A	2180	U	2.1
15	2T	112	ARG	2.1
39	2h	102	ARG	2.1
43	2l	19	ARG	2.1
45	2n	29	ARG	2.1
1	2A	2178	C	2.1
6	2G	145	THR	2.1
32	1a	1027	C	2.1
46	2o	4	THR	2.1
53	2y	7	SER	2.1
1	1A	569	G	2.1
1	1A	1088	G	2.1
1	1A	2147	G	2.1
1	2A	1068	G	2.1
21	2Z	184	ALA	2.1
24	12	15	LYS	2.1
33	1b	133	LYS	2.1
44	2m	18	ALA	2.1
51	1t	97	ALA	2.1
52	2u	3	LYS	2.1
15	1T	1	MET	2.1
21	1Z	1	MET	2.1
24	12	11	GLU	2.1
7	2H	65	HIS	2.1
12	1Q	135	ASP	2.1
33	2b	223	ILE	2.1
34	1c	28	GLN	2.1
34	2c	6	HIS	2.1
34	2c	157	ILE	2.1
40	2i	81	ILE	2.1
41	1j	84	GLN	2.1
6	2G	112	PRO	2.1
7	1H	126	PRO	2.1
7	2H	83	TYR	2.1
33	1b	148	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
35	1d	106	TYR	2.1
6	2G	28	VAL	2.1
7	2H	37	VAL	2.1
34	2c	130	VAL	2.1
35	1d	17	VAL	2.1
35	2d	170	VAL	2.1
38	2g	61	VAL	2.1
39	2h	19	VAL	2.1
41	2j	94	VAL	2.1
45	2n	56	VAL	2.1
6	2G	23	PHE	2.1
7	1H	123	PHE	2.1
8	2I	106	GLY	2.1
33	1b	18	GLY	2.1
34	2c	194	GLY	2.1
50	2s	72	GLY	2.1
32	1a	1040	U	2.1
32	2a	90	U	2.1
40	1i	66	ARG	2.1
40	1i	107	ARG	2.1
41	2j	45	ARG	2.1
20	2Y	81	LYS	2.0
45	1n	17	LYS	2.0
48	2q	100	LYS	2.0
50	2s	70	LYS	2.0
1	2A	888	C	2.0
1	2A	1079	C	2.0
20	2Y	52	SER	2.0
33	2b	192	SER	2.0
33	2b	235	SER	2.0
40	2i	64	THR	2.0
41	2j	92	THR	2.0
47	2p	69	THR	2.0
5	2F	22	ALA	2.0
8	1I	85	GLU	2.0
26	24	39	CYS	2.0
32	1a	1447	A	2.0
36	2e	86	ALA	2.0
38	2g	89	MET	2.0
34	1c	58	GLU	2.0
40	1i	52	ALA	2.0
41	2j	20	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
42	2k	92	GLU	2.0
44	2m	76	ALA	2.0
53	1y	68	GLU	2.0
1	1A	2149	G	2.0
1	2A	2159	G	2.0
21	1Z	91	LEU	2.0
38	2g	20	ASP	2.0
38	2g	99	LEU	2.0
39	2h	112	LEU	2.0
50	2s	42	PRO	2.0
44	2m	23	TYR	2.0
8	2I	92	VAL	2.0
26	14	55	ARG	2.0
38	1g	6	ARG	2.0
38	2g	17	VAL	2.0
41	2j	28	ARG	2.0
44	2m	74	VAL	2.0
52	2u	15	ARG	2.0
1	1A	12	U	2.0
6	2G	127	GLY	2.0
7	2H	48	GLY	2.0
34	2c	185	GLY	2.0
35	2d	44	GLY	2.0
42	2k	76	GLY	2.0
52	1u	2	GLY	2.0
14	2S	12	PHE	2.0
33	2b	105	PHE	2.0
35	1d	185	PHE	2.0
40	1i	18	PHE	2.0
45	2n	37	PHE	2.0
49	1r	29	PHE	2.0
49	1r	43	PHE	2.0
33	2b	156	LYS	2.0
46	1o	84	LYS	2.0
8	2I	129	THR	2.0
22	20	43	THR	2.0
23	21	83	GLU	2.0
40	2i	35	GLU	2.0
45	2n	32	SER	2.0
1	1A	2192	A	2.0
1	2A	652(T)	C	2.0
1	2A	2173	A	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2789	C	2.0
32	2a	1004	A	2.0
32	2a	1029	C	2.0
32	2a	1037	C	2.0
32	2a	1531	A	2.0
36	2e	94	ALA	2.0
51	1t	94	ALA	2.0
34	2c	176	HIS	2.0
38	2g	11	GLN	2.0
50	2s	47	HIS	2.0
1	1A	2171	G	2.0
1	2A	2131	G	2.0
6	2G	111	LEU	2.0
14	2S	32	LEU	2.0
14	2S	78	LEU	2.0
34	1c	12	LEU	2.0
34	1c	181	ASN	2.0
44	2m	19	LEU	2.0
3	1D	263	ARG	2.0
7	2H	8	PRO	2.0
7	2H	72	ILE	2.0
7	2H	128	PRO	2.0
35	2d	37	PRO	2.0
38	2g	79	ARG	2.0
45	2n	42	ILE	2.0
46	1o	19	PRO	2.0
46	1o	88	ARG	2.0
46	2o	17	ARG	2.0
47	1p	36	ILE	2.0
51	1t	86	ARG	2.0
43	1l	17	LYS	2.0
53	2y	8	LYS	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	5MU	2A	1915	21/22	0.80	0.15	70,82,87,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	PSU	2A	1917	20/21	0.85	0.13	62,74,84,89	0
1	5MU	1A	1937	21/22	0.87	0.13	65,79,86,95	0
32	M2G	2a	966	25/26	0.87	0.14	52,68,81,90	0
1	PSU	2A	1911	20/21	0.88	0.11	62,68,73,82	0
32	2MG	2a	1207	24/25	0.88	0.12	75,83,90,94	0
1	PSU	1A	1939	20/21	0.89	0.11	63,73,82,86	0
43	0TD	2l	92	10/11	0.91	0.12	57,63,66,74	0
32	PSU	2a	516	20/21	0.92	0.10	69,76,81,82	0
1	4OC	2A	1920	21/23	0.92	0.11	57,62,67,67	0
43	0TD	1l	92	10/11	0.93	0.14	54,59,68,68	0
32	5MC	2a	967	21/22	0.93	0.10	61,68,77,86	0
32	2MG	1a	1207	24/25	0.93	0.10	60,68,71,74	0
32	7MG	2a	527	24/25	0.93	0.12	57,66,70,73	0
32	4OC	2a	1402	22/23	0.94	0.10	53,64,74,82	0
32	5MC	1a	967	21/22	0.94	0.11	51,61,73,83	0
1	PSU	1A	1933	20/21	0.95	0.08	59,66,68,81	0
32	5MC	2a	1404	21/22	0.95	0.09	54,61,64,67	0
32	5MC	2a	1407	21/22	0.95	0.10	46,62,69,70	0
32	UR3	2a	1498	21/22	0.95	0.09	53,60,65,73	0
32	PSU	1a	516	20/21	0.95	0.08	49,58,65,67	0
32	5MC	1a	1400	21/22	0.96	0.09	37,50,57,58	0
32	5MC	1a	1407	21/22	0.96	0.09	41,48,54,56	0
32	5MC	2a	1400	21/22	0.96	0.10	62,68,74,77	0
32	UR3	1a	1498	21/22	0.96	0.08	35,46,53,56	0
1	5MC	2A	1942	21/22	0.96	0.08	36,45,52,53	0
32	MA6	1a	1519	24/25	0.96	0.10	40,45,52,52	0
1	4OC	1A	1942	21/23	0.96	0.11	52,60,63,65	0
32	MA6	2a	1518	24/25	0.96	0.08	47,58,65,68	0
32	7MG	1a	527	24/25	0.96	0.08	40,48,55,55	0
32	MA6	1a	1518	24/25	0.97	0.09	37,44,51,56	0
32	4OC	1a	1402	22/23	0.97	0.07	41,47,51,56	0
32	5MC	1a	1404	21/22	0.97	0.07	33,43,49,51	0
32	M2G	1a	966	25/26	0.97	0.08	48,53,59,65	0
32	MA6	2a	1519	24/25	0.97	0.09	51,61,64,69	0
1	5MC	1A	1964	21/22	0.97	0.07	34,41,47,52	0
1	5MU	1A	1961	21/22	0.98	0.06	24,30,34,37	0
1	5MC	1A	1984	21/22	0.98	0.06	29,36,41,47	0
1	5MU	2A	1939	21/22	0.98	0.06	28,33,37,42	0
1	2MA	1A	2515	23/24	0.98	0.07	17,23,28,31	0
1	5MC	2A	1962	21/22	0.98	0.08	32,38,44,54	0
1	OMG	2A	2251	24/25	0.98	0.07	27,31,35,37	0
1	2MA	2A	2503	23/24	0.98	0.06	21,28,32,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	2MU	2A	2552	21/23	0.98	0.06	27,33,38,38	0
1	PSU	2A	2605	20/21	0.98	0.06	27,31,39,41	0
1	2MU	1A	2564	21/23	0.98	0.06	24,29,33,36	0
1	PSU	1A	2617	20/21	0.98	0.07	23,29,35,38	0
1	OMG	1A	2263	24/25	0.99	0.06	22,28,29,33	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3990	1/1	0.44	0.29	83,83,83,83	0
54	MG	1a	1788	1/1	0.46	0.22	85,85,85,85	0
54	MG	1A	3747	1/1	0.52	0.16	62,62,62,62	0
54	MG	1a	1773	1/1	0.56	0.26	85,85,85,85	0
54	MG	1A	3513	1/1	0.57	0.21	58,58,58,58	0
54	MG	1a	1850	1/1	0.57	0.21	94,94,94,94	0
54	MG	2O	202	1/1	0.59	0.37	94,94,94,94	0
54	MG	1A	3295	1/1	0.60	0.28	84,84,84,84	0
54	MG	1A	3496	1/1	0.62	0.18	56,56,56,56	0
54	MG	1a	1719	1/1	0.62	0.19	94,94,94,94	0
54	MG	14	502	1/1	0.64	0.14	83,83,83,83	0
54	MG	1A	3528	1/1	0.64	0.23	61,61,61,61	0
54	MG	1A	3612	1/1	0.64	0.43	66,66,66,66	0
54	MG	2a	1787	1/1	0.64	0.27	82,82,82,82	0
54	MG	1a	1744	1/1	0.65	0.38	88,88,88,88	0
54	MG	1A	3579	1/1	0.65	0.22	74,74,74,74	0
54	MG	1T	8003	1/1	0.65	0.21	72,72,72,72	0
54	MG	1a	1836	1/1	0.66	0.24	83,83,83,83	0
54	MG	2A	3478	1/1	0.67	0.28	64,64,64,64	0
54	MG	2B	3015	1/1	0.68	0.18	87,87,87,87	0
54	MG	2A	3360	1/1	0.68	0.20	72,72,72,72	0
54	MG	2a	1667	1/1	0.68	0.23	83,83,83,83	0
54	MG	1A	3964	1/1	0.68	0.19	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3810	1/1	0.69	0.26	80,80,80,80	0
54	MG	2A	3408	1/1	0.70	0.33	74,74,74,74	0
54	MG	1B	221	1/1	0.70	0.15	48,48,48,48	0
54	MG	1A	3377	1/1	0.70	0.28	67,67,67,67	0
54	MG	2A	3509	1/1	0.71	0.19	75,75,75,75	0
54	MG	1A	3949	1/1	0.71	0.23	69,69,69,69	0
54	MG	1a	1732	1/1	0.71	0.24	92,92,92,92	0
54	MG	1a	1791	1/1	0.71	0.14	72,72,72,72	0
54	MG	1A	3593	1/1	0.71	0.15	62,62,62,62	0
54	MG	2A	3502	1/1	0.72	0.17	61,61,61,61	0
54	MG	1a	1872	1/1	0.72	0.26	83,83,83,83	0
54	MG	2A	3720	1/1	0.72	0.17	55,55,55,55	0
54	MG	2A	3231	1/1	0.72	0.14	61,61,61,61	0
54	MG	1a	1803	1/1	0.72	0.21	87,87,87,87	0
54	MG	1A	3664	1/1	0.72	0.13	60,60,60,60	0
54	MG	1A	3889	1/1	0.72	0.22	47,47,47,47	0
54	MG	1A	3788	1/1	0.73	0.27	66,66,66,66	0
54	MG	2A	3495	1/1	0.73	0.12	54,54,54,54	0
54	MG	1A	3577	1/1	0.73	0.23	41,41,41,41	0
54	MG	1A	3833	1/1	0.73	0.18	60,60,60,60	0
54	MG	2A	3582	1/1	0.73	0.16	70,70,70,70	0
54	MG	1A	3882	1/1	0.73	0.23	74,74,74,74	0
54	MG	1A	3643	1/1	0.73	0.21	72,72,72,72	0
54	MG	1A	3415	1/1	0.73	0.15	63,63,63,63	0
54	MG	1A	3694	1/1	0.73	0.25	69,69,69,69	0
54	MG	1A	3511	1/1	0.73	0.15	64,64,64,64	0
54	MG	2a	1788	1/1	0.73	0.15	102,102,102,102	0
54	MG	2A	3729	1/1	0.74	0.12	59,59,59,59	0
54	MG	2A	3438	1/1	0.74	0.16	56,56,56,56	0
54	MG	2A	3465	1/1	0.74	0.23	67,67,67,67	0
54	MG	1A	3331	1/1	0.74	0.23	75,75,75,75	0
54	MG	2a	1689	1/1	0.74	0.23	70,70,70,70	0
54	MG	2A	3593	1/1	0.74	0.14	48,48,48,48	0
54	MG	1a	1834	1/1	0.74	0.20	59,59,59,59	0
54	MG	1a	1751	1/1	0.75	0.22	67,67,67,67	0
54	MG	1A	3583	1/1	0.75	0.16	43,43,43,43	0
54	MG	1A	3631	1/1	0.75	0.38	74,74,74,74	0
54	MG	2A	3426	1/1	0.75	0.18	58,58,58,58	0
54	MG	2A	3157	1/1	0.75	0.24	68,68,68,68	0
54	MG	2A	3584	1/1	0.76	0.24	49,49,49,49	0
54	MG	1a	1815	1/1	0.76	0.16	75,75,75,75	0
54	MG	1A	3553	1/1	0.76	0.24	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1a	1752	1/1	0.76	0.20	73,73,73,73	0
54	MG	1B	207	1/1	0.76	0.23	68,68,68,68	0
54	MG	2E	303	1/1	0.76	0.27	72,72,72,72	0
54	MG	1A	3866	1/1	0.76	0.13	64,64,64,64	0
54	MG	1A	3573	1/1	0.76	0.21	59,59,59,59	0
54	MG	1a	1793	1/1	0.76	0.15	67,67,67,67	0
54	MG	2a	1693	1/1	0.76	0.35	88,88,88,88	0
54	MG	2a	1724	1/1	0.76	0.30	82,82,82,82	0
54	MG	2A	3306	1/1	0.76	0.14	56,56,56,56	0
54	MG	1a	1749	1/1	0.76	0.19	70,70,70,70	0
54	MG	1A	3328	1/1	0.77	0.16	19,19,19,19	0
54	MG	1A	3890	1/1	0.77	0.22	62,62,62,62	0
54	MG	1A	3432	1/1	0.77	0.19	67,67,67,67	0
54	MG	1a	1762	1/1	0.77	0.23	80,80,80,80	0
54	MG	2A	3534	1/1	0.77	0.29	78,78,78,78	0
54	MG	1A	3858	1/1	0.77	0.14	68,68,68,68	0
54	MG	1A	3639	1/1	0.77	0.11	65,65,65,65	0
54	MG	1A	3407	1/1	0.77	0.19	66,66,66,66	0
54	MG	2A	3598	1/1	0.77	0.15	72,72,72,72	0
54	MG	2A	3129	1/1	0.77	0.11	63,63,63,63	0
54	MG	1g	203	1/1	0.78	0.28	78,78,78,78	0
54	MG	2A	3609	1/1	0.78	0.13	58,58,58,58	0
54	MG	2A	3717	1/1	0.78	0.14	60,60,60,60	0
54	MG	2A	3464	1/1	0.78	0.23	63,63,63,63	0
54	MG	1q	202	1/1	0.78	0.25	73,73,73,73	0
54	MG	1A	3825	1/1	0.78	0.20	70,70,70,70	0
54	MG	1A	3224	1/1	0.78	0.15	69,69,69,69	0
54	MG	1a	1841	1/1	0.78	0.20	61,61,61,61	0
54	MG	2a	1649	1/1	0.78	0.17	75,75,75,75	0
54	MG	2a	1650	1/1	0.78	0.30	74,74,74,74	0
54	MG	2a	1656	1/1	0.78	0.22	69,69,69,69	0
54	MG	2A	3277	1/1	0.78	0.17	58,58,58,58	0
54	MG	2a	1668	1/1	0.78	0.31	77,77,77,77	0
54	MG	1a	1685	1/1	0.78	0.18	75,75,75,75	0
54	MG	2A	3569	1/1	0.78	0.20	55,55,55,55	0
54	MG	1a	1859	1/1	0.78	0.19	72,72,72,72	0
54	MG	1B	225	1/1	0.78	0.27	68,68,68,68	0
54	MG	1a	1878	1/1	0.78	0.20	66,66,66,66	0
54	MG	2A	3384	1/1	0.79	0.13	46,46,46,46	0
54	MG	1A	3973	1/1	0.79	0.15	44,44,44,44	0
54	MG	2G	3002	1/1	0.79	0.20	79,79,79,79	0
54	MG	2A	3418	1/1	0.79	0.17	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2a	1637	1/1	0.79	0.19	92,92,92,92	0
54	MG	2a	1641	1/1	0.79	0.29	70,70,70,70	0
54	MG	1A	3975	1/1	0.79	0.18	52,52,52,52	0
54	MG	2A	3576	1/1	0.79	0.14	49,49,49,49	0
54	MG	2A	3431	1/1	0.79	0.19	57,57,57,57	0
54	MG	2a	1666	1/1	0.79	0.30	78,78,78,78	0
54	MG	1A	3870	1/1	0.79	0.23	71,71,71,71	0
54	MG	1A	3171	1/1	0.79	0.14	56,56,56,56	0
54	MG	2a	1687	1/1	0.79	0.26	82,82,82,82	0
54	MG	1a	1874	1/1	0.79	0.14	66,66,66,66	0
54	MG	2A	3468	1/1	0.79	0.20	72,72,72,72	0
54	MG	2a	1719	1/1	0.79	0.22	76,76,76,76	0
54	MG	1A	3960	1/1	0.79	0.15	71,71,71,71	0
54	MG	2A	3481	1/1	0.79	0.15	69,69,69,69	0
54	MG	1A	3566	1/1	0.79	0.15	60,60,60,60	0
54	MG	2j	8001	1/1	0.79	0.12	82,82,82,82	0
54	MG	1A	4003	1/1	0.80	0.23	66,66,66,66	0
54	MG	1A	3365	1/1	0.80	0.19	69,69,69,69	0
54	MG	2A	3336	1/1	0.80	0.15	55,55,55,55	0
54	MG	1A	3752	1/1	0.80	0.21	57,57,57,57	0
54	MG	2A	3365	1/1	0.80	0.23	68,68,68,68	0
54	MG	1A	3763	1/1	0.80	0.18	53,53,53,53	0
54	MG	1B	227	1/1	0.80	0.14	76,76,76,76	0
54	MG	1a	1800	1/1	0.80	0.18	70,70,70,70	0
54	MG	1F	307	1/1	0.80	0.17	49,49,49,49	0
54	MG	1F	309	1/1	0.80	0.16	69,69,69,69	0
54	MG	2a	1633	1/1	0.80	0.32	69,69,69,69	0
54	MG	1A	3576	1/1	0.80	0.21	57,57,57,57	0
54	MG	1A	3916	1/1	0.80	0.30	68,68,68,68	0
54	MG	1a	1602	1/1	0.80	0.14	73,73,73,73	0
54	MG	1a	1659	1/1	0.80	0.28	76,76,76,76	0
54	MG	1a	1676	1/1	0.80	0.35	75,75,75,75	0
54	MG	2a	1664	1/1	0.80	0.29	79,79,79,79	0
54	MG	1A	3530	1/1	0.80	0.18	69,69,69,69	0
54	MG	2A	3486	1/1	0.80	0.13	63,63,63,63	0
54	MG	1a	1702	1/1	0.80	0.21	67,67,67,67	0
54	MG	1A	3426	1/1	0.80	0.14	34,34,34,34	0
54	MG	1A	3963	1/1	0.80	0.20	67,67,67,67	0
54	MG	2A	3526	1/1	0.80	0.18	66,66,66,66	0
54	MG	2a	1706	1/1	0.80	0.19	74,74,74,74	0
54	MG	2a	1710	1/1	0.80	0.30	71,71,71,71	0
54	MG	1A	3830	1/1	0.80	0.14	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2a	1721	1/1	0.80	0.24	71,71,71,71	0
54	MG	1A	3557	1/1	0.80	0.16	61,61,61,61	0
54	MG	2a	1778	1/1	0.80	0.14	79,79,79,79	0
54	MG	1A	3371	1/1	0.80	0.14	65,65,65,65	0
54	MG	2A	3174	1/1	0.80	0.22	61,61,61,61	0
54	MG	2a	1789	1/1	0.80	0.37	80,80,80,80	0
54	MG	1A	3706	1/1	0.80	0.17	64,64,64,64	0
55	MPD	1a	1880	8/8	0.80	0.22	48,59,72,72	0
54	MG	1A	3431	1/1	0.81	0.13	61,61,61,61	0
54	MG	1A	3688	1/1	0.81	0.26	80,80,80,80	0
54	MG	2B	3006	1/1	0.81	0.27	72,72,72,72	0
54	MG	2A	3414	1/1	0.81	0.26	65,65,65,65	0
54	MG	1a	1822	1/1	0.81	0.26	68,68,68,68	0
54	MG	2A	3527	1/1	0.81	0.13	66,66,66,66	0
54	MG	1A	3786	1/1	0.81	0.21	64,64,64,64	0
54	MG	2a	1630	1/1	0.81	0.24	71,71,71,71	0
54	MG	1a	1684	1/1	0.81	0.37	73,73,73,73	0
54	MG	1a	1768	1/1	0.81	0.17	71,71,71,71	0
54	MG	1A	3434	1/1	0.81	0.29	72,72,72,72	0
54	MG	1A	3450	1/1	0.81	0.15	57,57,57,57	0
54	MG	2A	3329	1/1	0.81	0.19	60,60,60,60	0
54	MG	1A	4051	1/1	0.81	0.22	52,52,52,52	0
54	MG	1W	3001	1/1	0.81	0.24	59,59,59,59	0
54	MG	1A	3646	1/1	0.81	0.31	81,81,81,81	0
54	MG	2A	3633	1/1	0.82	0.30	68,68,68,68	0
54	MG	2A	3513	1/1	0.82	0.22	58,58,58,58	0
54	MG	2A	3524	1/1	0.82	0.15	64,64,64,64	0
54	MG	1B	217	1/1	0.82	0.20	70,70,70,70	0
54	MG	2B	3001	1/1	0.82	0.13	68,68,68,68	0
54	MG	2B	3002	1/1	0.82	0.17	72,72,72,72	0
54	MG	2a	1686	1/1	0.82	0.26	66,66,66,66	0
54	MG	1a	1696	1/1	0.82	0.25	68,68,68,68	0
54	MG	2A	3528	1/1	0.82	0.29	67,67,67,67	0
54	MG	2D	301	1/1	0.82	0.24	55,55,55,55	0
54	MG	2A	3387	1/1	0.82	0.21	55,55,55,55	0
54	MG	1A	3625	1/1	0.82	0.16	63,63,63,63	0
54	MG	2A	3292	1/1	0.82	0.16	55,55,55,55	0
54	MG	2a	1609	1/1	0.82	0.33	74,74,74,74	0
54	MG	2a	1618	1/1	0.82	0.11	75,75,75,75	0
54	MG	1a	1811	1/1	0.82	0.26	78,78,78,78	0
54	MG	2A	3055	1/1	0.82	0.12	54,54,54,54	0
54	MG	2A	3498	1/1	0.82	0.16	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2a	1638	1/1	0.82	0.19	62,62,62,62	0
54	MG	1a	1705	1/1	0.82	0.16	56,56,56,56	0
54	MG	1a	1613	1/1	0.82	0.43	71,71,71,71	0
55	MPD	2B	3020	8/8	0.82	0.23	47,70,77,79	0
54	MG	1A	3680	1/1	0.83	0.12	66,66,66,66	0
54	MG	1A	3922	1/1	0.83	0.10	30,30,30,30	0
54	MG	1A	3571	1/1	0.83	0.13	65,65,65,65	0
54	MG	1a	1776	1/1	0.83	0.27	80,80,80,80	0
54	MG	2A	3388	1/1	0.83	0.17	55,55,55,55	0
54	MG	1a	1689	1/1	0.83	0.39	73,73,73,73	0
54	MG	1b	3001	1/1	0.83	0.18	87,87,87,87	0
54	MG	1d	506	1/1	0.83	0.10	93,93,93,93	0
54	MG	2A	3420	1/1	0.83	0.16	54,54,54,54	0
54	MG	2a	1661	1/1	0.83	0.34	74,74,74,74	0
54	MG	1A	3038	1/1	0.83	0.18	60,60,60,60	0
54	MG	1A	3697	1/1	0.83	0.20	53,53,53,53	0
54	MG	2A	3035	1/1	0.83	0.21	67,67,67,67	0
54	MG	1A	3400	1/1	0.83	0.18	61,61,61,61	0
54	MG	1A	3721	1/1	0.83	0.21	64,64,64,64	0
54	MG	2A	3467	1/1	0.83	0.19	67,67,67,67	0
54	MG	1a	1805	1/1	0.83	0.17	68,68,68,68	0
54	MG	1A	3294	1/1	0.83	0.15	74,74,74,74	0
54	MG	2a	1705	1/1	0.83	0.17	75,75,75,75	0
54	MG	2A	3226	1/1	0.83	0.31	69,69,69,69	0
54	MG	2A	3484	1/1	0.83	0.18	66,66,66,66	0
54	MG	2B	3010	1/1	0.83	0.23	80,80,80,80	0
54	MG	1a	1736	1/1	0.83	0.23	66,66,66,66	0
54	MG	1A	3219	1/1	0.83	0.21	65,65,65,65	0
54	MG	2a	1771	1/1	0.83	0.15	86,86,86,86	0
54	MG	2a	1774	1/1	0.83	0.18	66,66,66,66	0
54	MG	1a	1832	1/1	0.83	0.19	72,72,72,72	0
54	MG	1A	3418	1/1	0.83	0.15	55,55,55,55	0
54	MG	1A	3765	1/1	0.83	0.16	71,71,71,71	0
54	MG	2R	8001	1/1	0.83	0.15	52,52,52,52	0
54	MG	21	101	1/1	0.83	0.09	69,69,69,69	0
54	MG	2a	1603	1/1	0.83	0.17	69,69,69,69	0
55	MPD	2A	3747	8/8	0.83	0.27	37,47,59,61	0
54	MG	1A	3312	1/1	0.83	0.23	72,72,72,72	0
54	MG	1A	3590	1/1	0.84	0.19	72,72,72,72	0
54	MG	2A	3247	1/1	0.84	0.21	55,55,55,55	0
54	MG	2a	1640	1/1	0.84	0.30	66,66,66,66	0
54	MG	2A	3627	1/1	0.84	0.15	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3084	1/1	0.84	0.20	58,58,58,58	0
54	MG	1A	3768	1/1	0.84	0.19	67,67,67,67	0
54	MG	1A	3770	1/1	0.84	0.12	34,34,34,34	0
54	MG	2a	1659	1/1	0.84	0.32	75,75,75,75	0
54	MG	2A	3725	1/1	0.84	0.13	61,61,61,61	0
54	MG	2A	3310	1/1	0.84	0.17	62,62,62,62	0
54	MG	1A	3192	1/1	0.84	0.26	68,68,68,68	0
54	MG	1A	3621	1/1	0.84	0.15	65,65,65,65	0
54	MG	2B	3004	1/1	0.84	0.11	77,77,77,77	0
54	MG	2a	1672	1/1	0.84	0.35	73,73,73,73	0
54	MG	2a	1679	1/1	0.84	0.28	67,67,67,67	0
54	MG	1A	3405	1/1	0.84	0.25	65,65,65,65	0
54	MG	1A	3196	1/1	0.84	0.24	72,72,72,72	0
54	MG	2B	3014	1/1	0.84	0.14	65,65,65,65	0
54	MG	1a	1801	1/1	0.84	0.16	80,80,80,80	0
54	MG	1A	3561	1/1	0.84	0.18	62,62,62,62	0
54	MG	1A	3726	1/1	0.84	0.12	50,50,50,50	0
54	MG	1A	3581	1/1	0.84	0.17	67,67,67,67	0
54	MG	2a	1715	1/1	0.84	0.24	71,71,71,71	0
54	MG	1A	3409	1/1	0.84	0.16	58,58,58,58	0
54	MG	1a	1820	1/1	0.84	0.21	76,76,76,76	0
54	MG	1A	3754	1/1	0.84	0.23	59,59,59,59	0
54	MG	2a	1765	1/1	0.84	0.22	68,68,68,68	0
54	MG	2A	3171	1/1	0.84	0.16	56,56,56,56	0
54	MG	2a	1605	1/1	0.84	0.16	63,63,63,63	0
54	MG	2a	1608	1/1	0.84	0.37	69,69,69,69	0
54	MG	1a	1614	1/1	0.84	0.27	74,74,74,74	0
54	MG	2A	3191	1/1	0.84	0.11	53,53,53,53	0
54	MG	2a	1620	1/1	0.84	0.30	77,77,77,77	0
54	MG	2A	3455	1/1	0.84	0.17	62,62,62,62	0
55	MPD	1T	8004	8/8	0.84	0.24	56,61,69,80	0
54	MG	2a	1631	1/1	0.84	0.24	77,77,77,77	0
54	MG	1a	1648	1/1	0.84	0.30	56,56,56,56	0
54	MG	2a	1635	1/1	0.84	0.17	67,67,67,67	0
57	ZN	24	501	1/1	0.84	0.10	257,257,257,257	0
54	MG	1a	1673	1/1	0.85	0.25	71,71,71,71	0
54	MG	2a	1604	1/1	0.85	0.21	66,66,66,66	0
54	MG	1a	1675	1/1	0.85	0.47	70,70,70,70	0
54	MG	1A	3745	1/1	0.85	0.11	71,71,71,71	0
54	MG	2A	3499	1/1	0.85	0.11	47,47,47,47	0
54	MG	1A	3666	1/1	0.85	0.10	64,64,64,64	0
54	MG	1A	3956	1/1	0.85	0.22	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2a	1622	1/1	0.85	0.34	74,74,74,74	0
54	MG	2a	1626	1/1	0.85	0.22	70,70,70,70	0
54	MG	2A	3237	1/1	0.85	0.28	65,65,65,65	0
54	MG	2A	3516	1/1	0.85	0.13	58,58,58,58	0
54	MG	2A	3244	1/1	0.85	0.17	56,56,56,56	0
54	MG	1A	3267	1/1	0.85	0.10	82,82,82,82	0
54	MG	2A	3251	1/1	0.85	0.17	53,53,53,53	0
54	MG	1E	304	1/1	0.85	0.15	59,59,59,59	0
54	MG	1a	1699	1/1	0.85	0.29	73,73,73,73	0
54	MG	2A	3549	1/1	0.85	0.11	51,51,51,51	0
54	MG	1A	3454	1/1	0.85	0.15	31,31,31,31	0
54	MG	2A	3572	1/1	0.85	0.16	52,52,52,52	0
54	MG	1a	1829	1/1	0.85	0.30	70,70,70,70	0
54	MG	1A	3758	1/1	0.85	0.17	66,66,66,66	0
54	MG	1R	203	1/1	0.85	0.14	48,48,48,48	0
54	MG	2a	1663	1/1	0.85	0.27	67,67,67,67	0
54	MG	1a	1730	1/1	0.85	0.12	62,62,62,62	0
54	MG	1T	8002	1/1	0.85	0.19	61,61,61,61	0
54	MG	2A	3367	1/1	0.85	0.16	66,66,66,66	0
54	MG	2A	3620	1/1	0.85	0.12	42,42,42,42	0
54	MG	2A	3625	1/1	0.85	0.16	43,43,43,43	0
54	MG	1a	1845	1/1	0.85	0.30	68,68,68,68	0
54	MG	1A	3638	1/1	0.85	0.19	35,35,35,35	0
54	MG	2A	3668	1/1	0.85	0.15	73,73,73,73	0
54	MG	2A	3684	1/1	0.85	0.13	62,62,62,62	0
54	MG	1A	3274	1/1	0.85	0.25	74,74,74,74	0
54	MG	2A	3391	1/1	0.85	0.22	71,71,71,71	0
54	MG	1a	1863	1/1	0.85	0.14	64,64,64,64	0
54	MG	2a	1707	1/1	0.85	0.14	65,65,65,65	0
54	MG	1a	1869	1/1	0.85	0.23	74,74,74,74	0
54	MG	2A	3737	1/1	0.85	0.12	37,37,37,37	0
54	MG	2a	1718	1/1	0.85	0.32	82,82,82,82	0
54	MG	10	104	1/1	0.85	0.15	64,64,64,64	0
54	MG	1A	3506	1/1	0.85	0.19	36,36,36,36	0
54	MG	1A	3708	1/1	0.85	0.12	64,64,64,64	0
54	MG	2a	1733	1/1	0.85	0.12	83,83,83,83	0
54	MG	2a	1739	1/1	0.85	0.13	79,79,79,79	0
54	MG	1a	1753	1/1	0.85	0.16	62,62,62,62	0
54	MG	2B	3007	1/1	0.85	0.13	76,76,76,76	0
54	MG	1A	4004	1/1	0.85	0.10	56,56,56,56	0
54	MG	1A	3616	1/1	0.85	0.10	55,55,55,55	0
54	MG	1a	1631	1/1	0.85	0.33	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1a	1774	1/1	0.85	0.21	68,68,68,68	0
54	MG	2A	3048	1/1	0.85	0.18	66,66,66,66	0
54	MG	1B	202	1/1	0.85	0.18	63,63,63,63	0
54	MG	2N	8001	1/1	0.85	0.12	78,78,78,78	0
54	MG	1a	1658	1/1	0.85	0.29	61,61,61,61	0
54	MG	2A	3144	1/1	0.85	0.12	53,53,53,53	0
54	MG	1A	3531	1/1	0.85	0.20	66,66,66,66	0
54	MG	2a	1601	1/1	0.85	0.18	69,69,69,69	0
54	MG	1a	1677	1/1	0.86	0.30	63,63,63,63	0
54	MG	1a	1680	1/1	0.86	0.22	69,69,69,69	0
54	MG	1a	1837	1/1	0.86	0.18	74,74,74,74	0
54	MG	1a	1838	1/1	0.86	0.17	66,66,66,66	0
54	MG	1A	3998	1/1	0.86	0.28	51,51,51,51	0
54	MG	1A	3480	1/1	0.86	0.12	28,28,28,28	0
54	MG	2A	3437	1/1	0.86	0.16	52,52,52,52	0
54	MG	1A	3568	1/1	0.86	0.16	55,55,55,55	0
54	MG	1A	4030	1/1	0.86	0.33	53,53,53,53	0
54	MG	1A	4035	1/1	0.86	0.12	27,27,27,27	0
54	MG	1a	1866	1/1	0.86	0.19	69,69,69,69	0
54	MG	1A	3640	1/1	0.86	0.27	71,71,71,71	0
54	MG	1A	3485	1/1	0.86	0.13	72,72,72,72	0
54	MG	2A	3475	1/1	0.86	0.10	62,62,62,62	0
54	MG	1a	1707	1/1	0.86	0.21	74,74,74,74	0
54	MG	1a	1718	1/1	0.86	0.14	58,58,58,58	0
54	MG	1A	3399	1/1	0.86	0.18	54,54,54,54	0
54	MG	1B	216	1/1	0.86	0.26	58,58,58,58	0
54	MG	2a	1623	1/1	0.86	0.37	73,73,73,73	0
54	MG	2a	1625	1/1	0.86	0.31	73,73,73,73	0
54	MG	2A	3487	1/1	0.86	0.12	73,73,73,73	0
54	MG	2A	3490	1/1	0.86	0.14	66,66,66,66	0
54	MG	1A	3649	1/1	0.86	0.19	59,59,59,59	0
54	MG	1A	3655	1/1	0.86	0.10	40,40,40,40	0
54	MG	2A	3023	1/1	0.86	0.13	54,54,54,54	0
54	MG	1A	3501	1/1	0.86	0.12	69,69,69,69	0
54	MG	1A	3425	1/1	0.86	0.18	57,57,57,57	0
54	MG	2A	3511	1/1	0.86	0.14	62,62,62,62	0
54	MG	2A	3512	1/1	0.86	0.12	54,54,54,54	0
54	MG	2a	1644	1/1	0.86	0.21	75,75,75,75	0
54	MG	2a	1645	1/1	0.86	0.28	67,67,67,67	0
54	MG	2a	1646	1/1	0.86	0.22	77,77,77,77	0
54	MG	2a	1648	1/1	0.86	0.35	76,76,76,76	0
54	MG	1a	1750	1/1	0.86	0.14	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3124	1/1	0.86	0.10	66,66,66,66	0
54	MG	1A	3670	1/1	0.86	0.18	64,64,64,64	0
54	MG	1A	3679	1/1	0.86	0.13	69,69,69,69	0
54	MG	2a	1660	1/1	0.86	0.34	72,72,72,72	0
54	MG	1A	3507	1/1	0.86	0.14	32,32,32,32	0
54	MG	2a	1662	1/1	0.86	0.32	79,79,79,79	0
54	MG	2A	3162	1/1	0.86	0.19	57,57,57,57	0
54	MG	2A	3530	1/1	0.86	0.10	50,50,50,50	0
54	MG	1O	8001	1/1	0.86	0.14	62,62,62,62	0
54	MG	1A	3125	1/1	0.86	0.15	49,49,49,49	0
54	MG	2A	3182	1/1	0.86	0.12	49,49,49,49	0
54	MG	1A	3297	1/1	0.86	0.28	71,71,71,71	0
54	MG	2A	3206	1/1	0.86	0.20	56,56,56,56	0
54	MG	2A	3223	1/1	0.86	0.13	58,58,58,58	0
54	MG	1A	3525	1/1	0.86	0.11	57,57,57,57	0
54	MG	1A	3592	1/1	0.86	0.12	54,54,54,54	0
54	MG	1a	1783	1/1	0.86	0.11	87,87,87,87	0
54	MG	1A	3066	1/1	0.86	0.22	64,64,64,64	0
54	MG	2A	3614	1/1	0.86	0.12	42,42,42,42	0
54	MG	1A	3719	1/1	0.86	0.12	47,47,47,47	0
54	MG	1A	3597	1/1	0.86	0.12	62,62,62,62	0
54	MG	1a	1606	1/1	0.86	0.22	63,63,63,63	0
54	MG	2A	3289	1/1	0.86	0.17	69,69,69,69	0
54	MG	2A	3635	1/1	0.86	0.21	65,65,65,65	0
54	MG	2A	3642	1/1	0.86	0.13	77,77,77,77	0
54	MG	2A	3659	1/1	0.86	0.11	76,76,76,76	0
54	MG	2a	1727	1/1	0.86	0.17	69,69,69,69	0
54	MG	1A	3372	1/1	0.86	0.10	39,39,39,39	0
54	MG	2A	3303	1/1	0.86	0.21	61,61,61,61	0
54	MG	1A	3615	1/1	0.86	0.14	60,60,60,60	0
54	MG	1A	3443	1/1	0.86	0.10	48,48,48,48	0
54	MG	2A	3722	1/1	0.86	0.15	57,57,57,57	0
54	MG	1A	3413	1/1	0.86	0.17	68,68,68,68	0
54	MG	1A	3969	1/1	0.86	0.18	61,61,61,61	0
54	MG	1A	3753	1/1	0.86	0.13	57,57,57,57	0
54	MG	1A	3027	1/1	0.86	0.10	60,60,60,60	0
54	MG	1a	1823	1/1	0.86	0.16	75,75,75,75	0
54	MG	1a	1824	1/1	0.86	0.23	73,73,73,73	0
54	MG	1a	1827	1/1	0.86	0.28	73,73,73,73	0
54	MG	1A	3988	1/1	0.86	0.10	81,81,81,81	0
54	MG	1A	3462	1/1	0.86	0.12	60,60,60,60	0
54	MG	2B	3012	1/1	0.86	0.20	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1a	1701	1/1	0.87	0.26	64,64,64,64	0
54	MG	1A	3644	1/1	0.87	0.14	48,48,48,48	0
54	MG	1A	3375	1/1	0.87	0.13	49,49,49,49	0
54	MG	1A	3580	1/1	0.87	0.09	59,59,59,59	0
54	MG	1A	3522	1/1	0.87	0.19	61,61,61,61	0
54	MG	1G	3002	1/1	0.87	0.11	62,62,62,62	0
54	MG	2A	3288	1/1	0.87	0.13	51,51,51,51	0
54	MG	1A	3319	1/1	0.87	0.10	65,65,65,65	0
54	MG	1A	3965	1/1	0.87	0.12	63,63,63,63	0
54	MG	1a	1735	1/1	0.87	0.13	68,68,68,68	0
54	MG	1A	3321	1/1	0.87	0.14	50,50,50,50	0
54	MG	2A	3535	1/1	0.87	0.24	71,71,71,71	0
54	MG	2A	3537	1/1	0.87	0.10	55,55,55,55	0
54	MG	1A	3324	1/1	0.87	0.25	61,61,61,61	0
54	MG	2A	3551	1/1	0.87	0.12	61,61,61,61	0
54	MG	2A	3312	1/1	0.87	0.14	65,65,65,65	0
54	MG	1A	3292	1/1	0.87	0.18	58,58,58,58	0
54	MG	2A	3335	1/1	0.87	0.20	63,63,63,63	0
54	MG	10	102	1/1	0.87	0.10	51,51,51,51	0
54	MG	1A	3596	1/1	0.87	0.16	47,47,47,47	0
54	MG	1a	1873	1/1	0.87	0.13	65,65,65,65	0
54	MG	1A	3011	1/1	0.87	0.16	62,62,62,62	0
54	MG	1A	3995	1/1	0.87	0.16	44,44,44,44	0
54	MG	1A	3555	1/1	0.87	0.12	53,53,53,53	0
54	MG	1A	3344	1/1	0.87	0.17	59,59,59,59	0
54	MG	1A	3348	1/1	0.87	0.12	44,44,44,44	0
54	MG	2A	3626	1/1	0.87	0.18	47,47,47,47	0
54	MG	1A	4019	1/1	0.87	0.30	58,58,58,58	0
54	MG	2A	3628	1/1	0.87	0.12	56,56,56,56	0
54	MG	1a	1641	1/1	0.87	0.45	75,75,75,75	0
54	MG	1A	3261	1/1	0.87	0.11	64,64,64,64	0
54	MG	2A	3419	1/1	0.87	0.14	54,54,54,54	0
54	MG	1A	3367	1/1	0.87	0.14	54,54,54,54	0
54	MG	2A	3422	1/1	0.87	0.15	56,56,56,56	0
54	MG	1A	3570	1/1	0.87	0.19	71,71,71,71	0
54	MG	2A	3703	1/1	0.87	0.09	59,59,59,59	0
54	MG	2a	1685	1/1	0.87	0.29	64,64,64,64	0
54	MG	2A	3709	1/1	0.87	0.11	50,50,50,50	0
54	MG	2A	3057	1/1	0.87	0.19	63,63,63,63	0
54	MG	1a	1669	1/1	0.87	0.13	70,70,70,70	0
54	MG	1A	3725	1/1	0.87	0.13	51,51,51,51	0
54	MG	2A	3445	1/1	0.87	0.23	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3132	1/1	0.87	0.10	60,60,60,60	0
54	MG	2A	3462	1/1	0.87	0.18	53,53,53,53	0
54	MG	2A	3752	1/1	0.87	0.15	46,46,46,46	0
54	MG	2A	3136	1/1	0.87	0.24	64,64,64,64	0
54	MG	1B	203	1/1	0.87	0.16	70,70,70,70	0
54	MG	2A	3466	1/1	0.87	0.10	51,51,51,51	0
54	MG	2B	3005	1/1	0.87	0.24	60,60,60,60	0
54	MG	2A	3152	1/1	0.87	0.15	61,61,61,61	0
54	MG	1B	206	1/1	0.87	0.10	51,51,51,51	0
54	MG	2a	1731	1/1	0.87	0.16	73,73,73,73	0
54	MG	2B	3009	1/1	0.87	0.22	64,64,64,64	0
54	MG	1A	3419	1/1	0.87	0.15	49,49,49,49	0
54	MG	2a	1752	1/1	0.87	0.12	67,67,67,67	0
54	MG	2A	3476	1/1	0.87	0.12	55,55,55,55	0
54	MG	1B	208	1/1	0.87	0.35	72,72,72,72	0
54	MG	1B	211	1/1	0.87	0.22	69,69,69,69	0
54	MG	1A	3199	1/1	0.87	0.32	70,70,70,70	0
54	MG	2A	3187	1/1	0.87	0.24	61,61,61,61	0
54	MG	1A	3891	1/1	0.87	0.20	73,73,73,73	0
54	MG	2A	3488	1/1	0.87	0.11	58,58,58,58	0
54	MG	2A	3196	1/1	0.87	0.11	49,49,49,49	0
54	MG	2A	3200	1/1	0.87	0.31	57,57,57,57	0
54	MG	20	101	1/1	0.87	0.10	64,64,64,64	0
54	MG	1A	3128	1/1	0.87	0.38	65,65,65,65	0
54	MG	1A	3428	1/1	0.87	0.10	48,48,48,48	0
54	MG	1a	1700	1/1	0.87	0.13	66,66,66,66	0
54	MG	2A	3374	1/1	0.88	0.09	57,57,57,57	0
54	MG	2A	3380	1/1	0.88	0.11	35,35,35,35	0
54	MG	1A	3674	1/1	0.88	0.12	58,58,58,58	0
54	MG	1A	3439	1/1	0.88	0.13	49,49,49,49	0
54	MG	2A	3755	1/1	0.88	0.28	52,52,52,52	0
54	MG	1A	3402	1/1	0.88	0.20	73,73,73,73	0
54	MG	2A	3389	1/1	0.88	0.12	56,56,56,56	0
54	MG	1A	3836	1/1	0.88	0.11	57,57,57,57	0
54	MG	1A	3847	1/1	0.88	0.12	59,59,59,59	0
54	MG	2A	3410	1/1	0.88	0.12	57,57,57,57	0
54	MG	1A	3849	1/1	0.88	0.10	53,53,53,53	0
54	MG	1A	3447	1/1	0.88	0.13	53,53,53,53	0
54	MG	1a	1720	1/1	0.88	0.10	65,65,65,65	0
54	MG	1a	1728	1/1	0.88	0.18	56,56,56,56	0
54	MG	2B	3013	1/1	0.88	0.09	76,76,76,76	0
54	MG	1e	201	1/1	0.88	0.24	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3861	1/1	0.88	0.10	54,54,54,54	0
54	MG	2B	3018	1/1	0.88	0.18	76,76,76,76	0
54	MG	1A	3540	1/1	0.88	0.12	52,52,52,52	0
54	MG	1A	3695	1/1	0.88	0.13	51,51,51,51	0
54	MG	2E	305	1/1	0.88	0.20	65,65,65,65	0
54	MG	1A	3601	1/1	0.88	0.18	38,38,38,38	0
54	MG	2A	3040	1/1	0.88	0.18	58,58,58,58	0
54	MG	2A	3453	1/1	0.88	0.26	52,52,52,52	0
54	MG	1a	1740	1/1	0.88	0.30	69,69,69,69	0
54	MG	2T	3001	1/1	0.88	0.22	65,65,65,65	0
54	MG	1A	3884	1/1	0.88	0.08	27,27,27,27	0
54	MG	1A	3705	1/1	0.88	0.15	67,67,67,67	0
54	MG	28	8001	1/1	0.88	0.10	66,66,66,66	0
54	MG	2A	3080	1/1	0.88	0.11	50,50,50,50	0
54	MG	2A	3081	1/1	0.88	0.25	55,55,55,55	0
54	MG	2A	3082	1/1	0.88	0.21	59,59,59,59	0
54	MG	2A	3093	1/1	0.88	0.15	61,61,61,61	0
54	MG	2A	3474	1/1	0.88	0.22	65,65,65,65	0
54	MG	2A	3096	1/1	0.88	0.21	63,63,63,63	0
54	MG	2a	1617	1/1	0.88	0.23	65,65,65,65	0
54	MG	2A	3100	1/1	0.88	0.11	54,54,54,54	0
54	MG	1A	3150	1/1	0.88	0.18	58,58,58,58	0
54	MG	1P	202	1/1	0.88	0.14	73,73,73,73	0
54	MG	1A	3152	1/1	0.88	0.17	66,66,66,66	0
54	MG	2a	1624	1/1	0.88	0.35	73,73,73,73	0
54	MG	1A	3712	1/1	0.88	0.11	36,36,36,36	0
54	MG	2A	3140	1/1	0.88	0.12	54,54,54,54	0
54	MG	1A	3353	1/1	0.88	0.12	53,53,53,53	0
54	MG	1A	3938	1/1	0.88	0.14	56,56,56,56	0
54	MG	1a	1772	1/1	0.88	0.14	77,77,77,77	0
54	MG	1A	3939	1/1	0.88	0.12	61,61,61,61	0
54	MG	2a	1636	1/1	0.88	0.10	64,64,64,64	0
54	MG	2A	3163	1/1	0.88	0.20	62,62,62,62	0
54	MG	2A	3500	1/1	0.88	0.16	62,62,62,62	0
54	MG	1A	3474	1/1	0.88	0.13	35,35,35,35	0
54	MG	2A	3504	1/1	0.88	0.15	63,63,63,63	0
54	MG	2a	1642	1/1	0.88	0.24	80,80,80,80	0
54	MG	2A	3508	1/1	0.88	0.10	59,59,59,59	0
54	MG	1A	3360	1/1	0.88	0.17	55,55,55,55	0
54	MG	1A	3629	1/1	0.88	0.20	68,68,68,68	0
54	MG	1a	1605	1/1	0.88	0.15	61,61,61,61	0
54	MG	2A	3189	1/1	0.88	0.17	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3190	1/1	0.88	0.25	61,61,61,61	0
54	MG	2a	1654	1/1	0.88	0.23	60,60,60,60	0
54	MG	2a	1655	1/1	0.88	0.24	69,69,69,69	0
54	MG	1A	3567	1/1	0.88	0.13	49,49,49,49	0
54	MG	1A	3634	1/1	0.88	0.29	43,43,43,43	0
54	MG	1A	3166	1/1	0.88	0.24	61,61,61,61	0
54	MG	2A	3204	1/1	0.88	0.35	66,66,66,66	0
54	MG	1A	3492	1/1	0.88	0.08	60,60,60,60	0
54	MG	2A	3219	1/1	0.88	0.21	62,62,62,62	0
54	MG	1A	3100	1/1	0.88	0.12	50,50,50,50	0
54	MG	2A	3224	1/1	0.88	0.21	49,49,49,49	0
54	MG	1a	1644	1/1	0.88	0.12	57,57,57,57	0
54	MG	2A	3230	1/1	0.88	0.20	62,62,62,62	0
54	MG	2A	3553	1/1	0.88	0.13	76,76,76,76	0
54	MG	2A	3568	1/1	0.88	0.12	42,42,42,42	0
54	MG	1a	1809	1/1	0.88	0.18	62,62,62,62	0
54	MG	1A	3497	1/1	0.88	0.10	45,45,45,45	0
54	MG	1A	3762	1/1	0.88	0.16	52,52,52,52	0
54	MG	2A	3578	1/1	0.88	0.15	71,71,71,71	0
54	MG	1A	3369	1/1	0.88	0.09	39,39,39,39	0
54	MG	2a	1698	1/1	0.88	0.18	69,69,69,69	0
54	MG	1a	1664	1/1	0.88	0.18	58,58,58,58	0
54	MG	2A	3265	1/1	0.88	0.17	55,55,55,55	0
54	MG	1A	3262	1/1	0.88	0.22	60,60,60,60	0
54	MG	1A	3190	1/1	0.88	0.11	61,61,61,61	0
54	MG	1A	3067	1/1	0.88	0.17	60,60,60,60	0
54	MG	1A	3283	1/1	0.88	0.11	60,60,60,60	0
54	MG	2A	3624	1/1	0.88	0.12	66,66,66,66	0
54	MG	2A	3294	1/1	0.88	0.14	56,56,56,56	0
54	MG	2A	3302	1/1	0.88	0.10	57,57,57,57	0
54	MG	2a	1725	1/1	0.88	0.16	64,64,64,64	0
54	MG	1A	4008	1/1	0.88	0.14	33,33,33,33	0
54	MG	2a	1729	1/1	0.88	0.12	71,71,71,71	0
54	MG	1A	3062	1/1	0.88	0.18	46,46,46,46	0
54	MG	1A	3791	1/1	0.88	0.15	60,60,60,60	0
54	MG	1A	3794	1/1	0.88	0.18	65,65,65,65	0
54	MG	1A	3803	1/1	0.88	0.13	50,50,50,50	0
54	MG	1a	1690	1/1	0.88	0.37	71,71,71,71	0
54	MG	2A	3663	1/1	0.88	0.10	74,74,74,74	0
54	MG	1a	1694	1/1	0.88	0.26	67,67,67,67	0
54	MG	2A	3680	1/1	0.88	0.17	53,53,53,53	0
54	MG	2a	1780	1/1	0.88	0.19	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3346	1/1	0.88	0.10	55,55,55,55	0
54	MG	2A	3692	1/1	0.88	0.08	52,52,52,52	0
54	MG	2A	3696	1/1	0.88	0.08	56,56,56,56	0
54	MG	2e	201	1/1	0.88	0.18	71,71,71,71	0
54	MG	2A	3350	1/1	0.88	0.10	43,43,43,43	0
54	MG	2l	3001	1/1	0.88	0.42	64,64,64,64	0
54	MG	2A	3353	1/1	0.88	0.12	44,44,44,44	0
54	MG	2A	3713	1/1	0.88	0.13	57,57,57,57	0
54	MG	1a	1846	1/1	0.88	0.14	74,74,74,74	0
54	MG	1A	3808	1/1	0.88	0.10	55,55,55,55	0
56	ARG	1F	311	12/12	0.88	0.12	44,63,72,77	0
54	MG	1A	3341	1/1	0.88	0.12	46,46,46,46	0
54	MG	1a	1654	1/1	0.89	0.26	64,64,64,64	0
54	MG	2A	3279	1/1	0.89	0.17	37,37,37,37	0
54	MG	1a	1761	1/1	0.89	0.25	64,64,64,64	0
54	MG	2A	3519	1/1	0.89	0.15	60,60,60,60	0
54	MG	1A	3894	1/1	0.89	0.16	62,62,62,62	0
54	MG	1A	3516	1/1	0.89	0.15	60,60,60,60	0
54	MG	2a	1614	1/1	0.89	0.15	55,55,55,55	0
54	MG	1l	3002	1/1	0.89	0.20	72,72,72,72	0
54	MG	1A	3715	1/1	0.89	0.18	48,48,48,48	0
54	MG	1r	3001	1/1	0.89	0.19	65,65,65,65	0
54	MG	1y	204	1/1	0.89	0.15	93,93,93,93	0
54	MG	1A	3928	1/1	0.89	0.21	58,58,58,58	0
54	MG	1a	1671	1/1	0.89	0.31	63,63,63,63	0
54	MG	2A	3544	1/1	0.89	0.09	55,55,55,55	0
54	MG	1A	3799	1/1	0.89	0.10	51,51,51,51	0
54	MG	1a	1777	1/1	0.89	0.09	55,55,55,55	0
54	MG	2A	3049	1/1	0.89	0.15	50,50,50,50	0
54	MG	2A	3554	1/1	0.89	0.16	43,43,43,43	0
54	MG	2A	3342	1/1	0.89	0.12	45,45,45,45	0
54	MG	1A	3716	1/1	0.89	0.17	48,48,48,48	0
54	MG	2A	3348	1/1	0.89	0.09	62,62,62,62	0
54	MG	2A	3056	1/1	0.89	0.19	62,62,62,62	0
54	MG	1a	1785	1/1	0.89	0.21	76,76,76,76	0
54	MG	2A	3062	1/1	0.89	0.16	53,53,53,53	0
54	MG	2A	3063	1/1	0.89	0.17	61,61,61,61	0
54	MG	1a	1786	1/1	0.89	0.25	70,70,70,70	0
54	MG	2A	3368	1/1	0.89	0.14	64,64,64,64	0
54	MG	1B	218	1/1	0.89	0.13	48,48,48,48	0
54	MG	1A	3943	1/1	0.89	0.10	38,38,38,38	0
54	MG	2A	3383	1/1	0.89	0.17	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3595	1/1	0.89	0.12	48,48,48,48	0
54	MG	1a	1794	1/1	0.89	0.21	58,58,58,58	0
54	MG	1A	3668	1/1	0.89	0.17	52,52,52,52	0
54	MG	1A	3813	1/1	0.89	0.13	31,31,31,31	0
54	MG	1A	3819	1/1	0.89	0.21	76,76,76,76	0
54	MG	2A	3395	1/1	0.89	0.14	51,51,51,51	0
54	MG	1a	1804	1/1	0.89	0.11	65,65,65,65	0
54	MG	2A	3135	1/1	0.89	0.29	61,61,61,61	0
54	MG	1A	3382	1/1	0.89	0.07	32,32,32,32	0
54	MG	2A	3416	1/1	0.89	0.16	61,61,61,61	0
54	MG	2A	3138	1/1	0.89	0.24	61,61,61,61	0
54	MG	1A	3635	1/1	0.89	0.17	59,59,59,59	0
54	MG	1A	3967	1/1	0.89	0.12	81,81,81,81	0
54	MG	1a	1697	1/1	0.89	0.13	60,60,60,60	0
54	MG	2A	3693	1/1	0.89	0.09	57,57,57,57	0
54	MG	1A	3677	1/1	0.89	0.14	54,54,54,54	0
54	MG	1A	3835	1/1	0.89	0.10	47,47,47,47	0
54	MG	1A	3559	1/1	0.89	0.09	46,46,46,46	0
54	MG	1A	3838	1/1	0.89	0.09	55,55,55,55	0
54	MG	2A	3172	1/1	0.89	0.15	61,61,61,61	0
54	MG	1a	1825	1/1	0.89	0.20	77,77,77,77	0
54	MG	2a	1702	1/1	0.89	0.15	65,65,65,65	0
54	MG	2A	3454	1/1	0.89	0.11	58,58,58,58	0
54	MG	2A	3179	1/1	0.89	0.27	56,56,56,56	0
54	MG	2A	3461	1/1	0.89	0.17	52,52,52,52	0
54	MG	1A	3466	1/1	0.89	0.14	53,53,53,53	0
54	MG	2A	3186	1/1	0.89	0.14	53,53,53,53	0
54	MG	1A	3610	1/1	0.89	0.12	35,35,35,35	0
54	MG	1a	1715	1/1	0.89	0.25	65,65,65,65	0
54	MG	1a	1716	1/1	0.89	0.12	74,74,74,74	0
54	MG	2B	3003	1/1	0.89	0.26	71,71,71,71	0
54	MG	1A	3471	1/1	0.89	0.11	29,29,29,29	0
54	MG	1A	3451	1/1	0.89	0.11	48,48,48,48	0
54	MG	1A	3374	1/1	0.89	0.12	57,57,57,57	0
54	MG	1a	1723	1/1	0.89	0.14	64,64,64,64	0
54	MG	2A	3477	1/1	0.89	0.10	49,49,49,49	0
54	MG	1a	1603	1/1	0.89	0.23	77,77,77,77	0
54	MG	2A	3209	1/1	0.89	0.13	63,63,63,63	0
54	MG	2a	1755	1/1	0.89	0.11	82,82,82,82	0
54	MG	2A	3212	1/1	0.89	0.20	70,70,70,70	0
54	MG	2A	3214	1/1	0.89	0.29	49,49,49,49	0
54	MG	1A	3699	1/1	0.89	0.13	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	4017	1/1	0.89	0.17	62,62,62,62	0
54	MG	1a	1857	1/1	0.89	0.21	68,68,68,68	0
54	MG	2D	306	1/1	0.89	0.13	60,60,60,60	0
54	MG	1A	3878	1/1	0.89	0.12	65,65,65,65	0
54	MG	1A	3701	1/1	0.89	0.25	68,68,68,68	0
54	MG	2G	3001	1/1	0.89	0.18	76,76,76,76	0
54	MG	1A	3704	1/1	0.89	0.11	58,58,58,58	0
54	MG	1a	1637	1/1	0.89	0.24	68,68,68,68	0
54	MG	2A	3501	1/1	0.89	0.17	72,72,72,72	0
54	MG	1A	3455	1/1	0.89	0.10	50,50,50,50	0
54	MG	2A	3246	1/1	0.89	0.10	51,51,51,51	0
54	MG	1A	3459	1/1	0.89	0.15	55,55,55,55	0
54	MG	1A	3663	1/1	0.89	0.18	37,37,37,37	0
54	MG	1a	1653	1/1	0.89	0.21	64,64,64,64	0
54	MG	1A	3611	1/1	0.90	0.16	54,54,54,54	0
54	MG	1A	3982	1/1	0.90	0.20	62,62,62,62	0
54	MG	2A	3460	1/1	0.90	0.12	54,54,54,54	0
54	MG	1A	3987	1/1	0.90	0.10	44,44,44,44	0
54	MG	1A	3313	1/1	0.90	0.14	70,70,70,70	0
54	MG	1A	3318	1/1	0.90	0.13	44,44,44,44	0
54	MG	2B	3011	1/1	0.90	0.11	61,61,61,61	0
54	MG	1a	1706	1/1	0.90	0.10	47,47,47,47	0
54	MG	1A	3529	1/1	0.90	0.10	55,55,55,55	0
54	MG	1a	1714	1/1	0.90	0.18	62,62,62,62	0
54	MG	11	101	1/1	0.90	0.17	66,66,66,66	0
54	MG	2A	3469	1/1	0.90	0.10	62,62,62,62	0
54	MG	2A	3472	1/1	0.90	0.22	65,65,65,65	0
54	MG	2A	3194	1/1	0.90	0.11	53,53,53,53	0
54	MG	2D	309	1/1	0.90	0.24	65,65,65,65	0
54	MG	11	103	1/1	0.90	0.15	60,60,60,60	0
54	MG	1A	3488	1/1	0.90	0.12	45,45,45,45	0
54	MG	1a	1839	1/1	0.90	0.09	67,67,67,67	0
54	MG	17	102	1/1	0.90	0.15	63,63,63,63	0
54	MG	2G	3003	1/1	0.90	0.09	65,65,65,65	0
54	MG	2A	3480	1/1	0.90	0.18	53,53,53,53	0
54	MG	18	101	1/1	0.90	0.09	60,60,60,60	0
54	MG	1a	1721	1/1	0.90	0.17	71,71,71,71	0
54	MG	1a	1849	1/1	0.90	0.12	66,66,66,66	0
54	MG	1A	4000	1/1	0.90	0.17	78,78,78,78	0
54	MG	1a	1725	1/1	0.90	0.18	67,67,67,67	0
54	MG	1A	3690	1/1	0.90	0.14	51,51,51,51	0
54	MG	1A	3134	1/1	0.90	0.10	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3228	1/1	0.90	0.23	64,64,64,64	0
54	MG	1a	1864	1/1	0.90	0.15	70,70,70,70	0
54	MG	1A	3766	1/1	0.90	0.17	56,56,56,56	0
54	MG	1A	3578	1/1	0.90	0.28	58,58,58,58	0
54	MG	1A	3363	1/1	0.90	0.10	33,33,33,33	0
54	MG	1A	3545	1/1	0.90	0.32	64,64,64,64	0
54	MG	2A	3507	1/1	0.90	0.08	52,52,52,52	0
54	MG	1a	1742	1/1	0.90	0.21	55,55,55,55	0
54	MG	1a	1634	1/1	0.90	0.25	61,61,61,61	0
54	MG	2A	3253	1/1	0.90	0.12	50,50,50,50	0
54	MG	2A	3260	1/1	0.90	0.10	53,53,53,53	0
54	MG	2A	3264	1/1	0.90	0.23	59,59,59,59	0
54	MG	2A	3515	1/1	0.90	0.16	34,34,34,34	0
54	MG	1a	1745	1/1	0.90	0.21	73,73,73,73	0
54	MG	2A	3275	1/1	0.90	0.18	58,58,58,58	0
54	MG	2A	3520	1/1	0.90	0.24	38,38,38,38	0
54	MG	2A	3521	1/1	0.90	0.22	57,57,57,57	0
54	MG	2A	3522	1/1	0.90	0.12	55,55,55,55	0
54	MG	2A	3523	1/1	0.90	0.11	51,51,51,51	0
54	MG	1d	502	1/1	0.90	0.38	77,77,77,77	0
54	MG	1A	3549	1/1	0.90	0.15	63,63,63,63	0
54	MG	1A	3789	1/1	0.90	0.13	58,58,58,58	0
54	MG	1e	202	1/1	0.90	0.28	58,58,58,58	0
54	MG	2A	3529	1/1	0.90	0.12	54,54,54,54	0
54	MG	1A	4076	1/1	0.90	0.21	57,57,57,57	0
54	MG	1a	1647	1/1	0.90	0.29	57,57,57,57	0
54	MG	2A	3301	1/1	0.90	0.11	48,48,48,48	0
54	MG	2A	3536	1/1	0.90	0.08	63,63,63,63	0
54	MG	1q	201	1/1	0.90	0.17	55,55,55,55	0
54	MG	2A	3539	1/1	0.90	0.09	38,38,38,38	0
54	MG	2a	1652	1/1	0.90	0.21	57,57,57,57	0
54	MG	1A	3908	1/1	0.90	0.10	27,27,27,27	0
54	MG	2A	3546	1/1	0.90	0.09	58,58,58,58	0
54	MG	1a	1756	1/1	0.90	0.14	57,57,57,57	0
54	MG	2a	1658	1/1	0.90	0.16	60,60,60,60	0
54	MG	1a	1758	1/1	0.90	0.15	73,73,73,73	0
54	MG	2A	3010	1/1	0.90	0.22	60,60,60,60	0
54	MG	2A	3315	1/1	0.90	0.17	57,57,57,57	0
54	MG	2A	3556	1/1	0.90	0.10	62,62,62,62	0
54	MG	2A	3566	1/1	0.90	0.09	63,63,63,63	0
54	MG	1a	1759	1/1	0.90	0.15	65,65,65,65	0
54	MG	1A	3112	1/1	0.90	0.11	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1B	204	1/1	0.90	0.25	65,65,65,65	0
54	MG	1a	1764	1/1	0.90	0.18	65,65,65,65	0
54	MG	2a	1670	1/1	0.90	0.09	65,65,65,65	0
54	MG	1A	3585	1/1	0.90	0.11	54,54,54,54	0
54	MG	2a	1675	1/1	0.90	0.37	69,69,69,69	0
54	MG	2a	1678	1/1	0.90	0.12	66,66,66,66	0
54	MG	2A	3347	1/1	0.90	0.08	34,34,34,34	0
54	MG	2a	1680	1/1	0.90	0.13	75,75,75,75	0
54	MG	1A	3589	1/1	0.90	0.14	57,57,57,57	0
54	MG	1a	1660	1/1	0.90	0.17	69,69,69,69	0
54	MG	1A	3933	1/1	0.90	0.13	68,68,68,68	0
54	MG	1a	1665	1/1	0.90	0.11	67,67,67,67	0
54	MG	2A	3612	1/1	0.90	0.14	33,33,33,33	0
54	MG	1A	3554	1/1	0.90	0.16	58,58,58,58	0
54	MG	1A	3591	1/1	0.90	0.08	55,55,55,55	0
54	MG	1a	1784	1/1	0.90	0.09	66,66,66,66	0
54	MG	2A	3372	1/1	0.90	0.07	51,51,51,51	0
54	MG	1A	3174	1/1	0.90	0.19	57,57,57,57	0
54	MG	2A	3090	1/1	0.90	0.09	63,63,63,63	0
54	MG	2a	1711	1/1	0.90	0.19	79,79,79,79	0
54	MG	1A	3945	1/1	0.90	0.09	37,37,37,37	0
54	MG	2A	3629	1/1	0.90	0.10	62,62,62,62	0
54	MG	1a	1787	1/1	0.90	0.14	64,64,64,64	0
54	MG	2A	3097	1/1	0.90	0.13	57,57,57,57	0
54	MG	2A	3098	1/1	0.90	0.15	53,53,53,53	0
54	MG	1A	3429	1/1	0.90	0.20	57,57,57,57	0
54	MG	2A	3113	1/1	0.90	0.15	57,57,57,57	0
54	MG	2a	1728	1/1	0.90	0.12	77,77,77,77	0
54	MG	2A	3392	1/1	0.90	0.20	65,65,65,65	0
54	MG	2A	3671	1/1	0.90	0.09	36,36,36,36	0
54	MG	2A	3679	1/1	0.90	0.10	56,56,56,56	0
54	MG	2a	1736	1/1	0.90	0.15	67,67,67,67	0
54	MG	1A	3718	1/1	0.90	0.20	47,47,47,47	0
54	MG	2a	1740	1/1	0.90	0.10	80,80,80,80	0
54	MG	2a	1751	1/1	0.90	0.10	65,65,65,65	0
54	MG	1A	3821	1/1	0.90	0.15	36,36,36,36	0
54	MG	1a	1681	1/1	0.90	0.18	61,61,61,61	0
54	MG	2A	3411	1/1	0.90	0.16	62,62,62,62	0
54	MG	1a	1795	1/1	0.90	0.12	71,71,71,71	0
54	MG	1D	314	1/1	0.90	0.16	72,72,72,72	0
54	MG	2A	3137	1/1	0.90	0.17	57,57,57,57	0
54	MG	1A	3206	1/1	0.90	0.33	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1a	1688	1/1	0.90	0.37	70,70,70,70	0
54	MG	2A	3719	1/1	0.90	0.14	56,56,56,56	0
54	MG	1A	3130	1/1	0.90	0.17	55,55,55,55	0
54	MG	1A	3467	1/1	0.90	0.10	43,43,43,43	0
54	MG	2A	3427	1/1	0.90	0.12	51,51,51,51	0
54	MG	1a	1691	1/1	0.90	0.16	56,56,56,56	0
54	MG	2r	101	1/1	0.90	0.12	68,68,68,68	0
54	MG	1A	3304	1/1	0.90	0.26	62,62,62,62	0
54	MG	1A	3604	1/1	0.90	0.12	59,59,59,59	0
54	MG	2A	3444	1/1	0.90	0.15	61,61,61,61	0
55	MPD	2A	3748	8/8	0.90	0.18	54,65,67,73	0
54	MG	2A	3166	1/1	0.90	0.10	61,61,61,61	0
54	MG	2A	3448	1/1	0.90	0.16	66,66,66,66	0
57	ZN	2Y	501	1/1	0.90	0.16	169,169,169,169	0
54	MG	1A	3282	1/1	0.90	0.28	60,60,60,60	0
54	MG	1A	3632	1/1	0.91	0.13	56,56,56,56	0
54	MG	2A	3400	1/1	0.91	0.14	40,40,40,40	0
54	MG	2A	3405	1/1	0.91	0.13	53,53,53,53	0
54	MG	1A	4001	1/1	0.91	0.19	68,68,68,68	0
54	MG	2A	3409	1/1	0.91	0.09	44,44,44,44	0
54	MG	2A	3099	1/1	0.91	0.20	53,53,53,53	0
54	MG	1A	3453	1/1	0.91	0.12	40,40,40,40	0
54	MG	2A	3727	1/1	0.91	0.10	70,70,70,70	0
54	MG	2A	3413	1/1	0.91	0.19	59,59,59,59	0
54	MG	2A	3107	1/1	0.91	0.12	53,53,53,53	0
54	MG	2A	3751	1/1	0.91	0.25	48,48,48,48	0
54	MG	1a	1782	1/1	0.91	0.09	75,75,75,75	0
54	MG	2A	3119	1/1	0.91	0.12	49,49,49,49	0
54	MG	2A	3120	1/1	0.91	0.24	55,55,55,55	0
54	MG	1A	3713	1/1	0.91	0.13	33,33,33,33	0
54	MG	2A	3421	1/1	0.91	0.10	69,69,69,69	0
54	MG	1a	1649	1/1	0.91	0.22	58,58,58,58	0
54	MG	1A	3138	1/1	0.91	0.19	60,60,60,60	0
54	MG	2A	3133	1/1	0.91	0.34	57,57,57,57	0
54	MG	2A	3428	1/1	0.91	0.15	57,57,57,57	0
54	MG	2B	3008	1/1	0.91	0.09	66,66,66,66	0
54	MG	1A	3203	1/1	0.91	0.16	61,61,61,61	0
54	MG	1A	3527	1/1	0.91	0.11	32,32,32,32	0
54	MG	1A	4022	1/1	0.91	0.18	55,55,55,55	0
54	MG	2A	3442	1/1	0.91	0.14	51,51,51,51	0
54	MG	2A	3443	1/1	0.91	0.09	41,41,41,41	0
54	MG	1A	4026	1/1	0.91	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3456	1/1	0.91	0.15	62,62,62,62	0
54	MG	1A	3205	1/1	0.91	0.14	57,57,57,57	0
54	MG	2A	3148	1/1	0.91	0.12	51,51,51,51	0
54	MG	1A	3057	1/1	0.91	0.14	53,53,53,53	0
54	MG	1A	4064	1/1	0.91	0.23	40,40,40,40	0
54	MG	2A	3457	1/1	0.91	0.11	62,62,62,62	0
54	MG	2A	3458	1/1	0.91	0.08	57,57,57,57	0
54	MG	2A	3159	1/1	0.91	0.19	46,46,46,46	0
54	MG	1A	3864	1/1	0.91	0.13	48,48,48,48	0
54	MG	1A	3284	1/1	0.91	0.10	59,59,59,59	0
54	MG	2A	3164	1/1	0.91	0.20	58,58,58,58	0
54	MG	1A	3868	1/1	0.91	0.10	39,39,39,39	0
54	MG	1A	3737	1/1	0.91	0.13	57,57,57,57	0
54	MG	1A	3738	1/1	0.91	0.09	34,34,34,34	0
54	MG	2W	8001	1/1	0.91	0.15	50,50,50,50	0
54	MG	1A	3647	1/1	0.91	0.10	49,49,49,49	0
54	MG	1A	3207	1/1	0.91	0.12	60,60,60,60	0
54	MG	1a	1817	1/1	0.91	0.08	98,98,98,98	0
54	MG	2A	3473	1/1	0.91	0.08	51,51,51,51	0
54	MG	2a	1602	1/1	0.91	0.10	58,58,58,58	0
54	MG	2A	3183	1/1	0.91	0.10	66,66,66,66	0
54	MG	1A	3887	1/1	0.91	0.12	56,56,56,56	0
54	MG	1A	3468	1/1	0.91	0.16	64,64,64,64	0
54	MG	2a	1607	1/1	0.91	0.09	72,72,72,72	0
54	MG	1A	3657	1/1	0.91	0.12	55,55,55,55	0
54	MG	1A	3548	1/1	0.91	0.09	57,57,57,57	0
54	MG	2a	1610	1/1	0.91	0.18	61,61,61,61	0
54	MG	1B	219	1/1	0.91	0.09	44,44,44,44	0
54	MG	1a	1826	1/1	0.91	0.15	70,70,70,70	0
54	MG	2A	3483	1/1	0.91	0.09	37,37,37,37	0
54	MG	2A	3195	1/1	0.91	0.23	66,66,66,66	0
54	MG	2a	1621	1/1	0.91	0.10	56,56,56,56	0
54	MG	1A	3893	1/1	0.91	0.21	40,40,40,40	0
54	MG	1B	222	1/1	0.91	0.13	65,65,65,65	0
54	MG	2A	3202	1/1	0.91	0.14	49,49,49,49	0
54	MG	1A	3065	1/1	0.91	0.12	39,39,39,39	0
54	MG	2A	3491	1/1	0.91	0.09	51,51,51,51	0
54	MG	1A	3898	1/1	0.91	0.08	50,50,50,50	0
54	MG	1B	229	1/1	0.91	0.08	60,60,60,60	0
54	MG	1D	311	1/1	0.91	0.13	69,69,69,69	0
54	MG	2A	3213	1/1	0.91	0.10	60,60,60,60	0
54	MG	1A	3552	1/1	0.91	0.12	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3218	1/1	0.91	0.21	60,60,60,60	0
54	MG	1a	1703	1/1	0.91	0.33	66,66,66,66	0
54	MG	2A	3505	1/1	0.91	0.10	73,73,73,73	0
54	MG	2A	3506	1/1	0.91	0.11	59,59,59,59	0
54	MG	1a	1704	1/1	0.91	0.16	68,68,68,68	0
54	MG	2a	1643	1/1	0.91	0.17	76,76,76,76	0
54	MG	1A	3339	1/1	0.91	0.14	54,54,54,54	0
54	MG	1F	306	1/1	0.91	0.24	48,48,48,48	0
54	MG	1A	3191	1/1	0.91	0.18	55,55,55,55	0
54	MG	1a	1708	1/1	0.91	0.12	55,55,55,55	0
54	MG	1A	3600	1/1	0.91	0.12	57,57,57,57	0
54	MG	2A	3234	1/1	0.91	0.17	65,65,65,65	0
54	MG	2a	1651	1/1	0.91	0.34	67,67,67,67	0
54	MG	1A	3676	1/1	0.91	0.23	71,71,71,71	0
54	MG	1H	8001	1/1	0.91	0.17	62,62,62,62	0
54	MG	1H	8002	1/1	0.91	0.12	58,58,58,58	0
54	MG	1a	1865	1/1	0.91	0.12	46,46,46,46	0
54	MG	1N	202	1/1	0.91	0.12	61,61,61,61	0
54	MG	2A	3252	1/1	0.91	0.10	54,54,54,54	0
54	MG	1A	3380	1/1	0.91	0.09	26,26,26,26	0
54	MG	1A	3785	1/1	0.91	0.17	58,58,58,58	0
54	MG	1Q	203	1/1	0.91	0.13	50,50,50,50	0
54	MG	1A	3252	1/1	0.91	0.26	59,59,59,59	0
54	MG	2A	3272	1/1	0.91	0.13	46,46,46,46	0
54	MG	2a	1665	1/1	0.91	0.27	66,66,66,66	0
54	MG	1a	1726	1/1	0.91	0.13	65,65,65,65	0
54	MG	1A	3608	1/1	0.91	0.13	37,37,37,37	0
54	MG	1a	1729	1/1	0.91	0.07	56,56,56,56	0
54	MG	2A	3287	1/1	0.91	0.10	48,48,48,48	0
54	MG	1d	504	1/1	0.91	0.28	67,67,67,67	0
54	MG	2a	1674	1/1	0.91	0.16	74,74,74,74	0
54	MG	1A	3687	1/1	0.91	0.08	61,61,61,61	0
54	MG	1A	3950	1/1	0.91	0.09	77,77,77,77	0
54	MG	1A	3383	1/1	0.91	0.07	34,34,34,34	0
54	MG	1A	3435	1/1	0.91	0.17	52,52,52,52	0
54	MG	2a	1681	1/1	0.91	0.15	74,74,74,74	0
54	MG	1a	1738	1/1	0.91	0.10	64,64,64,64	0
54	MG	1n	502	1/1	0.91	0.07	46,46,46,46	0
54	MG	1A	3797	1/1	0.91	0.21	65,65,65,65	0
54	MG	1a	1741	1/1	0.91	0.21	65,65,65,65	0
54	MG	2A	3561	1/1	0.91	0.12	50,50,50,50	0
54	MG	2a	1695	1/1	0.91	0.14	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3345	1/1	0.91	0.17	61,61,61,61	0
54	MG	1A	3500	1/1	0.91	0.07	19,19,19,19	0
54	MG	2A	3319	1/1	0.91	0.09	42,42,42,42	0
54	MG	2A	3001	1/1	0.91	0.12	57,57,57,57	0
54	MG	17	101	1/1	0.91	0.14	64,64,64,64	0
54	MG	2a	1709	1/1	0.91	0.13	66,66,66,66	0
54	MG	1A	3806	1/1	0.91	0.19	62,62,62,62	0
54	MG	2A	3340	1/1	0.91	0.08	54,54,54,54	0
54	MG	2A	3024	1/1	0.91	0.21	49,49,49,49	0
54	MG	2A	3025	1/1	0.91	0.09	44,44,44,44	0
54	MG	1A	3441	1/1	0.91	0.16	64,64,64,64	0
54	MG	2A	3603	1/1	0.91	0.12	78,78,78,78	0
54	MG	2A	3605	1/1	0.91	0.09	36,36,36,36	0
54	MG	19	101	1/1	0.91	0.29	62,62,62,62	0
54	MG	2a	1726	1/1	0.91	0.18	57,57,57,57	0
54	MG	2A	3349	1/1	0.91	0.11	46,46,46,46	0
54	MG	1A	3158	1/1	0.91	0.10	49,49,49,49	0
54	MG	1A	3811	1/1	0.91	0.19	32,32,32,32	0
54	MG	2A	3355	1/1	0.91	0.13	49,49,49,49	0
54	MG	1a	1754	1/1	0.91	0.18	66,66,66,66	0
54	MG	1A	3623	1/1	0.91	0.14	29,29,29,29	0
54	MG	1A	3814	1/1	0.91	0.14	60,60,60,60	0
54	MG	2A	3060	1/1	0.91	0.24	42,42,42,42	0
54	MG	2a	1749	1/1	0.91	0.09	85,85,85,85	0
54	MG	2A	3061	1/1	0.91	0.16	50,50,50,50	0
54	MG	1A	3311	1/1	0.91	0.09	46,46,46,46	0
54	MG	2A	3634	1/1	0.91	0.13	50,50,50,50	0
54	MG	2A	3376	1/1	0.91	0.11	58,58,58,58	0
54	MG	2A	3636	1/1	0.91	0.12	66,66,66,66	0
54	MG	2A	3637	1/1	0.91	0.11	49,49,49,49	0
54	MG	2A	3638	1/1	0.91	0.09	55,55,55,55	0
54	MG	1A	3358	1/1	0.91	0.11	27,27,27,27	0
54	MG	2a	1786	1/1	0.91	0.19	67,67,67,67	0
54	MG	2A	3381	1/1	0.91	0.09	39,39,39,39	0
54	MG	2A	3382	1/1	0.91	0.10	58,58,58,58	0
54	MG	2A	3667	1/1	0.91	0.10	49,49,49,49	0
54	MG	2a	1791	1/1	0.91	0.09	61,61,61,61	0
54	MG	2a	1792	1/1	0.91	0.11	67,67,67,67	0
54	MG	1a	1618	1/1	0.91	0.11	65,65,65,65	0
54	MG	1A	3127	1/1	0.91	0.26	57,57,57,57	0
54	MG	2A	3385	1/1	0.91	0.16	43,43,43,43	0
54	MG	2A	3386	1/1	0.91	0.11	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MPD	1A	4028	8/8	0.91	0.16	39,59,65,70	0
54	MG	1a	1633	1/1	0.91	0.29	67,67,67,67	0
54	MG	2A	3086	1/1	0.91	0.18	57,57,57,57	0
54	MG	1a	1770	1/1	0.91	0.15	58,58,58,58	0
54	MG	2A	3694	1/1	0.91	0.10	41,41,41,41	0
54	MG	1A	3997	1/1	0.91	0.21	58,58,58,58	0
54	MG	2A	3697	1/1	0.91	0.10	67,67,67,67	0
54	MG	1A	3826	1/1	0.91	0.06	8,8,8,8	0
54	MG	2A	3708	1/1	0.91	0.15	51,51,51,51	0
54	MG	1A	4033	1/1	0.92	0.23	47,47,47,47	0
54	MG	1d	505	1/1	0.92	0.20	60,60,60,60	0
54	MG	1a	1625	1/1	0.92	0.11	53,53,53,53	0
54	MG	1A	3477	1/1	0.92	0.13	39,39,39,39	0
54	MG	2D	302	1/1	0.92	0.24	52,52,52,52	0
54	MG	1A	4044	1/1	0.92	0.32	52,52,52,52	0
54	MG	2D	308	1/1	0.92	0.07	31,31,31,31	0
54	MG	2A	3241	1/1	0.92	0.07	48,48,48,48	0
54	MG	2A	3243	1/1	0.92	0.27	46,46,46,46	0
54	MG	1A	3478	1/1	0.92	0.14	36,36,36,36	0
54	MG	1i	3001	1/1	0.92	0.15	62,62,62,62	0
54	MG	1A	3534	1/1	0.92	0.16	67,67,67,67	0
54	MG	2A	3250	1/1	0.92	0.09	62,62,62,62	0
54	MG	1a	1638	1/1	0.92	0.25	61,61,61,61	0
54	MG	1o	3001	1/1	0.92	0.29	65,65,65,65	0
54	MG	2Q	3002	1/1	0.92	0.10	63,63,63,63	0
54	MG	1a	1640	1/1	0.92	0.15	61,61,61,61	0
54	MG	2A	3256	1/1	0.92	0.42	61,61,61,61	0
54	MG	2T	3002	1/1	0.92	0.16	69,69,69,69	0
54	MG	2A	3259	1/1	0.92	0.08	51,51,51,51	0
54	MG	1A	3636	1/1	0.92	0.15	37,37,37,37	0
54	MG	20	102	1/1	0.92	0.10	60,60,60,60	0
54	MG	1a	1757	1/1	0.92	0.10	71,71,71,71	0
54	MG	26	502	1/1	0.92	0.15	68,68,68,68	0
54	MG	1y	201	1/1	0.92	0.26	72,72,72,72	0
54	MG	1A	3176	1/1	0.92	0.14	46,46,46,46	0
54	MG	1A	3905	1/1	0.92	0.14	55,55,55,55	0
54	MG	1A	3544	1/1	0.92	0.12	58,58,58,58	0
54	MG	1A	3914	1/1	0.92	0.12	49,49,49,49	0
54	MG	1a	1650	1/1	0.92	0.33	65,65,65,65	0
54	MG	1A	3411	1/1	0.92	0.15	35,35,35,35	0
54	MG	1a	1769	1/1	0.92	0.11	58,58,58,58	0
54	MG	2A	3036	1/1	0.92	0.13	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3038	1/1	0.92	0.16	53,53,53,53	0
54	MG	2A	3300	1/1	0.92	0.09	55,55,55,55	0
54	MG	2A	3517	1/1	0.92	0.11	57,57,57,57	0
54	MG	1A	3641	1/1	0.92	0.11	62,62,62,62	0
54	MG	2A	3041	1/1	0.92	0.10	50,50,50,50	0
54	MG	1a	1771	1/1	0.92	0.17	79,79,79,79	0
54	MG	1a	1655	1/1	0.92	0.38	69,69,69,69	0
54	MG	1B	210	1/1	0.92	0.10	56,56,56,56	0
54	MG	1A	3926	1/1	0.92	0.11	65,65,65,65	0
54	MG	2A	3313	1/1	0.92	0.12	52,52,52,52	0
54	MG	1a	1775	1/1	0.92	0.12	59,59,59,59	0
54	MG	2a	1629	1/1	0.92	0.16	61,61,61,61	0
54	MG	1A	3709	1/1	0.92	0.07	53,53,53,53	0
54	MG	2A	3323	1/1	0.92	0.11	59,59,59,59	0
54	MG	1A	3642	1/1	0.92	0.17	39,39,39,39	0
54	MG	2A	3333	1/1	0.92	0.10	38,38,38,38	0
54	MG	1a	1780	1/1	0.92	0.11	53,53,53,53	0
54	MG	1A	3934	1/1	0.92	0.08	35,35,35,35	0
54	MG	2A	3065	1/1	0.92	0.28	47,47,47,47	0
54	MG	2A	3068	1/1	0.92	0.14	61,61,61,61	0
54	MG	2A	3540	1/1	0.92	0.12	47,47,47,47	0
54	MG	1a	1667	1/1	0.92	0.14	63,63,63,63	0
54	MG	1A	3936	1/1	0.92	0.10	55,55,55,55	0
54	MG	1A	3177	1/1	0.92	0.14	52,52,52,52	0
54	MG	2A	3550	1/1	0.92	0.08	53,53,53,53	0
54	MG	1A	3352	1/1	0.92	0.10	53,53,53,53	0
54	MG	2a	1647	1/1	0.92	0.34	67,67,67,67	0
54	MG	1A	3550	1/1	0.92	0.12	57,57,57,57	0
54	MG	2A	3352	1/1	0.92	0.07	25,25,25,25	0
54	MG	2A	3092	1/1	0.92	0.19	59,59,59,59	0
54	MG	1A	3494	1/1	0.92	0.11	41,41,41,41	0
54	MG	1B	228	1/1	0.92	0.10	65,65,65,65	0
54	MG	2A	3363	1/1	0.92	0.08	64,64,64,64	0
54	MG	1A	3948	1/1	0.92	0.10	49,49,49,49	0
54	MG	2A	3571	1/1	0.92	0.10	44,44,44,44	0
54	MG	1A	3416	1/1	0.92	0.13	33,33,33,33	0
54	MG	1a	1683	1/1	0.92	0.11	58,58,58,58	0
54	MG	1a	1799	1/1	0.92	0.10	65,65,65,65	0
54	MG	2A	3580	1/1	0.92	0.10	39,39,39,39	0
54	MG	1A	3815	1/1	0.92	0.09	47,47,47,47	0
54	MG	1E	301	1/1	0.92	0.25	40,40,40,40	0
54	MG	2A	3587	1/1	0.92	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3118	1/1	0.92	0.19	45,45,45,45	0
54	MG	1a	1686	1/1	0.92	0.10	64,64,64,64	0
54	MG	1A	3272	1/1	0.92	0.16	30,30,30,30	0
54	MG	1A	3355	1/1	0.92	0.10	43,43,43,43	0
54	MG	2a	1669	1/1	0.92	0.13	77,77,77,77	0
54	MG	2A	3125	1/1	0.92	0.09	44,44,44,44	0
54	MG	2a	1671	1/1	0.92	0.34	70,70,70,70	0
54	MG	1A	3169	1/1	0.92	0.13	53,53,53,53	0
54	MG	2a	1673	1/1	0.92	0.09	68,68,68,68	0
54	MG	1A	3502	1/1	0.92	0.11	56,56,56,56	0
54	MG	2A	3618	1/1	0.92	0.12	37,37,37,37	0
54	MG	2a	1676	1/1	0.92	0.33	62,62,62,62	0
54	MG	2a	1677	1/1	0.92	0.24	66,66,66,66	0
54	MG	1a	1812	1/1	0.92	0.09	51,51,51,51	0
54	MG	1G	3001	1/1	0.92	0.07	72,72,72,72	0
54	MG	1A	3279	1/1	0.92	0.34	69,69,69,69	0
54	MG	1a	1818	1/1	0.92	0.08	69,69,69,69	0
54	MG	2a	1683	1/1	0.92	0.23	69,69,69,69	0
54	MG	1A	3744	1/1	0.92	0.17	51,51,51,51	0
54	MG	1A	3458	1/1	0.92	0.14	48,48,48,48	0
54	MG	2A	3396	1/1	0.92	0.12	50,50,50,50	0
54	MG	2a	1688	1/1	0.92	0.17	58,58,58,58	0
54	MG	2A	3398	1/1	0.92	0.18	56,56,56,56	0
54	MG	2A	3141	1/1	0.92	0.17	59,59,59,59	0
54	MG	2A	3404	1/1	0.92	0.20	70,70,70,70	0
54	MG	1A	3509	1/1	0.92	0.10	62,62,62,62	0
54	MG	2A	3407	1/1	0.92	0.12	41,41,41,41	0
54	MG	1A	3974	1/1	0.92	0.11	75,75,75,75	0
54	MG	1A	3361	1/1	0.92	0.09	47,47,47,47	0
54	MG	2A	3658	1/1	0.92	0.07	52,52,52,52	0
54	MG	1Q	202	1/1	0.92	0.12	55,55,55,55	0
54	MG	1A	3979	1/1	0.92	0.13	62,62,62,62	0
54	MG	1A	3846	1/1	0.92	0.09	47,47,47,47	0
54	MG	2a	1712	1/1	0.92	0.14	62,62,62,62	0
54	MG	1a	1830	1/1	0.92	0.13	84,84,84,84	0
54	MG	1a	1831	1/1	0.92	0.16	67,67,67,67	0
54	MG	2A	3165	1/1	0.92	0.19	64,64,64,64	0
54	MG	1T	8001	1/1	0.92	0.10	60,60,60,60	0
54	MG	2a	1723	1/1	0.92	0.15	68,68,68,68	0
54	MG	2A	3683	1/1	0.92	0.08	51,51,51,51	0
54	MG	1A	3460	1/1	0.92	0.12	55,55,55,55	0
54	MG	2A	3688	1/1	0.92	0.10	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1a	1835	1/1	0.92	0.21	60,60,60,60	0
54	MG	1A	3391	1/1	0.92	0.11	49,49,49,49	0
54	MG	1A	3854	1/1	0.92	0.09	42,42,42,42	0
54	MG	2A	3180	1/1	0.92	0.10	49,49,49,49	0
54	MG	1Z	8001	1/1	0.92	0.15	64,64,64,64	0
54	MG	2A	3700	1/1	0.92	0.09	49,49,49,49	0
54	MG	1A	3994	1/1	0.92	0.13	38,38,38,38	0
54	MG	1A	3855	1/1	0.92	0.09	62,62,62,62	0
54	MG	1A	3617	1/1	0.92	0.09	24,24,24,24	0
54	MG	2A	3712	1/1	0.92	0.07	67,67,67,67	0
54	MG	1A	3761	1/1	0.92	0.12	58,58,58,58	0
54	MG	2A	3716	1/1	0.92	0.10	54,54,54,54	0
54	MG	2a	1757	1/1	0.92	0.08	49,49,49,49	0
54	MG	1a	1848	1/1	0.92	0.13	64,64,64,64	0
54	MG	2a	1769	1/1	0.92	0.17	50,50,50,50	0
54	MG	1A	3305	1/1	0.92	0.19	54,54,54,54	0
54	MG	15	102	1/1	0.92	0.09	55,55,55,55	0
54	MG	2A	3447	1/1	0.92	0.20	48,48,48,48	0
54	MG	15	103	1/1	0.92	0.15	71,71,71,71	0
54	MG	2a	1782	1/1	0.92	0.11	65,65,65,65	0
54	MG	1A	3047	1/1	0.92	0.34	63,63,63,63	0
54	MG	1A	3254	1/1	0.92	0.13	53,53,53,53	0
54	MG	1A	3368	1/1	0.92	0.07	24,24,24,24	0
54	MG	2A	3203	1/1	0.92	0.26	58,58,58,58	0
54	MG	1A	3692	1/1	0.92	0.08	55,55,55,55	0
54	MG	1A	3769	1/1	0.92	0.12	57,57,57,57	0
54	MG	2A	3208	1/1	0.92	0.18	48,48,48,48	0
54	MG	2f	3001	1/1	0.92	0.15	53,53,53,53	0
54	MG	1A	3154	1/1	0.92	0.16	67,67,67,67	0
54	MG	2A	3463	1/1	0.92	0.12	55,55,55,55	0
54	MG	1a	1871	1/1	0.92	0.08	75,75,75,75	0
54	MG	1A	4020	1/1	0.92	0.09	63,63,63,63	0
54	MG	1A	3772	1/1	0.92	0.08	50,50,50,50	0
54	MG	2A	3216	1/1	0.92	0.23	64,64,64,64	0
54	MG	1a	1739	1/1	0.92	0.24	60,60,60,60	0
54	MG	1a	1607	1/1	0.92	0.21	54,54,54,54	0
54	MG	2A	3222	1/1	0.92	0.17	53,53,53,53	0
54	MG	1a	1879	1/1	0.92	0.08	72,72,72,72	0
57	ZN	14	501	1/1	0.92	0.11	225,225,225,225	0
54	MG	1A	3888	1/1	0.92	0.07	58,58,58,58	0
54	MG	1A	3779	1/1	0.92	0.10	29,29,29,29	0
54	MG	1a	1657	1/1	0.93	0.18	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3957	1/1	0.93	0.13	40,40,40,40	0
54	MG	2A	3482	1/1	0.93	0.14	36,36,36,36	0
54	MG	1A	3958	1/1	0.93	0.08	63,63,63,63	0
54	MG	1A	3959	1/1	0.93	0.08	70,70,70,70	0
54	MG	2A	3016	1/1	0.93	0.17	59,59,59,59	0
54	MG	1a	1661	1/1	0.93	0.24	44,44,44,44	0
54	MG	1A	3102	1/1	0.93	0.11	48,48,48,48	0
54	MG	1D	303	1/1	0.93	0.19	36,36,36,36	0
54	MG	2A	3029	1/1	0.93	0.15	47,47,47,47	0
54	MG	2A	3032	1/1	0.93	0.08	46,46,46,46	0
54	MG	2A	3034	1/1	0.93	0.12	49,49,49,49	0
54	MG	2A	3257	1/1	0.93	0.23	58,58,58,58	0
54	MG	1A	3449	1/1	0.93	0.11	54,54,54,54	0
54	MG	1a	1778	1/1	0.93	0.09	67,67,67,67	0
54	MG	2A	3037	1/1	0.93	0.26	52,52,52,52	0
54	MG	1a	1668	1/1	0.93	0.10	59,59,59,59	0
54	MG	2A	3267	1/1	0.93	0.12	60,60,60,60	0
54	MG	1a	1781	1/1	0.93	0.13	62,62,62,62	0
54	MG	1D	313	1/1	0.93	0.13	52,52,52,52	0
54	MG	1A	3837	1/1	0.93	0.07	29,29,29,29	0
54	MG	1A	3499	1/1	0.93	0.07	55,55,55,55	0
54	MG	2A	3280	1/1	0.93	0.09	48,48,48,48	0
54	MG	1a	1674	1/1	0.93	0.15	63,63,63,63	0
54	MG	1E	303	1/1	0.93	0.12	31,31,31,31	0
54	MG	2A	3514	1/1	0.93	0.15	60,60,60,60	0
54	MG	1A	3843	1/1	0.93	0.22	53,53,53,53	0
54	MG	2A	3058	1/1	0.93	0.15	58,58,58,58	0
54	MG	2a	1606	1/1	0.93	0.16	57,57,57,57	0
54	MG	2A	3293	1/1	0.93	0.10	42,42,42,42	0
54	MG	1E	305	1/1	0.93	0.08	38,38,38,38	0
54	MG	2A	3296	1/1	0.93	0.09	42,42,42,42	0
54	MG	1a	1679	1/1	0.93	0.22	55,55,55,55	0
54	MG	2a	1612	1/1	0.93	0.23	63,63,63,63	0
54	MG	2a	1613	1/1	0.93	0.23	68,68,68,68	0
54	MG	1A	3844	1/1	0.93	0.12	58,58,58,58	0
54	MG	1A	3751	1/1	0.93	0.10	27,27,27,27	0
54	MG	1A	3049	1/1	0.93	0.26	55,55,55,55	0
54	MG	1a	1797	1/1	0.93	0.09	74,74,74,74	0
54	MG	2A	3070	1/1	0.93	0.09	46,46,46,46	0
54	MG	2A	3071	1/1	0.93	0.21	52,52,52,52	0
54	MG	2A	3075	1/1	0.93	0.18	46,46,46,46	0
54	MG	1A	3410	1/1	0.93	0.09	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3533	1/1	0.93	0.13	58,58,58,58	0
54	MG	1A	3976	1/1	0.93	0.14	50,50,50,50	0
54	MG	1G	3003	1/1	0.93	0.09	63,63,63,63	0
54	MG	1a	1687	1/1	0.93	0.07	52,52,52,52	0
54	MG	1A	3672	1/1	0.93	0.09	68,68,68,68	0
54	MG	1A	3980	1/1	0.93	0.15	58,58,58,58	0
54	MG	1A	3981	1/1	0.93	0.11	58,58,58,58	0
54	MG	1a	1810	1/1	0.93	0.16	60,60,60,60	0
54	MG	1A	3609	1/1	0.93	0.13	54,54,54,54	0
54	MG	2A	3547	1/1	0.93	0.14	63,63,63,63	0
54	MG	2a	1639	1/1	0.93	0.20	73,73,73,73	0
54	MG	1A	3985	1/1	0.93	0.08	75,75,75,75	0
54	MG	1A	3035	1/1	0.93	0.17	57,57,57,57	0
54	MG	1A	3213	1/1	0.93	0.30	63,63,63,63	0
54	MG	2A	3105	1/1	0.93	0.16	55,55,55,55	0
54	MG	1R	201	1/1	0.93	0.14	53,53,53,53	0
54	MG	1A	3989	1/1	0.93	0.10	48,48,48,48	0
54	MG	2A	3558	1/1	0.93	0.08	32,32,32,32	0
54	MG	2A	3116	1/1	0.93	0.09	65,65,65,65	0
54	MG	2A	3117	1/1	0.93	0.12	52,52,52,52	0
54	MG	1A	3862	1/1	0.93	0.07	54,54,54,54	0
54	MG	1A	3991	1/1	0.93	0.07	50,50,50,50	0
54	MG	1A	3014	1/1	0.93	0.20	58,58,58,58	0
54	MG	2A	3366	1/1	0.93	0.08	53,53,53,53	0
54	MG	2a	1653	1/1	0.93	0.26	62,62,62,62	0
54	MG	2A	3121	1/1	0.93	0.15	58,58,58,58	0
54	MG	2A	3122	1/1	0.93	0.14	44,44,44,44	0
54	MG	2A	3369	1/1	0.93	0.10	51,51,51,51	0
54	MG	2A	3370	1/1	0.93	0.06	33,33,33,33	0
54	MG	1A	3563	1/1	0.93	0.15	53,53,53,53	0
54	MG	2A	3585	1/1	0.93	0.12	38,38,38,38	0
54	MG	1A	3684	1/1	0.93	0.10	39,39,39,39	0
54	MG	2A	3588	1/1	0.93	0.10	88,88,88,88	0
54	MG	2A	3591	1/1	0.93	0.08	43,43,43,43	0
54	MG	2A	3375	1/1	0.93	0.07	51,51,51,51	0
54	MG	1A	3221	1/1	0.93	0.18	54,54,54,54	0
54	MG	1A	3876	1/1	0.93	0.14	37,37,37,37	0
54	MG	10	105	1/1	0.93	0.09	65,65,65,65	0
54	MG	1A	3335	1/1	0.93	0.10	37,37,37,37	0
54	MG	1A	3689	1/1	0.93	0.11	71,71,71,71	0
54	MG	1A	3620	1/1	0.93	0.15	40,40,40,40	0
54	MG	2A	3616	1/1	0.93	0.10	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1a	1717	1/1	0.93	0.12	64,64,64,64	0
54	MG	1A	3089	1/1	0.93	0.12	47,47,47,47	0
54	MG	2A	3622	1/1	0.93	0.08	69,69,69,69	0
54	MG	1A	3783	1/1	0.93	0.12	37,37,37,37	0
54	MG	2A	3142	1/1	0.93	0.09	47,47,47,47	0
54	MG	1A	3515	1/1	0.93	0.12	34,34,34,34	0
54	MG	2A	3146	1/1	0.93	0.08	61,61,61,61	0
54	MG	1A	3247	1/1	0.93	0.28	61,61,61,61	0
54	MG	1A	3518	1/1	0.93	0.11	65,65,65,65	0
54	MG	1a	1842	1/1	0.93	0.17	64,64,64,64	0
54	MG	1a	1844	1/1	0.93	0.08	54,54,54,54	0
54	MG	1A	4025	1/1	0.93	0.08	70,70,70,70	0
54	MG	19	103	1/1	0.93	0.09	66,66,66,66	0
54	MG	1A	3129	1/1	0.93	0.13	49,49,49,49	0
54	MG	1A	3099	1/1	0.93	0.18	59,59,59,59	0
54	MG	1A	3257	1/1	0.93	0.19	51,51,51,51	0
54	MG	2A	3644	1/1	0.93	0.07	58,58,58,58	0
54	MG	2a	1694	1/1	0.93	0.11	50,50,50,50	0
54	MG	1a	1731	1/1	0.93	0.07	54,54,54,54	0
54	MG	2a	1696	1/1	0.93	0.13	73,73,73,73	0
54	MG	2a	1697	1/1	0.93	0.16	66,66,66,66	0
54	MG	1A	3170	1/1	0.93	0.08	38,38,38,38	0
54	MG	2A	3661	1/1	0.93	0.07	46,46,46,46	0
54	MG	2a	1703	1/1	0.93	0.15	69,69,69,69	0
54	MG	1a	1861	1/1	0.93	0.08	52,52,52,52	0
54	MG	2A	3178	1/1	0.93	0.12	59,59,59,59	0
54	MG	1a	1862	1/1	0.93	0.17	64,64,64,64	0
54	MG	2A	3415	1/1	0.93	0.20	49,49,49,49	0
54	MG	2A	3674	1/1	0.93	0.08	25,25,25,25	0
54	MG	1A	4043	1/1	0.93	0.10	32,32,32,32	0
54	MG	2A	3417	1/1	0.93	0.22	52,52,52,52	0
54	MG	2a	1714	1/1	0.93	0.09	69,69,69,69	0
54	MG	2A	3681	1/1	0.93	0.07	70,70,70,70	0
54	MG	1A	3200	1/1	0.93	0.30	63,63,63,63	0
54	MG	1A	3397	1/1	0.93	0.09	33,33,33,33	0
54	MG	1A	3002	1/1	0.93	0.09	54,54,54,54	0
54	MG	1a	1868	1/1	0.93	0.07	71,71,71,71	0
54	MG	1A	3584	1/1	0.93	0.11	47,47,47,47	0
54	MG	2A	3425	1/1	0.93	0.13	55,55,55,55	0
54	MG	1a	1870	1/1	0.93	0.07	93,93,93,93	0
54	MG	1a	1627	1/1	0.93	0.13	54,54,54,54	0
54	MG	2A	3698	1/1	0.93	0.10	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3437	1/1	0.93	0.13	41,41,41,41	0
54	MG	1A	3586	1/1	0.93	0.13	55,55,55,55	0
54	MG	1A	3932	1/1	0.93	0.06	55,55,55,55	0
54	MG	2A	3197	1/1	0.93	0.10	47,47,47,47	0
54	MG	2a	1737	1/1	0.93	0.08	67,67,67,67	0
54	MG	2A	3198	1/1	0.93	0.11	56,56,56,56	0
54	MG	2A	3199	1/1	0.93	0.09	56,56,56,56	0
54	MG	2a	1741	1/1	0.93	0.08	82,82,82,82	0
54	MG	1A	3812	1/1	0.93	0.10	46,46,46,46	0
54	MG	1A	3269	1/1	0.93	0.10	53,53,53,53	0
54	MG	1a	1639	1/1	0.93	0.14	47,47,47,47	0
54	MG	1A	3542	1/1	0.93	0.12	49,49,49,49	0
54	MG	2A	3449	1/1	0.93	0.11	60,60,60,60	0
54	MG	2A	3723	1/1	0.93	0.35	44,44,44,44	0
54	MG	2A	3205	1/1	0.93	0.32	66,66,66,66	0
54	MG	1A	3314	1/1	0.93	0.14	73,73,73,73	0
54	MG	2A	3207	1/1	0.93	0.09	46,46,46,46	0
54	MG	2A	3730	1/1	0.93	0.17	56,56,56,56	0
54	MG	1a	1642	1/1	0.93	0.24	70,70,70,70	0
54	MG	2A	3740	1/1	0.93	0.09	54,54,54,54	0
54	MG	2A	3746	1/1	0.93	0.10	55,55,55,55	0
54	MG	1a	1643	1/1	0.93	0.10	62,62,62,62	0
54	MG	1A	3442	1/1	0.93	0.14	61,61,61,61	0
54	MG	1B	215	1/1	0.93	0.09	59,59,59,59	0
54	MG	2A	3757	1/1	0.93	0.16	64,64,64,64	0
54	MG	1e	204	1/1	0.93	0.12	62,62,62,62	0
54	MG	1f	8001	1/1	0.93	0.14	52,52,52,52	0
54	MG	1A	3648	1/1	0.93	0.06	29,29,29,29	0
54	MG	1h	3001	1/1	0.93	0.29	65,65,65,65	0
54	MG	1h	3002	1/1	0.93	0.19	58,58,58,58	0
54	MG	1A	3547	1/1	0.93	0.08	41,41,41,41	0
54	MG	1A	3731	1/1	0.93	0.06	38,38,38,38	0
54	MG	2A	3225	1/1	0.93	0.16	54,54,54,54	0
54	MG	1A	3827	1/1	0.93	0.12	27,27,27,27	0
54	MG	1a	1765	1/1	0.93	0.14	48,48,48,48	0
54	MG	2A	3229	1/1	0.93	0.09	51,51,51,51	0
54	MG	1a	1767	1/1	0.93	0.07	79,79,79,79	0
54	MG	1A	3317	1/1	0.93	0.19	45,45,45,45	0
54	MG	2A	3232	1/1	0.93	0.12	52,52,52,52	0
54	MG	1A	3444	1/1	0.93	0.19	61,61,61,61	0
54	MG	2B	3017	1/1	0.93	0.08	68,68,68,68	0
54	MG	1A	4057	1/1	0.94	0.16	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3491	1/1	0.94	0.12	24,24,24,24	0
54	MG	2D	307	1/1	0.94	0.13	37,37,37,37	0
54	MG	2A	3258	1/1	0.94	0.23	44,44,44,44	0
54	MG	1A	3420	1/1	0.94	0.13	24,24,24,24	0
54	MG	2A	3046	1/1	0.94	0.11	48,48,48,48	0
54	MG	1A	3422	1/1	0.94	0.13	32,32,32,32	0
54	MG	2F	302	1/1	0.94	0.09	41,41,41,41	0
54	MG	1A	3572	1/1	0.94	0.09	30,30,30,30	0
54	MG	2A	3051	1/1	0.94	0.30	57,57,57,57	0
54	MG	2A	3052	1/1	0.94	0.16	43,43,43,43	0
54	MG	2I	3001	1/1	0.94	0.07	52,52,52,52	0
54	MG	2A	3274	1/1	0.94	0.11	53,53,53,53	0
54	MG	1A	3036	1/1	0.94	0.10	41,41,41,41	0
54	MG	2P	201	1/1	0.94	0.12	55,55,55,55	0
54	MG	2P	202	1/1	0.94	0.07	55,55,55,55	0
54	MG	1A	3022	1/1	0.94	0.08	46,46,46,46	0
54	MG	1A	3903	1/1	0.94	0.08	67,67,67,67	0
54	MG	1A	3182	1/1	0.94	0.16	61,61,61,61	0
54	MG	2A	3285	1/1	0.94	0.08	32,32,32,32	0
54	MG	2T	3003	1/1	0.94	0.14	68,68,68,68	0
54	MG	1A	3652	1/1	0.94	0.07	56,56,56,56	0
54	MG	1A	3653	1/1	0.94	0.14	40,40,40,40	0
54	MG	1A	3187	1/1	0.94	0.26	56,56,56,56	0
54	MG	1a	1789	1/1	0.94	0.06	67,67,67,67	0
54	MG	1a	1790	1/1	0.94	0.09	52,52,52,52	0
54	MG	1A	3656	1/1	0.94	0.07	26,26,26,26	0
54	MG	1A	3430	1/1	0.94	0.11	56,56,56,56	0
54	MG	2A	3297	1/1	0.94	0.07	43,43,43,43	0
54	MG	1A	3662	1/1	0.94	0.07	48,48,48,48	0
54	MG	1A	3076	1/1	0.94	0.07	44,44,44,44	0
54	MG	1A	3782	1/1	0.94	0.07	35,35,35,35	0
54	MG	1a	1798	1/1	0.94	0.08	48,48,48,48	0
54	MG	1A	3503	1/1	0.94	0.11	52,52,52,52	0
54	MG	2A	3308	1/1	0.94	0.17	56,56,56,56	0
54	MG	2A	3083	1/1	0.94	0.12	69,69,69,69	0
54	MG	2A	3532	1/1	0.94	0.14	47,47,47,47	0
54	MG	1A	3004	1/1	0.94	0.09	44,44,44,44	0
54	MG	1A	3030	1/1	0.94	0.06	33,33,33,33	0
54	MG	2A	3314	1/1	0.94	0.13	38,38,38,38	0
54	MG	1A	3669	1/1	0.94	0.06	46,46,46,46	0
54	MG	1A	3941	1/1	0.94	0.16	66,66,66,66	0
54	MG	2A	3538	1/1	0.94	0.08	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3321	1/1	0.94	0.05	33,33,33,33	0
54	MG	1B	231	1/1	0.94	0.06	59,59,59,59	0
54	MG	2A	3541	1/1	0.94	0.12	43,43,43,43	0
54	MG	2A	3326	1/1	0.94	0.09	30,30,30,30	0
54	MG	1a	1808	1/1	0.94	0.11	67,67,67,67	0
54	MG	1D	302	1/1	0.94	0.20	60,60,60,60	0
54	MG	2a	1628	1/1	0.94	0.20	66,66,66,66	0
54	MG	1A	3373	1/1	0.94	0.12	52,52,52,52	0
54	MG	1A	3944	1/1	0.94	0.05	24,24,24,24	0
54	MG	2A	3104	1/1	0.94	0.10	46,46,46,46	0
54	MG	2a	1632	1/1	0.94	0.30	59,59,59,59	0
54	MG	1A	3142	1/1	0.94	0.08	51,51,51,51	0
54	MG	2A	3106	1/1	0.94	0.17	56,56,56,56	0
54	MG	1a	1814	1/1	0.94	0.08	67,67,67,67	0
54	MG	2A	3109	1/1	0.94	0.10	47,47,47,47	0
54	MG	2A	3112	1/1	0.94	0.14	50,50,50,50	0
54	MG	2A	3562	1/1	0.94	0.07	50,50,50,50	0
54	MG	1A	3322	1/1	0.94	0.11	30,30,30,30	0
54	MG	1A	3052	1/1	0.94	0.18	44,44,44,44	0
54	MG	1A	3378	1/1	0.94	0.11	36,36,36,36	0
54	MG	2A	3354	1/1	0.94	0.07	56,56,56,56	0
54	MG	1a	1819	1/1	0.94	0.30	64,64,64,64	0
54	MG	2A	3358	1/1	0.94	0.19	69,69,69,69	0
54	MG	2A	3577	1/1	0.94	0.08	57,57,57,57	0
54	MG	1A	3955	1/1	0.94	0.10	60,60,60,60	0
54	MG	1A	3151	1/1	0.94	0.10	41,41,41,41	0
54	MG	1F	305	1/1	0.94	0.34	66,66,66,66	0
54	MG	1A	3804	1/1	0.94	0.18	37,37,37,37	0
54	MG	1A	3381	1/1	0.94	0.07	24,24,24,24	0
54	MG	1F	308	1/1	0.94	0.12	41,41,41,41	0
54	MG	1A	3682	1/1	0.94	0.10	59,59,59,59	0
54	MG	1a	1693	1/1	0.94	0.08	40,40,40,40	0
54	MG	1A	3594	1/1	0.94	0.10	58,58,58,58	0
54	MG	2A	3596	1/1	0.94	0.08	58,58,58,58	0
54	MG	1a	1695	1/1	0.94	0.38	67,67,67,67	0
54	MG	2A	3599	1/1	0.94	0.10	57,57,57,57	0
54	MG	1A	3278	1/1	0.94	0.10	56,56,56,56	0
54	MG	1A	3448	1/1	0.94	0.11	67,67,67,67	0
54	MG	1A	3032	1/1	0.94	0.19	56,56,56,56	0
54	MG	2A	3611	1/1	0.94	0.06	34,34,34,34	0
54	MG	1A	3598	1/1	0.94	0.10	35,35,35,35	0
54	MG	1N	201	1/1	0.94	0.12	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3390	1/1	0.94	0.09	42,42,42,42	0
54	MG	1A	3337	1/1	0.94	0.07	35,35,35,35	0
54	MG	2A	3619	1/1	0.94	0.07	53,53,53,53	0
54	MG	1A	3603	1/1	0.94	0.08	53,53,53,53	0
54	MG	1A	3696	1/1	0.94	0.27	38,38,38,38	0
54	MG	1a	1843	1/1	0.94	0.08	67,67,67,67	0
54	MG	2A	3153	1/1	0.94	0.14	48,48,48,48	0
54	MG	2A	3155	1/1	0.94	0.19	52,52,52,52	0
54	MG	1A	3394	1/1	0.94	0.08	26,26,26,26	0
54	MG	1A	3698	1/1	0.94	0.16	51,51,51,51	0
54	MG	1A	3395	1/1	0.94	0.16	32,32,32,32	0
54	MG	2A	3632	1/1	0.94	0.07	72,72,72,72	0
54	MG	1a	1711	1/1	0.94	0.13	69,69,69,69	0
54	MG	1A	3536	1/1	0.94	0.09	33,33,33,33	0
54	MG	1A	3338	1/1	0.94	0.09	46,46,46,46	0
54	MG	1A	3984	1/1	0.94	0.19	59,59,59,59	0
54	MG	2A	3170	1/1	0.94	0.16	59,59,59,59	0
54	MG	1U	201	1/1	0.94	0.35	61,61,61,61	0
54	MG	1V	202	1/1	0.94	0.14	64,64,64,64	0
54	MG	2A	3173	1/1	0.94	0.09	55,55,55,55	0
54	MG	2A	3655	1/1	0.94	0.06	54,54,54,54	0
54	MG	1V	203	1/1	0.94	0.18	63,63,63,63	0
54	MG	1A	3061	1/1	0.94	0.12	49,49,49,49	0
54	MG	1W	3002	1/1	0.94	0.09	52,52,52,52	0
54	MG	1A	3109	1/1	0.94	0.12	45,45,45,45	0
54	MG	1A	3110	1/1	0.94	0.08	43,43,43,43	0
54	MG	1A	3841	1/1	0.94	0.12	49,49,49,49	0
54	MG	2A	3185	1/1	0.94	0.23	50,50,50,50	0
54	MG	2a	1701	1/1	0.94	0.08	70,70,70,70	0
54	MG	1a	1727	1/1	0.94	0.12	54,54,54,54	0
54	MG	2A	3677	1/1	0.94	0.11	52,52,52,52	0
54	MG	2a	1704	1/1	0.94	0.18	67,67,67,67	0
54	MG	1A	3546	1/1	0.94	0.15	42,42,42,42	0
54	MG	1A	3285	1/1	0.94	0.13	53,53,53,53	0
54	MG	1A	3210	1/1	0.94	0.30	58,58,58,58	0
54	MG	11	104	1/1	0.94	0.07	41,41,41,41	0
54	MG	1A	3349	1/1	0.94	0.11	30,30,30,30	0
54	MG	2A	3687	1/1	0.94	0.07	39,39,39,39	0
54	MG	1a	1875	1/1	0.94	0.10	77,77,77,77	0
54	MG	1A	3996	1/1	0.94	0.13	59,59,59,59	0
54	MG	1A	3034	1/1	0.94	0.07	53,53,53,53	0
54	MG	1a	1737	1/1	0.94	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3433	1/1	0.94	0.09	32,32,32,32	0
54	MG	1A	3624	1/1	0.94	0.11	60,60,60,60	0
54	MG	1A	3999	1/1	0.94	0.16	39,39,39,39	0
54	MG	1A	3115	1/1	0.94	0.09	46,46,46,46	0
54	MG	1A	3857	1/1	0.94	0.10	23,23,23,23	0
54	MG	1A	4002	1/1	0.94	0.14	68,68,68,68	0
54	MG	1A	3469	1/1	0.94	0.11	25,25,25,25	0
54	MG	2A	3711	1/1	0.94	0.09	50,50,50,50	0
54	MG	1A	3860	1/1	0.94	0.07	48,48,48,48	0
54	MG	1a	1746	1/1	0.94	0.07	56,56,56,56	0
54	MG	1g	202	1/1	0.94	0.42	66,66,66,66	0
54	MG	1a	1604	1/1	0.94	0.15	54,54,54,54	0
54	MG	1A	3412	1/1	0.94	0.13	27,27,27,27	0
54	MG	1A	4010	1/1	0.94	0.07	34,34,34,34	0
54	MG	1A	3064	1/1	0.94	0.07	44,44,44,44	0
54	MG	1l	3001	1/1	0.94	0.23	62,62,62,62	0
54	MG	2a	1745	1/1	0.94	0.07	46,46,46,46	0
54	MG	1a	1608	1/1	0.94	0.20	54,54,54,54	0
54	MG	1a	1609	1/1	0.94	0.10	57,57,57,57	0
54	MG	2A	3728	1/1	0.94	0.12	58,58,58,58	0
54	MG	2A	3220	1/1	0.94	0.14	58,58,58,58	0
54	MG	1A	3728	1/1	0.94	0.12	68,68,68,68	0
54	MG	2a	1759	1/1	0.94	0.09	75,75,75,75	0
54	MG	2a	1761	1/1	0.94	0.09	65,65,65,65	0
54	MG	1A	3414	1/1	0.94	0.08	33,33,33,33	0
54	MG	2a	1768	1/1	0.94	0.07	52,52,52,52	0
54	MG	2A	3738	1/1	0.94	0.07	46,46,46,46	0
54	MG	1A	3357	1/1	0.94	0.09	51,51,51,51	0
54	MG	1a	1619	1/1	0.94	0.10	65,65,65,65	0
54	MG	2A	3750	1/1	0.94	0.18	48,48,48,48	0
54	MG	2a	1779	1/1	0.94	0.13	78,78,78,78	0
54	MG	1a	1620	1/1	0.94	0.07	48,48,48,48	0
54	MG	2A	3227	1/1	0.94	0.09	51,51,51,51	0
54	MG	2a	1784	1/1	0.94	0.11	64,64,64,64	0
54	MG	1a	1624	1/1	0.94	0.17	52,52,52,52	0
54	MG	2A	3471	1/1	0.94	0.10	30,30,30,30	0
54	MG	2A	3758	1/1	0.94	0.09	52,52,52,52	0
54	MG	1A	3298	1/1	0.94	0.09	62,62,62,62	0
54	MG	2A	3002	1/1	0.94	0.08	38,38,38,38	0
54	MG	1A	3873	1/1	0.94	0.08	48,48,48,48	0
54	MG	1a	1766	1/1	0.94	0.21	71,71,71,71	0
54	MG	2A	3017	1/1	0.94	0.15	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	4027	1/1	0.94	0.11	55,55,55,55	0
54	MG	2A	3239	1/1	0.94	0.18	49,49,49,49	0
54	MG	1A	3739	1/1	0.94	0.08	45,45,45,45	0
54	MG	1A	3562	1/1	0.94	0.08	54,54,54,54	0
54	MG	1A	3482	1/1	0.94	0.13	30,30,30,30	0
54	MG	1A	3746	1/1	0.94	0.10	59,59,59,59	0
54	MG	2A	3033	1/1	0.94	0.21	54,54,54,54	0
54	MG	2A	3248	1/1	0.94	0.10	43,43,43,43	0
54	MG	1A	3010	1/1	0.94	0.08	49,49,49,49	0
54	MG	1A	4047	1/1	0.94	0.09	59,59,59,59	0
54	MG	1A	3230	1/1	0.94	0.13	44,44,44,44	0
54	MG	1A	4055	1/1	0.94	0.15	42,42,42,42	0
54	MG	2A	3493	1/1	0.94	0.08	53,53,53,53	0
54	MG	1A	3162	1/1	0.95	0.19	40,40,40,40	0
54	MG	1A	3204	1/1	0.95	0.11	60,60,60,60	0
54	MG	2A	3255	1/1	0.95	0.15	45,45,45,45	0
54	MG	1D	304	1/1	0.95	0.13	61,61,61,61	0
54	MG	1a	1670	1/1	0.95	0.27	68,68,68,68	0
54	MG	2A	3497	1/1	0.95	0.08	47,47,47,47	0
54	MG	2D	304	1/1	0.95	0.11	36,36,36,36	0
54	MG	2A	3059	1/1	0.95	0.09	45,45,45,45	0
54	MG	1A	3954	1/1	0.95	0.07	24,24,24,24	0
54	MG	1A	3807	1/1	0.95	0.08	52,52,52,52	0
54	MG	1A	3618	1/1	0.95	0.10	32,32,32,32	0
54	MG	1A	3164	1/1	0.95	0.12	45,45,45,45	0
54	MG	1A	3558	1/1	0.95	0.06	62,62,62,62	0
54	MG	2A	3268	1/1	0.95	0.10	57,57,57,57	0
54	MG	2A	3067	1/1	0.95	0.07	49,49,49,49	0
54	MG	1a	1806	1/1	0.95	0.09	52,52,52,52	0
54	MG	1A	3622	1/1	0.95	0.12	53,53,53,53	0
54	MG	1A	3700	1/1	0.95	0.14	41,41,41,41	0
54	MG	2A	3278	1/1	0.95	0.06	50,50,50,50	0
54	MG	1E	306	1/1	0.95	0.19	68,68,68,68	0
54	MG	1F	302	1/1	0.95	0.20	40,40,40,40	0
54	MG	2A	3282	1/1	0.95	0.06	52,52,52,52	0
54	MG	2A	3283	1/1	0.95	0.10	19,19,19,19	0
54	MG	1A	3962	1/1	0.95	0.08	59,59,59,59	0
54	MG	1A	3058	1/1	0.95	0.15	49,49,49,49	0
54	MG	1A	3702	1/1	0.95	0.13	43,43,43,43	0
54	MG	2A	3084	1/1	0.95	0.09	49,49,49,49	0
54	MG	2A	3291	1/1	0.95	0.14	54,54,54,54	0
54	MG	2A	3085	1/1	0.95	0.07	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3560	1/1	0.95	0.08	57,57,57,57	0
54	MG	2A	3088	1/1	0.95	0.32	47,47,47,47	0
54	MG	1A	3493	1/1	0.95	0.11	53,53,53,53	0
54	MG	1F	310	1/1	0.95	0.09	53,53,53,53	0
54	MG	28	8002	1/1	0.95	0.12	51,51,51,51	0
54	MG	2A	3298	1/1	0.95	0.06	33,33,33,33	0
54	MG	1A	3388	1/1	0.95	0.14	31,31,31,31	0
54	MG	1A	3495	1/1	0.95	0.07	45,45,45,45	0
54	MG	2A	3531	1/1	0.95	0.09	62,62,62,62	0
54	MG	1A	3436	1/1	0.95	0.07	43,43,43,43	0
54	MG	1A	3711	1/1	0.95	0.06	40,40,40,40	0
54	MG	1A	3831	1/1	0.95	0.17	53,53,53,53	0
54	MG	1A	3059	1/1	0.95	0.14	26,26,26,26	0
54	MG	2A	3309	1/1	0.95	0.09	39,39,39,39	0
54	MG	1A	3090	1/1	0.95	0.12	55,55,55,55	0
54	MG	1A	3714	1/1	0.95	0.08	45,45,45,45	0
54	MG	1A	3392	1/1	0.95	0.12	27,27,27,27	0
54	MG	1A	3637	1/1	0.95	0.08	49,49,49,49	0
54	MG	2A	3108	1/1	0.95	0.10	60,60,60,60	0
54	MG	1A	3092	1/1	0.95	0.12	35,35,35,35	0
54	MG	1a	1833	1/1	0.95	0.09	48,48,48,48	0
54	MG	1A	3346	1/1	0.95	0.07	35,35,35,35	0
54	MG	1R	202	1/1	0.95	0.12	50,50,50,50	0
54	MG	1A	3293	1/1	0.95	0.07	50,50,50,50	0
54	MG	2A	3331	1/1	0.95	0.08	47,47,47,47	0
54	MG	1A	3218	1/1	0.95	0.26	48,48,48,48	0
54	MG	1A	3173	1/1	0.95	0.21	52,52,52,52	0
54	MG	2A	3555	1/1	0.95	0.07	52,52,52,52	0
54	MG	1A	3039	1/1	0.95	0.09	48,48,48,48	0
54	MG	2A	3338	1/1	0.95	0.07	33,33,33,33	0
54	MG	1a	1840	1/1	0.95	0.11	58,58,58,58	0
54	MG	1A	3133	1/1	0.95	0.08	42,42,42,42	0
54	MG	2A	3565	1/1	0.95	0.09	57,57,57,57	0
54	MG	2A	3343	1/1	0.95	0.07	56,56,56,56	0
54	MG	2A	3344	1/1	0.95	0.11	42,42,42,42	0
54	MG	1U	202	1/1	0.95	0.16	47,47,47,47	0
54	MG	1A	3041	1/1	0.95	0.11	54,54,54,54	0
54	MG	2A	3127	1/1	0.95	0.09	44,44,44,44	0
54	MG	2A	3128	1/1	0.95	0.13	45,45,45,45	0
54	MG	1A	3408	1/1	0.95	0.09	38,38,38,38	0
54	MG	1A	3001	1/1	0.95	0.08	33,33,33,33	0
54	MG	1A	3741	1/1	0.95	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3517	1/1	0.95	0.11	22,22,22,22	0
54	MG	10	101	1/1	0.95	0.07	52,52,52,52	0
54	MG	1A	3248	1/1	0.95	0.35	58,58,58,58	0
54	MG	10	103	1/1	0.95	0.08	53,53,53,53	0
54	MG	1a	1858	1/1	0.95	0.07	54,54,54,54	0
54	MG	1A	3186	1/1	0.95	0.34	43,43,43,43	0
54	MG	1a	1860	1/1	0.95	0.11	66,66,66,66	0
54	MG	1A	3654	1/1	0.95	0.07	34,34,34,34	0
54	MG	2A	3145	1/1	0.95	0.09	49,49,49,49	0
54	MG	1A	3587	1/1	0.95	0.12	50,50,50,50	0
54	MG	2A	3147	1/1	0.95	0.08	47,47,47,47	0
54	MG	2A	3371	1/1	0.95	0.10	70,70,70,70	0
54	MG	1A	3139	1/1	0.95	0.06	45,45,45,45	0
54	MG	2A	3373	1/1	0.95	0.06	50,50,50,50	0
54	MG	1A	4006	1/1	0.95	0.10	55,55,55,55	0
54	MG	13	101	1/1	0.95	0.10	62,62,62,62	0
54	MG	2A	3154	1/1	0.95	0.14	45,45,45,45	0
54	MG	2A	3378	1/1	0.95	0.08	47,47,47,47	0
54	MG	1A	3021	1/1	0.95	0.15	34,34,34,34	0
54	MG	1A	4009	1/1	0.95	0.11	41,41,41,41	0
54	MG	1A	3659	1/1	0.95	0.08	54,54,54,54	0
54	MG	1A	3757	1/1	0.95	0.07	50,50,50,50	0
54	MG	1A	3008	1/1	0.95	0.07	40,40,40,40	0
54	MG	1A	3759	1/1	0.95	0.12	45,45,45,45	0
54	MG	1A	4021	1/1	0.95	0.22	34,34,34,34	0
54	MG	1A	3056	1/1	0.95	0.08	47,47,47,47	0
54	MG	2A	3168	1/1	0.95	0.31	46,46,46,46	0
54	MG	2A	3631	1/1	0.95	0.06	64,64,64,64	0
54	MG	1A	3263	1/1	0.95	0.19	49,49,49,49	0
54	MG	1A	3417	1/1	0.95	0.13	40,40,40,40	0
54	MG	1A	3033	1/1	0.95	0.12	44,44,44,44	0
54	MG	1A	3119	1/1	0.95	0.31	47,47,47,47	0
54	MG	1A	3767	1/1	0.95	0.06	43,43,43,43	0
54	MG	2A	3176	1/1	0.95	0.12	45,45,45,45	0
54	MG	2A	3399	1/1	0.95	0.07	61,61,61,61	0
54	MG	1d	503	1/1	0.95	0.33	69,69,69,69	0
54	MG	2A	3402	1/1	0.95	0.09	52,52,52,52	0
54	MG	1A	3124	1/1	0.95	0.12	45,45,45,45	0
54	MG	2a	1684	1/1	0.95	0.39	59,59,59,59	0
54	MG	1a	1747	1/1	0.95	0.15	54,54,54,54	0
54	MG	2A	3406	1/1	0.95	0.08	42,42,42,42	0
54	MG	1a	1748	1/1	0.95	0.07	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3326	1/1	0.95	0.10	33,33,33,33	0
54	MG	2A	3665	1/1	0.95	0.07	53,53,53,53	0
54	MG	1A	3543	1/1	0.95	0.20	46,46,46,46	0
54	MG	1a	1612	1/1	0.95	0.35	62,62,62,62	0
54	MG	1A	3904	1/1	0.95	0.06	51,51,51,51	0
54	MG	2A	3188	1/1	0.95	0.06	57,57,57,57	0
54	MG	1A	4048	1/1	0.95	0.15	35,35,35,35	0
54	MG	2A	3678	1/1	0.95	0.07	54,54,54,54	0
54	MG	2a	1699	1/1	0.95	0.07	53,53,53,53	0
54	MG	1A	4050	1/1	0.95	0.17	29,29,29,29	0
54	MG	1A	3675	1/1	0.95	0.14	60,60,60,60	0
54	MG	1A	3776	1/1	0.95	0.07	21,21,21,21	0
54	MG	1a	1621	1/1	0.95	0.06	48,48,48,48	0
54	MG	1A	4056	1/1	0.95	0.25	41,41,41,41	0
54	MG	1A	3912	1/1	0.95	0.06	39,39,39,39	0
54	MG	1A	3777	1/1	0.95	0.07	40,40,40,40	0
54	MG	2A	3689	1/1	0.95	0.07	45,45,45,45	0
54	MG	2A	3690	1/1	0.95	0.06	63,63,63,63	0
54	MG	1n	503	1/1	0.95	0.13	59,59,59,59	0
54	MG	1a	1629	1/1	0.95	0.26	65,65,65,65	0
54	MG	2a	1713	1/1	0.95	0.11	61,61,61,61	0
54	MG	2A	3201	1/1	0.95	0.14	53,53,53,53	0
54	MG	2A	3695	1/1	0.95	0.10	57,57,57,57	0
54	MG	2a	1716	1/1	0.95	0.15	64,64,64,64	0
54	MG	1A	4070	1/1	0.95	0.13	32,32,32,32	0
54	MG	1A	4075	1/1	0.95	0.14	39,39,39,39	0
54	MG	2a	1720	1/1	0.95	0.07	63,63,63,63	0
54	MG	1A	3915	1/1	0.95	0.10	34,34,34,34	0
54	MG	2a	1722	1/1	0.95	0.15	64,64,64,64	0
54	MG	1A	3475	1/1	0.95	0.14	40,40,40,40	0
54	MG	2A	3701	1/1	0.95	0.09	63,63,63,63	0
54	MG	1y	203	1/1	0.95	0.07	61,61,61,61	0
54	MG	2A	3705	1/1	0.95	0.13	57,57,57,57	0
54	MG	1A	3919	1/1	0.95	0.11	35,35,35,35	0
54	MG	2A	3441	1/1	0.95	0.11	70,70,70,70	0
54	MG	2A	3710	1/1	0.95	0.07	45,45,45,45	0
54	MG	1A	3921	1/1	0.95	0.09	61,61,61,61	0
54	MG	1A	3780	1/1	0.95	0.13	48,48,48,48	0
54	MG	2A	3211	1/1	0.95	0.10	56,56,56,56	0
54	MG	2A	3715	1/1	0.95	0.10	50,50,50,50	0
54	MG	2A	3009	1/1	0.95	0.08	44,44,44,44	0
54	MG	1A	3476	1/1	0.95	0.08	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3014	1/1	0.95	0.08	53,53,53,53	0
54	MG	2A	3215	1/1	0.95	0.09	54,54,54,54	0
54	MG	2A	3721	1/1	0.95	0.11	59,59,59,59	0
54	MG	1A	3273	1/1	0.95	0.11	55,55,55,55	0
54	MG	2A	3217	1/1	0.95	0.27	61,61,61,61	0
54	MG	2a	1754	1/1	0.95	0.14	84,84,84,84	0
54	MG	1A	3930	1/1	0.95	0.09	60,60,60,60	0
54	MG	2A	3022	1/1	0.95	0.21	44,44,44,44	0
54	MG	1A	3605	1/1	0.95	0.23	40,40,40,40	0
54	MG	1a	1645	1/1	0.95	0.09	61,61,61,61	0
54	MG	2a	1763	1/1	0.95	0.07	51,51,51,51	0
54	MG	1A	3681	1/1	0.95	0.07	29,29,29,29	0
54	MG	2A	3735	1/1	0.95	0.09	38,38,38,38	0
54	MG	1A	3607	1/1	0.95	0.20	52,52,52,52	0
54	MG	1A	3935	1/1	0.95	0.08	53,53,53,53	0
54	MG	1A	3376	1/1	0.95	0.09	45,45,45,45	0
54	MG	2A	3741	1/1	0.95	0.16	50,50,50,50	0
54	MG	2A	3743	1/1	0.95	0.11	63,63,63,63	0
54	MG	2A	3745	1/1	0.95	0.35	67,67,67,67	0
54	MG	1A	3479	1/1	0.95	0.15	42,42,42,42	0
54	MG	2a	1783	1/1	0.95	0.06	62,62,62,62	0
54	MG	1B	220	1/1	0.95	0.06	34,34,34,34	0
54	MG	1A	3330	1/1	0.95	0.09	33,33,33,33	0
54	MG	1A	3940	1/1	0.95	0.05	43,43,43,43	0
54	MG	1B	223	1/1	0.95	0.07	69,69,69,69	0
54	MG	2A	3756	1/1	0.95	0.15	52,52,52,52	0
54	MG	2A	3039	1/1	0.95	0.13	55,55,55,55	0
54	MG	2A	3233	1/1	0.95	0.09	58,58,58,58	0
54	MG	2a	1793	1/1	0.95	0.13	51,51,51,51	0
54	MG	2A	3761	1/1	0.95	0.17	37,37,37,37	0
54	MG	2A	3763	1/1	0.95	0.08	40,40,40,40	0
54	MG	1A	3796	1/1	0.95	0.10	60,60,60,60	0
54	MG	2A	3236	1/1	0.95	0.09	49,49,49,49	0
54	MG	1A	3481	1/1	0.95	0.08	57,57,57,57	0
54	MG	2A	3238	1/1	0.95	0.21	47,47,47,47	0
54	MG	2A	3044	1/1	0.95	0.09	44,44,44,44	0
54	MG	2A	3045	1/1	0.95	0.11	41,41,41,41	0
54	MG	1A	3201	1/1	0.95	0.15	47,47,47,47	0
54	MG	2A	3047	1/1	0.95	0.10	46,46,46,46	0
54	MG	1a	1662	1/1	0.95	0.37	64,64,64,64	0
56	ARG	1B	230	12/12	0.95	0.08	29,41,51,51	0
54	MG	1a	1663	1/1	0.95	0.18	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3050	1/1	0.95	0.18	54,54,54,54	0
54	MG	1A	3800	1/1	0.95	0.08	38,38,38,38	0
54	MG	1A	3483	1/1	0.95	0.10	31,31,31,31	0
54	MG	1A	3651	1/1	0.96	0.10	58,58,58,58	0
54	MG	1A	3095	1/1	0.96	0.31	45,45,45,45	0
54	MG	2A	3742	1/1	0.96	0.11	56,56,56,56	0
54	MG	2A	3210	1/1	0.96	0.07	53,53,53,53	0
54	MG	1A	3564	1/1	0.96	0.10	26,26,26,26	0
54	MG	1A	3074	1/1	0.96	0.09	36,36,36,36	0
54	MG	2A	3450	1/1	0.96	0.15	58,58,58,58	0
54	MG	2A	3451	1/1	0.96	0.11	39,39,39,39	0
54	MG	1A	3051	1/1	0.96	0.22	48,48,48,48	0
54	MG	1A	3202	1/1	0.96	0.20	49,49,49,49	0
54	MG	1A	3484	1/1	0.96	0.08	41,41,41,41	0
54	MG	1A	3778	1/1	0.96	0.05	34,34,34,34	0
54	MG	1Q	201	1/1	0.96	0.08	33,33,33,33	0
54	MG	1A	3658	1/1	0.96	0.05	19,19,19,19	0
54	MG	2A	3762	1/1	0.96	0.08	53,53,53,53	0
54	MG	1y	202	1/1	0.96	0.09	59,59,59,59	0
54	MG	1A	3167	1/1	0.96	0.12	53,53,53,53	0
54	MG	1A	3781	1/1	0.96	0.08	48,48,48,48	0
54	MG	1A	3660	1/1	0.96	0.07	23,23,23,23	0
54	MG	1A	3168	1/1	0.96	0.06	32,32,32,32	0
54	MG	1A	3784	1/1	0.96	0.04	36,36,36,36	0
54	MG	1A	3489	1/1	0.96	0.08	61,61,61,61	0
54	MG	2A	3012	1/1	0.96	0.04	39,39,39,39	0
54	MG	1A	3574	1/1	0.96	0.10	31,31,31,31	0
54	MG	1A	3961	1/1	0.96	0.10	45,45,45,45	0
54	MG	1A	3787	1/1	0.96	0.06	25,25,25,25	0
54	MG	1V	201	1/1	0.96	0.07	55,55,55,55	0
54	MG	1A	3490	1/1	0.96	0.17	66,66,66,66	0
54	MG	1A	3101	1/1	0.96	0.08	47,47,47,47	0
54	MG	1A	3354	1/1	0.96	0.08	63,63,63,63	0
54	MG	2A	3026	1/1	0.96	0.09	45,45,45,45	0
54	MG	2B	3016	1/1	0.96	0.06	67,67,67,67	0
54	MG	2A	3027	1/1	0.96	0.10	45,45,45,45	0
54	MG	1A	3079	1/1	0.96	0.12	40,40,40,40	0
54	MG	1X	8001	1/1	0.96	0.11	43,43,43,43	0
54	MG	1A	3671	1/1	0.96	0.12	36,36,36,36	0
54	MG	2D	303	1/1	0.96	0.26	44,44,44,44	0
54	MG	1A	3012	1/1	0.96	0.08	38,38,38,38	0
54	MG	1A	3673	1/1	0.96	0.06	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3245	1/1	0.96	0.08	56,56,56,56	0
54	MG	1A	3209	1/1	0.96	0.07	44,44,44,44	0
54	MG	1a	1755	1/1	0.96	0.17	58,58,58,58	0
54	MG	1A	3802	1/1	0.96	0.06	47,47,47,47	0
54	MG	2A	3249	1/1	0.96	0.08	49,49,49,49	0
54	MG	2F	301	1/1	0.96	0.08	44,44,44,44	0
54	MG	1A	3977	1/1	0.96	0.07	24,24,24,24	0
54	MG	1A	3359	1/1	0.96	0.10	11,11,11,11	0
54	MG	11	102	1/1	0.96	0.07	49,49,49,49	0
54	MG	2A	3042	1/1	0.96	0.13	47,47,47,47	0
54	MG	1A	3288	1/1	0.96	0.14	57,57,57,57	0
54	MG	1A	3289	1/1	0.96	0.07	31,31,31,31	0
54	MG	2O	201	1/1	0.96	0.13	58,58,58,58	0
54	MG	1A	3362	1/1	0.96	0.09	39,39,39,39	0
54	MG	13	102	1/1	0.96	0.07	49,49,49,49	0
54	MG	1A	3172	1/1	0.96	0.22	48,48,48,48	0
54	MG	1A	3809	1/1	0.96	0.25	46,46,46,46	0
54	MG	2A	3261	1/1	0.96	0.17	47,47,47,47	0
54	MG	1A	3986	1/1	0.96	0.06	19,19,19,19	0
54	MG	1A	3364	1/1	0.96	0.06	33,33,33,33	0
54	MG	2A	3266	1/1	0.96	0.11	55,55,55,55	0
54	MG	2V	201	1/1	0.96	0.18	60,60,60,60	0
54	MG	2A	3510	1/1	0.96	0.09	47,47,47,47	0
54	MG	1A	3212	1/1	0.96	0.09	48,48,48,48	0
54	MG	1A	3504	1/1	0.96	0.11	26,26,26,26	0
54	MG	2A	3269	1/1	0.96	0.17	38,38,38,38	0
54	MG	2A	3271	1/1	0.96	0.24	47,47,47,47	0
54	MG	27	3001	1/1	0.96	0.12	43,43,43,43	0
54	MG	1A	3685	1/1	0.96	0.06	70,70,70,70	0
54	MG	1A	3366	1/1	0.96	0.09	46,46,46,46	0
54	MG	1A	3992	1/1	0.96	0.06	19,19,19,19	0
54	MG	1A	3993	1/1	0.96	0.29	54,54,54,54	0
54	MG	1A	3086	1/1	0.96	0.23	45,45,45,45	0
54	MG	1A	3818	1/1	0.96	0.06	47,47,47,47	0
54	MG	1A	3508	1/1	0.96	0.07	46,46,46,46	0
54	MG	1A	3820	1/1	0.96	0.11	31,31,31,31	0
54	MG	1A	3217	1/1	0.96	0.20	49,49,49,49	0
54	MG	2A	3525	1/1	0.96	0.09	51,51,51,51	0
54	MG	2A	3066	1/1	0.96	0.06	45,45,45,45	0
54	MG	2A	3286	1/1	0.96	0.05	31,31,31,31	0
54	MG	1A	3822	1/1	0.96	0.08	34,34,34,34	0
54	MG	1a	1610	1/1	0.96	0.12	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3691	1/1	0.96	0.08	54,54,54,54	0
54	MG	2a	1616	1/1	0.96	0.06	48,48,48,48	0
54	MG	1A	3510	1/1	0.96	0.13	31,31,31,31	0
54	MG	1A	3088	1/1	0.96	0.31	47,47,47,47	0
54	MG	2A	3078	1/1	0.96	0.09	56,56,56,56	0
54	MG	1A	3060	1/1	0.96	0.09	49,49,49,49	0
54	MG	1A	3514	1/1	0.96	0.08	23,23,23,23	0
54	MG	1A	3832	1/1	0.96	0.09	50,50,50,50	0
54	MG	1A	4007	1/1	0.96	0.12	17,17,17,17	0
54	MG	2A	3299	1/1	0.96	0.06	35,35,35,35	0
54	MG	1A	3301	1/1	0.96	0.23	48,48,48,48	0
54	MG	1A	3602	1/1	0.96	0.24	32,32,32,32	0
54	MG	1A	3147	1/1	0.96	0.17	46,46,46,46	0
54	MG	2A	3542	1/1	0.96	0.14	34,34,34,34	0
54	MG	2A	3543	1/1	0.96	0.05	42,42,42,42	0
54	MG	1A	4011	1/1	0.96	0.10	58,58,58,58	0
54	MG	1a	1630	1/1	0.96	0.18	64,64,64,64	0
54	MG	2A	3307	1/1	0.96	0.11	53,53,53,53	0
54	MG	2A	3548	1/1	0.96	0.06	55,55,55,55	0
54	MG	1A	4015	1/1	0.96	0.24	41,41,41,41	0
54	MG	1A	3116	1/1	0.96	0.11	49,49,49,49	0
54	MG	2A	3094	1/1	0.96	0.10	40,40,40,40	0
54	MG	2A	3552	1/1	0.96	0.09	57,57,57,57	0
54	MG	2A	3311	1/1	0.96	0.07	49,49,49,49	0
54	MG	1A	3225	1/1	0.96	0.10	49,49,49,49	0
54	MG	1a	1635	1/1	0.96	0.07	37,37,37,37	0
54	MG	1a	1636	1/1	0.96	0.10	47,47,47,47	0
54	MG	2A	3557	1/1	0.96	0.09	52,52,52,52	0
54	MG	1A	3839	1/1	0.96	0.22	60,60,60,60	0
54	MG	2A	3318	1/1	0.96	0.10	37,37,37,37	0
54	MG	1A	3069	1/1	0.96	0.10	37,37,37,37	0
54	MG	1A	3231	1/1	0.96	0.08	44,44,44,44	0
54	MG	1a	1807	1/1	0.96	0.08	73,73,73,73	0
54	MG	2A	3324	1/1	0.96	0.07	44,44,44,44	0
54	MG	2A	3325	1/1	0.96	0.07	50,50,50,50	0
54	MG	2A	3570	1/1	0.96	0.08	57,57,57,57	0
54	MG	1A	4024	1/1	0.96	0.22	36,36,36,36	0
54	MG	1A	3526	1/1	0.96	0.07	48,48,48,48	0
54	MG	2A	3575	1/1	0.96	0.06	43,43,43,43	0
54	MG	2A	3330	1/1	0.96	0.08	31,31,31,31	0
54	MG	1A	3234	1/1	0.96	0.12	37,37,37,37	0
54	MG	2A	3332	1/1	0.96	0.07	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3235	1/1	0.96	0.12	41,41,41,41	0
54	MG	2A	3111	1/1	0.96	0.07	54,54,54,54	0
54	MG	1A	3236	1/1	0.96	0.18	59,59,59,59	0
54	MG	1A	4031	1/1	0.96	0.24	38,38,38,38	0
54	MG	2A	3586	1/1	0.96	0.07	62,62,62,62	0
54	MG	1A	3850	1/1	0.96	0.10	33,33,33,33	0
54	MG	1a	1816	1/1	0.96	0.09	73,73,73,73	0
54	MG	1A	3852	1/1	0.96	0.08	46,46,46,46	0
54	MG	1A	3614	1/1	0.96	0.07	38,38,38,38	0
54	MG	2A	3345	1/1	0.96	0.05	35,35,35,35	0
54	MG	1A	3243	1/1	0.96	0.13	33,33,33,33	0
54	MG	1A	3320	1/1	0.96	0.14	33,33,33,33	0
54	MG	2A	3600	1/1	0.96	0.09	67,67,67,67	0
54	MG	1a	1821	1/1	0.96	0.09	72,72,72,72	0
54	MG	2A	3123	1/1	0.96	0.30	48,48,48,48	0
54	MG	2A	3607	1/1	0.96	0.09	67,67,67,67	0
54	MG	1A	3532	1/1	0.96	0.16	61,61,61,61	0
54	MG	2A	3351	1/1	0.96	0.04	35,35,35,35	0
54	MG	1A	3385	1/1	0.96	0.13	40,40,40,40	0
54	MG	1A	3386	1/1	0.96	0.10	41,41,41,41	0
54	MG	1A	4053	1/1	0.96	0.20	45,45,45,45	0
54	MG	1A	3717	1/1	0.96	0.18	39,39,39,39	0
54	MG	2A	3356	1/1	0.96	0.08	48,48,48,48	0
54	MG	2A	3130	1/1	0.96	0.32	42,42,42,42	0
54	MG	1A	3537	1/1	0.96	0.07	31,31,31,31	0
54	MG	1A	3538	1/1	0.96	0.06	36,36,36,36	0
54	MG	2A	3364	1/1	0.96	0.14	49,49,49,49	0
54	MG	2A	3134	1/1	0.96	0.14	49,49,49,49	0
54	MG	2a	1691	1/1	0.96	0.10	71,71,71,71	0
54	MG	2a	1692	1/1	0.96	0.06	77,77,77,77	0
54	MG	1A	4060	1/1	0.96	0.23	32,32,32,32	0
54	MG	1A	3246	1/1	0.96	0.13	54,54,54,54	0
54	MG	1A	4067	1/1	0.96	0.11	42,42,42,42	0
54	MG	2A	3630	1/1	0.96	0.06	52,52,52,52	0
54	MG	1A	3869	1/1	0.96	0.07	50,50,50,50	0
54	MG	1a	1666	1/1	0.96	0.08	53,53,53,53	0
54	MG	1A	4074	1/1	0.96	0.06	43,43,43,43	0
54	MG	1A	3457	1/1	0.96	0.10	51,51,51,51	0
54	MG	1A	3871	1/1	0.96	0.05	45,45,45,45	0
54	MG	1A	3073	1/1	0.96	0.07	38,38,38,38	0
54	MG	1A	3727	1/1	0.96	0.09	42,42,42,42	0
54	MG	1a	1672	1/1	0.96	0.14	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3639	1/1	0.96	0.08	59,59,59,59	0
54	MG	2A	3640	1/1	0.96	0.07	63,63,63,63	0
54	MG	2a	1708	1/1	0.96	0.09	55,55,55,55	0
54	MG	2A	3641	1/1	0.96	0.11	49,49,49,49	0
54	MG	2A	3377	1/1	0.96	0.08	57,57,57,57	0
54	MG	1A	3628	1/1	0.96	0.09	20,20,20,20	0
54	MG	2A	3646	1/1	0.96	0.09	71,71,71,71	0
54	MG	2A	3651	1/1	0.96	0.06	66,66,66,66	0
54	MG	2A	3379	1/1	0.96	0.06	30,30,30,30	0
54	MG	1A	3730	1/1	0.96	0.07	53,53,53,53	0
54	MG	1A	3323	1/1	0.96	0.13	28,28,28,28	0
54	MG	2a	1717	1/1	0.96	0.09	77,77,77,77	0
54	MG	1A	3886	1/1	0.96	0.04	29,29,29,29	0
54	MG	1A	3735	1/1	0.96	0.11	39,39,39,39	0
54	MG	2A	3156	1/1	0.96	0.05	36,36,36,36	0
54	MG	1a	1678	1/1	0.96	0.27	64,64,64,64	0
54	MG	1A	3736	1/1	0.96	0.06	54,54,54,54	0
54	MG	2A	3670	1/1	0.96	0.13	38,38,38,38	0
54	MG	1A	3630	1/1	0.96	0.04	41,41,41,41	0
54	MG	2A	3672	1/1	0.96	0.06	39,39,39,39	0
54	MG	2A	3673	1/1	0.96	0.06	38,38,38,38	0
54	MG	1A	3189	1/1	0.96	0.23	44,44,44,44	0
54	MG	1a	1855	1/1	0.96	0.06	59,59,59,59	0
54	MG	1a	1682	1/1	0.96	0.11	47,47,47,47	0
54	MG	2a	1730	1/1	0.96	0.07	55,55,55,55	0
54	MG	1A	3093	1/1	0.96	0.11	54,54,54,54	0
54	MG	1A	3892	1/1	0.96	0.12	38,38,38,38	0
54	MG	1A	3633	1/1	0.96	0.17	46,46,46,46	0
54	MG	2A	3397	1/1	0.96	0.05	36,36,36,36	0
54	MG	1A	3743	1/1	0.96	0.09	45,45,45,45	0
54	MG	2A	3685	1/1	0.96	0.06	60,60,60,60	0
54	MG	1A	3465	1/1	0.96	0.05	59,59,59,59	0
54	MG	1A	3253	1/1	0.96	0.24	34,34,34,34	0
54	MG	2a	1748	1/1	0.96	0.10	75,75,75,75	0
54	MG	2A	3401	1/1	0.96	0.07	43,43,43,43	0
54	MG	2a	1750	1/1	0.96	0.08	79,79,79,79	0
54	MG	1A	3126	1/1	0.96	0.09	44,44,44,44	0
54	MG	2A	3691	1/1	0.96	0.06	54,54,54,54	0
54	MG	2a	1753	1/1	0.96	0.08	74,74,74,74	0
54	MG	2A	3403	1/1	0.96	0.09	36,36,36,36	0
54	MG	2A	3175	1/1	0.96	0.07	52,52,52,52	0
54	MG	1A	3256	1/1	0.96	0.07	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3177	1/1	0.96	0.13	39,39,39,39	0
54	MG	2a	1760	1/1	0.96	0.08	63,63,63,63	0
54	MG	1A	3906	1/1	0.96	0.25	38,38,38,38	0
54	MG	1A	3907	1/1	0.96	0.05	13,13,13,13	0
54	MG	1A	3748	1/1	0.96	0.20	54,54,54,54	0
54	MG	1A	3911	1/1	0.96	0.10	28,28,28,28	0
54	MG	1A	3749	1/1	0.96	0.06	27,27,27,27	0
54	MG	1A	3913	1/1	0.96	0.06	22,22,22,22	0
54	MG	2A	3704	1/1	0.96	0.07	48,48,48,48	0
54	MG	2a	1775	1/1	0.96	0.17	57,57,57,57	0
54	MG	1a	1698	1/1	0.96	0.12	60,60,60,60	0
54	MG	2A	3706	1/1	0.96	0.06	51,51,51,51	0
54	MG	2A	3707	1/1	0.96	0.13	39,39,39,39	0
54	MG	1A	3750	1/1	0.96	0.11	33,33,33,33	0
54	MG	1D	310	1/1	0.96	0.08	52,52,52,52	0
54	MG	1a	1876	1/1	0.96	0.17	41,41,41,41	0
54	MG	1A	3551	1/1	0.96	0.12	50,50,50,50	0
54	MG	1A	3159	1/1	0.96	0.10	53,53,53,53	0
54	MG	1A	3401	1/1	0.96	0.08	32,32,32,32	0
54	MG	1A	3472	1/1	0.96	0.11	36,36,36,36	0
54	MG	1A	3756	1/1	0.96	0.07	47,47,47,47	0
54	MG	2A	3424	1/1	0.96	0.23	61,61,61,61	0
54	MG	2A	3718	1/1	0.96	0.08	67,67,67,67	0
54	MG	1A	3923	1/1	0.96	0.04	43,43,43,43	0
54	MG	1A	3473	1/1	0.96	0.06	33,33,33,33	0
54	MG	1A	3193	1/1	0.96	0.12	46,46,46,46	0
54	MG	1A	3403	1/1	0.96	0.07	25,25,25,25	0
54	MG	2A	3429	1/1	0.96	0.06	36,36,36,36	0
54	MG	2t	3001	1/1	0.96	0.15	52,52,52,52	0
54	MG	2A	3430	1/1	0.96	0.09	52,52,52,52	0
54	MG	2A	3726	1/1	0.96	0.08	58,58,58,58	0
55	MPD	18	102	8/8	0.96	0.09	30,34,40,47	0
54	MG	1A	3931	1/1	0.96	0.07	35,35,35,35	0
54	MG	1A	3194	1/1	0.96	0.26	42,42,42,42	0
54	MG	1A	3161	1/1	0.96	0.08	49,49,49,49	0
54	MG	1A	3198	1/1	0.96	0.28	56,56,56,56	0
54	MG	2A	3732	1/1	0.96	0.17	47,47,47,47	0
54	MG	1A	3764	1/1	0.96	0.06	29,29,29,29	0
54	MG	2A	3736	1/1	0.96	0.21	50,50,50,50	0
54	MG	1A	3343	1/1	0.96	0.06	31,31,31,31	0
54	MG	1A	3650	1/1	0.96	0.14	61,61,61,61	0
54	MG	2A	3496	1/1	0.97	0.06	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3064	1/1	0.97	0.04	38,38,38,38	0
54	MG	1A	4063	1/1	0.97	0.13	41,41,41,41	0
54	MG	1A	3521	1/1	0.97	0.20	31,31,31,31	0
54	MG	1A	4066	1/1	0.97	0.10	38,38,38,38	0
54	MG	1A	3083	1/1	0.97	0.08	38,38,38,38	0
54	MG	2A	3069	1/1	0.97	0.11	44,44,44,44	0
54	MG	1A	4069	1/1	0.97	0.21	40,40,40,40	0
54	MG	1A	3523	1/1	0.97	0.10	49,49,49,49	0
54	MG	2A	3276	1/1	0.97	0.06	40,40,40,40	0
54	MG	2A	3073	1/1	0.97	0.08	49,49,49,49	0
54	MG	1A	4071	1/1	0.97	0.06	39,39,39,39	0
54	MG	2A	3076	1/1	0.97	0.22	51,51,51,51	0
54	MG	2A	3077	1/1	0.97	0.18	48,48,48,48	0
54	MG	2A	3281	1/1	0.97	0.05	33,33,33,33	0
54	MG	1a	1802	1/1	0.97	0.06	63,63,63,63	0
54	MG	2A	3079	1/1	0.97	0.09	44,44,44,44	0
54	MG	2B	3019	1/1	0.97	0.07	51,51,51,51	0
54	MG	1A	4072	1/1	0.97	0.12	36,36,36,36	0
54	MG	1a	1646	1/1	0.97	0.10	39,39,39,39	0
54	MG	1A	3175	1/1	0.97	0.05	43,43,43,43	0
54	MG	1A	3918	1/1	0.97	0.07	52,52,52,52	0
54	MG	2D	305	1/1	0.97	0.17	49,49,49,49	0
54	MG	2A	3518	1/1	0.97	0.08	35,35,35,35	0
54	MG	1A	3255	1/1	0.97	0.25	45,45,45,45	0
54	MG	1B	201	1/1	0.97	0.22	44,44,44,44	0
54	MG	1a	1652	1/1	0.97	0.11	44,44,44,44	0
54	MG	2E	302	1/1	0.97	0.06	41,41,41,41	0
54	MG	1A	3920	1/1	0.97	0.04	47,47,47,47	0
54	MG	2A	3089	1/1	0.97	0.04	33,33,33,33	0
54	MG	1A	3070	1/1	0.97	0.21	43,43,43,43	0
54	MG	2A	3091	1/1	0.97	0.05	34,34,34,34	0
54	MG	2F	303	1/1	0.97	0.20	43,43,43,43	0
54	MG	1A	3153	1/1	0.97	0.12	46,46,46,46	0
54	MG	1a	1813	1/1	0.97	0.05	81,81,81,81	0
54	MG	1A	3384	1/1	0.97	0.08	43,43,43,43	0
54	MG	1A	3924	1/1	0.97	0.07	61,61,61,61	0
54	MG	1A	3259	1/1	0.97	0.09	40,40,40,40	0
54	MG	1B	209	1/1	0.97	0.04	39,39,39,39	0
54	MG	2A	3304	1/1	0.97	0.12	37,37,37,37	0
54	MG	1A	3927	1/1	0.97	0.07	63,63,63,63	0
54	MG	1A	3693	1/1	0.97	0.25	54,54,54,54	0
54	MG	2Q	3001	1/1	0.97	0.04	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1B	212	1/1	0.97	0.06	59,59,59,59	0
54	MG	1B	213	1/1	0.97	0.07	55,55,55,55	0
54	MG	1A	3792	1/1	0.97	0.06	26,26,26,26	0
54	MG	1A	3260	1/1	0.97	0.05	44,44,44,44	0
54	MG	1A	3327	1/1	0.97	0.04	32,32,32,32	0
54	MG	1A	3533	1/1	0.97	0.17	27,27,27,27	0
54	MG	1A	3613	1/1	0.97	0.19	42,42,42,42	0
54	MG	1A	3180	1/1	0.97	0.19	48,48,48,48	0
54	MG	1A	3801	1/1	0.97	0.05	45,45,45,45	0
54	MG	2A	3114	1/1	0.97	0.06	47,47,47,47	0
54	MG	2A	3545	1/1	0.97	0.05	75,75,75,75	0
54	MG	2A	3115	1/1	0.97	0.05	50,50,50,50	0
54	MG	2A	3322	1/1	0.97	0.05	40,40,40,40	0
54	MG	1A	3937	1/1	0.97	0.05	71,71,71,71	0
54	MG	1A	3535	1/1	0.97	0.04	26,26,26,26	0
54	MG	1B	224	1/1	0.97	0.04	44,44,44,44	0
54	MG	1A	3211	1/1	0.97	0.16	40,40,40,40	0
54	MG	1B	226	1/1	0.97	0.05	37,37,37,37	0
54	MG	1A	3072	1/1	0.97	0.10	37,37,37,37	0
54	MG	1A	3805	1/1	0.97	0.05	63,63,63,63	0
54	MG	1A	3464	1/1	0.97	0.09	47,47,47,47	0
54	MG	1A	3539	1/1	0.97	0.09	36,36,36,36	0
54	MG	2A	3334	1/1	0.97	0.06	31,31,31,31	0
54	MG	1D	301	1/1	0.97	0.16	37,37,37,37	0
54	MG	1A	3333	1/1	0.97	0.10	47,47,47,47	0
54	MG	1A	3946	1/1	0.97	0.12	56,56,56,56	0
54	MG	2A	3564	1/1	0.97	0.05	57,57,57,57	0
54	MG	2a	1615	1/1	0.97	0.21	63,63,63,63	0
54	MG	2A	3339	1/1	0.97	0.05	36,36,36,36	0
54	MG	1A	3947	1/1	0.97	0.06	50,50,50,50	0
54	MG	2A	3567	1/1	0.97	0.04	46,46,46,46	0
54	MG	2a	1619	1/1	0.97	0.08	48,48,48,48	0
54	MG	1D	309	1/1	0.97	0.13	40,40,40,40	0
54	MG	1A	3541	1/1	0.97	0.04	27,27,27,27	0
54	MG	1A	3707	1/1	0.97	0.10	43,43,43,43	0
54	MG	1D	312	1/1	0.97	0.08	54,54,54,54	0
54	MG	1A	3334	1/1	0.97	0.09	37,37,37,37	0
54	MG	1A	3396	1/1	0.97	0.08	26,26,26,26	0
54	MG	1A	3265	1/1	0.97	0.07	40,40,40,40	0
54	MG	2a	1627	1/1	0.97	0.09	49,49,49,49	0
54	MG	1a	1853	1/1	0.97	0.06	54,54,54,54	0
54	MG	1A	3627	1/1	0.97	0.11	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3579	1/1	0.97	0.09	56,56,56,56	0
54	MG	1A	3336	1/1	0.97	0.09	45,45,45,45	0
54	MG	2A	3581	1/1	0.97	0.08	48,48,48,48	0
54	MG	1A	3155	1/1	0.97	0.09	54,54,54,54	0
54	MG	2a	1634	1/1	0.97	0.07	37,37,37,37	0
54	MG	2A	3143	1/1	0.97	0.07	40,40,40,40	0
54	MG	1A	3268	1/1	0.97	0.12	45,45,45,45	0
54	MG	1A	3215	1/1	0.97	0.10	50,50,50,50	0
54	MG	1F	303	1/1	0.97	0.12	34,34,34,34	0
54	MG	1A	3340	1/1	0.97	0.06	25,25,25,25	0
54	MG	2A	3359	1/1	0.97	0.04	40,40,40,40	0
54	MG	2A	3592	1/1	0.97	0.10	47,47,47,47	0
54	MG	1A	3404	1/1	0.97	0.05	33,33,33,33	0
54	MG	2A	3594	1/1	0.97	0.07	46,46,46,46	0
54	MG	2A	3150	1/1	0.97	0.20	46,46,46,46	0
54	MG	2A	3151	1/1	0.97	0.04	48,48,48,48	0
54	MG	1A	3216	1/1	0.97	0.13	44,44,44,44	0
54	MG	1A	3107	1/1	0.97	0.21	38,38,38,38	0
54	MG	2A	3602	1/1	0.97	0.05	32,32,32,32	0
54	MG	1A	3722	1/1	0.97	0.05	32,32,32,32	0
54	MG	2A	3604	1/1	0.97	0.09	35,35,35,35	0
54	MG	1a	1867	1/1	0.97	0.05	47,47,47,47	0
54	MG	1A	3966	1/1	0.97	0.06	48,48,48,48	0
54	MG	1A	3724	1/1	0.97	0.07	66,66,66,66	0
54	MG	2A	3158	1/1	0.97	0.09	44,44,44,44	0
54	MG	1A	3968	1/1	0.97	0.14	44,44,44,44	0
54	MG	2A	3160	1/1	0.97	0.14	44,44,44,44	0
54	MG	2A	3161	1/1	0.97	0.10	51,51,51,51	0
54	MG	1A	3108	1/1	0.97	0.06	41,41,41,41	0
54	MG	1A	3970	1/1	0.97	0.08	62,62,62,62	0
54	MG	1a	1709	1/1	0.97	0.07	39,39,39,39	0
54	MG	2A	3621	1/1	0.97	0.10	56,56,56,56	0
54	MG	1A	3972	1/1	0.97	0.07	26,26,26,26	0
54	MG	2A	3623	1/1	0.97	0.15	61,61,61,61	0
54	MG	1a	1712	1/1	0.97	0.04	50,50,50,50	0
54	MG	2A	3167	1/1	0.97	0.21	41,41,41,41	0
54	MG	1A	3275	1/1	0.97	0.12	41,41,41,41	0
54	MG	2A	3169	1/1	0.97	0.16	41,41,41,41	0
54	MG	1A	3160	1/1	0.97	0.22	44,44,44,44	0
54	MG	1N	203	1/1	0.97	0.06	53,53,53,53	0
54	MG	1a	1881	1/1	0.97	0.06	68,68,68,68	0
54	MG	1A	3220	1/1	0.97	0.31	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3729	1/1	0.97	0.09	27,27,27,27	0
54	MG	1A	3026	1/1	0.97	0.22	34,34,34,34	0
54	MG	1A	3350	1/1	0.97	0.13	37,37,37,37	0
54	MG	1A	3733	1/1	0.97	0.05	55,55,55,55	0
54	MG	1A	3351	1/1	0.97	0.05	24,24,24,24	0
54	MG	2A	3393	1/1	0.97	0.08	43,43,43,43	0
54	MG	1A	3842	1/1	0.97	0.07	41,41,41,41	0
54	MG	1A	3983	1/1	0.97	0.09	74,74,74,74	0
54	MG	1e	203	1/1	0.97	0.09	58,58,58,58	0
54	MG	2a	1682	1/1	0.97	0.09	51,51,51,51	0
54	MG	1A	3222	1/1	0.97	0.09	36,36,36,36	0
54	MG	2A	3184	1/1	0.97	0.08	45,45,45,45	0
54	MG	1A	3132	1/1	0.97	0.05	39,39,39,39	0
54	MG	2A	3645	1/1	0.97	0.05	77,77,77,77	0
54	MG	1g	201	1/1	0.97	0.10	62,62,62,62	0
54	MG	2A	3650	1/1	0.97	0.05	61,61,61,61	0
54	MG	1A	3017	1/1	0.97	0.17	37,37,37,37	0
54	MG	2a	1690	1/1	0.97	0.05	71,71,71,71	0
54	MG	1A	3227	1/1	0.97	0.23	37,37,37,37	0
54	MG	2A	3656	1/1	0.97	0.15	61,61,61,61	0
54	MG	2A	3657	1/1	0.97	0.06	40,40,40,40	0
54	MG	1A	3229	1/1	0.97	0.08	47,47,47,47	0
54	MG	1A	3742	1/1	0.97	0.06	47,47,47,47	0
54	MG	1a	1734	1/1	0.97	0.09	47,47,47,47	0
54	MG	2A	3192	1/1	0.97	0.07	44,44,44,44	0
54	MG	1A	3851	1/1	0.97	0.10	44,44,44,44	0
54	MG	2A	3666	1/1	0.97	0.08	54,54,54,54	0
54	MG	2a	1700	1/1	0.97	0.24	47,47,47,47	0
54	MG	1A	3165	1/1	0.97	0.12	37,37,37,37	0
54	MG	1A	3853	1/1	0.97	0.08	40,40,40,40	0
54	MG	2A	3669	1/1	0.97	0.04	38,38,38,38	0
54	MG	1A	3068	1/1	0.97	0.23	49,49,49,49	0
54	MG	1A	3423	1/1	0.97	0.06	16,16,16,16	0
54	MG	1A	3856	1/1	0.97	0.10	33,33,33,33	0
54	MG	1A	3232	1/1	0.97	0.11	42,42,42,42	0
54	MG	1A	3197	1/1	0.97	0.06	52,52,52,52	0
54	MG	1A	3427	1/1	0.97	0.07	39,39,39,39	0
54	MG	1A	3498	1/1	0.97	0.07	50,50,50,50	0
54	MG	1A	3135	1/1	0.97	0.20	41,41,41,41	0
54	MG	1A	3863	1/1	0.97	0.06	51,51,51,51	0
54	MG	1A	3136	1/1	0.97	0.19	39,39,39,39	0
54	MG	1A	3237	1/1	0.97	0.12	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3423	1/1	0.97	0.05	33,33,33,33	0
54	MG	2A	3003	1/1	0.97	0.05	51,51,51,51	0
54	MG	2A	3686	1/1	0.97	0.06	43,43,43,43	0
54	MG	2A	3006	1/1	0.97	0.10	46,46,46,46	0
54	MG	2A	3007	1/1	0.97	0.08	36,36,36,36	0
54	MG	2A	3008	1/1	0.97	0.05	30,30,30,30	0
54	MG	1A	3302	1/1	0.97	0.13	34,34,34,34	0
54	MG	1A	4005	1/1	0.97	0.08	97,97,97,97	0
54	MG	1A	3077	1/1	0.97	0.15	53,53,53,53	0
54	MG	1A	3755	1/1	0.97	0.12	47,47,47,47	0
54	MG	2A	3015	1/1	0.97	0.22	36,36,36,36	0
54	MG	2A	3434	1/1	0.97	0.09	56,56,56,56	0
54	MG	2A	3436	1/1	0.97	0.14	49,49,49,49	0
54	MG	1A	3661	1/1	0.97	0.05	46,46,46,46	0
54	MG	1A	3433	1/1	0.97	0.06	10,10,10,10	0
54	MG	2A	3699	1/1	0.97	0.05	44,44,44,44	0
54	MG	2A	3439	1/1	0.97	0.05	46,46,46,46	0
54	MG	2A	3021	1/1	0.97	0.06	31,31,31,31	0
54	MG	2A	3702	1/1	0.97	0.07	55,55,55,55	0
54	MG	1A	3874	1/1	0.97	0.04	24,24,24,24	0
54	MG	2A	3221	1/1	0.97	0.25	45,45,45,45	0
54	MG	1A	3505	1/1	0.97	0.09	28,28,28,28	0
54	MG	1A	4013	1/1	0.97	0.06	43,43,43,43	0
54	MG	2a	1744	1/1	0.97	0.08	75,75,75,75	0
54	MG	2A	3446	1/1	0.97	0.07	58,58,58,58	0
54	MG	1A	3244	1/1	0.97	0.15	36,36,36,36	0
54	MG	1a	1760	1/1	0.97	0.13	63,63,63,63	0
54	MG	1A	3880	1/1	0.97	0.12	39,39,39,39	0
54	MG	2A	3028	1/1	0.97	0.06	33,33,33,33	0
54	MG	1A	3881	1/1	0.97	0.07	28,28,28,28	0
54	MG	2A	3031	1/1	0.97	0.11	27,27,27,27	0
54	MG	2A	3714	1/1	0.97	0.04	56,56,56,56	0
54	MG	1a	1763	1/1	0.97	0.13	59,59,59,59	0
54	MG	1A	3665	1/1	0.97	0.12	60,60,60,60	0
54	MG	1A	3307	1/1	0.97	0.06	46,46,46,46	0
54	MG	1A	3309	1/1	0.97	0.06	47,47,47,47	0
54	MG	2A	3459	1/1	0.97	0.13	49,49,49,49	0
54	MG	2a	1762	1/1	0.97	0.05	54,54,54,54	0
54	MG	1A	3370	1/1	0.97	0.09	54,54,54,54	0
54	MG	2A	3235	1/1	0.97	0.08	48,48,48,48	0
54	MG	2a	1767	1/1	0.97	0.09	70,70,70,70	0
54	MG	1A	3310	1/1	0.97	0.15	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3440	1/1	0.97	0.06	42,42,42,42	0
54	MG	2a	1770	1/1	0.97	0.06	82,82,82,82	0
54	MG	1A	3512	1/1	0.97	0.06	61,61,61,61	0
54	MG	2a	1772	1/1	0.97	0.05	58,58,58,58	0
54	MG	1A	3245	1/1	0.97	0.18	35,35,35,35	0
54	MG	1a	1611	1/1	0.97	0.05	38,38,38,38	0
54	MG	2A	3242	1/1	0.97	0.17	48,48,48,48	0
54	MG	1A	3048	1/1	0.97	0.04	28,28,28,28	0
54	MG	1A	3080	1/1	0.97	0.09	52,52,52,52	0
54	MG	1A	3771	1/1	0.97	0.06	44,44,44,44	0
54	MG	2A	3733	1/1	0.97	0.09	33,33,33,33	0
54	MG	2A	3734	1/1	0.97	0.24	41,41,41,41	0
54	MG	2a	1785	1/1	0.97	0.07	76,76,76,76	0
54	MG	1A	4036	1/1	0.97	0.15	35,35,35,35	0
54	MG	1A	3120	1/1	0.97	0.05	37,37,37,37	0
54	MG	1A	3902	1/1	0.97	0.05	69,69,69,69	0
54	MG	1A	4045	1/1	0.97	0.14	36,36,36,36	0
54	MG	1a	1622	1/1	0.97	0.05	47,47,47,47	0
54	MG	1A	3773	1/1	0.97	0.04	31,31,31,31	0
54	MG	1A	3774	1/1	0.97	0.10	43,43,43,43	0
54	MG	2A	3054	1/1	0.97	0.09	44,44,44,44	0
54	MG	2A	3744	1/1	0.97	0.10	40,40,40,40	0
54	MG	1A	3775	1/1	0.97	0.04	36,36,36,36	0
54	MG	1A	3251	1/1	0.97	0.12	52,52,52,52	0
54	MG	2A	3749	1/1	0.97	0.17	39,39,39,39	0
54	MG	1A	4052	1/1	0.97	0.15	45,45,45,45	0
54	MG	1A	3678	1/1	0.97	0.06	62,62,62,62	0
54	MG	2A	3485	1/1	0.97	0.05	54,54,54,54	0
54	MG	2A	3754	1/1	0.97	0.28	46,46,46,46	0
54	MG	1A	4054	1/1	0.97	0.13	44,44,44,44	0
54	MG	1A	3082	1/1	0.97	0.13	53,53,53,53	0
54	MG	1A	3909	1/1	0.97	0.04	28,28,28,28	0
54	MG	2A	3489	1/1	0.97	0.06	33,33,33,33	0
54	MG	2A	3759	1/1	0.97	0.21	46,46,46,46	0
54	MG	2A	3262	1/1	0.97	0.09	58,58,58,58	0
54	MG	2A	3263	1/1	0.97	0.06	41,41,41,41	0
54	MG	1A	3519	1/1	0.97	0.06	59,59,59,59	0
54	MG	1A	3599	1/1	0.97	0.09	50,50,50,50	0
57	ZN	29	501	1/1	0.97	0.14	131,131,131,131	0
58	SF4	1d	501	8/8	0.97	0.07	64,70,74,95	0
54	MG	1A	3520	1/1	0.98	0.07	32,32,32,32	0
54	MG	1A	3823	1/1	0.98	0.19	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1D	305	1/1	0.98	0.04	38,38,38,38	0
54	MG	2E	304	1/1	0.98	0.06	35,35,35,35	0
54	MG	1D	306	1/1	0.98	0.18	46,46,46,46	0
54	MG	1D	308	1/1	0.98	0.06	45,45,45,45	0
54	MG	1A	3824	1/1	0.98	0.19	33,33,33,33	0
54	MG	1A	3271	1/1	0.98	0.09	37,37,37,37	0
54	MG	1A	3113	1/1	0.98	0.12	34,34,34,34	0
54	MG	2A	3560	1/1	0.98	0.05	23,23,23,23	0
54	MG	1a	1692	1/1	0.98	0.11	44,44,44,44	0
54	MG	1A	3114	1/1	0.98	0.18	33,33,33,33	0
54	MG	2A	3563	1/1	0.98	0.04	50,50,50,50	0
54	MG	1A	3829	1/1	0.98	0.04	25,25,25,25	0
54	MG	1A	3524	1/1	0.98	0.08	29,29,29,29	0
54	MG	1A	3720	1/1	0.98	0.08	33,33,33,33	0
54	MG	1E	302	1/1	0.98	0.03	42,42,42,42	0
54	MG	1A	3045	1/1	0.98	0.08	33,33,33,33	0
54	MG	1A	3063	1/1	0.98	0.03	31,31,31,31	0
54	MG	1A	3276	1/1	0.98	0.16	29,29,29,29	0
54	MG	1A	3438	1/1	0.98	0.04	27,27,27,27	0
54	MG	1F	301	1/1	0.98	0.17	36,36,36,36	0
54	MG	2A	3574	1/1	0.98	0.05	30,30,30,30	0
54	MG	1a	1877	1/1	0.98	0.05	55,55,55,55	0
54	MG	1A	3214	1/1	0.98	0.17	42,42,42,42	0
54	MG	2W	8002	1/1	0.98	0.13	60,60,60,60	0
54	MG	2X	8001	1/1	0.98	0.04	47,47,47,47	0
54	MG	1A	3118	1/1	0.98	0.14	43,43,43,43	0
54	MG	1F	304	1/1	0.98	0.07	33,33,33,33	0
54	MG	1A	3280	1/1	0.98	0.10	48,48,48,48	0
54	MG	1A	3840	1/1	0.98	0.04	39,39,39,39	0
54	MG	1A	3003	1/1	0.98	0.12	24,24,24,24	0
54	MG	1A	3085	1/1	0.98	0.33	38,38,38,38	0
54	MG	2A	3583	1/1	0.98	0.04	34,34,34,34	0
54	MG	1a	1710	1/1	0.98	0.09	38,38,38,38	0
54	MG	1A	3121	1/1	0.98	0.09	35,35,35,35	0
54	MG	1A	3978	1/1	0.98	0.07	29,29,29,29	0
54	MG	1a	1713	1/1	0.98	0.07	44,44,44,44	0
54	MG	1A	3732	1/1	0.98	0.04	32,32,32,32	0
54	MG	1A	3123	1/1	0.98	0.09	23,23,23,23	0
54	MG	1A	3286	1/1	0.98	0.17	41,41,41,41	0
54	MG	1A	3848	1/1	0.98	0.06	41,41,41,41	0
54	MG	1A	3287	1/1	0.98	0.05	39,39,39,39	0
54	MG	1A	3006	1/1	0.98	0.03	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2a	1611	1/1	0.98	0.05	41,41,41,41	0
54	MG	2A	3597	1/1	0.98	0.06	72,72,72,72	0
54	MG	1A	3087	1/1	0.98	0.25	34,34,34,34	0
54	MG	1A	3452	1/1	0.98	0.07	56,56,56,56	0
54	MG	1A	3740	1/1	0.98	0.04	22,22,22,22	0
54	MG	2A	3601	1/1	0.98	0.03	50,50,50,50	0
54	MG	1A	3290	1/1	0.98	0.15	36,36,36,36	0
54	MG	1A	3291	1/1	0.98	0.21	43,43,43,43	0
54	MG	1A	3023	1/1	0.98	0.12	34,34,34,34	0
54	MG	1A	3223	1/1	0.98	0.11	32,32,32,32	0
54	MG	2A	3606	1/1	0.98	0.04	48,48,48,48	0
54	MG	1Q	204	1/1	0.98	0.14	55,55,55,55	0
54	MG	2A	3608	1/1	0.98	0.05	64,64,64,64	0
54	MG	1A	3050	1/1	0.98	0.08	44,44,44,44	0
54	MG	2A	3610	1/1	0.98	0.10	44,44,44,44	0
54	MG	1A	3859	1/1	0.98	0.04	33,33,33,33	0
54	MG	1A	3015	1/1	0.98	0.10	38,38,38,38	0
54	MG	2A	3613	1/1	0.98	0.12	49,49,49,49	0
54	MG	1t	3001	1/1	0.98	0.05	49,49,49,49	0
54	MG	2A	3615	1/1	0.98	0.03	34,34,34,34	0
54	MG	1A	3296	1/1	0.98	0.06	31,31,31,31	0
54	MG	2A	3617	1/1	0.98	0.04	23,23,23,23	0
54	MG	1A	3226	1/1	0.98	0.19	42,42,42,42	0
54	MG	2A	3394	1/1	0.98	0.07	33,33,33,33	0
54	MG	1A	3461	1/1	0.98	0.05	44,44,44,44	0
54	MG	1A	3016	1/1	0.98	0.15	42,42,42,42	0
54	MG	1A	3865	1/1	0.98	0.11	35,35,35,35	0
54	MG	2A	3193	1/1	0.98	0.06	41,41,41,41	0
54	MG	1A	3463	1/1	0.98	0.04	53,53,53,53	0
54	MG	1A	3867	1/1	0.98	0.08	32,32,32,32	0
54	MG	2A	3004	1/1	0.98	0.07	26,26,26,26	0
54	MG	2A	3005	1/1	0.98	0.13	45,45,45,45	0
54	MG	1A	3299	1/1	0.98	0.10	22,22,22,22	0
54	MG	1A	3228	1/1	0.98	0.21	41,41,41,41	0
54	MG	1a	1743	1/1	0.98	0.05	53,53,53,53	0
54	MG	1A	3053	1/1	0.98	0.17	36,36,36,36	0
54	MG	1A	3379	1/1	0.98	0.05	27,27,27,27	0
54	MG	1A	3872	1/1	0.98	0.04	42,42,42,42	0
54	MG	2A	3013	1/1	0.98	0.11	24,24,24,24	0
54	MG	1A	3303	1/1	0.98	0.22	31,31,31,31	0
54	MG	1A	3131	1/1	0.98	0.05	46,46,46,46	0
54	MG	2A	3412	1/1	0.98	0.04	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3875	1/1	0.98	0.04	50,50,50,50	0
54	MG	1A	3470	1/1	0.98	0.12	49,49,49,49	0
54	MG	2A	3018	1/1	0.98	0.15	35,35,35,35	0
54	MG	2A	3019	1/1	0.98	0.23	46,46,46,46	0
54	MG	2a	1657	1/1	0.98	0.09	52,52,52,52	0
54	MG	1A	3178	1/1	0.98	0.09	38,38,38,38	0
54	MG	2A	3643	1/1	0.98	0.05	63,63,63,63	0
54	MG	1A	3760	1/1	0.98	0.07	34,34,34,34	0
54	MG	1A	4014	1/1	0.98	0.03	33,33,33,33	0
54	MG	1A	3306	1/1	0.98	0.05	29,29,29,29	0
54	MG	2A	3647	1/1	0.98	0.14	58,58,58,58	0
54	MG	2A	3649	1/1	0.98	0.04	56,56,56,56	0
54	MG	1A	4016	1/1	0.98	0.06	62,62,62,62	0
54	MG	1A	3094	1/1	0.98	0.13	37,37,37,37	0
54	MG	1A	4018	1/1	0.98	0.05	44,44,44,44	0
54	MG	1A	3883	1/1	0.98	0.05	38,38,38,38	0
54	MG	1A	3308	1/1	0.98	0.08	46,46,46,46	0
54	MG	2A	3030	1/1	0.98	0.14	39,39,39,39	0
54	MG	1A	3885	1/1	0.98	0.04	67,67,67,67	0
54	MG	1A	3181	1/1	0.98	0.10	36,36,36,36	0
54	MG	2A	3662	1/1	0.98	0.05	59,59,59,59	0
54	MG	1A	4023	1/1	0.98	0.04	60,60,60,60	0
54	MG	2A	3664	1/1	0.98	0.05	61,61,61,61	0
54	MG	1A	3565	1/1	0.98	0.06	50,50,50,50	0
54	MG	1A	3387	1/1	0.98	0.09	25,25,25,25	0
54	MG	2A	3432	1/1	0.98	0.06	35,35,35,35	0
54	MG	1A	3055	1/1	0.98	0.26	42,42,42,42	0
54	MG	1a	1601	1/1	0.98	0.07	57,57,57,57	0
54	MG	1A	3389	1/1	0.98	0.13	35,35,35,35	0
54	MG	1A	4029	1/1	0.98	0.07	49,49,49,49	0
54	MG	1A	3569	1/1	0.98	0.06	37,37,37,37	0
54	MG	1A	3183	1/1	0.98	0.14	41,41,41,41	0
54	MG	2A	3440	1/1	0.98	0.04	45,45,45,45	0
54	MG	2A	3675	1/1	0.98	0.08	61,61,61,61	0
54	MG	2A	3676	1/1	0.98	0.04	48,48,48,48	0
54	MG	1A	4032	1/1	0.98	0.19	35,35,35,35	0
54	MG	2A	3043	1/1	0.98	0.03	23,23,23,23	0
54	MG	1A	3096	1/1	0.98	0.05	40,40,40,40	0
54	MG	1A	4034	1/1	0.98	0.10	31,31,31,31	0
54	MG	1A	3238	1/1	0.98	0.19	38,38,38,38	0
54	MG	1A	3895	1/1	0.98	0.03	35,35,35,35	0
54	MG	1A	4037	1/1	0.98	0.12	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	4038	1/1	0.98	0.04	37,37,37,37	0
54	MG	2A	3240	1/1	0.98	0.12	34,34,34,34	0
54	MG	1A	4039	1/1	0.98	0.08	41,41,41,41	0
54	MG	1a	1779	1/1	0.98	0.06	56,56,56,56	0
54	MG	2A	3452	1/1	0.98	0.07	48,48,48,48	0
54	MG	1A	4042	1/1	0.98	0.11	36,36,36,36	0
54	MG	2A	3053	1/1	0.98	0.04	39,39,39,39	0
54	MG	1a	1615	1/1	0.98	0.10	28,28,28,28	0
54	MG	1a	1616	1/1	0.98	0.08	48,48,48,48	0
54	MG	1a	1617	1/1	0.98	0.04	50,50,50,50	0
54	MG	1A	3239	1/1	0.98	0.13	43,43,43,43	0
54	MG	1A	3900	1/1	0.98	0.03	29,29,29,29	0
54	MG	1A	3901	1/1	0.98	0.08	46,46,46,46	0
54	MG	1A	3315	1/1	0.98	0.09	34,34,34,34	0
54	MG	1A	3575	1/1	0.98	0.06	33,33,33,33	0
54	MG	1a	1623	1/1	0.98	0.05	43,43,43,43	0
54	MG	2A	3254	1/1	0.98	0.27	39,39,39,39	0
54	MG	1A	3316	1/1	0.98	0.07	39,39,39,39	0
54	MG	1A	3241	1/1	0.98	0.14	37,37,37,37	0
54	MG	1a	1626	1/1	0.98	0.06	43,43,43,43	0
54	MG	1A	3486	1/1	0.98	0.09	31,31,31,31	0
54	MG	1a	1628	1/1	0.98	0.04	37,37,37,37	0
54	MG	1A	3487	1/1	0.98	0.06	25,25,25,25	0
54	MG	1A	3398	1/1	0.98	0.07	22,22,22,22	0
54	MG	1A	3242	1/1	0.98	0.13	40,40,40,40	0
54	MG	1a	1632	1/1	0.98	0.07	36,36,36,36	0
54	MG	2A	3072	1/1	0.98	0.18	36,36,36,36	0
54	MG	1A	3582	1/1	0.98	0.09	50,50,50,50	0
54	MG	1A	3097	1/1	0.98	0.12	42,42,42,42	0
54	MG	2A	3479	1/1	0.98	0.06	38,38,38,38	0
54	MG	1A	4058	1/1	0.98	0.07	37,37,37,37	0
54	MG	1A	3188	1/1	0.98	0.10	40,40,40,40	0
54	MG	1A	3683	1/1	0.98	0.08	57,57,57,57	0
54	MG	2A	3270	1/1	0.98	0.07	41,41,41,41	0
54	MG	1A	3037	1/1	0.98	0.13	39,39,39,39	0
54	MG	1A	4065	1/1	0.98	0.09	49,49,49,49	0
54	MG	1A	3137	1/1	0.98	0.18	42,42,42,42	0
54	MG	1A	3028	1/1	0.98	0.15	28,28,28,28	0
54	MG	2a	1734	1/1	0.98	0.06	64,64,64,64	0
54	MG	2a	1735	1/1	0.98	0.08	64,64,64,64	0
54	MG	1A	4068	1/1	0.98	0.27	43,43,43,43	0
54	MG	1A	3075	1/1	0.98	0.09	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3790	1/1	0.98	0.05	21,21,21,21	0
54	MG	1A	3406	1/1	0.98	0.03	30,30,30,30	0
54	MG	2A	3492	1/1	0.98	0.14	57,57,57,57	0
54	MG	2a	1743	1/1	0.98	0.06	61,61,61,61	0
54	MG	2A	3087	1/1	0.98	0.08	47,47,47,47	0
54	MG	1A	3325	1/1	0.98	0.05	21,21,21,21	0
54	MG	2a	1747	1/1	0.98	0.09	78,78,78,78	0
54	MG	2A	3731	1/1	0.98	0.14	23,23,23,23	0
54	MG	1A	4073	1/1	0.98	0.17	40,40,40,40	0
54	MG	1A	3793	1/1	0.98	0.09	55,55,55,55	0
54	MG	1A	3141	1/1	0.98	0.19	36,36,36,36	0
54	MG	1A	3795	1/1	0.98	0.05	68,68,68,68	0
54	MG	1a	1651	1/1	0.98	0.10	38,38,38,38	0
54	MG	1A	3007	1/1	0.98	0.11	35,35,35,35	0
54	MG	2A	3095	1/1	0.98	0.04	38,38,38,38	0
54	MG	2a	1756	1/1	0.98	0.05	57,57,57,57	0
54	MG	2A	3290	1/1	0.98	0.07	33,33,33,33	0
54	MG	2a	1758	1/1	0.98	0.10	50,50,50,50	0
54	MG	1A	3195	1/1	0.98	0.10	47,47,47,47	0
54	MG	1A	3929	1/1	0.98	0.04	52,52,52,52	0
54	MG	1A	3143	1/1	0.98	0.05	44,44,44,44	0
54	MG	1a	1656	1/1	0.98	0.04	37,37,37,37	0
54	MG	2A	3295	1/1	0.98	0.04	33,33,33,33	0
54	MG	1A	3144	1/1	0.98	0.14	41,41,41,41	0
54	MG	2a	1766	1/1	0.98	0.04	63,63,63,63	0
54	MG	2A	3101	1/1	0.98	0.05	34,34,34,34	0
54	MG	2A	3102	1/1	0.98	0.09	49,49,49,49	0
54	MG	2A	3103	1/1	0.98	0.13	37,37,37,37	0
54	MG	1A	3332	1/1	0.98	0.08	28,28,28,28	0
54	MG	2A	3753	1/1	0.98	0.20	39,39,39,39	0
54	MG	1A	3145	1/1	0.98	0.09	43,43,43,43	0
54	MG	2a	1773	1/1	0.98	0.12	59,59,59,59	0
54	MG	1a	1828	1/1	0.98	0.04	55,55,55,55	0
54	MG	1A	3103	1/1	0.98	0.14	44,44,44,44	0
54	MG	2a	1776	1/1	0.98	0.04	76,76,76,76	0
54	MG	2a	1777	1/1	0.98	0.04	72,72,72,72	0
54	MG	1A	3258	1/1	0.98	0.11	40,40,40,40	0
54	MG	1A	3104	1/1	0.98	0.19	41,41,41,41	0
54	MG	1A	3105	1/1	0.98	0.05	57,57,57,57	0
54	MG	2A	3760	1/1	0.98	0.43	40,40,40,40	0
54	MG	1A	3106	1/1	0.98	0.15	30,30,30,30	0
54	MG	1B	214	1/1	0.98	0.03	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3703	1/1	0.98	0.04	41,41,41,41	0
54	MG	1A	3040	1/1	0.98	0.10	39,39,39,39	0
54	MG	1A	3078	1/1	0.98	0.26	38,38,38,38	0
54	MG	1A	3942	1/1	0.98	0.05	59,59,59,59	0
54	MG	1A	3031	1/1	0.98	0.12	24,24,24,24	0
54	MG	2a	1790	1/1	0.98	0.06	61,61,61,61	0
54	MG	1A	3342	1/1	0.98	0.06	57,57,57,57	0
54	MG	2A	3316	1/1	0.98	0.04	40,40,40,40	0
54	MG	2A	3317	1/1	0.98	0.04	37,37,37,37	0
54	MG	1A	3266	1/1	0.98	0.15	28,28,28,28	0
54	MG	1A	3157	1/1	0.98	0.10	39,39,39,39	0
54	MG	2A	3320	1/1	0.98	0.06	47,47,47,47	0
54	MG	1A	3710	1/1	0.98	0.07	55,55,55,55	0
54	MG	1A	3816	1/1	0.98	0.05	32,32,32,32	0
54	MG	1A	3817	1/1	0.98	0.04	45,45,45,45	0
54	MG	1A	3043	1/1	0.98	0.08	17,17,17,17	0
54	MG	2A	3126	1/1	0.98	0.05	28,28,28,28	0
54	MG	1A	3951	1/1	0.98	0.06	31,31,31,31	0
54	MG	2A	3327	1/1	0.98	0.11	34,34,34,34	0
54	MG	2A	3328	1/1	0.98	0.12	36,36,36,36	0
54	MG	1A	3952	1/1	0.98	0.04	33,33,33,33	0
54	MG	1A	3953	1/1	0.98	0.06	19,19,19,19	0
54	MG	1A	3081	1/1	0.98	0.16	46,46,46,46	0
54	MG	2A	3131	1/1	0.98	0.12	39,39,39,39	0
54	MG	1a	1854	1/1	0.98	0.04	52,52,52,52	0
57	ZN	1n	501	1/1	0.98	0.04	65,65,65,65	0
54	MG	1A	3347	1/1	0.98	0.07	24,24,24,24	0
54	MG	1a	1856	1/1	0.98	0.04	58,58,58,58	0
57	ZN	25	101	1/1	0.98	0.04	64,64,64,64	0
54	MG	1A	3270	1/1	0.98	0.18	32,32,32,32	0
57	ZN	2n	501	1/1	0.98	0.06	84,84,84,84	0
54	MG	2A	3337	1/1	0.98	0.06	32,32,32,32	0
58	SF4	2d	501	8/8	0.98	0.05	61,78,84,104	0
54	MG	1A	3140	1/1	0.99	0.23	31,31,31,31	0
54	MG	1A	3645	1/1	0.99	0.09	30,30,30,30	0
54	MG	1A	4046	1/1	0.99	0.07	29,29,29,29	0
54	MG	1A	3798	1/1	0.99	0.04	71,71,71,71	0
54	MG	2A	3284	1/1	0.99	0.03	41,41,41,41	0
54	MG	2A	3020	1/1	0.99	0.16	44,44,44,44	0
54	MG	1a	1847	1/1	0.99	0.03	42,42,42,42	0
54	MG	1A	3122	1/1	0.99	0.17	37,37,37,37	0
54	MG	1A	4049	1/1	0.99	0.14	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3281	1/1	0.99	0.08	39,39,39,39	0
54	MG	2A	3110	1/1	0.99	0.07	28,28,28,28	0
54	MG	2A	3589	1/1	0.99	0.03	54,54,54,54	0
54	MG	2A	3590	1/1	0.99	0.03	49,49,49,49	0
54	MG	1a	1851	1/1	0.99	0.03	68,68,68,68	0
54	MG	1a	1852	1/1	0.99	0.03	52,52,52,52	0
54	MG	1A	3917	1/1	0.99	0.03	15,15,15,15	0
54	MG	2A	3390	1/1	0.99	0.04	31,31,31,31	0
54	MG	2A	3595	1/1	0.99	0.04	33,33,33,33	0
54	MG	1A	3556	1/1	0.99	0.09	39,39,39,39	0
54	MG	1A	3019	1/1	0.99	0.12	30,30,30,30	0
54	MG	1A	3249	1/1	0.99	0.18	35,35,35,35	0
54	MG	1A	3250	1/1	0.99	0.12	39,39,39,39	0
54	MG	2A	3494	1/1	0.99	0.07	27,27,27,27	0
54	MG	1A	3393	1/1	0.99	0.12	26,26,26,26	0
54	MG	1A	3356	1/1	0.99	0.03	11,11,11,11	0
54	MG	1A	3606	1/1	0.99	0.19	32,32,32,32	0
54	MG	1A	4059	1/1	0.99	0.16	28,28,28,28	0
54	MG	1A	3925	1/1	0.99	0.05	54,54,54,54	0
54	MG	1A	4061	1/1	0.99	0.09	37,37,37,37	0
54	MG	1A	4062	1/1	0.99	0.07	37,37,37,37	0
54	MG	2A	3305	1/1	0.99	0.06	19,19,19,19	0
54	MG	2A	3503	1/1	0.99	0.13	35,35,35,35	0
54	MG	1A	3020	1/1	0.99	0.19	39,39,39,39	0
54	MG	1A	3091	1/1	0.99	0.05	42,42,42,42	0
54	MG	2A	3724	1/1	0.99	0.03	66,66,66,66	0
54	MG	2a	1732	1/1	0.99	0.03	62,62,62,62	0
54	MG	1A	3029	1/1	0.99	0.04	40,40,40,40	0
54	MG	1G	3004	1/1	0.99	0.04	45,45,45,45	0
54	MG	1A	3146	1/1	0.99	0.13	28,28,28,28	0
54	MG	1A	3005	1/1	0.99	0.12	24,24,24,24	0
54	MG	1A	3149	1/1	0.99	0.05	28,28,28,28	0
54	MG	2a	1738	1/1	0.99	0.04	71,71,71,71	0
54	MG	1A	3013	1/1	0.99	0.04	17,17,17,17	0
54	MG	1A	3111	1/1	0.99	0.11	38,38,38,38	0
54	MG	1A	3009	1/1	0.99	0.04	26,26,26,26	0
54	MG	2a	1742	1/1	0.99	0.03	69,69,69,69	0
54	MG	1a	1792	1/1	0.99	0.05	62,62,62,62	0
54	MG	1P	201	1/1	0.99	0.15	26,26,26,26	0
54	MG	1A	3329	1/1	0.99	0.08	39,39,39,39	0
54	MG	2a	1746	1/1	0.99	0.06	56,56,56,56	0
54	MG	1A	3445	1/1	0.99	0.07	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	2A	3139	1/1	0.99	0.10	28,28,28,28	0
54	MG	1A	3446	1/1	0.99	0.09	30,30,30,30	0
54	MG	2A	3739	1/1	0.99	0.04	52,52,52,52	0
54	MG	1A	3667	1/1	0.99	0.06	47,47,47,47	0
54	MG	1A	3619	1/1	0.99	0.10	37,37,37,37	0
54	MG	1A	3877	1/1	0.99	0.07	40,40,40,40	0
54	MG	1A	3054	1/1	0.99	0.15	34,34,34,34	0
54	MG	1A	3879	1/1	0.99	0.05	38,38,38,38	0
54	MG	1a	1722	1/1	0.99	0.06	40,40,40,40	0
54	MG	1A	3042	1/1	0.99	0.04	24,24,24,24	0
54	MG	1B	205	1/1	0.99	0.09	39,39,39,39	0
54	MG	2A	3149	1/1	0.99	0.05	28,28,28,28	0
54	MG	1A	3024	1/1	0.99	0.11	18,18,18,18	0
54	MG	1A	3179	1/1	0.99	0.11	34,34,34,34	0
54	MG	1A	3723	1/1	0.99	0.04	44,44,44,44	0
54	MG	1A	3264	1/1	0.99	0.16	29,29,29,29	0
54	MG	2a	1764	1/1	0.99	0.04	64,64,64,64	0
54	MG	1A	4012	1/1	0.99	0.11	23,23,23,23	0
54	MG	1A	3828	1/1	0.99	0.06	27,27,27,27	0
54	MG	1A	3233	1/1	0.99	0.08	37,37,37,37	0
54	MG	2A	3435	1/1	0.99	0.08	43,43,43,43	0
54	MG	1a	1733	1/1	0.99	0.07	34,34,34,34	0
54	MG	1A	3626	1/1	0.99	0.10	30,30,30,30	0
54	MG	1A	3300	1/1	0.99	0.07	12,12,12,12	0
54	MG	2A	3341	1/1	0.99	0.06	36,36,36,36	0
54	MG	1A	3156	1/1	0.99	0.17	30,30,30,30	0
54	MG	2A	3648	1/1	0.99	0.04	48,48,48,48	0
54	MG	1A	3044	1/1	0.99	0.08	32,32,32,32	0
54	MG	2A	3074	1/1	0.99	0.05	23,23,23,23	0
54	MG	1A	3834	1/1	0.99	0.04	45,45,45,45	0
54	MG	2A	3652	1/1	0.99	0.06	38,38,38,38	0
54	MG	2A	3653	1/1	0.99	0.05	38,38,38,38	0
54	MG	2A	3654	1/1	0.99	0.03	56,56,56,56	0
54	MG	2a	1781	1/1	0.99	0.04	60,60,60,60	0
54	MG	1A	3208	1/1	0.99	0.14	42,42,42,42	0
54	MG	1A	3117	1/1	0.99	0.12	39,39,39,39	0
54	MG	1A	3071	1/1	0.99	0.16	32,32,32,32	0
54	MG	1A	3184	1/1	0.99	0.09	35,35,35,35	0
54	MG	1A	3896	1/1	0.99	0.05	49,49,49,49	0
54	MG	2A	3660	1/1	0.99	0.08	47,47,47,47	0
54	MG	1A	3897	1/1	0.99	0.12	44,44,44,44	0
54	MG	1A	3734	1/1	0.99	0.03	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	MG	1A	3899	1/1	0.99	0.04	47,47,47,47	0
54	MG	1A	3240	1/1	0.99	0.20	38,38,38,38	0
54	MG	1A	3588	1/1	0.99	0.06	21,21,21,21	0
54	MG	1A	3185	1/1	0.99	0.13	37,37,37,37	0
54	MG	2A	3357	1/1	0.99	0.06	41,41,41,41	0
54	MG	2A	3456	1/1	0.99	0.02	24,24,24,24	0
54	MG	1A	3025	1/1	0.99	0.16	40,40,40,40	0
54	MG	2A	3559	1/1	0.99	0.03	55,55,55,55	0
54	MG	1A	3421	1/1	0.99	0.08	24,24,24,24	0
54	MG	1A	3845	1/1	0.99	0.07	22,22,22,22	0
54	MG	2A	3362	1/1	0.99	0.04	34,34,34,34	0
54	MG	1A	3046	1/1	0.99	0.13	13,13,13,13	0
54	MG	1A	3018	1/1	0.99	0.11	33,33,33,33	0
54	MG	2E	301	1/1	0.99	0.04	50,50,50,50	0
54	MG	1A	3971	1/1	0.99	0.04	31,31,31,31	0
54	MG	2A	3181	1/1	0.99	0.03	46,46,46,46	0
54	MG	1A	3424	1/1	0.99	0.04	46,46,46,46	0
54	MG	1A	3277	1/1	0.99	0.18	29,29,29,29	0
54	MG	2A	3273	1/1	0.99	0.09	44,44,44,44	0
57	ZN	1Y	501	1/1	0.99	0.05	56,56,56,56	0
54	MG	1D	307	1/1	0.99	0.11	17,17,17,17	0
57	ZN	15	101	1/1	0.99	0.02	50,50,50,50	0
57	ZN	16	501	1/1	0.99	0.05	39,39,39,39	0
57	ZN	19	102	1/1	0.99	0.03	37,37,37,37	0
54	MG	2A	3682	1/1	0.99	0.03	40,40,40,40	0
54	MG	2A	3011	1/1	0.99	0.06	28,28,28,28	0
54	MG	2A	3470	1/1	0.99	0.11	50,50,50,50	0
54	MG	2A	3573	1/1	0.99	0.03	50,50,50,50	0
57	ZN	26	501	1/1	0.99	0.03	60,60,60,60	0
54	MG	1A	4040	1/1	0.99	0.14	37,37,37,37	0
54	MG	1A	4041	1/1	0.99	0.09	37,37,37,37	0
54	MG	1A	3910	1/1	0.99	0.03	42,42,42,42	0
54	MG	1A	3163	1/1	0.99	0.18	34,34,34,34	0
54	MG	1a	1796	1/1	1.00	0.02	68,68,68,68	0
54	MG	1a	1724	1/1	1.00	0.06	36,36,36,36	0
54	MG	1A	3098	1/1	1.00	0.07	12,12,12,12	0
54	MG	1A	3686	1/1	1.00	0.03	50,50,50,50	0
54	MG	1A	3148	1/1	1.00	0.02	33,33,33,33	0
54	MG	2A	3361	1/1	1.00	0.01	34,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.