Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2026 – 04:10 AM EDT

PDB ID	:	9D7S / pdb_00009d7s
Title	:	Crystal structure of the wild-type Thermus thermophilus 70S ribosome in complex with Api antimicrobial peptide, mRNA, A-site release factor 1, and deacylated P-site and E-site tRNAphe at 2.85A resolution
Authors	:	Aleksandrova, E.V.; Huang, W.; Baliga, C.; Atkinson, G.C.; Vazquez-Laslop, N.; Mankin, A.S.; Polikanov, Y.S.
Deposited on	:	2024-08-17
Resolution	:	2.85 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 (i) 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 (i)) were used in the production of this report:

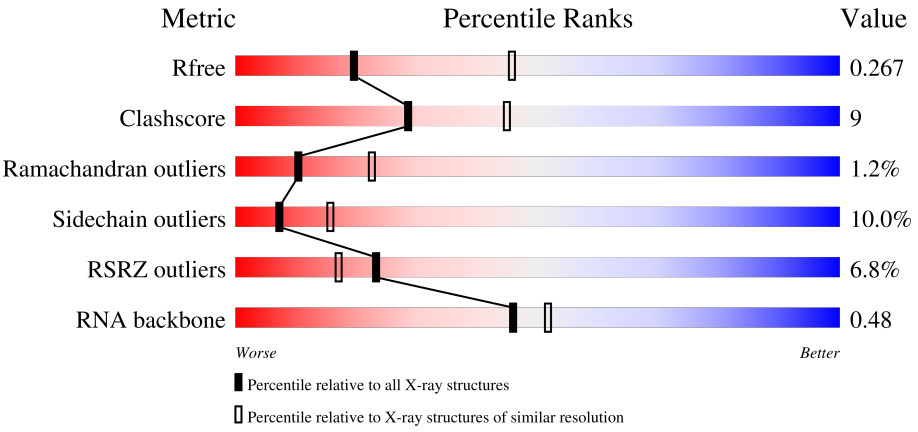
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)
RNA backbone	3983	1009 (3.06-2.66)

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

Mol	Chain	Length	Quality of chain
1	1A	2915	4% 64% 29% 6% .
1	2A	2915	4% 58% 31% 7% .
2	1B	121	76% 19% . .

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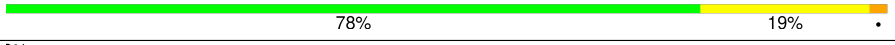
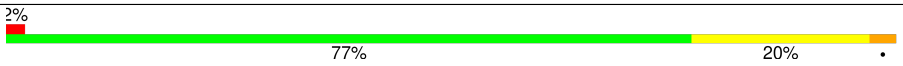
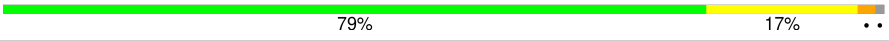
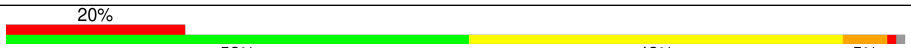
Mol	Chain	Length	Quality of chain
2	2B	121	
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	

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Mol	Chain	Length	Quality of chain
15	1T	146	3% 58% 30% 10%
15	2T	146	2% 59% 28% 10%
16	1U	118	81% 15%
16	2U	118	% 81% 16%
17	1V	101	80% 17%
17	2V	101	4% 83% 15%
18	1W	113	% 75% 23%
18	2W	113	77% 22%
19	1X	96	% 79% 17%
19	2X	96	6% 79% 18%
20	1Y	110	2% 63% 31%
20	2Y	110	15% 68% 25% 5%
21	1Z	206	5% 56% 31% 11%
21	2Z	206	7% 49% 33% 8% 10%
22	10	85	2% 72% 16% 11%
22	20	85	6% 67% 20% 9%
23	11	98	3% 73% 24%
23	21	98	4% 76% 21%
24	12	72	6% 76% 17%
24	22	72	4% 62% 35%
25	13	60	67% 30%
25	23	60	7% 77% 20%
26	14	71	25% 49% 35% 10%
26	24	71	39% 54% 32% 10%
27	15	60	80% 18%

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Mol	Chain	Length	Quality of chain
27	25	60	2% 75% 23%
28	16	54	81% 15%
28	26	54	4% 78% 19%
29	17	49	4% 71% 24%
29	27	49	8% 84% 12%
30	18	65	65% 32%
30	28	65	5% 66% 29%
31	19	37	68% 30%
31	29	37	70% 27%
32	1a	1521	5% 49% 42% 7%
32	2a	1521	6% 49% 41% 9%
33	1b	256	11% 45% 34% 11% 10%
33	2b	256	24% 46% 36% 9% 10%
34	1c	239	18% 55% 27% 5% 14%
34	2c	239	15% 56% 28% 14%
35	1d	209	11% 58% 36% 6%
35	2d	209	3% 60% 34% 5%
36	1e	162	% 59% 25% 6% 9%
36	2e	162	5% 56% 30% 6% 9%
37	1f	101	% 66% 33%
37	2f	101	3% 67% 26% 5%
38	1g	156	8% 71% 27%
38	2g	156	19% 56% 37% 6%
39	1h	138	% 74% 24%
39	2h	138	6% 71% 26%

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Mol	Chain	Length	Quality of chain
40	1i	128	18% 55% 38% 6%
40	2i	128	38% 52% 39%
41	1j	105	45% 53% 33% 7% 7%
41	2j	105	53% 48% 40% 9%
42	1k	129	2% 62% 25% 12%
42	2k	129	4% 64% 21% 12%
43	1l	132	4% 68% 22% 8%
43	2l	132	2% 70% 20% 8%
44	1m	126	11% 46% 43% 5% 6%
44	2m	126	37% 52% 35% 5% 9%
45	1n	61	25% 62% 34%
45	2n	61	38% 52% 43%
46	1o	89	2% 69% 29%
46	2o	89	6% 64% 33%
47	1p	88	19% 51% 35% 7% 7%
47	2p	88	3% 61% 30% 7%
48	1q	105	4% 69% 23% 6%
48	2q	105	6% 67% 27% 6%
49	1r	88	% 58% 17% 23%
49	2r	88	2% 50% 24% 23%
50	1s	93	23% 52% 37% 11%
50	2s	93	29% 49% 37% 11%
51	1t	106	10% 53% 30% 8% 9%
51	2t	106	8% 59% 25% 6% 9%
52	1u	27	37% 59% 22% 15%

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Mol	Chain	Length	Quality of chain
52	2u	27	41% 63% 19% 15%
53	1v	24	12% 21% 25% 8% 46%
53	2v	24	12% 33% 17% 46%
54	1w	354	% 47% 20% 30%
54	2w	354	5% 51% 17% 29%
55	1x	76	% 62% 30% 7%
55	1y	76	4% 41% 41% 14%
55	2x	76	% 54% 39% 5%
55	2y	76	8% 37% 42% 17%
56	1z	18	44% 56% 17% 6% 22%
56	2z	18	44% 56% 17% 6% 22%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	1A	3600	-	-	-	X
57	MG	1a	1662	-	-	-	X

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 299015 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2576	1146	476	834	120			
2	2B	120	Total	C	N	O	P	0	0	0
			2576	1146	476	834	120			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total 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
			771	495	140	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	1X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	2X	95	Total	C	N	O	S	0	0	0
			746	485	134	126	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	183	Total	C	N	O	S	0	0	0
			1437	919	256	260	2			
21	2Z	186	Total	C	N	O	S	0	0	0
			1451	928	256	265	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	76	Total	C	N	O	S	0	0	0
			604	373	128	102	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
			755	475	148	131	1			
23	21	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			548	347	99	97	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	68	Total	C	N	O	S	0	0	0
			517	330	92	90	5			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	18	64	Total	C	N	O	S	0	0	0
			511	328	99	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1554	977	302	274	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
			1659	1040	326	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1130	714	214	199	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			810	513	143	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
			1231	766	243	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			983	623	193	167			
40	2i	123	Total	C	N	O	0	0	0
			940	593	185	162			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	98	Total	C	N	O	0	0	0
			721	449	140	132			
41	2j	96	Total	C	N	O	0	0	0
			714	445	138	131			

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	118	Total	C	N	O	S	0	0	0
			923	569	191	161	2			
44	2m	115	Total	C	N	O	S	0	0	0
			889	546	183	158	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
			486	309	101	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
			551	353	108	90			

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

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

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

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

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

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

- Molecule 53 is a RNA chain called PHE-Stop mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	13	Total	C	N	O	P	0	0	0
			274	124	48	89	13			
53	2v	13	Total	C	N	O	P	0	0	0
			274	124	48	89	13			

- Molecule 54 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	249	Total	C	N	O	S	0	0	0
			1939	1199	360	371	9			
54	2w	253	Total	C	N	O	S	0	0	0
			1957	1210	361	377	9			

- Molecule 55 is a RNA chain called P-site and E-site Deacylated tRNAphe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	75	Total	C	N	O	P	S	0	0	0
			1612	722	288	525	75	2			
55	1y	74	Total	C	N	O	P	S	0	0	0
			1590	712	285	517	74	2			
55	2x	75	Total	C	N	O	P	S	0	0	0
			1612	722	288	525	75	2			
55	2y	74	Total	C	N	O	P	S	0	0	0
			1592	713	285	518	74	2			

- Molecule 56 is a protein called Api Antimicrobial Peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
56	1z	14	Total	C	N	O	0	0	0
			119	79	23	17			
56	2z	14	Total	C	N	O	0	0	0
			119	79	23	17			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	793	Total	Mg	0	0
			793	793		
57	1B	20	Total	Mg	0	0
			20	20		
57	1D	9	Total	Mg	0	0
			9	9		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1E	7	Total Mg 7 7	0	0
57	1F	14	Total Mg 14 14	0	0
57	1G	3	Total Mg 3 3	0	0
57	1N	3	Total Mg 3 3	0	0
57	1O	1	Total Mg 1 1	0	0
57	1P	4	Total Mg 4 4	0	0
57	1Q	5	Total Mg 5 5	0	0
57	1R	2	Total Mg 2 2	0	0
57	1T	1	Total Mg 1 1	0	0
57	1U	8	Total Mg 8 8	0	0
57	1V	5	Total Mg 5 5	0	0
57	1W	3	Total Mg 3 3	0	0
57	1X	3	Total Mg 3 3	0	0
57	1Z	2	Total Mg 2 2	0	0
57	10	4	Total Mg 4 4	0	0
57	11	3	Total Mg 3 3	0	0
57	12	1	Total Mg 1 1	0	0
57	13	1	Total Mg 1 1	0	0
57	15	7	Total Mg 7 7	0	0
57	16	1	Total Mg 1 1	0	0
57	17	7	Total Mg 7 7	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	18	2	Total Mg 2 2	0	0
57	19	1	Total Mg 1 1	0	0
57	1a	167	Total Mg 167 167	0	0
57	1f	1	Total Mg 1 1	0	0
57	1i	1	Total Mg 1 1	0	0
57	1k	1	Total Mg 1 1	0	0
57	1m	1	Total Mg 1 1	0	0
57	1n	1	Total Mg 1 1	0	0
57	1v	3	Total Mg 3 3	0	0
57	1w	3	Total Mg 3 3	0	0
57	1x	10	Total Mg 10 10	0	0
57	1y	3	Total Mg 3 3	0	0
57	2A	657	Total Mg 657 657	0	0
57	2B	10	Total Mg 10 10	0	0
57	2D	7	Total Mg 7 7	0	0
57	2E	7	Total Mg 7 7	0	0
57	2F	5	Total Mg 5 5	0	0
57	2O	1	Total Mg 1 1	0	0
57	2P	1	Total Mg 1 1	0	0
57	2Q	3	Total Mg 3 3	0	0
57	2R	1	Total Mg 1 1	0	0

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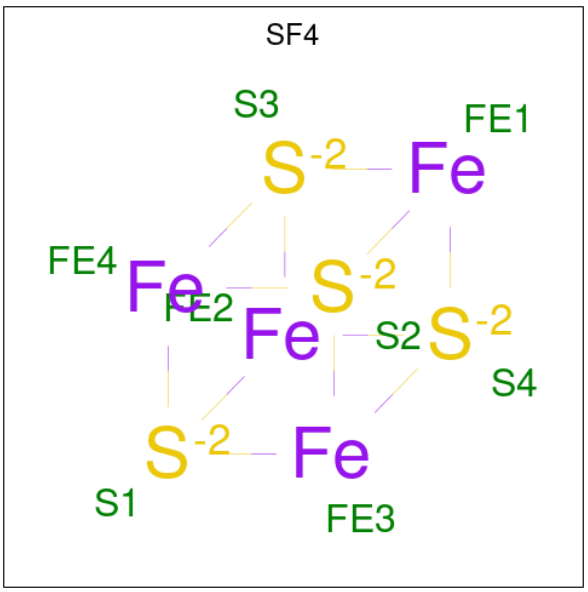
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2U	2	Total Mg 2 2	0	0
57	2V	2	Total Mg 2 2	0	0
57	2W	1	Total Mg 1 1	0	0
57	2X	1	Total Mg 1 1	0	0
57	2Y	1	Total Mg 1 1	0	0
57	20	1	Total Mg 1 1	0	0
57	21	1	Total Mg 1 1	0	0
57	23	2	Total Mg 2 2	0	0
57	25	2	Total Mg 2 2	0	0
57	26	1	Total Mg 1 1	0	0
57	28	1	Total Mg 1 1	0	0
57	2a	165	Total Mg 165 165	0	0
57	2e	3	Total Mg 3 3	0	0
57	2f	1	Total Mg 1 1	0	0
57	2j	1	Total Mg 1 1	0	0
57	2k	2	Total Mg 2 2	0	0
57	2t	1	Total Mg 1 1	0	0
57	2v	2	Total Mg 2 2	0	0
57	2x	9	Total Mg 9 9	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1Y	1	Total Zn 1 1	0	0
58	14	1	Total Zn 1 1	0	0
58	15	1	Total Zn 1 1	0	0
58	16	1	Total Zn 1 1	0	0
58	19	1	Total Zn 1 1	0	0
58	1n	1	Total Zn 1 1	0	0
58	2Y	1	Total Zn 1 1	0	0
58	24	1	Total Zn 1 1	0	0
58	25	1	Total Zn 1 1	0	0
58	26	1	Total Zn 1 1	0	0
58	29	1	Total Zn 1 1	0	0
58	2n	1	Total Zn 1 1	0	0

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



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

- Molecule 60 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	1368	Total O 1368 1368	0	0
60	1B	27	Total O 27 27	0	0
60	1D	14	Total O 14 14	0	0
60	1E	14	Total O 14 14	0	0
60	1F	10	Total O 10 10	0	0
60	1G	1	Total O 1 1	0	0
60	1N	3	Total O 3 3	0	0
60	1O	3	Total O 3 3	0	0
60	1P	18	Total O 18 18	0	0
60	1Q	7	Total O 7 7	0	0
60	1R	1	Total O 1 1	0	0
60	1T	1	Total O 1 1	0	0
60	1U	6	Total O 6 6	0	0
60	1V	2	Total O 2 2	0	0
60	1W	2	Total O 2 2	0	0
60	1X	3	Total O 3 3	0	0
60	10	3	Total O 3 3	0	0
60	11	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	13	2	Total O 2 2	0	0
60	15	6	Total O 6 6	0	0
60	16	1	Total O 1 1	0	0
60	17	3	Total O 3 3	0	0
60	18	6	Total O 6 6	0	0
60	19	1	Total O 1 1	0	0
60	1a	164	Total O 164 164	0	0
60	1d	2	Total O 2 2	0	0
60	1e	1	Total O 1 1	0	0
60	1l	2	Total O 2 2	0	0
60	1p	1	Total O 1 1	0	0
60	1v	3	Total O 3 3	0	0
60	1w	5	Total O 5 5	0	0
60	1x	20	Total O 20 20	0	0
60	1y	1	Total O 1 1	0	0
60	1z	3	Total O 3 3	0	0
60	2A	949	Total O 949 949	0	0
60	2B	5	Total O 5 5	0	0
60	2D	13	Total O 13 13	0	0
60	2E	8	Total O 8 8	0	0
60	2F	6	Total O 6 6	0	0

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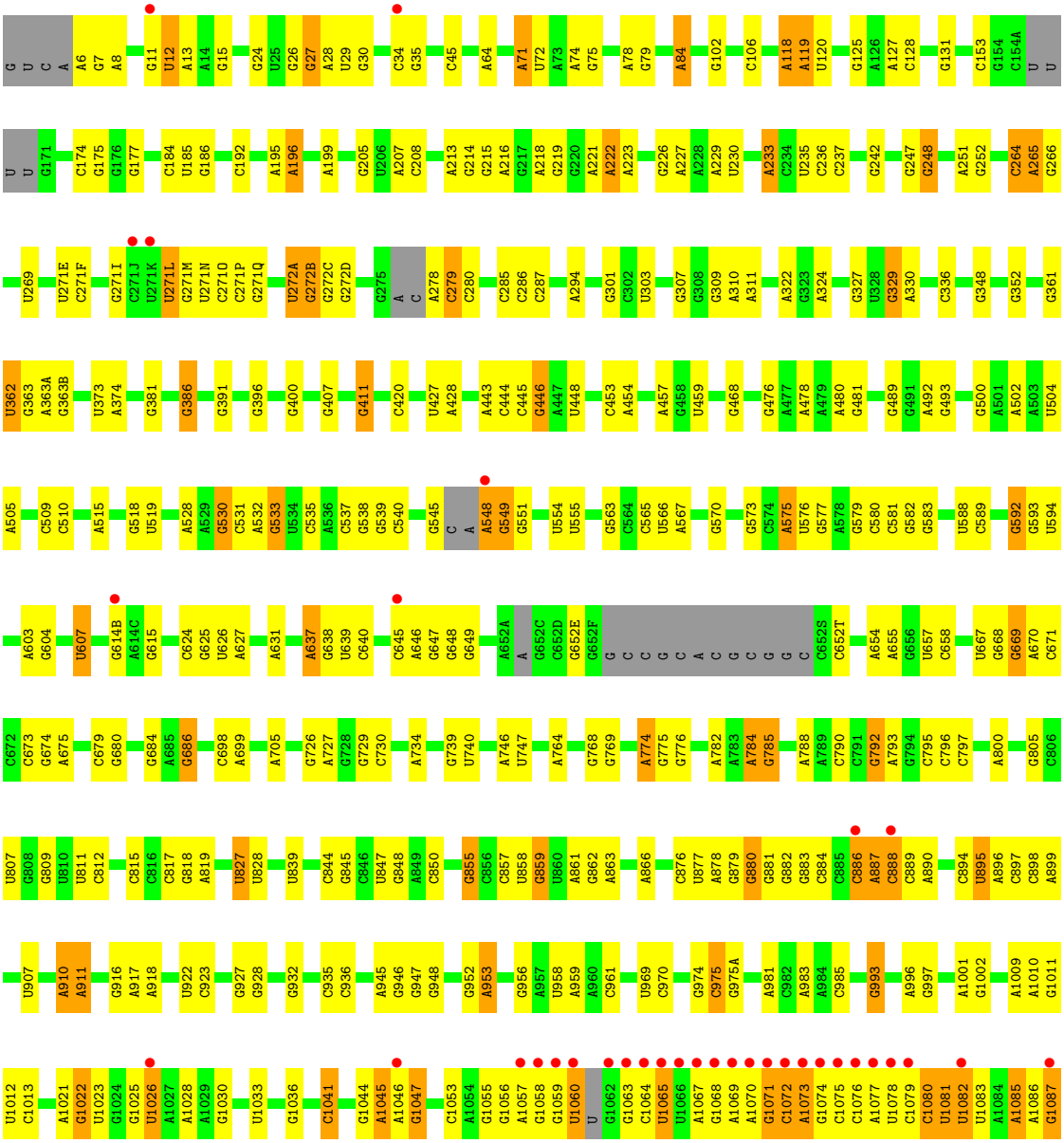
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	2N	2	Total O 2 2	0	0
60	2P	7	Total O 7 7	0	0
60	2R	2	Total O 2 2	0	0
60	2T	1	Total O 1 1	0	0
60	2U	1	Total O 1 1	0	0
60	2V	1	Total O 1 1	0	0
60	2W	1	Total O 1 1	0	0
60	2X	2	Total O 2 2	0	0
60	2Y	1	Total O 1 1	0	0
60	20	6	Total O 6 6	0	0
60	21	2	Total O 2 2	0	0
60	23	2	Total O 2 2	0	0
60	27	2	Total O 2 2	0	0
60	28	2	Total O 2 2	0	0
60	2a	154	Total O 154 154	0	0
60	2d	1	Total O 1 1	0	0
60	2q	1	Total O 1 1	0	0
60	2v	3	Total O 3 3	0	0
60	2w	2	Total O 2 2	0	0
60	2x	11	Total O 11 11	0	0
60	2z	1	Total O 1 1	0	0

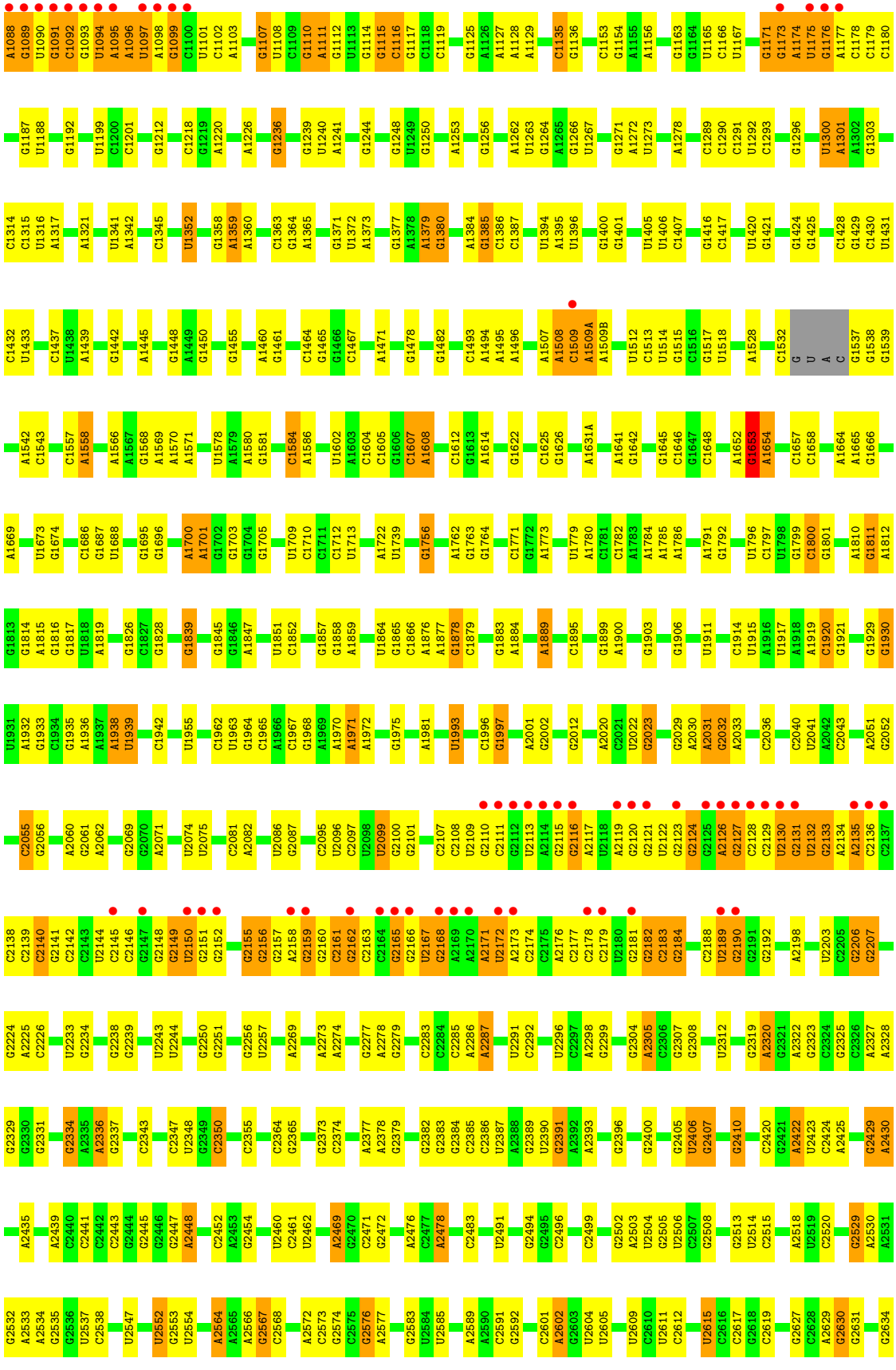
3 Residue-property plots (i)

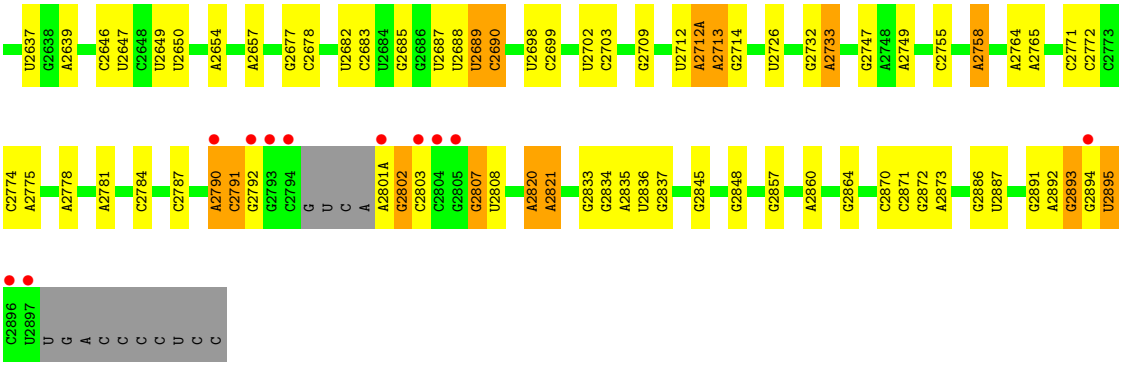
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 23S Ribosomal RNA

Chain 1A:

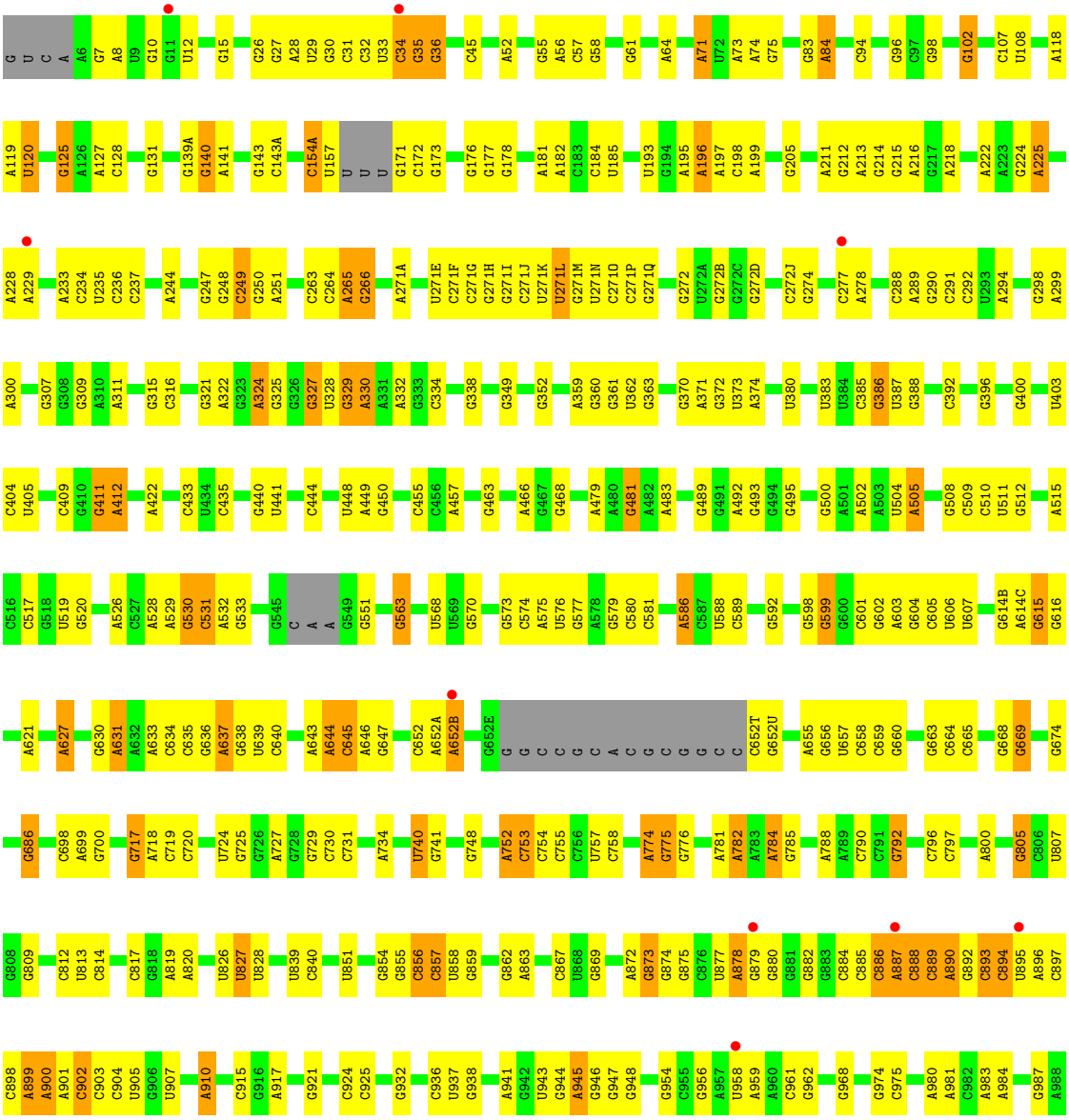


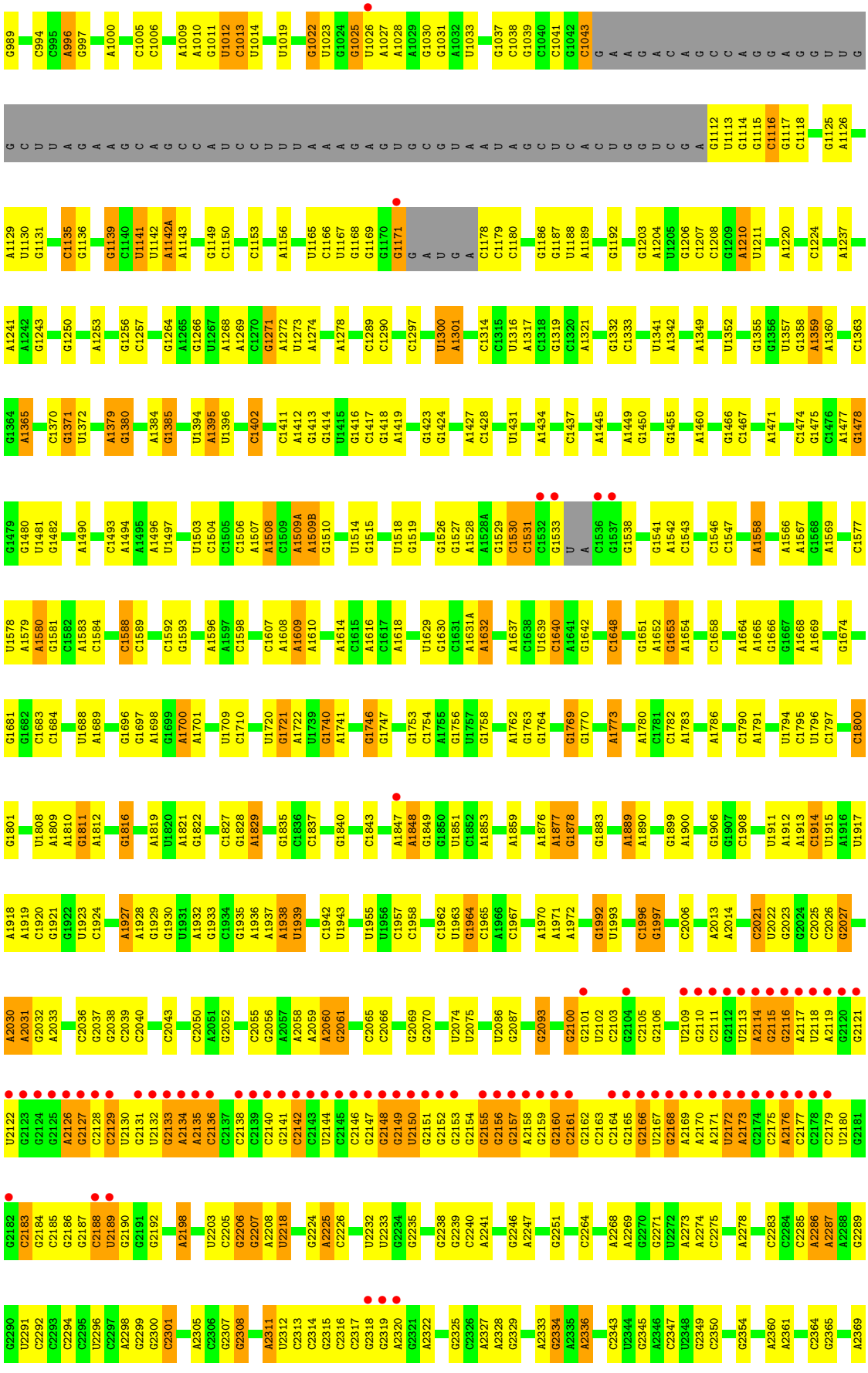


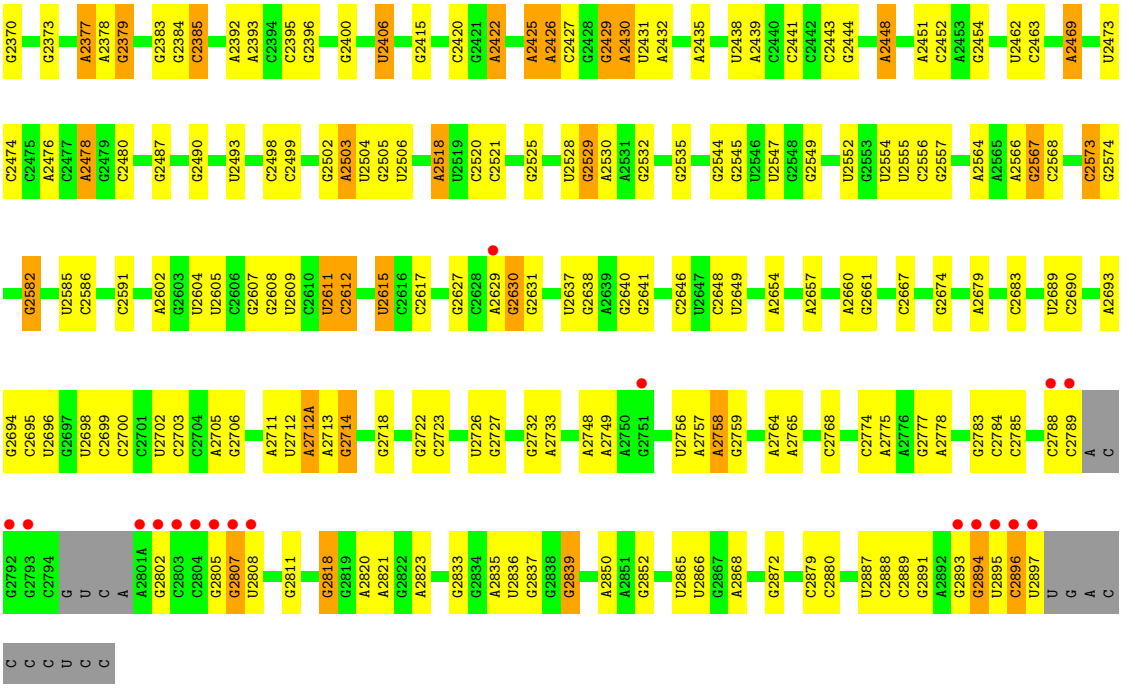


• Molecule 1: 23S Ribosomal RNA

Chain 2A:





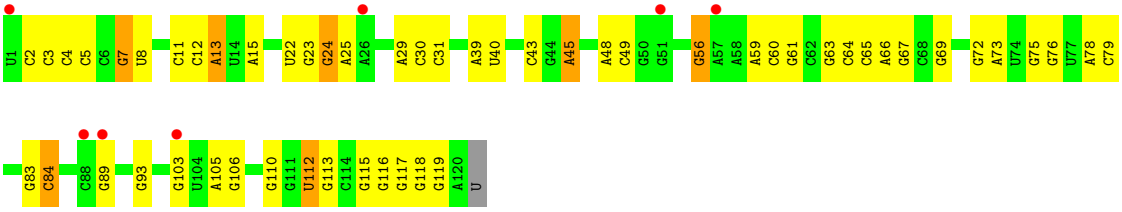


• Molecule 2: 5S Ribosomal RNA

Chain 1B:

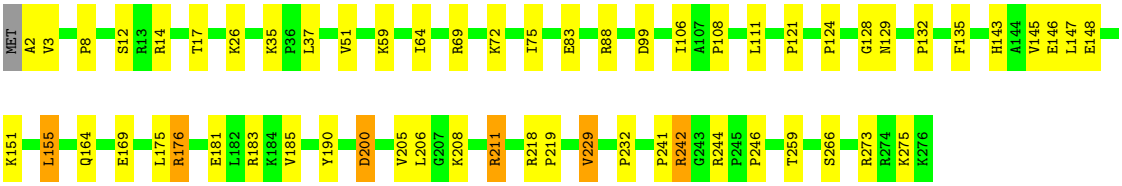
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



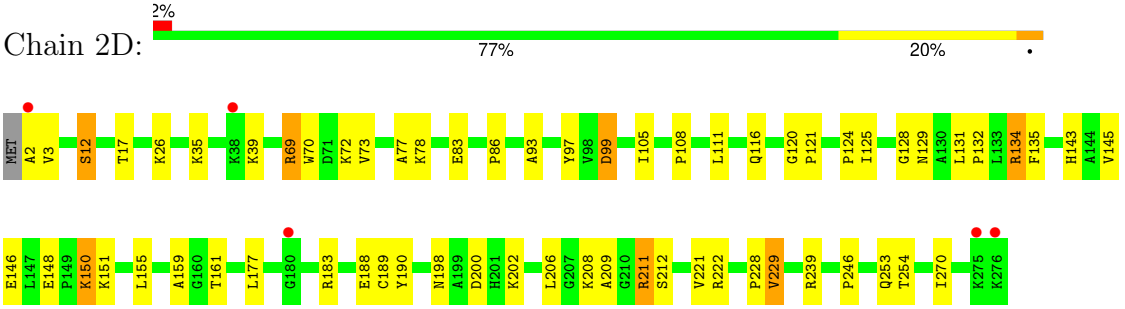
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



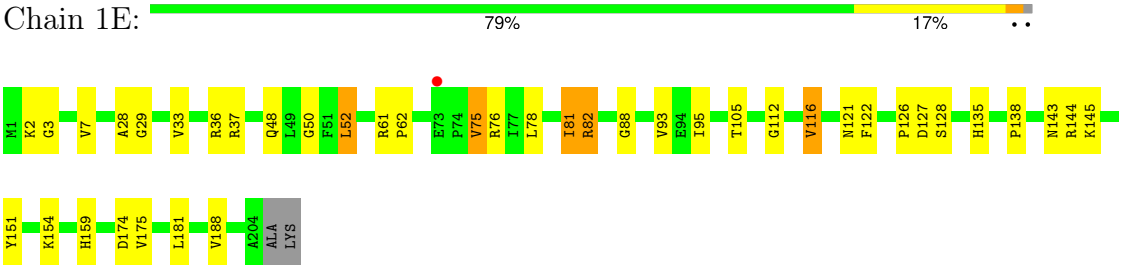
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



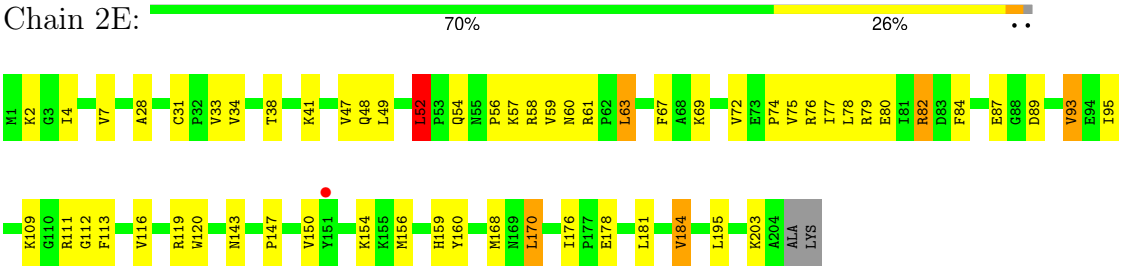
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



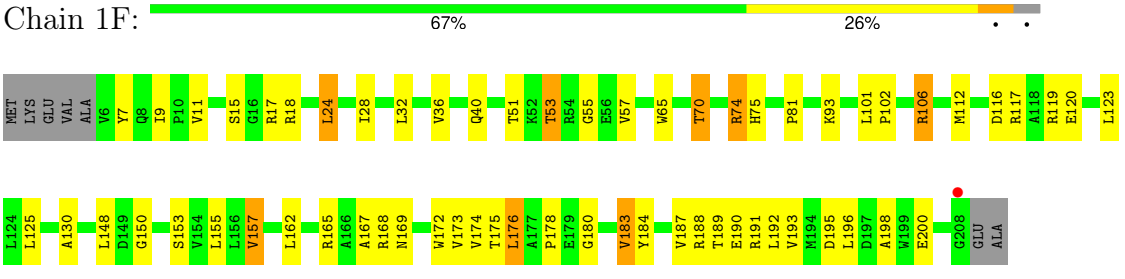
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



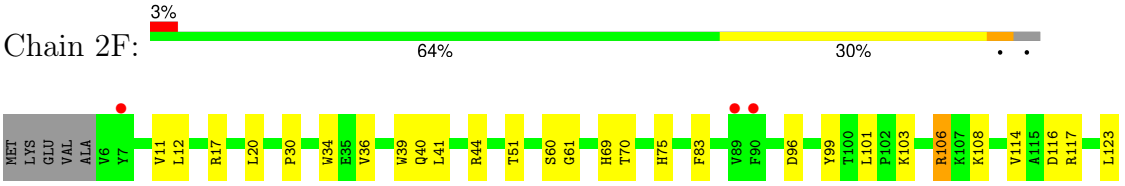
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



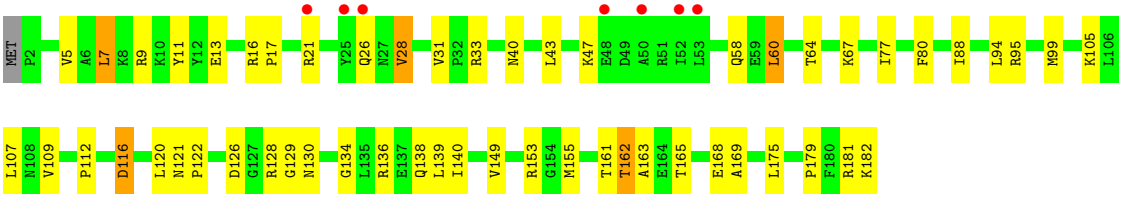
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



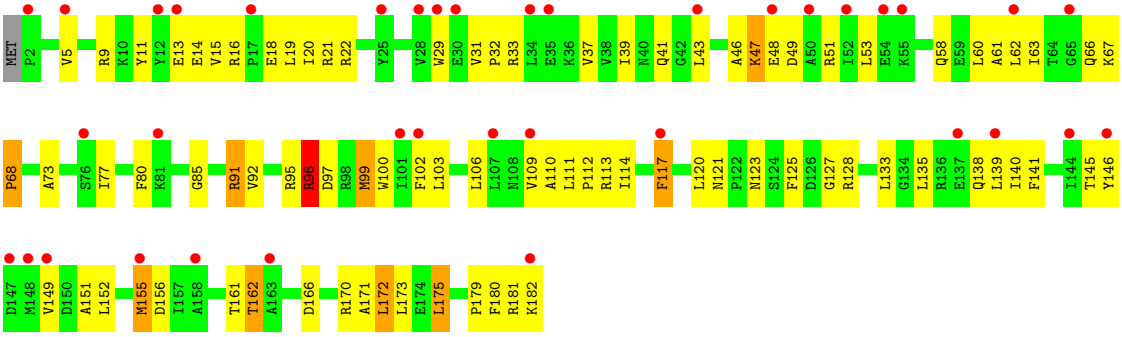
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



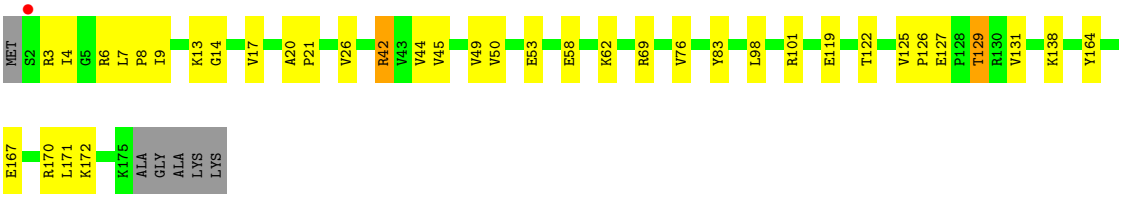
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



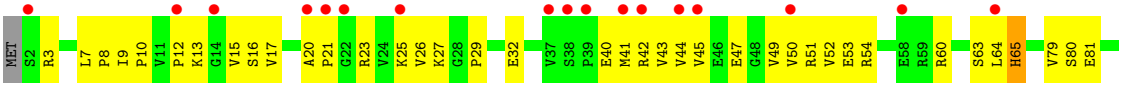
• Molecule 7: 50S ribosomal protein L6

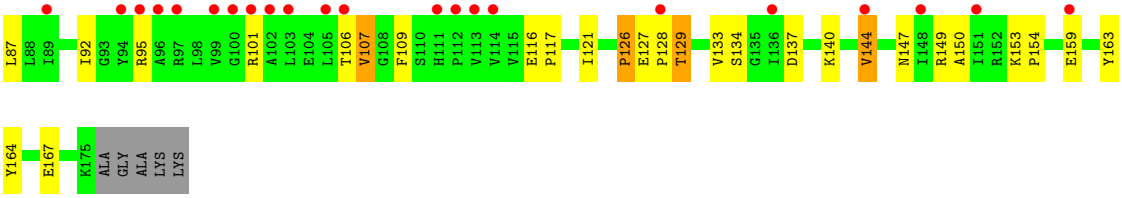
Chain 1H:



• Molecule 7: 50S ribosomal protein L6

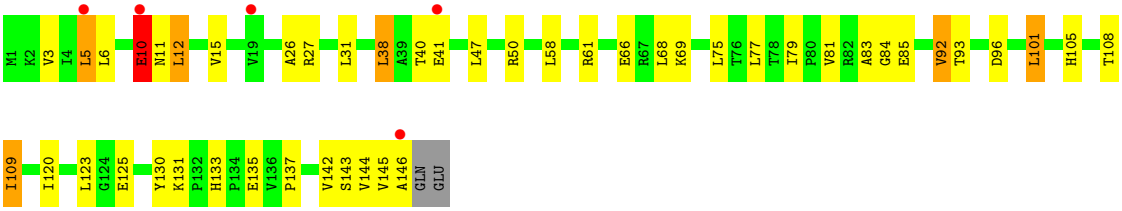
Chain 2H:





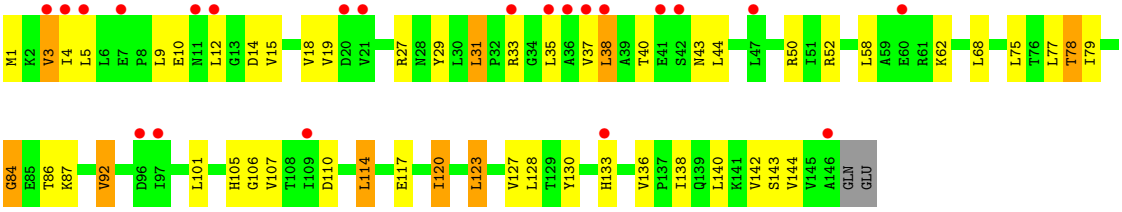
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



• Molecule 8: 50S ribosomal protein L9

Chain 2I:

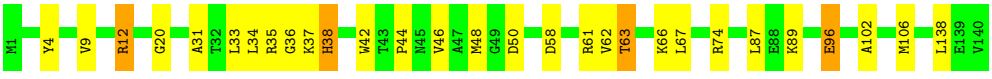


• Molecule 9: 50S ribosomal protein L13

Chain 1N:

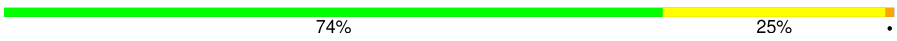
• Molecule 9: 50S ribosomal protein L13

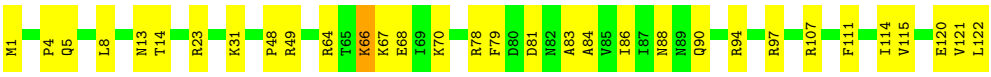
Chain 2N:



• Molecule 10: 50S ribosomal protein L14

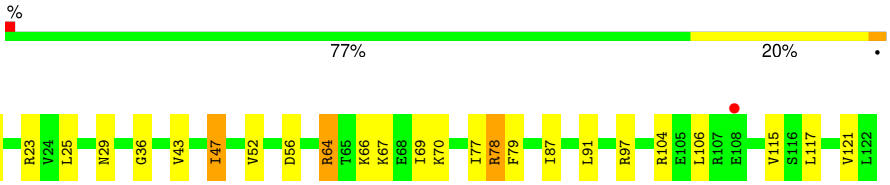
Chain 1O:





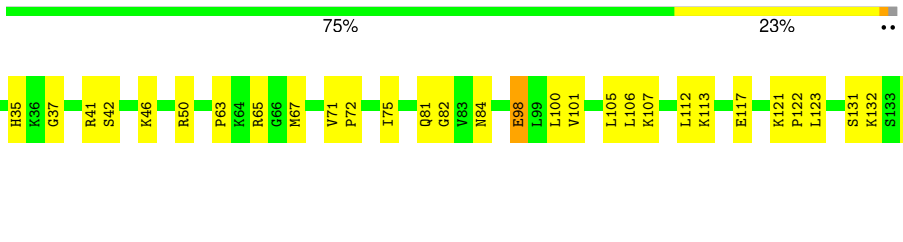
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



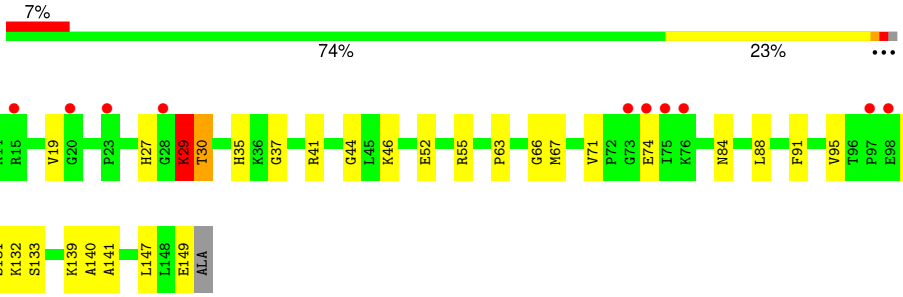
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



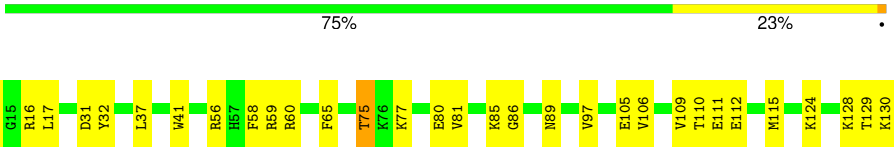
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



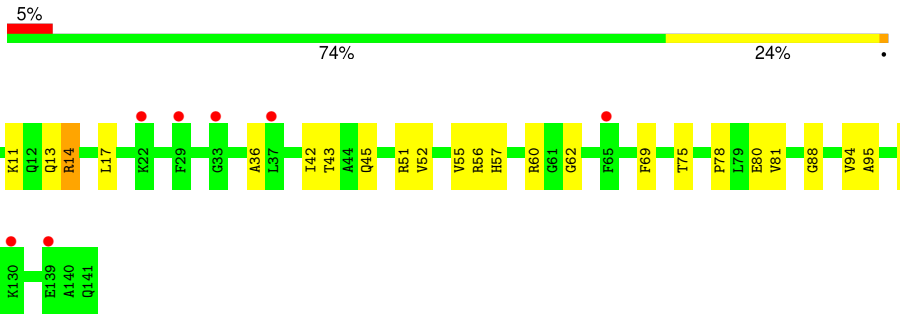
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



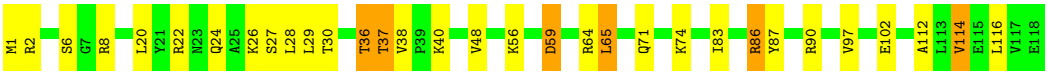
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



• Molecule 13: 50S ribosomal protein L17

Chain 1R:

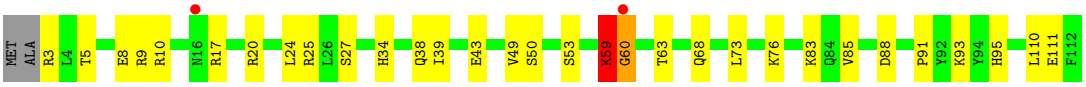


• Molecule 13: 50S ribosomal protein L17

Chain 2R:

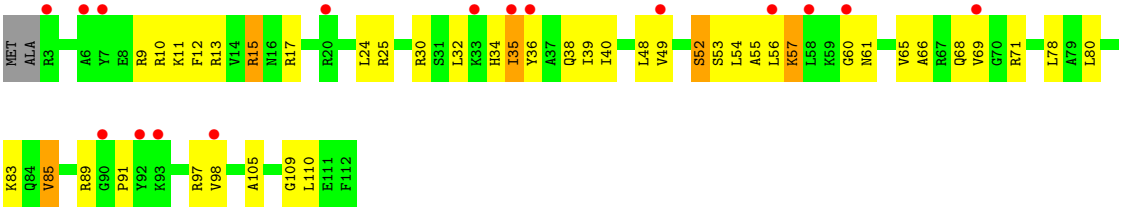
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



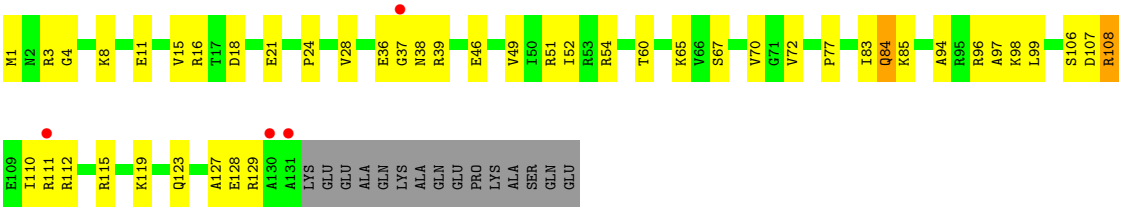
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



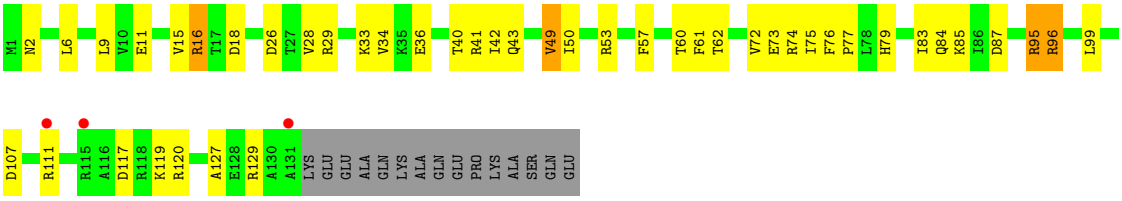
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



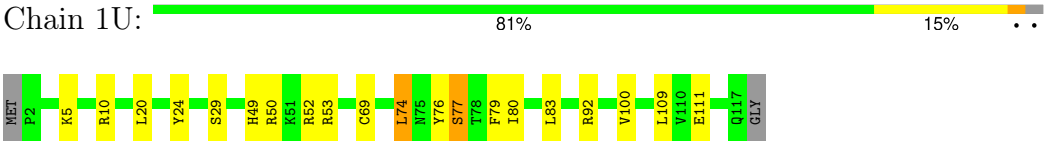
• Molecule 15: 50S ribosomal protein L19

Chain 2T:



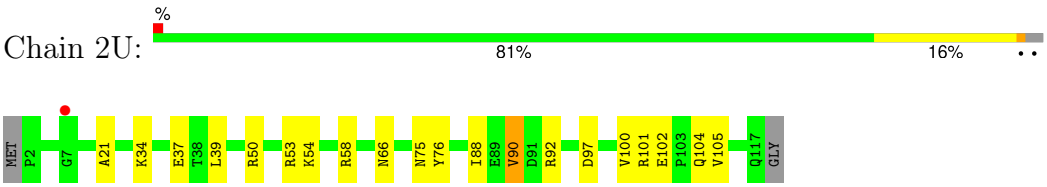
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



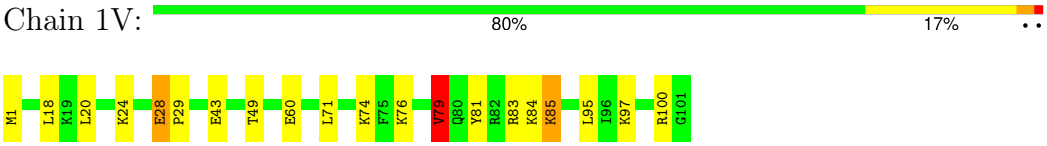
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



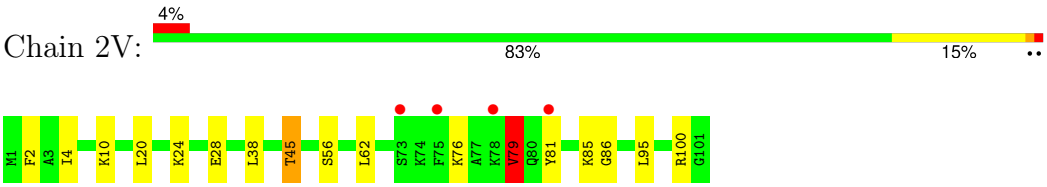
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



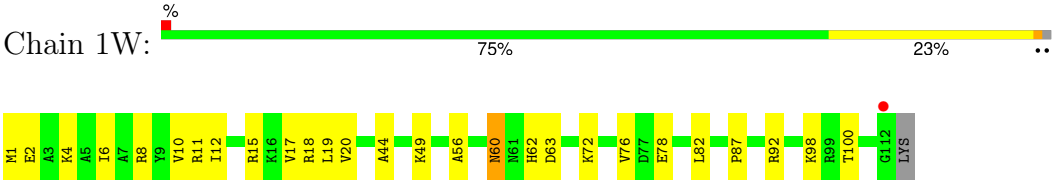
• Molecule 17: 50S ribosomal protein L21

Chain 2V:



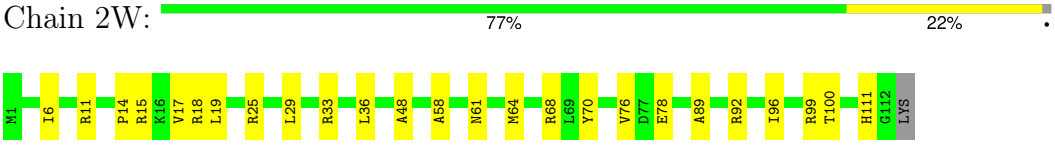
• Molecule 18: 50S ribosomal protein L22

Chain 1W:



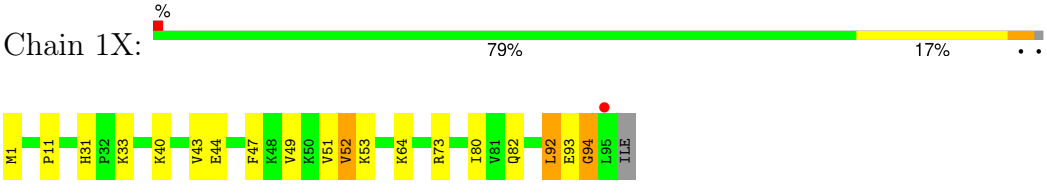
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



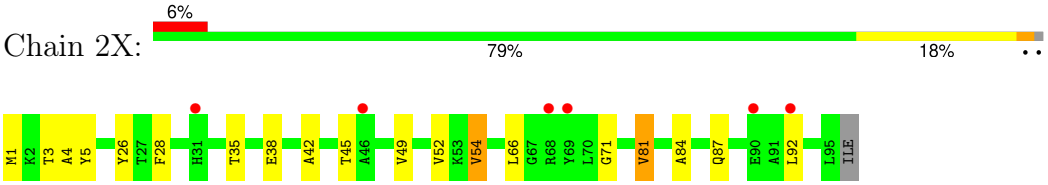
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



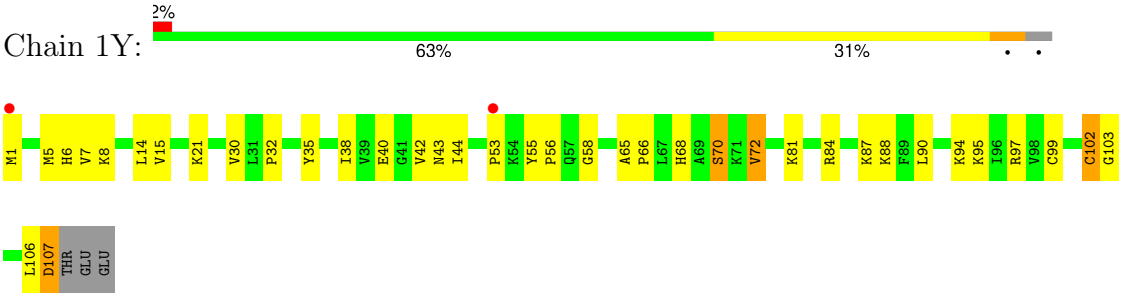
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



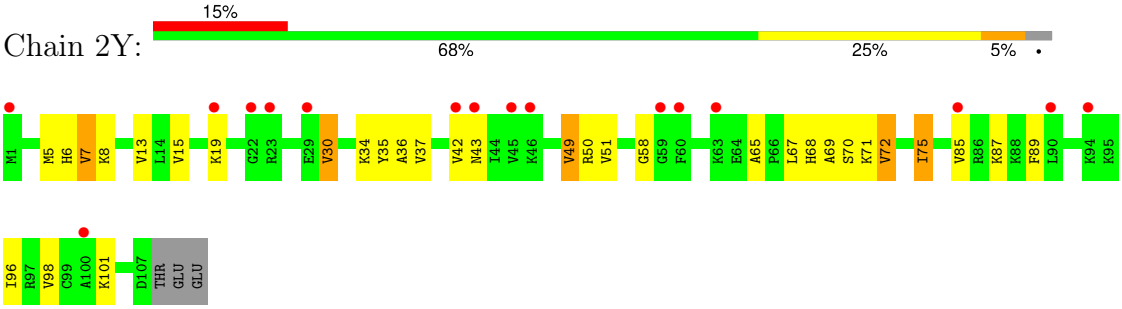
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



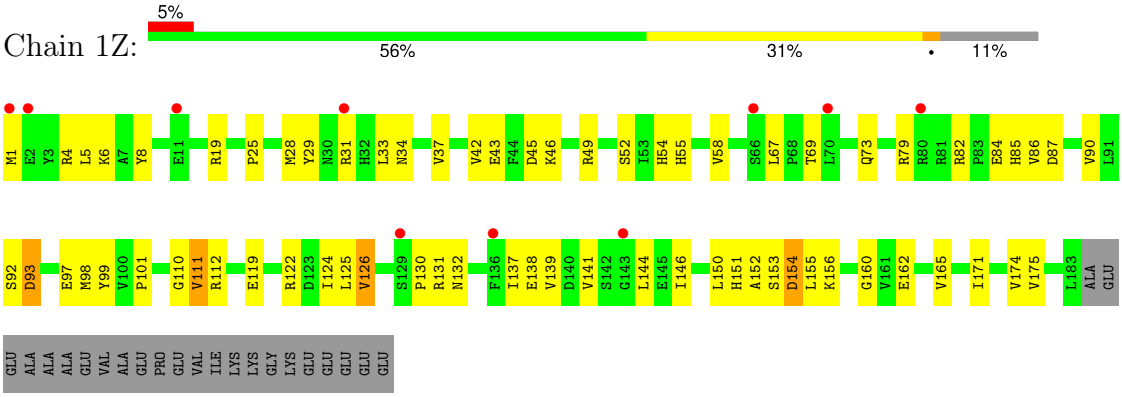
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



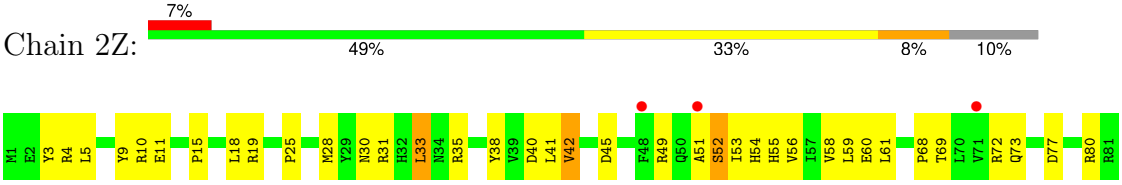
• Molecule 21: 50S ribosomal protein L25

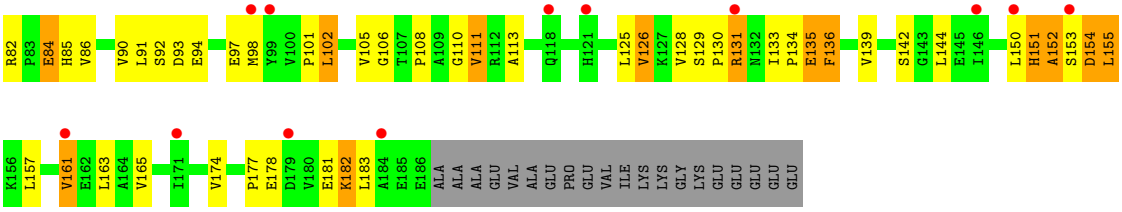
Chain 1Z:



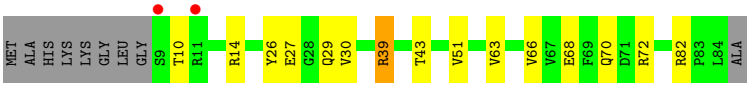
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:

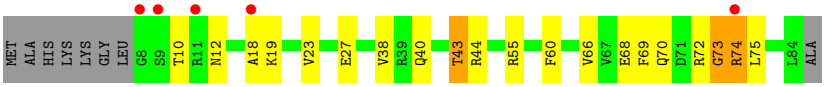




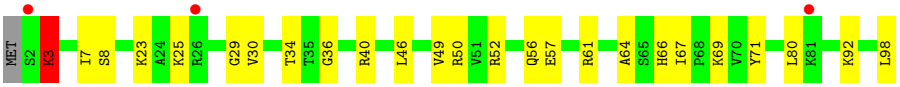
• Molecule 22: 50S ribosomal protein L27



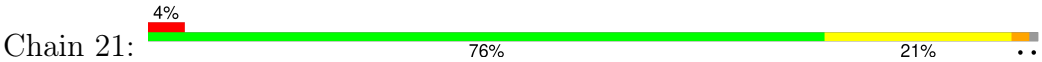
• Molecule 22: 50S ribosomal protein L27

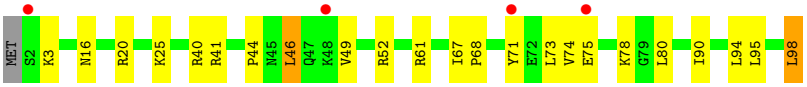


• Molecule 23: 50S ribosomal protein L28

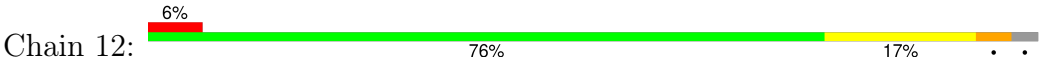


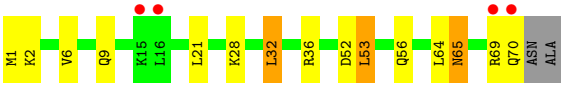
• Molecule 23: 50S ribosomal protein L28



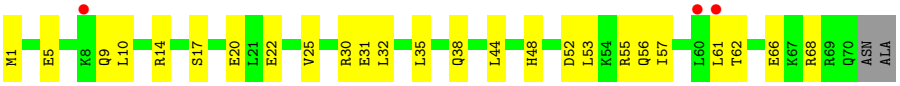


• Molecule 24: 50S ribosomal protein L29



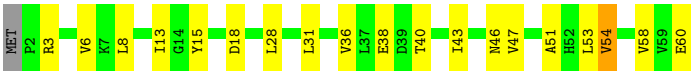


• Molecule 24: 50S ribosomal protein L29



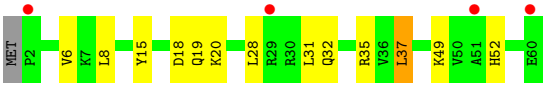
• Molecule 25: 50S ribosomal protein L30

Chain 13:



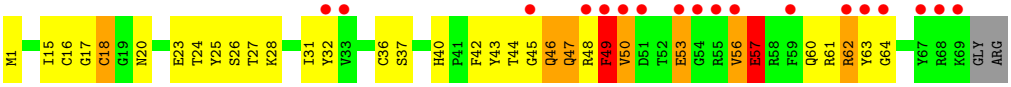
• Molecule 25: 50S ribosomal protein L30

Chain 23:



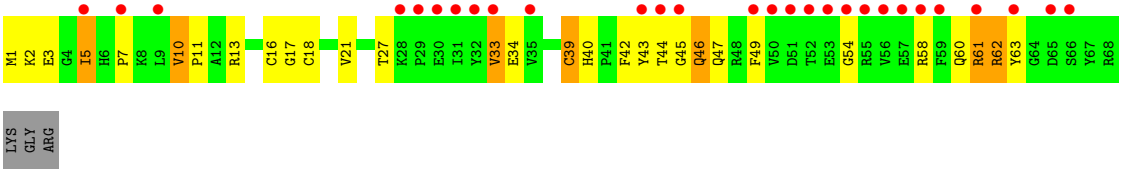
• Molecule 26: 50S ribosomal protein L31

Chain 14:



• Molecule 26: 50S ribosomal protein L31

Chain 24:

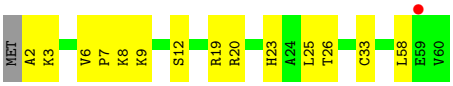


• Molecule 27: 50S ribosomal protein L32

Chain 15:

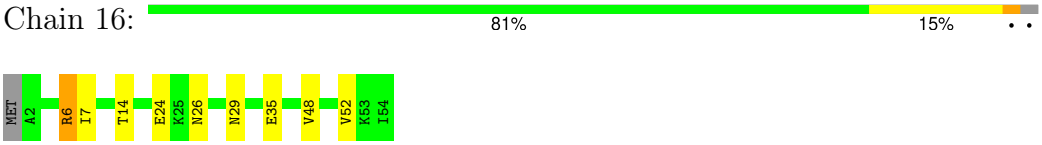
• Molecule 27: 50S ribosomal protein L32

Chain 25:



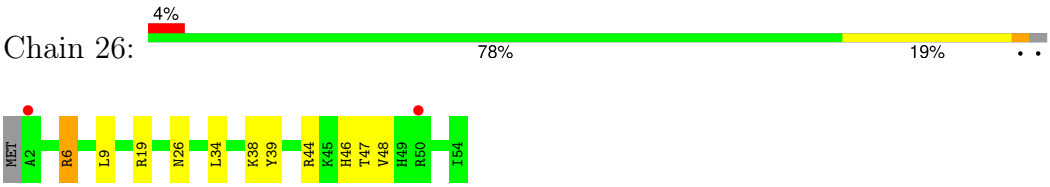
• Molecule 28: 50S ribosomal protein L33

Chain 16:



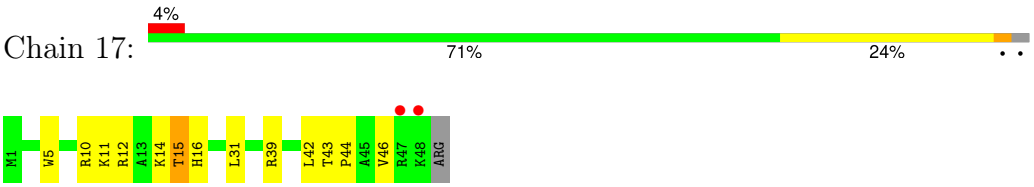
• Molecule 28: 50S ribosomal protein L33

Chain 26:



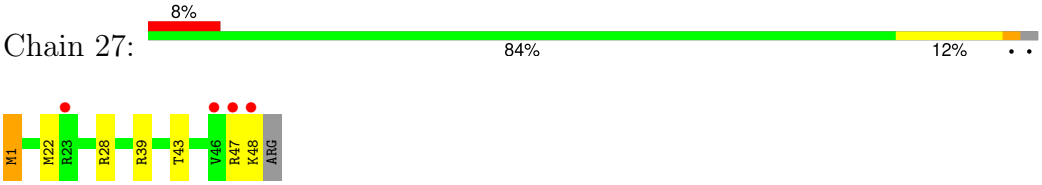
• Molecule 29: 50S ribosomal protein L34

Chain 17:



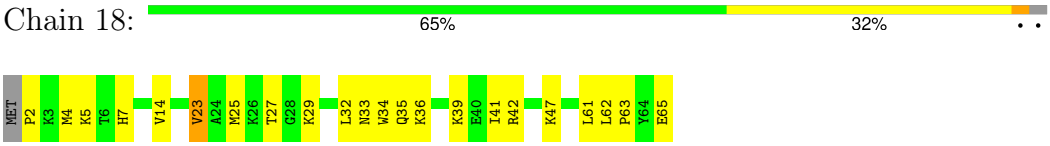
• Molecule 29: 50S ribosomal protein L34

Chain 27:



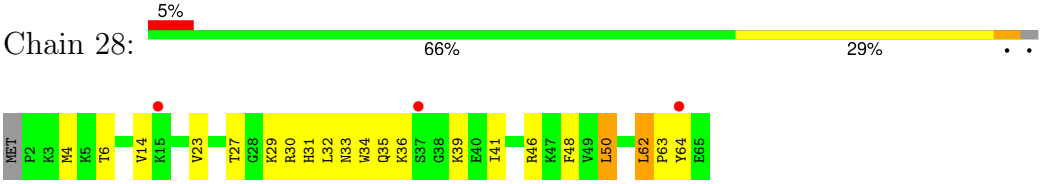
• Molecule 30: 50S ribosomal protein L35

Chain 18:



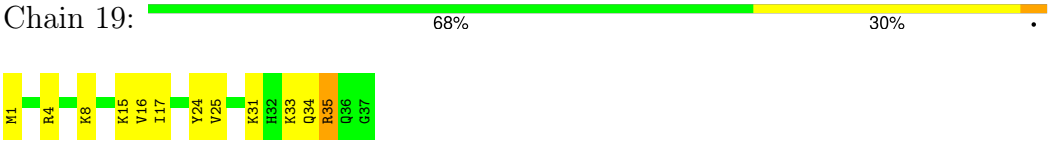
• Molecule 30: 50S ribosomal protein L35

Chain 28:



• Molecule 31: 50S ribosomal protein L36

Chain 19:

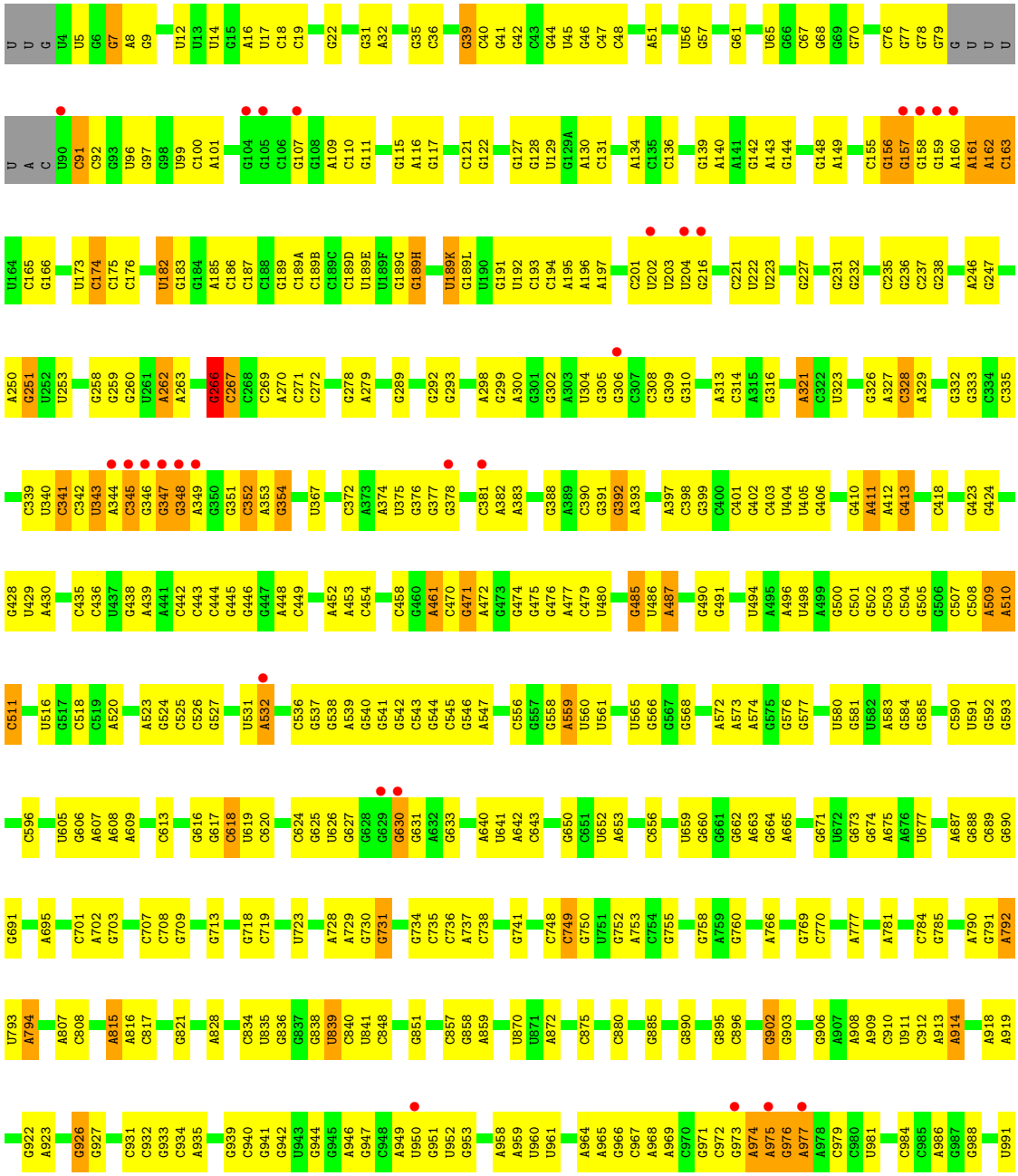


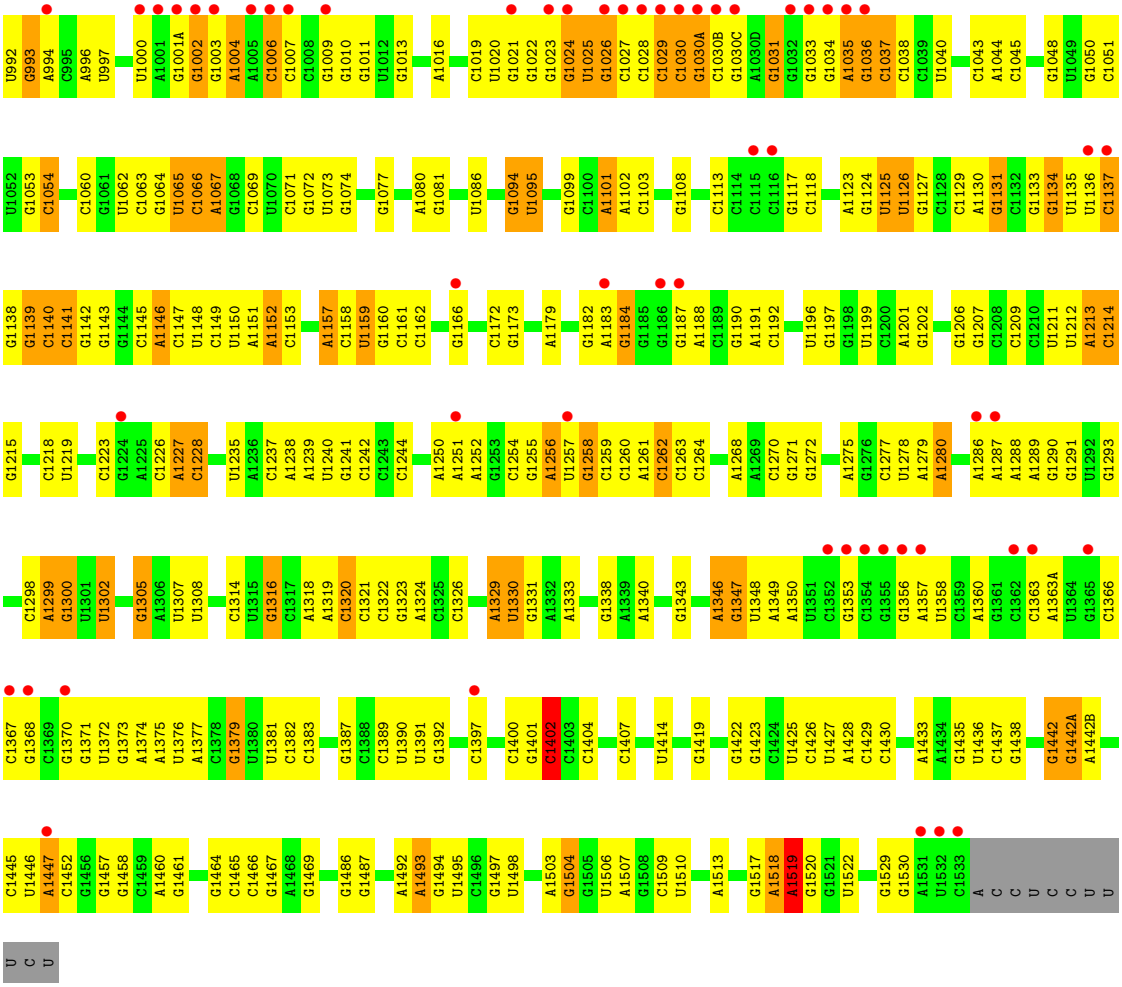
• Molecule 31: 50S ribosomal protein L36

Chain 29:

• Molecule 32: 16S Ribosomal RNA

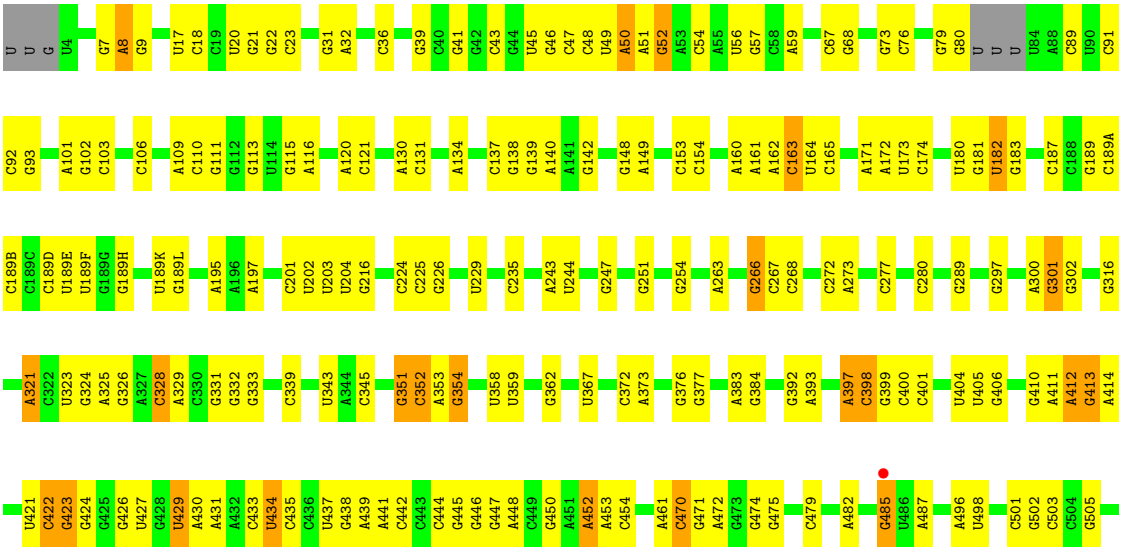
Chain 1a:

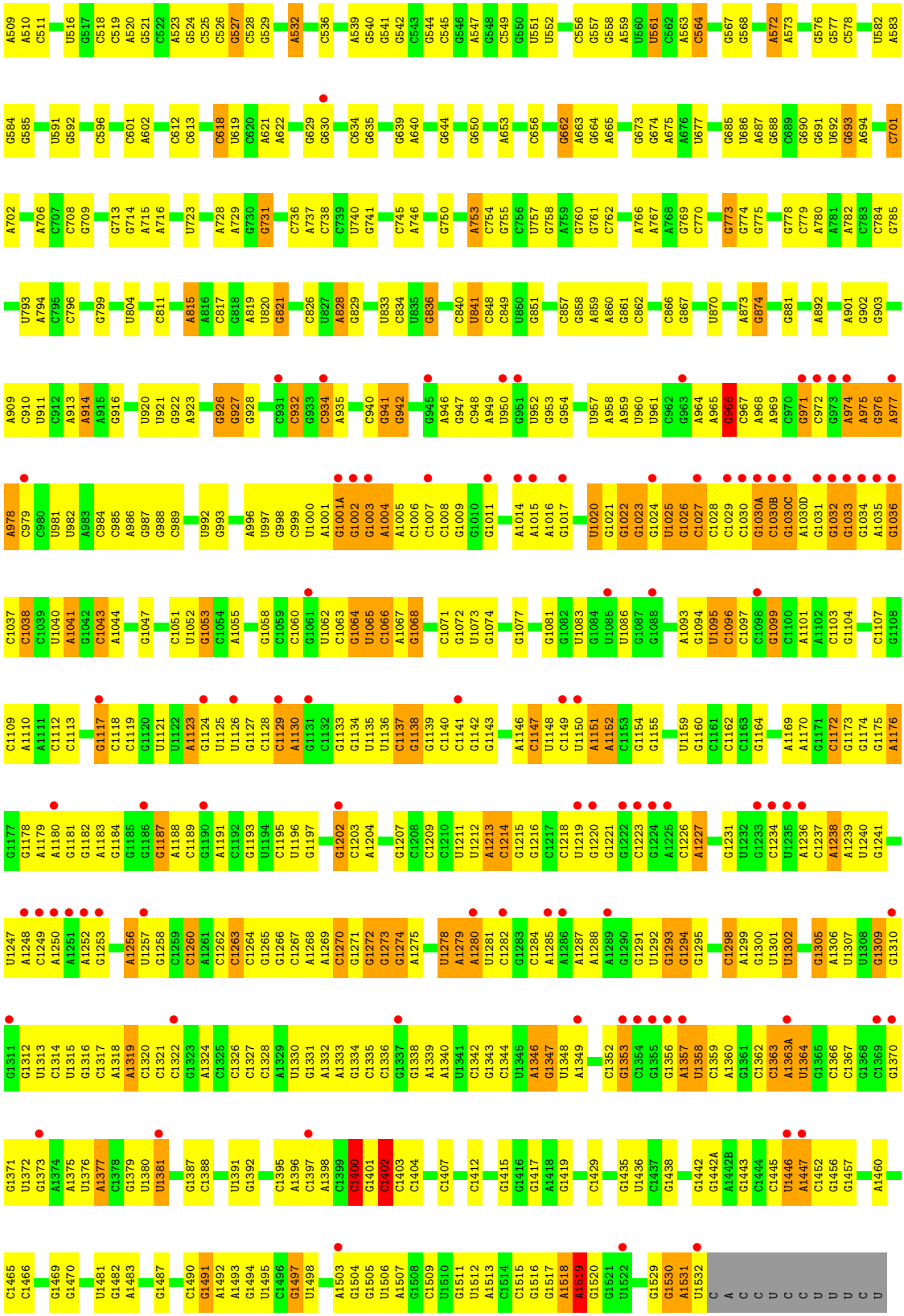




• Molecule 32: 16S Ribosomal RNA

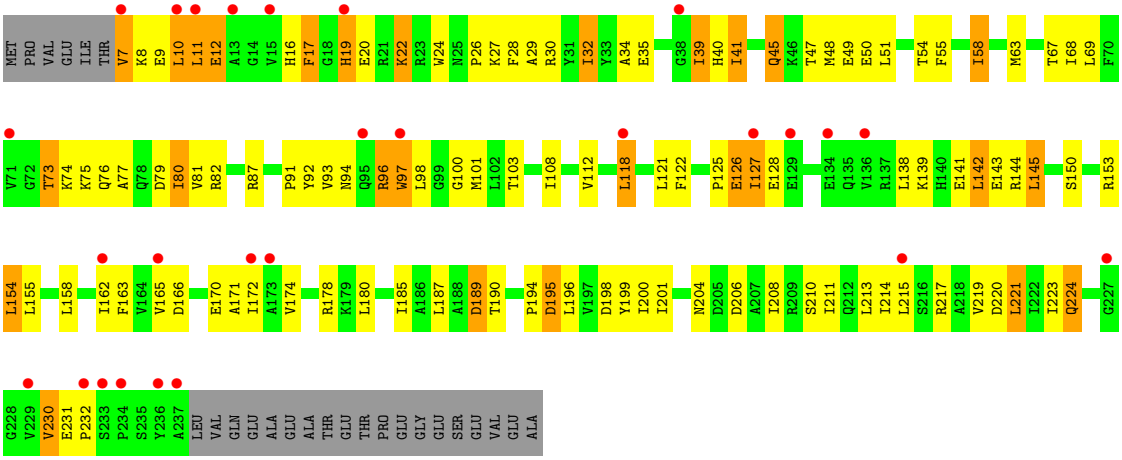
Chain 2a:





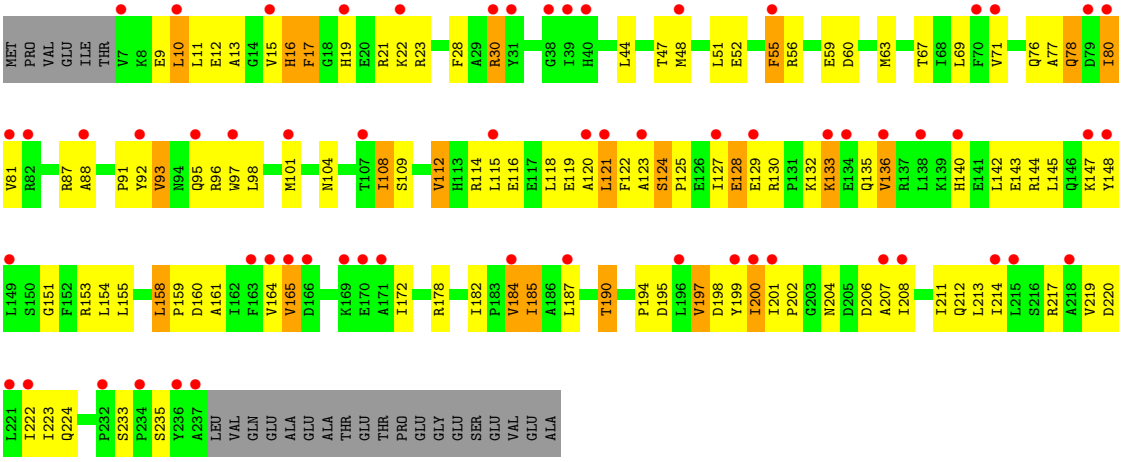
• Molecule 33: 30S ribosomal protein S2

Chain 1b:



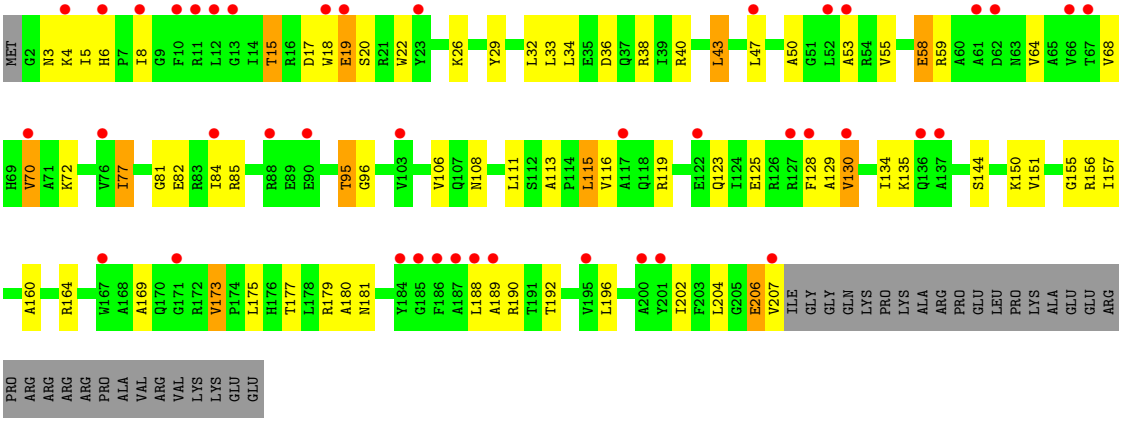
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



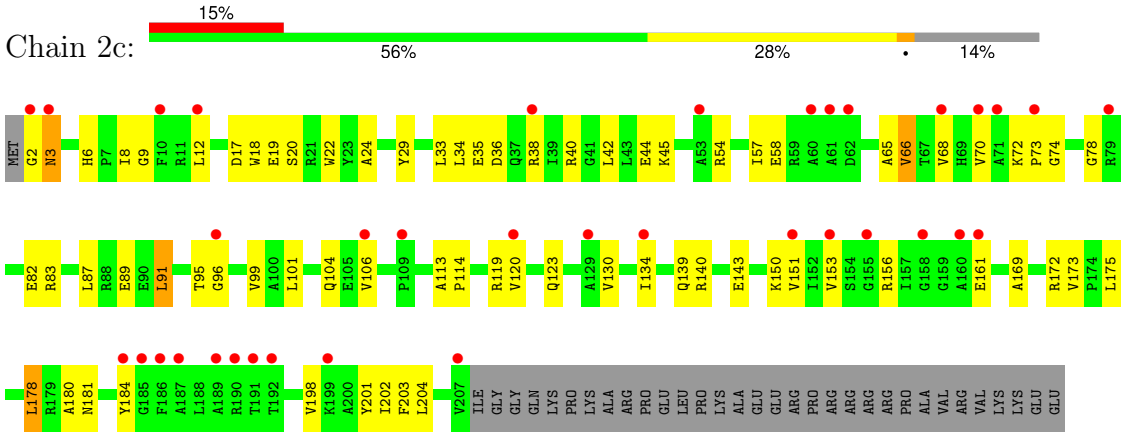
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



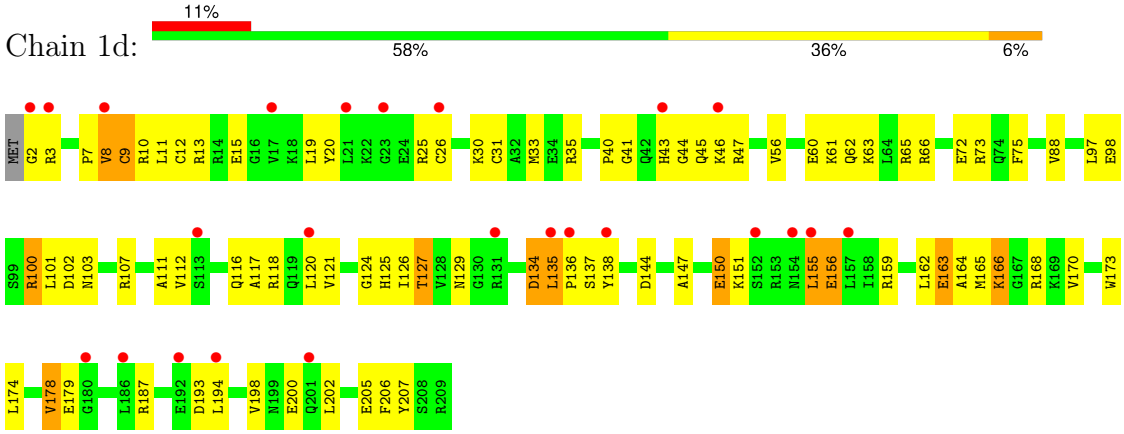
• Molecule 34: 30S ribosomal protein S3

Chain 2c:



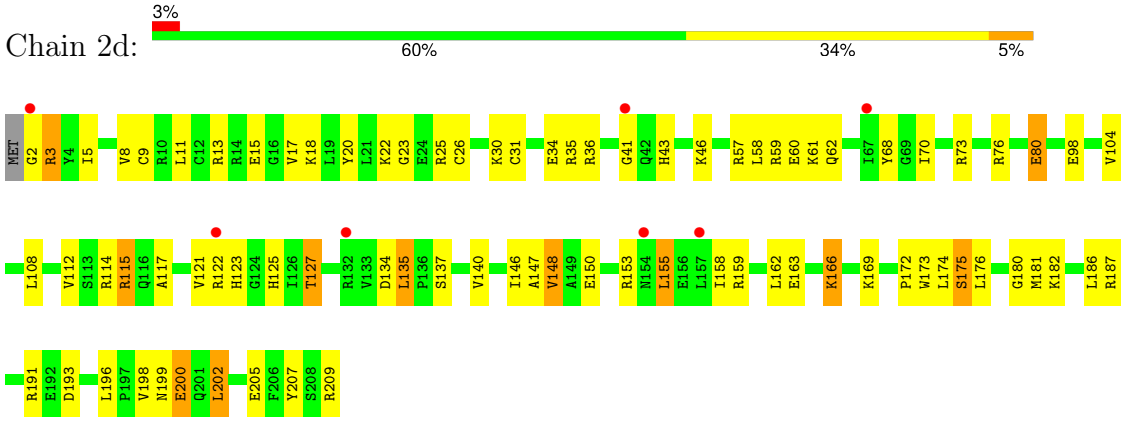
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



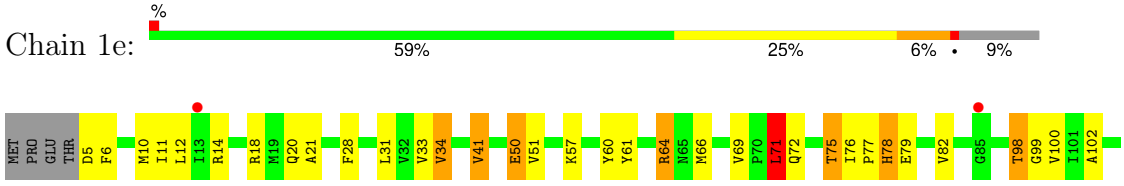
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



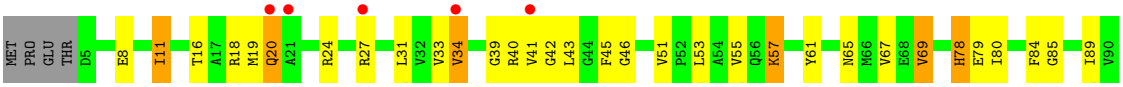
• Molecule 36: 30S ribosomal protein S5

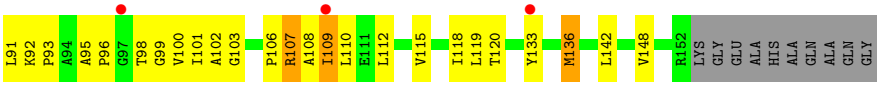
Chain 1e:



• Molecule 36: 30S ribosomal protein S5

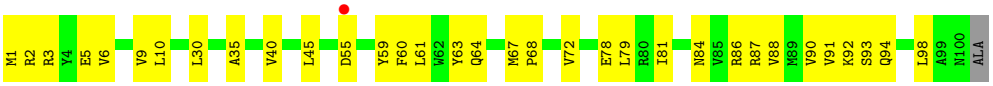
Chain 2e:





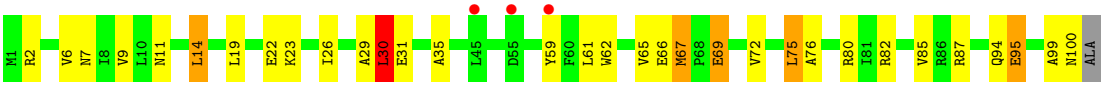
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



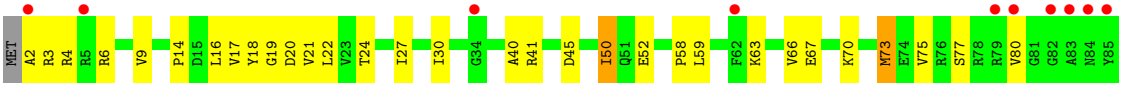
• Molecule 37: 30S ribosomal protein S6

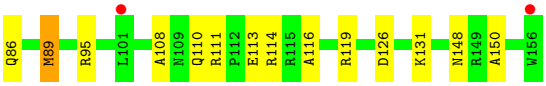
Chain 2f:



• Molecule 38: 30S ribosomal protein S7

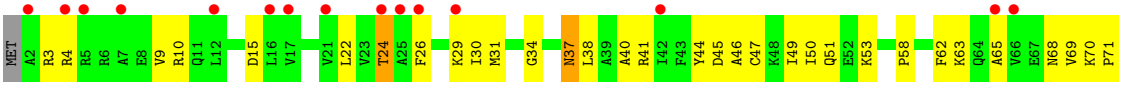
Chain 1g:

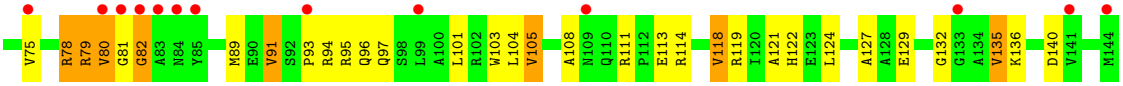


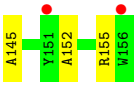


• Molecule 38: 30S ribosomal protein S7

Chain 2g:

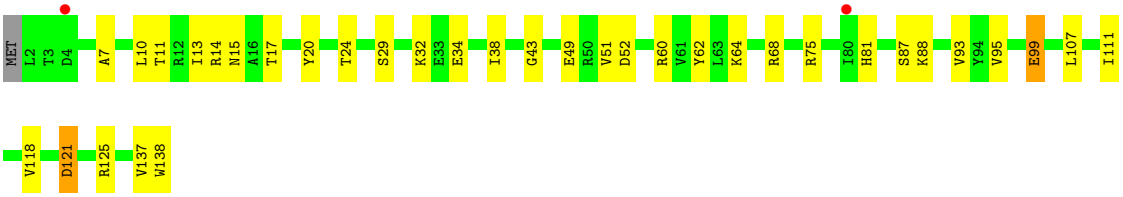






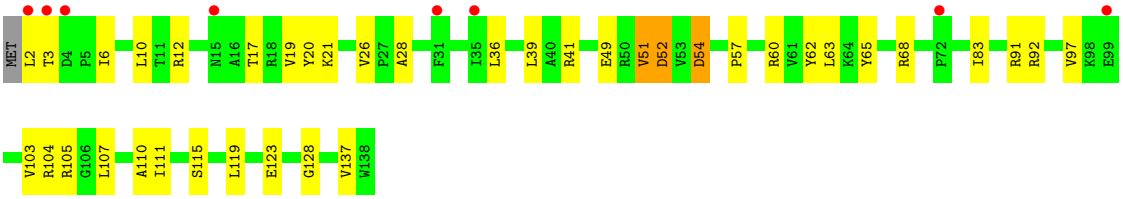
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



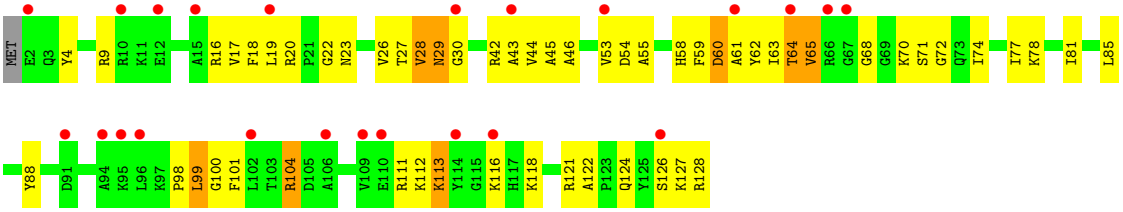
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



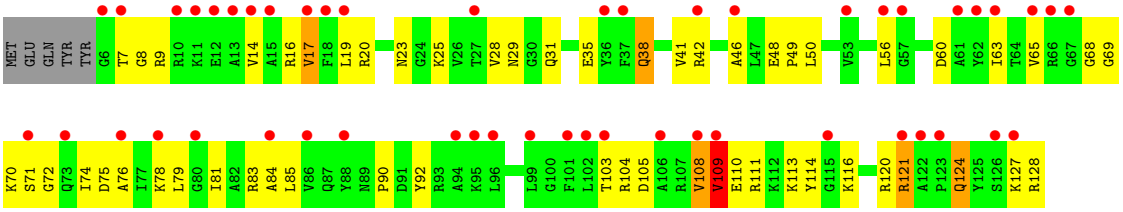
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



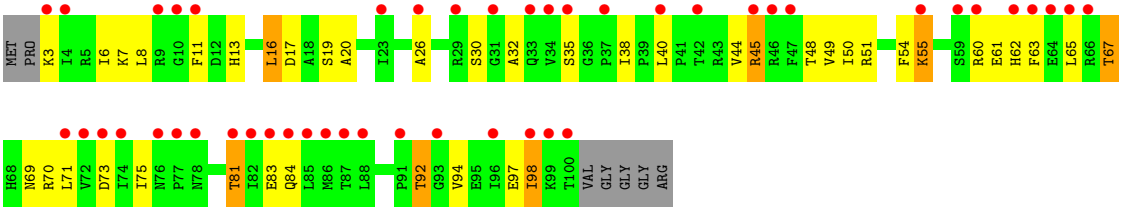
• Molecule 40: 30S ribosomal protein S9

Chain 2i:

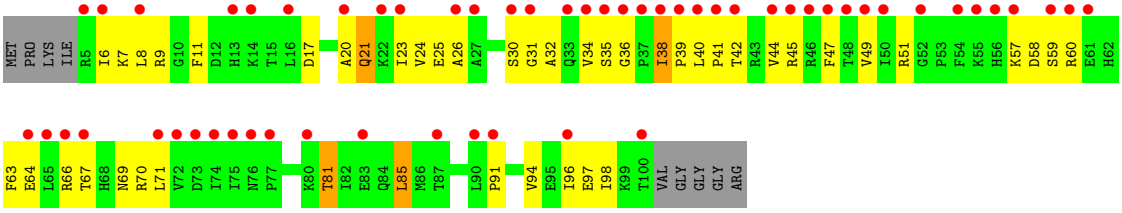


• Molecule 41: 30S ribosomal protein S10

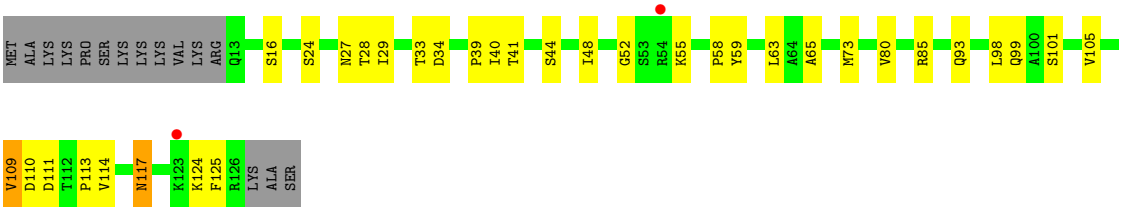
Chain 1j:



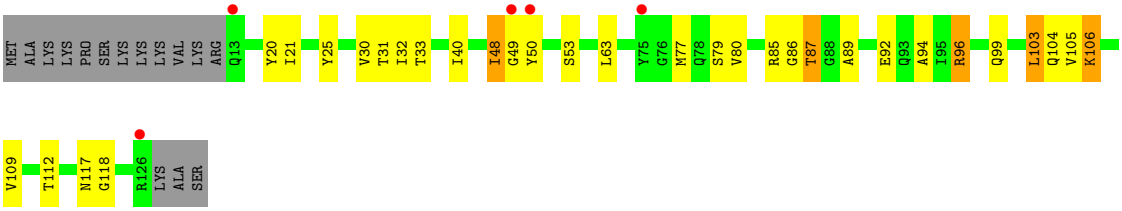
• Molecule 41: 30S ribosomal protein S10



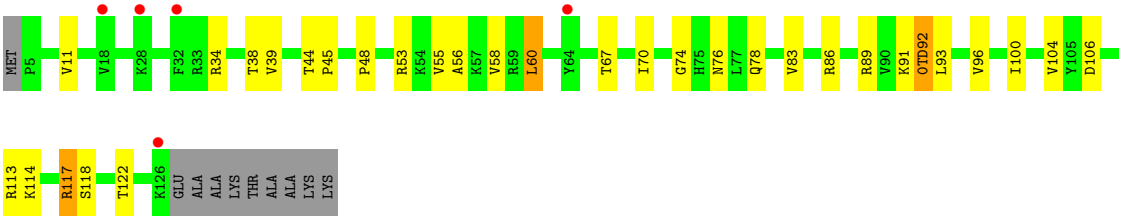
• Molecule 42: 30S ribosomal protein S11



• Molecule 42: 30S ribosomal protein S11

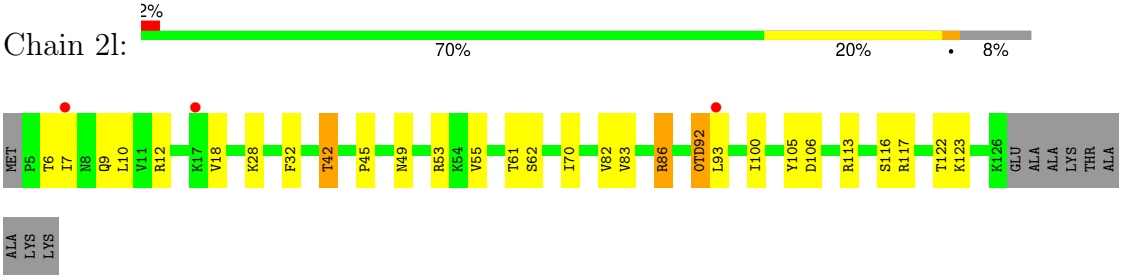


• Molecule 43: 30S ribosomal protein S12



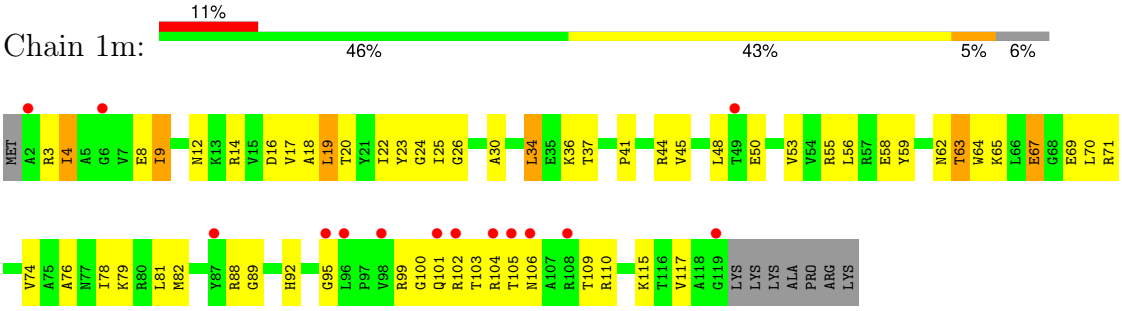
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



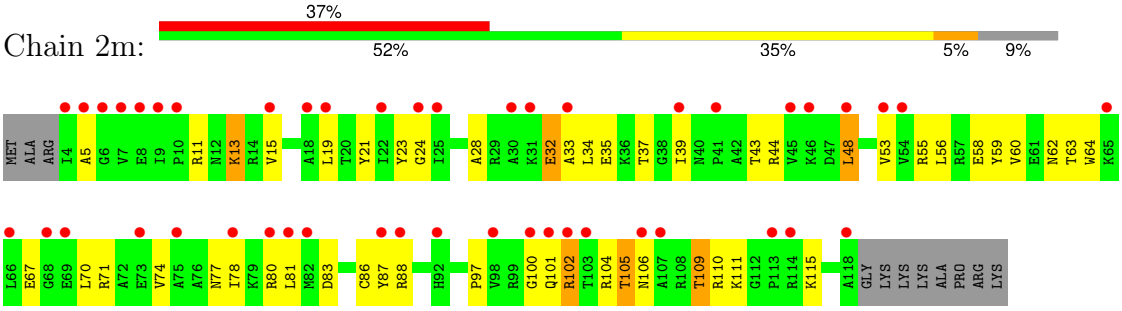
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



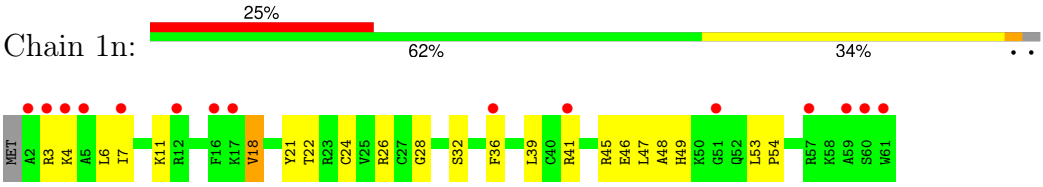
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



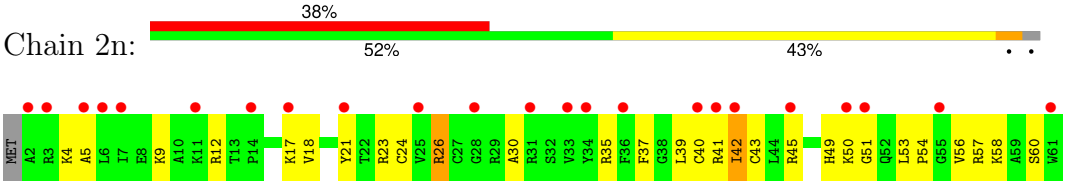
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:

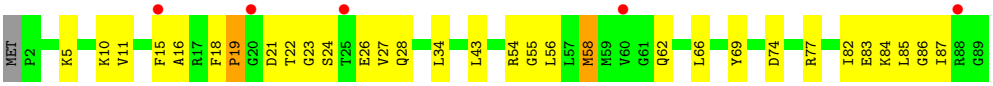


• Molecule 46: 30S ribosomal protein S15

Chain 1o:

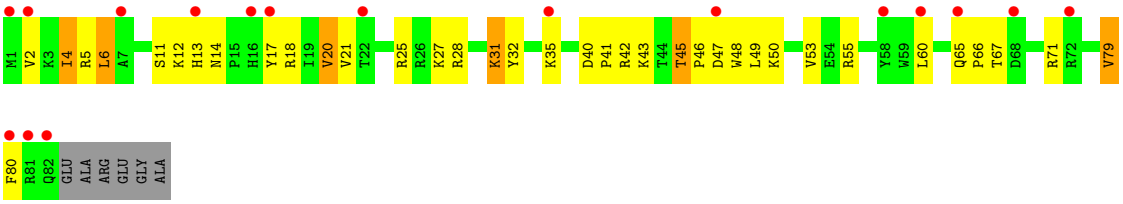
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



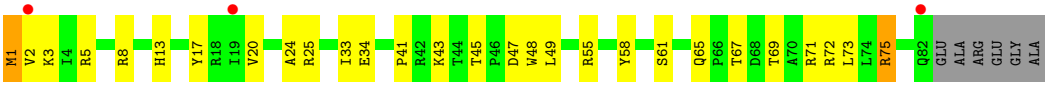
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



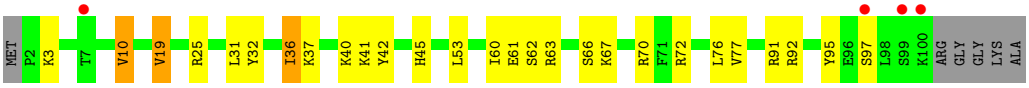
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



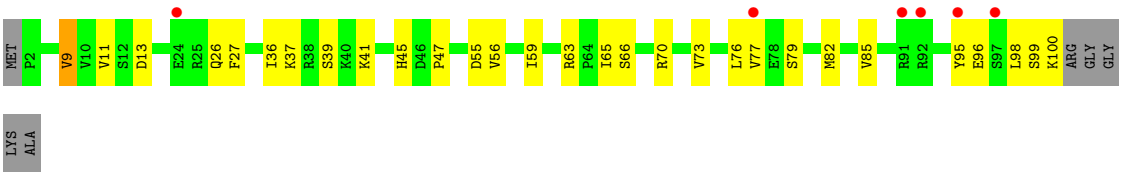
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



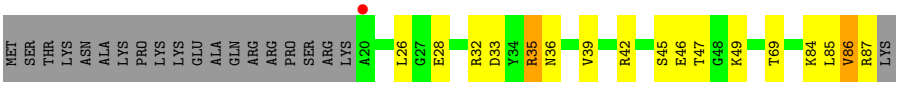
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



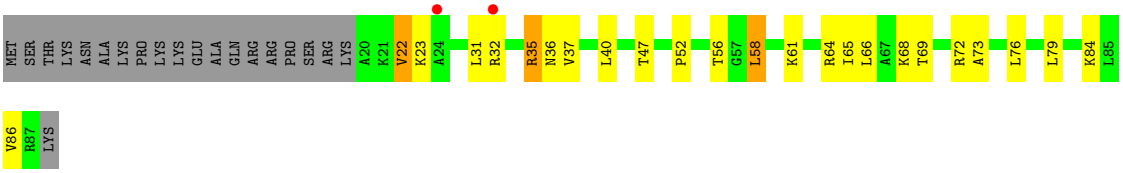
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



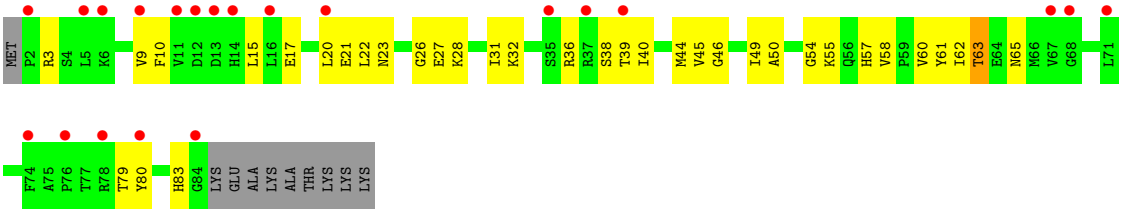
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



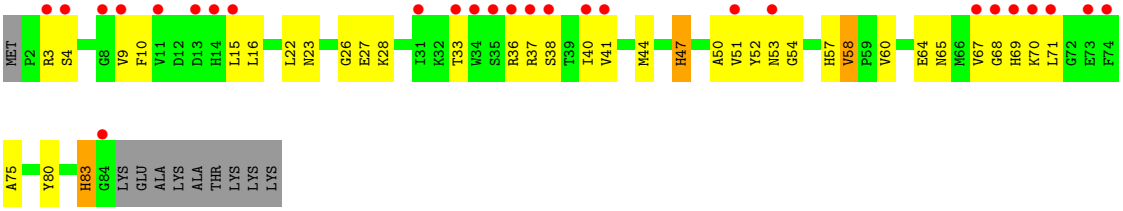
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



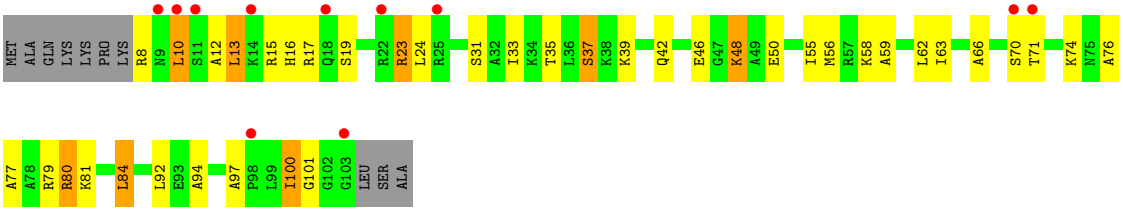
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



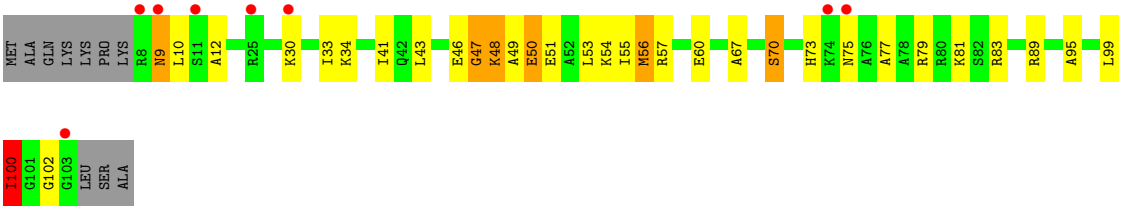
• Molecule 51: 30S ribosomal protein S20

Chain 1t:

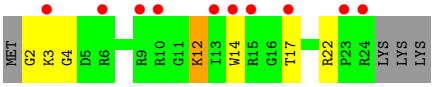


• Molecule 51: 30S ribosomal protein S20

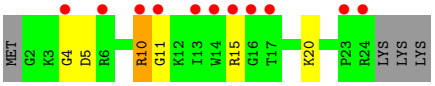
Chain 2t:



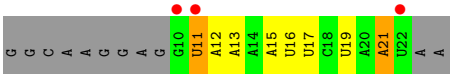
• Molecule 52: 30S ribosomal protein Thx



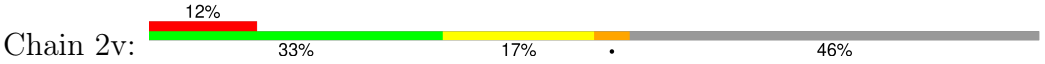
• Molecule 52: 30S ribosomal protein Thx

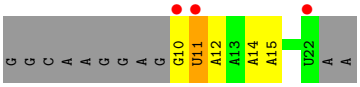


• Molecule 53: PHE-Stop mRNA

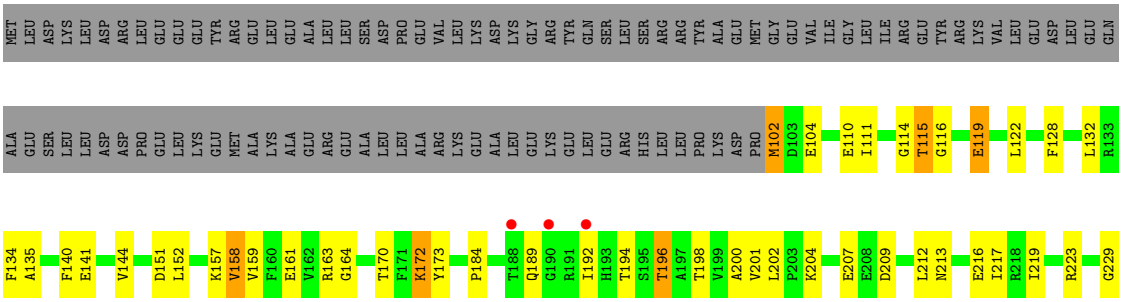


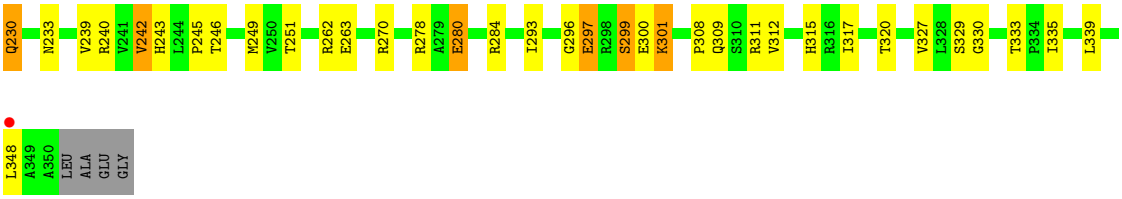
• Molecule 53: PHE-Stop mRNA



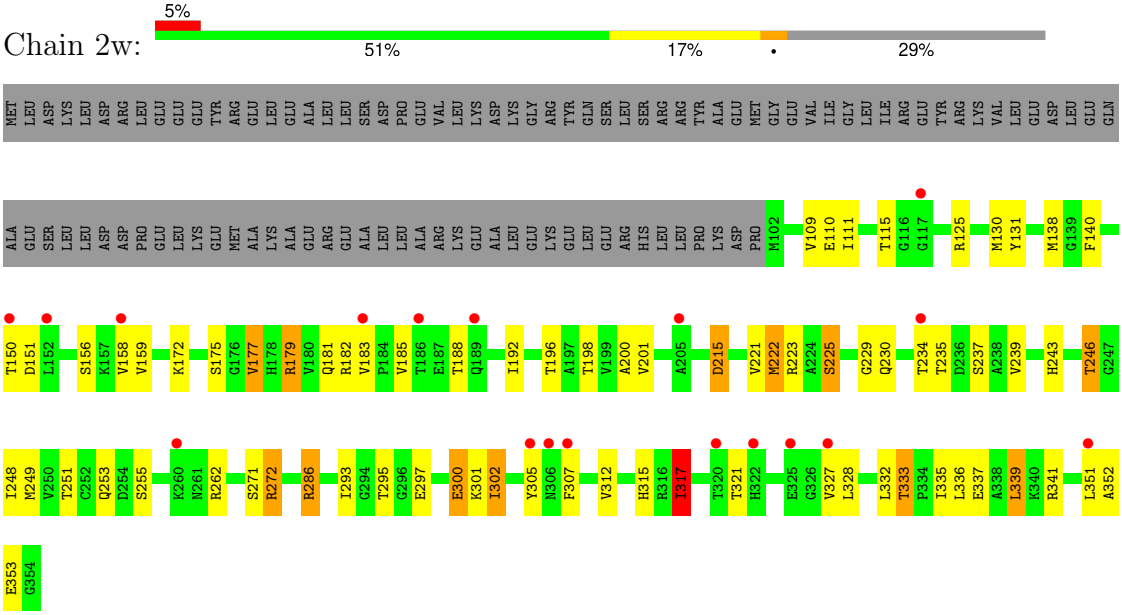


• Molecule 54: Peptide chain release factor 1

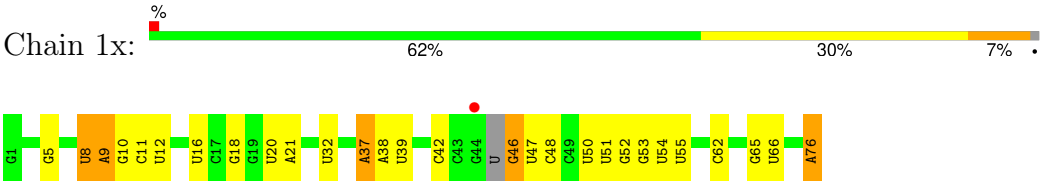




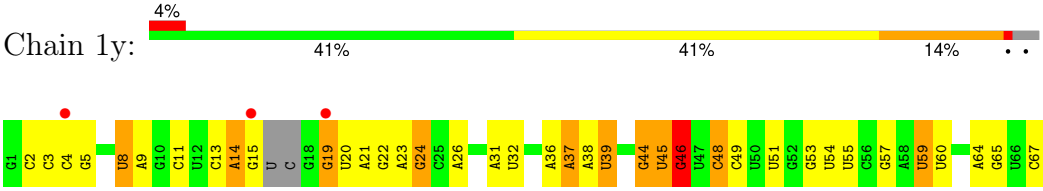
• Molecule 54: Peptide chain release factor 1



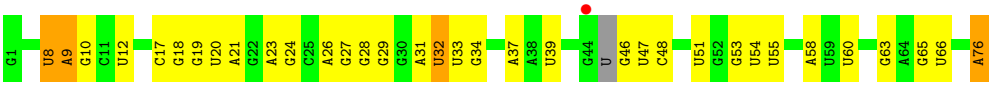
• Molecule 55: P-site and E-site Deacylated tRNAphe



• Molecule 55: P-site and E-site Deacylated tRNAphe

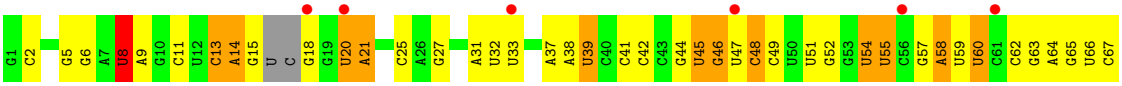


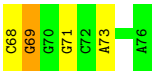
• Molecule 55: P-site and E-site Deacylated tRNAphe



• Molecule 55: P-site and E-site Deacylated tRNAphe

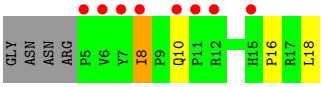
Chain 2y:





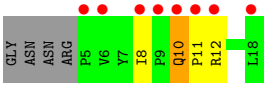
• Molecule 56: Api Antimicrobial Peptide

Chain 1z:



• Molecule 56: Api Antimicrobial Peptide

Chain 2z:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	210.35Å 451.32Å 625.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	102.43 – 2.85 102.43 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.1 (102.43-2.85) 99.1 (102.43-2.85)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.28 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.218 , 0.268 0.220 , 0.267	Depositor DCC
R_{free} test set	68034 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	48.2	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 58.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	299015	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.45% 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: SF4, 4OC, 2MG, MA6, OMG, 5MU, MG, G7M, MIA, 5MC, 4SU, OMU, ZN, OMC, PSU, 0TD, 2MA, UR3, M2G, MEQ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	1A	0.28	0/69011	0.45	1/107720 (0.0%)
1	2A	0.21	0/67295	0.39	1/105042 (0.0%)
2	1B	0.21	0/2881	0.38	0/4494
2	2B	0.18	0/2881	0.33	0/4494
3	1D	0.26	0/2186	0.50	0/2944
3	2D	0.22	0/2186	0.44	0/2944
4	1E	0.28	0/1592	0.49	0/2149
4	2E	0.21	0/1592	0.44	0/2149
5	1F	0.27	0/1619	0.51	0/2193
5	2F	0.21	0/1615	0.46	0/2188
6	1G	0.20	0/1450	0.44	0/1959
6	2G	0.21	0/1449	0.45	0/1958
7	1H	0.22	0/1356	0.43	0/1834
7	2H	0.18	0/1356	0.37	0/1834
8	1I	0.21	0/1100	0.49	1/1501 (0.1%)
8	2I	0.19	0/1076	0.44	0/1471
9	1N	0.27	0/1144	0.46	0/1543
9	2N	0.18	0/1144	0.39	0/1543
10	1O	0.28	0/943	0.50	0/1269
10	2O	0.21	0/943	0.42	0/1269
11	1P	0.26	0/1152	0.55	0/1533
11	2P	0.20	0/1152	0.44	0/1533
12	1Q	0.25	0/1143	0.48	0/1527
12	2Q	0.19	0/1143	0.41	0/1527
13	1R	0.27	0/982	0.52	0/1312
13	2R	0.20	0/982	0.45	0/1312
14	1S	0.22	0/887	0.55	1/1180 (0.1%)
14	2S	0.21	0/880	0.46	0/1172
15	1T	0.26	0/1105	0.48	0/1477
15	2T	0.20	0/1097	0.47	0/1468
16	1U	0.30	0/977	0.46	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.20	0/977	0.38	0/1301
17	1V	0.25	0/782	0.45	0/1049
17	2V	0.20	0/782	0.43	0/1049
18	1W	0.29	0/897	0.48	0/1205
18	2W	0.22	0/897	0.47	0/1205
19	1X	0.24	0/764	0.44	0/1025
19	2X	0.21	0/760	0.38	0/1021
20	1Y	0.24	0/819	0.50	0/1095
20	2Y	0.21	0/823	0.47	0/1100
21	1Z	0.21	0/1469	0.47	0/1998
21	2Z	0.19	0/1483	0.42	0/2018
22	10	0.25	0/612	0.53	0/816
22	20	0.21	0/616	0.48	0/821
23	11	0.23	0/762	0.41	0/1014
23	21	0.23	0/762	0.45	0/1014
24	12	0.25	0/590	0.38	0/781
24	22	0.18	0/590	0.36	0/781
25	13	0.27	0/474	0.48	0/635
25	23	0.21	0/469	0.40	0/630
26	14	0.25	0/561	0.61	0/756
26	24	0.28	0/530	0.66	1/719 (0.1%)
27	15	0.29	0/469	0.53	0/635
27	25	0.22	0/469	0.41	0/635
28	16	0.23	0/460	0.46	0/613
28	26	0.20	0/456	0.41	0/608
29	17	0.31	0/426	0.53	0/561
29	27	0.25	0/426	0.50	0/561
30	18	0.28	0/519	0.47	0/684
30	28	0.18	0/525	0.39	0/691
31	19	0.27	0/310	0.45	0/407
31	29	0.21	0/310	0.43	0/407
32	1a	0.20	0/35795	0.38	2/55864 (0.0%)
32	2a	0.20	0/35886	0.38	0/56005
33	1b	0.21	0/1881	0.48	0/2542
33	2b	0.24	0/1860	0.54	1/2518 (0.0%)
34	1c	0.19	0/1578	0.43	1/2133 (0.0%)
34	2c	0.20	0/1566	0.46	1/2119 (0.0%)
35	1d	0.19	0/1689	0.42	0/2267
35	2d	0.21	0/1704	0.43	0/2284
36	1e	0.20	0/1145	0.46	0/1543
36	2e	0.21	0/1146	0.45	0/1545
37	1f	0.20	0/823	0.45	0/1116
37	2f	0.19	0/829	0.39	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.21	0/1250	0.41	0/1679
38	2g	0.20	0/1254	0.45	0/1683
39	1h	0.19	0/1108	0.41	0/1494
39	2h	0.20	0/1108	0.42	0/1494
40	1i	0.21	0/1002	0.51	0/1346
40	2i	0.25	0/957	0.51	0/1288
41	1j	0.21	0/734	0.43	0/997
41	2j	0.22	0/727	0.44	0/988
42	1k	0.19	0/844	0.38	0/1145
42	2k	0.19	0/848	0.39	0/1149
43	1l	0.21	0/937	0.43	0/1260
43	2l	0.21	0/937	0.45	0/1260
44	1m	0.21	0/933	0.51	0/1254
44	2m	0.21	0/899	0.49	0/1212
45	1n	0.20	0/501	0.47	0/664
45	2n	0.21	0/495	0.44	0/657
46	1o	0.20	0/739	0.40	0/985
46	2o	0.18	0/739	0.37	0/985
47	1p	0.20	0/697	0.45	0/939
47	2p	0.21	0/693	0.45	0/935
48	1q	0.19	0/836	0.41	0/1117
48	2q	0.19	0/836	0.40	0/1117
49	1r	0.19	0/560	0.44	0/746
49	2r	0.21	0/556	0.47	0/741
50	1s	0.21	0/667	0.43	0/900
50	2s	0.19	0/661	0.40	0/893
51	1t	0.20	0/730	0.46	0/965
51	2t	0.19	0/729	0.41	0/965
52	1u	0.20	0/203	0.48	0/266
52	2u	0.19	0/203	0.44	0/266
53	1v	0.24	0/306	0.41	0/473
53	2v	0.22	0/306	0.38	0/473
54	1w	0.20	0/1956	0.41	0/2634
54	2w	0.19	0/1974	0.38	0/2657
55	1x	0.28	1/1629 (0.1%)	0.40	0/2535
55	1y	0.26	1/1602 (0.1%)	0.35	0/2488
55	2x	0.26	2/1629 (0.1%)	0.35	0/2535
55	2y	0.28	1/1606 (0.1%)	0.35	0/2497
56	1z	0.25	0/126	0.43	0/173
56	2z	0.23	0/126	0.41	0/173
All	All	0.23	5/317653 (0.0%)	0.42	10/474762 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
11	1P	0	1
11	2P	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2y	46	G7M	O3'-P	5.59	1.61	1.56
55	2x	46	G7M	O3'-P	5.35	1.61	1.56
55	1y	46	G7M	O3'-P	5.22	1.61	1.56
55	1x	8	4SU	O3'-P	5.11	1.61	1.56
55	2x	8	4SU	O3'-P	5.08	1.61	1.56

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	24	54	GLY	N-CA-C	-7.39	105.53	115.36
8	1I	68	LEU	N-CA-C	-7.16	106.46	114.62
14	1S	59	LYS	N-CA-C	6.48	118.42	108.12
34	2c	66	VAL	N-CA-C	6.28	112.93	106.21
34	1c	19	GLU	N-CA-C	-6.17	106.12	113.21
32	1a	266	G	C2'-C3'-O3'	5.86	118.29	109.50
1	2A	1992	G	C2'-C3'-O3'	5.70	118.05	109.50
1	1A	1653	G	C2'-C3'-O3'	5.51	117.77	109.50
32	1a	266	G	P-O3'-C3'	5.18	127.97	120.20
33	2b	30	ARG	N-CA-C	-5.11	107.02	113.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	1P	35	HIS	Peptide
11	2P	35	HIS	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31195	582	0
1	2A	60322	0	30426	659	0
2	1B	2576	0	1305	20	0
2	2B	2576	0	1305	39	0
3	1D	2136	0	2218	41	0
3	2D	2136	0	2218	45	0
4	1E	1559	0	1618	26	0
4	2E	1559	0	1618	38	0
5	1F	1584	0	1624	39	0
5	2F	1580	0	1619	46	0
6	1G	1425	0	1443	32	0
6	2G	1424	0	1434	54	0
7	1H	1330	0	1407	19	0
7	2H	1330	0	1407	35	0
8	1I	1085	0	1114	30	0
8	2I	1061	0	1080	33	0
9	1N	1117	0	1184	17	0
9	2N	1117	0	1184	18	0
10	1O	933	0	996	24	0
10	2O	933	0	996	21	0
11	1P	1135	0	1212	27	0
11	2P	1135	0	1212	28	0
12	1Q	1122	0	1178	19	0
12	2Q	1122	0	1179	21	0
13	1R	968	0	1033	18	0
13	2R	968	0	1033	17	0
14	1S	877	0	938	21	0
14	2S	870	0	923	32	0
15	1T	1091	0	1151	28	0
15	2T	1083	0	1136	30	0
16	1U	959	0	1019	15	0
16	2U	959	0	1019	17	0
17	1V	771	0	830	14	0
17	2V	771	0	830	12	0
18	1W	886	0	940	15	0
18	2W	886	0	940	14	0
19	1X	750	0	814	13	0
19	2X	746	0	803	10	0
20	1Y	806	0	881	23	0
20	2Y	810	0	887	20	0
21	1Z	1437	0	1446	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	2Z	1451	0	1450	54	0
22	10	604	0	619	10	0
22	20	608	0	622	15	0
23	11	755	0	826	16	0
23	21	755	0	826	14	0
24	12	588	0	643	10	0
24	22	588	0	643	16	0
25	13	469	0	518	11	0
25	23	464	0	514	8	0
26	14	548	0	529	22	0
26	24	517	0	479	23	0
27	15	455	0	465	6	0
27	25	455	0	465	8	0
28	16	453	0	472	4	0
28	26	449	0	469	8	0
29	17	418	0	467	8	0
29	27	418	0	467	6	0
30	18	511	0	571	20	0
30	28	517	0	582	14	0
31	19	307	0	335	8	0
31	29	307	0	335	8	0
32	1a	32246	0	16294	477	0
32	2a	32327	0	16338	509	0
33	1b	1846	0	1867	76	0
33	2b	1825	0	1828	83	0
34	1c	1554	0	1551	42	0
34	2c	1542	0	1517	44	0
35	1d	1659	0	1676	61	0
35	2d	1674	0	1714	61	0
36	1e	1129	0	1185	37	0
36	2e	1130	0	1184	32	0
37	1f	810	0	797	19	0
37	2f	816	0	808	23	0
38	1g	1231	0	1238	23	0
38	2g	1235	0	1249	46	0
39	1h	1088	0	1126	24	0
39	2h	1088	0	1126	26	0
40	1i	983	0	986	43	0
40	2i	940	0	938	40	0
41	1j	721	0	672	33	0
41	2j	714	0	672	37	0
42	1k	829	0	825	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	2k	833	0	836	20	0
43	1l	932	0	980	17	0
43	2l	932	0	980	18	0
44	1m	923	0	962	45	0
44	2m	889	0	901	35	0
45	1n	492	0	529	22	0
45	2n	486	0	518	30	0
46	1o	728	0	760	14	0
46	2o	728	0	760	20	0
47	1p	681	0	697	30	0
47	2p	677	0	686	21	0
48	1q	823	0	891	21	0
48	2q	823	0	891	17	0
49	1r	555	0	618	8	0
49	2r	551	0	614	21	0
50	1s	652	0	662	23	0
50	2s	646	0	644	28	0
51	1t	728	0	798	26	0
51	2t	727	0	796	19	0
52	1u	199	0	208	6	0
52	2u	199	0	208	4	0
53	1v	274	0	139	8	0
53	2v	274	0	139	4	0
54	1w	1939	0	1925	51	0
54	2w	1957	0	1937	37	0
55	1x	1612	0	829	12	0
55	1y	1590	0	815	19	0
55	2x	1612	0	829	14	0
55	2y	1592	0	818	19	0
56	1z	119	0	123	3	0
56	2z	119	0	123	2	0
57	10	4	0	0	0	0
57	11	3	0	0	0	0
57	12	1	0	0	0	0
57	13	1	0	0	0	0
57	15	7	0	0	0	0
57	16	1	0	0	0	0
57	17	7	0	0	0	0
57	18	2	0	0	0	0
57	19	1	0	0	0	0
57	1A	793	0	0	0	0
57	1B	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1D	9	0	0	0	0
57	1E	7	0	0	0	0
57	1F	14	0	0	0	0
57	1G	3	0	0	0	0
57	1N	3	0	0	0	0
57	1O	1	0	0	0	0
57	1P	4	0	0	0	0
57	1Q	5	0	0	0	0
57	1R	2	0	0	0	0
57	1T	1	0	0	0	0
57	1U	8	0	0	0	0
57	1V	5	0	0	0	0
57	1W	3	0	0	0	0
57	1X	3	0	0	0	0
57	1Z	2	0	0	0	0
57	1a	167	0	0	0	0
57	1f	1	0	0	0	0
57	1i	1	0	0	0	0
57	1k	1	0	0	0	0
57	1m	1	0	0	0	0
57	1n	1	0	0	0	0
57	1v	3	0	0	0	0
57	1w	3	0	0	0	0
57	1x	10	0	0	0	0
57	1y	3	0	0	0	0
57	20	1	0	0	0	0
57	21	1	0	0	0	0
57	23	2	0	0	0	0
57	25	2	0	0	0	0
57	26	1	0	0	0	0
57	28	1	0	0	0	0
57	2A	657	0	0	0	0
57	2B	10	0	0	0	0
57	2D	7	0	0	0	0
57	2E	7	0	0	0	0
57	2F	5	0	0	0	0
57	2O	1	0	0	0	0
57	2P	1	0	0	0	0
57	2Q	3	0	0	0	0
57	2R	1	0	0	0	0
57	2U	2	0	0	0	0
57	2V	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2W	1	0	0	0	0
57	2X	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2a	165	0	0	0	0
57	2e	3	0	0	0	0
57	2f	1	0	0	0	0
57	2j	1	0	0	0	0
57	2k	2	0	0	0	0
57	2t	1	0	0	0	0
57	2v	2	0	0	0	0
57	2x	9	0	0	0	0
58	14	1	0	0	0	0
58	15	1	0	0	0	0
58	16	1	0	0	0	0
58	19	1	0	0	0	0
58	1Y	1	0	0	0	0
58	1n	1	0	0	0	0
58	24	1	0	0	0	0
58	25	1	0	0	0	0
58	26	1	0	0	0	0
58	29	1	0	0	0	0
58	2Y	1	0	0	0	0
58	2n	1	0	0	0	0
59	1d	8	0	0	0	0
59	2d	8	0	0	1	0
60	10	3	0	0	0	0
60	11	2	0	0	0	0
60	13	2	0	0	1	0
60	15	6	0	0	0	0
60	16	1	0	0	0	0
60	17	3	0	0	0	0
60	18	6	0	0	0	0
60	19	1	0	0	1	0
60	1A	1368	0	0	78	0
60	1B	27	0	0	0	0
60	1D	14	0	0	0	0
60	1E	14	0	0	2	0
60	1F	10	0	0	0	0
60	1G	1	0	0	0	0
60	1N	3	0	0	0	0
60	1O	3	0	0	0	0
60	1P	18	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	1Q	7	0	0	0	0
60	1R	1	0	0	0	0
60	1T	1	0	0	0	0
60	1U	6	0	0	0	0
60	1V	2	0	0	0	0
60	1W	2	0	0	0	0
60	1X	3	0	0	0	0
60	1a	164	0	0	14	0
60	1d	2	0	0	0	0
60	1e	1	0	0	0	0
60	1l	2	0	0	0	0
60	1p	1	0	0	0	0
60	1v	3	0	0	0	0
60	1w	5	0	0	0	0
60	1x	20	0	0	2	0
60	1y	1	0	0	0	0
60	1z	3	0	0	0	0
60	20	6	0	0	0	0
60	21	2	0	0	0	0
60	23	2	0	0	0	0
60	27	2	0	0	0	0
60	28	2	0	0	0	0
60	2A	949	0	0	89	0
60	2B	5	0	0	0	0
60	2D	13	0	0	2	0
60	2E	8	0	0	0	0
60	2F	6	0	0	0	0
60	2N	2	0	0	0	0
60	2P	7	0	0	1	0
60	2R	2	0	0	0	0
60	2T	1	0	0	0	0
60	2U	1	0	0	0	0
60	2V	1	0	0	0	0
60	2W	1	0	0	0	0
60	2X	2	0	0	0	0
60	2Y	1	0	0	0	0
60	2a	154	0	0	14	0
60	2d	1	0	0	0	0
60	2q	1	0	0	0	0
60	2v	3	0	0	0	0
60	2w	2	0	0	1	0
60	2x	11	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	2z	1	0	0	0	0
All	All	299015	0	199299	4238	0

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

All (4238) 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)
1:2A:2129:C:N4	1:2A:2159:G:H1	1.47	1.12
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.26	1.00
1:1A:1057:A:N6	1:1A:1081:U:H3	1.60	0.99
1:1A:2124:G:H1	1:1A:2174:C:H42	1.07	0.97
32:1a:875:C:H1'	39:1h:15:ASN:HD21	1.33	0.93
2:2B:75:G:HO2'	21:2Z:85:HIS:HE2	1.07	0.93
32:2a:1316:G:H22	32:2a:1319:A:H5"	1.36	0.89
54:1w:119:GLU:HG3	54:1w:184:PRO:HB3	1.55	0.89
1:2A:2110:G:H1	1:2A:2179:C:H42	1.15	0.88
1:1A:2499:C:OP1	60:1A:3810:HOH:O	1.90	0.88
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.39	0.86
1:2A:1171:G:H1	1:2A:1178:C:H42	1.19	0.86
1:2A:2129:C:N3	1:2A:2159:G:N2	2.25	0.85
1:1A:2131:G:H5"	1:1A:2132:U:H3'	1.58	0.85
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.10	0.84
1:2A:449:A:OP2	60:2A:3706:HOH:O	1.95	0.84
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.59	0.84
42:2k:79:SER:HB2	42:2k:106:LYS:HD2	1.57	0.84
32:1a:1027:C:N4	32:1a:1034:G:C6	2.45	0.84
1:1A:1315:C:OP2	60:1A:3811:HOH:O	1.94	0.84
32:2a:1264:C:H42	32:2a:1271:G:H1	1.23	0.83
1:1A:2124:G:H1	1:1A:2174:C:N4	1.75	0.83
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.10	0.83
32:2a:376:G:H5"	47:2p:5:ARG:HB2	1.60	0.82
40:1i:53:VAL:O	40:1i:55:ALA:N	2.13	0.82
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.60	0.82
39:1h:34:GLU:HB3	39:1h:118:VAL:HG21	1.60	0.82
1:2A:2166:G:N7	1:2A:2168:G:N2	2.26	0.82
1:2A:2101:G:H1	1:2A:2188:C:H42	1.27	0.82
1:2A:2430:A:OP2	60:2A:3707:HOH:O	1.98	0.82
32:2a:266:G:H5"	32:2a:268:C:H41	1.45	0.81
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.60	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.14	0.81
26:14:16:CYS:SG	26:14:17:GLY:N	2.53	0.81
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.16	0.80
6:2G:13:GLU:HG3	6:2G:14:GLU:HG3	1.63	0.80
32:1a:1129:C:H5"	40:1i:16:ARG:HH12	1.45	0.80
1:1A:453:C:OP1	60:1A:3813:HOH:O	2.00	0.80
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.15	0.79
1:2A:422:A:OP2	60:2A:3708:HOH:O	1.99	0.79
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.16	0.79
1:1A:2136:C:H42	1:1A:2155:G:H1	1.29	0.79
1:2A:1616:A:O2'	60:2A:3709:HOH:O	2.00	0.79
1:2A:1689:A:H62	1:2A:1698:A:H2	1.30	0.79
32:2a:1164:G:H1	32:2a:1172:C:H42	1.27	0.79
32:1a:1035:A:N3	32:1a:1036:G:N2	2.31	0.79
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.30	0.79
1:1A:248:G:OP1	60:1A:3812:HOH:O	2.00	0.79
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.54	0.79
51:2t:10:LEU:HG	51:2t:12:ALA:H	1.47	0.79
32:2a:448:A:OP2	32:2a:485:G:N2	2.15	0.79
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.47	0.79
32:1a:509:A:OP2	60:1a:1801:HOH:O	2.00	0.78
32:1a:1004:A:H5"	32:1a:1024:G:H1	1.48	0.78
1:2A:1332:G:OP1	60:2A:3710:HOH:O	2.00	0.78
1:2A:2127:G:H1	1:2A:2161:C:H42	1.27	0.78
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H3'	1.65	0.78
40:2i:17:VAL:HB	40:2i:63:ILE:HG12	1.66	0.78
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.48	0.78
1:2A:2136:C:C4	1:2A:2155:G:N1	2.51	0.78
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.65	0.78
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.46	0.78
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.17	0.77
54:1w:317:ILE:HD13	54:1w:339:LEU:HG	1.67	0.77
1:2A:752:A:H3'	29:27:1:MET:HE1	1.65	0.77
1:2A:2133:G:O2'	1:2A:2157:G:N2	2.17	0.77
1:1A:1057:A:H61	1:1A:1081:U:H3	0.82	0.77
44:1m:19:LEU:HD21	44:1m:56:LEU:HD21	1.67	0.77
44:1m:45:VAL:HA	44:1m:48:LEU:HD12	1.67	0.77
1:1A:1093:G:H3'	1:1A:1094:U:H5"	1.65	0.77
32:2a:1256:A:N6	32:2a:1278:U:O2	2.18	0.77
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.50	0.76
26:14:40:HIS:HB3	26:14:43:TYR:HB2	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2452:C:OP1	60:1A:3814:HOH:O	2.01	0.76
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.67	0.76
35:1d:100:ARG:NH1	35:1d:137:SER:OG	2.18	0.76
1:1A:2504:U:OP2	60:1A:3815:HOH:O	2.03	0.76
40:1i:19:LEU:HD22	40:1i:59:PHE:HB3	1.67	0.76
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.16	0.76
1:1A:1267:U:OP1	60:1A:3818:HOH:O	2.04	0.76
44:2m:37:THR:HB	44:2m:55:ARG:HD2	1.67	0.76
1:1A:2447:G:OP2	60:1A:3816:HOH:O	2.03	0.76
33:2b:91:PRO:HG2	33:2b:155:LEU:HD13	1.68	0.75
32:1a:1027:C:C4	32:1a:1034:G:C2	2.75	0.75
51:1t:50:GLU:HG3	51:1t:100:ILE:HD11	1.69	0.75
1:2A:2499:C:OP2	60:2A:3712:HOH:O	2.04	0.75
32:2a:1133:G:H2'	32:2a:1134:G:H8	1.50	0.75
1:1A:1009:A:OP2	9:1N:37:LYS:NZ	2.18	0.75
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.69	0.75
32:1a:664:G:H22	32:1a:741:G:H1	1.35	0.75
1:1A:576:U:OP1	60:1A:3817:HOH:O	2.03	0.75
1:2A:2711:A:OP2	60:2A:3711:HOH:O	2.03	0.75
1:2A:1914:C:N3	54:2w:286:ARG:NH2	2.35	0.74
1:1A:400:G:N7	60:1A:3864:HOH:O	2.20	0.74
1:1A:2429:G:OP2	60:1A:3819:HOH:O	2.05	0.74
32:1a:558:G:OP1	60:1a:1803:HOH:O	2.05	0.74
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.20	0.74
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.70	0.74
13:1R:24:GLN:HE22	13:1R:36:THR:HG21	1.52	0.74
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	1.69	0.74
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.69	0.74
32:2a:903:G:OP1	60:2a:1802:HOH:O	2.06	0.74
42:2k:77:MET:HG3	42:2k:103:LEU:HD21	1.69	0.74
1:1A:1041:C:H42	1:1A:1114:G:H1	1.33	0.74
51:1t:39:LYS:HA	51:1t:42:GLN:HB3	1.68	0.74
1:2A:193:U:OP2	60:2A:3713:HOH:O	2.05	0.74
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.20	0.74
32:2a:501:C:H2'	32:2a:502:G:H8	1.51	0.74
1:1A:1069:A:H1'	1:1A:1096:A:H4'	1.68	0.74
32:1a:574:A:OP2	60:1a:1802:HOH:O	2.05	0.74
32:2a:975:A:H4'	32:2a:976:G:H5"	1.68	0.74
14:2S:105:ALA:HB1	14:2S:110:LEU:HD12	1.69	0.74
1:1A:958:U:O2	2:1B:90:A:O2'	2.05	0.73
12:2Q:110:THR:HB	12:2Q:113:GLN:H	1.51	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.70	0.73
1:2A:2110:G:H1	1:2A:2179:C:N4	1.85	0.73
1:1A:881:G:H1	1:1A:895:U:H3	1.33	0.73
32:2a:1006:C:H42	32:2a:1023:G:H1	1.36	0.73
40:2i:46:ALA:HA	40:2i:78:LYS:HB2	1.70	0.73
1:1A:2508:G:OP1	54:1w:223:ARG:NH2	2.20	0.73
11:2P:44:GLY:O	60:2P:301:HOH:O	2.06	0.73
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.06	0.73
55:1y:26:A:N6	55:1y:44:G:O6	2.20	0.73
1:2A:139(A):G:OP1	60:2A:3716:HOH:O	2.07	0.73
13:2R:28:LEU:HD23	13:2R:48:VAL:HG21	1.70	0.73
55:2y:8:4SU:H4'	55:2y:48:C:H4'	1.70	0.73
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.71	0.73
55:2x:12:U:OP2	60:2x:201:HOH:O	2.04	0.73
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	1.71	0.73
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.69	0.73
33:2b:127:ILE:HG12	33:2b:128:GLU:HG2	1.71	0.73
32:2a:1271:G:N2	32:2a:1272:G:N7	2.37	0.72
1:2A:2113:U:H3	1:2A:2170:A:H61	1.38	0.72
8:2I:92:VAL:HG23	8:2I:120:ILE:HG13	1.71	0.72
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.54	0.72
11:2P:63:PRO:HB2	30:28:30:ARG:HH21	1.53	0.72
32:2a:1047:G:HO2'	32:2a:1215:G:HO2'	1.36	0.72
24:12:65:ASN:HD22	24:12:69:ARG:HH11	1.34	0.72
34:2c:57:ILE:HG12	34:2c:66:VAL:HG12	1.71	0.72
41:1j:6:ILE:HA	41:1j:98:ILE:HG12	1.71	0.72
1:1A:2454:G:OP1	60:1A:3820:HOH:O	2.07	0.72
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.22	0.72
32:1a:347:G:H2'	32:1a:348:G:H8	1.53	0.72
47:1p:66:PRO:HD2	47:1p:71:ARG:HH21	1.54	0.72
1:1A:2285:C:OP2	28:16:6:ARG:NH1	2.22	0.72
40:1i:99:LEU:O	40:1i:101:PHE:N	2.22	0.72
1:2A:740:U:OP2	60:2A:3714:HOH:O	2.06	0.72
1:2A:962:G:OP1	60:2A:3715:HOH:O	2.07	0.72
1:2A:2140:C:H42	1:2A:2151:G:H1	1.37	0.72
1:2A:948:G:OP1	60:2A:3715:HOH:O	2.08	0.72
32:2a:1006:C:N4	32:2a:1023:G:H1	1.88	0.72
33:2b:11:LEU:HD21	33:2b:217:ARG:HH21	1.55	0.72
7:1H:101:ARG:HH22	7:1H:122:THR:HA	1.55	0.72
32:1a:1002:G:N2	32:1a:1004:A:O2'	2.23	0.72
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:229:GLY:HA3	55:1x:76:A:H3'	1.71	0.72
32:2a:979:C:OP1	32:2a:1223:C:N4	2.23	0.72
10:1O:1:MET:HE3	10:1O:67:LYS:HG2	1.72	0.71
34:1c:55:VAL:HG22	34:1c:68:VAL:HG12	1.71	0.71
33:2b:30:ARG:NH2	33:2b:195:ASP:OD1	2.23	0.71
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.25	0.71
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	1.71	0.71
32:1a:1350:A:N7	40:1i:118:LYS:NZ	2.37	0.71
1:2A:586:A:N1	1:2A:809:G:O2'	2.22	0.71
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.73	0.71
48:2q:95:TYR:HA	48:2q:98:LEU:HD12	1.70	0.71
1:2A:615:G:OP1	5:2F:40:GLN:NE2	2.24	0.71
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.56	0.71
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.24	0.71
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.54	0.71
8:2I:105:HIS:O	8:2I:107:VAL:N	2.23	0.71
1:1A:576:U:H2'	1:1A:577:G:C8	2.26	0.71
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.24	0.71
21:1Z:110:GLY:HA3	21:1Z:174:VAL:HG11	1.72	0.71
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.23	0.71
32:2a:1160:G:H1	32:2a:1176:A:H61	1.39	0.71
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.73	0.71
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	1.73	0.70
1:2A:505:A:OP2	60:2A:3719:HOH:O	2.09	0.70
18:2W:14:PRO:HG2	18:2W:78:GLU:HG3	1.71	0.70
34:1c:125:GLU:HG3	34:1c:189:ALA:HB1	1.73	0.70
50:1s:27:GLU:HB2	50:1s:28:LYS:HD3	1.73	0.70
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.27	0.70
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD21	1.72	0.70
1:2A:1355:G:O6	60:2A:3718:HOH:O	2.08	0.70
2:2B:40:U:O4	26:24:1:MET:N	2.23	0.70
1:1A:11:G:H2'	1:1A:12:U:H5"	1.74	0.70
1:1A:1023:U:OP2	60:1A:3823:HOH:O	2.09	0.70
31:19:15:LYS:HE2	31:19:17:ILE:HD11	1.71	0.70
1:1A:2602:A:OP1	60:1A:3826:HOH:O	2.10	0.70
3:1D:147:LEU:HD13	3:1D:155:LEU:HD21	1.73	0.70
7:2H:144:VAL:HA	7:2H:147:ASN:HB2	1.73	0.70
32:1a:1255:G:O2'	32:1a:1258:G:O2'	2.08	0.70
1:1A:1971:A:OP1	60:1A:3824:HOH:O	2.09	0.70
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.73	0.70
41:1j:50:ILE:HA	41:1j:60:ARG:HG2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:4:ILE:HG13	47:1p:66:PRO:HB3	1.74	0.70
33:2b:21:ARG:O	33:2b:23:ARG:N	2.24	0.70
1:1A:883:G:H21	1:1A:884:C:H41	1.41	0.69
1:1A:2131:G:H5'	1:1A:2133:G:C8	2.27	0.69
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.74	0.69
33:2b:133:LYS:HE2	33:2b:133:LYS:H	1.57	0.69
1:2A:370:G:OP2	60:2A:3708:HOH:O	2.10	0.69
1:2A:2789:C:O2	1:2A:2894:G:N2	2.23	0.69
1:2A:805:G:OP1	60:2A:3723:HOH:O	2.11	0.69
32:2a:1324:A:H4'	32:2a:1362:C:H4'	1.74	0.69
1:1A:1395:A:OP1	60:1A:3827:HOH:O	2.11	0.69
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	1.73	0.69
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.25	0.69
32:1a:975:A:H4'	32:1a:976:G:H5"	1.74	0.69
32:2a:946:A:H2'	32:2a:947:G:C8	2.28	0.69
41:1j:16:LEU:HD21	41:1j:70:ARG:HG2	1.74	0.69
1:2A:563:G:OP2	60:2A:3717:HOH:O	2.08	0.69
1:2A:1827:C:OP2	3:2D:222:ARG:NH1	2.26	0.69
7:2H:17:VAL:HG22	7:2H:26:VAL:HG13	1.73	0.69
1:1A:2712:U:O2'	1:1A:2712(A):A:OP2	2.10	0.69
32:1a:1025:U:O2	32:1a:1036:G:O6	2.11	0.69
1:1A:1345:C:OP2	60:1A:3822:HOH:O	2.09	0.69
1:1A:2292:C:OP1	14:1S:17:ARG:NH2	2.26	0.69
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.75	0.69
32:2a:976:G:N2	32:2a:1363:C:OP2	2.23	0.69
38:2g:78:ARG:HH22	38:2g:79:ARG:HD3	1.58	0.68
1:1A:2243:U:OP1	60:1A:3828:HOH:O	2.11	0.68
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.26	0.68
1:2A:392:C:H5"	1:2A:409:C:H5"	1.76	0.68
1:2A:1189:A:OP2	60:2A:3722:HOH:O	2.10	0.68
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.26	0.68
38:2g:80:VAL:O	38:2g:82:GLY:N	2.25	0.68
33:1b:91:PRO:HG3	33:1b:154:LEU:HB3	1.76	0.68
32:2a:1298:C:H2'	38:2g:114:ARG:HH12	1.57	0.68
1:1A:827:U:OP1	60:1A:3819:HOH:O	2.11	0.68
32:1a:1139:G:H4'	32:1a:1140:C:H5'	1.74	0.68
32:1a:1402:4OC:OP2	60:1a:1804:HOH:O	2.09	0.68
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.75	0.68
1:1A:2547:U:O2	10:1O:23:ARG:NH2	2.27	0.68
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.26	0.68
33:2b:178:ARG:HH22	39:2h:68:ARG:HH22	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2y:62:C:H2'	55:2y:63:G:C8	2.29	0.68
5:1F:101:LEU:O	5:1F:106:ARG:NH1	2.26	0.68
37:1f:3:ARG:HB3	37:1f:93:SER:HB2	1.75	0.68
1:2A:2218:U:O2	23:21:52:ARG:NH1	2.27	0.68
1:2A:1153:C:OP2	60:2A:3726:HOH:O	2.11	0.68
1:2A:1271:G:OP2	60:2A:3724:HOH:O	2.11	0.68
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.57	0.68
14:2S:10:ARG:NE	14:2S:91:PRO:O	2.25	0.68
32:2a:8:A:N6	35:2d:205:GLU:O	2.27	0.68
32:1a:382:A:H2'	32:1a:383:A:C8	2.29	0.67
1:1A:1602:U:O4	60:1A:3821:HOH:O	2.09	0.67
1:2A:1418:G:OP2	60:2A:3730:HOH:O	2.12	0.67
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.42	0.67
32:2a:501:C:H2'	32:2a:502:G:C8	2.30	0.67
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.77	0.67
42:2k:85:ARG:HA	42:2k:112:THR:HG22	1.77	0.67
33:1b:55:PHE:HA	33:1b:58:ILE:HG13	1.77	0.67
1:2A:249:C:OP1	60:2A:3733:HOH:O	2.13	0.67
1:2A:731:C:OP2	60:2A:3728:HOH:O	2.12	0.67
1:2A:944:G:O3'	60:2A:3732:HOH:O	2.12	0.67
1:1A:1673:U:OP1	60:1A:3829:HOH:O	2.12	0.67
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.76	0.67
40:1i:28:VAL:HA	40:1i:63:ILE:HB	1.77	0.67
1:2A:826:U:OP1	60:2A:3727:HOH:O	2.12	0.67
1:2A:1022:G:N2	1:2A:1023:U:O4	2.24	0.67
34:2c:120:VAL:HA	34:2c:123:GLN:HE21	1.58	0.67
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.77	0.67
5:1F:9:ILE:HD12	5:1F:123:LEU:HD23	1.76	0.67
32:2a:1142:G:H2'	32:2a:1143:G:O4'	1.95	0.67
32:2a:1209:C:O2'	32:2a:1214:C:N4	2.27	0.67
1:1A:1439:A:OP1	60:1A:3832:HOH:O	2.13	0.67
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.75	0.67
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.27	0.67
1:1A:1342:A:OP2	60:1A:3821:HOH:O	2.11	0.67
32:1a:673:G:H2'	32:1a:674:G:C8	2.29	0.67
35:1d:159:ARG:O	35:1d:163:GLU:N	2.27	0.67
1:2A:1614:A:OP1	60:2A:3725:HOH:O	2.11	0.67
32:1a:266:G:H3'	48:1q:67:LYS:HB2	1.77	0.66
32:2a:881:G:P	43:2l:12:ARG:HH22	2.18	0.66
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.30	0.66
33:2b:10:LEU:HB2	33:2b:13:ALA:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:927:G:N7	60:1A:3905:HOH:O	2.29	0.66
32:1a:1069:C:OP2	60:1a:1805:HOH:O	2.11	0.66
32:2a:1004:A:N6	32:2a:1036:G:N7	2.43	0.66
41:2j:38:ILE:HG23	41:2j:71:LEU:HB3	1.76	0.66
32:1a:117:G:OP2	60:1a:1807:HOH:O	2.13	0.66
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.30	0.66
1:2A:2349:G:OP1	60:2A:3735:HOH:O	2.14	0.66
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.10	0.66
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.29	0.66
32:1a:972:C:OP1	60:1a:1806:HOH:O	2.13	0.66
44:1m:34:LEU:HD23	44:1m:41:PRO:HB3	1.75	0.66
1:2A:981:A:OP1	60:2A:3734:HOH:O	2.13	0.66
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.78	0.66
1:1A:2036:C:OP1	60:1A:3831:HOH:O	2.13	0.66
1:1A:2305:A:H5"	6:1G:134:GLY:HA3	1.76	0.66
46:2o:54:ARG:NH1	46:2o:58:MET:SD	2.69	0.66
54:2w:172:LYS:HA	54:2w:201:VAL:HG21	1.77	0.66
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.42	0.66
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.77	0.66
1:2A:309:G:N3	1:2A:329:G:O2'	2.29	0.66
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.77	0.66
21:2Z:151:HIS:O	21:2Z:153:SER:N	2.26	0.66
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.77	0.66
32:2a:235:C:H5'	48:2q:70:ARG:HG2	1.77	0.66
1:1A:1701:A:OP2	60:1A:3834:HOH:O	2.14	0.66
1:2A:686:G:N2	1:2A:788:A:H61	1.93	0.66
1:2A:781:A:OP1	60:2A:3737:HOH:O	2.14	0.66
1:2A:1023:U:OP2	60:2A:3736:HOH:O	2.14	0.66
26:24:2:LYS:HB2	26:24:5:ILE:HD11	1.78	0.66
32:2a:1164:G:H1	32:2a:1172:C:N4	1.93	0.66
44:2m:39:ILE:HD12	44:2m:56:LEU:HD13	1.78	0.66
55:1y:68:C:H2'	55:1y:69:G:C8	2.30	0.66
1:2A:630:G:N2	1:2A:633:A:OP2	2.27	0.66
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.76	0.66
54:2w:175:SER:HB3	54:2w:201:VAL:HG22	1.76	0.66
1:1A:1072:C:H2'	1:1A:1094:U:H3	1.60	0.66
1:1A:1352:U:OP2	60:1A:3830:HOH:O	2.12	0.66
1:2A:271(H):G:H1	1:2A:271(P):C:H42	1.44	0.66
32:2a:1264:C:N4	32:2a:1271:G:H1	1.94	0.66
1:2A:2345:G:OP2	28:26:38:LYS:NZ	2.22	0.65
32:2a:410:G:OP1	35:2d:30:LYS:NZ	2.21	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:310:A:OP2	20:1Y:21:LYS:NZ	2.29	0.65
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.29	0.65
1:2A:1658:C:OP1	60:2A:3740:HOH:O	2.14	0.65
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.59	0.65
19:2X:26:TYR:HB3	19:2X:92:LEU:HD22	1.78	0.65
1:1A:818:G:OP2	60:1A:3837:HOH:O	2.15	0.65
1:1A:1359:A:H61	1:1A:1372:U:H3	1.43	0.65
54:1w:161:GLU:OE2	54:1w:204:LYS:NZ	2.29	0.65
1:2A:2151:G:H2'	1:2A:2152:G:C8	2.32	0.65
46:2o:82:ILE:O	46:2o:86:GLY:N	2.29	0.65
60:2A:3759:HOH:O	9:2N:37:LYS:NZ	2.29	0.65
32:2a:36:C:OP1	43:2l:123:LYS:NZ	2.25	0.65
32:2a:677:U:H3	32:2a:713:G:H22	1.44	0.65
32:2a:1320:C:O2	50:2s:36:ARG:NH2	2.28	0.65
1:2A:2298:A:H62	1:2A:2318:G:H8	1.44	0.65
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.78	0.65
42:2k:86:GLY:H	42:2k:112:THR:HG22	1.61	0.65
54:1w:161:GLU:OE1	54:1w:163:ARG:NH2	2.28	0.65
1:2A:1631(A):A:OP1	60:2A:3738:HOH:O	2.14	0.65
1:2A:2127:G:H1	1:2A:2161:C:N4	1.94	0.65
2:2B:8:U:O3'	14:2S:25:ARG:NH2	2.30	0.65
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.32	0.65
16:2U:34:LYS:NZ	16:2U:37:GLU:OE1	2.27	0.65
32:1a:1401:G:OP1	60:1a:1804:HOH:O	2.14	0.65
1:2A:526:A:OP1	60:2A:3739:HOH:O	2.14	0.65
42:2k:87:THR:O	42:2k:87:THR:OG1	2.12	0.65
1:1A:1604:C:OP2	60:1A:3827:HOH:O	2.13	0.65
1:2A:2101:G:H1	1:2A:2188:C:N4	1.94	0.65
37:2f:2:ARG:HE	37:2f:69:GLU:HB3	1.62	0.65
1:1A:2171:A:HO2'	1:1A:2172:U:H6	1.43	0.65
1:1A:2355:C:H1'	22:10:39:ARG:HH21	1.61	0.65
2:1B:66:A:H61	2:1B:108:U:H2'	1.61	0.65
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.29	0.65
32:1a:944:G:OP1	60:1a:1809:HOH:O	2.15	0.65
32:1a:964:A:OP1	60:1a:1808:HOH:O	2.14	0.65
43:1l:76:ASN:ND2	43:1l:106:ASP:O	2.28	0.65
26:14:28:LYS:HB2	26:14:31:ILE:HD11	1.79	0.65
32:1a:959:A:HO2'	32:1a:984:C:HO2'	1.39	0.65
1:2A:1125:G:H5'	31:29:37:GLY:HA2	1.78	0.65
4:2E:78:LEU:O	4:2E:79:ARG:NH1	2.28	0.65
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2589:A:OP1	60:1A:3835:HOH:O	2.14	0.64
1:1A:2836:U:H2'	1:1A:2837:G:C8	2.32	0.64
42:1k:33:THR:HA	42:1k:39:PRO:HA	1.79	0.64
21:2Z:9:TYR:HE1	21:2Z:35:ARG:HG2	1.62	0.64
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.30	0.64
32:1a:148:G:H2'	32:1a:149:A:C8	2.32	0.64
42:1k:65:ALA:HB1	42:1k:98:LEU:HG	1.77	0.64
53:1v:11:U:H3'	53:1v:12:A:H8	1.62	0.64
32:2a:1271:G:C2	32:2a:1272:G:N7	2.65	0.64
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.62	0.64
42:1k:111:ASP:HB2	49:1r:84:LYS:HE3	1.78	0.64
30:28:29:LYS:NZ	30:28:41:ILE:O	2.26	0.64
1:1A:530:G:N1	1:1A:2023:G:OP1	2.22	0.64
8:1I:5:LEU:HD21	8:1I:12:LEU:HB3	1.79	0.64
1:2A:1632:A:OP2	60:2A:3741:HOH:O	2.14	0.64
1:2A:2612:C:OP2	27:25:2:ALA:N	2.30	0.64
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.78	0.64
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.33	0.64
19:1X:64:LYS:HE3	19:1X:73:ARG:HH12	1.63	0.64
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.44	0.64
41:2j:63:PHE:HE1	45:2n:58:LYS:HG2	1.62	0.64
7:2H:101:ARG:NH2	7:2H:121:ILE:O	2.31	0.64
22:20:27:GLU:HB2	22:20:69:PHE:HD1	1.63	0.64
32:2a:664:G:H22	32:2a:741:G:H1	1.46	0.64
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.30	0.64
33:2b:95:GLN:NE2	33:2b:147:LYS:O	2.26	0.64
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.80	0.64
32:1a:490:G:H2'	32:1a:491:G:H8	1.62	0.64
1:2A:2499:C:O2	60:2A:3729:HOH:O	2.12	0.64
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.13	0.64
1:1A:195:A:OP1	11:1P:46:LYS:NZ	2.27	0.64
1:1A:510:C:OP1	60:1A:3838:HOH:O	2.15	0.64
1:1A:975:C:OP1	60:1A:3839:HOH:O	2.15	0.64
26:14:61:ARG:HH12	50:1s:9:VAL:HG11	1.62	0.64
32:1a:1117:G:O3'	40:1i:104:ARG:NE	2.31	0.64
1:2A:1359:A:H61	1:2A:1372:U:H3	1.44	0.64
32:2a:572:A:OP1	60:2a:1803:HOH:O	2.14	0.64
32:1a:17:U:H2'	32:1a:18:C:C6	2.33	0.64
32:1a:159:G:H21	32:1a:161:A:H3'	1.61	0.64
1:2A:2393:A:H5"	11:2P:63:PRO:HB3	1.80	0.64
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:76:ARG:NH1	35:2d:80:GLU:OE1	2.31	0.64
32:1a:538:G:H5"	43:1l:114:LYS:HB2	1.80	0.64
1:2A:1783:A:OP1	60:2A:3714:HOH:O	2.15	0.64
41:2j:57:LYS:HE2	41:2j:60:ARG:NH2	2.13	0.64
44:1m:88:ARG:O	44:1m:92:HIS:ND1	2.31	0.63
1:2A:1187:G:OP2	60:2A:3742:HOH:O	2.15	0.63
40:2i:79:LEU:HG	40:2i:83:ARG:HD2	1.79	0.63
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.81	0.63
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.17	0.63
4:1E:127:ASP:OD2	60:1E:401:HOH:O	2.15	0.63
1:2A:2121:G:H1	1:2A:2177:C:H42	1.47	0.63
1:2A:2429:G:OP2	60:2A:3707:HOH:O	2.16	0.63
8:2I:40:THR:O	8:2I:44:LEU:HB2	1.98	0.63
32:2a:444:C:H2'	32:2a:445:G:H8	1.63	0.63
32:1a:1086:U:H3	32:1a:1099:G:H22	1.45	0.63
32:1a:1346:A:N6	32:1a:1375:A:OP2	2.32	0.63
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	1.80	0.63
1:2A:674:G:OP2	60:2A:3743:HOH:O	2.15	0.63
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.81	0.63
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.80	0.63
50:2s:53:ASN:HB3	50:2s:75:ALA:HB1	1.80	0.63
1:1A:588:U:H2'	1:1A:589:C:C6	2.34	0.63
13:1R:38:VAL:HG22	13:1R:112:ALA:HB2	1.81	0.63
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.29	0.63
32:1a:472:A:H5"	47:1p:80:PHE:HB3	1.80	0.63
32:1a:953:G:H5'	32:1a:965:A:H61	1.63	0.63
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.31	0.63
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.32	0.63
44:1m:59:TYR:O	44:1m:63:THR:OG1	2.15	0.63
1:2A:450:G:O6	60:2A:3731:HOH:O	2.12	0.63
32:2a:17:U:H2'	32:2a:18:C:C6	2.34	0.63
32:2a:1179:A:H4'	40:2i:103:THR:HA	1.81	0.63
26:14:46:GLN:HG2	26:14:48:ARG:HG3	1.79	0.63
32:1a:1209:C:O2'	32:1a:1214:C:N4	2.29	0.63
48:2q:59:ILE:HG22	48:2q:73:VAL:HA	1.80	0.63
1:1A:1056:G:H4'	1:1A:1086:A:C8	2.33	0.63
1:2A:994:C:O2'	1:2A:996:A:OP1	2.15	0.63
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.32	0.63
7:2H:129:THR:O	7:2H:129:THR:OG1	2.17	0.63
32:2a:405:U:O4	35:2d:2:GLY:N	2.31	0.63
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:6:ILE:HG23	41:2j:98:ILE:HG13	1.81	0.63
32:1a:1298:C:OP2	38:1g:114:ARG:NH2	2.32	0.63
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.16	0.63
1:2A:663:G:O6	60:2A:3721:HOH:O	2.10	0.63
32:2a:612:C:O2	32:2a:629:G:N2	2.32	0.63
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.22	0.63
34:2c:139:GLN:HE21	34:2c:143:GLU:HG3	1.64	0.63
41:2j:17:ASP:OD1	41:2j:70:ARG:NH1	2.31	0.63
48:2q:26:GLN:HG2	48:2q:37:LYS:HG2	1.80	0.63
1:1A:2637:U:OP1	4:1E:82:ARG:NH1	2.31	0.62
6:1G:126:ASP:OD2	6:1G:130:ASN:ND2	2.26	0.62
32:1a:1027:C:N3	32:1a:1034:G:C2	2.67	0.62
32:1a:1349:A:H5"	40:1i:121:ARG:HB2	1.81	0.62
50:1s:39:THR:HG22	50:1s:40:ILE:H	1.64	0.62
35:2d:18:LYS:NZ	35:2d:26:CYS:O	2.32	0.62
40:1i:18:PHE:HD2	40:1i:62:TYR:HD2	1.47	0.62
3:2D:239:ARG:NE	60:2D:403:HOH:O	2.31	0.62
6:2G:32:PRO:HB2	6:2G:172:LEU:HD13	1.79	0.62
1:1A:2337:G:OP1	60:1A:3840:HOH:O	2.16	0.62
1:1A:2791:C:H2'	1:1A:2792:G:H8	1.64	0.62
34:1c:33:LEU:HD21	45:1n:53:LEU:HD22	1.81	0.62
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.34	0.62
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.82	0.62
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.00	0.62
32:1a:192:U:H2'	32:1a:193:C:C6	2.35	0.62
39:1h:11:THR:HG23	39:1h:14:ARG:HH12	1.65	0.62
2:2B:43:C:O2	6:2G:95:ARG:NE	2.27	0.62
20:2Y:30:VAL:HG22	20:2Y:37:VAL:HG12	1.81	0.62
32:2a:472:A:OP1	47:2p:75:ARG:NH2	2.31	0.62
32:2a:1123:A:H4'	41:2j:36:GLY:HA3	1.81	0.62
32:1a:718:G:H5'	42:1k:117:ASN:HB2	1.82	0.62
32:1a:41:G:H2'	32:1a:42:G:H8	1.64	0.62
34:1c:50:ALA:HB1	34:1c:72:LYS:HB2	1.80	0.62
21:2Z:134:PRO:HG3	21:2Z:161:VAL:HG21	1.81	0.62
33:2b:15:VAL:HG12	33:2b:16:HIS:H	1.65	0.62
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.82	0.62
32:1a:1343:G:O2'	40:1i:121:ARG:HD2	2.00	0.62
33:1b:10:LEU:C	33:1b:12:GLU:H	2.07	0.62
38:1g:67:GLU:HA	38:1g:70:LYS:HD2	1.80	0.62
32:1a:1256:A:OP2	34:1c:26:LYS:NZ	2.33	0.62
45:1n:24:CYS:HB3	45:1n:28:GLY:H	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:68:GLN:HG2	14:2S:71:ARG:HH12	1.63	0.62
38:2g:46:ALA:HB1	38:2g:121:ALA:HB2	1.82	0.62
24:12:28:LYS:HD2	24:12:53:LEU:HD21	1.81	0.62
1:2A:1648:C:OP1	60:2A:3724:HOH:O	2.16	0.62
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.29	0.62
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.65	0.62
1:1A:1839:G:N7	60:1A:3912:HOH:O	2.31	0.61
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.35	0.61
36:1e:152:ARG:HB3	39:1h:43:GLY:HA3	1.81	0.61
7:2H:3:ARG:HA	7:2H:3:ARG:HH11	1.64	0.61
1:1A:2136:C:N4	1:1A:2155:G:H1	1.97	0.61
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.82	0.61
1:2A:574:C:OP1	60:2A:3747:HOH:O	2.16	0.61
49:2r:32:ARG:HH12	49:2r:65:ILE:HD12	1.65	0.61
33:1b:118:LEU:HD22	33:1b:142:LEU:HB2	1.81	0.61
32:2a:1291:G:OP1	38:2g:37:ASN:ND2	2.31	0.61
39:2h:51:VAL:HG11	39:2h:60:ARG:HH12	1.66	0.61
1:1A:2430:A:OP2	60:1A:3819:HOH:O	2.16	0.61
32:1a:584:G:H5'	48:1q:91:ARG:HH22	1.66	0.61
33:1b:24:TRP:HZ3	33:1b:29:ALA:HB2	1.66	0.61
35:1d:43:HIS:O	35:1d:45:GLN:N	2.33	0.61
39:1h:121:ASP:HB2	39:1h:125:ARG:HH21	1.65	0.61
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.65	0.61
33:2b:184:VAL:HG13	33:2b:198:ASP:H	1.64	0.61
47:2p:1:MET:HE2	47:2p:65:GLN:HG3	1.81	0.61
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.33	0.61
32:1a:155:C:H2'	32:1a:156:G:C8	2.35	0.61
42:1k:34:ASP:HB3	42:1k:40:ILE:HD11	1.83	0.61
32:2a:578:C:OP1	60:2a:1807:HOH:O	2.16	0.61
33:1b:48:MET:HA	33:1b:51:LEU:HD12	1.81	0.61
10:2O:97:ARG:NH1	32:2a:339:C:OP2	2.30	0.61
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.16	0.61
32:2a:8:A:C6	35:2d:209:ARG:HB2	2.36	0.61
1:1A:2407:G:OP1	60:1A:3842:HOH:O	2.16	0.61
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.65	0.61
32:1a:110:C:O2'	47:1p:25:ARG:O	2.16	0.61
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.83	0.61
32:1a:1004:A:N6	32:1a:1037:C:O2	2.34	0.61
3:2D:202:LYS:NZ	32:2a:773:G:O3'	2.33	0.61
32:2a:1272:G:N2	32:2a:1273:G:C8	2.68	0.61
33:2b:48:MET:HA	33:2b:51:LEU:HD12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:181:ARG:HG3	6:1G:182:LYS:H	1.65	0.61
7:1H:101:ARG:HH12	7:1H:122:THR:HG23	1.65	0.61
32:1a:1030(A):G:O2'	32:1a:1031:G:N2	2.33	0.61
39:1h:20:TYR:HE2	39:1h:75:ARG:HD2	1.66	0.61
39:1h:29:SER:HB3	39:1h:32:LYS:HD3	1.82	0.61
51:1t:100:ILE:HG22	51:1t:101:GLY:H	1.65	0.61
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.48	0.61
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.34	0.61
6:2G:67:LYS:HD3	26:24:5:ILE:HB	1.83	0.61
42:2k:32:ILE:O	42:2k:40:ILE:N	2.30	0.61
44:2m:80:ARG:HH12	50:2s:69:HIS:HE1	1.48	0.61
55:2y:5:G:H1	55:2y:68:C:H42	1.49	0.61
28:16:14:THR:OG1	28:16:48:VAL:O	2.12	0.61
50:2s:22:LEU:HA	50:2s:26:GLY:H	1.65	0.61
1:1A:2128:C:H42	1:1A:2160:G:H1	1.47	0.61
1:1A:2135:A:N6	1:1A:2156:G:O2'	2.34	0.61
1:1A:2462:U:H1'	1:1A:2491:U:O4	2.01	0.61
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.36	0.61
36:1e:102:ALA:HB1	36:1e:106:PRO:HB2	1.82	0.61
1:2A:1243:G:O2'	11:2P:7:ARG:NH2	2.32	0.61
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.35	0.61
32:2a:946:A:H2'	32:2a:947:G:H8	1.64	0.61
35:2d:180:GLY:HA3	35:2d:182:LYS:HE2	1.83	0.61
44:2m:23:TYR:HB3	44:2m:67:GLU:HG2	1.83	0.61
1:1A:1065:U:O2	1:1A:1073:A:N6	2.34	0.60
32:1a:946:A:O2'	32:1a:1333:A:N3	2.30	0.60
1:2A:10:G:N7	60:2A:3821:HOH:O	2.31	0.60
1:2A:2006:C:OP2	60:2A:3748:HOH:O	2.16	0.60
32:2a:1124:G:H5"	41:2j:35:SER:HB2	1.81	0.60
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.25	0.60
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.34	0.60
35:1d:100:ARG:HG2	35:1d:137:SER:HA	1.82	0.60
36:1e:78:HIS:HE1	36:1e:142:LEU:HA	1.66	0.60
41:1j:3:LYS:HA	41:1j:75:ILE:HA	1.83	0.60
1:2A:1113:U:H2'	1:2A:1114:G:C8	2.36	0.60
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.66	0.60
7:2H:42:ARG:NH2	7:2H:53:GLU:OE1	2.30	0.60
32:2a:1278:U:H5'	32:2a:1279:A:H5'	1.84	0.60
2:1B:106:G:H5'	21:1Z:31:ARG:HB3	1.81	0.60
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.83	0.60
1:2A:1890:A:OP2	60:2A:3746:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2175:C:H2'	1:2A:2176:A:C8	2.36	0.60
2:2B:13:A:N1	2:2B:69:G:O2'	2.33	0.60
7:2H:40:GLU:OE1	7:2H:60:ARG:NH1	2.33	0.60
32:2a:187:C:O2'	51:2t:89:ARG:NH2	2.34	0.60
40:2i:28:VAL:HG12	40:2i:63:ILE:HB	1.83	0.60
1:1A:674:G:H1'	5:1F:74:ARG:HD3	1.83	0.60
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.84	0.60
55:1y:68:C:H2'	55:1y:69:G:H8	1.65	0.60
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	1.83	0.60
6:2G:33:ARG:HE	6:2G:162:THR:HG21	1.66	0.60
32:2a:1381:U:H1'	38:2g:79:ARG:HB2	1.82	0.60
1:1A:1087:G:H22	1:1A:1103:A:H1'	1.67	0.60
9:1N:73:THR:HG22	9:1N:84:LYS:HG2	1.82	0.60
1:2A:392:C:OP1	60:2A:3744:HOH:O	2.15	0.60
1:2A:2128:C:H1'	1:2A:2173:A:O2'	2.02	0.60
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	1.82	0.60
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.83	0.60
44:2m:86:CYS:SG	44:2m:87:TYR:N	2.74	0.60
46:2o:15:PHE:HE1	46:2o:84:LYS:HG2	1.66	0.60
1:1A:2379:G:O2'	14:1S:17:ARG:NH1	2.33	0.60
1:1A:2448:A:OP1	60:1A:3810:HOH:O	2.16	0.60
8:1I:77:LEU:HD22	8:1I:101:LEU:HD22	1.84	0.60
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.84	0.60
23:11:23:LYS:HB3	23:11:29:GLY:HA3	1.84	0.60
37:1f:86:ARG:O	37:1f:87:ARG:HG2	2.02	0.60
2:2B:76:G:O3'	21:2Z:19:ARG:NH2	2.33	0.60
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.82	0.60
32:2a:775:G:N2	32:2a:804:U:O4	2.35	0.60
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.83	0.60
1:1A:1495:A:OP2	60:1A:3845:HOH:O	2.17	0.60
32:1a:430:A:OP1	35:1d:9:CYS:HB2	2.02	0.60
32:1a:1030(A):G:H1'	32:1a:1031:G:H1	1.65	0.60
1:2A:886:C:H1'	1:2A:890:A:N1	2.17	0.60
1:2A:2370:G:H4'	28:26:44:ARG:HH22	1.67	0.60
1:2A:31:C:OP1	60:2A:3745:HOH:O	2.16	0.60
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.34	0.60
33:2b:69:LEU:HD13	33:2b:155:LEU:HD22	1.83	0.60
46:2o:5:LYS:H	46:2o:5:LYS:HD2	1.66	0.60
1:1A:883:G:N2	1:1A:884:C:H41	1.99	0.60
11:1P:37:GLY:N	60:1P:304:HOH:O	2.34	0.60
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.84	0.60
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.84	0.60
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.37	0.60
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.02	0.60
5:2F:132:VAL:HA	5:2F:138:GLU:HB3	1.83	0.60
7:2H:3:ARG:HE	7:2H:54:ARG:HH12	1.48	0.60
32:2a:470:C:OP2	60:2a:1806:HOH:O	2.16	0.60
46:2o:74:ASP:HB3	46:2o:77:ARG:HB2	1.84	0.60
1:1A:301:G:OP2	20:1Y:84:ARG:NH2	2.35	0.60
1:1A:588:U:OP2	60:1A:3846:HOH:O	2.17	0.60
1:1A:2099:U:H3	1:1A:2190:G:H1	1.49	0.60
15:1T:127:ALA:C	15:1T:129:ARG:H	2.10	0.60
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.83	0.60
32:2a:1029:C:H42	32:2a:1032:G:H1	1.48	0.60
1:1A:649:G:O6	60:1A:3833:HOH:O	2.14	0.59
3:1D:108:PRO:HD2	3:1D:111:LEU:HD22	1.84	0.59
9:1N:86:PRO:HD2	9:1N:89:LYS:HB2	1.83	0.59
32:1a:19:C:OP1	36:1e:130:ASN:ND2	2.35	0.59
32:2a:585:G:OP1	48:2q:37:LYS:NZ	2.31	0.59
32:2a:815:A:N7	32:2a:1509:C:O2'	2.30	0.59
38:2g:22:LEU:HD23	38:2g:63:LYS:HE3	1.82	0.59
38:2g:62:PHE:HA	38:2g:124:LEU:HD22	1.83	0.59
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.83	0.59
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.24	0.59
3:2D:78:LYS:HE2	3:2D:116:GLN:HE21	1.67	0.59
1:2A:827:U:OP1	60:2A:3707:HOH:O	2.17	0.59
1:2A:2430:A:H2'	1:2A:2430:A:N3	2.16	0.59
32:2a:959:A:O2'	32:2a:984:C:O2'	2.21	0.59
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.67	0.59
1:2A:568:U:O4	60:2A:3720:HOH:O	2.10	0.59
7:2H:29:PRO:HD2	7:2H:80:SER:HA	1.84	0.59
32:2a:673:G:H2'	32:2a:674:G:C8	2.36	0.59
32:2a:674:G:H2'	32:2a:675:A:H8	1.66	0.59
32:2a:770:C:OP1	60:2a:1805:HOH:O	2.16	0.59
32:2a:1083:U:OP2	60:2a:1804:HOH:O	2.16	0.59
54:2w:317:ILE:HD11	54:2w:339:LEU:HD12	1.84	0.59
14:1S:59:LYS:HE3	14:1S:60:GLY:H	1.67	0.59
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.83	0.59
54:1w:280:GLU:OE1	54:1w:284:ARG:NH1	2.35	0.59
1:2A:599:G:N7	60:2A:3823:HOH:O	2.31	0.59
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2427:C:OP1	60:2A:3727:HOH:O	2.17	0.59
25:23:8:LEU:HB2	25:23:28:LEU:HD13	1.85	0.59
24:12:9:GLN:HE22	24:12:56:GLN:HG2	1.67	0.59
35:1d:129:ASN:HD21	35:1d:144:ASP:HA	1.67	0.59
40:1i:28:VAL:O	40:1i:30:GLY:N	2.36	0.59
1:2A:483:A:H5"	20:2Y:50:ARG:HE	1.68	0.59
14:2S:11:LYS:HD3	14:2S:91:PRO:HD3	1.84	0.59
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.84	0.59
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.68	0.59
32:2a:1291:G:O2'	40:2i:38:GLN:NE2	2.33	0.59
1:1A:847:U:OP2	60:1A:3848:HOH:O	2.17	0.59
44:1m:3:ARG:HE	44:1m:8:GLU:HG3	1.67	0.59
1:2A:2504:U:OP2	60:2A:3751:HOH:O	2.16	0.59
8:2I:31:LEU:HD21	8:2I:38:LEU:HD12	1.85	0.59
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.38	0.59
32:2a:972:C:OP1	60:2a:1808:HOH:O	2.17	0.59
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.38	0.59
33:1b:231:GLU:HB3	33:1b:232:PRO:HD2	1.84	0.59
35:1d:8:VAL:HA	35:1d:11:LEU:HD13	1.84	0.59
50:1s:22:LEU:HD22	50:1s:27:GLU:HA	1.83	0.59
1:2A:212:G:H2'	1:2A:213:A:O4'	2.03	0.59
32:2a:701:C:OP1	32:2a:702:A:O2'	2.11	0.59
1:1A:883:G:N3	1:1A:884:C:N4	2.50	0.59
1:1A:2032:G:O2'	4:1E:145:LYS:NZ	2.24	0.59
5:1F:117:ARG:NH2	5:1F:189:THR:O	2.35	0.59
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.83	0.59
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.21	0.59
30:28:6:THR:HG23	30:28:62:LEU:HA	1.85	0.59
32:2a:316:G:OP2	32:2a:351:G:O2'	2.21	0.59
32:2a:1053:G:N2	32:2a:1058:G:O6	2.36	0.59
37:2f:2:ARG:HG2	37:2f:69:GLU:HG2	1.85	0.59
41:2j:7:LYS:HB2	41:2j:97:GLU:HB2	1.85	0.59
38:1g:16:LEU:HD11	40:1i:45:ALA:HB2	1.85	0.59
54:1w:115:THR:H	54:1w:196:THR:HG22	1.68	0.59
1:2A:131:G:OP1	60:2A:3749:HOH:O	2.16	0.59
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.36	0.59
2:2B:5:C:OP1	2:2B:61:G:O2'	2.20	0.59
7:2H:13:LYS:HA	7:2H:15:VAL:H	1.68	0.59
14:2S:25:ARG:O	14:2S:39:ILE:HA	2.02	0.59
32:2a:1270:C:HO2'	32:2a:1313:U:HO2'	1.51	0.59
44:2m:23:TYR:O	44:2m:67:GLU:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:41:G:H2'	32:1a:42:G:C8	2.38	0.58
33:1b:118:LEU:HD21	33:1b:138:LEU:HB3	1.83	0.58
54:1w:111:ILE:HB	54:1w:158:VAL:HG23	1.84	0.58
1:2A:956:G:OP2	12:2Q:14:ARG:NH2	2.36	0.58
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.84	0.58
32:2a:113:G:H1'	32:2a:354:G:H5'	1.84	0.58
32:2a:164:U:H2'	32:2a:165:C:C6	2.38	0.58
56:2z:10:GLN:HG2	56:2z:11:PRO:HD2	1.85	0.58
1:1A:1509(A):A:H3'	1:1A:1509(B):A:H8	1.69	0.58
20:1Y:5:MET:HE3	20:1Y:32:PRO:HA	1.85	0.58
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.18	0.58
33:1b:230:VAL:HG12	33:1b:231:GLU:H	1.67	0.58
1:2A:370:G:N7	60:2A:3828:HOH:O	2.32	0.58
1:2A:1395:A:OP1	60:2A:3753:HOH:O	2.17	0.58
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.68	0.58
1:2A:1853:A:N3	1:2A:2233:U:O2'	2.35	0.58
7:2H:25:LYS:HD2	7:2H:27:LYS:HE2	1.85	0.58
8:2I:101:LEU:HD12	8:2I:105:HIS:HB2	1.85	0.58
32:2a:56:U:H2'	32:2a:57:G:C8	2.37	0.58
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.34	0.58
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.68	0.58
40:2i:110:GLU:OE2	40:2i:113:LYS:NZ	2.37	0.58
1:1A:1653:G:H3'	13:1R:2:ARG:HD3	1.84	0.58
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.66	0.58
32:1a:1318:A:H5"	50:1s:3:ARG:HH11	1.67	0.58
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.39	0.58
32:2a:148:G:H2'	32:2a:149:A:C8	2.38	0.58
32:2a:523:A:N1	43:2l:92:0TD:H6	2.18	0.58
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.38	0.58
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.18	0.58
32:2a:1375:A:H4'	38:2g:29:LYS:HE3	1.84	0.58
1:1A:953:A:OP2	12:1Q:16:ARG:HD3	2.02	0.58
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.37	0.58
21:1Z:151:HIS:O	21:1Z:153:SER:N	2.32	0.58
32:1a:376:G:H4'	47:1p:5:ARG:HH11	1.68	0.58
35:1d:61:LYS:NZ	35:1d:72:GLU:OE1	2.35	0.58
4:2E:56:PRO:HG3	4:2E:74:PRO:HG2	1.85	0.58
32:2a:392:G:H2'	32:2a:393:A:H8	1.67	0.58
32:2a:1154:G:H2'	32:2a:1155:G:H8	1.69	0.58
35:2d:162:LEU:HD13	35:2d:181:MET:HG2	1.85	0.58
36:2e:98:THR:HG22	36:2e:99:GLY:H	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.39	0.58
1:1A:2124:G:N2	1:1A:2174:C:N3	2.46	0.58
1:1A:1359:A:N6	1:1A:1372:U:H3	2.01	0.58
1:1A:1756:G:O6	60:1A:3836:HOH:O	2.14	0.58
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.36	0.58
47:1p:53:VAL:HG12	47:1p:79:VAL:HG22	1.84	0.58
53:1v:11:U:H3'	53:1v:12:A:C8	2.38	0.58
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.85	0.58
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.39	0.58
5:2F:117:ARG:NH2	11:2P:1:MET:O	2.37	0.58
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.38	0.58
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.86	0.58
1:1A:1981:A:OP1	60:1A:3849:HOH:O	2.17	0.58
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.69	0.58
25:13:8:LEU:HB2	25:13:28:LEU:HD13	1.85	0.58
32:1a:391:G:OP1	47:1p:28:ARG:NH2	2.32	0.58
32:1a:1457:G:OP1	51:1t:39:LYS:NZ	2.35	0.58
1:1A:72:U:OP1	60:1A:3847:HOH:O	2.17	0.58
21:1Z:138:GLU:H	21:1Z:156:LYS:HZ1	1.50	0.58
44:1m:9:ILE:HG13	44:1m:45:VAL:HG11	1.84	0.58
1:2A:387:U:OP2	23:21:20:ARG:NH2	2.36	0.58
1:2A:1531:C:H42	1:2A:1538:G:H1	1.51	0.58
1:2A:2749:A:OP1	7:2H:3:ARG:NH1	2.37	0.58
2:2B:12:C:H2'	22:20:73:GLY:HA3	1.86	0.58
40:2i:19:LEU:O	40:2i:20:ARG:NH1	2.36	0.58
32:1a:271:C:H2'	32:1a:272:C:C6	2.39	0.58
32:1a:939:G:OP1	38:1g:95:ARG:NH2	2.32	0.58
32:1a:1318:A:H2'	32:1a:1319:A:H5"	1.85	0.58
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.37	0.58
37:1f:6:VAL:HG22	37:1f:90:VAL:HG22	1.86	0.58
44:1m:9:ILE:HB	44:1m:18:ALA:HB1	1.84	0.58
54:1w:135:ALA:HB1	54:1w:140:PHE:HB2	1.86	0.58
1:2A:646:A:H2'	1:2A:647:G:O4'	2.04	0.58
54:2w:243:HIS:ND1	54:2w:246:THR:OG1	2.37	0.58
1:1A:579:G:H2'	1:1A:580:C:C6	2.39	0.58
1:2A:601:C:OP1	5:2F:108:LYS:NZ	2.36	0.58
1:2A:2032:G:OP2	1:2A:2454:G:O2'	2.19	0.58
32:2a:950:U:H3	32:2a:1231:G:H1	1.52	0.58
32:2a:1221:G:OP1	32:2a:1320:C:N4	2.34	0.58
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.85	0.58
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1092:C:H42	1:1A:1099:G:H1	1.52	0.57
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	1.84	0.57
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.09	0.57
32:2a:1262:C:H2'	32:2a:1263:C:H5'	1.85	0.57
44:2m:19:LEU:HD11	44:2m:56:LEU:HD21	1.85	0.57
5:1F:70:THR:HB	56:1z:8:ILE:HG21	1.86	0.57
32:1a:490:G:H2'	32:1a:491:G:C8	2.38	0.57
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.37	0.57
54:1w:114:GLY:HA3	54:1w:196:THR:HG22	1.86	0.57
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.39	0.57
32:2a:1187:G:O2'	40:2i:111:ARG:NH1	2.37	0.57
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.85	0.57
33:1b:24:TRP:CE3	33:1b:26:PRO:HA	2.39	0.57
32:2a:450:G:H4'	47:2p:41:PRO:HB2	1.86	0.57
32:2a:728:A:H2'	32:2a:729:A:C8	2.39	0.57
1:1A:2790:A:H5'	1:1A:2893:G:H21	1.69	0.57
13:1R:36:THR:HG22	13:1R:37:THR:H	1.70	0.57
32:1a:1009:G:N2	32:1a:1021:G:O4'	2.38	0.57
34:1c:157:ILE:HD12	34:1c:164:ARG:HB3	1.86	0.57
42:1k:52:GLY:H	42:1k:55:LYS:HE2	1.69	0.57
1:2A:1341:U:OP2	1:2A:1394:U:O2'	2.22	0.57
6:2G:73:ALA:HB3	6:2G:85:GLY:H	1.68	0.57
1:1A:2790:A:H3'	1:1A:2790:A:N3	2.19	0.57
32:1a:100:C:H2'	32:1a:101:A:C8	2.39	0.57
32:1a:382:A:H2'	32:1a:383:A:H8	1.67	0.57
1:2A:2667:C:H1'	7:2H:109:PHE:HD1	1.67	0.57
32:2a:433:C:H2'	32:2a:434:U:C6	2.40	0.57
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.86	0.57
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	1.86	0.57
1:1A:184:C:H2'	1:1A:185:U:C6	2.39	0.57
1:1A:2206:G:H5"	1:1A:2207:G:C5	2.39	0.57
32:1a:1307:U:OP1	44:1m:101:GLN:NE2	2.37	0.57
35:1d:155:LEU:HD22	35:1d:156:GLU:H	1.70	0.57
1:2A:479:A:N3	1:2A:481:G:H5"	2.19	0.57
1:2A:987:G:O2'	1:2A:1000:A:N3	2.34	0.57
3:2D:93:ALA:HB3	3:2D:105:ILE:HG13	1.86	0.57
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.84	0.57
32:2a:45:U:H2'	32:2a:46:G:C8	2.39	0.57
33:2b:197:VAL:HB	33:2b:200:ILE:HG12	1.86	0.57
55:2x:9:A:O2'	55:2x:10:G:N7	2.37	0.57
12:1Q:14:ARG:HG2	12:1Q:41:TRP:CH2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.39	0.57
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.40	0.57
33:1b:208:ILE:HA	33:1b:211:ILE:HD12	1.87	0.57
1:2A:1365:A:OP1	23:21:41:ARG:NH1	2.33	0.57
32:2a:189(K):U:H2'	32:2a:189(L):G:H8	1.70	0.57
32:2a:411:A:OP2	35:2d:25:ARG:NH2	2.37	0.57
32:2a:413:G:H22	32:2a:429:U:H5"	1.69	0.57
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.86	0.57
5:1F:148:LEU:HD11	5:1F:193:VAL:HG21	1.86	0.57
21:1Z:93:ASP:HB3	21:1Z:131:ARG:HH22	1.69	0.57
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.21	0.57
1:2A:247:G:H4'	1:2A:386:G:C5	2.40	0.57
1:2A:1026:U:OP1	60:2A:3736:HOH:O	2.17	0.57
1:2A:1957:C:OP1	60:2A:3752:HOH:O	2.17	0.57
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.86	0.57
1:1A:1508:A:O2'	1:1A:1509:C:H5"	2.05	0.57
1:1A:1996:C:OP1	10:1O:31:LYS:NZ	2.34	0.57
1:1A:2454:G:OP2	60:1A:3844:HOH:O	2.17	0.57
1:1A:2499:C:N3	60:1A:3924:HOH:O	2.33	0.57
47:1p:45:THR:HG23	47:1p:47:ASP:H	1.68	0.57
1:2A:579:G:H2'	1:2A:580:C:C6	2.40	0.57
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.32	0.57
33:2b:9:GLU:O	33:2b:11:LEU:N	2.32	0.57
38:2g:91:VAL:HG23	38:2g:95:ARG:HB3	1.86	0.57
54:2w:182:ARG:HB3	54:2w:307:PHE:HB2	1.87	0.57
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.38	0.57
32:1a:620:C:C2	35:1d:135:LEU:HG	2.40	0.57
32:1a:1445:C:H2'	32:1a:1446:U:O4'	2.05	0.57
32:1a:1469:G:N7	60:1a:1819:HOH:O	2.32	0.57
60:1a:1804:HOH:O	53:1v:19:U:OP1	2.17	0.57
33:1b:223:ILE:HD12	33:1b:230:VAL:H	1.70	0.57
36:1e:144:THR:OG1	36:1e:147:ASP:OD2	2.20	0.57
38:1g:111:ARG:NH2	38:1g:126:ASP:OD2	2.38	0.57
1:2A:1349:A:OP1	60:2A:3750:HOH:O	2.16	0.57
1:2A:1394:U:OP1	60:2A:3754:HOH:O	2.18	0.57
1:2A:2060:A:N3	60:2A:3829:HOH:O	2.33	0.57
6:2G:37:VAL:HG21	6:2G:103:LEU:HD21	1.87	0.57
35:2d:163:GLU:O	35:2d:166:LYS:HG2	2.05	0.57
32:1a:834:C:H2'	32:1a:835:U:C6	2.39	0.56
1:2A:1642:G:N7	60:2A:3830:HOH:O	2.33	0.56
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:1:MET:N	24:22:52:ASP:OD1	2.27	0.56
1:1A:271(L):U:H4'	8:1I:50:ARG:HH22	1.70	0.56
5:1F:195:ASP:HB2	5:1F:198:ALA:H	1.68	0.56
32:1a:1379:G:O6	38:1g:2:ALA:N	2.38	0.56
32:2a:1310:G:OP2	44:2m:88:ARG:NH2	2.37	0.56
33:2b:76:GLN:OE1	33:2b:76:GLN:N	2.38	0.56
35:2d:57:ARG:NH2	35:2d:205:GLU:OE1	2.31	0.56
1:1A:1296:G:OP1	1:1A:2709:G:O2'	2.17	0.56
1:1A:2206:G:H3'	1:1A:2207:G:N7	2.19	0.56
1:1A:2469:A:H4'	12:1Q:56:ARG:HG2	1.86	0.56
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.40	0.56
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.23	0.56
32:1a:1048:G:H5"	45:1n:3:ARG:HB3	1.86	0.56
32:1a:1402:4OC:OP1	60:1a:1810:HOH:O	2.17	0.56
41:1j:13:HIS:H	41:1j:13:HIS:CD2	2.21	0.56
51:1t:33:ILE:O	51:1t:37:SER:OG	2.23	0.56
1:2A:30:G:H2'	1:2A:31:C:C6	2.39	0.56
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.23	0.56
13:2R:96:ARG:NH1	13:2R:115:GLU:OE2	2.37	0.56
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.34	0.56
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HG	1.85	0.56
26:24:16:CYS:SG	26:24:17:GLY:N	2.79	0.56
34:2c:6:HIS:CD2	34:2c:8:ILE:HG12	2.41	0.56
34:2c:184:TYR:HD1	34:2c:201:TYR:HE1	1.51	0.56
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.27	0.56
1:1A:1088:A:H4'	1:1A:1089:G:C8	2.39	0.56
32:1a:975:A:N1	41:1j:48:THR:HB	2.20	0.56
44:1m:76:ALA:HA	44:1m:79:LYS:HB3	1.88	0.56
14:2S:52:SER:HB2	14:2S:55:ALA:H	1.71	0.56
14:2S:66:ALA:O	14:2S:69:VAL:HG12	2.04	0.56
18:2W:18:ARG:HG2	18:2W:76:VAL:HB	1.88	0.56
8:1I:123:LEU:HA	8:1I:144:VAL:HG23	1.87	0.56
55:1x:5:G:O6	60:1x:201:HOH:O	2.18	0.56
1:2A:800:A:H8	1:2A:800:A:OP1	1.89	0.56
3:2D:26:LYS:HB3	3:2D:83:GLU:HG2	1.86	0.56
16:2U:76:TYR:HH	16:2U:92:ARG:HE	1.53	0.56
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.53	0.56
34:2c:66:VAL:HG23	34:2c:101:LEU:HA	1.88	0.56
1:1A:592:G:O6	60:1A:3843:HOH:O	2.16	0.56
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.40	0.56
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:76:G:O3'	21:1Z:19:ARG:NH2	2.39	0.56
12:1Q:31:ASP:OD1	12:1Q:134:ARG:NH1	2.37	0.56
32:1a:1027:C:C2	32:1a:1034:G:N2	2.73	0.56
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.69	0.56
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.40	0.56
4:2E:34:VAL:HB	4:2E:48:GLN:HE21	1.69	0.56
5:2F:40:GLN:HE22	5:2F:182:ASN:HB2	1.70	0.56
15:2T:16:ARG:NH1	15:2T:18:ASP:OD2	2.38	0.56
32:2a:1133:G:H1	32:2a:1141:C:H42	1.54	0.56
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.41	0.56
32:1a:236:G:H5"	48:1q:42:TYR:OH	2.05	0.56
1:2A:315:G:H2'	1:2A:316:C:C6	2.41	0.56
14:2S:61:ASN:O	14:2S:65:VAL:HG12	2.05	0.56
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.86	0.56
32:2a:43:C:H42	32:2a:399:G:H1	1.54	0.56
32:2a:532:A:H2	34:2c:156:ARG:HH22	1.51	0.56
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.05	0.56
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.38	0.56
1:1A:322:A:OP1	5:1F:168:ARG:NH1	2.39	0.56
1:1A:593:G:H4'	30:18:4:MET:HE2	1.88	0.56
1:1A:1163:G:OP1	17:1V:24:LYS:NZ	2.37	0.56
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.40	0.56
3:1D:145:VAL:HB	3:1D:155:LEU:HD12	1.87	0.56
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.88	0.56
23:11:50:ARG:NH1	23:11:57:GLU:OE2	2.34	0.56
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.40	0.56
1:2A:643:A:N1	1:2A:2369:A:O2'	2.37	0.56
1:2A:2148:G:H2'	1:2A:2149:G:C8	2.41	0.56
32:2a:1263:C:C4	32:2a:1272:G:O6	2.59	0.56
35:2d:175:SER:HB3	35:2d:186:LEU:HD21	1.87	0.56
55:2y:67:C:H2'	55:2y:68:C:C6	2.40	0.56
8:1I:27:ARG:HD3	23:11:71:TYR:CE2	2.41	0.56
1:2A:652(B):A:H61	1:2A:655:A:H1'	1.71	0.56
1:2A:2136:C:N3	1:2A:2155:G:N2	2.53	0.56
7:2H:3:ARG:HH21	7:2H:65:HIS:HB3	1.70	0.56
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.68	0.56
34:2c:18:TRP:CD1	45:2n:54:PRO:HA	2.41	0.56
55:2x:58:A:O2'	55:2x:60:U:OP2	2.24	0.56
1:1A:271(L):U:H4'	8:1I:50:ARG:HH12	1.71	0.56
1:1A:1652:A:OP1	13:1R:8:ARG:NH1	2.39	0.56
3:1D:26:LYS:HB3	3:1D:83:GLU:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.88	0.56
32:1a:1063:C:H3'	32:1a:1064:G:H2'	1.87	0.56
35:1d:163:GLU:C	35:1d:165:MET:H	2.13	0.56
55:1y:45:U:H3'	55:1y:46:G7M:H5"	1.88	0.56
1:2A:1609:A:OP2	60:2A:3755:HOH:O	2.18	0.56
4:2E:143:ASN:HB2	4:2E:147:PRO:HD2	1.88	0.56
7:2H:27:LYS:NZ	7:2H:32:GLU:OE1	2.33	0.56
21:2Z:133:ILE:HG22	21:2Z:135:GLU:HG2	1.88	0.56
32:2a:1371:G:H5"	40:2i:69:GLY:H	1.70	0.56
29:17:11:LYS:O	29:17:15:THR:OG1	2.23	0.55
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.06	0.55
32:1a:1137:C:O2'	32:1a:1138:G:N2	2.39	0.55
33:1b:9:GLU:H	33:1b:217:ARG:HH12	1.54	0.55
1:2A:856:C:H2'	1:2A:857:C:C6	2.41	0.55
1:2A:2454:G:O6	60:2A:3757:HOH:O	2.18	0.55
11:2P:29:LYS:HD3	11:2P:30:THR:HG23	1.87	0.55
14:2S:39:ILE:HB	14:2S:49:VAL:HG12	1.87	0.55
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.04	0.55
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.06	0.55
4:2E:168:MET:HE2	4:2E:203:LYS:HE2	1.88	0.55
21:2Z:4:ARG:NH1	21:2Z:60:GLU:OE2	2.38	0.55
32:2a:1320:C:OP1	50:2s:70:LYS:NZ	2.34	0.55
1:1A:1056:G:H5'	1:1A:1085:A:N1	2.21	0.55
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.88	0.55
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.40	0.55
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	1.88	0.55
12:2Q:78:PRO:HD2	12:2Q:81:VAL:HG21	1.88	0.55
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.39	0.55
32:2a:736:C:H2'	32:2a:737:A:C8	2.42	0.55
55:2x:31:A:H2'	55:2x:32:PSU:H6	1.72	0.55
1:1A:272(D):G:N7	60:1A:3929:HOH:O	2.33	0.55
24:12:65:ASN:O	24:12:69:ARG:HG3	2.07	0.55
33:1b:76:GLN:HB3	33:1b:208:ILE:HG13	1.88	0.55
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.32	0.55
43:1l:117:ARG:HB3	43:1l:122:THR:HB	1.89	0.55
47:1p:18:ARG:NH1	47:1p:32:TYR:OH	2.39	0.55
1:2A:2141:G:N2	1:2A:2151:G:H1'	2.21	0.55
16:2U:88:ILE:HG22	16:2U:90:VAL:HG22	1.89	0.55
37:2f:11:ASN:HB3	37:2f:14:LEU:HD13	1.89	0.55
38:2g:94:ARG:O	38:2g:97:GLN:HB3	2.06	0.55
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:13:HIS:O	41:1j:17:ASP:N	2.39	0.55
32:2a:91:C:H2'	32:2a:92:C:C6	2.42	0.55
35:2d:172:PRO:HB2	35:2d:187:ARG:HH21	1.72	0.55
15:1T:84:GLN:HG2	15:1T:85:LYS:HG2	1.86	0.55
26:14:40:HIS:CE1	26:14:42:PHE:HB3	2.41	0.55
32:1a:1130:A:OP1	40:1i:16:ARG:NH2	2.39	0.55
32:1a:1291:G:OP1	38:1g:41:ARG:NH1	2.37	0.55
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.71	0.55
1:2A:668:G:H5'	1:2A:669:G:OP2	2.06	0.55
1:2A:1300:U:H4'	1:2A:1301:A:H5"	1.89	0.55
6:2G:11:TYR:HA	6:2G:15:VAL:HG12	1.89	0.55
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.88	0.55
33:2b:93:VAL:HG21	33:2b:97:TRP:HD1	1.71	0.55
39:2h:51:VAL:HG12	39:2h:52:ASP:H	1.72	0.55
1:1A:947:G:OP2	60:1A:3852:HOH:O	2.18	0.55
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.42	0.55
1:1A:2808:U:H5"	1:1A:2891:G:O6	2.07	0.55
33:1b:19:HIS:HB3	33:1b:204:ASN:HD22	1.71	0.55
1:2A:1039:G:H1	1:2A:1116:C:H42	1.55	0.55
1:2A:1937:A:H1'	1:2A:1939:5MU:H72	1.88	0.55
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.89	0.55
21:2Z:51:ALA:HA	21:2Z:55:HIS:HD2	1.72	0.55
38:2g:49:ILE:HG23	38:2g:53:LYS:HE3	1.89	0.55
55:2y:68:C:C2'	55:2y:69:G:H5'	2.36	0.55
17:1V:95:LEU:HD23	17:1V:97:LYS:HE3	1.89	0.55
32:1a:1027:C:N4	32:1a:1034:G:C5	2.74	0.55
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	1.89	0.55
1:2A:1932:A:OP2	60:2A:3756:HOH:O	2.18	0.55
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.07	0.55
8:2I:75:LEU:HD11	8:2I:105:HIS:NE2	2.21	0.55
32:2a:134:A:H61	47:2p:25:ARG:NH1	2.05	0.55
32:2a:539:A:H2'	32:2a:540:G:C8	2.41	0.55
55:2x:51:U:H3	55:2x:63:G:H1	1.54	0.55
17:1V:60:GLU:OE1	17:1V:97:LYS:NZ	2.30	0.55
23:11:7:ILE:HG21	23:11:69:LYS:HG2	1.89	0.55
32:1a:585:G:OP1	48:1q:37:LYS:NZ	2.40	0.55
32:1a:1288:A:N1	32:1a:1371:G:H1'	2.22	0.55
1:2A:127:A:H5"	1:2A:128:C:C6	2.42	0.55
1:2A:211:A:H2'	1:2A:212:G:O4'	2.05	0.55
32:2a:601:C:H2'	32:2a:602:A:C8	2.42	0.55
32:2a:979:C:H42	45:2n:18:VAL:HG12	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:68:TYR:OH	35:2d:98:GLU:OE1	2.23	0.55
35:2d:153:ARG:NH1	35:2d:180:GLY:O	2.40	0.55
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.40	0.55
32:1a:613:C:H42	32:1a:627:G:H1	1.55	0.55
32:1a:1103:C:OP1	33:1b:96:ARG:NH2	2.40	0.55
32:1a:1389:C:H2'	32:1a:1390:U:O4'	2.07	0.55
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.07	0.55
21:2Z:134:PRO:C	21:2Z:136:PHE:H	2.13	0.55
32:2a:67:C:H2'	32:2a:68:G:C8	2.41	0.55
32:2a:716:A:N3	42:2k:118:GLY:HA2	2.21	0.55
32:2a:1072:G:H2'	32:2a:1073:U:C6	2.42	0.55
1:1A:1082:U:O4	1:1A:1086:A:N1	2.40	0.54
32:1a:96:U:H2'	32:1a:97:G:C8	2.42	0.54
32:1a:165:C:H2'	32:1a:166:G:C8	2.41	0.54
33:1b:10:LEU:O	33:1b:12:GLU:N	2.37	0.54
33:1b:126:GLU:HG3	33:1b:127:ILE:HG13	1.89	0.54
41:1j:45:ARG:HB3	41:1j:65:LEU:HB3	1.88	0.54
2:2B:117:G:H4'	14:2S:54:LEU:HG	1.88	0.54
32:2a:171:A:H2'	32:2a:172:A:C8	2.41	0.54
32:2a:392:G:H2'	32:2a:393:A:C8	2.41	0.54
32:2a:558:G:O6	60:2a:1809:HOH:O	2.18	0.54
33:2b:178:ARG:NH2	39:2h:68:ARG:HH22	2.03	0.54
37:2f:82:ARG:HB2	37:2f:85:VAL:HG23	1.88	0.54
32:1a:1134:G:H2'	32:1a:1135:U:H5'	1.89	0.54
32:1a:1182:G:H4'	32:1a:1183:A:H5"	1.90	0.54
51:1t:77:ALA:O	51:1t:81:LYS:HG3	2.06	0.54
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.41	0.54
1:2A:2140:C:N4	1:2A:2151:G:H1	2.05	0.54
8:2I:75:LEU:HD21	8:2I:105:HIS:CD2	2.42	0.54
9:2N:35:ARG:HB2	9:2N:37:LYS:HG3	1.89	0.54
26:24:61:ARG:HH21	50:2s:41:VAL:HG12	1.72	0.54
32:2a:444:C:H2'	32:2a:445:G:C8	2.42	0.54
32:2a:1052:U:O2'	32:2a:1055:A:OP2	2.12	0.54
44:2m:23:TYR:CE2	44:2m:71:ARG:HG2	2.42	0.54
1:1A:2161:C:O2'	1:1A:2162:G:H5"	2.08	0.54
1:1A:2400:G:O6	60:1A:3841:HOH:O	2.16	0.54
1:1A:2870:C:H5"	13:1R:65:LEU:HD21	1.88	0.54
32:1a:1466:C:H2'	32:1a:1467:G:O4'	2.07	0.54
2:2B:3:C:H2'	2:2B:4:C:C6	2.43	0.54
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.42	0.54
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:68:ASN:ND2	38:2g:127:ALA:O	2.30	0.54
1:1A:809:G:OP2	60:1A:3853:HOH:O	2.18	0.54
1:1A:1263:U:OP1	27:15:16:ARG:NH1	2.37	0.54
1:1A:1665:A:OP2	60:1A:3854:HOH:O	2.18	0.54
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.08	0.54
1:1A:2238:G:N3	1:1A:2238:G:H2'	2.23	0.54
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.07	0.54
32:1a:504:C:H2'	32:1a:511:C:H5	1.73	0.54
32:1a:544:G:OP1	35:1d:62:GLN:NE2	2.38	0.54
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.40	0.54
1:2A:1434:A:H61	1:2A:1558:A:H62	1.56	0.54
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.42	0.54
32:2a:377:G:OP1	47:2p:3:LYS:HD2	2.08	0.54
32:2a:1150:U:O4	32:2a:1151:A:N6	2.41	0.54
32:2a:1264:C:H2'	32:2a:1265:G:C8	2.43	0.54
32:2a:1267:C:H1'	52:2u:20:LYS:HE3	1.89	0.54
32:2a:1273:G:H3'	32:2a:1274:G:O4'	2.06	0.54
1:1A:2140:C:O2	1:1A:2152:G:N1	2.40	0.54
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.40	0.54
32:1a:136:C:O3'	47:1p:65:GLN:NE2	2.41	0.54
1:2A:515:A:H1'	1:2A:581:C:H1'	1.90	0.54
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.23	0.54
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.43	0.54
1:1A:793:A:OP2	1:1A:2071:A:O2'	2.24	0.54
6:1G:21:ARG:HA	6:1G:21:ARG:NH1	2.23	0.54
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.07	0.54
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.43	0.54
8:2I:77:LEU:HD13	8:2I:101:LEU:HD13	1.90	0.54
32:2a:1006:C:N3	32:2a:1023:G:N2	2.47	0.54
32:2a:1316:G:H5"	45:2n:17:LYS:HD3	1.90	0.54
41:2j:57:LYS:O	41:2j:59:SER:N	2.38	0.54
18:1W:19:LEU:HB3	27:15:25:LEU:HG	1.88	0.54
32:1a:347:G:H2'	32:1a:348:G:C8	2.39	0.54
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.88	0.54
46:1o:26:GLU:HG3	46:1o:81:LEU:HD13	1.90	0.54
2:2B:60:C:H2'	2:2B:61:G:C8	2.43	0.54
6:2G:96:ARG:HA	6:2G:99:MET:HE2	1.90	0.54
32:2a:325:A:OP2	51:2t:70:SER:HB3	2.08	0.54
1:1A:1199:U:OP1	60:1A:3850:HOH:O	2.18	0.54
32:1a:1289:A:N1	32:1a:1371:G:O2'	2.39	0.54
54:1w:200:ALA:HB2	54:1w:293:ILE:HG13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2529:G:H5"	1:2A:2530:A:H5"	1.90	0.54
1:2A:2627:G:N2	1:2A:2777:G:OP2	2.41	0.54
20:2Y:13:VAL:HB	20:2Y:72:VAL:HG13	1.90	0.54
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.42	0.54
32:1a:192:U:H2'	32:1a:193:C:H6	1.73	0.54
43:1l:44:THR:HG21	54:1w:297:GLU:HG2	1.89	0.54
1:2A:2316:C:H2'	1:2A:2317:C:C6	2.43	0.54
6:2G:16:ARG:NH1	6:2G:31:VAL:HB	2.23	0.54
22:20:72:ARG:HB3	22:20:75:LEU:HB2	1.90	0.54
40:2i:46:ALA:O	40:2i:49:PRO:HD2	2.07	0.54
6:1G:21:ARG:HA	6:1G:21:ARG:HH11	1.73	0.54
32:1a:67:C:H2'	32:1a:68:G:C8	2.42	0.54
32:1a:979:C:OP1	32:1a:1223:C:N4	2.41	0.54
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.23	0.54
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.42	0.54
42:1k:59:TYR:CZ	42:1k:63:LEU:HD11	2.43	0.54
54:1w:198:THR:HG21	54:1w:293:ILE:HG23	1.89	0.54
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.90	0.54
32:2a:1346:A:H2'	38:2g:10:ARG:HH22	1.73	0.54
38:2g:113:GLU:HB2	38:2g:119:ARG:HG2	1.90	0.54
44:2m:48:LEU:HD22	44:2m:53:VAL:HG23	1.90	0.54
1:1A:264:C:O2'	1:1A:265:A:H2'	2.08	0.53
1:1A:1289:C:H2'	1:1A:1290:C:H6	1.72	0.53
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.43	0.53
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.07	0.53
33:1b:178:ARG:NH2	39:1h:68:ARG:HH22	2.06	0.53
34:1c:77:ILE:O	34:1c:84:ILE:N	2.35	0.53
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.41	0.53
6:2G:125:PHE:HB3	6:2G:166:ASP:OD1	2.07	0.53
6:2G:135:LEU:HD21	6:2G:140:ILE:HD11	1.90	0.53
39:2h:36:LEU:HD23	39:2h:39:LEU:HD12	1.90	0.53
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.91	0.53
22:10:30:VAL:HG22	22:10:66:VAL:HG22	1.90	0.53
32:1a:749:C:H2'	32:1a:750:G:H8	1.73	0.53
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.34	0.53
3:2D:70:TRP:NE1	3:2D:146:GLU:OE2	2.34	0.53
12:2Q:55:VAL:HG11	21:2Z:183:LEU:HD21	1.90	0.53
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.42	0.53
33:2b:87:ARG:HB3	33:2b:219:VAL:HG11	1.89	0.53
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.90	0.53
35:2d:122:ARG:NH2	35:2d:134:ASP:O	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:97:PRO:HA	44:2m:110:ARG:HG2	1.89	0.53
49:2r:58:LEU:HD23	49:2r:58:LEU:H	1.73	0.53
54:2w:225:SER:H	54:2w:253:GLN:HE22	1.54	0.53
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.43	0.53
27:15:47:PRO:O	27:15:60:VAL:HG11	2.08	0.53
32:1a:1067:A:H3'	32:1a:1094:G:OP1	2.08	0.53
36:1e:148:VAL:HG21	39:1h:107:LEU:HD23	1.89	0.53
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.90	0.53
32:2a:1000:U:H3	32:2a:1041:A:H61	1.55	0.53
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.44	0.53
32:2a:1400:5MC:O2	54:2w:188:THR:HG21	2.08	0.53
1:1A:2108:C:H2'	1:1A:2109:U:H6	1.74	0.53
1:1A:2494:G:O2'	12:1Q:80:GLU:HA	2.08	0.53
1:1A:2637:U:H5"	4:1E:82:ARG:NH1	2.23	0.53
5:1F:150:GLY:HA2	5:1F:172:TRP:CD2	2.43	0.53
20:1Y:8:LYS:HD2	20:1Y:97:ARG:HH21	1.73	0.53
25:13:38:GLU:O	25:13:43:ILE:HD12	2.09	0.53
32:1a:435:C:H2'	32:1a:436:C:C6	2.44	0.53
32:1a:539:A:H2'	32:1a:540:G:C8	2.43	0.53
48:1q:45:HIS:HB3	48:1q:72:ARG:HB3	1.90	0.53
4:2E:176:ILE:HB	4:2E:181:LEU:HB2	1.89	0.53
34:2c:8:ILE:HD11	45:2n:50:LYS:HA	1.89	0.53
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.43	0.53
1:1A:1460:A:H4'	1:1A:1461:G:OP2	2.08	0.53
1:1A:2149:G:C2	1:1A:2150:U:H1'	2.43	0.53
18:1W:10:VAL:HG12	18:1W:12:ILE:HG22	1.90	0.53
21:1Z:73:GLN:HB3	21:1Z:87:ASP:HB2	1.90	0.53
32:1a:781:A:O2'	32:1a:1522:U:O2	2.26	0.53
32:1a:1446:U:H4'	32:1a:1447:A:C5	2.44	0.53
33:1b:16:HIS:CD2	33:1b:17:PHE:H	2.27	0.53
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.25	0.53
8:2I:27:ARG:HD3	23:21:71:TYR:CE2	2.43	0.53
12:2Q:52:VAL:HG13	21:2Z:183:LEU:HD13	1.90	0.53
25:23:8:LEU:O	25:23:32:GLN:N	2.38	0.53
33:2b:128:GLU:OE1	33:2b:135:GLN:NE2	2.40	0.53
46:2o:62:GLN:O	46:2o:66:LEU:HG	2.09	0.53
9:1N:38:HIS:NE2	9:1N:50:ASP:OD2	2.41	0.53
32:1a:130:A:OP2	48:1q:63:ARG:NH1	2.36	0.53
52:1u:3:LYS:HD3	52:1u:14:TRP:CD1	2.44	0.53
55:1y:3:C:H42	55:1y:70:G:H1	1.56	0.53
1:2A:1204:A:H2	1:2A:1241:A:H62	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.74	0.53
2:2B:11:C:H2'	2:2B:15:A:H61	1.74	0.53
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.89	0.53
50:2s:22:LEU:O	50:2s:27:GLU:N	2.41	0.53
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.23	0.53
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.91	0.53
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.24	0.53
33:1b:220:ASP:O	33:1b:223:ILE:HG12	2.09	0.53
34:1c:29:TYR:CE2	45:1n:54:PRO:HD2	2.44	0.53
1:2A:1908:C:O2	55:2x:12:U:H4'	2.09	0.53
2:2B:59:A:H2'	2:2B:60:C:O4'	2.08	0.53
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.44	0.53
32:2a:149:A:OP2	60:2a:1811:HOH:O	2.19	0.53
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.09	0.53
38:2g:118:VAL:HG13	38:2g:122:HIS:CE1	2.43	0.53
50:2s:38:SER:HB2	50:2s:71:LEU:HD13	1.91	0.53
1:1A:1056:G:H1'	1:1A:1103:A:H61	1.73	0.53
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.91	0.53
32:1a:278:G:OP2	48:1q:41:LYS:NZ	2.41	0.53
54:1w:110:GLU:HG2	54:1w:159:VAL:HG13	1.91	0.53
1:2A:154(A):C:H42	1:2A:171:G:H1	1.57	0.53
1:2A:463:G:N2	1:2A:466:A:OP2	2.40	0.53
1:2A:1819:A:H5"	3:2D:161:THR:HG21	1.90	0.53
32:2a:404:U:H2'	32:2a:405:U:C6	2.44	0.53
33:2b:114:ARG:O	33:2b:118:LEU:HB2	2.09	0.53
41:2j:57:LYS:C	41:2j:59:SER:H	2.17	0.53
1:1A:2115:G:H21	1:1A:2171:A:H61	1.57	0.53
32:1a:435:C:H2'	32:1a:436:C:H6	1.73	0.53
32:1a:503:C:H2'	32:1a:504:C:H6	1.74	0.53
32:1a:539:A:H2'	32:1a:540:G:H8	1.74	0.53
54:1w:216:GLU:HB2	54:1w:245:PRO:HD3	1.91	0.53
1:2A:330:A:H2	1:2A:1210:A:H2'	1.73	0.53
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.89	0.53
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.41	0.53
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.90	0.53
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.43	0.53
38:2g:29:LYS:HB3	38:2g:105:VAL:HG21	1.90	0.53
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.44	0.53
1:1A:911:A:OP1	60:1A:3856:HOH:O	2.19	0.53
22:10:26:TYR:H	22:10:29:GLN:NE2	2.07	0.53
32:1a:1004:A:H2'	32:1a:1038:C:H1'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1069:C:O2'	32:1a:1192:C:H1'	2.08	0.53
36:1e:77:PRO:HD2	36:1e:142:LEU:HD22	1.89	0.53
1:2A:858:U:O2	1:2A:2268:A:H2'	2.09	0.53
1:2A:2129:C:H42	1:2A:2159:G:H1	0.69	0.53
39:2h:41:ARG:NH2	39:2h:123:GLU:OE2	2.42	0.53
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.07	0.52
32:1a:1367:C:H5'	41:1j:60:ARG:CZ	2.39	0.52
36:1e:152:ARG:HA	39:1h:64:LYS:NZ	2.24	0.52
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.44	0.52
1:2A:686:G:H21	1:2A:788:A:H61	1.56	0.52
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.22	0.52
4:2E:28:ALA:HB3	4:2E:93:VAL:HG13	1.90	0.52
20:2Y:34:LYS:HE3	20:2Y:36:ALA:HB2	1.91	0.52
20:2Y:51:VAL:HG22	20:2Y:58:GLY:HA3	1.91	0.52
22:20:43:THR:O	22:20:43:THR:OG1	2.22	0.52
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.19	0.52
32:1a:1064:G:H1'	32:1a:1190:G:N2	2.25	0.52
1:2A:892:G:H2'	1:2A:893:C:H4'	1.91	0.52
1:2A:2582:G:OP2	60:2A:3758:HOH:O	2.18	0.52
14:2S:35:ILE:HG23	14:2S:69:VAL:HG11	1.91	0.52
32:2a:266:G:H2'	32:2a:266:G:N3	2.25	0.52
32:2a:1086:U:H3	32:2a:1099:G:H22	1.55	0.52
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.44	0.52
34:2c:91:LEU:HD21	34:2c:101:LEU:HD22	1.90	0.52
41:2j:32:ALA:HB2	41:2j:81:THR:HG21	1.91	0.52
41:2j:64:GLU:OE2	41:2j:66:ARG:NH1	2.43	0.52
23:11:7:ILE:HG23	23:11:98:LEU:HD11	1.91	0.52
32:1a:377:G:H2'	32:1a:378:G:C8	2.44	0.52
1:2A:2478:A:H5'	31:29:31:LYS:HE2	1.90	0.52
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.91	0.52
32:2a:715:A:H2'	32:2a:716:A:C8	2.43	0.52
1:1A:1930:G:O2'	1:1A:1968:G:O6	2.20	0.52
1:1A:2097:C:H42	1:1A:2192:G:H1	1.57	0.52
2:1B:13:A:N1	2:1B:69:G:O2'	2.40	0.52
6:1G:109:VAL:C	6:1G:112:PRO:HD2	2.35	0.52
15:1T:108:ARG:HH21	15:1T:112:ARG:HD3	1.74	0.52
32:1a:807:A:H2'	32:1a:808:C:C6	2.44	0.52
32:1a:1172:C:H2'	32:1a:1173:G:H8	1.75	0.52
33:1b:16:HIS:HB3	33:1b:210:SER:HB3	1.91	0.52
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.34	0.52
51:1t:63:ILE:HD13	51:1t:80:ARG:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:954:G:H5"	12:2Q:13:GLN:HB3	1.92	0.52
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.43	0.52
5:2F:34:TRP:HA	11:2P:6:LEU:HD13	1.90	0.52
8:2I:40:THR:OG1	8:2I:43:ASN:OD1	2.22	0.52
32:2a:7:G:H2'	36:2e:119:LEU:HD22	1.91	0.52
32:2a:352:C:H4'	32:2a:354:G:OP1	2.10	0.52
32:2a:1109:C:H2'	32:2a:1110:A:O4'	2.09	0.52
51:2t:50:GLU:H	51:2t:99:LEU:HD12	1.74	0.52
1:1A:1289:C:H2'	1:1A:1290:C:C6	2.44	0.52
21:1Z:28:MET:O	21:1Z:34:ASN:HA	2.10	0.52
32:1a:159:G:N2	32:1a:161:A:H3'	2.25	0.52
32:1a:448:A:P	32:1a:485:G:H22	2.32	0.52
32:1a:1095:U:P	32:1a:1108:G:H1	2.32	0.52
44:1m:37:THR:HB	44:1m:55:ARG:HD3	1.92	0.52
1:2A:2289:G:OP1	60:2A:3761:HOH:O	2.19	0.52
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.44	0.52
1:2A:2722:G:OP2	60:2A:3760:HOH:O	2.19	0.52
3:2D:134:ARG:NH2	3:2D:188:GLU:OE2	2.43	0.52
3:2D:155:LEU:HD13	3:2D:177:LEU:HD22	1.91	0.52
14:2S:34:HIS:CD2	14:2S:54:LEU:HB2	2.45	0.52
21:2Z:157:LEU:HD11	21:2Z:163:LEU:HB2	1.92	0.52
26:24:49:PHE:HE1	44:2m:62:ASN:HA	1.74	0.52
32:2a:634:C:H2'	32:2a:635:G:H8	1.74	0.52
32:2a:811:C:O2'	32:2a:901:A:N1	2.43	0.52
35:2d:159:ARG:O	35:2d:163:GLU:N	2.38	0.52
55:2x:65:G:H2'	55:2x:66:U:C6	2.43	0.52
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.25	0.52
32:1a:35:G:O2'	43:1l:118:SER:O	2.22	0.52
32:1a:70:G:H1	32:1a:99:U:H3	1.57	0.52
32:1a:352:C:O2'	32:1a:354:G:OP1	2.23	0.52
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.39	0.52
33:1b:16:HIS:CG	33:1b:17:PHE:H	2.28	0.52
1:2A:372:G:O2'	1:2A:400:G:O6	2.22	0.52
1:2A:1009:A:OP2	60:2A:3759:HOH:O	2.19	0.52
1:2A:2818:G:OP1	1:2A:2837:G:O2'	2.26	0.52
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.56	0.52
5:2F:117:ARG:HH21	5:2F:187:VAL:HA	1.73	0.52
10:2O:36:GLY:HA2	10:2O:106:LEU:HD23	1.92	0.52
32:2a:434:U:H2'	32:2a:435:C:C6	2.45	0.52
32:2a:1173:G:H2'	32:2a:1174:G:C8	2.44	0.52
32:2a:1314:C:H2'	32:2a:1315:U:H6	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:52:TYR:HB2	50:2s:57:HIS:CE1	2.44	0.52
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.92	0.52
53:1v:15:A:H2	55:1x:37:MIA:H131	1.75	0.52
1:2A:2300:G:H2'	1:2A:2301:C:H6	1.74	0.52
32:2a:957:U:H2'	32:2a:959:A:OP2	2.10	0.52
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.44	0.52
33:2b:185:ILE:HA	33:2b:199:TYR:O	2.10	0.52
34:2c:29:TYR:OH	45:2n:54:PRO:O	2.24	0.52
54:2w:333:THR:O	54:2w:337:GLU:HG2	2.09	0.52
1:1A:747:U:H1'	18:1W:92:ARG:HH22	1.75	0.52
1:1A:1876:A:H2'	1:1A:1877:A:C8	2.45	0.52
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.91	0.52
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.18	0.52
20:1Y:68:HIS:ND1	20:1Y:70:SER:HB3	2.25	0.52
32:1a:926:G:O2'	53:1v:13:A:N3	2.38	0.52
40:1i:81:ILE:O	40:1i:85:LEU:HG	2.09	0.52
1:2A:644:A:H4'	1:2A:645:C:C4	2.45	0.52
1:2A:1012:U:OP1	16:2U:75:ASN:ND2	2.42	0.52
1:2A:2641:G:OP2	9:2N:74:ARG:NH2	2.39	0.52
2:2B:112:U:H2'	2:2B:113:G:H8	1.75	0.52
4:2E:48:GLN:HA	4:2E:80:GLU:HA	1.92	0.52
19:2X:54:VAL:HG13	19:2X:81:VAL:HG13	1.91	0.52
32:2a:736:C:H5"	49:2r:72:ARG:HE	1.74	0.52
55:2y:9:A:OP2	55:2y:13:C:N4	2.43	0.52
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.21	0.52
4:1E:29:GLY:HA3	60:1E:402:HOH:O	2.09	0.52
32:1a:890:G:O2'	32:1a:906:G:O6	2.17	0.52
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.24	0.52
48:1q:3:LYS:HB3	48:1q:61:GLU:HB3	1.92	0.52
50:1s:3:ARG:CZ	50:1s:10:PHE:HB2	2.39	0.52
50:1s:58:VAL:HG12	50:1s:60:VAL:HG13	1.92	0.52
55:1y:48:C:O2'	55:1y:59:U:O2'	2.25	0.52
32:2a:731:G:H5'	32:2a:766:A:H4'	1.91	0.52
32:2a:811:C:N4	60:2a:1836:HOH:O	2.42	0.52
32:2a:946:A:O2'	32:2a:1333:A:N3	2.39	0.52
32:2a:1263:C:N3	32:2a:1272:G:O6	2.42	0.52
32:2a:1274:G:N2	32:2a:1275:A:N7	2.45	0.52
33:2b:30:ARG:NH2	33:2b:194:PRO:HB2	2.24	0.52
35:2d:3:ARG:HH12	35:2d:115:ARG:HD2	1.75	0.52
36:2e:148:VAL:HG21	39:2h:107:LEU:HD23	1.92	0.52
1:1A:286:C:H2'	1:1A:287:C:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.75	0.52
32:1a:299:G:H2'	32:1a:300:A:C8	2.44	0.52
32:1a:381:C:H2'	32:1a:382:A:O4'	2.10	0.52
32:1a:1060:C:H5"	41:1j:51:ARG:HG2	1.90	0.52
53:1v:21:A:N7	54:1w:194:THR:OG1	2.41	0.52
1:2A:885:C:H2'	1:2A:886:C:O4'	2.10	0.52
1:2A:2300:G:H2'	1:2A:2301:C:C6	2.45	0.52
6:2G:46:ALA:HB2	6:2G:53:LEU:HD12	1.92	0.52
15:2T:29:ARG:HB3	15:2T:87:ASP:HB2	1.92	0.52
32:2a:280:C:N3	48:2q:39:SER:OG	2.40	0.52
32:2a:1342:C:H2'	32:2a:1343:G:H8	1.74	0.52
48:2q:82:MET:HA	48:2q:85:VAL:HB	1.92	0.52
55:2y:20:U:H1'	55:2y:21:A:H4'	1.92	0.52
1:1A:7:G:H2'	1:1A:8:A:O4'	2.10	0.51
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.24	0.51
32:1a:1366:C:O3'	41:1j:60:ARG:NH2	2.43	0.51
33:1b:7:VAL:HG11	33:1b:221:LEU:HD21	1.90	0.51
36:1e:75:THR:OG1	36:1e:76:ILE:N	2.40	0.51
32:2a:404:U:H2'	32:2a:405:U:H6	1.74	0.51
32:2a:664:G:P	49:2r:64:ARG:HH21	2.33	0.51
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.42	0.51
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.46	0.51
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.10	0.51
1:1A:1826:G:H4'	3:1D:242:ARG:NH1	2.25	0.51
15:1T:107:ASP:O	15:1T:111:ARG:HG3	2.10	0.51
20:1Y:90:LEU:HD12	20:1Y:94:LYS:HB2	1.93	0.51
32:1a:309:G:O2'	32:1a:607:A:N1	2.43	0.51
32:1a:652:U:O4	32:1a:752:G:O2'	2.26	0.51
32:1a:946:A:H2'	32:1a:947:G:C8	2.44	0.51
32:1a:1029:C:H41	32:1a:1030(A):G:H21	1.58	0.51
1:2A:271(A):A:N1	1:2A:272(D):G:O2'	2.41	0.51
4:2E:52:LEU:HB3	4:2E:76:ARG:HD3	1.92	0.51
4:2E:56:PRO:C	4:2E:58:ARG:H	2.18	0.51
21:2Z:3:TYR:CD2	21:2Z:51:ALA:HB2	2.45	0.51
32:2a:243:A:H4'	32:2a:244:U:H5"	1.93	0.51
32:2a:254:G:OP1	48:2q:66:SER:OG	2.18	0.51
32:2a:975:A:H5'	32:2a:975:A:H8	1.75	0.51
32:2a:1302:U:OP2	44:2m:21:TYR:OH	2.19	0.51
41:2j:44:VAL:HG22	41:2j:66:ARG:HG2	1.92	0.51
50:2s:27:GLU:HG3	50:2s:28:LYS:HG2	1.91	0.51
1:1A:859:G:O2'	1:1A:916:G:O6	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1935:G:H1'	1:1A:1964:G:N2	2.25	0.51
21:1Z:141:VAL:HB	21:1Z:144:LEU:HD12	1.92	0.51
32:1a:770:C:OP1	60:1a:1811:HOH:O	2.18	0.51
32:1a:857:C:H2'	32:1a:858:G:O4'	2.11	0.51
32:1a:1073:U:H2'	32:1a:1074:G:H8	1.75	0.51
32:1a:1251:A:H2'	32:1a:1252:A:H8	1.72	0.51
36:1e:69:VAL:O	36:1e:71:LEU:HD22	2.10	0.51
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.91	0.51
40:1i:4:TYR:CZ	40:1i:88:TYR:HA	2.45	0.51
40:1i:16:ARG:HB2	40:1i:64:THR:HB	1.91	0.51
41:1j:38:ILE:HB	41:1j:71:LEU:HB3	1.91	0.51
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.21	0.51
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.45	0.51
2:2B:84:C:H42	2:2B:93:G:H1	1.58	0.51
1:1A:956:G:OP2	12:1Q:14:ARG:NH2	2.40	0.51
38:1g:20:ASP:OD2	38:1g:63:LYS:NZ	2.44	0.51
55:1x:65:G:H2'	55:1x:66:U:C6	2.44	0.51
1:2A:1358:G:O2'	1:2A:1359:A:H5"	2.10	0.51
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.27	0.51
32:2a:1146:A:H3'	32:2a:1147:C:H5"	1.91	0.51
35:2d:148:VAL:HG12	35:2d:153:ARG:HG2	1.91	0.51
1:1A:1091:G:C2	1:1A:1101:U:H1'	2.46	0.51
32:1a:616:G:H2'	32:1a:617:G:H8	1.76	0.51
32:1a:736:C:H2'	32:1a:737:A:C8	2.46	0.51
32:1a:1071:C:H2'	32:1a:1072:G:H8	1.76	0.51
33:1b:34:ALA:HB3	33:1b:41:ILE:HD11	1.92	0.51
33:1b:178:ARG:NH2	33:1b:198:ASP:OD1	2.43	0.51
36:1e:41:VAL:O	36:1e:66:MET:HA	2.11	0.51
48:1q:66:SER:OG	48:1q:67:LYS:N	2.43	0.51
1:2A:84:A:N1	1:2A:98:G:O2'	2.38	0.51
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.45	0.51
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.93	0.51
32:2a:398:C:OP2	60:2a:1810:HOH:O	2.18	0.51
32:2a:618:C:H5'	32:2a:619:U:H5"	1.92	0.51
35:2d:60:GLU:OE1	35:2d:199:ASN:N	2.37	0.51
1:1A:2637:U:H5"	4:1E:82:ARG:HH12	1.75	0.51
5:1F:17:ARG:HG2	5:1F:18:ARG:H	1.76	0.51
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.91	0.51
32:1a:973:G:H1'	41:1j:54:PHE:CE1	2.46	0.51
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.93	0.51
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.46	0.51
8:2I:9:LEU:HD21	8:2I:35:LEU:HD12	1.93	0.51
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.43	0.51
32:2a:137:C:H2'	32:2a:138:G:H8	1.75	0.51
32:2a:523:A:H61	43:2l:53:ARG:NH1	2.09	0.51
32:2a:1279:A:H4'	32:2a:1281:U:H5	1.76	0.51
1:1A:862:G:H2'	1:1A:863:A:O4'	2.11	0.51
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.10	0.51
7:1H:129:THR:O	7:1H:129:THR:OG1	2.29	0.51
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.39	0.51
23:11:50:ARG:HD2	23:11:57:GLU:OE2	2.10	0.51
32:1a:235:C:H5'	48:1q:70:ARG:HG2	1.92	0.51
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.29	0.51
54:1w:243:HIS:ND1	54:1w:246:THR:OG1	2.43	0.51
1:2A:2783:G:H2'	1:2A:2784:C:C6	2.46	0.51
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.51	0.51
21:2Z:58:VAL:HG22	21:2Z:68:PRO:HA	1.92	0.51
1:1A:1478:G:O2'	1:1A:1558:A:N7	2.42	0.51
1:1A:2532:G:O2'	1:1A:2657:A:N1	2.40	0.51
10:1O:13:ASN:ND2	10:1O:97:ARG:HG2	2.26	0.51
32:1a:107:G:O6	51:1t:15:ARG:NE	2.38	0.51
32:1a:537:G:H5"	43:1l:113:ARG:NH1	2.26	0.51
3:2D:72:LYS:NZ	3:2D:99:ASP:OD2	2.39	0.51
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	1.92	0.51
6:2G:121:ASN:HD21	6:2G:123:ASN:HB2	1.75	0.51
8:2I:62:LYS:HG3	8:2I:133:HIS:HD2	1.76	0.51
12:2Q:43:THR:HA	12:2Q:94:VAL:HA	1.91	0.51
13:2R:72:ASP:HB3	13:2R:75:LEU:HB3	1.93	0.51
21:2Z:126:VAL:HG11	21:2Z:161:VAL:HG22	1.92	0.51
26:24:33:VAL:HG12	26:24:34:GLU:H	1.76	0.51
46:2o:43:LEU:HD12	46:2o:56:LEU:HD13	1.91	0.51
1:1A:24:G:O2'	18:1W:78:GLU:O	2.25	0.51
3:1D:35:LYS:HD2	3:1D:64:ILE:HD11	1.92	0.51
32:1a:509:A:N3	32:1a:543:C:O2'	2.39	0.51
32:1a:592:G:H2'	32:1a:593:G:H8	1.75	0.51
33:1b:45:GLN:O	33:1b:49:GLU:HG3	2.11	0.51
36:1e:98:THR:HG22	36:1e:99:GLY:H	1.75	0.51
50:1s:20:LEU:HA	50:1s:23:ASN:HB2	1.93	0.51
1:2A:71:A:H5"	1:2A:73:A:C8	2.46	0.51
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.43	0.51
1:2A:1139:G:O2'	1:2A:1143:A:N1	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2493:U:O2'	12:2Q:80:GLU:OE2	2.26	0.51
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.44	0.51
19:2X:35:THR:HG23	19:2X:38:GLU:H	1.75	0.51
20:2Y:15:VAL:HG21	20:2Y:42:VAL:HG11	1.93	0.51
32:2a:1051:C:H2'	32:2a:1052:U:H6	1.75	0.51
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.46	0.51
33:2b:120:ALA:O	33:2b:121:LEU:HB2	2.11	0.51
34:2c:20:SER:HB2	34:2c:40:ARG:HH22	1.75	0.51
40:2i:70:LYS:O	40:2i:74:ILE:HG13	2.11	0.51
1:1A:1507:A:H2'	1:1A:1508:A:H8	1.76	0.51
1:1A:1669:A:OP2	60:1A:3857:HOH:O	2.20	0.51
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.46	0.51
7:1H:98:LEU:HG	7:1H:125:VAL:HG23	1.93	0.51
37:1f:67:MET:HG3	37:1f:68:PRO:HD2	1.93	0.51
44:1m:99:ARG:O	44:1m:101:GLN:N	2.44	0.51
1:2A:327:G:N2	20:2Y:70:SER:OG	2.44	0.51
19:2X:28:PHE:HE1	19:2X:92:LEU:HD11	1.76	0.51
32:2a:414:A:N6	32:2a:431:A:N3	2.59	0.51
32:2a:1001:A:H2'	32:2a:1001(A):G:H8	1.76	0.51
35:2d:31:CYS:O	35:2d:35:ARG:HG3	2.10	0.51
1:1A:279:C:H42	1:1A:361:G:H1	1.60	0.50
1:1A:1709:U:H2'	1:1A:1710:C:C6	2.47	0.50
17:1V:71:LEU:HD22	17:1V:84:LYS:HE2	1.93	0.50
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.26	0.50
32:1a:1172:C:H2'	32:1a:1173:G:C8	2.46	0.50
33:1b:163:PHE:CD1	33:1b:185:ILE:HG13	2.46	0.50
43:1l:56:ALA:HB2	43:1l:70:ILE:HD11	1.93	0.50
49:1r:33:ASP:CG	49:1r:36:ASN:HB2	2.36	0.50
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.46	0.50
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.29	0.50
32:2a:757:U:H2'	32:2a:758:G:O4'	2.10	0.50
32:2a:1107:C:OP1	34:2c:173:VAL:N	2.44	0.50
32:2a:1380:U:C4	38:2g:3:ARG:HG2	2.46	0.50
36:2e:109:ILE:HG12	36:2e:136:MET:HE1	1.93	0.50
55:2x:23:A:H2'	55:2x:24:G:C8	2.46	0.50
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.46	0.50
1:1A:2167:U:H2'	1:1A:2168:G:H4'	1.92	0.50
2:1B:66:A:N6	2:1B:108:U:H2'	2.24	0.50
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.11	0.50
39:1h:11:THR:HG23	39:1h:14:ARG:NH1	2.25	0.50
6:2G:77:ILE:HG22	6:2G:80:PHE:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:673:G:O3'	37:2f:87:ARG:NH2	2.44	0.50
32:2a:1004:A:H1'	32:2a:1038:C:O2	2.11	0.50
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.11	0.50
40:2i:71:SER:HA	40:2i:74:ILE:HD12	1.92	0.50
42:2k:92:GLU:C	42:2k:94:ALA:H	2.18	0.50
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.46	0.50
1:1A:2386:C:H2'	1:1A:2387:U:C6	2.46	0.50
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.46	0.50
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.92	0.50
32:1a:262:A:H2'	32:1a:263:A:C8	2.46	0.50
32:1a:618:C:H5'	32:1a:619:U:H5"	1.93	0.50
32:1a:1318:A:H5"	50:1s:3:ARG:NH1	2.26	0.50
1:2A:1359:A:N6	1:2A:1372:U:H3	2.09	0.50
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.46	0.50
2:2B:78:A:H2'	2:2B:79:C:O4'	2.10	0.50
31:29:1:MET:SD	31:29:33:LYS:HG2	2.52	0.50
32:2a:736:C:H5"	49:2r:72:ARG:HH21	1.76	0.50
32:2a:1372:U:H2'	32:2a:1373:G:O4'	2.12	0.50
1:1A:213:A:H2'	1:1A:214:G:O4'	2.12	0.50
1:1A:624:C:O2'	1:1A:657:U:OP1	2.26	0.50
1:1A:2639:A:OP2	60:1A:3855:HOH:O	2.19	0.50
32:1a:444:C:H2'	32:1a:445:G:H8	1.76	0.50
35:1d:9:CYS:O	35:1d:13:ARG:HG3	2.12	0.50
39:1h:34:GLU:HB3	39:1h:118:VAL:CG2	2.39	0.50
1:2A:576:U:H2'	1:2A:577:G:C8	2.47	0.50
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.45	0.50
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.12	0.50
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.47	0.50
2:2B:29:A:H2'	2:2B:30:C:C6	2.46	0.50
13:2R:30:THR:HG22	13:2R:31:HIS:CD2	2.46	0.50
14:2S:10:ARG:HH21	14:2S:91:PRO:HB2	1.76	0.50
31:29:17:ILE:HG13	31:29:26:ILE:HD11	1.94	0.50
32:2a:1372:U:H5"	40:2i:71:SER:HB2	1.93	0.50
34:2c:9:GLY:HA2	34:2c:12:LEU:HD13	1.93	0.50
47:2p:3:LYS:HG3	47:2p:24:ALA:HB2	1.94	0.50
50:2s:3:ARG:NH1	50:2s:10:PHE:HB2	2.26	0.50
54:2w:109:VAL:HG22	54:2w:201:VAL:HG12	1.93	0.50
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.93	0.50
1:1A:2845:G:H5"	15:1T:54:ARG:O	2.10	0.50
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.93	0.50
21:1Z:43:GLU:O	21:1Z:46:LYS:HG2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:142:G:H2'	32:1a:143:A:C8	2.46	0.50
32:1a:160:A:C2	32:1a:343:U:H5'	2.47	0.50
32:1a:540:G:H2'	32:1a:541:G:O4'	2.12	0.50
33:1b:19:HIS:HB3	33:1b:204:ASN:ND2	2.27	0.50
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.93	0.50
44:1m:23:TYR:HE2	44:1m:70:LEU:HB3	1.76	0.50
45:1n:39:LEU:HD11	45:1n:47:LEU:HD12	1.92	0.50
1:2A:1043:C:N4	1:2A:1112:G:H1	2.08	0.50
1:2A:2162:G:H2'	1:2A:2163:C:O4'	2.11	0.50
21:2Z:134:PRO:O	21:2Z:136:PHE:N	2.40	0.50
32:2a:433:C:H2'	32:2a:434:U:H6	1.77	0.50
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.45	0.50
33:2b:93:VAL:HG21	33:2b:97:TRP:CD1	2.47	0.50
36:2e:78:HIS:CD2	39:2h:104:ARG:HD3	2.47	0.50
41:2j:40:LEU:HB2	41:2j:69:ASN:HB2	1.93	0.50
5:1F:195:ASP:CB	5:1F:198:ALA:H	2.25	0.50
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.92	0.50
13:1R:56:LYS:NZ	13:1R:90:ARG:O	2.45	0.50
15:1T:51:ARG:HG3	15:1T:98:LYS:HD2	1.94	0.50
25:13:18:ASP:OD1	25:13:18:ASP:N	2.45	0.50
32:1a:269:C:H2'	32:1a:270:A:C8	2.46	0.50
32:1a:630:G:H2'	32:1a:631:G:C8	2.46	0.50
32:1a:1006:C:H2'	32:1a:1007:C:C6	2.47	0.50
32:1a:1414:U:H3	32:1a:1486:G:H1	1.60	0.50
1:2A:403:U:H4'	1:2A:404:C:H5'	1.94	0.50
1:2A:740:U:H2'	1:2A:741:G:C8	2.47	0.50
1:2A:1821:A:H2'	1:2A:1822:G:C8	2.46	0.50
6:2G:61:ALA:HA	6:2G:66:GLN:O	2.10	0.50
21:2Z:152:ALA:O	21:2Z:155:LEU:HB3	2.10	0.50
32:2a:662:G:H2'	32:2a:663:A:C8	2.47	0.50
32:2a:932:C:H5"	38:2g:4:ARG:CZ	2.42	0.50
33:2b:71:VAL:O	33:2b:165:VAL:HG23	2.12	0.50
33:2b:115:LEU:HD22	33:2b:145:LEU:HB3	1.94	0.50
42:2k:79:SER:HB3	42:2k:104:GLN:HB3	1.94	0.50
1:1A:6:A:H2'	1:1A:7:G:O4'	2.12	0.50
15:1T:112:ARG:HG2	15:1T:115:ARG:NH2	2.27	0.50
32:1a:142:G:H1	32:1a:221:C:H42	1.58	0.50
32:1a:1054:C:H41	54:1w:192:ILE:HG22	1.77	0.50
32:1a:1157:A:H5'	32:1a:1158:C:C6	2.46	0.50
33:1b:122:PHE:CE1	33:1b:139:LYS:HD2	2.47	0.50
35:1d:12:CYS:SG	35:1d:19:LEU:HB2	2.52	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:166:LYS:H	35:1d:166:LYS:HZ3	1.60	0.50
1:2A:657:U:H2'	1:2A:658:C:C6	2.46	0.50
1:2A:1025:G:O2'	60:2A:3736:HOH:O	2.14	0.50
20:2Y:37:VAL:O	20:2Y:67:LEU:N	2.44	0.50
32:2a:766:A:H2'	32:2a:767:A:O4'	2.12	0.50
33:2b:197:VAL:HG11	33:2b:200:ILE:HG23	1.93	0.50
36:2e:78:HIS:HE1	36:2e:142:LEU:HA	1.77	0.50
36:2e:80:ILE:HG21	36:2e:142:LEU:HD21	1.93	0.50
47:2p:8:ARG:HA	47:2p:17:TYR:HD1	1.77	0.50
49:2r:61:LYS:O	49:2r:65:ILE:HG12	2.11	0.50
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.30	0.50
1:1A:2319:G:H22	14:1S:3:ARG:NE	2.10	0.50
1:1A:2619:C:H4'	4:1E:151:TYR:O	2.12	0.50
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.12	0.50
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.93	0.50
19:1X:92:LEU:O	19:1X:94:GLY:N	2.45	0.50
32:1a:1141:C:H2'	32:1a:1142:G:H8	1.75	0.50
34:1c:155:GLY:HA3	34:1c:196:LEU:HG	1.94	0.50
1:2A:1192:G:OP1	60:2A:3762:HOH:O	2.19	0.50
32:2a:972:C:O3'	41:2j:57:LYS:HD2	2.11	0.50
32:2a:1263:C:N4	32:2a:1271:G:O6	2.45	0.50
46:2o:11:VAL:HG21	46:2o:34:LEU:HD12	1.94	0.50
2:1B:29:A:H2'	2:1B:30:C:C6	2.47	0.50
5:1F:7:TYR:CD2	5:1F:24:LEU:HB2	2.47	0.50
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.47	0.50
32:1a:445:G:H2'	32:1a:446:G:C8	2.46	0.50
39:1h:81:HIS:N	39:1h:138:TRP:O	2.43	0.50
55:1y:14:A:H61	55:1y:21:A:H2	1.59	0.50
1:2A:1943:U:OP1	54:2w:272:ARG:NH1	2.45	0.50
1:2A:2888:C:H2'	1:2A:2889:C:H6	1.77	0.50
6:2G:63:ILE:HD12	6:2G:141:PHE:HB3	1.94	0.50
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.94	0.50
8:2I:87:LYS:H	8:2I:87:LYS:HD3	1.76	0.50
14:2S:9:ARG:O	14:2S:13:ARG:HG3	2.12	0.50
32:2a:426:G:OP1	35:2d:36:ARG:HD2	2.11	0.50
32:2a:540:G:H2'	32:2a:541:G:O4'	2.12	0.50
41:2j:49:VAL:HG21	45:2n:45:ARG:HB2	1.93	0.50
42:2k:48:ILE:O	42:2k:50:TYR:N	2.43	0.50
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.47	0.49
32:1a:316:G:OP2	32:1a:351:G:O2'	2.30	0.49
32:1a:931:C:H1'	32:1a:1387:G:N2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:973:G:H3'	32:1a:974:A:H5"	1.94	0.49
32:1a:1004:A:N6	32:1a:1037:C:C2	2.79	0.49
33:1b:81:VAL:HG11	33:1b:165:VAL:HG21	1.94	0.49
1:2A:1357:U:H2'	1:2A:1358:G:O4'	2.12	0.49
1:2A:1821:A:H2'	1:2A:1822:G:H8	1.77	0.49
26:24:44:THR:O	26:24:46:GLN:N	2.45	0.49
32:2a:640:A:O2'	39:2h:115:SER:O	2.26	0.49
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.12	0.49
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.93	0.49
1:1A:800:A:H8	1:1A:800:A:OP1	1.95	0.49
1:1A:1070:A:N6	1:1A:1097:U:H1'	2.28	0.49
1:1A:1377:G:H2'	60:1A:4432:HOH:O	2.12	0.49
1:1A:1625:C:H2'	1:1A:1626:G:O4'	2.12	0.49
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.77	0.49
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.46	0.49
32:1a:110:C:H2'	32:1a:111:G:O4'	2.13	0.49
32:1a:411:A:OP1	35:1d:30:LYS:NZ	2.45	0.49
34:1c:177:THR:HG22	34:1c:180:ALA:H	1.77	0.49
54:1w:230:MEQ:HG2	56:1z:18:LEU:O	2.12	0.49
1:2A:182:A:N3	1:2A:433:C:O2'	2.40	0.49
1:2A:698:C:O2'	1:2A:734:A:N6	2.45	0.49
1:2A:700:G:O2'	1:2A:1632:A:N3	2.42	0.49
1:2A:856:C:H2'	1:2A:857:C:H6	1.77	0.49
1:2A:882:G:H1	1:2A:894:C:H42	1.59	0.49
1:2A:2159:G:H2'	1:2A:2160:G:H8	1.77	0.49
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.45	0.49
4:2E:47:VAL:HG12	4:2E:84:PHE:HB3	1.93	0.49
32:2a:1060:C:C5	34:2c:2:GLY:HA2	2.47	0.49
46:2o:15:PHE:CE1	46:2o:84:LYS:HG2	2.46	0.49
46:2o:18:PHE:HB2	46:2o:19:PRO:HD2	1.94	0.49
48:2q:9:VAL:HB	48:2q:56:VAL:HG22	1.95	0.49
32:1a:520:A:N1	32:1a:536:C:H1'	2.27	0.49
1:2A:2206:G:H8	1:2A:2207:G:N7	2.10	0.49
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.11	0.49
11:2P:88:LEU:HA	11:2P:91:PHE:CE2	2.48	0.49
1:1A:381:G:O6	60:1A:3858:HOH:O	2.20	0.49
1:1A:1082:U:H3	1:1A:1086:A:H61	1.57	0.49
1:1A:1631(A):A:OP1	60:1A:3859:HOH:O	2.20	0.49
1:1A:2126:A:N6	1:1A:2163:C:H4'	2.27	0.49
1:1A:2422:A:O4'	55:1y:76:A:N6	2.45	0.49
19:1X:52:VAL:HG12	19:1X:82:GLN:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:719:C:O2'	49:1r:49:LYS:HB3	2.13	0.49
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.28	0.49
41:1j:32:ALA:HB2	41:1j:81:THR:HG21	1.95	0.49
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.95	0.49
54:1w:240:ARG:HB2	54:1w:251:THR:HG22	1.94	0.49
1:2A:107:C:H2'	1:2A:108:U:H6	1.77	0.49
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.45	0.49
3:2D:228:PRO:O	60:2D:401:HOH:O	2.20	0.49
32:2a:164:U:H2'	32:2a:165:C:H6	1.76	0.49
54:2w:229:GLY:HA3	55:2x:76:A:H3'	1.93	0.49
54:2w:307:PHE:CZ	54:2w:328:LEU:HD11	2.46	0.49
1:1A:1026:U:OP1	60:1A:3823:HOH:O	2.19	0.49
15:1T:119:LYS:O	15:1T:123:GLN:HG3	2.12	0.49
20:1Y:107:ASP:OD1	20:1Y:107:ASP:N	2.46	0.49
32:1a:91:C:H2'	32:1a:92:C:C6	2.47	0.49
34:1c:188:LEU:HD11	34:1c:190:ARG:NH2	2.28	0.49
35:1d:65:ARG:HH11	35:1d:72:GLU:HB2	1.78	0.49
41:1j:40:LEU:HB2	41:1j:69:ASN:HB3	1.95	0.49
51:1t:56:MET:HG3	51:1t:84:LEU:HD22	1.93	0.49
1:2A:892:G:N2	1:2A:893:C:O3'	2.45	0.49
1:2A:2365:G:H4'	22:20:60:PHE:CZ	2.46	0.49
6:2G:123:ASN:C	6:2G:125:PHE:H	2.21	0.49
32:2a:662:G:O2'	32:2a:836:G:OP1	2.30	0.49
39:2h:54:ASP:OD1	39:2h:54:ASP:N	2.44	0.49
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	1.94	0.49
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.93	0.49
32:1a:689:C:H2'	32:1a:690:G:O4'	2.13	0.49
32:1a:1029:C:N4	32:1a:1030:C:H41	2.10	0.49
33:1b:68:ILE:O	33:1b:91:PRO:HD2	2.12	0.49
43:1l:11:VAL:HG11	48:1q:36:ILE:HG21	1.95	0.49
1:2A:1203:G:OP2	1:2A:1204:A:O2'	2.18	0.49
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.78	0.49
1:2A:2224:G:H4'	1:2A:2226:C:C2	2.47	0.49
5:2F:103:LYS:HA	5:2F:106:ARG:HD3	1.94	0.49
12:2Q:51:ARG:HH12	21:2Z:182:LYS:HE3	1.77	0.49
18:2W:68:ARG:HH21	18:2W:111:HIS:HE1	1.61	0.49
32:2a:1212:U:H5'	32:2a:1213:A:C8	2.47	0.49
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.95	0.49
54:2w:246:THR:HB	54:2w:248:ILE:HG23	1.94	0.49
1:1A:185:U:H4'	1:1A:218:A:H4'	1.93	0.49
1:1A:796:C:H2'	1:1A:797:C:C6	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:817:C:O2'	1:1A:839:U:H5"	2.13	0.49
1:1A:1092:C:N4	1:1A:1099:G:H1	2.10	0.49
15:1T:1:MET:HE2	15:1T:3:ARG:HG2	1.95	0.49
21:1Z:138:GLU:H	21:1Z:156:LYS:NZ	2.10	0.49
32:1a:403:C:H5"	35:1d:136:PRO:HD2	1.93	0.49
32:1a:500:G:N2	32:1a:546:G:H1'	2.27	0.49
40:1i:28:VAL:HG12	40:1i:29:ASN:H	1.76	0.49
1:2A:945:A:C4	1:2A:2448:A:C2	3.00	0.49
1:2A:2126:A:N3	1:2A:2127:G:H1'	2.27	0.49
1:2A:2141:G:H22	1:2A:2151:G:H1'	1.78	0.49
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.94	0.49
9:2N:31:ALA:HA	9:2N:34:LEU:HD12	1.94	0.49
14:2S:38:GLN:HB3	14:2S:40:ILE:HD11	1.94	0.49
21:2Z:9:TYR:CE1	21:2Z:35:ARG:HG2	2.44	0.49
35:2d:9:CYS:O	35:2d:13:ARG:HG3	2.12	0.49
37:2f:62:TRP:CD1	49:2r:35:ARG:HE	2.31	0.49
1:1A:2304:G:H22	1:1A:2312:U:H3	1.60	0.49
1:1A:2406:U:C4	11:1P:72:PRO:HD2	2.48	0.49
21:1Z:54:HIS:HB3	21:1Z:101:PRO:HD3	1.95	0.49
32:1a:977:A:O2'	32:1a:979:C:OP2	2.31	0.49
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.59	0.49
33:1b:210:SER:O	33:1b:214:ILE:HG12	2.13	0.49
35:1d:159:ARG:HA	35:1d:162:LEU:HB2	1.94	0.49
43:1l:58:VAL:HG12	43:1l:60:LEU:HD12	1.93	0.49
1:2A:2638:G:P	4:2E:82:ARG:HH22	2.35	0.49
3:2D:2:ALA:N	3:2D:200:ASP:OD2	2.46	0.49
9:2N:20:GLY:HA2	9:2N:61:ARG:HG2	1.93	0.49
32:2a:1118:C:H2'	32:2a:1119:C:C6	2.48	0.49
32:2a:1335:C:H4'	32:2a:1336:C:H6	1.77	0.49
36:2e:18:ARG:HH12	36:2e:20:GLN:HG2	1.78	0.49
36:2e:80:ILE:HG23	36:2e:91:LEU:HD23	1.94	0.49
39:2h:97:VAL:HG21	39:2h:128:GLY:HA2	1.94	0.49
54:2w:200:ALA:HB2	54:2w:293:ILE:HG13	1.95	0.49
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.12	0.49
1:1A:2747:G:O6	1:1A:2755:C:H5"	2.13	0.49
1:1A:2758:A:OP2	60:1A:3851:HOH:O	2.18	0.49
32:1a:1064:G:H4'	32:1a:1065:U:OP1	2.11	0.49
32:1a:1131:G:OP1	40:1i:20:ARG:NH2	2.46	0.49
34:1c:188:LEU:HD11	34:1c:190:ARG:HH21	1.77	0.49
35:1d:173:TRP:CD1	35:1d:174:LEU:HG	2.48	0.49
39:1h:95:VAL:HG23	39:1h:99:GLU:HB2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:1x:50:U:H2'	55:1x:51:U:C6	2.48	0.49
1:2A:263:C:H2'	1:2A:264:C:O4'	2.13	0.49
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.28	0.49
3:2D:124:PRO:O	3:2D:129:ASN:ND2	2.46	0.49
7:2H:149:ARG:HH21	7:2H:154:PRO:HG2	1.78	0.49
17:2V:4:ILE:HG22	17:2V:38:LEU:HD12	1.95	0.49
21:2Z:93:ASP:HA	21:2Z:131:ARG:HH22	1.77	0.49
32:2a:1006:C:N4	32:2a:1022:G:O6	2.46	0.49
45:2n:26:ARG:HB3	45:2n:43:CYS:SG	2.53	0.49
54:2w:130:MET:HE1	54:2w:305:TYR:CE1	2.47	0.49
55:2y:58:A:O2'	55:2y:60:U:OP2	2.21	0.49
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.13	0.49
1:1A:2121:G:H1	1:1A:2177:C:H42	1.60	0.49
4:1E:52:LEU:O	4:1E:76:ARG:N	2.42	0.49
8:1I:77:LEU:HB3	8:1I:142:VAL:HG22	1.95	0.49
19:1X:43:VAL:HG13	19:1X:47:PHE:HD2	1.78	0.49
21:1Z:119:GLU:OE1	21:1Z:122:ARG:NH1	2.46	0.49
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.42	0.49
32:1a:96:U:H2'	32:1a:97:G:H8	1.76	0.49
32:1a:1187:G:H2'	32:1a:1188:A:C8	2.47	0.49
32:1a:1211:U:H1'	32:1a:1213:A:C2	2.48	0.49
33:1b:69:LEU:HD13	33:1b:91:PRO:HB2	1.95	0.49
35:1d:101:LEU:HD12	35:1d:138:TYR:HB3	1.94	0.49
21:2Z:77:ASP:N	21:2Z:82:ARG:O	2.35	0.49
32:2a:102:G:H2'	32:2a:103:C:C6	2.47	0.49
33:2b:44:LEU:O	33:2b:47:THR:OG1	2.31	0.49
33:2b:121:LEU:H	33:2b:125:PRO:HD2	1.77	0.49
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.28	0.49
37:2f:19:LEU:HD11	37:2f:59:TYR:CZ	2.48	0.49
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.13	0.49
44:2m:74:VAL:HA	44:2m:77:ASN:HB2	1.93	0.49
48:2q:99:SER:OG	48:2q:100:LYS:N	2.45	0.49
1:1A:219:G:OP2	60:1A:3862:HOH:O	2.20	0.48
1:1A:679:C:H2'	1:1A:680:G:C8	2.48	0.48
1:1A:2250:G:O2'	1:1A:2496:C:OP1	2.30	0.48
11:1P:3:LEU:HD23	11:1P:6:LEU:HD12	1.95	0.48
15:1T:4:GLY:O	15:1T:8:LYS:HG2	2.13	0.48
33:1b:16:HIS:HB2	33:1b:204:ASN:H	1.78	0.48
55:1y:46:G7M:H4'	55:1y:46:G7M:OP1	2.12	0.48
6:2G:172:LEU:HD23	6:2G:173:LEU:HG	1.94	0.48
32:2a:56:U:H2'	32:2a:57:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:300:A:H2'	32:2a:301:G:O4'	2.12	0.48
32:2a:779:C:H2'	32:2a:780:A:O4'	2.13	0.48
35:2d:104:VAL:HG11	35:2d:146:ILE:HD12	1.95	0.48
1:1A:1226:A:OP1	17:1V:84:LYS:NZ	2.40	0.48
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.48	0.48
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.13	0.48
32:1a:1013:G:N2	32:1a:1016:A:OP2	2.42	0.48
32:1a:1372:U:OP1	40:1i:72:GLY:N	2.45	0.48
50:1s:40:ILE:HD13	50:1s:62:ILE:HD12	1.96	0.48
1:2A:858:U:OP1	22:20:44:ARG:NH1	2.30	0.48
1:2A:2336:A:N3	1:2A:2385:C:H1'	2.28	0.48
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.28	0.48
32:2a:966:M2G:HM22	55:2x:34:G:H5'	1.96	0.48
34:2c:22:TRP:HZ3	34:2c:24:ALA:HB2	1.76	0.48
34:2c:119:ARG:HG2	34:2c:140:ARG:HH22	1.78	0.48
49:2r:58:LEU:HD11	49:2r:66:LEU:HD22	1.95	0.48
1:1A:784:A:C5	3:1D:229:VAL:HG21	2.48	0.48
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.28	0.48
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.14	0.48
1:1A:2291:U:O2'	1:1A:2374:C:O2	2.28	0.48
11:1P:131:SER:HB3	11:1P:134:ALA:H	1.78	0.48
32:1a:1124:G:N2	32:1a:1125:U:O4	2.44	0.48
32:1a:1346:A:H5'	32:1a:1348:U:H1'	1.95	0.48
34:1c:29:TYR:HE2	45:1n:54:PRO:HD2	1.78	0.48
35:1d:65:ARG:HB2	35:1d:75:PHE:CE2	2.48	0.48
36:1e:60:TYR:CE2	36:1e:64:ARG:HD3	2.47	0.48
40:1i:42:ARG:NH1	40:1i:71:SER:O	2.45	0.48
41:1j:8:LEU:HB2	41:1j:70:ARG:HB2	1.94	0.48
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.94	0.48
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.95	0.48
55:1y:19:G:H1'	55:1y:57:G:H22	1.78	0.48
55:1y:48:C:C2	55:1y:59:U:H1'	2.49	0.48
1:2A:236:C:H2'	1:2A:237:C:C6	2.48	0.48
1:2A:1496:A:N3	1:2A:1577:C:O2'	2.45	0.48
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.47	0.48
1:2A:2888:C:H2'	1:2A:2889:C:C6	2.48	0.48
10:2O:43:VAL:HG23	10:2O:56:ASP:O	2.13	0.48
32:2a:302:G:N3	32:2a:556:C:H4'	2.28	0.48
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.14	0.48
32:2a:1292:U:OP2	38:2g:41:ARG:NH1	2.46	0.48
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:118:LEU:HG	33:2b:142:LEU:HD12	1.95	0.48
1:1A:625:G:N7	11:1P:107:LYS:NZ	2.57	0.48
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.12	0.48
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.13	0.48
1:1A:2506:U:O4	56:1z:16:PRO:HD2	2.13	0.48
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.49	0.48
12:1Q:65:PHE:HB2	12:1Q:105:GLU:HB2	1.95	0.48
26:14:46:GLN:HE21	26:14:48:ARG:H	1.60	0.48
31:19:16:VAL:HG22	31:19:25:VAL:HG22	1.94	0.48
32:1a:401:C:P	35:1d:73:ARG:HH22	2.37	0.48
32:1a:624:C:H2'	32:1a:625:G:H8	1.78	0.48
39:1h:81:HIS:HB2	39:1h:138:TRP:CD1	2.48	0.48
51:1t:10:LEU:HD23	51:1t:12:ALA:H	1.76	0.48
54:1w:141:GLU:HB3	54:1w:163:ARG:HB2	1.94	0.48
1:2A:775:G:O3'	60:2A:3763:HOH:O	2.20	0.48
2:2B:7:G:H21	14:2S:38:GLN:NE2	2.11	0.48
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.95	0.48
9:2N:36:GLY:HA2	9:2N:38:HIS:CE1	2.48	0.48
21:2Z:52:SER:C	21:2Z:54:HIS:H	2.22	0.48
32:2a:1123:A:C2	41:2j:39:PRO:HD2	2.49	0.48
32:2a:1239:A:H4'	32:2a:1240:U:H5"	1.94	0.48
32:2a:1359:C:H3'	45:2n:35:ARG:NH2	2.28	0.48
39:2h:19:VAL:HG23	39:2h:21:LYS:HG3	1.95	0.48
32:1a:7:G:H5'	32:1a:298:A:O4'	2.12	0.48
32:1a:374:A:C6	32:1a:375:U:C4	3.02	0.48
33:1b:103:THR:HA	33:1b:180:LEU:HD11	1.94	0.48
38:1g:113:GLU:HB2	38:1g:119:ARG:HG2	1.95	0.48
51:1t:42:GLN:NE2	51:1t:46:GLU:OE2	2.46	0.48
2:2B:49:C:OP2	14:2S:30:ARG:NH1	2.47	0.48
2:2B:60:C:H2'	2:2B:61:G:H8	1.79	0.48
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.94	0.48
32:2a:189(A):C:H2'	32:2a:189(B):C:C6	2.48	0.48
32:2a:1103:C:H4'	33:2b:98:LEU:HD21	1.96	0.48
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.29	0.48
32:2a:1150:U:C2'	32:2a:1151:A:H5'	2.44	0.48
42:2k:48:ILE:HD11	42:2k:50:TYR:CD2	2.48	0.48
55:2x:26:A:H2'	55:2x:27:G:O4'	2.14	0.48
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.28	0.48
1:1A:2471:C:H2'	1:1A:2472:G:O4'	2.13	0.48
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	1.96	0.48
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:444:C:H2'	32:1a:445:G:C8	2.49	0.48
32:1a:1027:C:N4	32:1a:1034:G:N1	2.62	0.48
32:1a:1305:G:H5"	52:1u:4:GLY:HA3	1.95	0.48
35:1d:166:LYS:HZ3	35:1d:166:LYS:N	2.11	0.48
39:1h:38:ILE:HD12	39:1h:111:ILE:HG23	1.95	0.48
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.77	0.48
1:2A:2521:C:O2'	1:2A:2564:A:N3	2.42	0.48
4:2E:150:VAL:HG13	4:2E:154:LYS:HE3	1.95	0.48
15:2T:16:ARG:NH2	15:2T:83:ILE:O	2.47	0.48
32:2a:20:U:H2'	32:2a:21:G:O4'	2.12	0.48
32:2a:713:G:H2'	32:2a:714:G:C8	2.49	0.48
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.31	0.48
32:2a:1247:U:H2'	32:2a:1248:A:O4'	2.14	0.48
1:1A:286:C:H2'	1:1A:287:C:C6	2.48	0.48
1:1A:2784:C:H1'	4:1E:37:ARG:HH12	1.78	0.48
2:1B:50:G:OP1	14:1S:63:THR:OG1	2.28	0.48
32:1a:292:G:C5	32:1a:293:G:H1'	2.49	0.48
32:1a:503:C:H2'	32:1a:504:C:C6	2.49	0.48
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.95	0.48
35:1d:117:ALA:O	35:1d:121:VAL:HG23	2.14	0.48
1:2A:307:G:H21	1:2A:330:A:H62	1.62	0.48
1:2A:1141:U:OP2	9:2N:63:THR:OG1	2.24	0.48
1:2A:1224:C:O2'	17:2V:86:GLY:N	2.43	0.48
3:2D:246:PRO:O	3:2D:254:THR:HG22	2.13	0.48
5:2F:155:LEU:HD12	5:2F:174:VAL:O	2.14	0.48
7:2H:101:ARG:NE	7:2H:117:PRO:HG2	2.28	0.48
14:2S:34:HIS:HB3	14:2S:53:SER:HB3	1.96	0.48
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.48	0.48
32:2a:862:C:H1'	32:2a:874:G:H5"	1.95	0.48
32:2a:1001:A:H2'	32:2a:1001(A):G:C8	2.48	0.48
32:2a:1178:G:N2	32:2a:1180:A:H3'	2.28	0.48
37:2f:26:ILE:HG22	37:2f:30:LEU:HD11	1.95	0.48
43:2l:45:PRO:HB2	43:2l:92:0TD:OD2	2.13	0.48
51:2t:53:LEU:O	51:2t:57:ARG:HG3	2.14	0.48
1:1A:242:G:C8	30:18:5:LYS:HG2	2.49	0.48
1:1A:815:C:H42	1:1A:1192:G:H1	1.61	0.48
1:1A:2478:A:H5'	31:19:31:LYS:HE2	1.95	0.48
1:1A:2864:G:OP1	15:1T:119:LYS:HD2	2.14	0.48
8:1I:66:GLU:OE1	8:1I:69:LYS:HD3	2.13	0.48
11:1P:84:ASN:HB3	11:1P:117:GLU:O	2.13	0.48
13:1R:83:ILE:O	13:1R:86:ARG:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:18:LEU:HD22	17:1V:20:LEU:HB2	1.95	0.48
32:1a:981:U:OP1	45:1n:6:LEU:HD21	2.13	0.48
35:1d:150:GLU:OE1	35:1d:151:LYS:N	2.47	0.48
38:1g:17:VAL:HG12	38:1g:18:TYR:CD2	2.48	0.48
44:1m:3:ARG:HG3	44:1m:4:ILE:HD12	1.96	0.48
1:2A:288:C:H2'	1:2A:289:A:H8	1.78	0.48
1:2A:994:C:OP2	16:2U:54:LYS:NZ	2.40	0.48
1:2A:1167:U:H2'	1:2A:1168:G:H8	1.79	0.48
1:2A:1851:U:H4'	55:2y:71:G:H4'	1.95	0.48
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	1.95	0.48
24:22:35:LEU:HD22	24:22:44:LEU:HD11	1.95	0.48
32:2a:1118:C:H2'	32:2a:1119:C:H6	1.79	0.48
32:2a:1178:G:N2	32:2a:1181:G:OP2	2.34	0.48
32:2a:1279:A:H5"	32:2a:1280:A:OP1	2.13	0.48
33:2b:207:ALA:O	33:2b:211:ILE:HG13	2.13	0.48
35:2d:162:LEU:CD1	35:2d:181:MET:HG2	2.44	0.48
38:2g:108:ALA:O	38:2g:111:ARG:HB2	2.13	0.48
55:2x:8:4SU:O5'	55:2x:8:4SU:H6	2.14	0.48
1:1A:478:A:N1	1:1A:500:G:H4'	2.29	0.48
1:1A:1779:U:H2'	60:1A:3975:HOH:O	2.13	0.48
1:1A:1815:A:H8	1:1A:1815:A:OP1	1.97	0.48
10:1O:111:PHE:HB3	10:1O:114:ILE:HD13	1.95	0.48
20:1Y:68:HIS:CE1	20:1Y:70:SER:HB3	2.49	0.48
32:1a:134:A:H61	47:1p:25:ARG:HH12	1.62	0.48
32:1a:308:C:H2'	32:1a:309:G:C8	2.49	0.48
32:1a:674:G:H2'	32:1a:675:A:H8	1.79	0.48
32:1a:677:U:H3	32:1a:713:G:H22	1.60	0.48
32:1a:902:G:H2'	32:1a:903:G:H8	1.79	0.48
35:1d:11:LEU:O	35:1d:15:GLU:HG2	2.13	0.48
35:1d:102:ASP:N	35:1d:102:ASP:OD1	2.47	0.48
1:2A:729:G:C5	3:2D:208:LYS:HB2	2.49	0.48
1:2A:2121:G:H1	1:2A:2177:C:N4	2.12	0.48
8:2I:62:LYS:HG3	8:2I:133:HIS:CD2	2.49	0.48
8:2I:77:LEU:HB3	8:2I:142:VAL:HG22	1.96	0.48
20:2Y:67:LEU:HD22	20:2Y:71:LYS:HD3	1.94	0.48
21:2Z:45:ASP:O	21:2Z:49:ARG:HG3	2.14	0.48
30:28:4:MET:HE3	30:28:63:PRO:HG3	1.95	0.48
32:2a:998:G:H1	32:2a:1043:C:H42	1.62	0.48
32:2a:1314:C:H2'	32:2a:1315:U:C6	2.49	0.48
34:2c:19:GLU:HA	34:2c:54:ARG:HH12	1.79	0.48
44:2m:32:GLU:HA	44:2m:35:GLU:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1291:C:H2'	1:1A:1292:U:H6	1.79	0.48
1:1A:1889:A:O2'	1:1A:2087:G:H5'	2.14	0.48
1:1A:2001:A:H2'	1:1A:2002:G:C8	2.49	0.48
32:1a:8:A:N6	35:1d:205:GLU:O	2.46	0.48
32:1a:182:U:C4	32:1a:183:G:H1'	2.49	0.48
32:1a:448:A:H2'	32:1a:449:C:H6	1.79	0.48
33:1b:171:ALA:HA	33:1b:174:VAL:HG22	1.95	0.48
44:1m:44:ARG:HD3	44:1m:44:ARG:HA	1.62	0.48
55:1x:12:U:OP2	60:1x:202:HOH:O	2.20	0.48
1:2A:1876:A:OP2	1:2A:1876:A:H8	1.97	0.48
1:2A:1927:A:H2'	1:2A:1928:A:C8	2.49	0.48
1:2A:2038:G:H2'	1:2A:2039:C:O4'	2.14	0.48
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.12	0.48
30:28:48:PHE:HE1	30:28:50:LEU:HD23	1.78	0.48
32:2a:1016:A:H2'	32:2a:1017:G:O4'	2.14	0.48
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.13	0.48
36:2e:107:ARG:HG2	36:2e:108:ALA:N	2.28	0.48
47:2p:58:TYR:O	47:2p:61:SER:OG	2.28	0.48
1:1A:1059:G:H2'	1:1A:1060:U:H5	1.77	0.47
1:1A:1102:C:H2'	1:1A:1103:A:O4'	2.14	0.47
1:1A:1495:A:H2'	1:1A:1496:A:C8	2.48	0.47
1:1A:1792:G:H5'	3:1D:205:VAL:HG13	1.96	0.47
1:1A:2159:G:H2'	1:1A:2160:G:C8	2.49	0.47
1:1A:2833:G:H4'	1:1A:2834:G:OP2	2.14	0.47
7:1H:170:ARG:O	7:1H:171:LEU:HD23	2.14	0.47
18:1W:4:LYS:HE3	18:1W:6:ILE:HD11	1.96	0.47
24:12:21:LEU:HB2	24:12:64:LEU:HD13	1.95	0.47
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.96	0.47
26:14:26:SER:OG	26:14:27:THR:N	2.47	0.47
46:1o:43:LEU:HD13	46:1o:53:HIS:HD2	1.79	0.47
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.48	0.47
1:2A:902:C:H2'	1:2A:903:C:C6	2.49	0.47
1:2A:2850:A:OP2	1:2A:2866:U:H5	1.97	0.47
1:2A:2893:G:H5"	1:2A:2894:G:O4'	2.13	0.47
2:2B:11:C:H3'	2:2B:12:C:C6	2.49	0.47
5:2F:125:LEU:HD13	5:2F:194:MET:HB2	1.95	0.47
13:2R:31:HIS:C	13:2R:33:ARG:H	2.22	0.47
26:24:10:VAL:HG22	26:24:11:PRO:HD2	1.96	0.47
32:2a:438:G:H4'	35:2d:123:HIS:CD2	2.49	0.47
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.47	0.47
32:2a:909:A:H2'	32:2a:910:C:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:668:G:H5'	1:1A:669:G:OP2	2.13	0.47
3:1D:132:PRO:HD3	3:1D:190:TYR:CZ	2.50	0.47
14:1S:83:LYS:HG2	14:1S:111:GLU:HG3	1.96	0.47
26:14:18:CYS:SG	26:14:20:ASN:HB2	2.54	0.47
31:19:8:LYS:H	31:19:34:GLN:HE22	1.60	0.47
36:1e:147:ASP:O	36:1e:151:LEU:HG	2.13	0.47
55:1x:9:A:H5'	55:1x:46:G7M:H22	1.79	0.47
1:2A:171:G:H2'	1:2A:172:C:C6	2.49	0.47
1:2A:2135:A:N1	1:2A:2156:G:O2'	2.46	0.47
5:2F:185:ASP:OD1	5:2F:188:ARG:NH1	2.43	0.47
24:22:25:VAL:HG13	24:22:57:ILE:HG23	1.97	0.47
29:27:22:MET:O	29:27:28:ARG:NH1	2.44	0.47
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C5	2.49	0.47
32:2a:1446:U:H4'	32:2a:1447:A:C6	2.49	0.47
34:2c:12:LEU:HD21	45:2n:51:GLY:HA2	1.95	0.47
42:2k:109:VAL:HG22	49:2r:86:VAL:HA	1.96	0.47
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.49	0.47
1:1A:2319:G:H22	14:1S:3:ARG:HE	1.62	0.47
6:1G:116:ASP:OD1	6:1G:116:ASP:N	2.46	0.47
10:1O:14:THR:HG21	10:1O:86:ILE:HB	1.95	0.47
32:1a:41:G:C6	32:1a:402:G:C6	3.02	0.47
32:1a:189(D):C:H1'	32:1a:189(H):G:N2	2.28	0.47
32:1a:509:A:O2'	32:1a:510:A:OP1	2.22	0.47
33:1b:30:ARG:HH21	33:1b:194:PRO:HB2	1.79	0.47
34:1c:108:ASN:HB3	34:1c:111:LEU:HD13	1.95	0.47
54:1w:299:SER:C	54:1w:301:LYS:H	2.23	0.47
1:2A:7:G:H1	1:2A:2896:C:H42	1.62	0.47
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.49	0.47
60:2A:3931:HOH:O	11:2P:37:GLY:HA3	2.13	0.47
11:2P:52:GLU:HB3	11:2P:55:ARG:HE	1.80	0.47
11:2P:84:ASN:HB3	11:2P:117:GLU:HB3	1.96	0.47
21:2Z:98:MET:O	21:2Z:126:VAL:N	2.46	0.47
32:2a:229:U:H5"	47:2p:33:ILE:HD13	1.96	0.47
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.95	0.47
45:2n:9:LYS:HE3	45:2n:12:ARG:HH21	1.79	0.47
54:2w:239:VAL:HG11	54:2w:262:ARG:HA	1.96	0.47
1:1A:535:C:O3'	16:1U:53:ARG:NH1	2.45	0.47
1:1A:679:C:H2'	1:1A:680:G:H8	1.79	0.47
1:1A:1087:G:N2	1:1A:1103:A:H1'	2.28	0.47
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.15	0.47
9:1N:39:ARG:HE	9:1N:39:ARG:HB3	1.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:112:ARG:O	15:1T:115:ARG:NE	2.45	0.47
23:11:3:LYS:HZ2	23:11:3:LYS:HG3	1.55	0.47
24:12:65:ASN:ND2	24:12:69:ARG:HH11	2.09	0.47
26:14:49:PHE:HB3	26:14:50:VAL:H	1.58	0.47
32:1a:7:G:O2'	36:1e:120:THR:O	2.32	0.47
32:1a:507:C:OP2	32:1a:508:C:O2'	2.28	0.47
32:1a:940:C:H2'	32:1a:941:G:C8	2.49	0.47
37:1f:61:LEU:HD23	37:1f:63:TYR:OH	2.14	0.47
54:1w:217:ILE:HD13	54:1w:243:HIS:HA	1.96	0.47
1:2A:34:C:O2'	1:2A:35:G:OP1	2.30	0.47
1:2A:185:U:H4'	1:2A:218:A:H4'	1.97	0.47
1:2A:265:A:C8	1:2A:266:G:H1'	2.50	0.47
1:2A:1843:C:H5'	3:2D:253:GLN:OE1	2.15	0.47
1:2A:2298:A:H2'	1:2A:2299:G:O4'	2.15	0.47
2:2B:39:A:H2'	2:2B:40:U:C6	2.50	0.47
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.14	0.47
32:2a:102:G:H2'	32:2a:103:C:H6	1.80	0.47
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.49	0.47
34:2c:72:LYS:NZ	34:2c:73:PRO:HD2	2.29	0.47
53:2v:10:G:H21	53:2v:11:U:H6	1.61	0.47
54:2w:337:GLU:O	54:2w:341:ARG:HB2	2.15	0.47
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.14	0.47
1:1A:2298:A:H2'	1:1A:2299:G:O4'	2.15	0.47
26:14:60:GLN:C	26:14:62:ARG:H	2.23	0.47
32:1a:162:A:C8	32:1a:163:C:H1'	2.49	0.47
42:1k:63:LEU:H	42:1k:63:LEU:HD12	1.78	0.47
54:1w:172:LYS:HE2	54:1w:172:LYS:HB3	1.55	0.47
1:2A:635:C:H2'	1:2A:636:G:O4'	2.14	0.47
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.14	0.47
1:2A:2865:U:OP2	15:2T:119:LYS:NZ	2.46	0.47
2:2B:83:G:H4'	25:23:52:HIS:CG	2.49	0.47
32:2a:182:U:C4	32:2a:183:G:H1'	2.49	0.47
32:2a:948:C:OP1	44:2m:109:THR:OG1	2.33	0.47
33:2b:187:LEU:HD12	33:2b:201:ILE:O	2.15	0.47
38:2g:31:MET:SD	38:2g:34:GLY:HA2	2.54	0.47
53:2v:12:A:O5'	53:2v:12:A:H8	1.97	0.47
1:1A:583:G:OP2	16:1U:10:ARG:HD2	2.14	0.47
5:1F:32:LEU:HB3	5:1F:112:MET:HE1	1.96	0.47
32:1a:501:C:H2'	32:1a:502:G:C8	2.50	0.47
32:1a:986:A:H1'	50:1s:54:GLY:O	2.13	0.47
32:1a:1262:C:H2'	32:1a:1263:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:11:SER:HB2	47:1p:14:ASN:HB3	1.96	0.47
1:2A:519:U:H2'	1:2A:520:G:H8	1.79	0.47
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.50	0.47
1:2A:839:U:H2'	1:2A:840:C:C6	2.49	0.47
1:2A:900:A:H2'	1:2A:901:A:O4'	2.14	0.47
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.14	0.47
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.14	0.47
5:2F:39:TRP:CD1	5:2F:101:LEU:HB2	2.50	0.47
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.97	0.47
32:2a:1117:G:H4'	40:2i:104:ARG:NH1	2.30	0.47
32:2a:1445:C:O2'	32:2a:1447:A:N6	2.45	0.47
40:2i:128:ARG:NH1	55:2x:33:U:OP2	2.28	0.47
54:2w:221:VAL:HG12	54:2w:239:VAL:HG22	1.97	0.47
1:1A:271(L):U:H4'	8:1I:50:ARG:NH2	2.30	0.47
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.50	0.47
1:1A:1975:G:OP2	60:1A:3860:HOH:O	2.20	0.47
21:1Z:1:MET:HA	21:1Z:55:HIS:HB3	1.96	0.47
32:1a:139:G:H2'	32:1a:140:A:H8	1.79	0.47
32:1a:580:U:H2'	32:1a:581:G:O4'	2.14	0.47
32:1a:659:U:H2'	32:1a:660:G:H8	1.79	0.47
32:1a:950:U:H2'	32:1a:951:G:C8	2.50	0.47
32:1a:976:G:OP1	45:1n:32:SER:N	2.43	0.47
32:1a:1004:A:H5"	32:1a:1024:G:N1	2.23	0.47
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.31	0.47
33:1b:20:GLU:H	33:1b:39:ILE:HG23	1.80	0.47
34:1c:113:ALA:HB2	34:1c:202:ILE:HG13	1.96	0.47
36:1e:78:HIS:CE1	36:1e:142:LEU:HA	2.49	0.47
40:1i:43:ALA:C	40:1i:45:ALA:H	2.22	0.47
55:1x:51:U:H2'	55:1x:52:G:C8	2.49	0.47
1:2A:224:G:H2'	1:2A:225:A:O4'	2.14	0.47
1:2A:234:C:H2'	1:2A:235:U:H6	1.80	0.47
1:2A:271(L):U:H5'	8:2I:50:ARG:NH1	2.29	0.47
1:2A:887:A:H2'	1:2A:887:A:N3	2.30	0.47
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.50	0.47
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.49	0.47
1:2A:2591:C:OP1	3:2D:239:ARG:HD2	2.15	0.47
6:2G:41:GLN:HB2	6:2G:60:LEU:HD21	1.97	0.47
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.50	0.47
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.83	0.47
33:2b:116:GLU:HG3	33:2b:153:ARG:HD3	1.96	0.47
34:2c:22:TRP:CZ3	34:2c:24:ALA:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:127:THR:HG23	35:2d:147:ALA:HB3	1.96	0.47
37:2f:99:ALA:HB2	49:2r:31:LEU:HD11	1.97	0.47
1:1A:131:G:OP1	60:1A:3863:HOH:O	2.20	0.47
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.15	0.47
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.97	0.47
21:1Z:132:ASN:ND2	21:1Z:160:GLY:HA3	2.30	0.47
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.95	0.47
32:1a:193:C:H2'	32:1a:194:C:H6	1.80	0.47
32:1a:390:C:H2'	32:1a:391:G:C8	2.49	0.47
32:1a:546:G:OP1	35:1d:73:ARG:HG2	2.13	0.47
32:1a:1226:C:H2'	44:1m:103:THR:HB	1.97	0.47
34:1c:15:THR:HG22	34:1c:181:ASN:HD22	1.80	0.47
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.43	0.47
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.97	0.47
1:2A:32:C:O2'	1:2A:33:U:H5'	2.15	0.47
1:2A:289:A:H2'	1:2A:290:G:O4'	2.15	0.47
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.50	0.47
6:2G:19:LEU:HD13	6:2G:32:PRO:HD2	1.95	0.47
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.97	0.47
16:2U:21:ALA:HB2	16:2U:39:LEU:HD11	1.96	0.47
32:2a:76:C:H42	32:2a:93:G:H1	1.62	0.47
40:2i:108:VAL:HG12	40:2i:109:VAL:HG12	1.95	0.47
44:2m:24:GLY:N	44:2m:70:LEU:HD23	2.29	0.47
49:2r:73:ALA:HB1	49:2r:79:LEU:HD23	1.97	0.47
1:1A:2171:A:O2'	1:1A:2172:U:H6	1.98	0.47
32:1a:36:C:O2'	43:1l:117:ARG:NH2	2.48	0.47
32:1a:186:C:H2'	32:1a:187:C:H6	1.80	0.47
32:1a:418:C:H1'	32:1a:540:G:O2'	2.15	0.47
34:1c:181:ASN:OD1	34:1c:204:LEU:HD12	2.15	0.47
40:1i:55:ALA:HB1	40:1i:58:HIS:HB2	1.97	0.47
42:1k:73:MET:HE1	42:1k:101:SER:O	2.15	0.47
47:1p:6:LEU:HG	47:1p:17:TYR:HB3	1.96	0.47
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.50	0.47
1:2A:1301:A:OP1	60:2A:3766:HOH:O	2.21	0.47
1:2A:2161:C:H2'	1:2A:2162:G:O4'	2.15	0.47
1:2A:2823:A:OP1	4:2E:113:PHE:HB2	2.14	0.47
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.96	0.47
8:2I:78:THR:HA	8:2I:143:SER:O	2.15	0.47
20:2Y:7:VAL:HG12	20:2Y:8:LYS:H	1.80	0.47
32:2a:848:C:H2'	32:2a:849:C:C6	2.50	0.47
32:2a:921:U:O2'	36:2e:19:MET:O	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1481:U:H2'	32:2a:1482:G:C8	2.50	0.47
54:2w:198:THR:HB	54:2w:293:ILE:HG12	1.97	0.47
1:1A:2627:G:O2'	1:1A:2781:A:N1	2.44	0.47
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.33	0.47
8:1I:109:ILE:HD12	8:1I:130:TYR:CZ	2.50	0.47
13:1R:87:TYR:OH	13:1R:116:LEU:HB3	2.15	0.47
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.49	0.47
32:1a:1437:C:H2'	32:1a:1438:G:H8	1.79	0.47
33:1b:35:GLU:HB3	33:1b:40:HIS:CD2	2.49	0.47
33:1b:141:GLU:O	33:1b:145:LEU:HD12	2.15	0.47
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.50	0.47
32:2a:1063:C:H3'	32:2a:1064:G:H2'	1.97	0.47
32:2a:1511:G:H2'	32:2a:1512:U:O4'	2.16	0.47
36:2e:11:ILE:HD11	36:2e:108:ALA:HB3	1.96	0.47
1:1A:1036:G:H1	1:1A:1119:C:H42	1.63	0.46
1:1A:1071:G:O2'	1:1A:1089:G:OP2	2.30	0.46
1:1A:2615:U:OP1	60:1A:3865:HOH:O	2.21	0.46
5:1F:51:THR:O	5:1F:93:LYS:NZ	2.30	0.46
11:1P:100:LEU:HD22	11:1P:105:LEU:HD12	1.97	0.46
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.50	0.46
35:1d:20:TYR:CD1	35:1d:26:CYS:HB3	2.50	0.46
35:1d:134:ASP:N	35:1d:134:ASP:OD1	2.48	0.46
38:1g:108:ALA:O	38:1g:111:ARG:HB2	2.15	0.46
51:1t:13:LEU:O	51:1t:17:ARG:HG3	2.15	0.46
55:1y:64:A:H2'	55:1y:65:G:C8	2.49	0.46
1:2A:7:G:H2'	1:2A:8:A:C8	2.50	0.46
1:2A:903:C:H2'	1:2A:904:C:H6	1.80	0.46
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.44	0.46
4:2E:2:LYS:HB2	4:2E:95:ILE:HD12	1.95	0.46
4:2E:31:CYS:HB3	4:2E:49:LEU:HB3	1.97	0.46
5:2F:195:ASP:HB3	5:2F:198:ALA:H	1.80	0.46
21:2Z:10:ARG:HD3	21:2Z:18:LEU:HD21	1.97	0.46
32:2a:153:C:H2'	32:2a:154:C:C6	2.49	0.46
32:2a:524:G:H2'	32:2a:525:C:C6	2.49	0.46
32:2a:644:G:H4'	39:2h:92:ARG:HH21	1.80	0.46
33:2b:92:TYR:CD2	33:2b:151:GLY:HA3	2.51	0.46
38:2g:132:GLY:O	38:2g:136:LYS:HG3	2.15	0.46
1:1A:29:U:H2'	1:1A:30:G:C8	2.51	0.46
1:1A:567:A:OP2	11:1P:29:LYS:NZ	2.45	0.46
1:1A:1364:G:OP2	23:11:3:LYS:HB2	2.14	0.46
1:1A:1537:G:H2'	1:1A:1538:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2373:G:H2'	1:1A:2374:C:C6	2.50	0.46
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.97	0.46
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.15	0.46
13:1R:29:LEU:HD11	13:1R:48:VAL:HG13	1.97	0.46
27:15:18:ALA:O	27:15:21:SER:HB2	2.15	0.46
32:1a:253:U:OP1	48:1q:67:LYS:NZ	2.43	0.46
32:1a:266:G:N3	32:1a:266:G:H5"	2.31	0.46
32:1a:1065:U:H4'	32:1a:1066:C:O5'	2.16	0.46
40:1i:46:ALA:HA	40:1i:78:LYS:HB2	1.96	0.46
1:2A:1114:G:H2'	1:2A:1115:G:H8	1.78	0.46
1:2A:2059:A:H2'	1:2A:2503:2MA:HM23	1.97	0.46
1:2A:2136:C:N4	1:2A:2155:G:N1	2.62	0.46
1:2A:2518:A:H2'	1:2A:2518:A:N3	2.29	0.46
1:2A:2768:C:O2'	9:2N:89:LYS:NZ	2.46	0.46
4:2E:4:ILE:HD13	4:2E:28:ALA:HB1	1.97	0.46
7:2H:26:VAL:O	7:2H:79:VAL:HG11	2.15	0.46
32:2a:1160:G:H1	32:2a:1176:A:N6	2.08	0.46
34:2c:113:ALA:HB2	34:2c:202:ILE:HG13	1.98	0.46
35:2d:11:LEU:O	35:2d:15:GLU:HG2	2.16	0.46
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.48	0.46
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.98	0.46
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.98	0.46
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.80	0.46
43:2l:82:VAL:O	43:2l:106:ASP:HB2	2.15	0.46
51:2t:73:HIS:ND1	51:2t:75:ASN:HB2	2.30	0.46
2:1B:43:C:H5"	26:14:1:MET:HG2	1.97	0.46
8:1I:125:GLU:OE2	8:1I:143:SER:HB2	2.14	0.46
10:1O:120:GLU:HG2	10:1O:122:LEU:HG	1.97	0.46
18:1W:18:ARG:HG2	18:1W:76:VAL:HB	1.98	0.46
32:1a:232:G:H1'	32:1a:262:A:N1	2.30	0.46
32:1a:393:A:OP2	47:1p:12:LYS:HD3	2.14	0.46
32:1a:1159:U:O4'	32:1a:1182:G:N2	2.49	0.46
34:1c:53:ALA:HB2	34:1c:115:LEU:HD22	1.96	0.46
36:1e:78:HIS:CE1	36:1e:142:LEU:HD23	2.51	0.46
43:1l:48:PRO:HD2	43:1l:92:0TD:H3	1.98	0.46
54:1w:243:HIS:CD2	54:1w:245:PRO:HD2	2.50	0.46
1:2A:120:U:OP2	60:2A:3768:HOH:O	2.21	0.46
1:2A:727:A:OP1	1:2A:1431:U:O2'	2.33	0.46
1:2A:1114:G:H2'	1:2A:1115:G:C8	2.50	0.46
1:2A:2058:A:N7	60:2A:3849:HOH:O	2.36	0.46
1:2A:2198:A:H5'	8:2I:33:ARG:NH2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2240:C:H2'	1:2A:2241:A:H8	1.80	0.46
5:2F:140:LEU:HD11	5:2F:170:LEU:HD21	1.96	0.46
32:2a:224:C:H2'	32:2a:225:C:H6	1.79	0.46
32:2a:272:C:H2'	32:2a:273:A:H8	1.81	0.46
35:2d:200:GLU:H	35:2d:200:GLU:HG3	1.44	0.46
1:1A:127:A:H5"	1:1A:128:C:C6	2.50	0.46
1:1A:207:A:H2'	1:1A:208:C:O4'	2.16	0.46
1:1A:631:A:OP1	11:1P:65:ARG:NE	2.35	0.46
1:1A:1073:A:C8	1:1A:1074:G:C8	3.04	0.46
1:1A:1153:C:OP1	16:1U:76:TYR:OH	2.30	0.46
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.98	0.46
8:1I:5:LEU:O	8:1I:6:LEU:HD23	2.16	0.46
10:1O:107:ARG:NE	15:1T:36:GLU:HG2	2.30	0.46
11:1P:106:LEU:HD22	11:1P:112:LEU:HD13	1.98	0.46
49:1r:86:VAL:HG12	49:1r:87:ARG:H	1.81	0.46
1:2A:1269:A:OP2	60:2A:3765:HOH:O	2.20	0.46
1:2A:1773:A:C5	1:2A:1829:A:H1'	2.50	0.46
2:2B:115:G:H2'	2:2B:116:G:C8	2.50	0.46
9:2N:102:ALA:O	9:2N:106:MET:HG3	2.15	0.46
15:2T:33:LYS:HE3	15:2T:40:THR:HG21	1.98	0.46
15:2T:62:THR:HG23	15:2T:75:ILE:HG12	1.97	0.46
21:2Z:97:GLU:HB3	21:2Z:125:LEU:HD11	1.96	0.46
32:2a:981:U:H5'	45:2n:21:TYR:CE2	2.50	0.46
32:2a:1234:C:H1'	32:2a:1364:U:O2	2.15	0.46
32:2a:1315:U:H2'	32:2a:1316:G:O4'	2.15	0.46
33:2b:124:SER:N	33:2b:125:PRO:HD3	2.29	0.46
41:2j:21:GLN:HA	41:2j:21:GLN:HE21	1.80	0.46
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.14	0.46
1:1A:1652:A:C2'	1:1A:1653:G:H5'	2.45	0.46
1:1A:2116:G:H2'	1:1A:2117:A:C5	2.50	0.46
1:1A:2390:U:O2'	1:1A:2391:G:H5'	2.16	0.46
2:1B:92:C:OP1	21:1Z:79:ARG:NH1	2.48	0.46
18:1W:82:LEU:HB2	18:1W:98:LYS:HB2	1.98	0.46
21:1Z:125:LEU:HB3	21:1Z:165:VAL:HG13	1.96	0.46
30:18:61:LEU:O	30:18:63:PRO:HD3	2.16	0.46
32:1a:404:U:H2'	32:1a:405:U:C6	2.51	0.46
49:1r:39:VAL:O	49:1r:42:ARG:HB2	2.16	0.46
50:1s:46:GLY:HA2	50:1s:61:TYR:CE1	2.50	0.46
1:2A:1697:G:OP2	1:2A:1698:A:O2'	2.20	0.46
1:2A:2115:G:H2'	1:2A:2117:A:C8	2.51	0.46
4:2E:60:ASN:OD1	4:2E:63:LEU:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:50:ILE:HA	15:2T:99:LEU:HD12	1.97	0.46
32:2a:1335:C:H4'	32:2a:1336:C:C6	2.50	0.46
1:1A:774:A:N3	1:1A:774:A:H2'	2.29	0.46
1:1A:1059:G:H2'	1:1A:1060:U:C5	2.51	0.46
1:1A:1507:A:H2'	1:1A:1508:A:C8	2.50	0.46
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.16	0.46
32:1a:707:C:OP1	42:1k:85:ARG:NH1	2.48	0.46
41:1j:63:PHE:HZ	45:1n:49:HIS:CE1	2.33	0.46
48:1q:41:LYS:NZ	48:1q:92:ARG:HH21	2.14	0.46
1:2A:981:A:HO2'	1:2A:2036:C:HO2'	1.59	0.46
1:2A:1385:G:H1	1:2A:1402:C:H42	1.63	0.46
1:2A:1528:A:OP2	60:2A:3767:HOH:O	2.21	0.46
1:2A:1541:G:H3'	1:2A:1542:A:H2'	1.97	0.46
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.30	0.46
1:2A:2110:G:N2	1:2A:2179:C:N3	2.51	0.46
5:2F:164:ARG:HD2	5:2F:175:THR:HG23	1.98	0.46
6:2G:9:ARG:O	6:2G:13:GLU:HG2	2.16	0.46
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.15	0.46
21:2Z:106:GLY:HA3	21:2Z:142:SER:HB3	1.97	0.46
24:22:31:GLU:HB3	24:22:53:LEU:HD11	1.97	0.46
32:2a:422:C:H5"	32:2a:423:G:C5	2.50	0.46
32:2a:1142:G:C2	32:2a:1143:G:H1'	2.50	0.46
32:2a:1272:G:N2	32:2a:1273:G:N7	2.63	0.46
33:2b:19:HIS:HB3	33:2b:204:ASN:CG	2.40	0.46
36:2e:84:PHE:CZ	36:2e:133:TYR:HD2	2.33	0.46
38:2g:50:ILE:HD11	38:2g:58:PRO:HB3	1.96	0.46
1:1A:218:A:C2	1:1A:235:U:H4'	2.51	0.46
1:1A:2552:OMU:O5'	1:1A:2552:OMU:H6	2.16	0.46
2:1B:45:A:O4'	6:1G:95:ARG:NH1	2.48	0.46
8:1I:123:LEU:HD13	8:1I:145:VAL:HA	1.98	0.46
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.50	0.46
11:1P:132:LYS:HB2	11:1P:132:LYS:HE3	1.66	0.46
15:1T:18:ASP:OD1	15:1T:18:ASP:N	2.48	0.46
31:19:1:MET:SD	31:19:33:LYS:HG2	2.56	0.46
32:1a:109:A:C6	32:1a:326:G:C6	3.04	0.46
32:1a:430:A:H4'	35:1d:7:PRO:HG3	1.97	0.46
32:1a:1146:A:H2'	32:1a:1147:C:O4'	2.16	0.46
43:1l:45:PRO:HB2	43:1l:92:0TD:OD2	2.15	0.46
54:1w:223:ARG:HD2	54:1w:233:ASN:O	2.15	0.46
55:1x:9:A:H8	55:1x:11:C:H41	1.64	0.46
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2203:U:H2'	1:2A:2205:C:H6	1.80	0.46
22:20:23:VAL:HG22	22:20:38:VAL:HG22	1.97	0.46
32:2a:708:C:H2'	32:2a:709:G:H8	1.81	0.46
32:2a:740:U:H2'	32:2a:741:G:C8	2.51	0.46
32:2a:1338:G:H2'	32:2a:1339:A:C8	2.50	0.46
33:2b:52:GLU:HG2	33:2b:56:ARG:HH22	1.81	0.46
33:2b:109:SER:HA	33:2b:112:VAL:HG13	1.96	0.46
34:2c:184:TYR:CD1	34:2c:201:TYR:HE1	2.32	0.46
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.16	0.46
39:2h:17:THR:HG22	39:2h:63:LEU:HD13	1.97	0.46
47:2p:8:ARG:HD2	47:2p:17:TYR:HE1	1.81	0.46
1:1A:739:G:OP1	60:1A:3866:HOH:O	2.21	0.46
1:1A:792:G:H5"	1:1A:793:A:H5'	1.98	0.46
1:1A:1291:C:H2'	1:1A:1292:U:C6	2.50	0.46
1:1A:1797:C:O2'	3:1D:259:THR:OG1	2.31	0.46
1:1A:2389:G:H5"	1:1A:2390:U:O4'	2.16	0.46
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.46	0.46
3:1D:273:ARG:O	3:1D:275:LYS:HE3	2.16	0.46
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.62	0.46
32:1a:1152:A:H2'	32:1a:1153:C:C6	2.51	0.46
34:1c:179:ARG:HD2	34:1c:206:GLU:HB3	1.97	0.46
41:1j:8:LEU:O	41:1j:70:ARG:N	2.45	0.46
44:1m:20:THR:C	44:1m:22:ILE:H	2.24	0.46
49:1r:35:ARG:H	49:1r:35:ARG:HG2	1.52	0.46
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.16	0.46
1:2A:2113:U:H2'	1:2A:2114:A:H8	1.81	0.46
1:2A:2425:A:H4'	1:2A:2426:A:H5"	1.97	0.46
11:2P:52:GLU:OE1	11:2P:55:ARG:NE	2.46	0.46
18:2W:29:LEU:HD21	18:2W:33:ARG:NH2	2.31	0.46
24:22:1:MET:HE1	24:22:9:GLN:NE2	2.30	0.46
32:2a:8:A:N6	35:2d:209:ARG:HB2	2.31	0.46
32:2a:542:G:H5'	35:2d:41:GLY:HA3	1.97	0.46
33:2b:87:ARG:HD2	33:2b:233:SER:HB3	1.97	0.46
38:2g:65:ALA:O	38:2g:69:VAL:HG23	2.16	0.46
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.81	0.46
1:1A:850:C:O2'	25:13:46:ASN:OD1	2.20	0.46
1:1A:2279:G:N7	22:10:14:ARG:NH1	2.63	0.46
3:1D:169:GLU:O	3:1D:169:GLU:HG3	2.16	0.46
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE1	2.27	0.46
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.46	0.46
32:1a:950:U:OP2	44:1m:102:ARG:HD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:95:THR:HG23	34:1c:96:GLY:H	1.81	0.46
41:1j:17:ASP:HA	41:1j:20:ALA:HB3	1.97	0.46
41:1j:63:PHE:HZ	45:1n:49:HIS:HE1	1.62	0.46
47:1p:41:PRO:O	47:1p:43:LYS:HE2	2.16	0.46
1:2A:265:A:H1'	1:2A:266:G:O4'	2.16	0.46
1:2A:2021:C:OP1	27:25:12:SER:OG	2.25	0.46
1:2A:2171:A:H1'	1:2A:2172:U:C6	2.50	0.46
5:2F:160:ASN:HB3	5:2F:163:VAL:HB	1.98	0.46
6:2G:18:GLU:HG2	6:2G:175:LEU:HD11	1.98	0.46
13:2R:36:THR:HG22	13:2R:37:THR:H	1.81	0.46
20:2Y:35:TYR:CE2	20:2Y:69:ALA:HB3	2.51	0.46
32:2a:421:U:O2'	32:2a:423:G:N7	2.49	0.46
32:2a:520:A:H61	32:2a:529:G:H1'	1.81	0.46
32:2a:532:A:H5'	34:2c:161:GLU:OE2	2.15	0.46
32:2a:952:U:H4'	32:2a:964:A:N1	2.31	0.46
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.51	0.46
32:2a:1226:C:O2	50:2s:83:HIS:HE1	1.99	0.46
36:2e:40:ARG:HA	36:2e:67:VAL:O	2.15	0.46
37:2f:95:GLU:H	37:2f:95:GLU:HG2	1.52	0.46
43:2l:28:LYS:NZ	43:2l:62:SER:HB2	2.31	0.46
1:1A:78:A:H2'	1:1A:79:G:H8	1.81	0.46
1:1A:880:G:N2	1:1A:898:C:N3	2.63	0.46
1:1A:1514:U:H2'	1:1A:1515:G:H8	1.81	0.46
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.31	0.46
5:1F:40:GLN:NE2	5:1F:183:VAL:HG13	2.31	0.46
5:1F:101:LEU:HB3	5:1F:106:ARG:HD3	1.97	0.46
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	1.97	0.46
15:1T:24:PRO:HA	15:1T:49:VAL:O	2.16	0.46
32:1a:165:C:H2'	32:1a:166:G:H8	1.80	0.46
32:1a:1347:G:O2'	32:1a:1373:G:O6	2.34	0.46
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.51	0.46
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.45	0.46
34:1c:119:ARG:O	34:1c:123:GLN:HB2	2.16	0.46
37:1f:10:LEU:HD13	37:1f:61:LEU:HD13	1.98	0.46
44:1m:23:TYR:HA	44:1m:24:GLY:HA2	1.63	0.46
54:1w:128:PHE:CZ	54:1w:132:LEU:HD11	2.51	0.46
54:1w:140:PHE:HD1	54:1w:164:GLY:HA3	1.80	0.46
1:2A:570:G:H5"	60:2A:4516:HOH:O	2.16	0.46
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.51	0.46
12:2Q:42:ILE:O	12:2Q:95:ALA:N	2.35	0.46
32:2a:1030(A):G:N2	32:2a:1030(D):A:OP2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1250:A:H4'	40:2i:68:GLY:H	1.81	0.46
32:2a:1348:U:H2'	32:2a:1349:A:H8	1.81	0.46
36:2e:42:GLY:HA2	36:2e:65:ASN:O	2.16	0.46
54:2w:332:LEU:HB3	54:2w:336:LEU:HD12	1.97	0.46
1:1A:476:G:H4'	1:1A:502:A:N1	2.31	0.45
1:1A:1300:U:H4'	1:1A:1301:A:H5'	1.98	0.45
1:1A:2127:G:H2'	1:1A:2128:C:C6	2.50	0.45
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.16	0.45
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.81	0.45
8:1I:109:ILE:HA	8:1I:109:ILE:HD13	1.78	0.45
11:1P:37:GLY:O	11:1P:41:ARG:HG2	2.16	0.45
12:1Q:75:THR:HA	12:1Q:89:ASN:O	2.16	0.45
32:1a:148:G:H2'	32:1a:149:A:H8	1.79	0.45
32:1a:238:G:OP1	48:1q:25:ARG:NH2	2.49	0.45
36:1e:75:THR:HB	36:1e:117:ASP:O	2.16	0.45
37:1f:60:PHE:C	37:1f:61:LEU:HD12	2.41	0.45
45:1n:4:LYS:HA	45:1n:7:ILE:HD12	1.97	0.45
54:1w:299:SER:O	54:1w:301:LYS:N	2.49	0.45
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.15	0.45
1:2A:902:C:H2'	1:2A:903:C:H6	1.81	0.45
1:2A:1418:G:OP1	1:2A:1588:C:O2'	2.33	0.45
1:2A:1598:C:O3'	19:2X:35:THR:OG1	2.34	0.45
1:2A:1919:A:N1	32:2a:1495:U:O2'	2.41	0.45
10:2O:104:ARG:NH1	15:2T:34:VAL:HG21	2.30	0.45
21:2Z:105:VAL:N	21:2Z:139:VAL:O	2.36	0.45
32:2a:1022:G:H3'	32:2a:1023:G:C8	2.51	0.45
32:2a:1372:U:OP1	40:2i:72:GLY:N	2.48	0.45
38:2g:15:ASP:OD2	38:2g:44:TYR:OH	2.33	0.45
54:2w:110:GLU:HG2	54:2w:159:VAL:HG22	1.98	0.45
54:2w:215:ASP:N	54:2w:215:ASP:OD1	2.47	0.45
1:1A:222:A:C2	1:1A:233:A:H5"	2.52	0.45
1:1A:1358:G:O2'	1:1A:1359:A:H5"	2.15	0.45
1:1A:2095:C:H2'	1:1A:2096:U:O4'	2.16	0.45
7:1H:58:GLU:O	7:1H:62:LYS:HG3	2.16	0.45
32:1a:401:C:OP1	35:1d:73:ARG:NH2	2.50	0.45
32:1a:895:G:H2'	32:1a:896:C:C6	2.52	0.45
32:1a:1019:C:H2'	32:1a:1020:U:O4'	2.15	0.45
33:1b:69:LEU:HD22	33:1b:155:LEU:HD11	1.99	0.45
33:1b:166:ASP:O	33:1b:170:GLU:HG2	2.17	0.45
40:1i:65:VAL:HG21	40:1i:77:ILE:HD11	1.97	0.45
54:1w:198:THR:HB	54:1w:293:ILE:HG12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:234:C:H2'	1:2A:235:U:C6	2.52	0.45
1:2A:981:A:N1	1:2A:2027:G:O2'	2.46	0.45
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.15	0.45
1:2A:2317:C:H2'	1:2A:2318:G:H5'	1.98	0.45
1:2A:2695:C:H2'	1:2A:2696:U:H6	1.81	0.45
32:2a:1015:A:N3	32:2a:1218:C:O2'	2.45	0.45
33:2b:67:THR:HG23	33:2b:159:PRO:HA	1.97	0.45
35:2d:59:ARG:HD3	35:2d:59:ARG:HA	1.46	0.45
54:2w:222:MET:HE3	54:2w:222:MET:HB3	1.86	0.45
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.17	0.45
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.51	0.45
1:1A:1920:OMC:HM22	1:1A:1921:G:O4'	2.17	0.45
1:1A:2250:G:OP1	12:1Q:85:LYS:NZ	2.45	0.45
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.97	0.45
1:1A:2533:A:H2'	1:1A:2534:A:O4'	2.15	0.45
21:1Z:154:ASP:OD1	21:1Z:154:ASP:N	2.48	0.45
32:1a:630:G:H2'	32:1a:631:G:H8	1.81	0.45
41:1j:61:GLU:OE1	45:1n:45:ARG:NE	2.41	0.45
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.40	0.45
1:2A:1506:C:H2'	1:2A:1507:A:H5'	1.99	0.45
1:2A:1637:A:H4'	1:2A:2711:A:O2'	2.16	0.45
1:2A:1651:G:OP1	13:2R:40:LYS:NZ	2.44	0.45
1:2A:2114:A:H61	1:2A:2171:A:H61	1.64	0.45
1:2A:2808:U:H5"	1:2A:2891:G:O6	2.16	0.45
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.25	0.45
13:2R:13:HIS:CE1	13:2R:16:HIS:HB2	2.51	0.45
24:22:17:SER:HB2	24:22:20:GLU:H	1.80	0.45
32:2a:1191:A:OP1	34:2c:3:ASN:ND2	2.44	0.45
32:2a:1318:A:O2'	50:2s:37:ARG:HB3	2.16	0.45
36:2e:8:GLU:HG2	36:2e:34:VAL:HG23	1.98	0.45
50:2s:58:VAL:O	50:2s:60:VAL:HG23	2.15	0.45
1:1A:271(L):U:H4'	8:1I:50:ARG:NH1	2.30	0.45
1:1A:1071:G:O4'	1:1A:1088:A:O2'	2.29	0.45
17:1V:85:LYS:NZ	17:1V:85:LYS:HB3	2.30	0.45
21:1Z:152:ALA:HA	21:1Z:155:LEU:HG	1.97	0.45
23:11:34:THR:HG22	23:11:36:GLY:H	1.81	0.45
32:1a:189(A):C:H2'	32:1a:189(B):C:C6	2.51	0.45
38:1g:131:LYS:HE3	38:1g:131:LYS:HB2	1.84	0.45
39:1h:29:SER:CB	39:1h:32:LYS:HD3	2.46	0.45
47:1p:40:ASP:HB3	47:1p:48:TRP:HB2	1.98	0.45
54:1w:312:VAL:HG21	54:1w:327:VAL:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.52	0.45
9:2N:12:ARG:NH1	9:2N:50:ASP:OD2	2.49	0.45
24:22:25:VAL:HG11	24:22:61:LEU:HD21	1.99	0.45
30:28:34:TRP:CG	30:28:35:GLN:N	2.85	0.45
32:2a:160:A:H2'	32:2a:161:A:O4'	2.16	0.45
32:2a:162:A:C5	32:2a:163:C:H1'	2.51	0.45
32:2a:393:A:OP1	47:2p:13:HIS:HE1	1.99	0.45
32:2a:544:G:P	35:2d:62:GLN:HE21	2.35	0.45
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.16	0.45
33:2b:123:ALA:O	33:2b:124:SER:OG	2.31	0.45
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.99	0.45
38:2g:40:ALA:HB1	38:2g:44:TYR:CE2	2.51	0.45
8:1I:12:LEU:HD13	8:1I:12:LEU:HA	1.80	0.45
14:1S:93:LYS:HB3	14:1S:93:LYS:HE2	1.71	0.45
21:1Z:45:ASP:O	21:1Z:49:ARG:HB2	2.16	0.45
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.39	0.45
32:1a:139:G:H2'	32:1a:140:A:C8	2.51	0.45
32:1a:237:C:OP2	48:1q:40:LYS:NZ	2.45	0.45
32:1a:401:C:OP2	35:1d:73:ARG:NH1	2.44	0.45
32:1a:405:U:O4	35:1d:2:GLY:N	2.50	0.45
32:1a:730:G:C5	32:1a:731:G:H1'	2.52	0.45
32:1a:815:A:N7	32:1a:1509:C:O2'	2.49	0.45
32:1a:1228:C:OP1	44:1m:115:LYS:N	2.45	0.45
32:1a:1460:A:H2'	32:1a:1461:G:O4'	2.16	0.45
35:1d:163:GLU:O	35:1d:165:MET:N	2.49	0.45
40:1i:22:GLY:HA3	40:1i:60:ASP:HB2	1.97	0.45
48:1q:76:LEU:HD12	48:1q:77:VAL:H	1.81	0.45
1:2A:910:A:N3	1:2A:2264:C:O2'	2.45	0.45
1:2A:1289:C:H2'	1:2A:1290:C:H6	1.80	0.45
1:2A:1371:G:C2'	1:2A:1372:U:H5	2.30	0.45
1:2A:2811:G:N2	1:2A:2891:G:H1'	2.32	0.45
3:2D:70:TRP:HB3	3:2D:190:TYR:CZ	2.51	0.45
6:2G:62:LEU:HD22	26:24:7:PRO:HG2	1.99	0.45
15:2T:36:GLU:HG3	15:2T:41:ARG:HE	1.82	0.45
32:2a:1238:A:H2	32:2a:1241:G:N3	2.15	0.45
32:2a:1273:G:C5	32:2a:1274:G:H1'	2.52	0.45
33:2b:59:GLU:O	33:2b:63:MET:HB2	2.17	0.45
33:2b:155:LEU:HD12	33:2b:155:LEU:HA	1.83	0.45
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.98	0.45
35:2d:153:ARG:HH11	35:2d:181:MET:HE3	1.82	0.45
36:2e:95:ALA:HB1	36:2e:96:PRO:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:22:GLU:H	37:2f:22:GLU:HG2	1.58	0.45
44:2m:23:TYR:HA	44:2m:24:GLY:HA2	1.63	0.45
54:2w:249:MET:HE2	54:2w:249:MET:HB3	1.79	0.45
55:2y:68:C:H2'	55:2y:69:G:H5'	1.98	0.45
1:1A:1771:C:OP1	60:1A:3867:HOH:O	2.21	0.45
1:1A:2139:C:H2'	1:1A:2140:C:O4'	2.16	0.45
1:1A:2807:G:N2	1:1A:2893:G:O6	2.44	0.45
8:1I:75:LEU:HD13	8:1I:105:HIS:CE1	2.52	0.45
32:1a:258:G:H2'	32:1a:259:G:H8	1.82	0.45
39:1h:87:SER:HB2	39:1h:93:VAL:HB	1.98	0.45
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.97	0.45
52:1u:12:LYS:HB2	52:1u:22:ARG:HD3	1.99	0.45
54:1w:239:VAL:HG11	54:1w:262:ARG:HA	1.97	0.45
1:2A:125:G:O2'	29:27:48:LYS:HE3	2.16	0.45
1:2A:1207:C:H2'	1:2A:1208:C:C6	2.52	0.45
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.52	0.45
1:2A:1810:A:H2'	1:2A:1811:G:O4'	2.16	0.45
1:2A:2334:G:O6	22:20:74:ARG:NH2	2.50	0.45
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.51	0.45
5:2F:197:ASP:N	5:2F:197:ASP:OD1	2.49	0.45
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.81	0.45
14:2S:30:ARG:HD2	14:2S:97:ARG:HD3	1.97	0.45
15:2T:42:ILE:HG13	15:2T:84:GLN:NE2	2.32	0.45
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.97	0.45
17:2V:56:SER:OG	17:2V:100:ARG:HG3	2.16	0.45
32:2a:564:C:O2'	39:2h:91:ARG:NH1	2.31	0.45
32:2a:989:C:HO2'	32:2a:1017:G:HO2'	1.65	0.45
32:2a:1124:G:N2	32:2a:1125:U:O4	2.39	0.45
33:2b:144:ARG:HG3	33:2b:148:TYR:HE2	1.80	0.45
38:2g:47:CYS:HA	38:2g:50:ILE:HG12	1.98	0.45
41:2j:57:LYS:HE2	41:2j:60:ARG:HH22	1.81	0.45
42:2k:21:ILE:HG12	42:2k:30:VAL:HG22	1.99	0.45
51:2t:50:GLU:HG2	51:2t:100:ILE:HD11	1.99	0.45
1:1A:675:A:N3	1:1A:2443:C:O2'	2.47	0.45
1:1A:1095:A:H2'	1:1A:1096:A:O4'	2.17	0.45
21:1Z:138:GLU:HG3	21:1Z:156:LYS:HZ3	1.82	0.45
29:17:31:LEU:HD22	29:17:42:LEU:HD13	1.99	0.45
32:1a:302:G:N3	32:1a:556:C:H4'	2.32	0.45
32:1a:737:A:H5"	37:1f:92:LYS:HG3	1.98	0.45
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.16	0.45
32:1a:1226:C:H4'	50:1s:80:TYR:CZ	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:195:ASP:OD1	33:1b:195:ASP:N	2.49	0.45
1:2A:370:G:OP1	1:2A:403:U:N3	2.36	0.45
1:2A:862:G:H2'	1:2A:863:A:O4'	2.17	0.45
1:2A:1169:G:H1	1:2A:1180:C:H42	1.64	0.45
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.52	0.45
11:2P:132:LYS:HE3	11:2P:132:LYS:HB2	1.64	0.45
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.16	0.45
32:2a:383:A:OP1	32:2a:454:C:O2'	2.26	0.45
32:2a:1279:A:OP2	41:2j:9:ARG:NH1	2.49	0.45
36:2e:43:LEU:HD22	36:2e:136:MET:HE3	1.98	0.45
39:2h:2:LEU:HD12	39:2h:3:THR:H	1.82	0.45
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.31	0.45
44:2m:33:ALA:HB1	44:2m:60:VAL:HG12	1.99	0.45
44:2m:59:TYR:CZ	44:2m:63:THR:HG21	2.51	0.45
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.51	0.45
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.52	0.45
15:1T:94:ALA:HB1	15:1T:99:LEU:HD21	1.98	0.45
15:1T:106:SER:O	15:1T:110:ILE:HG13	2.17	0.45
23:11:8:SER:HB3	23:11:66:HIS:CD2	2.51	0.45
32:1a:142:G:H2'	32:1a:143:A:H8	1.82	0.45
34:1c:6:HIS:HB2	45:1n:49:HIS:HD2	1.82	0.45
40:1i:43:ALA:O	40:1i:45:ALA:N	2.49	0.45
54:1w:242:VAL:HG13	54:1w:249:MET:HB3	1.98	0.45
1:2A:1508:A:H4'	1:2A:1509(A):A:C4	2.52	0.45
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.49	0.45
1:2A:2452:C:H4'	54:2w:234:THR:HG21	1.98	0.45
1:2A:2850:A:N7	1:2A:2868:A:O2'	2.49	0.45
6:2G:46:ALA:HA	6:2G:49:ASP:HB2	1.98	0.45
6:2G:155:MET:HE2	6:2G:155:MET:HB3	1.88	0.45
8:2I:29:TYR:O	8:2I:33:ARG:HD2	2.17	0.45
20:2Y:6:HIS:CD2	20:2Y:7:VAL:HG23	2.52	0.45
21:2Z:10:ARG:HB3	21:2Z:38:TYR:HD2	1.82	0.45
32:2a:181:G:H4'	32:2a:182:U:H5'	1.98	0.45
35:2d:205:GLU:OE2	36:2e:100:VAL:HG12	2.16	0.45
48:2q:76:LEU:HD12	48:2q:77:VAL:H	1.82	0.45
1:1A:795:C:H2'	1:1A:796:C:H6	1.82	0.45
10:1O:8:LEU:HD22	10:1O:84:ALA:HB2	1.99	0.45
30:18:29:LYS:HB2	30:18:33:ASN:HD21	1.81	0.45
32:1a:279:A:OP2	48:1q:95:TYR:OH	2.30	0.45
32:1a:613:C:N4	32:1a:627:G:H1	2.14	0.45
32:1a:659:U:H2'	32:1a:660:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:738:C:OP1	37:1f:2:ARG:NH1	2.48	0.45
41:1j:7:LYS:NZ	41:1j:71:LEU:HD13	2.32	0.45
1:2A:299:A:N1	1:2A:322:A:O2'	2.45	0.45
1:2A:468:G:N7	29:27:39:ARG:NH2	2.60	0.45
1:2A:602:G:O2'	1:2A:655:A:N6	2.50	0.45
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.52	0.45
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.22	0.45
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.15	0.45
8:2I:123:LEU:HD22	8:2I:123:LEU:HA	1.79	0.45
32:2a:110:C:H2'	32:2a:111:G:O4'	2.17	0.45
32:2a:857:C:H2'	32:2a:858:G:O4'	2.17	0.45
32:2a:985:C:H2'	32:2a:986:A:C8	2.52	0.45
32:2a:1271:G:H5'	32:2a:1314:C:H5"	1.98	0.45
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.51	0.45
39:2h:20:TYR:HA	39:2h:65:TYR:CE1	2.52	0.45
41:2j:42:THR:HG21	41:2j:66:ARG:HD3	1.97	0.45
43:2l:117:ARG:HB3	43:2l:122:THR:HB	1.99	0.45
1:1A:226:G:C2	1:1A:227:A:C6	3.05	0.45
1:1A:848:G:O6	1:1A:928:G:H2'	2.17	0.45
1:1A:1800:C:OP2	3:1D:183:ARG:NH2	2.50	0.45
1:1A:1859:A:N6	1:1A:1883:G:O2'	2.50	0.45
3:1D:72:LYS:HE3	3:1D:75:ILE:HD12	1.99	0.45
8:1I:109:ILE:HG23	8:1I:130:TYR:OH	2.17	0.45
14:1S:5:THR:OG1	14:1S:8:GLU:HG3	2.16	0.45
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.52	0.45
20:1Y:8:LYS:HD2	20:1Y:97:ARG:NH2	2.31	0.45
32:1a:201:C:H2'	32:1a:202:U:H2'	1.98	0.45
32:1a:310:G:H5"	47:1p:31:LYS:HB2	1.99	0.45
32:1a:728:A:C5	46:1o:54:ARG:HD2	2.52	0.45
37:1f:84:ASN:O	37:1f:86:ARG:HG3	2.17	0.45
44:1m:14:ARG:HH21	44:1m:41:PRO:HB2	1.81	0.45
44:1m:50:GLU:HA	44:1m:53:VAL:HB	1.99	0.45
48:1q:31:LEU:HD23	48:1q:32:TYR:CZ	2.52	0.45
53:1v:16:U:H2'	53:1v:17:U:O4'	2.16	0.45
1:2A:1289:C:H2'	1:2A:1290:C:C6	2.52	0.45
1:2A:1790:C:O2'	3:2D:209:ALA:HB2	2.17	0.45
1:2A:2013:A:H4'	18:2W:96:ILE:HD13	1.99	0.45
5:2F:125:LEU:HD11	5:2F:199:TRP:HB2	1.98	0.45
32:2a:582:U:C2	32:2a:760:G:C6	3.05	0.45
32:2a:691:G:H2'	32:2a:692:U:C6	2.51	0.45
32:2a:828:A:H2'	32:2a:829:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1025:U:H1'	32:2a:1026:G:N7	2.31	0.45
32:2a:1395:C:O2'	32:2a:1401:G:O2'	2.30	0.45
37:2f:23:LYS:HD3	37:2f:61:LEU:HD21	1.98	0.45
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.98	0.45
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.17	0.45
1:1A:673:C:H5"	5:1F:81:PRO:HD2	1.99	0.44
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.17	0.44
1:1A:1686:C:H2'	1:1A:1687:G:O4'	2.17	0.44
1:1A:1845:G:H1	1:1A:1895:C:H42	1.65	0.44
4:1E:116:VAL:HG21	4:1E:138:PRO:HB3	2.00	0.44
16:1U:79:PHE:CE2	16:1U:83:LEU:HD11	2.52	0.44
18:1W:2:GLU:OE2	18:1W:72:LYS:NZ	2.20	0.44
32:1a:565:U:OP2	32:1a:566:G:O2'	2.34	0.44
32:1a:626:U:C2	32:1a:627:G:C8	3.05	0.44
32:1a:993:G:H2'	32:1a:993:G:N3	2.32	0.44
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	1.99	0.44
38:1g:150:ALA:HA	42:1k:59:TYR:HB3	1.98	0.44
54:1w:151:ASP:OD1	54:1w:151:ASP:N	2.50	0.44
1:2A:271(F):C:H2'	1:2A:271(G):C:C6	2.52	0.44
1:2A:360:G:H2'	1:2A:361:G:O4'	2.16	0.44
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	2.00	0.44
6:2G:138:GLN:NE2	6:2G:151:ALA:O	2.51	0.44
21:2Z:102:LEU:HA	21:2Z:102:LEU:HD13	1.72	0.44
32:2a:321:A:C2	32:2a:333:G:C2	3.06	0.44
32:2a:437:U:O2'	35:2d:125:HIS:HE1	2.00	0.44
32:2a:452:A:O2'	32:2a:453:A:OP2	2.30	0.44
32:2a:1002:G:H1	32:2a:1038:C:H42	1.63	0.44
32:2a:1137:C:H4'	32:2a:1138:G:C5	2.52	0.44
42:2k:92:GLU:HB3	42:2k:96:ARG:NH2	2.31	0.44
43:2l:32:PHE:CE1	43:2l:86:ARG:HB3	2.52	0.44
1:1A:7:G:H4'	9:1N:13:TRP:CH2	2.52	0.44
1:1A:459:U:OP2	29:17:39:ARG:NH1	2.49	0.44
1:1A:593:G:C4'	30:18:4:MET:HE2	2.47	0.44
1:1A:886:C:O2	1:1A:887:A:H8	1.99	0.44
1:1A:2787:C:H1'	4:1E:62:PRO:HB3	1.99	0.44
1:1A:2820:A:O2'	1:1A:2821:A:OP1	2.34	0.44
5:1F:7:TYR:CE2	5:1F:24:LEU:HB2	2.53	0.44
6:1G:105:LYS:HG2	26:14:24:THR:HG21	1.98	0.44
9:1N:123:TYR:HH	9:1N:130:HIS:CE1	2.32	0.44
26:14:57:GLU:HA	26:14:60:GLN:HB2	1.99	0.44
32:1a:737:A:H2'	32:1a:738:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:792:A:O2'	32:1a:794:A:N7	2.48	0.44
32:1a:1429:C:H2'	32:1a:1430:C:C6	2.53	0.44
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.99	0.44
36:1e:110:LEU:HD13	36:1e:118:ILE:HD13	1.98	0.44
39:1h:13:ILE:O	39:1h:17:THR:HG23	2.18	0.44
41:1j:30:SER:OG	41:1j:81:THR:HG22	2.17	0.44
42:1k:58:PRO:O	42:1k:93:GLN:HG2	2.17	0.44
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.50	0.44
2:2B:24:G:H4'	2:2B:25:A:C8	2.53	0.44
5:2F:60:SER:OG	5:2F:61:GLY:N	2.50	0.44
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.82	0.44
26:24:58:ARG:HE	26:24:58:ARG:N	2.15	0.44
32:2a:67:C:H2'	32:2a:68:G:H8	1.82	0.44
51:2t:79:ARG:HD2	51:2t:83:ARG:NH2	2.33	0.44
1:1A:84:A:H5'	20:1Y:8:LYS:HB2	1.98	0.44
1:1A:807:U:OP2	11:1P:41:ARG:NH2	2.47	0.44
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.30	0.44
1:1A:2774:C:H2'	1:1A:2775:A:O4'	2.16	0.44
10:1O:49:ARG:NH2	32:1a:1423:G:OP1	2.28	0.44
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HE2	1.98	0.44
32:1a:250:A:H4'	32:1a:251:G:O5'	2.17	0.44
32:1a:1302:U:O4	44:1m:14:ARG:HD3	2.17	0.44
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.52	0.44
39:1h:51:VAL:HG21	39:1h:60:ARG:NH1	2.33	0.44
41:1j:70:ARG:HD3	41:1j:70:ARG:HA	1.65	0.44
45:1n:6:LEU:HD22	45:1n:21:TYR:OH	2.17	0.44
1:2A:27:G:N2	1:2A:512:G:H1'	2.32	0.44
1:2A:658:C:H2'	1:2A:659:C:C6	2.52	0.44
1:2A:989:G:O2'	60:2A:3771:HOH:O	2.21	0.44
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.52	0.44
3:2D:145:VAL:HB	3:2D:155:LEU:HB2	1.99	0.44
5:2F:123:LEU:HD12	5:2F:124:LEU:H	1.81	0.44
6:2G:146:TYR:O	6:2G:149:VAL:HG22	2.17	0.44
7:2H:3:ARG:HE	7:2H:54:ARG:NH1	2.13	0.44
7:2H:60:ARG:HG2	7:2H:64:LEU:HD11	1.98	0.44
18:2W:19:LEU:HB3	27:25:25:LEU:HG	1.99	0.44
20:2Y:5:MET:HE1	20:2Y:35:TYR:HA	1.99	0.44
24:22:10:LEU:HB3	24:22:14:ARG:HH11	1.82	0.44
24:22:53:LEU:O	24:22:57:ILE:HG13	2.17	0.44
25:23:35:ARG:HH21	25:23:37:LEU:HD21	1.82	0.44
32:2a:714:G:H2'	32:2a:715:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:952:U:O4	44:2m:104:ARG:HD3	2.17	0.44
32:2a:1027:C:C4	32:2a:1034:G:N1	2.86	0.44
32:2a:1151:A:H5"	41:2j:41:PRO:HA	1.99	0.44
35:2d:15:GLU:OE2	35:2d:59:ARG:HD2	2.18	0.44
35:2d:153:ARG:HD3	35:2d:181:MET:SD	2.57	0.44
37:2f:100:ASN:HD21	49:2r:23:LYS:HE3	1.81	0.44
44:2m:11:ARG:H	44:2m:11:ARG:HD2	1.82	0.44
54:2w:177:VAL:HG21	54:2w:300:GLU:HB2	1.99	0.44
1:1A:667:U:O2	30:18:2:PRO:HD2	2.17	0.44
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.23	0.44
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.18	0.44
1:1A:2052:G:H4'	4:1E:143:ASN:O	2.17	0.44
7:1H:101:ARG:NH2	7:1H:122:THR:HA	2.28	0.44
11:1P:98:GLU:O	11:1P:101:VAL:HG22	2.18	0.44
20:1Y:40:GLU:O	20:1Y:42:VAL:HG23	2.18	0.44
44:1m:67:GLU:O	44:1m:71:ARG:HG3	2.17	0.44
1:2A:83:G:N1	1:2A:102:G:O2'	2.40	0.44
1:2A:448:U:H5"	60:2A:4017:HOH:O	2.16	0.44
1:2A:813:U:H2'	1:2A:814:C:C6	2.52	0.44
1:2A:1257:C:H4'	5:2F:83:PHE:CD1	2.52	0.44
1:2A:2591:C:P	3:2D:239:ARG:HB2	2.58	0.44
2:2B:45:A:O4'	6:2G:95:ARG:NH1	2.50	0.44
2:2B:83:G:H5'	25:23:52:HIS:CE1	2.53	0.44
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.50	0.44
32:2a:551:U:H2'	32:2a:552:U:C6	2.52	0.44
32:2a:685:G:O2'	32:2a:686:U:H5'	2.17	0.44
32:2a:971:G:N2	32:2a:1363(A):A:OP2	2.45	0.44
32:2a:1093:A:H2'	32:2a:1095:U:H5'	1.98	0.44
33:2b:12:GLU:HB2	33:2b:213:LEU:HD23	2.00	0.44
33:2b:133:LYS:H	33:2b:133:LYS:CE	2.29	0.44
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.52	0.44
45:2n:57:ARG:HG2	45:2n:58:LYS:H	1.81	0.44
45:2n:58:LYS:HE2	45:2n:58:LYS:HB3	1.82	0.44
1:1A:272(C):G:H2'	1:1A:272(D):G:O4'	2.17	0.44
1:1A:855:G:O2'	22:10:27:GLU:OE2	2.28	0.44
1:1A:1568:G:H4'	3:1D:59:LYS:HB3	1.98	0.44
4:1E:181:LEU:HD23	4:1E:181:LEU:HA	1.77	0.44
5:1F:36:VAL:HG12	5:1F:40:GLN:HE21	1.81	0.44
10:1O:88:ASN:ND2	10:1O:90:GLN:OE1	2.50	0.44
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.99	0.44
30:18:34:TRP:CG	30:18:35:GLN:N	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:735:C:H2'	32:1a:736:C:H6	1.81	0.44
32:1a:973:G:H1'	41:1j:54:PHE:HE1	1.81	0.44
32:1a:1509:C:H2'	32:1a:1510:U:O4'	2.17	0.44
44:1m:16:ASP:HA	44:1m:30:ALA:HB1	1.97	0.44
1:2A:994:C:O2	17:2V:10:LYS:NZ	2.46	0.44
1:2A:1629:U:H2'	1:2A:1630:G:C8	2.52	0.44
1:2A:2198:A:H5'	8:2I:33:ARG:HH21	1.82	0.44
1:2A:2774:C:H2'	1:2A:2775:A:O4'	2.17	0.44
24:22:9:GLN:HE22	24:22:56:GLN:HG2	1.82	0.44
32:2a:446:G:H2'	32:2a:447:G:O4'	2.18	0.44
32:2a:820:U:O2'	32:2a:821:G:OP1	2.35	0.44
32:2a:866:C:C4	32:2a:867:G:H1'	2.52	0.44
32:2a:922:G:H2'	32:2a:923:A:C8	2.53	0.44
35:2d:43:HIS:HA	35:2d:46:LYS:HE3	2.00	0.44
37:2f:6:VAL:C	37:2f:7:ASN:HD22	2.26	0.44
38:2g:93:PRO:HA	38:2g:96:GLN:HB2	1.99	0.44
55:2y:62:C:H2'	55:2y:63:G:H8	1.78	0.44
1:1A:626:U:O4	11:1P:107:LYS:HE2	2.16	0.44
1:1A:887:A:H4'	1:1A:888:C:OP1	2.15	0.44
1:1A:1314:C:OP1	60:1A:3811:HOH:O	2.21	0.44
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.98	0.44
3:1D:121:PRO:HB3	3:1D:135:PHE:CE2	2.52	0.44
6:1G:9:ARG:O	6:1G:13:GLU:HG2	2.17	0.44
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	1.99	0.44
32:1a:1244:C:H42	32:1a:1293:G:H1	1.65	0.44
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.52	0.44
32:1a:1519:MA6:H102	32:1a:1520:G:O2'	2.17	0.44
33:1b:35:GLU:HB3	33:1b:40:HIS:HD2	1.80	0.44
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.53	0.44
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	2.00	0.44
22:20:40:GLN:OE1	22:20:44:ARG:N	2.50	0.44
32:2a:109:A:C6	32:2a:326:G:C6	3.06	0.44
32:2a:519:C:OP1	54:2w:179:ARG:NH2	2.51	0.44
32:2a:986:A:H1'	50:2s:54:GLY:O	2.18	0.44
32:2a:1366:C:H2'	32:2a:1367:C:H6	1.80	0.44
41:2j:85:LEU:HD12	41:2j:85:LEU:HA	1.71	0.44
42:2k:20:TYR:O	42:2k:30:VAL:HA	2.17	0.44
55:2y:51:U:H3	55:2y:63:G:H1	1.65	0.44
1:1A:1400:G:H2'	1:1A:1401:G:C8	2.52	0.44
1:1A:1424:G:H2'	1:1A:1425:G:O4'	2.18	0.44
1:1A:2040:C:H2'	1:1A:2041:U:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2513:G:H2'	1:1A:2514:U:C6	2.53	0.44
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.53	0.44
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.53	0.44
4:1E:2:LYS:NZ	4:1E:95:ILE:O	2.50	0.44
8:1I:84:GLY:O	8:1I:85:GLU:HB3	2.18	0.44
20:1Y:43:ASN:HB3	20:1Y:65:ALA:HB3	2.00	0.44
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.18	0.44
32:1a:375:U:C2	32:1a:376:G:C8	3.06	0.44
32:1a:583:A:H2'	32:1a:584:G:O4'	2.18	0.44
32:1a:690:G:C6	32:1a:691:G:C6	3.06	0.44
33:1b:208:ILE:H	33:1b:208:ILE:HD12	1.82	0.44
34:1c:34:LEU:HG	34:1c:38:ARG:HE	1.81	0.44
35:1d:98:GLU:OE2	35:1d:103:ASN:ND2	2.46	0.44
38:1g:75:VAL:HG11	38:1g:86:GLN:HB3	2.00	0.44
40:1i:19:LEU:HB3	40:1i:59:PHE:CD1	2.53	0.44
43:1l:89:ARG:NH2	43:1l:91:LYS:HG3	2.33	0.44
1:2A:796:C:H2'	1:2A:797:C:C6	2.52	0.44
1:2A:1859:A:N6	1:2A:1883:G:O2'	2.51	0.44
1:2A:2607:G:H2'	1:2A:2608:G:O4'	2.18	0.44
6:2G:99:MET:O	6:2G:103:LEU:HG	2.18	0.44
8:2I:140:LEU:HG	8:2I:142:VAL:HG23	2.00	0.44
15:2T:11:GLU:OE1	15:2T:57:PHE:HB3	2.18	0.44
15:2T:107:ASP:O	15:2T:111:ARG:HG3	2.18	0.44
16:2U:97:ASP:OD2	16:2U:101:ARG:HD2	2.18	0.44
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	2.00	0.44
34:2c:42:LEU:HA	34:2c:45:LYS:NZ	2.32	0.44
40:2i:127:LYS:O	40:2i:128:ARG:HG2	2.17	0.44
53:2v:10:G:N3	53:2v:10:G:H2'	2.33	0.44
1:1A:184:C:H2'	1:1A:185:U:H6	1.81	0.44
1:1A:1091:G:N2	1:1A:1101:U:H1'	2.33	0.44
6:1G:120:LEU:N	6:1G:179:PRO:O	2.42	0.44
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	2.00	0.44
15:1T:127:ALA:C	15:1T:129:ARG:N	2.74	0.44
26:14:53:GLU:HA	26:14:56:VAL:HG13	1.99	0.44
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.99	0.44
32:1a:475:G:H2'	32:1a:476:G:C8	2.52	0.44
32:1a:640:A:C6	32:1a:641:U:C4	3.06	0.44
32:1a:952:U:C5	44:1m:104:ARG:HD3	2.52	0.44
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.17	0.44
38:1g:73:MET:HG3	38:1g:89:MET:O	2.17	0.44
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:119:GLU:HA	54:1w:122:LEU:HB2	2.00	0.44
1:2A:817:C:O2'	1:2A:839:U:H5"	2.17	0.44
1:2A:873:G:N2	1:2A:905:U:C2	2.86	0.44
1:2A:2307:G:H4'	1:2A:2308:G:O4'	2.17	0.44
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.46	0.44
6:2G:58:GLN:O	6:2G:62:LEU:HD23	2.17	0.44
21:2Z:111:VAL:C	21:2Z:113:ALA:H	2.25	0.44
32:2a:1024:G:H2'	32:2a:1024:G:N3	2.33	0.44
32:2a:1249:C:O2'	40:2i:68:GLY:O	2.33	0.44
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	1.99	0.44
32:2a:1306:A:H1'	32:2a:1332:A:C2	2.53	0.44
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.47	0.44
37:2f:35:ALA:HB2	37:2f:67:MET:SD	2.58	0.44
55:2y:66:U:H2'	55:2y:67:C:O4'	2.18	0.44
1:1A:336:C:O2'	20:1Y:35:TYR:OH	2.26	0.44
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.66	0.44
1:1A:533:G:H5'	16:1U:24:TYR:CE1	2.52	0.44
1:1A:1088:A:H4'	1:1A:1089:G:H8	1.79	0.44
1:1A:2130:U:H1'	1:1A:2159:G:N2	2.33	0.44
1:1A:2630:G:O2'	1:1A:2631:G:H5'	2.18	0.44
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.16	0.44
6:1G:33:ARG:O	6:1G:162:THR:HG23	2.18	0.44
8:1I:135:GLU:C	8:1I:137:PRO:HD3	2.43	0.44
18:1W:56:ALA:O	18:1W:60:ASN:HB2	2.18	0.44
26:14:50:VAL:HG11	44:1m:64:TRP:C	2.43	0.44
27:15:21:SER:HB3	27:15:22:HIS:CD2	2.53	0.44
32:1a:175:C:H2'	32:1a:176:C:H6	1.83	0.44
32:1a:196:A:N3	32:1a:222:U:H1'	2.33	0.44
34:1c:77:ILE:H	34:1c:77:ILE:HG13	1.50	0.44
34:1c:135:LYS:NZ	36:1e:50:GLU:HG2	2.32	0.44
35:1d:127:THR:HG23	35:1d:147:ALA:HB3	1.99	0.44
36:1e:5:ASP:OD1	36:1e:5:ASP:N	2.51	0.44
40:1i:28:VAL:HG22	40:1i:63:ILE:HD12	2.00	0.44
44:1m:65:LYS:HD2	44:1m:69:GLU:CD	2.42	0.44
1:2A:55:G:H2'	1:2A:56:A:H8	1.83	0.44
1:2A:324:A:H2'	1:2A:325:G:O4'	2.18	0.44
1:2A:1840:G:N7	60:2A:3851:HOH:O	2.36	0.44
1:2A:2141:G:H2'	1:2A:2142:C:O4'	2.17	0.44
6:2G:120:LEU:HB2	6:2G:180:PHE:CD1	2.53	0.44
10:2O:78:ARG:HG2	15:2T:73:GLU:HB2	2.00	0.44
13:2R:59:ASP:OD1	13:2R:59:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:753:A:OP1	46:2o:69:TYR:OH	2.35	0.44
34:2c:72:LYS:NZ	34:2c:74:GLY:H	2.16	0.44
38:2g:89:MET:HE2	38:2g:89:MET:HB3	1.85	0.44
40:2i:17:VAL:HG12	40:2i:63:ILE:HG23	1.99	0.44
41:2j:20:ALA:HA	41:2j:23:ILE:HB	2.00	0.44
46:2o:24:SER:O	46:2o:28:GLN:HG3	2.18	0.44
1:1A:817:C:H2'	1:1A:818:G:O4'	2.17	0.43
1:1A:1053:C:C2	1:1A:1107:G:C2	3.06	0.43
1:1A:1068:G:H2'	1:1A:1096:A:O2'	2.18	0.43
1:1A:1557:C:H5"	1:1A:1558:A:OP2	2.18	0.43
1:1A:1664:A:OP1	60:1A:3869:HOH:O	2.21	0.43
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.33	0.43
1:1A:2365:G:O6	30:18:39:LYS:HE3	2.18	0.43
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.53	0.43
1:1A:2801(A):A:H5"	1:1A:2802:G:C8	2.53	0.43
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.36	0.43
24:12:2:LYS:O	24:12:6:VAL:HG23	2.18	0.43
26:14:16:CYS:HB3	26:14:20:ASN:HB3	2.00	0.43
32:1a:438:G:O2'	32:1a:494:U:O4	2.24	0.43
32:1a:790:A:OP1	55:1x:38:A:O2'	2.33	0.43
32:1a:909:A:H2'	32:1a:910:C:O4'	2.18	0.43
32:1a:1073:U:H2'	32:1a:1074:G:C8	2.51	0.43
32:1a:1316:G:H4'	45:1n:18:VAL:CG1	2.48	0.43
34:1c:26:LYS:HA	45:1n:36:PHE:HE1	1.83	0.43
35:1d:166:LYS:HA	35:1d:178:VAL:HG21	2.00	0.43
36:1e:82:VAL:HG21	36:1e:138:ALA:HA	1.99	0.43
37:1f:30:LEU:O	37:1f:35:ALA:HB3	2.18	0.43
45:1n:6:LEU:HA	45:1n:6:LEU:HD23	1.63	0.43
1:2A:197:A:N6	1:2A:2430:A:O2'	2.46	0.43
1:2A:1167:U:H2'	1:2A:1168:G:C8	2.53	0.43
1:2A:1607:C:N4	60:2A:3939:HOH:O	2.51	0.43
1:2A:1720:U:H2'	1:2A:1721:G:O4'	2.17	0.43
1:2A:1721:G:H8	1:2A:1741:A:H62	1.66	0.43
1:2A:2030:A:H4'	1:2A:2031:A:H8	1.82	0.43
1:2A:2271:G:OP1	22:20:18:ALA:HB1	2.18	0.43
1:2A:2615:U:C2	27:25:7:PRO:HA	2.53	0.43
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.53	0.43
4:2E:2:LYS:H	4:2E:2:LYS:HG2	1.65	0.43
6:2G:111:LEU:HB3	6:2G:117:PHE:CE2	2.53	0.43
15:2T:127:ALA:C	15:2T:129:ARG:H	2.24	0.43
31:29:11:CYS:HB3	31:29:32:HIS:HE1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:949:A:N7	44:2m:106:ASN:ND2	2.66	0.43
32:2a:1029:C:N4	32:2a:1032:G:H1	2.14	0.43
32:2a:1074:G:H4'	33:2b:104:ASN:HB2	2.00	0.43
33:2b:51:LEU:O	33:2b:55:PHE:HB2	2.17	0.43
33:2b:71:VAL:HB	33:2b:164:VAL:HG13	2.00	0.43
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	2.01	0.43
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.53	0.43
40:2i:31:GLN:HE21	40:2i:35:GLU:HB3	1.83	0.43
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.16	0.43
1:1A:411:G:C5	11:1P:72:PRO:HB3	2.53	0.43
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.53	0.43
1:1A:1815:A:N1	60:1A:3951:HOH:O	2.36	0.43
10:1O:66:LYS:HD2	10:1O:81:ASP:HA	1.99	0.43
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	1.99	0.43
21:1Z:29:TYR:OH	21:1Z:87:ASP:OD2	2.17	0.43
31:19:4:ARG:NH1	60:19:201:HOH:O	2.50	0.43
32:1a:343:U:H1'	32:1a:346:G:H1	1.84	0.43
32:1a:1129:C:H42	32:1a:1143:G:H1	1.65	0.43
32:1a:1133:G:C6	32:1a:1142:G:C6	3.05	0.43
33:1b:96:ARG:HG2	33:1b:98:LEU:HD23	2.00	0.43
34:1c:18:TRP:C	34:1c:20:SER:H	2.25	0.43
35:1d:63:LYS:HE3	35:1d:198:VAL:HG22	2.00	0.43
35:1d:173:TRP:CZ3	35:1d:193:ASP:HB3	2.53	0.43
44:1m:82:MET:HA	44:1m:89:GLY:HA3	1.99	0.43
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.19	0.43
1:2A:2109:U:H3	1:2A:2180:U:H3	1.63	0.43
1:2A:2114:A:C4	1:2A:2168:G:H1'	2.54	0.43
1:2A:2133:G:HO2'	1:2A:2157:G:H22	1.64	0.43
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.54	0.43
1:2A:2343:C:O2'	1:2A:2373:G:O2'	2.33	0.43
1:2A:2392:A:OP2	30:28:31:HIS:NE2	2.36	0.43
5:2F:137:LYS:HE2	5:2F:137:LYS:HB3	1.77	0.43
6:2G:18:GLU:O	6:2G:22:ARG:N	2.51	0.43
6:2G:102:PHE:HD2	6:2G:103:LEU:HD23	1.83	0.43
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	2.00	0.43
19:2X:5:TYR:CE2	24:22:30:ARG:HB2	2.53	0.43
28:26:39:TYR:HA	28:26:46:HIS:HA	2.00	0.43
32:2a:399:G:H2'	32:2a:400:C:C6	2.53	0.43
32:2a:833:U:H2'	32:2a:834:C:C6	2.53	0.43
32:2a:1202:G:C4	45:2n:42:ILE:HD12	2.53	0.43
32:2a:1530:G:H2'	32:2a:1531:A:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:78:GLN:O	33:2b:81:VAL:HG22	2.18	0.43
35:2d:135:LEU:C	35:2d:137:SER:H	2.25	0.43
36:2e:93:PRO:HG2	39:2h:105:ARG:CZ	2.48	0.43
36:2e:103:GLY:O	36:2e:107:ARG:HB3	2.18	0.43
36:2e:110:LEU:HB3	36:2e:115:VAL:HB	2.00	0.43
38:2g:101:LEU:O	38:2g:105:VAL:HG22	2.18	0.43
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.32	0.43
50:2s:27:GLU:CG	50:2s:28:LYS:HG2	2.47	0.43
54:2w:111:ILE:HD11	54:2w:131:TYR:HD2	1.81	0.43
1:1A:468:G:N7	29:17:39:ARG:NH2	2.59	0.43
1:1A:844:C:C2'	1:1A:845:G:H5'	2.48	0.43
1:1A:1028:A:H61	1:1A:1125:G:H2'	1.83	0.43
1:1A:1091:G:H2'	1:1A:1092:C:C6	2.53	0.43
1:1A:1537:G:H2'	1:1A:1538:G:C8	2.53	0.43
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.33	0.43
1:1A:2336:A:H61	22:10:43:THR:CG2	2.32	0.43
4:1E:126:PRO:O	4:1E:135:HIS:ND1	2.46	0.43
24:12:32:LEU:O	24:12:36:ARG:HG3	2.19	0.43
26:14:44:THR:O	26:14:47:GLN:HB2	2.18	0.43
32:1a:1319:A:OP1	50:1s:3:ARG:HB2	2.19	0.43
37:1f:45:LEU:HD12	37:1f:59:TYR:CD1	2.53	0.43
44:1m:95:GLY:O	44:1m:110:ARG:HG2	2.17	0.43
51:1t:76:ALA:O	51:1t:80:ARG:HG2	2.18	0.43
54:1w:301:LYS:H	54:1w:301:LYS:HG3	1.56	0.43
1:2A:291:C:H42	1:2A:349:G:H1	1.65	0.43
1:2A:468:G:H5"	5:2F:60:SER:HB2	2.00	0.43
1:2A:1363:C:OP1	23:21:61:ARG:NH2	2.52	0.43
1:2A:1411:C:H2'	1:2A:1412:A:C8	2.54	0.43
1:2A:2311:A:H5'	6:2G:80:PHE:HE2	1.83	0.43
1:2A:2705:A:O2'	1:2A:2852:G:OP1	2.23	0.43
6:2G:11:TYR:HA	6:2G:15:VAL:CG1	2.48	0.43
12:2Q:45:GLN:OE1	12:2Q:45:GLN:N	2.46	0.43
23:21:75:GLU:O	23:21:78:LYS:HG2	2.18	0.43
26:24:61:ARG:HH22	50:2s:9:VAL:HG11	1.83	0.43
28:26:6:ARG:HH12	28:26:26:ASN:HB2	1.81	0.43
32:2a:412:A:H4'	32:2a:413:G:H5'	2.00	0.43
32:2a:986:A:N3	50:2s:52:TYR:OH	2.40	0.43
32:2a:1151:A:H5"	41:2j:40:LEU:O	2.17	0.43
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.18	0.43
32:2a:1278:U:H5'	32:2a:1279:A:C5'	2.47	0.43
35:2d:26:CYS:HB3	59:2d:501:SF4:S1	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:58:LEU:O	35:2d:62:GLN:HG2	2.18	0.43
38:2g:69:VAL:HG21	38:2g:104:LEU:HD11	1.99	0.43
1:1A:272(A):U:O2'	1:1A:272(B):G:O5'	2.30	0.43
1:1A:303:U:O4	60:1A:3868:HOH:O	2.21	0.43
1:1A:548:A:H4'	1:1A:549:G:OP2	2.18	0.43
1:1A:948:G:H21	1:1A:985:C:P	2.41	0.43
1:1A:1094:U:H2'	1:1A:1096:A:OP2	2.18	0.43
1:1A:1919:A:N1	32:1a:1495:U:O2'	2.40	0.43
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	2.00	0.43
5:1F:196:LEU:HD23	5:1F:196:LEU:HA	1.90	0.43
6:1G:16:ARG:NH2	6:1G:28:VAL:HG22	2.34	0.43
16:1U:49:HIS:HA	16:1U:52:ARG:HB2	2.00	0.43
20:1Y:44:ILE:HD13	20:1Y:44:ILE:HA	1.84	0.43
26:14:15:ILE:HB	26:14:32:TYR:HD1	1.83	0.43
32:1a:189:G:C2	32:1a:189(L):G:C2	3.06	0.43
32:1a:523:A:H61	43:1l:53:ARG:NH1	2.16	0.43
32:1a:731:G:OP1	32:1a:766:A:H1'	2.17	0.43
32:1a:1118:C:OP1	40:1i:9:ARG:HD2	2.18	0.43
50:1s:40:ILE:HG23	50:1s:44:MET:SD	2.58	0.43
1:2A:184:C:H2'	1:2A:185:U:C6	2.54	0.43
1:2A:627:A:O4'	1:2A:637:A:N6	2.52	0.43
1:2A:898:C:H2'	1:2A:899:A:O4'	2.18	0.43
1:2A:1683:C:H2'	1:2A:1684:C:C6	2.53	0.43
1:2A:2030:A:H4'	1:2A:2031:A:C8	2.53	0.43
1:2A:2384:G:OP2	22:20:55:ARG:NH2	2.29	0.43
23:21:95:LEU:O	23:21:98:LEU:HB2	2.18	0.43
26:24:40:HIS:HB3	26:24:43:TYR:CD2	2.52	0.43
26:24:62:ARG:HD3	26:24:62:ARG:HA	1.73	0.43
32:2a:401:C:H1'	32:2a:622:A:H1'	2.00	0.43
32:2a:940:C:H2'	32:2a:941:G:C8	2.53	0.43
32:2a:942:G:H21	40:2i:124:GLN:HE22	1.66	0.43
32:2a:1497:G:H1'	32:2a:1518:MA6:H2	2.00	0.43
33:2b:132:LYS:O	33:2b:136:VAL:N	2.42	0.43
37:2f:69:GLU:H	37:2f:69:GLU:HG3	1.37	0.43
38:2g:75:VAL:HG13	38:2g:145:ALA:HA	2.00	0.43
40:2i:116:LYS:HB3	40:2i:121:ARG:O	2.19	0.43
46:2o:21:ASP:OD2	46:2o:24:SER:HB2	2.19	0.43
1:1A:784:A:C8	1:1A:792:G:C5	3.06	0.43
1:1A:876:C:H2'	1:1A:877:U:O4'	2.17	0.43
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.53	0.43
2:1B:89:G:H2'	2:1B:90:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:116:ASP:O	5:1F:120:GLU:HG2	2.18	0.43
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.53	0.43
11:1P:121:LYS:O	11:1P:123:LEU:N	2.52	0.43
33:1b:97:TRP:CH2	33:1b:101:MET:HB2	2.53	0.43
44:1m:71:ARG:HA	44:1m:74:VAL:HG22	2.00	0.43
46:1o:61:GLY:O	46:1o:65:ARG:HG3	2.18	0.43
1:2A:30:G:C5	1:2A:31:C:C4	3.07	0.43
1:2A:411:G:OP2	1:2A:2406:U:O2'	2.21	0.43
1:2A:854:G:H2'	1:2A:855:G:H8	1.83	0.43
1:2A:884:C:H3'	1:2A:885:C:C6	2.54	0.43
1:2A:904:C:H2'	1:2A:905:U:C6	2.53	0.43
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.32	0.43
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.53	0.43
1:2A:2203:U:O4'	3:2D:151:LYS:HE2	2.18	0.43
6:2G:113:ARG:HD3	6:2G:140:ILE:HA	1.99	0.43
7:2H:150:ALA:HA	7:2H:153:LYS:HG2	2.00	0.43
10:2O:104:ARG:HH12	15:2T:43:GLN:HE22	1.65	0.43
13:2R:92:GLY:HA2	13:2R:94:TYR:CZ	2.53	0.43
21:2Z:40:ASP:OD2	21:2Z:42:VAL:HG12	2.18	0.43
24:22:62:THR:O	24:22:66:GLU:HG3	2.18	0.43
26:24:58:ARG:O	50:2s:64:GLU:HB2	2.19	0.43
32:2a:591:U:H2'	32:2a:592:G:C8	2.53	0.43
32:2a:1237:C:H3'	32:2a:1336:C:H41	1.84	0.43
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	2.00	0.43
40:2i:20:ARG:O	40:2i:60:ASP:HB2	2.18	0.43
47:2p:34:GLU:OE2	47:2p:55:ARG:HD3	2.19	0.43
1:1A:478:A:C6	1:1A:480:A:C6	3.06	0.43
1:1A:857:C:N4	1:1A:858:U:O4	2.51	0.43
6:1G:138:GLN:HE22	6:1G:153:ARG:CZ	2.31	0.43
18:1W:20:VAL:HG11	18:1W:44:ALA:HA	2.00	0.43
21:1Z:111:VAL:O	21:1Z:112:ARG:HB2	2.18	0.43
32:1a:321:A:N7	32:1a:328:C:O2'	2.45	0.43
32:1a:391:G:P	47:1p:28:ARG:HH22	2.39	0.43
32:1a:1141:C:H2'	32:1a:1142:G:C8	2.53	0.43
33:1b:50:GLU:HB3	33:1b:200:ILE:O	2.18	0.43
33:1b:122:PHE:HE1	33:1b:139:LYS:HD2	1.82	0.43
33:1b:224:GLN:H	33:1b:224:GLN:HG2	1.52	0.43
34:1c:5:ILE:HG12	34:1c:6:HIS:N	2.33	0.43
35:1d:3:ARG:HG2	35:1d:118:ARG:NH2	2.33	0.43
47:1p:49:LEU:HD23	47:1p:50:LYS:N	2.34	0.43
51:1t:8:ARG:HD3	51:1t:8:ARG:HA	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:59:ALA:O	51:1t:63:ILE:HG13	2.18	0.43
1:2A:383:U:H2'	1:2A:385:C:H5	1.82	0.43
1:2A:510:C:H2'	1:2A:511:U:O4'	2.18	0.43
1:2A:731:C:OP1	60:2A:3775:HOH:O	2.22	0.43
1:2A:2674:G:O2'	10:2O:29:ASN:OD1	2.24	0.43
6:2G:68:PRO:HA	6:2G:92:VAL:HB	1.99	0.43
12:2Q:62:GLY:O	21:2Z:178:GLU:HG2	2.18	0.43
14:2S:57:LYS:HE2	14:2S:57:LYS:HB2	1.71	0.43
21:2Z:19:ARG:HH12	21:2Z:84:GLU:HB2	1.83	0.43
32:2a:693:G:H2'	32:2a:694:A:C8	2.53	0.43
32:2a:826:C:H4'	39:2h:12:ARG:HD3	1.99	0.43
32:2a:1065:U:H1'	32:2a:1066:C:OP2	2.18	0.43
32:2a:1268:A:H2'	32:2a:1269:A:C8	2.53	0.43
32:2a:1316:G:N2	32:2a:1319:A:H5"	2.18	0.43
32:2a:1469:G:H2'	32:2a:1470:G:C8	2.54	0.43
32:2a:1490:C:C2'	32:2a:1491:G:H5'	2.48	0.43
33:2b:80:ILE:HD11	33:2b:211:ILE:HG22	2.01	0.43
35:2d:23:GLY:HA3	35:2d:112:VAL:HG12	2.01	0.43
39:2h:51:VAL:HG11	39:2h:60:ARG:NH1	2.31	0.43
44:2m:67:GLU:O	44:2m:71:ARG:HG3	2.18	0.43
45:2n:9:LYS:HA	45:2n:12:ARG:HB2	2.00	0.43
45:2n:53:LEU:HD23	45:2n:53:LEU:HA	1.90	0.43
46:2o:85:LEU:HB2	46:2o:87:ILE:HG13	2.01	0.43
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	2.00	0.43
1:1A:2189:U:H2'	1:1A:2190:G:H8	1.81	0.43
1:1A:2256:G:H2'	1:1A:2257:U:O4'	2.19	0.43
1:1A:2322:A:H2'	1:1A:2323:G:O4'	2.18	0.43
1:1A:2685:G:H5'	10:1O:68:GLU:OE2	2.19	0.43
5:1F:11:VAL:HB	5:1F:18:ARG:HB3	2.00	0.43
32:1a:701:C:O2	32:1a:703:G:N1	2.51	0.43
32:1a:838:G:H2'	32:1a:839:U:H5"	2.01	0.43
33:1b:10:LEU:C	33:1b:12:GLU:N	2.72	0.43
33:1b:34:ALA:O	33:1b:41:ILE:HG13	2.19	0.43
34:1c:150:LYS:HG3	34:1c:169:ALA:HB2	2.00	0.43
35:1d:25:ARG:NH1	35:1d:30:LYS:O	2.52	0.43
35:1d:30:LYS:HA	35:1d:35:ARG:HH21	1.83	0.43
35:1d:112:VAL:H	35:1d:116:GLN:NE2	2.16	0.43
51:1t:80:ARG:HG2	51:1t:80:ARG:H	1.56	0.43
1:2A:12:U:O2	1:2A:12:U:H2'	2.19	0.43
1:2A:27:G:O2'	1:2A:28:A:OP2	2.34	0.43
1:2A:997:G:OP2	16:2U:58:ARG:NH1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.53	0.43
1:2A:1923:U:H2'	1:2A:1924:C:C6	2.54	0.43
1:2A:2451:A:C2	54:2w:230:MEQ:HE1	2.54	0.43
1:2A:2615:U:OP1	60:2A:3769:HOH:O	2.21	0.43
20:2Y:43:ASN:HB3	20:2Y:65:ALA:HB3	2.00	0.43
21:2Z:15:PRO:O	21:2Z:19:ARG:HG3	2.19	0.43
32:2a:302:G:O2'	32:2a:556:C:H5"	2.19	0.43
32:2a:328:C:H4'	32:2a:329:A:H5'	2.00	0.43
32:2a:618:C:N4	32:2a:621:A:N7	2.66	0.43
32:2a:910:C:H2'	32:2a:911:U:O4'	2.18	0.43
32:2a:985:C:H2'	32:2a:986:A:H8	1.84	0.43
55:2y:38:A:H2'	55:2y:39:PSU:O4'	2.19	0.43
1:1A:285:C:H2'	1:1A:286:C:C6	2.54	0.43
1:1A:918:A:H5"	2:1B:98:G:O2'	2.18	0.43
1:1A:1851:U:H2'	1:1A:1852:C:O4'	2.19	0.43
1:1A:1865:G:OP1	60:1A:3861:HOH:O	2.20	0.43
6:1G:7:LEU:HD11	6:1G:107:LEU:HD12	2.01	0.43
9:1N:102:ALA:O	9:1N:106:MET:HG3	2.19	0.43
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.51	0.43
21:1Z:99:TYR:CE2	21:1Z:125:LEU:HD13	2.54	0.43
25:13:51:ALA:HA	25:13:54:VAL:HG12	1.99	0.43
32:1a:486:U:H2'	32:1a:487:A:C8	2.54	0.43
32:1a:769:G:H4'	32:1a:1513:A:H4'	2.00	0.43
32:1a:1237:C:O2'	32:1a:1300:G:N2	2.41	0.43
32:1a:1437:C:H2'	32:1a:1438:G:C8	2.54	0.43
34:1c:22:TRP:CE2	45:1n:54:PRO:HG2	2.54	0.43
39:1h:7:ALA:O	39:1h:11:THR:OG1	2.34	0.43
1:2A:530:G:C5	1:2A:2022:U:H5"	2.53	0.43
1:2A:664:C:H2'	1:2A:665:C:H6	1.84	0.43
1:2A:719:C:H2'	1:2A:720:C:C6	2.53	0.43
1:2A:782:A:N7	3:2D:221:VAL:HG21	2.33	0.43
1:2A:1848:A:H2'	1:2A:1849:G:O4'	2.18	0.43
1:2A:2712:U:OP1	1:2A:2714:G:H4'	2.19	0.43
7:2H:41:MET:HE3	7:2H:64:LEU:HB2	2.00	0.43
32:2a:323:U:H2'	32:2a:324:G:O4'	2.18	0.43
32:2a:761:G:C6	32:2a:762:C:C4	3.07	0.43
32:2a:1003:G:N3	32:2a:1003:G:H2'	2.33	0.43
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.34	0.43
34:2c:134:ILE:HD11	34:2c:153:VAL:HB	2.01	0.43
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.19	0.43
35:2d:155:LEU:O	35:2d:159:ARG:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:138:MET:HE3	54:2w:140:PHE:CD2	2.54	0.43
1:1A:492:A:H2'	1:1A:493:G:O4'	2.19	0.43
1:1A:554:U:O2'	1:1A:555:U:H5'	2.19	0.43
1:1A:657:U:H2'	1:1A:658:C:C6	2.53	0.43
1:1A:684:G:OP1	29:17:16:HIS:ND1	2.47	0.43
1:1A:1174:A:H1'	1:1A:1175:U:O5'	2.19	0.43
1:1A:2732:G:H3'	1:1A:2733:A:O4'	2.18	0.43
2:1B:43:C:O2'	6:1G:95:ARG:HD2	2.18	0.43
4:1E:36:ARG:NH2	4:1E:88:GLY:O	2.48	0.43
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.84	0.43
21:1Z:6:LYS:HD3	21:1Z:8:TYR:OH	2.19	0.43
33:1b:73:THR:HG23	33:1b:94:ASN:O	2.17	0.43
36:1e:57:LYS:HD3	36:1e:61:TYR:HE2	1.84	0.43
37:1f:79:LEU:HD12	37:1f:88:VAL:HG11	2.01	0.43
42:1k:109:VAL:HG13	49:1r:86:VAL:HG22	2.01	0.43
42:1k:124:LYS:C	42:1k:125:PHE:HD2	2.26	0.43
46:1o:43:LEU:HD12	46:1o:56:LEU:HD13	2.01	0.43
51:1t:58:LYS:NZ	51:1t:62:LEU:HD11	2.34	0.43
1:2A:412:A:OP2	1:2A:412:A:H8	2.02	0.43
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.65	0.43
1:2A:652:C:C2'	1:2A:652(A):A:H5'	2.49	0.43
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.19	0.43
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.17	0.43
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.54	0.43
3:2D:132:PRO:HG3	3:2D:190:TYR:CE2	2.54	0.43
3:2D:159:ALA:HB1	3:2D:198:ASN:HB3	2.01	0.43
5:2F:114:VAL:HG21	5:2F:202:PHE:CZ	2.54	0.43
7:2H:40:GLU:CD	7:2H:60:ARG:HH12	2.25	0.43
7:2H:107:VAL:HG23	7:2H:109:PHE:CD2	2.54	0.43
32:2a:106:C:N4	60:2a:1846:HOH:O	2.51	0.43
32:2a:153:C:H2'	32:2a:154:C:H6	1.84	0.43
32:2a:736:C:OP1	49:2r:68:LYS:HD2	2.19	0.43
32:2a:1096:C:O2'	32:2a:1170:A:O2'	2.33	0.43
32:2a:1123:A:H4'	41:2j:36:GLY:CA	2.49	0.43
33:2b:97:TRP:HZ3	33:2b:172:ILE:HG22	1.83	0.43
48:2q:27:PHE:CZ	48:2q:36:ILE:HD11	2.54	0.43
55:2x:65:G:H2'	55:2x:66:U:H6	1.83	0.43
1:1A:1071:G:N3	1:1A:1089:G:O2'	2.39	0.43
1:1A:1153:C:H2'	1:1A:1154:G:O4'	2.19	0.43
1:1A:1857:G:C6	1:1A:1858:G:C6	3.06	0.43
1:1A:2029:G:H2'	1:1A:2031:A:OP1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:81:GLN:NE2	11:1P:106:LEU:HA	2.33	0.43
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	2.00	0.43
24:12:1:MET:HG3	24:12:52:ASP:OD1	2.19	0.43
30:18:61:LEU:C	30:18:63:PRO:HD3	2.43	0.43
32:1a:157:G:H2'	32:1a:157:G:N3	2.32	0.43
32:1a:259:G:H2'	32:1a:260:G:C8	2.54	0.43
32:1a:271:C:H2'	32:1a:272:C:H6	1.82	0.43
32:1a:346:G:H3'	32:1a:346:G:N3	2.34	0.43
32:1a:559:A:H4'	32:1a:560:U:H5"	2.01	0.43
32:1a:708:C:H2'	32:1a:709:G:H8	1.84	0.43
32:1a:1330:U:O4	32:1a:1331:G:N1	2.52	0.43
32:1a:1464:G:H2'	32:1a:1465:C:C6	2.54	0.43
34:1c:111:LEU:HD11	34:1c:144:SER:O	2.18	0.43
55:1y:38:A:H2'	55:1y:39:PSU:O4'	2.18	0.43
55:1y:59:U:H5'	55:1y:60:U:OP2	2.19	0.43
1:2A:271(L):U:H4'	8:2I:50:ARG:NH2	2.34	0.43
1:2A:820:A:H1'	1:2A:943:U:H1'	2.01	0.43
1:2A:1746:G:C2	1:2A:1747:G:C8	3.07	0.43
1:2A:2014:A:H4'	18:2W:92:ARG:HH21	1.84	0.43
1:2A:2116:G:O2'	1:2A:2117:A:O4'	2.28	0.43
1:2A:2134:A:H2'	1:2A:2134:A:N3	2.34	0.43
1:2A:2555:U:O2	54:2w:223:ARG:HB2	2.18	0.43
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.54	0.43
1:2A:2723:C:OP2	4:2E:109:LYS:NZ	2.52	0.43
2:2B:75:G:O2'	21:2Z:85:HIS:NE2	2.24	0.43
4:2E:48:GLN:NE2	4:2E:78:LEU:HD23	2.34	0.43
21:2Z:154:ASP:OD1	21:2Z:154:ASP:N	2.33	0.43
32:2a:429:U:O2'	35:2d:22:LYS:NZ	2.46	0.43
32:2a:528:C:N4	43:2l:49:ASN:OD1	2.52	0.43
32:2a:674:G:H2'	32:2a:675:A:C8	2.50	0.43
32:2a:860:A:OP2	60:2a:1813:HOH:O	2.20	0.43
32:2a:1009:G:H1	32:2a:1020:U:H3	1.65	0.43
32:2a:1033:G:H2'	32:2a:1034:G:H8	1.84	0.43
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.19	0.43
33:2b:158:LEU:HD23	33:2b:182:ILE:HD11	2.01	0.43
34:2c:34:LEU:HD11	34:2c:38:ARG:HE	1.83	0.43
50:2s:51:VAL:O	50:2s:57:HIS:HA	2.19	0.43
51:2t:30:LYS:HA	51:2t:33:ILE:HD12	2.00	0.43
51:2t:50:GLU:N	51:2t:99:LEU:HD12	2.33	0.43
1:1A:247:G:H4'	1:1A:386:G:C5	2.54	0.42
1:1A:768:G:C6	1:1A:769:G:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1363:C:OP1	23:11:61:ARG:NH2	2.52	0.42
1:1A:1584:C:H6	1:1A:1584:C:H2'	1.65	0.42
1:1A:2514:U:H2'	1:1A:2515:C:C6	2.54	0.42
6:1G:155:MET:HE2	6:1G:155:MET:HB3	1.96	0.42
13:1R:22:ARG:O	13:1R:26:LYS:HG3	2.19	0.42
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	2.00	0.42
14:1S:10:ARG:HG2	14:1S:91:PRO:HA	2.01	0.42
14:1S:39:ILE:HB	14:1S:49:VAL:HG12	2.00	0.42
21:1Z:98:MET:O	21:1Z:125:LEU:HD12	2.19	0.42
25:13:13:ILE:O	60:13:201:HOH:O	2.22	0.42
32:1a:56:U:H2'	32:1a:57:G:C8	2.54	0.42
32:1a:191:G:H2'	32:1a:192:U:C6	2.53	0.42
32:1a:1037:C:H2'	32:1a:1038:C:C5	2.54	0.42
32:1a:1149:C:H2'	32:1a:1150:U:O4'	2.18	0.42
32:1a:1187:G:H2'	32:1a:1188:A:H8	1.83	0.42
32:1a:1382:C:H2'	32:1a:1383:C:H6	1.85	0.42
32:1a:1382:C:H2'	32:1a:1383:C:C6	2.53	0.42
33:1b:100:GLY:HA2	33:1b:103:THR:OG1	2.18	0.42
37:1f:1:MET:HE2	37:1f:68:PRO:HG3	2.01	0.42
37:1f:3:ARG:HG2	37:1f:64:GLN:HE21	1.84	0.42
44:1m:36:LYS:HE3	44:1m:36:LYS:HB3	1.84	0.42
44:1m:78:ILE:HG22	44:1m:82:MET:HE2	2.00	0.42
51:1t:66:ALA:HB1	51:1t:71:THR:HB	1.99	0.42
54:1w:212:LEU:HD21	54:1w:270:ARG:HA	2.01	0.42
55:1y:23:A:C6	55:1y:24:G:C6	3.07	0.42
1:2A:1394:U:H2'	1:2A:1395:A:O4'	2.18	0.42
1:2A:1639:U:H2'	1:2A:1640:C:H5"	1.99	0.42
5:2F:41:LEU:O	5:2F:44:ARG:HG2	2.19	0.42
6:2G:181:ARG:HG2	6:2G:182:LYS:N	2.34	0.42
9:2N:42:TRP:CH2	9:2N:44:PRO:HB3	2.54	0.42
12:2Q:2:LEU:HD13	12:2Q:69:PHE:CD1	2.54	0.42
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.23	0.42
15:2T:15:VAL:HG13	15:2T:79:HIS:CE1	2.54	0.42
26:24:60:GLN:C	26:24:62:ARG:H	2.27	0.42
32:2a:427:U:OP1	35:2d:13:ARG:NH1	2.52	0.42
32:2a:1004:A:H3'	32:2a:1025:U:O4	2.18	0.42
32:2a:1265:G:C6	32:2a:1266:G:C5	3.07	0.42
32:2a:1268:A:N3	32:2a:1326:C:O2'	2.52	0.42
33:2b:12:GLU:HA	33:2b:15:VAL:HG23	2.01	0.42
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.51	0.42
41:2j:91:PRO:HD2	41:2j:94:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:40:CYS:SG	45:2n:42:ILE:HG13	2.59	0.42
49:2r:52:PRO:O	49:2r:56:THR:HG23	2.19	0.42
1:1A:1041:C:N4	1:1A:1114:G:H1	2.07	0.42
1:1A:1067:A:H3'	1:1A:1067:A:N3	2.33	0.42
1:1A:1657:C:H2'	1:1A:1658:C:C6	2.54	0.42
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.19	0.42
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.57	0.42
8:1I:26:ALA:O	8:1I:31:LEU:HB2	2.20	0.42
21:1Z:138:GLU:O	21:1Z:156:LYS:HE3	2.19	0.42
32:1a:160:A:N3	32:1a:343:U:H5'	2.34	0.42
32:1a:784:C:H2'	32:1a:785:G:H8	1.85	0.42
32:1a:1191:A:H2'	32:1a:1192:C:C6	2.54	0.42
32:1a:1305:G:OP2	52:1u:2:GLY:N	2.51	0.42
39:1h:49:GLU:HG2	39:1h:62:TYR:HE2	1.84	0.42
53:1v:16:U:C2	55:1x:37:MIA:H112	2.54	0.42
1:2A:563:G:H21	16:2U:37:GLU:CD	2.27	0.42
1:2A:1026:U:H4'	1:2A:1027:A:OP1	2.18	0.42
1:2A:2556:C:H2'	1:2A:2557:G:O4'	2.19	0.42
3:2D:148:GLU:OE1	3:2D:151:LYS:NZ	2.39	0.42
7:2H:80:SER:OG	7:2H:81:GLU:N	2.52	0.42
8:2I:5:LEU:HD21	8:2I:12:LEU:HB3	2.01	0.42
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.52	0.42
21:2Z:108:PRO:HB3	21:2Z:144:LEU:HB2	2.01	0.42
26:24:44:THR:HB	26:24:47:GLN:CB	2.48	0.42
32:2a:272:C:H2'	32:2a:273:A:C8	2.54	0.42
32:2a:1112:C:N3	34:2c:178:LEU:HD12	2.34	0.42
32:2a:1305:G:C2	32:2a:1331:G:N3	2.87	0.42
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.54	0.42
33:2b:204:ASN:HD21	33:2b:206:ASP:HB2	1.83	0.42
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.19	0.42
40:2i:90:PRO:C	40:2i:92:TYR:H	2.27	0.42
43:2l:6:THR:O	43:2l:10:LEU:HG	2.18	0.42
1:1A:1359:A:N1	1:1A:1372:U:O4	2.52	0.42
1:1A:1517:G:C6	1:1A:1518:U:C4	3.06	0.42
1:1A:2119:A:O2'	1:1A:2120:G:H5'	2.19	0.42
2:1B:66:A:H61	2:1B:109:C:H5'	1.84	0.42
3:1D:8:PRO:HB3	3:1D:14:ARG:HG3	2.00	0.42
32:1a:267:C:OP1	48:1q:67:LYS:HG3	2.20	0.42
32:1a:728:A:H2'	32:1a:729:A:C8	2.55	0.42
32:1a:949:A:C6	32:1a:950:U:C4	3.07	0.42
32:1a:1493:A:C5	54:1w:115:THR:HG23	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:148:ASN:OD1	38:1g:148:ASN:N	2.52	0.42
41:1j:67:THR:O	41:1j:67:THR:OG1	2.35	0.42
46:1o:58:MET:O	46:1o:62:GLN:N	2.44	0.42
54:1w:196:THR:HG21	54:1w:296:GLY:O	2.20	0.42
1:2A:784:A:C8	1:2A:792:G:C5	3.07	0.42
1:2A:875:G:O3'	21:2Z:151:HIS:HE1	2.02	0.42
1:2A:884:C:H3'	1:2A:885:C:H6	1.84	0.42
1:2A:1385:G:H1	1:2A:1402:C:N4	2.18	0.42
1:2A:1466:G:O2'	1:2A:1546:C:O2'	2.27	0.42
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.36	0.42
1:2A:2573:C:N4	54:2w:234:THR:O	2.48	0.42
2:2B:29:A:P	14:2S:32:LEU:HD12	2.60	0.42
5:2F:116:ASP:CG	11:2P:1:MET:HB2	2.44	0.42
20:2Y:67:LEU:HD23	20:2Y:67:LEU:HA	1.89	0.42
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.52	0.42
24:22:1:MET:HE3	24:22:1:MET:HB2	1.79	0.42
28:26:34:LEU:HA	28:26:34:LEU:HD23	1.82	0.42
29:27:47:ARG:NH1	29:27:47:ARG:HB2	2.34	0.42
32:2a:109:A:H2'	32:2a:326:G:N2	2.35	0.42
32:2a:297:G:H4'	32:2a:557:G:H4'	2.00	0.42
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.53	0.42
32:2a:1067:A:H8	32:2a:1067:A:O5'	2.01	0.42
32:2a:1169:A:H2'	32:2a:1170:A:C8	2.55	0.42
32:2a:1360:A:H8	32:2a:1360:A:OP1	2.02	0.42
32:2a:1401:G:H2'	32:2a:1402:4OC:O4'	2.19	0.42
1:1A:118:A:O5'	1:1A:119:A:H5"	2.19	0.42
1:1A:537:C:H2'	1:1A:538:G:C8	2.54	0.42
1:1A:539:G:H2'	1:1A:540:C:C6	2.55	0.42
1:1A:969:U:H2'	1:1A:970:C:C6	2.54	0.42
1:1A:1001:A:H2'	1:1A:1002:G:O4'	2.20	0.42
1:1A:1993:U:H4'	4:1E:128:SER:OG	2.18	0.42
1:1A:2406:U:H2'	1:1A:2406:U:H6	1.68	0.42
4:1E:127:ASP:HA	4:1E:135:HIS:HD1	1.83	0.42
6:1G:43:LEU:HA	6:1G:43:LEU:HD23	1.77	0.42
21:1Z:139:VAL:HG22	21:1Z:155:LEU:HD22	2.01	0.42
32:1a:269:C:H2'	32:1a:270:A:H8	1.84	0.42
32:1a:474:G:H3'	32:1a:475:G:H8	1.84	0.42
32:1a:758:G:H4'	32:1a:880:C:H4'	2.00	0.42
32:1a:1002:G:N1	32:1a:1004:A:H1'	2.34	0.42
32:1a:1025:U:O2	32:1a:1036:G:C6	2.72	0.42
32:1a:1442:G:O2'	32:1a:1442(A):G:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:124:GLY:C	35:1d:126:ILE:H	2.27	0.42
1:2A:634:C:H2'	1:2A:635:C:C6	2.55	0.42
1:2A:753:C:O5'	1:2A:753:C:H6	2.02	0.42
1:2A:921:G:H4'	1:2A:2269:A:C5	2.54	0.42
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.55	0.42
1:2A:2050:C:H1'	4:2E:156:MET:HE2	2.02	0.42
1:2A:2159:G:H2'	1:2A:2160:G:C8	2.53	0.42
5:2F:185:ASP:HA	5:2F:188:ARG:HB3	2.00	0.42
6:2G:109:VAL:C	6:2G:112:PRO:HD2	2.45	0.42
10:2O:25:LEU:HD23	10:2O:25:LEU:HA	1.93	0.42
10:2O:97:ARG:HA	10:2O:117:LEU:HD22	2.01	0.42
11:2P:63:PRO:HB2	30:28:30:ARG:NH2	2.27	0.42
32:2a:474:G:H2'	32:2a:475:G:H8	1.84	0.42
32:2a:502:G:C2	32:2a:503:C:C2	3.07	0.42
32:2a:1250:A:H4'	40:2i:68:GLY:N	2.34	0.42
32:2a:1353:G:OP1	52:2u:10:ARG:NH1	2.52	0.42
33:2b:160:ASP:OD1	33:2b:160:ASP:N	2.52	0.42
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	2.00	0.42
43:2l:42:THR:HA	43:2l:53:ARG:O	2.19	0.42
51:2t:43:LEU:HD12	51:2t:55:ILE:HD12	2.01	0.42
54:2w:235:THR:OG1	60:2w:401:HOH:O	2.20	0.42
1:1A:373:U:H2'	1:1A:374:A:H8	1.84	0.42
1:1A:1090:U:O2	1:1A:1090:U:H2'	2.18	0.42
1:1A:1432:C:H2'	1:1A:1433:U:O4'	2.20	0.42
1:1A:2081:C:H2'	1:1A:2082:A:H8	1.84	0.42
1:1A:2886:G:H2'	1:1A:2887:U:H6	1.84	0.42
5:1F:155:LEU:HD12	5:1F:174:VAL:O	2.20	0.42
21:1Z:110:GLY:N	21:1Z:144:LEU:O	2.49	0.42
32:1a:14:U:O2'	32:1a:16:A:N7	2.49	0.42
32:1a:148:G:H1	32:1a:174:C:H42	1.68	0.42
32:1a:262:A:C6	32:1a:263:A:C6	3.07	0.42
32:1a:748:C:H4'	32:1a:749:C:O5'	2.19	0.42
32:1a:1323:G:H2'	32:1a:1324:A:C8	2.55	0.42
36:1e:28:PHE:CD1	36:1e:51:VAL:HG22	2.55	0.42
37:1f:5:GLU:HA	37:1f:63:TYR:O	2.20	0.42
38:1g:14:PRO:HB3	38:1g:19:GLY:C	2.44	0.42
40:1i:111:ARG:O	40:1i:113:LYS:NZ	2.50	0.42
47:1p:55:ARG:HA	47:1p:55:ARG:HD2	1.91	0.42
54:1w:102:MET:C	54:1w:104:GLU:H	2.27	0.42
54:1w:134:PHE:HB2	54:1w:330:GLY:HA2	2.02	0.42
1:2A:598:G:H2'	1:2A:599:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:601:C:O2'	1:2A:605:C:H5"	2.20	0.42
1:2A:631:A:H1'	11:2P:66:GLY:HA2	2.01	0.42
1:2A:873:G:N2	1:2A:905:U:O2	2.52	0.42
1:2A:936:C:H2'	1:2A:937:U:C6	2.54	0.42
1:2A:1013:C:H2'	1:2A:1014:U:H6	1.85	0.42
1:2A:1837:C:O2'	1:2A:1927:A:N3	2.43	0.42
5:2F:69:HIS:HB3	56:2z:11:PRO:CD	2.49	0.42
6:2G:127:GLY:HA2	6:2G:166:ASP:CG	2.44	0.42
26:24:61:ARG:NH2	50:2s:9:VAL:HG11	2.35	0.42
32:2a:784:C:H2'	32:2a:785:G:C8	2.54	0.42
32:2a:921:U:H2'	32:2a:922:G:O4'	2.20	0.42
32:2a:953:G:H5'	32:2a:965:A:H61	1.84	0.42
40:2i:19:LEU:HG	40:2i:84:ALA:HB1	2.00	0.42
44:2m:102:ARG:NH1	44:2m:105:THR:OG1	2.52	0.42
55:2y:64:A:H2'	55:2y:65:G:C8	2.54	0.42
1:1A:12:U:O2	1:1A:12:U:H2'	2.19	0.42
1:1A:391:G:H1'	1:1A:411:G:O4'	2.20	0.42
1:1A:654:A:H2	1:1A:655:A:C2	2.38	0.42
1:1A:795:C:H2'	1:1A:796:C:C6	2.54	0.42
1:1A:2348:U:O4	1:1A:2382:G:N1	2.53	0.42
1:1A:2506:U:C2	1:1A:2585:U:O4	2.73	0.42
1:1A:2553:G:C2	1:1A:2583:G:H1'	2.55	0.42
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	2.00	0.42
5:1F:178:PRO:C	5:1F:180:GLY:H	2.27	0.42
21:1Z:4:ARG:NH2	21:1Z:58:VAL:HG11	2.35	0.42
32:1a:328:C:H4'	32:1a:329:A:H5'	2.02	0.42
32:1a:335:C:O2	32:1a:1433:A:H2	2.01	0.42
32:1a:479:C:H2'	32:1a:480:U:C6	2.53	0.42
32:1a:1053:G:N7	32:1a:1199:U:H3'	2.35	0.42
32:1a:1307:U:H2'	32:1a:1308:U:H6	1.84	0.42
33:1b:22:LYS:H	33:1b:22:LYS:HG3	1.45	0.42
34:1c:130:VAL:O	34:1c:134:ILE:HD12	2.19	0.42
48:1q:62:SER:OG	48:1q:72:ARG:HG2	2.19	0.42
1:2A:195:A:H61	1:2A:198:C:H3'	1.84	0.42
1:2A:298:G:OP2	20:2Y:87:LYS:HD2	2.20	0.42
1:2A:300:A:H2'	1:2A:334:C:H1'	2.02	0.42
1:2A:719:C:H6	1:2A:719:C:O5'	2.02	0.42
1:2A:754:C:H2'	1:2A:755:C:C6	2.54	0.42
1:2A:947:G:O2'	1:2A:984:A:N1	2.48	0.42
10:2O:10:VAL:HG11	10:2O:16:ALA:HB3	2.00	0.42
32:2a:130:A:H5'	48:2q:63:ARG:HH11	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1417:G:O2'	32:2a:1483:A:N6	2.49	0.42
33:2b:123:ALA:C	33:2b:125:PRO:HD3	2.43	0.42
33:2b:159:PRO:HB2	33:2b:161:ALA:O	2.19	0.42
33:2b:184:VAL:HG22	33:2b:197:VAL:HG13	2.02	0.42
35:2d:8:VAL:HG23	35:2d:11:LEU:HD22	2.00	0.42
43:2l:113:ARG:HH21	43:2l:116:SER:HB2	1.84	0.42
1:1A:106:C:O2'	1:1A:294:A:O2'	2.33	0.42
1:1A:251:A:C5	1:1A:252:G:H1'	2.54	0.42
1:1A:445:C:O2'	1:1A:446:G:H5'	2.20	0.42
1:1A:565:C:H2'	1:1A:566:U:O4'	2.20	0.42
1:1A:784:A:H5'	1:1A:785:G:OP1	2.20	0.42
1:1A:1093:G:N1	1:1A:1098:A:OP2	2.51	0.42
1:1A:2576:G:H5"	1:1A:2577:A:OP1	2.20	0.42
5:1F:32:LEU:HD22	5:1F:112:MET:HE2	2.02	0.42
22:10:43:THR:O	22:10:43:THR:HG23	2.20	0.42
36:1e:60:TYR:O	36:1e:64:ARG:HG3	2.20	0.42
38:1g:126:ASP:HB3	38:1g:131:LYS:HB3	2.02	0.42
44:1m:78:ILE:HA	44:1m:81:LEU:HB2	2.01	0.42
1:2A:373:U:H2'	1:2A:374:A:H8	1.84	0.42
1:2A:606:U:H4'	1:2A:658:C:H4'	2.01	0.42
1:2A:924:C:H2'	1:2A:925:C:C6	2.55	0.42
1:2A:1365:A:P	23:21:41:ARG:HH12	2.42	0.42
1:2A:1935:G:H1'	1:2A:1964:G:N2	2.35	0.42
1:2A:2186:G:C2	1:2A:2187:G:C5	3.07	0.42
26:24:18:CYS:HB3	26:24:39:CYS:SG	2.59	0.42
32:2a:519:C:O5'	54:2w:301:LYS:NZ	2.43	0.42
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.54	0.42
33:2b:115:LEU:HB2	33:2b:145:LEU:HD23	2.00	0.42
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	2.01	0.42
38:2g:69:VAL:HG22	38:2g:135:VAL:HG13	2.01	0.42
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	2.02	0.42
49:2r:22:VAL:CG2	49:2r:56:THR:HA	2.49	0.42
49:2r:36:ASN:O	49:2r:40:LEU:HG	2.20	0.42
55:2y:13:C:H5'	55:2y:14:A:OP2	2.19	0.42
1:1A:7:G:H4'	9:1N:13:TRP:HH2	1.85	0.42
1:1A:265:A:N1	1:1A:427:U:O2'	2.45	0.42
1:1A:593:G:C6	1:1A:594:U:C4	3.08	0.42
1:1A:2149:G:N1	1:1A:2150:U:O2	2.53	0.42
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.55	0.42
26:14:36:CYS:SG	26:14:37:SER:N	2.93	0.42
32:1a:45:U:H2'	32:1a:46:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:148:G:N2	32:1a:175:C:C2	2.88	0.42
32:1a:461:A:C5	32:1a:471:G:C6	3.08	0.42
32:1a:1026:G:H8	32:1a:1027:C:O2	2.02	0.42
32:1a:1142:G:H3'	32:1a:1143:G:H8	1.84	0.42
32:1a:1226:C:H4'	50:1s:80:TYR:OH	2.19	0.42
32:1a:1326:C:H5"	52:1u:12:LYS:HZ3	1.85	0.42
33:1b:19:HIS:O	33:1b:20:GLU:HG2	2.20	0.42
33:1b:29:ALA:O	33:1b:32:ILE:HG22	2.20	0.42
34:1c:156:ARG:NE	34:1c:160:ALA:O	2.48	0.42
35:1d:107:ARG:HH22	35:1d:194:LEU:HD22	1.84	0.42
41:1j:26:ALA:HB1	41:1j:84:GLN:NE2	2.35	0.42
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.54	0.42
1:2A:359:A:H2'	1:2A:360:G:O4'	2.20	0.42
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.33	0.42
1:2A:724:U:H2'	1:2A:725:G:O4'	2.19	0.42
1:2A:784:A:C5	3:2D:229:VAL:HG21	2.54	0.42
1:2A:877:U:H2'	1:2A:878:A:H5"	2.01	0.42
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.54	0.42
1:2A:2528:U:H2'	1:2A:2530:A:O5'	2.19	0.42
4:2E:67:PHE:CE2	4:2E:74:PRO:HA	2.55	0.42
7:2H:95:ARG:HB2	7:2H:128:PRO:HB3	2.00	0.42
23:21:44:PRO:HB2	23:21:46:LEU:HD13	2.01	0.42
32:2a:189(D):C:H1'	32:2a:189(H):G:C2	2.55	0.42
32:2a:358:U:H2'	32:2a:359:U:C6	2.55	0.42
32:2a:448:A:C4	32:2a:487:A:C2	3.07	0.42
33:2b:28:PHE:CD2	33:2b:190:THR:HA	2.55	0.42
34:2c:34:LEU:O	34:2c:38:ARG:HG3	2.19	0.42
40:2i:42:ARG:NH2	40:2i:75:ASP:OD2	2.53	0.42
40:2i:48:GLU:C	40:2i:50:LEU:H	2.27	0.42
45:2n:23:ARG:HB3	45:2n:24:CYS:H	1.70	0.42
1:1A:570:G:H2'	1:1A:2030:A:N7	2.35	0.42
1:1A:935:C:H2'	1:1A:936:C:H6	1.85	0.42
1:1A:2801(A):A:H1'	1:1A:2895:U:C1'	2.49	0.42
5:1F:153:SER:OG	5:1F:190:GLU:HG3	2.19	0.42
6:1G:11:TYR:CZ	6:1G:16:ARG:HD3	2.55	0.42
7:1H:9:ILE:HD11	7:1H:69:ARG:HG2	2.02	0.42
19:1X:44:GLU:HG2	19:1X:49:VAL:O	2.20	0.42
21:1Z:28:MET:HE2	21:1Z:37:VAL:HG11	2.02	0.42
28:16:26:ASN:HB3	28:16:29:ASN:HB2	2.02	0.42
32:1a:509:A:H2'	32:1a:510:A:C8	2.54	0.42
32:1a:1239:A:H62	32:1a:1299:A:N6	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.20	0.42
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.54	0.42
33:1b:80:ILE:HD11	33:1b:215:LEU:HD12	2.02	0.42
40:1i:127:LYS:O	40:1i:128:ARG:HG2	2.20	0.42
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	2.01	0.42
44:1m:9:ILE:H	44:1m:9:ILE:HG12	1.60	0.42
46:1o:82:ILE:O	46:1o:86:GLY:N	2.53	0.42
51:1t:74:LYS:HE2	51:1t:74:LYS:HB3	1.83	0.42
54:1w:172:LYS:HE3	54:1w:173:TYR:CE2	2.55	0.42
4:2E:119:ARG:HG2	4:2E:120:TRP:CE2	2.55	0.42
10:2O:64:ARG:HD3	10:2O:79:PHE:CD1	2.55	0.42
21:2Z:25:PRO:O	21:2Z:85:HIS:HA	2.20	0.42
32:2a:182:U:N3	32:2a:183:G:H1'	2.35	0.42
32:2a:926:G:C6	32:2a:1505:G:C6	3.07	0.42
32:2a:1262:C:H2'	32:2a:1263:C:C5'	2.49	0.42
32:2a:1298:C:H2'	38:2g:114:ARG:NH1	2.29	0.42
32:2a:1298:C:C4	38:2g:114:ARG:HD3	2.55	0.42
32:2a:1346:A:C8	32:2a:1348:U:C2	3.08	0.42
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.20	0.42
37:2f:100:ASN:ND2	49:2r:23:LYS:HE3	2.35	0.42
54:2w:302:ILE:HD12	54:2w:302:ILE:HA	1.89	0.42
1:1A:518:G:H2'	1:1A:519:U:C6	2.55	0.42
1:1A:1166:C:H2'	1:1A:1167:U:C6	2.55	0.42
1:1A:1666:G:OP1	10:1O:66:LYS:HD3	2.19	0.42
1:1A:2396:G:OP1	23:11:25:LYS:NZ	2.39	0.42
1:1A:2420:C:OP1	30:18:34:TRP:HB3	2.19	0.42
1:1A:2677:G:H2'	1:1A:2678:C:C6	2.55	0.42
3:1D:164:GLN:NE2	3:1D:176:ARG:HH21	2.18	0.42
5:1F:53:THR:HG22	5:1F:55:GLY:N	2.20	0.42
6:1G:60:LEU:HD12	6:1G:60:LEU:HA	1.78	0.42
21:1Z:97:GLU:HA	21:1Z:126:VAL:O	2.20	0.42
32:1a:323:U:H5'	51:1t:23:ARG:HB2	2.01	0.42
35:1d:107:ARG:NH1	35:1d:194:LEU:HD13	2.35	0.42
35:1d:120:LEU:HB3	35:1d:126:ILE:HD11	2.02	0.42
38:1g:22:LEU:HD21	38:1g:66:VAL:HG11	2.01	0.42
48:1q:10:VAL:HG22	48:1q:19:VAL:HB	2.01	0.42
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.52	0.42
7:2H:10:PRO:O	7:2H:12:PRO:HD3	2.20	0.42
10:2O:79:PHE:CD1	15:2T:72:VAL:HG22	2.55	0.42
12:2Q:2:LEU:HD22	12:2Q:69:PHE:HE1	1.84	0.42
21:2Z:128:VAL:HG21	21:2Z:161:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:27:47:ARG:HB2	29:27:47:ARG:HH11	1.85	0.42
32:2a:224:C:H2'	32:2a:225:C:C6	2.55	0.42
32:2a:913:A:H4'	32:2a:914:A:O5'	2.20	0.42
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.55	0.42
32:2a:1515:C:H2'	32:2a:1516:G:C8	2.54	0.42
35:2d:20:TYR:HA	35:2d:26:CYS:SG	2.60	0.42
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	2.02	0.42
37:2f:94:GLN:NE2	49:2r:72:ARG:HH12	2.18	0.42
41:2j:63:PHE:CE1	45:2n:58:LYS:HG2	2.49	0.42
46:2o:55:GLY:HA2	46:2o:58:MET:HG3	2.02	0.42
51:2t:56:MET:HE2	51:2t:56:MET:HB3	1.61	0.42
55:2y:55:PSU:N3	55:2y:57:G:H5"	2.34	0.42
1:1A:26:G:C6	1:1A:27:G:N1	2.88	0.41
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.55	0.41
1:1A:592:G:O2'	30:18:4:MET:HG3	2.20	0.41
1:1A:1316:U:H2'	1:1A:1317:A:C8	2.55	0.41
1:1A:2848:G:C8	15:1T:97:ALA:HB2	2.54	0.41
7:1H:26:VAL:HG11	7:1H:76:VAL:HA	2.02	0.41
11:1P:135:LEU:HD23	11:1P:135:LEU:HA	1.76	0.41
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	2.02	0.41
15:1T:39:ARG:NH2	32:1a:346:G:O4'	2.53	0.41
17:1V:49:THR:O	17:1V:49:THR:OG1	2.36	0.41
20:1Y:38:ILE:HD13	20:1Y:66:PRO:HA	2.02	0.41
25:13:31:LEU:HD23	25:13:31:LEU:HA	1.79	0.41
29:17:10:ARG:O	29:17:14:LYS:HG3	2.20	0.41
32:1a:532:A:N3	32:1a:532:A:H2'	2.35	0.41
32:1a:641:U:H1'	32:1a:642:A:N7	2.35	0.41
32:1a:790:A:C6	32:1a:791:G:C6	3.08	0.41
32:1a:922:G:C6	32:1a:923:A:C6	3.07	0.41
32:1a:958:A:C2	50:1s:55:LYS:HB2	2.55	0.41
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.39	0.41
34:1c:58:GLU:O	34:1c:59:ARG:HG3	2.19	0.41
35:1d:3:ARG:HG2	35:1d:118:ARG:CZ	2.50	0.41
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.19	0.41
1:2A:271(P):C:H2'	1:2A:271(Q):G:O4'	2.20	0.41
1:2A:2025:C:H2'	1:2A:2026:C:C6	2.55	0.41
1:2A:2115:G:OP2	1:2A:2115:G:H8	2.03	0.41
1:2A:2141:G:C6	1:2A:2151:G:C2	3.08	0.41
1:2A:2246:G:H2'	1:2A:2247:A:C8	2.54	0.41
1:2A:2640:G:O6	60:2A:3774:HOH:O	2.21	0.41
2:2B:48:A:H2'	2:2B:49:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:77:ALA:HA	3:2D:97:TYR:HA	2.02	0.41
7:2H:126:PRO:HB2	7:2H:127:GLU:H	1.70	0.41
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.50	0.41
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	2.01	0.41
18:2W:36:LEU:HD13	18:2W:48:ALA:HA	2.01	0.41
32:2a:745:C:H2'	32:2a:746:A:H8	1.84	0.41
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.53	0.41
32:2a:1371:G:C6	32:2a:1372:U:C4	3.08	0.41
1:1A:27:G:O2'	1:1A:28:A:OP2	2.34	0.41
1:1A:1047:G:H1'	1:1A:1111:A:N6	2.35	0.41
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.42	0.41
3:1D:106:ILE:O	3:1D:108:PRO:HD3	2.21	0.41
13:1R:20:LEU:HD21	13:1R:40:LYS:HD3	2.01	0.41
32:1a:393:A:OP1	47:1p:13:HIS:HE1	2.03	0.41
32:1a:918:A:H2'	32:1a:919:A:C8	2.55	0.41
32:1a:1239:A:H62	32:1a:1299:A:H61	1.68	0.41
32:1a:1250:A:H4'	40:1i:68:GLY:N	2.35	0.41
32:1a:1425:U:H2'	32:1a:1426:C:H6	1.85	0.41
35:1d:163:GLU:C	35:1d:165:MET:N	2.78	0.41
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	2.01	0.41
38:1g:27:ILE:HD13	38:1g:40:ALA:HA	2.02	0.41
44:1m:16:ASP:OD1	44:1m:16:ASP:N	2.54	0.41
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.53	0.41
55:1y:8:4SU:H4'	55:1y:48:C:H4'	2.00	0.41
1:2A:64:A:O3'	19:2X:71:GLY:HA3	2.20	0.41
1:2A:140:G:N2	1:2A:1596:A:H4'	2.35	0.41
1:2A:380:U:H4'	23:21:16:ASN:O	2.20	0.41
1:2A:886:C:H2'	1:2A:887:A:H4'	2.02	0.41
1:2A:1027:A:N6	1:2A:1126:A:C4	2.88	0.41
1:2A:1031:G:O2'	31:29:7:VAL:HG23	2.20	0.41
1:2A:2443:C:H2'	1:2A:2444:G:H8	1.85	0.41
1:2A:2532:G:O2'	1:2A:2657:A:N1	2.50	0.41
32:2a:545:C:O2'	32:2a:549:C:OP1	2.37	0.41
32:2a:583:A:N6	32:2a:758:G:O2'	2.53	0.41
32:2a:920:U:H2'	32:2a:921:U:C6	2.55	0.41
32:2a:996:A:H2'	32:2a:997:U:O4'	2.20	0.41
32:2a:1212:U:H5"	32:2a:1213:A:C5'	2.50	0.41
32:2a:1317:C:O2	50:2s:37:ARG:NH1	2.53	0.41
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.56	0.41
38:2g:70:LYS:HG2	38:2g:96:GLN:HB3	2.02	0.41
42:2k:80:VAL:HG22	42:2k:103:LEU:HD22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:43:LYS:HA	47:2p:48:TRP:HB3	2.01	0.41
50:2s:27:GLU:HA	50:2s:47:HIS:HE1	1.84	0.41
50:2s:40:ILE:HA	50:2s:44:MET:SD	2.60	0.41
51:2t:67:ALA:HB2	51:2t:77:ALA:HB2	2.02	0.41
4:1E:50:GLY:HA3	4:1E:75:VAL:HG11	2.01	0.41
32:1a:39:G:H2'	32:1a:40:C:C6	2.55	0.41
32:1a:501:C:H2'	32:1a:502:G:H8	1.84	0.41
32:1a:616:G:N2	32:1a:625:G:C4	2.89	0.41
32:1a:908:A:H2'	32:1a:909:A:C8	2.55	0.41
32:1a:923:A:OP1	36:1e:21:ALA:HB2	2.20	0.41
32:1a:1080:A:H5'	36:1e:14:ARG:NH2	2.35	0.41
35:1d:11:LEU:HD23	35:1d:66:ARG:HB3	2.01	0.41
1:2A:26:G:C6	1:2A:27:G:N1	2.88	0.41
1:2A:271(H):G:H1	1:2A:271(P):C:N4	2.16	0.41
1:2A:717:G:H2'	1:2A:718:A:O4'	2.21	0.41
1:2A:797:C:H6	1:2A:797:C:O5'	2.04	0.41
1:2A:1567:A:H3'	3:2D:86:PRO:HG3	2.03	0.41
1:2A:1770:G:O6	60:2A:3773:HOH:O	2.21	0.41
1:2A:1809:A:H2'	1:2A:1810:A:C8	2.55	0.41
1:2A:2712:U:H1'	1:2A:2712(A):A:C8	2.55	0.41
2:2B:22:U:H2'	2:2B:23:G:C8	2.54	0.41
6:2G:16:ARG:HA	6:2G:16:ARG:HD2	1.89	0.41
14:2S:24:LEU:HB2	14:2S:85:VAL:HG23	2.01	0.41
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.49	0.41
21:2Z:111:VAL:C	21:2Z:113:ALA:N	2.78	0.41
21:2Z:131:ARG:HB2	21:2Z:131:ARG:HH11	1.84	0.41
32:2a:49:U:O2	32:2a:362:G:H1'	2.19	0.41
32:2a:397:A:H3'	32:2a:397:A:N3	2.34	0.41
32:2a:737:A:H2'	32:2a:738:C:C6	2.55	0.41
32:2a:927:G:H2'	32:2a:928:G:O4'	2.20	0.41
32:2a:1324:A:C4'	32:2a:1362:C:H4'	2.45	0.41
1:1A:551:G:O2'	1:1A:1220:A:N3	2.46	0.41
1:1A:729:G:C5	3:1D:208:LYS:HB2	2.55	0.41
1:1A:880:G:N2	1:1A:898:C:C2	2.88	0.41
1:1A:1784:A:H4'	1:1A:1785:A:O5'	2.21	0.41
1:1A:2203:U:O4'	3:1D:151:LYS:HE2	2.20	0.41
2:1B:48:A:H2'	2:1B:49:C:C6	2.55	0.41
3:1D:124:PRO:HG2	3:1D:129:ASN:ND2	2.35	0.41
6:1G:105:LYS:HD3	26:14:25:TYR:O	2.19	0.41
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.55	0.41
17:1V:28:GLU:HG2	17:1V:29:PRO:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:40:HIS:HE1	26:14:42:PHE:HB3	1.86	0.41
32:1a:345:C:H4'	32:1a:346:G:H5"	2.02	0.41
32:1a:382:A:H8	32:1a:382:A:O5'	2.03	0.41
32:1a:445:G:H2'	32:1a:446:G:H8	1.84	0.41
32:1a:590:C:H2'	32:1a:591:U:H6	1.85	0.41
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.20	0.41
32:1a:1142:G:H2'	32:1a:1143:G:O4'	2.21	0.41
34:1c:173:VAL:O	34:1c:175:LEU:HD12	2.21	0.41
1:2A:888:C:H2'	1:2A:889:C:C5	2.55	0.41
1:2A:1019:U:H3	1:2A:1142(A):A:N6	2.15	0.41
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.55	0.41
1:2A:2151:G:C2	1:2A:2152:G:C5	3.08	0.41
1:2A:2183:C:H2'	1:2A:2184:G:C8	2.55	0.41
6:2G:171:ALA:O	6:2G:175:LEU:N	2.26	0.41
11:2P:139:LYS:C	11:2P:141:ALA:H	2.28	0.41
20:2Y:75:ILE:HD13	20:2Y:75:ILE:HA	1.80	0.41
32:2a:977:A:H2'	32:2a:978:A:H5"	2.03	0.41
32:2a:1298:C:C5	38:2g:114:ARG:HD3	2.56	0.41
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.21	0.41
34:2c:18:TRP:HD1	45:2n:54:PRO:HA	1.83	0.41
41:2j:24:VAL:C	41:2j:26:ALA:H	2.28	0.41
50:2s:67:VAL:HG23	50:2s:68:GLY:H	1.85	0.41
1:1A:174:C:H2'	1:1A:175:G:O4'	2.20	0.41
1:1A:307:G:N2	1:1A:309:G:H3'	2.35	0.41
1:1A:1301:A:C8	1:1A:1303:G:C8	3.08	0.41
1:1A:1448:G:H1'	1:1A:1528:A:N1	2.36	0.41
1:1A:1903:G:OP1	3:1D:241:PRO:HB2	2.20	0.41
1:1A:2182:G:C6	1:1A:2183:C:C4	3.08	0.41
1:1A:2630:G:HO2'	1:1A:2631:G:H5'	1.86	0.41
1:1A:2690:C:N4	1:1A:2713:A:H1'	2.35	0.41
4:1E:48:GLN:NE2	4:1E:78:LEU:HD13	2.35	0.41
6:1G:16:ARG:NH1	6:1G:31:VAL:HB	2.35	0.41
6:1G:99:MET:HE2	6:1G:99:MET:HB3	1.97	0.41
32:1a:413:G:N2	32:1a:428:G:H1'	2.36	0.41
32:1a:532:A:N6	32:1a:1206:G:O2'	2.53	0.41
32:1a:662:G:H2'	32:1a:663:A:C8	2.56	0.41
32:1a:1129:C:H5"	40:1i:16:ARG:NH1	2.24	0.41
35:1d:10:ARG:HB2	35:1d:40:PRO:HG3	2.02	0.41
36:1e:11:ILE:HG21	36:1e:105:VAL:HG22	2.02	0.41
40:1i:116:LYS:HB3	40:1i:121:ARG:O	2.21	0.41
51:1t:16:HIS:O	51:1t:19:SER:OG	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:299:SER:C	54:1w:301:LYS:N	2.78	0.41
54:1w:317:ILE:HG21	54:1w:339:LEU:HA	2.03	0.41
1:2A:55:G:H2'	1:2A:56:A:C8	2.56	0.41
1:2A:639:U:H2'	1:2A:640:C:C6	2.55	0.41
1:2A:757:U:H2'	1:2A:758:C:O4'	2.20	0.41
1:2A:1494:A:H2	1:2A:1579:A:H1'	1.85	0.41
1:2A:1808:U:H2'	1:2A:1809:A:O4'	2.21	0.41
8:2I:75:LEU:HD21	8:2I:105:HIS:CG	2.56	0.41
11:2P:88:LEU:HA	11:2P:91:PHE:HE2	1.85	0.41
32:2a:277:C:OP1	48:2q:41:LYS:HE3	2.21	0.41
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.21	0.41
32:2a:957:U:O2	32:2a:959:A:H8	2.03	0.41
32:2a:1189:C:O2	60:2a:1812:HOH:O	2.19	0.41
33:2b:185:ILE:CG2	33:2b:199:TYR:HB2	2.49	0.41
35:2d:191:ARG:HE	35:2d:200:GLU:CD	2.29	0.41
36:2e:45:PHE:HD1	36:2e:46:GLY:H	1.69	0.41
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	2.01	0.41
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	2.02	0.41
43:2l:6:THR:HB	43:2l:9:GLN:HG3	2.03	0.41
47:2p:43:LYS:HD3	47:2p:48:TRP:CE2	2.55	0.41
47:2p:72:ARG:HG2	47:2p:73:LEU:HD23	2.02	0.41
1:1A:196:A:N3	1:1A:196:A:H2'	2.36	0.41
1:1A:647:G:N3	1:1A:2350:C:O2'	2.54	0.41
1:1A:686:G:N2	1:1A:788:A:H61	2.18	0.41
1:1A:1607:C:N4	1:1A:1622:G:OP2	2.43	0.41
1:1A:1878:G:H2'	1:1A:1879:C:C6	2.54	0.41
1:1A:2296:U:OP2	14:1S:9:ARG:NH2	2.53	0.41
2:1B:78:A:C2	2:1B:100:A:C4	3.08	0.41
12:1Q:3:MET:HE2	12:1Q:3:MET:HB3	1.97	0.41
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.50	0.41
32:1a:298:A:H3'	32:1a:299:G:C8	2.55	0.41
32:1a:472:A:H4'	47:1p:80:PHE:O	2.20	0.41
32:1a:1329:A:H5'	44:1m:26:GLY:N	2.34	0.41
41:1j:81:THR:C	41:1j:83:GLU:H	2.28	0.41
44:1m:20:THR:HA	44:1m:25:ILE:O	2.20	0.41
54:1w:140:PHE:CD1	54:1w:164:GLY:HA3	2.55	0.41
54:1w:192:ILE:HD12	54:1w:308:PRO:HG2	2.03	0.41
54:1w:213:ASN:O	54:1w:216:GLU:HG2	2.20	0.41
1:2A:492:A:H2'	1:2A:493:G:O4'	2.21	0.41
1:2A:589:C:H42	1:2A:668:G:H1	1.68	0.41
1:2A:664:C:H2'	1:2A:665:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:774:A:H2'	1:2A:774:A:N3	2.36	0.41
1:2A:1224:C:O2'	17:2V:85:LYS:HA	2.21	0.41
1:2A:2061:G:H5"	1:2A:2503:2MA:C2	2.51	0.41
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.56	0.41
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.52	0.41
2:2B:72:G:O2'	2:2B:105:A:N6	2.53	0.41
2:2B:84:C:OP1	25:23:15:TYR:OH	2.23	0.41
25:23:18:ASP:OD1	25:23:19:GLN:N	2.54	0.41
26:24:13:ARG:NH1	26:24:21:VAL:HG11	2.35	0.41
28:26:38:LYS:HB3	28:26:38:LYS:HE3	1.86	0.41
31:29:7:VAL:HG12	31:29:34:GLN:HB3	2.02	0.41
32:2a:567:G:H2'	32:2a:568:G:O4'	2.21	0.41
32:2a:690:G:H2'	32:2a:691:G:O4'	2.19	0.41
32:2a:1096:C:H2'	32:2a:1097:C:H6	1.86	0.41
1:1A:493:G:HO2'	18:1W:8:ARG:H	1.69	0.41
1:1A:881:G:H2'	1:1A:882:G:O4'	2.20	0.41
1:1A:1115:G:H3'	1:1A:1116:C:H5"	2.01	0.41
1:1A:1212:G:N2	1:1A:1236:G:O2'	2.54	0.41
1:1A:2081:C:H2'	1:1A:2082:A:C8	2.55	0.41
5:1F:187:VAL:HG13	11:1P:1:MET:O	2.20	0.41
7:1H:42:ARG:NH2	7:1H:53:GLU:OE1	2.53	0.41
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD12	2.02	0.41
23:11:64:ALA:HA	23:11:67:ILE:HG13	2.02	0.41
32:1a:263:A:OP1	51:1t:79:ARG:NH1	2.53	0.41
32:1a:784:C:H2'	32:1a:785:G:C8	2.56	0.41
32:1a:1237:C:HO2'	32:1a:1300:G:H22	1.65	0.41
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.56	0.41
33:1b:27:LYS:HE2	33:1b:27:LYS:HB2	1.97	0.41
43:1l:38:THR:OG1	43:1l:39:VAL:N	2.54	0.41
51:1t:92:LEU:C	51:1t:94:ALA:H	2.28	0.41
1:2A:35:G:H2'	1:2A:36:G:O4'	2.21	0.41
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.56	0.41
1:2A:440:G:H2'	1:2A:441:U:C6	2.56	0.41
1:2A:1022:G:N7	9:2N:66:LYS:HE2	2.36	0.41
1:2A:1480:G:C6	1:2A:1481:U:N3	2.89	0.41
1:2A:1652:A:C2'	1:2A:1653:G:H5'	2.50	0.41
1:2A:1668:A:H4'	1:2A:1669:A:O5'	2.21	0.41
1:2A:2052:G:H4'	4:2E:143:ASN:O	2.21	0.41
1:2A:2093:G:C6	1:2A:2225:A:C8	3.08	0.41
1:2A:2127:G:N2	1:2A:2161:C:N3	2.63	0.41
1:2A:2164:C:H3'	1:2A:2165:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.21	0.41
1:2A:2395:C:H2'	1:2A:2396:G:O4'	2.21	0.41
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.45	0.41
3:2D:120:GLY:O	3:2D:131:LEU:HG	2.20	0.41
4:2E:112:GLY:O	4:2E:159:HIS:HA	2.21	0.41
8:2I:3:VAL:O	8:2I:18:VAL:HA	2.20	0.41
9:2N:61:ARG:HA	9:2N:61:ARG:HD3	1.72	0.41
16:2U:104:GLN:OE1	16:2U:104:GLN:N	2.50	0.41
21:2Z:92:SER:O	21:2Z:130:PRO:HG2	2.21	0.41
32:2a:583:A:H2'	32:2a:584:G:O4'	2.20	0.41
32:2a:612:C:H2'	32:2a:613:C:C6	2.56	0.41
32:2a:754:C:H1'	46:2o:69:TYR:CD2	2.55	0.41
32:2a:1068:G:OP2	32:2a:1068:G:H8	2.04	0.41
32:2a:1095:U:H5"	32:2a:1109:C:O2	2.20	0.41
32:2a:1213:A:C8	32:2a:1215:G:C5	3.09	0.41
32:2a:1443:G:N2	32:2a:1460:A:H1'	2.35	0.41
34:2c:181:ASN:ND2	34:2c:204:LEU:HD12	2.35	0.41
44:2m:115:LYS:H	44:2m:115:LYS:HG2	1.73	0.41
53:2v:15:A:H8	53:2v:15:A:O5'	2.03	0.41
1:1A:861:A:C2	1:1A:917:A:C4	3.09	0.41
1:1A:1262:A:H1'	60:1A:4227:HOH:O	2.19	0.41
1:1A:1386:C:H2'	1:1A:1387:C:C6	2.56	0.41
1:1A:1712:C:H2'	1:1A:1713:U:O4'	2.20	0.41
1:1A:2109:U:H1'	1:1A:2181:G:N2	2.36	0.41
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.56	0.41
7:1H:83:TYR:CE2	7:1H:138:LYS:HB2	2.56	0.41
17:1V:1:MET:HB2	17:1V:43:GLU:OE1	2.21	0.41
25:13:43:ILE:O	25:13:47:VAL:HG23	2.21	0.41
32:1a:193:C:H2'	32:1a:194:C:C6	2.55	0.41
32:1a:605:U:H2'	32:1a:606:G:C8	2.56	0.41
32:1a:885:G:O2'	32:1a:914:A:N1	2.50	0.41
32:1a:1157:A:H4'	32:1a:1158:C:O4'	2.21	0.41
32:1a:1182:G:H5'	32:1a:1184:G:H5'	2.03	0.41
36:1e:150:ARG:HE	36:1e:150:ARG:HB2	1.56	0.41
54:1w:309:GLN:OE1	54:1w:311:ARG:NH1	2.54	0.41
1:2A:250:G:H2'	1:2A:251:A:C8	2.56	0.41
4:2E:111:ARG:HA	13:2R:1:MET:SD	2.61	0.41
14:2S:11:LYS:O	14:2S:15:ARG:HB2	2.21	0.41
15:2T:2:ASN:O	15:2T:6:LEU:HG	2.21	0.41
15:2T:61:PHE:CE2	15:2T:76:PHE:HB2	2.55	0.41
16:2U:105:VAL:HG22	17:2V:45:THR:CG2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:2W:58:ALA:HB1	18:2W:64:MET:HB2	2.02	0.41
20:2Y:19:LYS:HE2	20:2Y:19:LYS:HB3	1.96	0.41
22:20:72:ARG:O	22:20:75:LEU:N	2.52	0.41
32:2a:130:A:H5'	48:2q:63:ARG:NH1	2.36	0.41
32:2a:137:C:H2'	32:2a:138:G:C8	2.54	0.41
32:2a:376:G:P	47:2p:67:THR:HG21	2.61	0.41
32:2a:526:C:C4	32:2a:527:G7M:H1'	2.56	0.41
32:2a:706:A:N3	42:2k:31:THR:HG21	2.35	0.41
32:2a:934:C:H5	32:2a:1344:C:H2'	1.86	0.41
32:2a:1154:G:H2'	32:2a:1155:G:C8	2.51	0.41
40:2i:23:ASN:HD21	40:2i:25:LYS:HE2	1.86	0.41
41:2j:8:LEU:HD13	41:2j:20:ALA:HB2	2.03	0.41
42:2k:92:GLU:C	42:2k:94:ALA:N	2.78	0.41
42:2k:92:GLU:O	42:2k:94:ALA:N	2.53	0.41
49:2r:69:THR:HA	49:2r:72:ARG:HB2	2.01	0.41
1:1A:236:C:H2'	1:1A:237:C:C6	2.56	0.41
1:1A:581:C:H2'	1:1A:582:G:C8	2.56	0.41
1:1A:698:C:O2'	1:1A:734:A:N6	2.54	0.41
1:1A:705:A:C2	1:1A:727:A:H1'	2.56	0.41
1:1A:1127:A:O2'	1:1A:1128:A:H5'	2.21	0.41
1:1A:1173:G:N1	1:1A:1176:G:OP1	2.54	0.41
1:1A:1179:C:H2'	1:1A:1180:C:C6	2.55	0.41
1:1A:1341:U:O2	19:1X:80:ILE:HD13	2.21	0.41
1:1A:1394:U:H2'	1:1A:1395:A:O4'	2.21	0.41
1:1A:2128:C:N4	1:1A:2160:G:H1	2.14	0.41
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.56	0.41
1:1A:2857:G:N2	1:1A:2860:A:OP2	2.48	0.41
5:1F:11:VAL:HG22	5:1F:125:LEU:HB2	2.03	0.41
5:1F:106:ARG:H	5:1F:106:ARG:HG2	1.61	0.41
5:1F:157:VAL:HA	5:1F:176:LEU:O	2.21	0.41
6:1G:121:ASN:HA	6:1G:122:PRO:HD3	1.95	0.41
7:1H:17:VAL:HG21	7:1H:50:VAL:HG21	2.03	0.41
9:1N:61:ARG:HD3	9:1N:61:ARG:HA	1.78	0.41
13:1R:36:THR:HG22	13:1R:37:THR:N	2.35	0.41
23:11:52:ARG:HA	23:11:56:GLN:O	2.21	0.41
25:13:3:ARG:HD2	25:13:60:GLU:HG3	2.03	0.41
25:13:15:TYR:CZ	25:13:53:LEU:HD21	2.56	0.41
32:1a:327:A:H1'	32:1a:329:A:O4'	2.20	0.41
32:1a:392:G:H2'	32:1a:393:A:C8	2.56	0.41
32:1a:443:C:H2'	32:1a:444:C:C6	2.56	0.41
32:1a:449:C:O2	47:1p:42:ARG:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1027:C:N3	32:1a:1034:G:N2	2.68	0.41
32:1a:1227:A:C8	50:1s:83:HIS:HB3	2.55	0.41
32:1a:1258:G:H2'	32:1a:1259:C:C6	2.55	0.41
32:1a:1271:G:H2'	32:1a:1272:G:C8	2.56	0.41
32:1a:1307:U:H2'	32:1a:1308:U:C6	2.56	0.41
32:1a:1316:G:H22	32:1a:1319:A:C5'	2.33	0.41
32:1a:1346:A:H61	32:1a:1374:A:H3'	1.86	0.41
33:1b:82:ARG:HG3	33:1b:92:TYR:CZ	2.56	0.41
33:1b:196:LEU:HA	33:1b:196:LEU:HD23	1.74	0.41
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	2.03	0.41
40:1i:70:LYS:O	40:1i:74:ILE:HG13	2.20	0.41
40:1i:112:LYS:HG3	40:1i:118:LYS:O	2.21	0.41
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	2.02	0.41
44:1m:70:LEU:O	44:1m:74:VAL:HG13	2.21	0.41
44:1m:70:LEU:HD23	44:1m:70:LEU:HA	1.79	0.41
47:1p:27:LYS:HB3	47:1p:27:LYS:HE2	1.83	0.41
47:1p:66:PRO:HG2	47:1p:71:ARG:HE	1.86	0.41
51:1t:46:GLU:HB2	51:1t:48:LYS:HG2	2.03	0.41
54:1w:115:THR:N	54:1w:196:THR:HG22	2.36	0.41
55:1y:45:U:H3'	55:1y:46:G7M:C5'	2.50	0.41
1:2A:500:G:N2	1:2A:502:A:H3'	2.36	0.41
1:2A:631:A:N3	1:2A:2415:G:O2'	2.44	0.41
1:2A:660:G:H5'	5:2F:99:TYR:CE1	2.56	0.41
1:2A:872:A:OP1	12:2Q:5:ARG:NH1	2.45	0.41
1:2A:994:C:OP2	16:2U:50:ARG:HG2	2.21	0.41
1:2A:1257:C:H5'	5:2F:75:HIS:CE1	2.56	0.41
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.21	0.41
1:2A:2103:C:H42	1:2A:2186:G:H1	1.68	0.41
1:2A:2168:G:H8	1:2A:2170:A:N7	2.19	0.41
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.44	0.41
1:2A:2660:A:H2'	1:2A:2661:G:O4'	2.21	0.41
1:2A:2699:C:H2'	1:2A:2700:C:O4'	2.20	0.41
1:2A:2749:A:H1'	7:2H:63:SER:OG	2.21	0.41
4:2E:67:PHE:CD2	4:2E:74:PRO:HA	2.55	0.41
4:2E:79:ARG:HD3	4:2E:79:ARG:HA	1.84	0.41
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.55	0.41
10:2O:13:ASN:ND2	10:2O:97:ARG:HG2	2.36	0.41
14:2S:83:LYS:HE3	14:2S:83:LYS:HB2	1.72	0.41
15:2T:42:ILE:HG13	15:2T:84:GLN:HE22	1.84	0.41
17:2V:24:LYS:HE2	17:2V:24:LYS:HB3	1.92	0.41
32:2a:263:A:OP1	51:2t:79:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:563:A:H2'	32:2a:567:G:C8	2.56	0.41
32:2a:860:A:H2'	32:2a:861:G:O4'	2.20	0.41
32:2a:1117:G:O3'	40:2i:104:ARG:HD2	2.21	0.41
32:2a:1227:A:OP2	44:2m:111:LYS:NZ	2.53	0.41
32:2a:1295:G:O2'	32:2a:1302:U:O4	2.35	0.41
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.56	0.41
33:2b:19:HIS:HB3	33:2b:204:ASN:ND2	2.36	0.41
33:2b:115:LEU:O	33:2b:119:GLU:HG2	2.21	0.41
33:2b:122:PHE:HD1	33:2b:122:PHE:HA	1.79	0.41
33:2b:213:LEU:O	33:2b:217:ARG:HG3	2.20	0.41
34:2c:113:ALA:HB3	34:2c:114:PRO:HD3	2.03	0.41
36:2e:53:LEU:HD12	36:2e:53:LEU:H	1.85	0.41
40:2i:23:ASN:ND2	40:2i:25:LYS:HE2	2.35	0.41
45:2n:37:PHE:HB3	45:2n:39:LEU:HD12	2.02	0.41
46:2o:74:ASP:CG	46:2o:77:ARG:HD3	2.46	0.41
47:2p:47:ASP:C	47:2p:49:LEU:H	2.28	0.41
48:2q:45:HIS:CD2	48:2q:47:PRO:HD3	2.56	0.41
51:2t:46:GLU:C	51:2t:48:LYS:H	2.29	0.41
1:1A:309:G:N3	1:1A:329:G:O2'	2.48	0.41
1:1A:1047:G:H2'	1:1A:1110:G:N1	2.36	0.41
1:1A:1358:G:O2'	1:1A:1373:A:N6	2.54	0.41
1:1A:1654:A:OP1	13:1R:1:MET:N	2.36	0.41
1:1A:1889:A:N1	1:1A:2234:G:H1'	2.35	0.41
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.55	0.41
1:1A:2405:G:H5'	11:1P:75:ILE:HD13	2.03	0.41
3:1D:183:ARG:NH2	3:1D:266:SER:HB2	2.36	0.41
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	2.02	0.41
4:1E:112:GLY:O	4:1E:159:HIS:HA	2.21	0.41
6:1G:129:GLY:HA2	6:1G:169:ALA:HB2	2.02	0.41
8:1I:5:LEU:HD12	8:1I:5:LEU:HA	1.73	0.41
12:1Q:130:LYS:HE2	12:1Q:130:LYS:HB3	1.72	0.41
20:1Y:30:VAL:O	20:1Y:32:PRO:HD3	2.21	0.41
22:10:70:GLN:HG2	22:10:72:ARG:HG3	2.03	0.41
31:19:17:ILE:HD13	31:19:17:ILE:HA	1.93	0.41
32:1a:22:G:H4'	32:1a:885:G:C8	2.56	0.41
32:1a:524:G:H2'	32:1a:525:C:C6	2.56	0.41
32:1a:1064:G:H1'	32:1a:1190:G:H21	1.85	0.41
37:1f:9:VAL:HB	37:1f:87:ARG:HB2	2.03	0.41
54:1w:301:LYS:HD2	54:1w:301:LYS:O	2.21	0.41
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.21	0.41
55:1y:67:C:H2'	55:1y:68:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:29:U:H2'	1:2A:30:G:C8	2.56	0.41
1:2A:196:A:N3	1:2A:196:A:H2'	2.36	0.41
1:2A:244:A:H4'	11:2P:74:GLU:HB2	2.02	0.41
1:2A:531:C:H5'	60:2A:4040:HOH:O	2.20	0.41
1:2A:1013:C:H2'	1:2A:1014:U:C6	2.56	0.41
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.48	0.41
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.86	0.41
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.56	0.41
1:2A:2544:G:H2'	1:2A:2545:G:O4'	2.20	0.41
19:2X:1:MET:HE2	19:2X:3:THR:HG22	2.03	0.41
30:28:50:LEU:HD23	30:28:50:LEU:HA	1.71	0.41
32:2a:343:U:H2'	32:2a:345:C:C5	2.56	0.41
32:2a:552:U:H4'	43:2l:86:ARG:HB2	2.02	0.41
32:2a:1123:A:C2	41:2j:38:ILE:HD12	2.56	0.41
32:2a:1293:G:H5"	32:2a:1294:G:OP2	2.20	0.41
32:2a:1322:C:H5"	44:2m:100:GLY:HA3	2.02	0.41
33:2b:77:ALA:O	33:2b:81:VAL:HG13	2.21	0.41
38:2g:15:ASP:HB3	38:2g:24:THR:HG22	2.03	0.41
41:2j:47:PHE:N	41:2j:63:PHE:O	2.41	0.41
44:2m:24:GLY:H	44:2m:70:LEU:HD23	1.85	0.41
47:2p:48:TRP:CD1	47:2p:48:TRP:H	2.38	0.41
1:1A:271(P):C:H2'	1:1A:271(Q):G:O4'	2.21	0.40
1:1A:362:U:H6	1:1A:362:U:H2'	1.73	0.40
1:1A:670:A:H4'	1:1A:671:C:O5'	2.21	0.40
1:1A:922:U:H2'	1:1A:923:C:C6	2.56	0.40
1:1A:1021:A:OP2	9:1N:65:LYS:NZ	2.50	0.40
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.56	0.40
14:1S:59:LYS:H	14:1S:59:LYS:HG3	1.46	0.40
20:1Y:53:PRO:C	20:1Y:55:TYR:H	2.29	0.40
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	2.04	0.40
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.21	0.40
32:1a:12:U:H4'	32:1a:526:C:H4'	2.03	0.40
32:1a:44:G:N2	32:1a:399:G:C4	2.89	0.40
32:1a:160:A:H2	32:1a:342:C:H2'	1.87	0.40
32:1a:174:C:H2'	32:1a:175:C:H6	1.85	0.40
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.56	0.40
32:1a:911:U:H2'	32:1a:912:C:C6	2.56	0.40
32:1a:1254:C:H2'	32:1a:1255:G:O4'	2.20	0.40
40:1i:9:ARG:HB3	40:1i:104:ARG:NH2	2.36	0.40
42:1k:29:ILE:HG23	42:1k:44:SER:HB3	2.02	0.40
1:2A:176:G:O2'	1:2A:177:G:H5'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1010:A:H1'	1:2A:1153:C:H1'	2.03	0.40
1:2A:1423:G:H2'	1:2A:1424:G:O4'	2.21	0.40
1:2A:1474:C:H2'	1:2A:1475:G:C8	2.56	0.40
1:2A:1529:G:C2'	1:2A:1530:C:H5'	2.51	0.40
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.55	0.40
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.56	0.40
1:2A:2705:A:H2'	1:2A:2706:G:O4'	2.21	0.40
2:2B:24:G:N7	2:2B:56:G:H2'	2.36	0.40
5:2F:34:TRP:NE1	11:2P:8:PRO:HD3	2.36	0.40
10:2O:87:ILE:HD12	10:2O:91:LEU:HA	2.04	0.40
19:2X:84:ALA:HB3	19:2X:87:GLN:CD	2.45	0.40
23:21:67:ILE:N	23:21:68:PRO:HD2	2.36	0.40
23:21:73:LEU:HD13	23:21:94:LEU:O	2.21	0.40
32:2a:23:C:H5	32:2a:561:U:O4	2.04	0.40
32:2a:974:A:P	45:2n:41:ARG:HH21	2.44	0.40
32:2a:1187:G:N2	45:2n:60:SER:OG	2.33	0.40
33:2b:69:LEU:HD12	33:2b:69:LEU:HA	1.87	0.40
34:2c:173:VAL:HG12	34:2c:175:LEU:HD21	2.02	0.40
37:2f:7:ASN:HD22	37:2f:7:ASN:N	2.19	0.40
38:2g:71:PRO:HG3	38:2g:103:TRP:CH2	2.55	0.40
39:2h:103:VAL:HG21	39:2h:110:ALA:HB2	2.03	0.40
40:2i:114:TYR:HE1	41:2j:59:SER:HA	1.85	0.40
41:2j:45:ARG:O	41:2j:64:GLU:HA	2.21	0.40
51:2t:43:LEU:HD13	51:2t:51:GLU:HB3	2.03	0.40
1:1A:192:C:OP1	60:1A:3828:HOH:O	2.21	0.40
1:1A:223:A:O2'	1:1A:420:C:O2	2.37	0.40
1:1A:952:G:OP1	12:1Q:16:ARG:NH1	2.54	0.40
1:1A:981:A:OP1	60:1A:3870:HOH:O	2.21	0.40
1:1A:1371:G:H2'	1:1A:1372:U:H5	1.85	0.40
1:1A:1612:C:H4'	29:17:5:TRP:O	2.22	0.40
1:1A:1645:G:H5"	1:1A:1646:C:H5'	2.03	0.40
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.48	0.40
1:1A:2233:U:H2'	1:1A:2234:G:C8	2.56	0.40
60:1A:3881:HOH:O	11:1P:37:GLY:HA3	2.21	0.40
60:1A:4615:HOH:O	30:18:42:ARG:HD2	2.21	0.40
7:1H:3:ARG:HG2	7:1H:6:ARG:HG3	2.03	0.40
8:1I:61:ARG:NE	8:1I:61:ARG:HA	2.37	0.40
15:1T:11:GLU:O	15:1T:15:VAL:HG23	2.21	0.40
15:1T:46:GLU:O	15:1T:65:LYS:HD2	2.20	0.40
16:1U:24:TYR:HB2	16:1U:29:SER:HB3	2.02	0.40
16:1U:69:CYS:HB3	16:1U:74:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	2.03	0.40
24:12:53:LEU:HD23	24:12:53:LEU:HA	1.91	0.40
32:1a:304:U:H2'	32:1a:305:G:C8	2.56	0.40
32:1a:340:U:H2'	32:1a:341:C:C6	2.57	0.40
32:1a:453:A:C5	32:1a:454:C:C4	3.10	0.40
32:1a:616:G:H2'	32:1a:617:G:C8	2.55	0.40
32:1a:642:A:H2'	32:1a:643:C:C6	2.56	0.40
32:1a:1235:U:O2'	32:1a:1305:G:OP1	2.35	0.40
34:1c:70:VAL:O	34:1c:106:VAL:HG23	2.21	0.40
44:1m:81:LEU:HD23	44:1m:81:LEU:HA	1.80	0.40
50:1s:45:VAL:HG13	50:1s:63:THR:HA	2.02	0.40
1:2A:57:C:H2'	1:2A:58:G:O4'	2.21	0.40
1:2A:321:G:N3	5:2F:165:ARG:HD2	2.37	0.40
1:2A:601:C:O2	1:2A:605:C:H4'	2.22	0.40
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.57	0.40
1:2A:2100:G:C2	1:2A:2190:G:C5	3.09	0.40
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.56	0.40
6:2G:111:LEU:HB2	6:2G:112:PRO:HD3	2.03	0.40
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.43	0.40
32:2a:59:A:H3'	32:2a:331:G:H22	1.86	0.40
32:2a:113:G:C1'	32:2a:354:G:H5'	2.49	0.40
32:2a:376:G:OP2	47:2p:67:THR:HG21	2.20	0.40
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	2.03	0.40
34:2c:87:LEU:O	34:2c:91:LEU:HD22	2.20	0.40
35:2d:176:LEU:HD12	35:2d:182:LYS:O	2.22	0.40
37:2f:29:ALA:C	37:2f:31:GLU:H	2.29	0.40
38:2g:152:ALA:O	38:2g:155:ARG:HG2	2.21	0.40
1:1A:26:G:H1'	1:1A:515:A:H61	1.86	0.40
1:1A:35:G:H1'	1:1A:454:A:C4	2.57	0.40
1:1A:647:G:H2'	1:1A:648:G:O4'	2.21	0.40
1:1A:910:A:N1	1:1A:2277:G:H1'	2.36	0.40
1:1A:997:G:OP1	16:1U:92:ARG:HD2	2.21	0.40
1:1A:1010:A:N3	1:1A:1153:C:H1'	2.36	0.40
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.21	0.40
1:1A:1604:C:H2'	1:1A:1605:C:H6	1.86	0.40
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.21	0.40
3:1D:242:ARG:HG3	3:1D:242:ARG:NH1	2.33	0.40
8:1I:10:GLU:OE1	8:1I:11:ASN:N	2.45	0.40
12:1Q:77:LYS:NZ	12:1Q:86:GLY:O	2.53	0.40
23:11:49:VAL:HG21	23:11:67:ILE:HG23	2.04	0.40
31:19:24:TYR:CE1	31:19:35:ARG:HB2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1161:C:H2'	32:1a:1162:C:C6	2.56	0.40
32:1a:1316:G:N2	32:1a:1318:A:H3'	2.36	0.40
34:1c:33:LEU:O	34:1c:36:ASP:HB2	2.20	0.40
34:1c:43:LEU:HA	34:1c:47:LEU:HD23	2.03	0.40
37:1f:78:GLU:O	37:1f:81:ILE:HG22	2.21	0.40
41:1j:17:ASP:OD1	41:1j:70:ARG:NH1	2.53	0.40
44:1m:14:ARG:HE	44:1m:14:ARG:HB3	1.66	0.40
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.21	0.40
50:1s:3:ARG:NH2	50:1s:10:PHE:HB2	2.36	0.40
1:2A:52:A:N1	1:2A:178:G:O2'	2.48	0.40
1:2A:272:G:H1	1:2A:404:C:H42	1.68	0.40
1:2A:636:G:OP2	11:2P:113:LYS:NZ	2.44	0.40
1:2A:851:U:H5'	25:23:49:LYS:HD2	2.04	0.40
1:2A:1526:G:C6	1:2A:1527:G:C2	3.10	0.40
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.56	0.40
1:2A:1753:G:OP1	15:2T:95:ARG:HD3	2.22	0.40
1:2A:2406:U:H6	1:2A:2406:U:H2'	1.74	0.40
2:2B:8:U:H5"	14:2S:15:ARG:NH1	2.35	0.40
9:2N:67:LEU:HA	9:2N:87:LEU:HD23	2.03	0.40
14:2S:78:LEU:HD21	14:2S:109:GLY:HA3	2.02	0.40
23:21:49:VAL:HG21	23:21:67:ILE:HG23	2.03	0.40
26:24:40:HIS:O	26:24:43:TYR:N	2.55	0.40
27:25:8:LYS:O	27:25:9:LYS:HD2	2.22	0.40
32:2a:736:C:H2'	32:2a:737:A:H8	1.85	0.40
32:2a:1032:G:H2'	32:2a:1033:G:C8	2.56	0.40
32:2a:1162:C:H42	32:2a:1174:G:H1	1.69	0.40
32:2a:1203:C:H2'	32:2a:1204:A:O4'	2.21	0.40
33:2b:118:LEU:HD12	33:2b:118:LEU:HA	1.91	0.40
36:2e:80:ILE:CG2	36:2e:91:LEU:HB2	2.51	0.40
51:2t:47:GLY:O	51:2t:49:ALA:N	2.55	0.40
54:2w:352:ALA:HB3	54:2w:353:GLU:OE1	2.22	0.40
1:1A:185:U:H2'	1:1A:186:G:H8	1.87	0.40
1:1A:1030:G:OP2	12:1Q:128:LYS:NZ	2.50	0.40
1:1A:1604:C:H2'	1:1A:1605:C:C6	2.56	0.40
1:1A:2529:G:H5"	1:1A:2530:A:H5"	2.03	0.40
2:1B:78:A:H2'	2:1B:79:C:O4'	2.22	0.40
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.22	0.40
14:1S:24:LEU:HB2	14:1S:85:VAL:HG23	2.03	0.40
16:1U:109:LEU:HD23	16:1U:109:LEU:HA	1.79	0.40
21:1Z:67:LEU:HD23	21:1Z:67:LEU:HA	1.97	0.40
33:1b:150:SER:O	33:1b:153:ARG:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:61:LYS:HD3	35:1d:206:PHE:CE2	2.57	0.40
35:1d:65:ARG:NH1	35:1d:72:GLU:HB2	2.36	0.40
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.56	0.40
45:1n:26:ARG:HH12	45:1n:46:GLU:HB2	1.86	0.40
46:1o:15:PHE:CE1	46:1o:84:LYS:HE3	2.57	0.40
47:1p:4:ILE:H	47:1p:4:ILE:HG12	1.64	0.40
1:2A:1037:G:H1	1:2A:1118:C:H42	1.67	0.40
1:2A:1580:A:H3'	1:2A:1581:G:H8	1.87	0.40
1:2A:2144:U:O2'	1:2A:2147:G:O6	2.32	0.40
1:2A:2420:C:P	30:28:33:ASN:H	2.43	0.40
1:2A:2422:A:H8	1:2A:2422:A:H2'	1.80	0.40
3:2D:121:PRO:HB3	3:2D:135:PHE:CE2	2.57	0.40
4:2E:54:GLN:NE2	4:2E:76:ARG:HG2	2.36	0.40
5:2F:30:PRO:HB3	11:2P:1:MET:CE	2.52	0.40
8:2I:84:GLY:C	8:2I:86:THR:H	2.27	0.40
10:2O:77:ILE:HG13	15:2T:74:ARG:HG2	2.03	0.40
11:2P:46:LYS:HE2	11:2P:46:LYS:HB3	1.76	0.40
16:2U:76:TYR:OH	16:2U:92:ARG:NE	2.34	0.40
18:2W:68:ARG:HH21	18:2W:111:HIS:CE1	2.40	0.40
21:2Z:150:LEU:HD23	21:2Z:150:LEU:HA	1.92	0.40
32:2a:958:A:N6	32:2a:1221:G:O2'	2.55	0.40
32:2a:1187:G:H21	45:2n:60:SER:HG	1.62	0.40
34:2c:19:GLU:HA	34:2c:54:ARG:NH1	2.37	0.40
38:2g:47:CYS:C	38:2g:49:ILE:H	2.29	0.40
55:2y:9:A:O3'	55:2y:45:U:O2'	2.40	0.40
55:2y:18:G:O2'	55:2y:57:G:N2	2.42	0.40
1:1A:322:A:OP2	5:1F:169:ASN:HB2	2.21	0.40
1:1A:575:A:OP2	1:1A:2055:C:N4	2.48	0.40
1:1A:637:A:H4'	1:1A:638:G:O5'	2.22	0.40
1:1A:639:U:H2'	1:1A:640:C:C6	2.56	0.40
1:1A:1021:A:N3	1:1A:1021:A:H3'	2.36	0.40
1:1A:1080:C:C2	1:1A:1081:U:H1'	2.57	0.40
1:1A:1171:G:OP2	1:1A:1174:A:N6	2.55	0.40
1:1A:1614:A:N1	18:1W:87:PRO:HB3	2.36	0.40
1:1A:2107:C:H2'	1:1A:2108:C:C6	2.56	0.40
3:1D:218:ARG:HB3	3:1D:219:PRO:HD2	2.04	0.40
6:1G:64:THR:HB	6:1G:94:LEU:HD11	2.04	0.40
32:1a:127:G:C2	32:1a:128:G:C8	3.09	0.40
32:1a:186:C:H2'	32:1a:187:C:C6	2.57	0.40
32:1a:313:A:H2'	32:1a:314:C:C6	2.57	0.40
32:1a:608:A:H2'	32:1a:609:A:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1367:C:P	40:1i:112:LYS:HZ1	2.43	0.40
35:1d:111:ALA:HA	35:1d:116:GLN:HE21	1.86	0.40
47:1p:45:THR:HA	47:1p:46:PRO:HD3	1.96	0.40
55:1y:4:C:H2'	55:1y:5:G:O4'	2.22	0.40
1:2A:568:U:H5'	1:2A:945:A:N1	2.37	0.40
1:2A:637:A:H4'	1:2A:638:G:O5'	2.22	0.40
1:2A:1912:A:C8	1:2A:1918:A:C2	3.09	0.40
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	2.04	0.40
5:2F:34:TRP:CZ2	11:2P:8:PRO:HB3	2.57	0.40
5:2F:179:GLU:H	5:2F:179:GLU:CD	2.28	0.40
14:2S:68:GLN:HG2	14:2S:71:ARG:NH1	2.33	0.40
15:2T:26:ASP:O	15:2T:49:VAL:HG12	2.22	0.40
16:2U:102:GLU:HG3	17:2V:2:PHE:CZ	2.57	0.40
21:2Z:54:HIS:HB3	21:2Z:101:PRO:HG3	2.03	0.40
22:20:19:LYS:HD3	22:20:19:LYS:HA	1.76	0.40
24:22:1:MET:HB3	24:22:5:GLU:OE1	2.21	0.40
32:2a:50:A:H4'	32:2a:52:G:OP1	2.22	0.40
32:2a:139:G:H2'	32:2a:140:A:C8	2.57	0.40
32:2a:841:U:O4'	32:2a:841:U:P	2.80	0.40
32:2a:1438:G:OP2	51:2t:34:LYS:NZ	2.53	0.40
33:2b:108:ILE:HD13	33:2b:108:ILE:HA	1.89	0.40
33:2b:127:ILE:O	33:2b:129:GLU:N	2.54	0.40
44:2m:33:ALA:HB2	44:2m:64:TRP:HH2	1.87	0.40
47:2p:67:THR:O	47:2p:71:ARG:N	2.54	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%)	259 (95%)	14 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	2D	273/276 (99%)	258 (94%)	14 (5%)	1 (0%)	30 48
4	1E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	24 42
4	2E	202/206 (98%)	187 (93%)	13 (6%)	2 (1%)	12 25
5	1F	201/210 (96%)	194 (96%)	6 (3%)	1 (0%)	24 42
5	2F	201/210 (96%)	191 (95%)	8 (4%)	2 (1%)	12 25
6	1G	179/182 (98%)	160 (89%)	18 (10%)	1 (1%)	21 38
6	2G	179/182 (98%)	156 (87%)	20 (11%)	3 (2%)	7 16
7	1H	172/180 (96%)	159 (92%)	12 (7%)	1 (1%)	21 38
7	2H	172/180 (96%)	152 (88%)	16 (9%)	4 (2%)	5 11
8	1I	144/148 (97%)	126 (88%)	15 (10%)	3 (2%)	5 13
8	2I	144/148 (97%)	121 (84%)	19 (13%)	4 (3%)	4 9
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100 100
9	2N	138/140 (99%)	131 (95%)	7 (5%)	0	100 100
10	1O	120/122 (98%)	115 (96%)	5 (4%)	0	100 100
10	2O	120/122 (98%)	112 (93%)	8 (7%)	0	100 100
11	1P	147/150 (98%)	137 (93%)	8 (5%)	2 (1%)	9 19
11	2P	147/150 (98%)	137 (93%)	7 (5%)	3 (2%)	6 13
12	1Q	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	18 35
12	2Q	139/141 (99%)	130 (94%)	8 (6%)	1 (1%)	18 35
13	1R	116/118 (98%)	113 (97%)	2 (2%)	1 (1%)	14 28
13	2R	116/118 (98%)	110 (95%)	6 (5%)	0	100 100
14	1S	108/112 (96%)	99 (92%)	8 (7%)	1 (1%)	14 28
14	2S	108/112 (96%)	93 (86%)	13 (12%)	2 (2%)	6 14
15	1T	129/146 (88%)	121 (94%)	8 (6%)	0	100 100
15	2T	129/146 (88%)	122 (95%)	7 (5%)	0	100 100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
16	2U	114/118 (97%)	110 (96%)	4 (4%)	0	100 100
17	1V	99/101 (98%)	94 (95%)	3 (3%)	2 (2%)	6 13
17	2V	99/101 (98%)	91 (92%)	7 (7%)	1 (1%)	12 25
18	1W	110/113 (97%)	108 (98%)	2 (2%)	0	100 100
18	2W	110/113 (97%)	106 (96%)	3 (3%)	1 (1%)	14 28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
19	1X	93/96 (97%)	91 (98%)	0	2 (2%)	5 12
19	2X	93/96 (97%)	90 (97%)	3 (3%)	0	100 100
20	1Y	105/110 (96%)	95 (90%)	9 (9%)	1 (1%)	12 25
20	2Y	105/110 (96%)	95 (90%)	9 (9%)	1 (1%)	12 25
21	1Z	181/206 (88%)	159 (88%)	20 (11%)	2 (1%)	11 24
21	2Z	184/206 (89%)	153 (83%)	26 (14%)	5 (3%)	4 9
22	10	74/85 (87%)	67 (90%)	6 (8%)	1 (1%)	9 19
22	20	75/85 (88%)	67 (89%)	7 (9%)	1 (1%)	9 21
23	11	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 24
23	21	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 24
24	12	68/72 (94%)	64 (94%)	4 (6%)	0	100 100
24	22	68/72 (94%)	66 (97%)	2 (3%)	0	100 100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
25	23	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
26	14	67/71 (94%)	42 (63%)	18 (27%)	7 (10%)	0 0
26	24	66/71 (93%)	44 (67%)	20 (30%)	2 (3%)	3 8
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
27	25	57/60 (95%)	54 (95%)	3 (5%)	0	100 100
28	16	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
28	26	51/54 (94%)	47 (92%)	4 (8%)	0	100 100
29	17	46/49 (94%)	44 (96%)	2 (4%)	0	100 100
29	27	46/49 (94%)	44 (96%)	2 (4%)	0	100 100
30	18	62/65 (95%)	62 (100%)	0	0	100 100
30	28	62/65 (95%)	59 (95%)	3 (5%)	0	100 100
31	19	35/37 (95%)	33 (94%)	2 (6%)	0	100 100
31	29	35/37 (95%)	34 (97%)	1 (3%)	0	100 100
33	1b	229/256 (90%)	187 (82%)	37 (16%)	5 (2%)	5 12
33	2b	229/256 (90%)	193 (84%)	27 (12%)	9 (4%)	2 4
34	1c	204/239 (85%)	178 (87%)	24 (12%)	2 (1%)	12 25
34	2c	204/239 (85%)	180 (88%)	21 (10%)	3 (2%)	8 18
35	1d	206/209 (99%)	185 (90%)	16 (8%)	5 (2%)	4 10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
35	2d	206/209 (99%)	189 (92%)	15 (7%)	2 (1%)	12 25
36	1e	146/162 (90%)	133 (91%)	11 (8%)	2 (1%)	9 19
36	2e	146/162 (90%)	133 (91%)	10 (7%)	3 (2%)	5 13
37	1f	98/101 (97%)	89 (91%)	9 (9%)	0	100 100
37	2f	98/101 (97%)	89 (91%)	8 (8%)	1 (1%)	12 25
38	1g	153/156 (98%)	138 (90%)	12 (8%)	3 (2%)	6 13
38	2g	153/156 (98%)	134 (88%)	16 (10%)	3 (2%)	6 13
39	1h	135/138 (98%)	127 (94%)	8 (6%)	0	100 100
39	2h	135/138 (98%)	124 (92%)	11 (8%)	0	100 100
40	1i	125/128 (98%)	103 (82%)	16 (13%)	6 (5%)	2 3
40	2i	121/128 (94%)	96 (79%)	23 (19%)	2 (2%)	7 16
41	1j	96/105 (91%)	84 (88%)	11 (12%)	1 (1%)	12 25
41	2j	94/105 (90%)	80 (85%)	12 (13%)	2 (2%)	5 13
42	1k	112/129 (87%)	98 (88%)	14 (12%)	0	100 100
42	2k	112/129 (87%)	98 (88%)	10 (9%)	4 (4%)	2 5
43	1l	119/132 (90%)	111 (93%)	7 (6%)	1 (1%)	16 31
43	2l	119/132 (90%)	107 (90%)	11 (9%)	1 (1%)	16 31
44	1m	116/126 (92%)	102 (88%)	11 (10%)	3 (3%)	4 9
44	2m	113/126 (90%)	94 (83%)	17 (15%)	2 (2%)	6 15
45	1n	58/61 (95%)	50 (86%)	8 (14%)	0	100 100
45	2n	58/61 (95%)	52 (90%)	6 (10%)	0	100 100
46	1o	86/89 (97%)	79 (92%)	7 (8%)	0	100 100
46	2o	86/89 (97%)	81 (94%)	4 (5%)	1 (1%)	10 22
47	1p	80/88 (91%)	64 (80%)	15 (19%)	1 (1%)	9 21
47	2p	80/88 (91%)	67 (84%)	13 (16%)	0	100 100
48	1q	97/105 (92%)	90 (93%)	7 (7%)	0	100 100
48	2q	97/105 (92%)	84 (87%)	12 (12%)	1 (1%)	12 25
49	1r	66/88 (75%)	61 (92%)	5 (8%)	0	100 100
49	2r	66/88 (75%)	59 (89%)	7 (11%)	0	100 100
50	1s	81/93 (87%)	68 (84%)	12 (15%)	1 (1%)	10 22
50	2s	81/93 (87%)	68 (84%)	13 (16%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
51	1t	94/106 (89%)	82 (87%)	10 (11%)	2 (2%)	5 13
51	2t	94/106 (89%)	83 (88%)	5 (5%)	6 (6%)	1 1
52	1u	21/27 (78%)	21 (100%)	0	0	100 100
52	2u	21/27 (78%)	19 (90%)	2 (10%)	0	100 100
54	1w	246/354 (70%)	228 (93%)	14 (6%)	4 (2%)	7 17
54	2w	250/354 (71%)	229 (92%)	20 (8%)	1 (0%)	30 48
56	1z	12/18 (67%)	10 (83%)	2 (17%)	0	100 100
56	2z	12/18 (67%)	10 (83%)	2 (17%)	0	100 100
All	All	11922/12872 (93%)	10834 (91%)	949 (8%)	139 (1%)	10 22

All (139) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
8	1I	10	GLU
14	1S	60	GLY
17	1V	79	VAL
23	1l	3	LYS
26	14	62	ARG
33	1b	96	ARG
35	1d	44	GLY
38	1g	80	VAL
40	1i	29	ASN
40	1i	54	ASP
44	1m	67	GLU
6	2G	96	ARG
7	2H	126	PRO
23	21	3	LYS
33	2b	10	LEU
33	2b	16	HIS
33	2b	17	PHE
6	1G	47	LYS
12	1Q	59	ARG
26	14	18	CYS
26	14	49	PHE
26	14	53	GLU
26	14	57	GLU
33	1b	11	LEU
33	1b	17	PHE

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Mol	Chain	Res	Type
35	1d	164	ALA
40	1i	100	GLY
41	1j	55	LYS
44	1m	100	GLY
47	1p	31	LYS
54	1w	299	SER
6	2G	117	PHE
8	2I	10	GLU
8	2I	106	GLY
14	2S	35	ILE
17	2V	79	VAL
22	20	73	GLY
26	24	45	GLY
33	2b	22	LYS
33	2b	78	GLN
33	2b	96	ARG
33	2b	124	SER
33	2b	165	VAL
38	2g	81	GLY
41	2j	31	GLY
44	2m	5	ALA
48	2q	55	ASP
19	1X	94	GLY
20	1Y	102	CYS
21	1Z	52	SER
22	10	10	THR
36	1e	72	GLN
40	1i	98	PRO
44	1m	106	ASN
54	1w	207	GLU
7	2H	92	ILE
7	2H	159	GLU
8	2I	84	GLY
14	2S	60	GLY
21	2Z	52	SER
21	2Z	135	GLU
21	2Z	152	ALA
26	24	62	ARG
33	2b	128	GLU
38	2g	80	VAL
40	2i	29	ASN
41	2j	58	ASP

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Mol	Chain	Res	Type
43	2l	105	TYR
44	2m	28	ALA
51	2t	9	ASN
4	1E	52	LEU
7	1H	126	PRO
8	1I	83	ALA
11	1P	29	LYS
19	1X	93	GLU
33	1b	126	GLU
34	1c	129	ALA
35	1d	46	LYS
40	1i	44	VAL
50	1s	26	GLY
51	1t	48	LYS
54	1w	116	GLY
4	2E	52	LEU
20	2Y	101	LYS
34	2c	95	THR
42	2k	25	TYR
42	2k	117	ASN
13	1R	71	GLN
26	14	64	GLY
35	1d	125	HIS
40	1i	126	SER
54	1w	300	GLU
4	2E	57	LYS
5	2F	130	ALA
7	2H	65	HIS
8	2I	117	GLU
11	2P	29	LYS
11	2P	140	ALA
18	2W	25	ARG
37	2f	30	LEU
40	2i	109	VAL
42	2k	89	ALA
51	2t	47	GLY
51	2t	95	ALA
51	2t	102	GLY
11	1P	122	PRO
17	1V	100	ARG
35	1d	156	GLU
36	1e	71	LEU

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Mol	Chain	Res	Type
38	1g	4	ARG
3	2D	125	ILE
5	2F	17	ARG
35	2d	166	LYS
36	2e	85	GLY
38	2g	82	GLY
42	2k	49	GLY
46	2o	19	PRO
51	2t	48	LYS
26	14	45	GLY
43	1l	74	GLY
12	2Q	3	MET
34	2c	99	VAL
36	2e	39	GLY
54	2w	317	ILE
8	1I	131	LYS
21	1Z	146	ILE
6	2G	68	PRO
21	2Z	53	ILE
34	2c	96	GLY
34	1c	81	GLY
36	2e	69	VAL
51	2t	100	ILE
38	1g	9	VAL
51	1t	97	ALA
11	2P	122	PRO
21	2Z	177	PRO
35	2d	5	ILE
33	1b	125	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	1D	215/218 (99%)	206 (96%)	9 (4%)	26 51
3	2D	215/218 (99%)	204 (95%)	11 (5%)	21 43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	1E	164/166 (99%)	153 (93%)	11 (7%)	15 31
4	2E	164/166 (99%)	146 (89%)	18 (11%)	6 12
5	1F	160/166 (96%)	142 (89%)	18 (11%)	5 11
5	2F	159/166 (96%)	143 (90%)	16 (10%)	7 15
6	1G	143/156 (92%)	126 (88%)	17 (12%)	5 10
6	2G	142/156 (91%)	120 (84%)	22 (16%)	2 5
7	1H	144/148 (97%)	135 (94%)	9 (6%)	16 34
7	2H	144/148 (97%)	127 (88%)	17 (12%)	5 10
8	1I	110/124 (89%)	96 (87%)	14 (13%)	4 8
8	2I	104/124 (84%)	86 (83%)	18 (17%)	2 3
9	1N	118/119 (99%)	110 (93%)	8 (7%)	14 30
9	2N	118/119 (99%)	110 (93%)	8 (7%)	14 30
10	1O	100/100 (100%)	98 (98%)	2 (2%)	48 71
10	2O	100/100 (100%)	94 (94%)	6 (6%)	17 36
11	1P	115/116 (99%)	109 (95%)	6 (5%)	21 43
11	2P	115/116 (99%)	103 (90%)	12 (10%)	7 14
12	1Q	111/111 (100%)	98 (88%)	13 (12%)	5 10
12	2Q	111/111 (100%)	101 (91%)	10 (9%)	9 19
13	1R	101/101 (100%)	89 (88%)	12 (12%)	5 10
13	2R	101/101 (100%)	97 (96%)	4 (4%)	28 53
14	1S	87/88 (99%)	77 (88%)	10 (12%)	5 10
14	2S	85/88 (97%)	75 (88%)	10 (12%)	5 10
15	1T	115/127 (91%)	108 (94%)	7 (6%)	17 35
15	2T	113/127 (89%)	107 (95%)	6 (5%)	20 42
16	1U	93/94 (99%)	88 (95%)	5 (5%)	20 42
16	2U	93/94 (99%)	92 (99%)	1 (1%)	65 81
17	1V	80/82 (98%)	77 (96%)	3 (4%)	29 54
17	2V	80/82 (98%)	76 (95%)	4 (5%)	22 44
18	1W	90/92 (98%)	85 (94%)	5 (6%)	19 40
18	2W	90/92 (98%)	85 (94%)	5 (6%)	19 40
19	1X	77/78 (99%)	74 (96%)	3 (4%)	28 54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
19	2X	76/78 (97%)	70 (92%)	6 (8%)	11 24
20	1Y	85/91 (93%)	76 (89%)	9 (11%)	6 13
20	2Y	86/91 (94%)	77 (90%)	9 (10%)	6 13
21	1Z	155/179 (87%)	141 (91%)	14 (9%)	9 19
21	2Z	155/179 (87%)	127 (82%)	28 (18%)	2 2
22	10	61/67 (91%)	58 (95%)	3 (5%)	22 45
22	20	61/67 (91%)	55 (90%)	6 (10%)	7 16
23	11	80/83 (96%)	75 (94%)	5 (6%)	16 34
23	21	80/83 (96%)	74 (92%)	6 (8%)	12 26
24	12	65/67 (97%)	61 (94%)	4 (6%)	16 34
24	22	65/67 (97%)	62 (95%)	3 (5%)	24 48
25	13	51/52 (98%)	46 (90%)	5 (10%)	7 16
25	23	50/52 (96%)	46 (92%)	4 (8%)	11 24
26	14	58/63 (92%)	50 (86%)	8 (14%)	3 7
26	24	51/63 (81%)	42 (82%)	9 (18%)	2 3
27	15	50/52 (96%)	47 (94%)	3 (6%)	17 36
27	25	50/52 (96%)	46 (92%)	4 (8%)	11 24
28	16	51/52 (98%)	47 (92%)	4 (8%)	11 25
28	26	50/52 (96%)	45 (90%)	5 (10%)	7 16
29	17	41/42 (98%)	38 (93%)	3 (7%)	13 27
29	27	41/42 (98%)	39 (95%)	2 (5%)	22 45
30	18	53/55 (96%)	49 (92%)	4 (8%)	12 26
30	28	54/55 (98%)	48 (89%)	6 (11%)	6 12
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 61
31	29	34/34 (100%)	33 (97%)	1 (3%)	37 61
33	1b	192/220 (87%)	150 (78%)	42 (22%)	1 1
33	2b	187/220 (85%)	162 (87%)	25 (13%)	4 7
34	1c	144/188 (77%)	122 (85%)	22 (15%)	3 5
34	2c	140/188 (74%)	123 (88%)	17 (12%)	5 9
35	1d	170/181 (94%)	148 (87%)	22 (13%)	4 7
35	2d	173/181 (96%)	153 (88%)	20 (12%)	5 10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
36	1e	113/123 (92%)	97 (86%)	16 (14%)	3 6
36	2e	113/123 (92%)	94 (83%)	19 (17%)	2 3
37	1f	84/90 (93%)	78 (93%)	6 (7%)	13 28
37	2f	85/90 (94%)	76 (89%)	9 (11%)	6 13
38	1g	119/127 (94%)	107 (90%)	12 (10%)	7 15
38	2g	120/127 (94%)	106 (88%)	14 (12%)	5 10
39	1h	114/119 (96%)	107 (94%)	7 (6%)	17 35
39	2h	114/119 (96%)	108 (95%)	6 (5%)	20 42
40	1i	90/99 (91%)	80 (89%)	10 (11%)	6 12
40	2i	86/99 (87%)	73 (85%)	13 (15%)	3 5
41	1j	68/92 (74%)	56 (82%)	12 (18%)	2 3
41	2j	69/92 (75%)	61 (88%)	8 (12%)	5 10
42	1k	82/99 (83%)	73 (89%)	9 (11%)	6 12
42	2k	83/99 (84%)	75 (90%)	8 (10%)	8 17
43	1l	96/108 (89%)	86 (90%)	10 (10%)	7 14
43	2l	96/108 (89%)	89 (93%)	7 (7%)	13 27
44	1m	90/101 (89%)	81 (90%)	9 (10%)	7 16
44	2m	85/101 (84%)	74 (87%)	11 (13%)	4 7
45	1n	49/50 (98%)	46 (94%)	3 (6%)	17 35
45	2n	48/50 (96%)	44 (92%)	4 (8%)	10 22
46	1o	78/80 (98%)	75 (96%)	3 (4%)	29 54
46	2o	78/80 (98%)	72 (92%)	6 (8%)	12 25
47	1p	69/74 (93%)	60 (87%)	9 (13%)	4 7
47	2p	68/74 (92%)	62 (91%)	6 (9%)	9 20
48	1q	94/97 (97%)	88 (94%)	6 (6%)	16 33
48	2q	94/97 (97%)	88 (94%)	6 (6%)	16 33
49	1r	59/77 (77%)	51 (86%)	8 (14%)	3 7
49	2r	58/77 (75%)	51 (88%)	7 (12%)	5 9
50	1s	69/80 (86%)	60 (87%)	9 (13%)	4 7
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4 7
51	1t	70/82 (85%)	59 (84%)	11 (16%)	2 4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
51	2t	70/82 (85%)	63 (90%)	7 (10%)	7 16
52	1u	18/22 (82%)	17 (94%)	1 (6%)	19 40
52	2u	18/22 (82%)	16 (89%)	2 (11%)	6 12
54	1w	203/298 (68%)	176 (87%)	27 (13%)	4 7
54	2w	203/298 (68%)	167 (82%)	36 (18%)	2 3
56	1z	14/17 (82%)	12 (86%)	2 (14%)	3 6
56	2z	14/17 (82%)	11 (79%)	3 (21%)	1 1
All	All	9748/10694 (91%)	8777 (90%)	971 (10%)	7 16

All (971) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	37	LEU
3	1D	99	ASP
3	1D	155	LEU
3	1D	176	ARG
3	1D	200	ASP
3	1D	211	ARG
3	1D	229	VAL
3	1D	242	ARG
4	1E	7	VAL
4	1E	33	VAL
4	1E	61	ARG
4	1E	75	VAL
4	1E	81	ILE
4	1E	82	ARG
4	1E	105	THR
4	1E	116	VAL
4	1E	121	ASN
4	1E	154	LYS
4	1E	188	VAL
5	1F	15	SER
5	1F	24	LEU
5	1F	28	ILE
5	1F	53	THR
5	1F	57	VAL
5	1F	70	THR
5	1F	74	ARG
5	1F	106	ARG

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Mol	Chain	Res	Type
5	1F	119	ARG
5	1F	157	VAL
5	1F	162	LEU
5	1F	165	ARG
5	1F	175	THR
5	1F	176	LEU
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU
5	1F	200	GLU
6	1G	5	VAL
6	1G	7	LEU
6	1G	26	GLN
6	1G	28	VAL
6	1G	40	ASN
6	1G	58	GLN
6	1G	60	LEU
6	1G	67	LYS
6	1G	116	ASP
6	1G	136	ARG
6	1G	139	LEU
6	1G	140	ILE
6	1G	149	VAL
6	1G	162	THR
6	1G	165	THR
6	1G	168	GLU
6	1G	175	LEU
7	1H	42	ARG
7	1H	44	VAL
7	1H	45	VAL
7	1H	49	VAL
7	1H	119	GLU
7	1H	127	GLU
7	1H	129	THR
7	1H	131	VAL
7	1H	172	LYS
8	1I	5	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	15	VAL
8	1I	38	LEU
8	1I	40	THR

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Mol	Chain	Res	Type
8	1I	41	GLU
8	1I	47	LEU
8	1I	58	LEU
8	1I	92	VAL
8	1I	101	LEU
8	1I	108	THR
8	1I	109	ILE
8	1I	133	HIS
9	1N	10	GLU
9	1N	33	LEU
9	1N	39	ARG
9	1N	46	VAL
9	1N	48	MET
9	1N	58	ASP
9	1N	62	VAL
9	1N	68	GLU
10	1O	66	LYS
10	1O	94	ARG
11	1P	42	SER
11	1P	67	MET
11	1P	71	VAL
11	1P	98	GLU
11	1P	148	LEU
11	1P	149	GLU
12	1Q	3	MET
12	1Q	7	MET
12	1Q	8	LYS
12	1Q	17	LEU
12	1Q	75	THR
12	1Q	81	VAL
12	1Q	97	VAL
12	1Q	106	VAL
12	1Q	109	VAL
12	1Q	110	THR
12	1Q	112	GLU
12	1Q	115	MET
12	1Q	129	THR
13	1R	6	SER
13	1R	27	SER
13	1R	30	THR
13	1R	36	THR
13	1R	37	THR

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Mol	Chain	Res	Type
13	1R	59	ASP
13	1R	64	ARG
13	1R	65	LEU
13	1R	74	LYS
13	1R	86	ARG
13	1R	102	GLU
13	1R	114	VAL
14	1S	27	SER
14	1S	38	GLN
14	1S	43	GLU
14	1S	50	SER
14	1S	59	LYS
14	1S	68	GLN
14	1S	73	LEU
14	1S	76	LYS
14	1S	88	ASP
14	1S	110	LEU
15	1T	21	GLU
15	1T	28	VAL
15	1T	70	VAL
15	1T	84	GLN
15	1T	96	ARG
15	1T	108	ARG
15	1T	128	GLU
16	1U	5	LYS
16	1U	20	LEU
16	1U	74	LEU
16	1U	77	SER
16	1U	111	GLU
17	1V	28	GLU
17	1V	79	VAL
17	1V	85	LYS
18	1W	11	ARG
18	1W	17	VAL
18	1W	60	ASN
18	1W	63	ASP
18	1W	100	THR
19	1X	1	MET
19	1X	52	VAL
19	1X	92	LEU
20	1Y	1	MET
20	1Y	14	LEU

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Mol	Chain	Res	Type
20	1Y	70	SER
20	1Y	72	VAL
20	1Y	81	LYS
20	1Y	88	LYS
20	1Y	99	CYS
20	1Y	106	LEU
20	1Y	107	ASP
21	1Z	5	LEU
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	82	ARG
21	1Z	86	VAL
21	1Z	93	ASP
21	1Z	111	VAL
21	1Z	124	ILE
21	1Z	126	VAL
21	1Z	137	ILE
21	1Z	154	ASP
21	1Z	162	GLU
21	1Z	171	ILE
21	1Z	175	VAL
22	10	39	ARG
22	10	63	VAL
22	10	82	ARG
23	11	3	LYS
23	11	30	VAL
23	11	40	ARG
23	11	46	LEU
23	11	80	LEU
24	12	32	LEU
24	12	53	LEU
24	12	65	ASN
24	12	70	GLN
25	13	6	VAL
25	13	36	VAL
25	13	40	THR
25	13	54	VAL
25	13	58	VAL
26	14	23	GLU
26	14	46	GLN
26	14	47	GLN
26	14	49	PHE

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Mol	Chain	Res	Type
26	14	50	VAL
26	14	56	VAL
26	14	57	GLU
26	14	63	TYR
27	15	6	VAL
27	15	26	THR
27	15	59	GLU
28	16	6	ARG
28	16	7	ILE
28	16	35	GLU
28	16	52	VAL
29	17	15	THR
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	23	VAL
30	18	32	LEU
30	18	41	ILE
31	19	35	ARG
33	1b	7	VAL
33	1b	8	LYS
33	1b	10	LEU
33	1b	11	LEU
33	1b	12	GLU
33	1b	19	HIS
33	1b	22	LYS
33	1b	32	ILE
33	1b	39	ILE
33	1b	41	ILE
33	1b	45	GLN
33	1b	47	THR
33	1b	58	ILE
33	1b	63	MET
33	1b	67	THR
33	1b	73	THR
33	1b	75	LYS
33	1b	79	ASP
33	1b	80	ILE
33	1b	93	VAL
33	1b	97	TRP
33	1b	108	ILE
33	1b	112	VAL

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Mol	Chain	Res	Type
33	1b	118	LEU
33	1b	121	LEU
33	1b	127	ILE
33	1b	128	GLU
33	1b	142	LEU
33	1b	143	GLU
33	1b	144	ARG
33	1b	145	LEU
33	1b	154	LEU
33	1b	158	LEU
33	1b	172	ILE
33	1b	187	LEU
33	1b	189	ASP
33	1b	195	ASP
33	1b	213	LEU
33	1b	219	VAL
33	1b	221	LEU
33	1b	224	GLN
33	1b	230	VAL
34	1c	3	ASN
34	1c	4	LYS
34	1c	8	ILE
34	1c	15	THR
34	1c	17	ASP
34	1c	32	LEU
34	1c	43	LEU
34	1c	58	GLU
34	1c	64	VAL
34	1c	70	VAL
34	1c	77	ILE
34	1c	82	GLU
34	1c	85	ARG
34	1c	95	THR
34	1c	115	LEU
34	1c	128	PHE
34	1c	130	VAL
34	1c	151	VAL
34	1c	173	VAL
34	1c	192	THR
34	1c	206	GLU
34	1c	207	VAL
35	1d	8	VAL

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Mol	Chain	Res	Type
35	1d	9	CYS
35	1d	31	CYS
35	1d	33	MET
35	1d	47	ARG
35	1d	56	VAL
35	1d	88	VAL
35	1d	97	LEU
35	1d	100	ARG
35	1d	127	THR
35	1d	134	ASP
35	1d	135	LEU
35	1d	150	GLU
35	1d	155	LEU
35	1d	163	GLU
35	1d	166	LYS
35	1d	168	ARG
35	1d	170	VAL
35	1d	178	VAL
35	1d	179	GLU
35	1d	187	ARG
35	1d	200	GLU
36	1e	10	MET
36	1e	12	LEU
36	1e	18	ARG
36	1e	31	LEU
36	1e	34	VAL
36	1e	41	VAL
36	1e	50	GLU
36	1e	64	ARG
36	1e	71	LEU
36	1e	75	THR
36	1e	78	HIS
36	1e	79	GLU
36	1e	98	THR
36	1e	120	THR
36	1e	147	ASP
36	1e	150	ARG
37	1f	40	VAL
37	1f	55	ASP
37	1f	72	VAL
37	1f	91	VAL
37	1f	94	GLN

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Mol	Chain	Res	Type
37	1f	98	LEU
38	1g	6	ARG
38	1g	21	VAL
38	1g	24	THR
38	1g	30	ILE
38	1g	45	ASP
38	1g	50	ILE
38	1g	52	GLU
38	1g	59	LEU
38	1g	73	MET
38	1g	77	SER
38	1g	89	MET
38	1g	110	GLN
39	1h	10	LEU
39	1h	24	THR
39	1h	52	ASP
39	1h	88	LYS
39	1h	99	GLU
39	1h	121	ASP
39	1h	137	VAL
40	1i	17	VAL
40	1i	23	ASN
40	1i	27	THR
40	1i	28	VAL
40	1i	60	ASP
40	1i	64	THR
40	1i	65	VAL
40	1i	99	LEU
40	1i	104	ARG
40	1i	113	LYS
41	1j	16	LEU
41	1j	19	SER
41	1j	44	VAL
41	1j	45	ARG
41	1j	55	LYS
41	1j	62	HIS
41	1j	67	THR
41	1j	81	THR
41	1j	92	THR
41	1j	94	VAL
41	1j	97	GLU
41	1j	98	ILE

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Mol	Chain	Res	Type
42	1k	16	SER
42	1k	24	SER
42	1k	41	THR
42	1k	48	ILE
42	1k	80	VAL
42	1k	109	VAL
42	1k	110	ASP
42	1k	114	VAL
42	1k	117	ASN
43	1l	34	ARG
43	1l	55	VAL
43	1l	60	LEU
43	1l	67	THR
43	1l	78	GLN
43	1l	83	VAL
43	1l	86	ARG
43	1l	96	VAL
43	1l	104	VAL
43	1l	117	ARG
44	1m	4	ILE
44	1m	9	ILE
44	1m	12	ASN
44	1m	19	LEU
44	1m	34	LEU
44	1m	63	THR
44	1m	105	THR
44	1m	109	THR
44	1m	117	VAL
45	1n	11	LYS
45	1n	18	VAL
45	1n	22	THR
46	1o	26	GLU
46	1o	64	ARG
46	1o	87	ILE
47	1p	2	VAL
47	1p	4	ILE
47	1p	6	LEU
47	1p	20	VAL
47	1p	21	VAL
47	1p	45	THR
47	1p	60	LEU
47	1p	67	THR

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Mol	Chain	Res	Type
47	1p	79	VAL
48	1q	10	VAL
48	1q	19	VAL
48	1q	36	ILE
48	1q	53	LEU
48	1q	60	ILE
48	1q	97	SER
49	1r	26	LEU
49	1r	28	GLU
49	1r	35	ARG
49	1r	45	SER
49	1r	46	GLU
49	1r	47	THR
49	1r	85	LEU
49	1r	86	VAL
50	1s	15	LEU
50	1s	17	GLU
50	1s	21	GLU
50	1s	31	ILE
50	1s	36	ARG
50	1s	38	SER
50	1s	49	ILE
50	1s	63	THR
50	1s	79	THR
51	1t	10	LEU
51	1t	13	LEU
51	1t	23	ARG
51	1t	24	LEU
51	1t	31	SER
51	1t	37	SER
51	1t	55	ILE
51	1t	70	SER
51	1t	80	ARG
51	1t	84	LEU
51	1t	100	ILE
52	1u	12	LYS
54	1w	102	MET
54	1w	115	THR
54	1w	119	GLU
54	1w	144	VAL
54	1w	152	LEU
54	1w	157	LYS

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Mol	Chain	Res	Type
54	1w	158	VAL
54	1w	170	THR
54	1w	172	LYS
54	1w	189	GLN
54	1w	196	THR
54	1w	201	VAL
54	1w	202	LEU
54	1w	209	ASP
54	1w	219	ILE
54	1w	242	VAL
54	1w	263	GLU
54	1w	278	ARG
54	1w	280	GLU
54	1w	297	GLU
54	1w	301	LYS
54	1w	315	HIS
54	1w	320	THR
54	1w	329	SER
54	1w	333	THR
54	1w	335	ILE
54	1w	348	LEU
56	1z	8	ILE
56	1z	10	GLN
3	2D	3	VAL
3	2D	12	SER
3	2D	39	LYS
3	2D	69	ARG
3	2D	99	ASP
3	2D	134	ARG
3	2D	150	LYS
3	2D	211	ARG
3	2D	212	SER
3	2D	229	VAL
3	2D	270	ILE
4	2E	7	VAL
4	2E	33	VAL
4	2E	38	THR
4	2E	52	LEU
4	2E	63	LEU
4	2E	69	LYS
4	2E	72	VAL
4	2E	75	VAL

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Mol	Chain	Res	Type
4	2E	77	ILE
4	2E	82	ARG
4	2E	87	GLU
4	2E	89	ASP
4	2E	93	VAL
4	2E	116	VAL
4	2E	170	LEU
4	2E	178	GLU
4	2E	184	VAL
4	2E	195	LEU
5	2F	12	LEU
5	2F	20	LEU
5	2F	51	THR
5	2F	70	THR
5	2F	96	ASP
5	2F	106	ARG
5	2F	132	VAL
5	2F	148	LEU
5	2F	151	SER
5	2F	153	SER
5	2F	154	VAL
5	2F	158	THR
5	2F	175	THR
5	2F	183	VAL
5	2F	192	LEU
5	2F	197	ASP
6	2G	5	VAL
6	2G	20	ILE
6	2G	21	ARG
6	2G	39	ILE
6	2G	43	LEU
6	2G	47	LYS
6	2G	51	ARG
6	2G	91	ARG
6	2G	96	ARG
6	2G	99	MET
6	2G	128	ARG
6	2G	133	LEU
6	2G	139	LEU
6	2G	145	THR
6	2G	152	LEU
6	2G	155	MET

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Mol	Chain	Res	Type
6	2G	156	ASP
6	2G	161	THR
6	2G	162	THR
6	2G	170	ARG
6	2G	172	LEU
6	2G	175	LEU
7	2H	7	LEU
7	2H	16	SER
7	2H	23	ARG
7	2H	43	VAL
7	2H	44	VAL
7	2H	45	VAL
7	2H	47	GLU
7	2H	49	VAL
7	2H	52	VAL
7	2H	87	LEU
7	2H	106	THR
7	2H	107	VAL
7	2H	116	GLU
7	2H	129	THR
7	2H	133	VAL
7	2H	134	SER
7	2H	144	VAL
8	2I	1	MET
8	2I	3	VAL
8	2I	31	LEU
8	2I	37	VAL
8	2I	38	LEU
8	2I	52	ARG
8	2I	58	LEU
8	2I	68	LEU
8	2I	78	THR
8	2I	79	ILE
8	2I	92	VAL
8	2I	110	ASP
8	2I	114	LEU
8	2I	120	ILE
8	2I	123	LEU
8	2I	127	VAL
8	2I	136	VAL
8	2I	144	VAL
9	2N	9	VAL

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Mol	Chain	Res	Type
9	2N	12	ARG
9	2N	33	LEU
9	2N	38	HIS
9	2N	62	VAL
9	2N	63	THR
9	2N	96	GLU
9	2N	138	LEU
10	2O	47	ILE
10	2O	52	VAL
10	2O	64	ARG
10	2O	66	LYS
10	2O	69	ILE
10	2O	78	ARG
11	2P	1	MET
11	2P	13	ASN
11	2P	29	LYS
11	2P	30	THR
11	2P	67	MET
11	2P	71	VAL
11	2P	95	VAL
11	2P	99	LEU
11	2P	131	SER
11	2P	133	SER
11	2P	147	LEU
11	2P	149	GLU
12	2Q	6	ARG
12	2Q	7	MET
12	2Q	14	ARG
12	2Q	17	LEU
12	2Q	60	ARG
12	2Q	75	THR
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	111	GLU
12	2Q	112	GLU
13	2R	65	LEU
13	2R	74	LYS
13	2R	113	LEU
13	2R	114	VAL
14	2S	12	PHE
14	2S	15	ARG
14	2S	36	TYR

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Mol	Chain	Res	Type
14	2S	48	LEU
14	2S	52	SER
14	2S	56	LEU
14	2S	57	LYS
14	2S	80	LEU
14	2S	85	VAL
14	2S	98	VAL
15	2T	9	LEU
15	2T	16	ARG
15	2T	28	VAL
15	2T	49	VAL
15	2T	95	ARG
15	2T	96	ARG
16	2U	90	VAL
17	2V	20	LEU
17	2V	28	GLU
17	2V	45	THR
17	2V	79	VAL
18	2W	6	ILE
18	2W	11	ARG
18	2W	17	VAL
18	2W	70	TYR
18	2W	100	THR
19	2X	45	THR
19	2X	49	VAL
19	2X	52	VAL
19	2X	54	VAL
19	2X	66	LEU
19	2X	81	VAL
20	2Y	7	VAL
20	2Y	30	VAL
20	2Y	49	VAL
20	2Y	72	VAL
20	2Y	75	ILE
20	2Y	85	VAL
20	2Y	89	PHE
20	2Y	96	ILE
20	2Y	98	VAL
21	2Z	5	LEU
21	2Z	11	GLU
21	2Z	30	ASN
21	2Z	31	ARG

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Mol	Chain	Res	Type
21	2Z	33	LEU
21	2Z	41	LEU
21	2Z	42	VAL
21	2Z	56	VAL
21	2Z	59	LEU
21	2Z	69	THR
21	2Z	80	ARG
21	2Z	84	GLU
21	2Z	86	VAL
21	2Z	91	LEU
21	2Z	94	GLU
21	2Z	102	LEU
21	2Z	111	VAL
21	2Z	126	VAL
21	2Z	129	SER
21	2Z	131	ARG
21	2Z	136	PHE
21	2Z	151	HIS
21	2Z	154	ASP
21	2Z	155	LEU
21	2Z	161	VAL
21	2Z	165	VAL
21	2Z	181	GLU
21	2Z	182	LYS
22	20	10	THR
22	20	12	ASN
22	20	43	THR
22	20	66	VAL
22	20	70	GLN
22	20	74	ARG
23	21	40	ARG
23	21	46	LEU
23	21	74	VAL
23	21	80	LEU
23	21	90	ILE
23	21	98	LEU
24	22	32	LEU
24	22	38	GLN
24	22	55	ARG
25	23	6	VAL
25	23	20	LYS
25	23	31	LEU

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Mol	Chain	Res	Type
25	23	37	LEU
26	24	3	GLU
26	24	5	ILE
26	24	10	VAL
26	24	27	THR
26	24	33	VAL
26	24	39	CYS
26	24	46	GLN
26	24	61	ARG
26	24	63	TYR
27	25	6	VAL
27	25	26	THR
27	25	33	CYS
27	25	58	LEU
28	26	6	ARG
28	26	9	LEU
28	26	19	ARG
28	26	47	THR
28	26	48	VAL
29	27	1	MET
29	27	43	THR
30	28	14	VAL
30	28	23	VAL
30	28	32	LEU
30	28	46	ARG
30	28	50	LEU
30	28	62	LEU
31	29	7	VAL
33	2b	55	PHE
33	2b	60	ASP
33	2b	80	ILE
33	2b	93	VAL
33	2b	108	ILE
33	2b	112	VAL
33	2b	121	LEU
33	2b	130	ARG
33	2b	133	LYS
33	2b	136	VAL
33	2b	140	HIS
33	2b	143	GLU
33	2b	154	LEU
33	2b	158	LEU

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Mol	Chain	Res	Type
33	2b	184	VAL
33	2b	185	ILE
33	2b	190	THR
33	2b	197	VAL
33	2b	200	ILE
33	2b	208	ILE
33	2b	212	GLN
33	2b	214	ILE
33	2b	223	ILE
33	2b	224	GLN
33	2b	235	SER
34	2c	3	ASN
34	2c	17	ASP
34	2c	33	LEU
34	2c	35	GLU
34	2c	36	ASP
34	2c	44	GLU
34	2c	68	VAL
34	2c	70	VAL
34	2c	82	GLU
34	2c	89	GLU
34	2c	91	LEU
34	2c	104	GLN
34	2c	106	VAL
34	2c	130	VAL
34	2c	172	ARG
34	2c	178	LEU
34	2c	198	VAL
35	2d	3	ARG
35	2d	17	VAL
35	2d	34	GLU
35	2d	70	ILE
35	2d	73	ARG
35	2d	80	GLU
35	2d	108	LEU
35	2d	115	ARG
35	2d	127	THR
35	2d	135	LEU
35	2d	148	VAL
35	2d	150	GLU
35	2d	155	LEU
35	2d	158	ILE

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Mol	Chain	Res	Type
35	2d	169	LYS
35	2d	175	SER
35	2d	196	LEU
35	2d	198	VAL
35	2d	200	GLU
35	2d	202	LEU
36	2e	11	ILE
36	2e	16	THR
36	2e	20	GLN
36	2e	24	ARG
36	2e	27	ARG
36	2e	31	LEU
36	2e	34	VAL
36	2e	41	VAL
36	2e	51	VAL
36	2e	55	VAL
36	2e	57	LYS
36	2e	69	VAL
36	2e	78	HIS
36	2e	79	GLU
36	2e	89	ILE
36	2e	107	ARG
36	2e	109	ILE
36	2e	120	THR
36	2e	136	MET
37	2f	14	LEU
37	2f	30	LEU
37	2f	65	VAL
37	2f	66	GLU
37	2f	67	MET
37	2f	69	GLU
37	2f	72	VAL
37	2f	75	LEU
37	2f	95	GLU
38	2g	9	VAL
38	2g	24	THR
38	2g	37	ASN
38	2g	38	LEU
38	2g	45	ASP
38	2g	51	GLN
38	2g	78	ARG
38	2g	79	ARG

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Mol	Chain	Res	Type
38	2g	91	VAL
38	2g	105	VAL
38	2g	118	VAL
38	2g	129	GLU
38	2g	135	VAL
38	2g	140	ASP
39	2h	26	VAL
39	2h	51	VAL
39	2h	52	ASP
39	2h	54	ASP
39	2h	111	ILE
39	2h	137	VAL
40	2i	7	THR
40	2i	16	ARG
40	2i	17	VAL
40	2i	38	GLN
40	2i	41	VAL
40	2i	56	LEU
40	2i	65	VAL
40	2i	81	ILE
40	2i	105	ASP
40	2i	108	VAL
40	2i	109	VAL
40	2i	121	ARG
40	2i	124	GLN
41	2j	21	GLN
41	2j	25	GLU
41	2j	30	SER
41	2j	34	VAL
41	2j	38	ILE
41	2j	81	THR
41	2j	85	LEU
41	2j	96	ILE
42	2k	33	THR
42	2k	48	ILE
42	2k	53	SER
42	2k	63	LEU
42	2k	87	THR
42	2k	96	ARG
42	2k	103	LEU
42	2k	106	LYS
43	2l	7	ILE

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Mol	Chain	Res	Type
43	2l	18	VAL
43	2l	42	THR
43	2l	55	VAL
43	2l	61	THR
43	2l	83	VAL
43	2l	86	ARG
44	2m	13	LYS
44	2m	15	VAL
44	2m	32	GLU
44	2m	34	LEU
44	2m	43	THR
44	2m	48	LEU
44	2m	83	ASP
44	2m	101	GLN
44	2m	102	ARG
44	2m	105	THR
44	2m	109	THR
45	2n	4	LYS
45	2n	26	ARG
45	2n	42	ILE
45	2n	56	VAL
46	2o	10	LYS
46	2o	22	THR
46	2o	26	GLU
46	2o	27	VAL
46	2o	58	MET
46	2o	83	GLU
47	2p	1	MET
47	2p	2	VAL
47	2p	20	VAL
47	2p	45	THR
47	2p	69	THR
47	2p	75	ARG
48	2q	9	VAL
48	2q	11	VAL
48	2q	13	ASP
48	2q	65	ILE
48	2q	79	SER
48	2q	96	GLU
49	2r	22	VAL
49	2r	35	ARG
49	2r	37	VAL

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Mol	Chain	Res	Type
49	2r	47	THR
49	2r	58	LEU
49	2r	76	LEU
49	2r	84	LYS
50	2s	4	SER
50	2s	15	LEU
50	2s	16	LEU
50	2s	23	ASN
50	2s	33	THR
50	2s	47	HIS
50	2s	58	VAL
50	2s	65	ASN
50	2s	83	HIS
51	2t	9	ASN
51	2t	41	ILE
51	2t	50	GLU
51	2t	54	LYS
51	2t	56	MET
51	2t	70	SER
51	2t	100	ILE
52	2u	10	ARG
52	2u	15	ARG
54	2w	115	THR
54	2w	125	ARG
54	2w	150	THR
54	2w	151	ASP
54	2w	156	SER
54	2w	158	VAL
54	2w	177	VAL
54	2w	179	ARG
54	2w	181	GLN
54	2w	183	VAL
54	2w	185	VAL
54	2w	192	ILE
54	2w	196	THR
54	2w	215	ASP
54	2w	222	MET
54	2w	225	SER
54	2w	237	SER
54	2w	246	THR
54	2w	251	THR
54	2w	255	SER

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Mol	Chain	Res	Type
54	2w	271	SER
54	2w	272	ARG
54	2w	286	ARG
54	2w	295	THR
54	2w	297	GLU
54	2w	300	GLU
54	2w	302	ILE
54	2w	312	VAL
54	2w	315	HIS
54	2w	317	ILE
54	2w	321	THR
54	2w	327	VAL
54	2w	333	THR
54	2w	335	ILE
54	2w	339	LEU
54	2w	351	LEU
56	2z	8	ILE
56	2z	10	GLN
56	2z	12	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (156) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	164	GLN
3	1D	166	GLN
4	1E	48	GLN
4	1E	121	ASN
5	1F	40	GLN
6	1G	58	GLN
6	1G	66	GLN
8	1I	43	ASN
8	1I	105	HIS
9	1N	131	GLN
9	1N	133	GLN
12	1Q	57	HIS
12	1Q	113	GLN
13	1R	24	GLN
13	1R	50	HIS
13	1R	71	GLN
15	1T	58	ASN
15	1T	84	GLN
16	1U	94	ASN

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Mol	Chain	Res	Type
17	1V	80	GLN
18	1W	111	HIS
19	1X	31	HIS
20	1Y	43	ASN
21	1Z	34	ASN
21	1Z	50	GLN
21	1Z	55	HIS
21	1Z	73	GLN
22	10	29	GLN
24	12	9	GLN
24	12	65	ASN
25	13	32	GLN
26	14	46	GLN
30	18	35	GLN
31	19	34	GLN
33	1b	40	HIS
33	1b	78	GLN
33	1b	113	HIS
33	1b	146	GLN
33	1b	212	GLN
34	1c	136	GLN
34	1c	181	ASN
35	1d	116	GLN
35	1d	129	ASN
36	1e	20	GLN
37	1f	94	GLN
37	1f	100	ASN
38	1g	28	ASN
38	1g	64	GLN
38	1g	109	ASN
39	1h	15	ASN
40	1i	3	GLN
40	1i	58	HIS
40	1i	124	GLN
41	1j	13	HIS
41	1j	62	HIS
41	1j	69	ASN
42	1k	93	GLN
43	1l	99	HIS
44	1m	62	ASN
45	1n	49	HIS
45	1n	52	GLN

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Mol	Chain	Res	Type
46	1o	13	GLN
46	1o	28	GLN
46	1o	50	HIS
47	1p	13	HIS
47	1p	76	GLN
48	1q	26	GLN
48	1q	29	HIS
50	1s	83	HIS
51	1t	16	HIS
51	1t	73	HIS
51	1t	90	GLN
54	1w	258	GLN
54	1w	322	HIS
3	2D	116	GLN
3	2D	164	GLN
4	2E	35	GLN
4	2E	48	GLN
5	2F	69	HIS
5	2F	75	HIS
6	2G	66	GLN
6	2G	121	ASN
6	2G	123	ASN
8	2I	74	ASN
8	2I	104	GLN
8	2I	133	HIS
9	2N	94	HIS
9	2N	131	GLN
9	2N	133	GLN
10	2O	5	GLN
10	2O	89	ASN
11	2P	35	HIS
12	2Q	113	GLN
12	2Q	141	GLN
13	2R	24	GLN
13	2R	31	HIS
13	2R	71	GLN
14	2S	38	GLN
15	2T	43	GLN
15	2T	58	ASN
15	2T	84	GLN
16	2U	94	ASN
18	2W	60	ASN

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Mol	Chain	Res	Type
18	2W	111	HIS
21	2Z	30	ASN
21	2Z	34	ASN
21	2Z	50	GLN
21	2Z	54	HIS
21	2Z	55	HIS
21	2Z	73	GLN
22	20	29	GLN
22	20	70	GLN
24	22	9	GLN
24	22	38	GLN
24	22	65	ASN
26	24	46	GLN
27	25	22	HIS
27	25	23	HIS
31	29	34	GLN
33	2b	19	HIS
33	2b	40	HIS
33	2b	204	ASN
33	2b	212	GLN
34	2c	63	ASN
34	2c	108	ASN
34	2c	123	GLN
34	2c	139	GLN
34	2c	170	GLN
34	2c	181	ASN
35	2d	77	ASN
36	2e	73	ASN
36	2e	78	HIS
37	2f	18	GLN
37	2f	73	ASN
37	2f	94	GLN
37	2f	100	ASN
38	2g	51	GLN
38	2g	64	GLN
38	2g	109	ASN
38	2g	148	ASN
40	2i	31	GLN
40	2i	38	GLN
40	2i	87	GLN
41	2j	21	GLN
44	2m	12	ASN

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Mol	Chain	Res	Type
44	2m	77	ASN
46	2o	13	GLN
46	2o	28	GLN
47	2p	13	HIS
48	2q	26	GLN
49	2r	63	GLN
50	2s	56	GLN
50	2s	69	HIS
54	2w	148	HIS
54	2w	253	GLN
56	2z	10	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	446 (15%)	27 (0%)
1	2A	2791/2915 (95%)	484 (17%)	22 (0%)
2	1B	119/121 (98%)	11 (9%)	0
2	2B	119/121 (98%)	19 (15%)	0
32	1a	1497/1521 (98%)	294 (19%)	0
32	2a	1501/1521 (98%)	315 (20%)	0
53	1v	10/24 (41%)	2 (20%)	0
53	2v	10/24 (41%)	2 (20%)	0
55	1x	73/76 (96%)	12 (16%)	0
55	1y	71/76 (93%)	23 (32%)	0
55	2x	73/76 (96%)	12 (16%)	0
55	2y	72/76 (94%)	28 (38%)	0
All	All	9200/9466 (97%)	1648 (17%)	49 (0%)

All (1648) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	13	A
1	1A	15	G
1	1A	27	G
1	1A	34	C
1	1A	45	C
1	1A	64	A
1	1A	71	A
1	1A	74	A

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Mol	Chain	Res	Type
1	1A	75	G
1	1A	84	A
1	1A	102	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	177	G
1	1A	196	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	221	A
1	1A	222	A
1	1A	229	A
1	1A	230	U
1	1A	233	A
1	1A	248	G
1	1A	264	C
1	1A	265	A
1	1A	266	G
1	1A	269	U
1	1A	271(I)	G
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	279	C
1	1A	280	C
1	1A	311	A
1	1A	324	A
1	1A	327	G
1	1A	329	G
1	1A	330	A
1	1A	352	G
1	1A	362	U
1	1A	363	G
1	1A	363(A)	A
1	1A	363(B)	G
1	1A	386	G
1	1A	396	G

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Mol	Chain	Res	Type
1	1A	407	G
1	1A	411	G
1	1A	428	A
1	1A	444	C
1	1A	446	G
1	1A	448	U
1	1A	457	A
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	509	C
1	1A	528	A
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	592	G
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(E)	G
1	1A	652(T)	C
1	1A	669	G
1	1A	686	G
1	1A	699	A
1	1A	726	G
1	1A	730	C
1	1A	740	U
1	1A	775	G
1	1A	776	G
1	1A	782	A

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Mol	Chain	Res	Type
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	811	U
1	1A	812	C
1	1A	819	A
1	1A	827	U
1	1A	828	U
1	1A	855	G
1	1A	859	G
1	1A	866	A
1	1A	878	A
1	1A	879	G
1	1A	880	G
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	894	C
1	1A	896	A
1	1A	897	C
1	1A	899	A
1	1A	907	U
1	1A	910	A
1	1A	911	A
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	975(A)	G
1	1A	983	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1022	G

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Mol	Chain	Res	Type
1	1A	1026	U
1	1A	1033	U
1	1A	1041	C
1	1A	1044	G
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1055	G
1	1A	1058	G
1	1A	1060	U
1	1A	1063	G
1	1A	1064	C
1	1A	1065	U
1	1A	1071	G
1	1A	1072	C
1	1A	1073	A
1	1A	1075	C
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U
1	1A	1079	C
1	1A	1080	C
1	1A	1081	U
1	1A	1082	U
1	1A	1083	U
1	1A	1085	A
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1091	G
1	1A	1092	C
1	1A	1094	U
1	1A	1095	A
1	1A	1096	A
1	1A	1097	U
1	1A	1099	G
1	1A	1108	U
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G
1	1A	1115	G
1	1A	1116	C

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Mol	Chain	Res	Type
1	1A	1117	G
1	1A	1129	A
1	1A	1135	C
1	1A	1136	G
1	1A	1156	A
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1218	C
1	1A	1236	G
1	1A	1241	A
1	1A	1244	G
1	1A	1248	G
1	1A	1250	G
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1321	A
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1437	C
1	1A	1445	A
1	1A	1450	G
1	1A	1455	G

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Mol	Chain	Res	Type
1	1A	1464	C
1	1A	1465	G
1	1A	1467	C
1	1A	1471	A
1	1A	1482	G
1	1A	1493	C
1	1A	1494	A
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1532	C
1	1A	1539	G
1	1A	1543	C
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1607	C
1	1A	1608	A
1	1A	1648	C
1	1A	1653	G
1	1A	1654	A
1	1A	1674	G
1	1A	1695	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1705	G
1	1A	1722	A
1	1A	1739	U
1	1A	1756	G
1	1A	1762	A
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C

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Mol	Chain	Res	Type
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1811	G
1	1A	1812	A
1	1A	1816	G
1	1A	1819	A
1	1A	1828	G
1	1A	1839	G
1	1A	1847	A
1	1A	1878	G
1	1A	1884	A
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1914	C
1	1A	1929	G
1	1A	1930	G
1	1A	1936	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A
1	1A	2043	C
1	1A	2051	A
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A
1	1A	2069	G

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Mol	Chain	Res	Type
1	1A	2099	U
1	1A	2100	G
1	1A	2101	G
1	1A	2110	G
1	1A	2111	C
1	1A	2113	U
1	1A	2116	G
1	1A	2122	U
1	1A	2123	G
1	1A	2124	G
1	1A	2126	A
1	1A	2127	G
1	1A	2129	C
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2135	A
1	1A	2138	C
1	1A	2140	C
1	1A	2141	G
1	1A	2142	C
1	1A	2144	U
1	1A	2145	C
1	1A	2146	C
1	1A	2148	G
1	1A	2149	G
1	1A	2150	U
1	1A	2151	G
1	1A	2155	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G
1	1A	2161	C
1	1A	2162	G
1	1A	2165	G
1	1A	2166	G
1	1A	2167	U
1	1A	2168	G
1	1A	2171	A
1	1A	2172	U

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Mol	Chain	Res	Type
1	1A	2173	A
1	1A	2176	A
1	1A	2178	C
1	1A	2179	C
1	1A	2182	G
1	1A	2184	G
1	1A	2188	C
1	1A	2189	U
1	1A	2190	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2225	A
1	1A	2239	G
1	1A	2269	A
1	1A	2278	A
1	1A	2283	C
1	1A	2287	A
1	1A	2305	A
1	1A	2307	G
1	1A	2308	G
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2343	C
1	1A	2347	C
1	1A	2350	C
1	1A	2383	G
1	1A	2384	G
1	1A	2385	C
1	1A	2391	G
1	1A	2393	A
1	1A	2406	U
1	1A	2407	G
1	1A	2410	G
1	1A	2422	A
1	1A	2423	U
1	1A	2424	C
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A

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Mol	Chain	Res	Type
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2460	U
1	1A	2469	A
1	1A	2476	A
1	1A	2478	A
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2520	C
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2564	A
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2576	G
1	1A	2601	C
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2615	U
1	1A	2629	A
1	1A	2630	G
1	1A	2634	G
1	1A	2654	A
1	1A	2682	U
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2758	A

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Mol	Chain	Res	Type
1	1A	2764	A
1	1A	2765	A
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2803	C
1	1A	2807	G
1	1A	2820	A
1	1A	2821	A
1	1A	2835	A
1	1A	2872	G
1	1A	2873	A
1	1A	2892	A
1	1A	2893	G
1	1A	2894	G
1	1A	2895	U
2	1B	2	C
2	1B	13	A
2	1B	45	A
2	1B	50	G
2	1B	56	G
2	1B	63	G
2	1B	66	A
2	1B	73	A
2	1B	93	G
2	1B	106	G
2	1B	110	G
32	1a	5	U
32	1a	7	G
32	1a	9	G
32	1a	31	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	65	U
32	1a	76	C
32	1a	77	G
32	1a	78	G

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Mol	Chain	Res	Type
32	1a	79	G
32	1a	91	C
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	122	G
32	1a	129	U
32	1a	131	C
32	1a	144	G
32	1a	156	G
32	1a	157	G
32	1a	158	G
32	1a	161	A
32	1a	162	A
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	185	A
32	1a	189(E)	U
32	1a	189(G)	G
32	1a	189(H)	G
32	1a	189(K)	U
32	1a	195	A
32	1a	197	A
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	223	U
32	1a	227	G
32	1a	231	G
32	1a	246	A
32	1a	247	G
32	1a	251	G
32	1a	262	A
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	306	G
32	1a	321	A
32	1a	328	C
32	1a	332	G

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Mol	Chain	Res	Type
32	1a	341	C
32	1a	343	U
32	1a	344	A
32	1a	345	C
32	1a	347	G
32	1a	348	G
32	1a	349	A
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	388	G
32	1a	392	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	410	G
32	1a	411	A
32	1a	412	A
32	1a	413	G
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	471	G
32	1a	477	A
32	1a	485	G
32	1a	487	A
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	531	U

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Mol	Chain	Res	Type
32	1a	532	A
32	1a	545	C
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	618	C
32	1a	630	G
32	1a	633	G
32	1a	650	G
32	1a	653	A
32	1a	665	A
32	1a	671	G
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	702	A
32	1a	723	U
32	1a	731	G
32	1a	734	G
32	1a	749	C
32	1a	753	A
32	1a	755	G
32	1a	760	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	836	G
32	1a	839	U
32	1a	840	C
32	1a	841	U

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Mol	Chain	Res	Type
32	1a	848	C
32	1a	851	G
32	1a	859	A
32	1a	870	U
32	1a	872	A
32	1a	902	G
32	1a	913	A
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	932	C
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	988	G
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	994	A
32	1a	996	A
32	1a	997	U
32	1a	1000	U
32	1a	1001(A)	G
32	1a	1002	G
32	1a	1003	G
32	1a	1004	A
32	1a	1006	C
32	1a	1011	G
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1028	C

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Mol	Chain	Res	Type
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(B)	C
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1035	A
32	1a	1036	G
32	1a	1037	C
32	1a	1040	U
32	1a	1043	C
32	1a	1044	A
32	1a	1045	C
32	1a	1050	G
32	1a	1051	C
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1067	A
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1113	C
32	1a	1123	A
32	1a	1125	U
32	1a	1126	U
32	1a	1127	G
32	1a	1131	G
32	1a	1134	G
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1141	C
32	1a	1146	A
32	1a	1151	A
32	1a	1152	A
32	1a	1157	A
32	1a	1159	U
32	1a	1160	G

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Mol	Chain	Res	Type
32	1a	1166	G
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1212	U
32	1a	1213	A
32	1a	1214	C
32	1a	1215	G
32	1a	1227	A
32	1a	1228	C
32	1a	1238	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1261	A
32	1a	1262	C
32	1a	1264	C
32	1a	1268	A
32	1a	1270	C
32	1a	1275	A
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1290	G
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1305	G
32	1a	1314	C
32	1a	1316	G
32	1a	1320	C
32	1a	1322	C
32	1a	1329	A
32	1a	1330	U
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G

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Mol	Chain	Res	Type
32	1a	1353	G
32	1a	1360	A
32	1a	1363	C
32	1a	1363(A)	A
32	1a	1368	G
32	1a	1370	G
32	1a	1379	G
32	1a	1381	U
32	1a	1397	C
32	1a	1402	4OC
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1442(B)	A
32	1a	1447	A
32	1a	1452	C
32	1a	1487	G
32	1a	1492	A
32	1a	1493	A
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1517	G
32	1a	1519	MA6
32	1a	1529	G
32	1a	1530	G
53	1v	11	U
53	1v	21	A
55	1x	9	A
55	1x	10	G
55	1x	16	U
55	1x	18	G
55	1x	20	U
55	1x	21	A
55	1x	42	C
55	1x	47	U
55	1x	48	C
55	1x	53	G
55	1x	62	C
55	1x	76	A

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Mol	Chain	Res	Type
55	1y	2	C
55	1y	9	A
55	1y	11	C
55	1y	13	C
55	1y	14	A
55	1y	15	G
55	1y	19	G
55	1y	20	U
55	1y	22	G
55	1y	24	G
55	1y	31	A
55	1y	36	A
55	1y	37	MIA
55	1y	44	G
55	1y	45	U
55	1y	46	G7M
55	1y	48	C
55	1y	49	C
55	1y	51	U
55	1y	53	G
55	1y	59	U
55	1y	68	C
55	1y	71	G
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	36	G
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	94	C
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	125	G
1	2A	140	G
1	2A	141	A
1	2A	154(A)	C

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Mol	Chain	Res	Type
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	233	A
1	2A	248	G
1	2A	249	C
1	2A	265	A
1	2A	266	G
1	2A	271(J)	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G
1	2A	272(J)	C
1	2A	274	G
1	2A	277	C
1	2A	278	A
1	2A	292	C
1	2A	294	A
1	2A	311	A
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	332	A
1	2A	338	G
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	371	A

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Mol	Chain	Res	Type
1	2A	386	G
1	2A	388	G
1	2A	396	G
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	435	C
1	2A	444	C
1	2A	455	C
1	2A	457	A
1	2A	481	G
1	2A	489	G
1	2A	504	U
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	517	C
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	551	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	588	U
1	2A	592	G
1	2A	599	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	631	A
1	2A	637	A
1	2A	644	A
1	2A	645	C
1	2A	652(B)	A

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Mol	Chain	Res	Type
1	2A	656	G
1	2A	669	G
1	2A	686	G
1	2A	699	A
1	2A	717	G
1	2A	730	C
1	2A	740	U
1	2A	752	A
1	2A	753	C
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	819	A
1	2A	827	U
1	2A	828	U
1	2A	857	C
1	2A	859	G
1	2A	867	C
1	2A	869	G
1	2A	873	G
1	2A	874	G
1	2A	878	A
1	2A	879	G
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	894	C
1	2A	895	U
1	2A	896	A
1	2A	897	C
1	2A	899	A

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Mol	Chain	Res	Type
1	2A	900	A
1	2A	902	C
1	2A	907	U
1	2A	910	A
1	2A	915	C
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	959	A
1	2A	961	C
1	2A	968	G
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	996	A
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1025	G
1	2A	1033	U
1	2A	1038	C
1	2A	1041	C
1	2A	1043	C
1	2A	1116	C
1	2A	1117	G
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1141	U
1	2A	1142	U
1	2A	1142(A)	A
1	2A	1156	A
1	2A	1171	G
1	2A	1186	G
1	2A	1206	G
1	2A	1210	A

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Mol	Chain	Res	Type
1	2A	1211	U
1	2A	1220	A
1	2A	1237	A
1	2A	1250	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	1314	C
1	2A	1319	G
1	2A	1321	A
1	2A	1333	C
1	2A	1342	A
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1370	C
1	2A	1371	G
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1395	A
1	2A	1402	C
1	2A	1413	G
1	2A	1414	G
1	2A	1416	G
1	2A	1417	C
1	2A	1419	A
1	2A	1427	A
1	2A	1428	C
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A

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Mol	Chain	Res	Type
1	2A	1478	G
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1497	U
1	2A	1508	A
1	2A	1509(A)	A
1	2A	1509(B)	A
1	2A	1530	C
1	2A	1531	C
1	2A	1533	G
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1588	C
1	2A	1589	C
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1618	A
1	2A	1632	A
1	2A	1640	C
1	2A	1648	C
1	2A	1653	G
1	2A	1654	A
1	2A	1664	A
1	2A	1674	G
1	2A	1681	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1746	G
1	2A	1756	G

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Mol	Chain	Res	Type
1	2A	1758	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1769	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1811	G
1	2A	1812	A
1	2A	1816	G
1	2A	1828	G
1	2A	1829	A
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1927	A
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1964	G
1	2A	1965	C
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1996	C

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Mol	Chain	Res	Type
1	2A	1997	G
1	2A	2021	C
1	2A	2023	G
1	2A	2027	G
1	2A	2030	A
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2070	G
1	2A	2093	G
1	2A	2100	G
1	2A	2111	C
1	2A	2114	A
1	2A	2115	G
1	2A	2116	G
1	2A	2118	U
1	2A	2119	A
1	2A	2122	U
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2130	U
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2138	C
1	2A	2142	C
1	2A	2146	C
1	2A	2148	G
1	2A	2149	G
1	2A	2150	U
1	2A	2153	G
1	2A	2154	G
1	2A	2155	G

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Mol	Chain	Res	Type
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2160	G
1	2A	2161	C
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2172	U
1	2A	2173	A
1	2A	2176	A
1	2A	2183	C
1	2A	2185	C
1	2A	2188	C
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2232	U
1	2A	2235	G
1	2A	2238	G
1	2A	2239	G
1	2A	2275	C
1	2A	2278	A
1	2A	2283	C
1	2A	2286	A
1	2A	2287	A
1	2A	2301	C
1	2A	2305	A
1	2A	2308	G
1	2A	2311	A
1	2A	2312	U
1	2A	2319	G
1	2A	2320	A
1	2A	2322	A
1	2A	2325	G
1	2A	2333	A

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Mol	Chain	Res	Type
1	2A	2334	G
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2377	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2400	G
1	2A	2406	U
1	2A	2422	A
1	2A	2425	A
1	2A	2426	A
1	2A	2429	G
1	2A	2430	A
1	2A	2431	U
1	2A	2432	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2469	A
1	2A	2473	U
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2480	C
1	2A	2487	G
1	2A	2490	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2535	G
1	2A	2549	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G

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Mol	Chain	Res	Type
1	2A	2573	C
1	2A	2574	G
1	2A	2582	G
1	2A	2585	U
1	2A	2586	C
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2615	U
1	2A	2629	A
1	2A	2630	G
1	2A	2654	A
1	2A	2679	A
1	2A	2689	U
1	2A	2690	C
1	2A	2702	U
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2718	G
1	2A	2726	U
1	2A	2733	A
1	2A	2748	A
1	2A	2757	A
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2802	G
1	2A	2807	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2839	G
1	2A	2872	G
1	2A	2879	C
1	2A	2880	C
1	2A	2894	G

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Mol	Chain	Res	Type
1	2A	2895	U
1	2A	2896	C
1	2A	2897	U
2	2B	2	C
2	2B	7	G
2	2B	13	A
2	2B	24	G
2	2B	45	A
2	2B	56	G
2	2B	63	G
2	2B	64	C
2	2B	65	C
2	2B	66	A
2	2B	67	G
2	2B	73	A
2	2B	84	C
2	2B	89	G
2	2B	106	G
2	2B	110	G
2	2B	112	U
2	2B	118	G
2	2B	119	G
32	2a	8	A
32	2a	9	G
32	2a	22	G
32	2a	31	G
32	2a	32	A
32	2a	39	G
32	2a	41	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	52	G
32	2a	54	C
32	2a	73	G
32	2a	79	G
32	2a	80	G
32	2a	89	C
32	2a	101	A
32	2a	115	G
32	2a	116	A

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Mol	Chain	Res	Type
32	2a	120	A
32	2a	121	C
32	2a	131	C
32	2a	142	G
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	180	U
32	2a	182	U
32	2a	189	G
32	2a	189(E)	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	226	G
32	2a	247	G
32	2a	251	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	301	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G

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Mol	Chain	Res	Type
32	2a	422	C
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	434	U
32	2a	439	A
32	2a	441	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	479	C
32	2a	482	A
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	521	G
32	2a	532	A
32	2a	536	C
32	2a	547	A
32	2a	559	A
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	618	C
32	2a	630	G
32	2a	639	G
32	2a	650	G
32	2a	653	A
32	2a	662	G
32	2a	665	A

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Mol	Chain	Res	Type
32	2a	687	A
32	2a	688	G
32	2a	693	G
32	2a	701	C
32	2a	723	U
32	2a	731	G
32	2a	753	A
32	2a	755	G
32	2a	773	G
32	2a	774	G
32	2a	778	G
32	2a	793	U
32	2a	794	A
32	2a	796	C
32	2a	799	G
32	2a	815	A
32	2a	817	C
32	2a	819	A
32	2a	821	G
32	2a	828	A
32	2a	836	G
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	859	A
32	2a	870	U
32	2a	873	A
32	2a	874	G
32	2a	902	G
32	2a	914	A
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	932	C
32	2a	934	C
32	2a	935	A
32	2a	941	G
32	2a	942	G
32	2a	954	G
32	2a	960	U
32	2a	961	U
32	2a	966	M2G

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Mol	Chain	Res	Type
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	978	A
32	2a	982	U
32	2a	987	G
32	2a	988	G
32	2a	992	U
32	2a	993	G
32	2a	999	C
32	2a	1001(A)	G
32	2a	1002	G
32	2a	1003	G
32	2a	1004	A
32	2a	1005	A
32	2a	1007	C
32	2a	1008	C
32	2a	1011	G
32	2a	1020	U
32	2a	1021	G
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	1030	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1030(C)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1033	G
32	2a	1035	A
32	2a	1036	G
32	2a	1037	C
32	2a	1038	C
32	2a	1040	U

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Mol	Chain	Res	Type
32	2a	1041	A
32	2a	1043	C
32	2a	1044	A
32	2a	1053	G
32	2a	1064	G
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1081	G
32	2a	1094	G
32	2a	1095	U
32	2a	1096	C
32	2a	1099	G
32	2a	1101	A
32	2a	1104	G
32	2a	1113	C
32	2a	1117	G
32	2a	1121	U
32	2a	1123	A
32	2a	1126	U
32	2a	1127	G
32	2a	1128	C
32	2a	1129	C
32	2a	1130	A
32	2a	1135	U
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1147	C
32	2a	1151	A
32	2a	1152	A
32	2a	1159	U
32	2a	1172	C
32	2a	1175	G
32	2a	1176	A
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1187	G

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Mol	Chain	Res	Type
32	2a	1188	A
32	2a	1193	G
32	2a	1195	C
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1211	U
32	2a	1213	A
32	2a	1214	C
32	2a	1220	G
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1263	C
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1274	G
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1282	C
32	2a	1285	A
32	2a	1287	A
32	2a	1293	G
32	2a	1294	G
32	2a	1298	C
32	2a	1299	A
32	2a	1300	G
32	2a	1301	U
32	2a	1302	U
32	2a	1305	G
32	2a	1307	U
32	2a	1309	G
32	2a	1312	G
32	2a	1319	A
32	2a	1340	A
32	2a	1346	A

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Mol	Chain	Res	Type
32	2a	1347	G
32	2a	1353	G
32	2a	1357	A
32	2a	1358	U
32	2a	1363	C
32	2a	1363(A)	A
32	2a	1364	U
32	2a	1370	G
32	2a	1377	A
32	2a	1379	G
32	2a	1381	U
32	2a	1396	A
32	2a	1397	C
32	2a	1398	A
32	2a	1400	5MC
32	2a	1402	4OC
32	2a	1412	C
32	2a	1419	G
32	2a	1429	C
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G
32	2a	1487	G
32	2a	1491	G
32	2a	1492	A
32	2a	1493	A
32	2a	1494	G
32	2a	1497	G
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1519	MA6
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A

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Mol	Chain	Res	Type
32	2a	1532	U
53	2v	11	U
53	2v	14	A
55	2x	9	A
55	2x	17	C
55	2x	18	G
55	2x	19	G
55	2x	20	U
55	2x	21	A
55	2x	28	G
55	2x	29	G
55	2x	47	U
55	2x	48	C
55	2x	53	G
55	2x	76	A
55	2y	2	C
55	2y	6	G
55	2y	8	4SU
55	2y	11	C
55	2y	13	C
55	2y	14	A
55	2y	15	G
55	2y	20	U
55	2y	21	A
55	2y	25	C
55	2y	27	G
55	2y	31	A
55	2y	33	U
55	2y	41	C
55	2y	42	C
55	2y	44	G
55	2y	45	U
55	2y	46	G7M
55	2y	47	U
55	2y	48	C
55	2y	49	C
55	2y	52	G
55	2y	54	5MU
55	2y	58	A
55	2y	59	U
55	2y	60	U
55	2y	69	G

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Mol	Chain	Res	Type
55	2y	73	A

All (49) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	199	A
1	1A	266	G
1	1A	278	A
1	1A	348	G
1	1A	548	A
1	1A	746	A
1	1A	764	A
1	1A	774	A
1	1A	827	U
1	1A	887	A
1	1A	895	U
1	1A	993	G
1	1A	1065	U
1	1A	1107	G
1	1A	1174	A
1	1A	1176	G
1	1A	1379	A
1	1A	1442	G
1	1A	1508	A
1	1A	1653	G
1	1A	2134	A
1	1A	2183	C
1	1A	2406	U
1	1A	2422	A
1	1A	2439	A
1	1A	2689	U
1	2A	34	C
1	2A	228	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	752	A
1	2A	774	A
1	2A	856	C
1	2A	888	C

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Mol	Chain	Res	Type
1	2A	1210	A
1	2A	1379	A
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2126	A
1	2A	2406	U
1	2A	2430	A
1	2A	2438	U
1	2A	2473	U
1	2A	2689	U
1	2A	2756	U

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

78 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	$\#\|Z\| > 2$
43	0TD	1l	92	43	8,9,10	4.24	1 (12%)	6,11,13	13.49	1 (16%)
1	OMG	2A	2251	55,1	23,26,27	1.22	3 (13%)	32,38,41	1.97	6 (18%)
55	4SU	1y	8	55	18,21,22	1.78	4 (22%)	25,30,33	2.20	5 (20%)
55	MIA	2x	37	55	28,31,32	2.37	6 (21%)	38,44,47	2.73	14 (36%)
1	5MC	2A	1962	57,1	19,22,23	1.62	3 (15%)	26,32,35	1.07	2 (7%)
1	OMC	2A	1920	1	19,22,23	0.79	0	25,31,34	0.90	0
32	PSU	2a	516	57,32	18,21,22	1.35	2 (11%)	21,30,33	1.90	4 (19%)
32	MA6	1a	1519	32	23,26,27	0.44	0	33,38,41	2.01	10 (30%)
55	G7M	2y	46	55	23,26,27	1.54	4 (17%)	34,39,42	1.79	5 (14%)
32	2MG	2a	1207	32	23,26,27	1.22	2 (8%)	33,38,41	2.21	8 (24%)
1	5MU	2A	1939	57,1	19,22,23	1.42	4 (21%)	27,32,35	2.30	6 (22%)
1	OMU	2A	2552	57,1	19,22,23	1.28	3 (15%)	25,31,34	1.78	5 (20%)
32	5MC	1a	1400	32	19,22,23	1.69	3 (15%)	26,32,35	1.13	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	OMU	1A	2552	57,1	19,22,23	1.21	3 (15%)	25,31,34	1.92	5 (20%)
55	PSU	1x	32	55	18,21,22	1.35	2 (11%)	21,30,33	2.03	3 (14%)
55	4SU	2x	8	55	18,21,22	1.83	5 (27%)	25,30,33	1.73	5 (20%)
55	PSU	1y	39	55	18,21,22	1.42	2 (11%)	21,30,33	1.99	3 (14%)
32	G7M	1a	527	32	23,26,27	1.54	3 (13%)	34,39,42	1.79	5 (14%)
32	4OC	2a	1402	57,32	20,23,24	0.80	0	25,32,35	0.99	2 (8%)
55	G7M	1y	46	55	23,26,27	1.58	4 (17%)	34,39,42	1.84	5 (14%)
32	MA6	2a	1519	32	23,26,27	0.43	0	33,38,41	2.09	9 (27%)
54	MEQ	2w	230	54	8,9,10	0.69	0	5,10,12	0.67	0
1	5MU	1A	1939	57,1	19,22,23	1.38	5 (26%)	27,32,35	2.26	6 (22%)
55	PSU	2x	32	55	18,21,22	1.38	2 (11%)	21,30,33	2.02	4 (19%)
55	PSU	2y	32	55	18,21,22	1.34	2 (11%)	21,30,33	1.95	3 (14%)
1	PSU	2A	2605	1	18,21,22	1.32	3 (16%)	21,30,33	2.18	5 (23%)
32	2MG	1a	1207	32	23,26,27	1.25	4 (17%)	33,38,41	2.10	7 (21%)
55	PSU	2x	39	55	18,21,22	1.42	2 (11%)	21,30,33	1.70	4 (19%)
32	UR3	2a	1498	32	19,22,23	0.98	0	26,32,35	1.69	2 (7%)
1	5MU	1A	1915	54,57,1	19,22,23	1.46	6 (31%)	27,32,35	2.31	6 (22%)
1	PSU	1A	1917	1	18,21,22	1.44	2 (11%)	21,30,33	2.05	3 (14%)
32	5MC	2a	1407	32	19,22,23	1.52	2 (10%)	26,32,35	1.05	3 (11%)
55	PSU	1y	32	55	18,21,22	1.38	2 (11%)	21,30,33	1.95	4 (19%)
55	G7M	1x	46	55	23,26,27	1.53	3 (13%)	34,39,42	1.71	5 (14%)
1	2MA	1A	2503	57,1	22,25,26	1.42	5 (22%)	32,37,40	2.39	9 (28%)
32	5MC	2a	1404	32	19,22,23	1.76	3 (15%)	26,32,35	1.24	3 (11%)
1	OMG	1A	2251	55,57,1	23,26,27	1.21	3 (13%)	32,38,41	2.04	6 (18%)
32	MA6	2a	1518	32	23,26,27	0.41	0	33,38,41	2.03	8 (24%)
55	4SU	1x	8	55	18,21,22	1.71	4 (22%)	25,30,33	1.69	4 (16%)
55	5MU	2x	54	55	19,22,23	1.38	5 (26%)	27,32,35	2.08	8 (29%)
55	PSU	2x	55	55	18,21,22	1.38	2 (11%)	21,30,33	2.05	4 (19%)
32	G7M	2a	527	32	23,26,27	1.51	3 (13%)	34,39,42	1.67	5 (14%)
32	5MC	2a	967	32	19,22,23	1.73	3 (15%)	26,32,35	1.18	2 (7%)
55	G7M	2x	46	55	23,26,27	1.55	3 (13%)	34,39,42	1.81	5 (14%)
55	MIA	1x	37	55	28,31,32	2.49	7 (25%)	38,44,47	2.53	13 (34%)
55	PSU	1x	55	55	18,21,22	1.29	2 (11%)	21,30,33	1.93	4 (19%)
55	5MU	2y	54	55	19,22,23	1.49	4 (21%)	27,32,35	1.97	7 (25%)
55	PSU	2y	55	55	18,21,22	1.38	2 (11%)	21,30,33	1.97	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	PSU	2A	1917	1	18,21,22	1.36	2 (11%)	21,30,33	2.03	3 (14%)
55	MIA	2y	37	55	28,31,32	2.33	6 (21%)	38,44,47	2.91	15 (39%)
1	PSU	2A	1911	1	18,21,22	1.40	2 (11%)	21,30,33	2.04	4 (19%)
32	M2G	1a	966	32	24,27,28	1.28	4 (16%)	33,40,43	1.91	6 (18%)
32	5MC	1a	1407	32	19,22,23	1.50	2 (10%)	26,32,35	1.05	2 (7%)
54	MEQ	1w	230	54	8,9,10	0.78	0	5,10,12	1.34	1 (20%)
1	PSU	1A	1911	1	18,21,22	1.40	2 (11%)	21,30,33	2.13	4 (19%)
32	5MC	1a	967	32	19,22,23	1.72	3 (15%)	26,32,35	1.14	3 (11%)
1	5MC	1A	1942	1	19,22,23	1.44	3 (15%)	26,32,35	1.19	2 (7%)
32	M2G	2a	966	32	24,27,28	1.27	4 (16%)	33,40,43	1.92	6 (18%)
32	5MC	1a	1404	32	19,22,23	1.61	3 (15%)	26,32,35	1.07	2 (7%)
32	UR3	1a	1498	57,32	19,22,23	1.05	2 (10%)	26,32,35	1.65	3 (11%)
1	5MU	2A	1915	57,1	19,22,23	1.50	6 (31%)	27,32,35	2.14	6 (22%)
1	PSU	1A	2605	57,1	18,21,22	1.39	2 (11%)	21,30,33	2.19	3 (14%)
55	PSU	2y	39	55	18,21,22	1.35	2 (11%)	21,30,33	1.94	3 (14%)
43	0TD	2l	92	43	8,9,10	4.66	2 (25%)	6,11,13	1.61	1 (16%)
1	5MC	2A	1942	1	19,22,23	1.53	3 (15%)	26,32,35	1.12	2 (7%)
1	2MA	2A	2503	57,1	22,25,26	1.47	4 (18%)	32,37,40	2.35	7 (21%)
32	4OC	1a	1402	57,32	20,23,24	0.76	0	25,32,35	1.04	2 (8%)
55	4SU	2y	8	55	18,21,22	1.70	3 (16%)	25,30,33	2.34	5 (20%)
55	5MU	1y	54	55	19,22,23	1.46	5 (26%)	27,32,35	2.02	7 (25%)
55	PSU	1y	55	55	18,21,22	1.36	2 (11%)	21,30,33	2.05	3 (14%)
32	PSU	1a	516	57,32	18,21,22	1.42	2 (11%)	21,30,33	2.04	5 (23%)
32	MA6	1a	1518	32	23,26,27	0.37	0	33,38,41	2.07	9 (27%)
55	5MU	1x	54	55	19,22,23	1.42	4 (21%)	27,32,35	1.88	6 (22%)
32	5MC	2a	1400	32	19,22,23	1.59	3 (15%)	26,32,35	1.16	2 (7%)
1	OMC	1A	1920	1	19,22,23	0.80	0	25,31,34	0.93	1 (4%)
1	5MC	1A	1962	57,1	19,22,23	1.44	3 (15%)	26,32,35	1.16	4 (15%)
55	PSU	1x	39	55	18,21,22	1.42	3 (16%)	21,30,33	1.78	3 (14%)
55	MIA	1y	37	55	28,31,32	2.24	6 (21%)	38,44,47	2.69	13 (34%)

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
43	0TD	1l	92	43	-	5/7/12/14	-
1	OMG	2A	2251	55,1	-	0/9/27/28	0/3/3/3
55	4SU	1y	8	55	-	1/7/25/26	0/2/2/2
55	MIA	2x	37	55	-	6/15/33/34	0/3/3/3
1	5MC	2A	1962	57,1	-	1/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
32	PSU	2a	516	57,32	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
55	G7M	2y	46	55	-	2/7/25/26	0/3/3/3
32	2MG	2a	1207	32	-	2/9/27/28	0/3/3/3
1	5MU	2A	1939	57,1	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	57,1	-	0/9/27/28	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	57,1	-	0/9/27/28	0/2/2/2
55	PSU	1x	32	55	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
55	PSU	1y	39	55	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	32	-	3/7/25/26	0/3/3/3
32	4OC	2a	1402	57,32	-	2/9/29/30	0/2/2/2
55	G7M	1y	46	55	-	3/7/25/26	0/3/3/3
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
54	MEQ	2w	230	54	-	2/8/9/11	-
1	5MU	1A	1939	57,1	-	0/7/25/26	0/2/2/2
55	PSU	2x	32	55	-	0/7/25/26	0/2/2/2
55	PSU	2y	32	55	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
55	PSU	2x	39	55	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	54,57,1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
55	PSU	1y	32	55	-	0/7/25/26	0/2/2/2
55	G7M	1x	46	55	-	3/7/25/26	0/3/3/3
1	2MA	1A	2503	57,1	-	0/7/25/26	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	55,57,1	-	0/9/27/28	0/3/3/3
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	G7M	2a	527	32	-	1/7/25/26	0/3/3/3
32	5MC	2a	967	32	-	1/7/25/26	0/2/2/2
55	G7M	2x	46	55	-	3/7/25/26	0/3/3/3
55	MIA	1x	37	55	-	5/15/33/34	0/3/3/3
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
55	5MU	2y	54	55	-	2/7/25/26	0/2/2/2
55	PSU	2y	55	55	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
55	MIA	2y	37	55	-	2/15/33/34	0/3/3/3
1	PSU	2A	1911	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
54	MEQ	1w	230	54	-	4/8/9/11	-
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	57,32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	57,1	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	57,1	-	0/7/25/26	0/2/2/2
55	PSU	2y	39	55	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	4/7/12/14	-
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	57,1	-	2/7/25/26	0/3/3/3
32	4OC	1a	1402	57,32	-	2/9/29/30	0/2/2/2
55	4SU	2y	8	55	-	0/7/25/26	0/2/2/2
55	5MU	1y	54	55	-	0/7/25/26	0/2/2/2
55	PSU	1y	55	55	-	2/7/25/26	0/2/2/2
32	PSU	1a	516	57,32	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
55	5MU	1x	54	55	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	2/7/25/26	0/2/2/2
1	OMC	1A	1920	1	-	0/9/27/28	0/2/2/2
1	5MC	1A	1962	57,1	-	0/7/25/26	0/2/2/2
55	PSU	1x	39	55	-	0/7/25/26	0/2/2/2
55	MIA	1y	37	55	-	6/15/33/34	0/3/3/3

All (216) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.60	1.69	1.82
43	1l	92	0TD	CB-SB	-11.52	1.70	1.82
55	1x	37	MIA	C2-S10	-8.24	1.68	1.75
55	1x	37	MIA	C13-C14	7.08	1.53	1.32
55	2x	37	MIA	C13-C14	6.96	1.53	1.32
55	2x	37	MIA	C2-S10	-6.92	1.70	1.75
55	2y	37	MIA	C13-C14	6.83	1.52	1.32
55	1y	37	MIA	C13-C14	6.82	1.52	1.32
55	2y	37	MIA	C2-S10	-6.74	1.70	1.75
32	2a	967	5MC	C5-C4	6.35	1.48	1.44
32	2a	1404	5MC	C5-C4	6.32	1.48	1.44
32	1a	967	5MC	C5-C4	6.20	1.48	1.44
32	1a	1400	5MC	C5-C4	6.18	1.48	1.44
32	2a	1400	5MC	C5-C4	5.90	1.48	1.44
1	2A	1962	5MC	C5-C4	5.89	1.48	1.44
32	1a	1404	5MC	C5-C4	5.80	1.48	1.44
55	1y	37	MIA	C2-S10	-5.57	1.71	1.75
1	2A	1942	5MC	C5-C4	5.32	1.48	1.44
32	2a	1407	5MC	C5-C4	5.29	1.48	1.44
32	1a	1407	5MC	C5-C4	5.18	1.48	1.44
55	2x	37	MIA	C5-C4	5.00	1.48	1.39
1	1A	1942	5MC	C5-C4	4.93	1.47	1.44
55	1x	46	G7M	C5-N7	-4.89	1.33	1.39
55	1y	37	MIA	C5-C4	4.86	1.47	1.39
55	2x	46	G7M	C5-N7	-4.85	1.33	1.39
32	1a	527	G7M	C5-N7	-4.84	1.33	1.39
1	1A	1962	5MC	C5-C4	4.83	1.47	1.44
55	2y	8	4SU	C4-S4	-4.82	1.60	1.68
55	1y	46	G7M	C5-N7	-4.82	1.33	1.39
55	1y	8	4SU	C4-S4	-4.78	1.60	1.68
55	2y	37	MIA	C5-C4	4.70	1.47	1.39
55	2x	8	4SU	C4-S4	-4.65	1.60	1.68
32	2a	527	G7M	C5-N7	-4.53	1.34	1.39
55	2y	46	G7M	C5-N7	-4.52	1.34	1.39
55	1x	37	MIA	C5-C4	4.51	1.47	1.39
1	2A	2503	2MA	C5-C4	4.43	1.47	1.39
55	1x	8	4SU	C4-S4	-4.28	1.61	1.68
55	2x	55	PSU	C6-C5	4.07	1.39	1.35
55	1y	32	PSU	C6-C5	3.94	1.39	1.35
1	1A	2503	2MA	C5-C4	3.92	1.46	1.39
1	1A	1917	PSU	C6-C5	3.89	1.39	1.35
55	1y	55	PSU	C6-C5	3.87	1.39	1.35
1	2A	1911	PSU	C6-C5	3.84	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2x	39	PSU	C6-C5	3.82	1.39	1.35
55	1y	39	PSU	C6-C5	3.80	1.39	1.35
1	1A	1911	PSU	C6-C5	3.78	1.39	1.35
55	2y	55	PSU	C6-C5	3.77	1.39	1.35
32	1a	516	PSU	C6-C5	3.72	1.39	1.35
55	1x	39	PSU	C6-C5	3.61	1.39	1.35
55	2y	32	PSU	C6-C5	3.61	1.39	1.35
55	2y	46	G7M	C5-C4	3.57	1.47	1.38
55	2y	39	PSU	C6-C5	3.57	1.39	1.35
55	2x	32	PSU	C6-C5	3.57	1.39	1.35
55	1y	46	G7M	C5-C4	3.52	1.47	1.38
1	1A	2605	PSU	C6-C5	3.41	1.39	1.35
55	2x	46	G7M	C5-C4	3.41	1.46	1.38
1	2A	1917	PSU	C6-C5	3.40	1.39	1.35
55	2x	8	4SU	C4-N3	-3.35	1.34	1.37
55	1x	8	4SU	C4-N3	-3.31	1.34	1.37
32	2a	527	G7M	C5-C4	3.29	1.46	1.38
32	1a	527	G7M	C5-C4	3.26	1.46	1.38
1	1A	2251	OMG	C5-C4	3.22	1.47	1.38
32	2a	1404	5MC	C6-C5	3.22	1.39	1.34
32	2a	966	M2G	C5-C4	3.22	1.47	1.38
32	2a	516	PSU	C6-C5	3.20	1.38	1.35
55	1x	46	G7M	C5-C4	3.18	1.46	1.38
32	2a	1207	2MG	C5-C4	3.17	1.47	1.38
55	2y	54	5MU	C6-C5	3.14	1.39	1.34
55	1x	32	PSU	C6-C5	3.13	1.38	1.35
55	1x	54	5MU	C6-C5	3.11	1.39	1.34
1	2A	2251	OMG	C5-C4	3.11	1.47	1.38
1	2A	2605	PSU	C6-C5	3.05	1.38	1.35
1	2A	2552	OMU	C4-N3	-3.05	1.33	1.38
32	1a	1207	2MG	C5-C4	3.05	1.47	1.38
55	1y	8	4SU	C4-N3	-3.03	1.34	1.37
32	1a	967	5MC	C6-C5	3.03	1.39	1.34
1	2A	1915	5MU	C6-C5	3.02	1.39	1.34
32	1a	966	M2G	C5-C4	3.02	1.47	1.38
32	2a	1407	5MC	C6-C5	3.00	1.39	1.34
1	1A	1915	5MU	C6-C5	2.99	1.39	1.34
55	1x	55	PSU	C6-C5	2.99	1.38	1.35
1	2A	1939	5MU	C6-C5	2.97	1.39	1.34
32	1a	966	M2G	C2-N2	2.97	1.40	1.35
1	1A	1915	5MU	C4-N3	-2.97	1.33	1.38
55	2x	8	4SU	C5-C4	-2.93	1.39	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	1939	5MU	C4-N3	-2.92	1.33	1.38
1	2A	1942	5MC	C6-C5	2.91	1.39	1.34
55	1y	37	MIA	C5-C6	2.91	1.48	1.41
55	1x	37	MIA	C5-C6	2.89	1.48	1.41
1	2A	2605	PSU	C4-N3	-2.87	1.33	1.38
55	1y	54	5MU	C6-C5	2.86	1.39	1.34
55	2x	37	MIA	C5-C6	2.86	1.48	1.41
55	2y	37	MIA	C5-C6	2.86	1.48	1.41
32	2a	967	5MC	C6-C5	2.86	1.39	1.34
1	2A	1915	5MU	C4-N3	-2.86	1.33	1.38
32	1a	1407	5MC	C6-C5	2.85	1.39	1.34
55	2y	54	5MU	C4-C5	2.84	1.49	1.44
55	1x	39	PSU	C4-N3	-2.82	1.33	1.38
55	1y	54	5MU	C4-C5	2.80	1.49	1.44
55	2x	54	5MU	C4-N3	-2.79	1.33	1.38
1	2A	1962	5MC	C6-C5	2.77	1.39	1.34
1	1A	2605	PSU	C4-N3	-2.75	1.33	1.38
55	1x	54	5MU	C4-N3	-2.74	1.33	1.38
1	2A	1915	5MU	C2-N1	2.73	1.42	1.38
1	1A	1939	5MU	C6-C5	2.72	1.39	1.34
55	2y	54	5MU	C2-N1	2.71	1.42	1.38
1	1A	2552	OMU	C4-N3	-2.70	1.34	1.38
32	1a	1400	5MC	C6-C5	2.69	1.39	1.34
1	2A	1911	PSU	C4-N3	-2.68	1.33	1.38
32	1a	516	PSU	C4-N3	-2.66	1.33	1.38
55	2y	8	4SU	C4-N3	-2.64	1.34	1.37
1	1A	1962	5MC	C6-N1	-2.61	1.33	1.38
1	2A	2503	2MA	C5-N7	-2.60	1.34	1.39
32	1a	1404	5MC	C6-C5	2.59	1.38	1.34
55	1x	32	PSU	C4-N3	-2.58	1.34	1.38
1	1A	1942	5MC	C6-N1	-2.58	1.33	1.38
1	2A	2251	OMG	C6-N1	-2.58	1.34	1.38
55	1y	39	PSU	C4-N3	-2.58	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.57	1.34	1.38
55	2x	39	PSU	C4-N3	-2.56	1.34	1.38
55	1x	55	PSU	C4-N3	-2.55	1.34	1.38
32	2a	516	PSU	C4-N3	-2.55	1.34	1.38
32	2a	966	M2G	C2-N2	2.55	1.39	1.35
32	1a	527	G7M	C6-N1	-2.55	1.34	1.38
1	1A	1917	PSU	C4-N3	-2.55	1.34	1.38
32	2a	966	M2G	C6-N1	-2.55	1.34	1.38
55	2x	54	5MU	C6-C5	2.54	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2251	OMG	C6-N1	-2.53	1.34	1.38
1	1A	1962	5MC	C6-C5	2.52	1.38	1.34
55	2y	55	PSU	C4-N3	-2.51	1.34	1.38
1	1A	1939	5MU	C4-N3	-2.51	1.34	1.38
55	1y	8	4SU	C5-C4	-2.50	1.39	1.42
1	1A	2503	2MA	C5-N7	-2.50	1.34	1.39
32	2a	1400	5MC	C6-C5	2.50	1.38	1.34
1	2A	1915	5MU	C4-C5	2.49	1.48	1.44
1	1A	1915	5MU	C2-N1	2.46	1.42	1.38
32	1a	1207	2MG	C6-N1	-2.45	1.34	1.38
55	2y	39	PSU	C4-N3	-2.45	1.34	1.38
55	1x	8	4SU	C5-C4	-2.44	1.39	1.42
1	1A	1939	5MU	C6-N1	-2.44	1.33	1.38
55	2x	55	PSU	C4-N3	-2.43	1.34	1.38
55	2y	32	PSU	C4-N3	-2.42	1.34	1.38
55	1y	8	4SU	C2-N1	2.42	1.42	1.38
55	1y	54	5MU	C2-N1	2.41	1.42	1.38
55	1x	8	4SU	C2-N3	-2.41	1.33	1.38
55	1y	55	PSU	C4-N3	-2.41	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.40	1.33	1.38
32	2a	527	G7M	C6-N1	-2.40	1.34	1.38
55	2x	37	MIA	C8-N7	2.40	1.36	1.31
1	1A	2503	2MA	C5-C6	2.40	1.47	1.41
55	2y	37	MIA	C8-N7	2.39	1.36	1.31
55	2x	54	5MU	C4-C5	2.39	1.48	1.44
1	2A	2251	OMG	C5-N7	-2.38	1.34	1.39
55	2y	8	4SU	C5-C4	-2.38	1.39	1.42
55	1x	46	G7M	C6-N1	-2.38	1.34	1.38
55	1y	54	5MU	C4-N3	-2.37	1.34	1.38
1	1A	1939	5MU	C4-C5	2.37	1.48	1.44
55	2y	54	5MU	C4-N3	-2.37	1.34	1.38
1	2A	2552	OMU	C2-N3	-2.37	1.33	1.38
1	1A	1911	PSU	C4-N3	-2.37	1.34	1.38
1	2A	2503	2MA	C5-C6	2.36	1.47	1.41
55	2x	54	5MU	C6-N1	-2.35	1.34	1.38
55	1x	37	MIA	C8-N7	2.35	1.36	1.31
55	2x	32	PSU	C4-N3	-2.34	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.33	1.34	1.38
32	1a	966	M2G	C6-N1	-2.33	1.34	1.38
1	1A	1942	5MC	C6-C5	2.32	1.38	1.34
55	1x	54	5MU	C4-C5	2.31	1.48	1.44
55	1y	37	MIA	C8-N7	2.30	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1y	46	G7M	C6-N1	-2.27	1.34	1.38
55	1x	37	MIA	C4-N9	-2.26	1.33	1.37
32	2a	1404	5MC	C6-N1	-2.26	1.34	1.38
55	2x	37	MIA	C5-N7	-2.25	1.35	1.39
32	1a	967	5MC	C6-N1	-2.24	1.34	1.38
55	1x	37	MIA	C5-N7	-2.21	1.35	1.39
55	2x	8	4SU	C2-N1	2.21	1.41	1.38
55	2x	8	4SU	C2-N3	-2.21	1.34	1.38
1	2A	2552	OMU	C5-C4	-2.20	1.38	1.43
55	1y	37	MIA	C5-N7	-2.20	1.35	1.39
1	1A	1939	5MU	C2-N3	-2.20	1.34	1.38
55	1y	46	G7M	C5-C6	2.20	1.49	1.43
55	1y	32	PSU	C4-N3	-2.20	1.34	1.38
32	1a	1404	5MC	C6-N1	-2.19	1.34	1.38
1	1A	1915	5MU	C2-N3	-2.19	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.19	1.34	1.38
32	2a	1400	5MC	C6-N1	-2.19	1.34	1.38
55	2y	46	G7M	C6-N1	-2.18	1.34	1.38
1	1A	1915	5MU	C4-C5	2.18	1.48	1.44
32	1a	1207	2MG	C4-N9	-2.18	1.32	1.38
43	2l	92	0TD	CB-CA	2.18	1.55	1.54
32	1a	1400	5MC	C6-N1	-2.17	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.16	1.34	1.38
55	2x	46	G7M	C6-N1	-2.12	1.34	1.38
32	1a	1498	UR3	C2-N1	2.12	1.41	1.38
1	2A	2605	PSU	C2-N3	-2.11	1.34	1.37
1	1A	2552	OMU	C2-N1	2.11	1.41	1.38
1	1A	2251	OMG	C5-N7	-2.11	1.34	1.39
32	1a	1207	2MG	C5-N7	-2.10	1.34	1.39
1	2A	1942	5MC	C6-N1	-2.10	1.34	1.38
55	2y	37	MIA	C5-N7	-2.10	1.35	1.39
1	1A	2503	2MA	C4-N9	-2.10	1.33	1.37
32	2a	967	5MC	C6-N1	-2.09	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.09	1.34	1.38
55	2y	46	G7M	C5-C6	2.09	1.49	1.43
55	1y	54	5MU	C6-N1	-2.08	1.34	1.38
1	1A	2552	OMU	C5-C4	-2.08	1.39	1.43
55	2x	54	5MU	C2-N3	-2.08	1.34	1.38
55	1x	39	PSU	C2-N3	-2.06	1.34	1.37
55	1x	54	5MU	C2-N3	-2.06	1.34	1.38
1	2A	2503	2MA	C8-N7	2.05	1.35	1.31
32	2a	966	M2G	C5-N7	-2.05	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1498	UR3	C6-C5	2.04	1.39	1.35
1	2A	1915	5MU	C6-N1	-2.03	1.34	1.38
1	2A	1915	5MU	C2-N3	-2.03	1.34	1.38
1	1A	2503	2MA	C8-N9	-2.03	1.34	1.37
32	1a	966	M2G	C5-N7	-2.01	1.35	1.39

All (372) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	1l	92	0TD	CSB-SB-CB	32.94	161.58	102.36
55	2y	37	MIA	C12-C13-C14	-10.01	109.05	127.01
1	2A	2503	2MA	C5-C4-N3	-8.59	118.14	127.18
1	1A	2503	2MA	C5-C4-N3	-8.25	118.49	127.18
55	2x	37	MIA	C5-C4-N3	-8.18	118.56	127.18
55	1y	37	MIA	C5-C4-N3	-8.17	118.58	127.18
55	2x	37	MIA	C12-C13-C14	-8.02	112.61	127.01
55	1y	37	MIA	C12-C13-C14	-7.55	113.45	127.01
55	2y	37	MIA	C5-C4-N3	-7.49	119.29	127.18
55	1x	37	MIA	C12-C13-C14	-7.37	113.78	127.01
55	1x	37	MIA	C5-C4-N3	-7.30	119.50	127.18
55	2y	8	4SU	C4-N3-C2	-7.01	120.60	127.31
1	2A	2503	2MA	N3-C4-N9	6.95	135.81	126.99
1	2A	2605	PSU	N1-C2-N3	6.76	122.30	115.17
1	1A	1911	PSU	N1-C2-N3	6.76	122.30	115.17
32	2a	1207	2MG	C2-N3-C4	6.73	120.42	112.00
1	1A	2605	PSU	N1-C2-N3	6.63	122.16	115.17
32	2a	1498	UR3	C4-N3-C2	-6.58	119.28	124.58
1	1A	2251	OMG	C5-C4-N3	-6.57	117.93	128.39
55	1y	37	MIA	N3-C4-N9	6.56	135.32	126.99
55	2x	37	MIA	N3-C4-N9	6.55	135.31	126.99
1	1A	1917	PSU	N1-C2-N3	6.53	122.05	115.17
55	1y	55	PSU	N1-C2-N3	6.48	122.01	115.17
32	1a	1207	2MG	C2-N3-C4	6.47	120.09	112.00
32	1a	1498	UR3	C4-N3-C2	-6.46	119.38	124.58
32	2a	966	M2G	C5-C4-N3	-6.43	118.16	128.39
1	2A	2251	OMG	C5-C4-N3	-6.43	118.16	128.39
55	1y	8	4SU	C4-N3-C2	-6.39	121.19	127.31
1	1A	2503	2MA	N3-C4-N9	6.38	135.09	126.99
1	2A	1917	PSU	N1-C2-N3	6.37	121.89	115.17
1	2A	1911	PSU	N1-C2-N3	6.33	121.85	115.17
55	1y	39	PSU	N1-C2-N3	6.28	121.79	115.17
55	1x	32	PSU	N1-C2-N3	6.24	121.75	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2x	32	PSU	N1-C2-N3	6.24	121.75	115.17
32	1a	516	PSU	N1-C2-N3	6.23	121.75	115.17
55	2x	55	PSU	N1-C2-N3	6.15	121.66	115.17
55	2y	55	PSU	N1-C2-N3	6.13	121.64	115.17
55	1y	32	PSU	N1-C2-N3	6.03	121.53	115.17
55	2y	39	PSU	N1-C2-N3	6.02	121.52	115.17
55	2y	32	PSU	N1-C2-N3	5.97	121.47	115.17
55	1y	46	G7M	C5-C4-N3	-5.97	116.87	128.15
55	2y	8	4SU	C5-C4-N3	5.96	120.30	114.75
55	1y	46	G7M	N9-C4-N3	5.93	137.82	125.95
32	1a	966	M2G	C5-C4-N3	-5.88	119.03	128.39
1	1A	1915	5MU	C4-N3-C2	-5.85	119.67	127.34
55	2y	37	MIA	N3-C4-N9	5.83	134.39	126.99
32	2a	516	PSU	N1-C2-N3	5.83	121.31	115.17
1	1A	1915	5MU	N3-C2-N1	5.79	122.43	114.89
55	2y	46	G7M	C5-C4-N3	-5.73	117.33	128.15
55	2y	46	G7M	N9-C4-N3	5.64	137.24	125.95
55	1x	55	PSU	N1-C2-N3	5.64	121.12	115.17
55	2x	46	G7M	N9-C4-N3	5.64	137.23	125.95
55	2x	46	G7M	C5-C4-N3	-5.63	117.51	128.15
32	1a	527	G7M	C5-C4-N3	-5.60	117.57	128.15
55	1x	39	PSU	N1-C2-N3	5.60	121.07	115.17
1	2A	1939	5MU	C4-N3-C2	-5.58	120.03	127.34
1	2A	1939	5MU	N3-C2-N1	5.57	122.14	114.89
32	1a	527	G7M	N9-C4-N3	5.54	137.03	125.95
55	1y	8	4SU	C5-C4-N3	5.51	119.88	114.75
32	1a	1207	2MG	C5-C4-N3	-5.51	119.62	128.39
1	1A	1939	5MU	C4-N3-C2	-5.45	120.20	127.34
32	2a	1207	2MG	C5-C4-N3	-5.43	119.75	128.39
1	2A	1915	5MU	N3-C2-N1	5.38	121.90	114.89
55	1x	46	G7M	C5-C4-N3	-5.36	118.02	128.15
1	2A	1915	5MU	C4-N3-C2	-5.33	120.36	127.34
55	1x	46	G7M	N9-C4-N3	5.31	136.58	125.95
1	1A	2251	OMG	C2-N3-C4	5.22	121.29	112.30
55	2x	54	5MU	N3-C2-N1	5.18	121.63	114.89
1	1A	2552	OMU	C4-N3-C2	-5.16	120.21	126.61
1	1A	1915	5MU	C5-C4-N3	5.15	119.80	115.32
55	1x	37	MIA	N3-C4-N9	5.15	133.53	126.99
32	2a	527	G7M	N9-C4-N3	5.12	136.19	125.95
32	2a	527	G7M	C5-C4-N3	-5.09	118.53	128.15
55	2x	39	PSU	N1-C2-N3	5.09	120.54	115.17
1	1A	1939	5MU	C5-C4-N3	5.08	119.74	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1x	54	5MU	N3-C2-N1	5.04	121.46	114.89
55	2y	54	5MU	N3-C2-N1	5.01	121.41	114.89
32	2a	1518	MA6	N1-C2-N3	-5.00	121.02	128.58
55	2x	54	5MU	C4-N3-C2	-4.98	120.81	127.34
55	1y	46	G7M	C2-N3-C4	4.97	120.86	112.30
32	1a	1518	MA6	N1-C2-N3	-4.95	121.09	128.58
32	2a	1519	MA6	N1-C2-N3	-4.95	121.10	128.58
1	2A	2251	OMG	N9-C4-N3	4.91	135.77	125.95
55	2y	46	G7M	C2-N3-C4	4.90	120.74	112.30
55	1y	54	5MU	N3-C2-N1	4.89	121.26	114.89
32	1a	527	G7M	C2-N3-C4	4.89	120.72	112.30
55	2x	46	G7M	C2-N3-C4	4.88	120.70	112.30
55	1y	54	5MU	C4-N3-C2	-4.88	120.94	127.34
1	2A	2251	OMG	C2-N3-C4	4.88	120.70	112.30
55	1x	46	G7M	C2-N3-C4	4.85	120.65	112.30
1	2A	1939	5MU	O4-C4-C5	-4.84	119.38	124.92
1	1A	2251	OMG	N9-C4-N3	4.83	135.61	125.95
1	2A	2605	PSU	C4-N3-C2	-4.81	119.75	126.37
55	2y	8	4SU	C5-C4-S4	-4.78	118.85	124.31
55	2y	54	5MU	C4-N3-C2	-4.77	121.08	127.34
1	1A	1939	5MU	O4-C4-C5	-4.72	119.52	124.92
1	1A	1939	5MU	N3-C2-N1	4.67	120.97	114.89
32	2a	966	M2G	N9-C4-N3	4.67	135.29	125.95
55	1x	8	4SU	C4-N3-C2	-4.67	122.84	127.31
1	2A	2552	OMU	C4-N3-C2	-4.67	120.82	126.61
32	1a	966	M2G	C2-N3-C4	4.66	121.12	112.51
32	2a	527	G7M	C2-N3-C4	4.65	120.30	112.30
55	2x	8	4SU	C5-C4-N3	4.62	119.05	114.75
1	2A	1939	5MU	C5-C4-N3	4.62	119.34	115.32
32	2a	966	M2G	C2-N3-C4	4.61	121.03	112.51
1	2A	1915	5MU	C5-C4-N3	4.59	119.31	115.32
32	1a	1519	MA6	N1-C2-N3	-4.43	121.88	128.58
55	1x	8	4SU	C5-C4-N3	4.42	118.86	114.75
1	1A	2552	OMU	N3-C2-N1	4.40	120.61	114.89
32	2a	1519	MA6	C5-C4-N3	-4.37	120.69	126.72
1	2A	1939	5MU	C5-C6-N1	-4.37	118.57	123.31
55	1x	54	5MU	C4-N3-C2	-4.33	121.66	127.34
55	2x	55	PSU	C4-N3-C2	-4.32	120.42	126.37
1	1A	2605	PSU	C4-N3-C2	-4.27	120.49	126.37
55	1y	37	MIA	C15-C14-C13	-4.24	109.93	122.66
1	2A	1911	PSU	C4-N3-C2	-4.23	120.54	126.37
32	1a	1518	MA6	C5-C4-N3	-4.22	120.90	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	516	PSU	C4-N3-C2	-4.22	120.56	126.37
1	1A	1911	PSU	C4-N3-C2	-4.21	120.57	126.37
32	1a	1519	MA6	C5-C4-N3	-4.20	120.93	126.72
55	1x	55	PSU	C4-N3-C2	-4.19	120.59	126.37
1	1A	1939	5MU	C5-C6-N1	-4.16	118.79	123.31
1	1A	1917	PSU	C4-N3-C2	-4.12	120.69	126.37
55	1y	54	5MU	C5-C4-N3	4.12	118.90	115.32
1	1A	2605	PSU	O2-C2-N1	-4.12	118.54	122.79
32	2a	1518	MA6	C2-N1-C6	4.11	121.88	111.83
55	1x	32	PSU	C4-N3-C2	-4.09	120.73	126.37
1	2A	2552	OMU	C5-C4-N3	4.09	120.52	114.80
1	1A	1915	5MU	O4-C4-C5	-4.06	120.27	124.92
32	2a	1518	MA6	C5-C4-N3	-4.06	121.13	126.72
1	2A	1917	PSU	C4-N3-C2	-4.05	120.78	126.37
55	1y	8	4SU	C5-C4-S4	-4.05	119.68	124.31
55	2y	54	5MU	C5-C4-N3	4.04	118.84	115.32
1	1A	1915	5MU	C5-C6-N1	-4.03	118.93	123.31
32	1a	966	M2G	N9-C4-N3	4.03	134.01	125.95
32	2a	1519	MA6	C2-N1-C6	4.02	121.65	111.83
32	1a	1518	MA6	C5-N7-C8	4.02	109.76	103.45
55	2y	55	PSU	C4-N3-C2	-3.98	120.88	126.37
55	1y	55	PSU	O2-C2-N1	-3.97	118.69	122.79
1	1A	2552	OMU	C5-C4-N3	3.96	120.35	114.80
55	2y	37	MIA	C15-C14-C13	-3.96	110.78	122.66
55	2x	8	4SU	C4-N3-C2	-3.96	123.52	127.31
32	1a	1519	MA6	C5-N7-C8	3.94	109.65	103.45
55	2y	32	PSU	C4-N3-C2	-3.94	120.94	126.37
1	2A	2552	OMU	N3-C2-N1	3.94	120.02	114.89
32	2a	1519	MA6	C5-N7-C8	3.94	109.64	103.45
55	2y	37	MIA	C16-C14-C13	-3.93	110.87	122.66
32	2a	1518	MA6	C5-N7-C8	3.91	109.59	103.45
55	1y	39	PSU	C4-N3-C2	-3.88	121.02	126.37
32	2a	516	PSU	C4-N3-C2	-3.88	121.03	126.37
55	1x	37	MIA	C6-C5-N7	3.87	136.65	132.43
32	2a	1207	2MG	C6-C5-N7	3.86	137.32	130.29
32	1a	1518	MA6	C2-N1-C6	3.85	121.24	111.83
32	1a	1519	MA6	C2-N1-C6	3.85	121.24	111.83
55	2x	32	PSU	C4-N3-C2	-3.85	121.07	126.37
1	2A	1915	5MU	C5-C6-N1	-3.84	119.14	123.31
55	1y	32	PSU	C4-N3-C2	-3.83	121.09	126.37
32	2a	1207	2MG	N1-C2-N2	3.83	120.47	116.56
32	1a	1207	2MG	N9-C4-N3	3.82	133.59	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1518	MA6	N9-C8-N7	-3.82	108.52	113.94
55	1y	55	PSU	C4-N3-C2	-3.81	121.12	126.37
55	2y	8	4SU	N3-C2-N1	3.81	119.85	114.89
32	2a	1518	MA6	C4-C5-N7	-3.80	106.24	110.58
55	2x	54	5MU	C5-C4-N3	3.78	118.61	115.32
55	2x	37	MIA	C16-C14-C13	-3.78	111.32	122.66
55	1x	37	MIA	C4-C5-N7	-3.78	106.26	110.58
1	1A	2503	2MA	C4-C5-N7	-3.76	106.28	110.58
1	1A	1911	PSU	O2-C2-N1	-3.76	118.91	122.79
55	2y	37	MIA	C11-S10-C2	-3.76	99.43	102.25
1	2A	1962	5MC	C5-C6-N1	-3.76	119.23	123.31
55	2y	39	PSU	C4-N3-C2	-3.76	121.19	126.37
32	2a	1519	MA6	C4-C5-N7	-3.75	106.29	110.58
55	2x	37	MIA	C15-C14-C13	-3.75	111.42	122.66
55	1y	8	4SU	N3-C2-N1	3.74	119.75	114.89
55	2x	32	PSU	O2-C2-N1	-3.73	118.95	122.79
32	2a	1400	5MC	C5-C6-N1	-3.71	119.28	123.31
1	2A	1915	5MU	O4-C4-C5	-3.70	120.69	124.92
55	1x	37	MIA	C16-C14-C13	-3.68	111.62	122.66
32	1a	1518	MA6	C4-C5-N7	-3.67	106.38	110.58
32	1a	966	M2G	C6-C5-N7	3.66	136.96	130.29
32	1a	1519	MA6	C4-C5-N7	-3.66	106.40	110.58
32	1a	1519	MA6	N9-C8-N7	-3.66	108.74	113.94
32	2a	967	5MC	C5-C6-N1	-3.60	119.40	123.31
32	2a	1519	MA6	N9-C8-N7	-3.60	108.83	113.94
55	1y	54	5MU	O4-C4-C5	-3.57	120.83	124.92
55	1y	37	MIA	C2-N3-C4	3.56	121.63	112.29
32	2a	1404	5MC	C5-C6-N1	-3.56	119.45	123.31
55	1x	32	PSU	O2-C2-N1	-3.55	119.12	122.79
55	2x	54	5MU	C5-C6-N1	-3.55	119.46	123.31
55	1y	37	MIA	C16-C14-C13	-3.53	112.06	122.66
32	2a	1518	MA6	N9-C8-N7	-3.51	108.95	113.94
55	2x	54	5MU	O2-C2-N1	-3.51	118.23	122.80
1	2A	1917	PSU	O2-C2-N1	-3.50	119.18	122.79
55	1x	37	MIA	C15-C14-C13	-3.49	112.19	122.66
55	2x	37	MIA	C4-C5-N7	-3.47	106.61	110.58
32	1a	1207	2MG	C6-C5-N7	3.46	136.59	130.29
55	2y	37	MIA	N6-C6-N1	3.46	122.98	118.33
32	1a	1518	MA6	C2-N3-C4	3.46	120.28	111.83
32	2a	1519	MA6	C2-N3-C4	3.45	120.25	111.83
32	2a	1207	2MG	N9-C4-N3	3.44	132.83	125.95
55	2y	37	MIA	C4-C5-N7	-3.43	106.66	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1400	5MC	C5-C6-N1	-3.42	119.60	123.31
55	1x	37	MIA	C2-N3-C4	3.40	121.21	112.29
55	1x	54	5MU	O4-C4-C5	-3.40	121.03	124.92
1	1A	1939	5MU	O2-C2-N1	-3.40	118.38	122.80
55	2y	32	PSU	O2-C2-N1	-3.39	119.30	122.79
55	1y	37	MIA	C4-C5-N7	-3.38	106.72	110.58
43	2l	92	0TD	CSB-SB-CB	-3.37	96.31	102.36
55	1x	8	4SU	N3-C2-N1	3.36	119.27	114.89
55	2y	39	PSU	O2-C2-N1	-3.36	119.32	122.79
55	2y	54	5MU	O4-C4-C5	-3.35	121.08	124.92
55	1x	39	PSU	C4-N3-C2	-3.35	121.75	126.37
1	1A	1942	5MC	C5-C6-N1	-3.35	119.68	123.31
55	2y	37	MIA	C2-N3-C4	3.35	121.06	112.29
32	2a	1518	MA6	C2-N3-C4	3.33	119.96	111.83
1	1A	1962	5MC	C5-C6-N1	-3.30	119.72	123.31
55	1x	54	5MU	C5-C6-N1	-3.30	119.73	123.31
55	2x	54	5MU	O4-C4-C5	-3.30	121.15	124.92
55	2x	37	MIA	C2-N3-C4	3.29	120.92	112.29
1	1A	1917	PSU	O2-C2-N1	-3.29	119.39	122.79
55	1x	54	5MU	C5-C4-N3	3.28	118.17	115.32
1	2A	2503	2MA	C4-C5-N7	-3.28	106.84	110.58
1	1A	2552	OMU	O4-C4-C5	-3.25	119.55	125.16
1	2A	1942	5MC	C5-C6-N1	-3.25	119.79	123.31
32	2a	1498	UR3	C5-C4-N3	3.25	119.31	115.04
55	1y	54	5MU	C5-C6-N1	-3.25	119.79	123.31
1	2A	1939	5MU	O2-C2-N1	-3.25	118.57	122.80
55	2y	55	PSU	O2-C2-N1	-3.24	119.45	122.79
55	2x	8	4SU	C5-C4-S4	-3.24	120.61	124.31
32	1a	967	5MC	C5-C6-N1	-3.23	119.81	123.31
55	1y	32	PSU	O2-C2-N1	-3.22	119.47	122.79
32	1a	1498	UR3	C5-C4-N3	3.20	119.25	115.04
55	2y	37	MIA	C6-C5-N7	3.17	135.89	132.43
32	2a	516	PSU	O2-C2-N1	-3.14	119.55	122.79
32	1a	1519	MA6	C2-N3-C4	3.13	119.48	111.83
55	2x	39	PSU	C4-N3-C2	-3.12	122.08	126.37
32	1a	967	5MC	C5-C4-N3	-3.12	118.56	121.75
1	1A	1942	5MC	C5-C4-N3	-3.11	118.57	121.75
32	2a	966	M2G	C6-C5-N7	3.11	135.94	130.29
55	1y	39	PSU	O2-C2-N1	-3.09	119.60	122.79
32	2a	1207	2MG	N2-C2-N3	-3.09	116.58	120.51
55	1y	37	MIA	C6-C5-N7	3.08	135.78	132.43
55	2y	54	5MU	C5-C6-N1	-3.05	120.00	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1y	8	4SU	C1'-N1-C2	3.03	123.03	117.59
55	2x	37	MIA	C11-S10-C2	-3.02	99.98	102.25
1	1A	2503	2MA	N6-C6-N1	3.01	121.09	117.03
1	1A	2251	OMG	C6-C5-N7	3.00	135.75	130.29
32	1a	1404	5MC	C5-C6-N1	-2.99	120.06	123.31
55	2x	55	PSU	O2-C2-N1	-2.99	119.70	122.79
32	2a	1404	5MC	C5-C4-N3	-2.99	118.69	121.75
55	1x	55	PSU	O2-C2-N1	-2.99	119.71	122.79
32	2a	1207	2MG	C4-C5-N7	-2.98	105.95	110.67
1	1A	2503	2MA	C4-N9-C8	2.97	108.86	105.74
1	2A	1942	5MC	C5-C4-N3	-2.95	118.73	121.75
55	1x	54	5MU	O2-C2-N1	-2.92	119.00	122.80
1	2A	1911	PSU	O2-C2-N1	-2.90	119.79	122.79
32	1a	516	PSU	O2-C2-N1	-2.90	119.79	122.79
55	2x	37	MIA	C6-C5-N7	2.87	135.56	132.43
1	1A	2503	2MA	C5-N7-C8	2.86	107.94	103.45
32	1a	1407	5MC	C5-C6-N1	-2.84	120.23	123.31
55	2x	8	4SU	N3-C2-N1	2.83	118.57	114.89
32	1a	966	M2G	C4-C5-N7	-2.83	106.19	110.67
32	1a	1518	MA6	N3-C4-N9	2.81	131.94	127.17
55	2y	37	MIA	C4-N9-C8	2.81	108.68	105.74
32	1a	1207	2MG	N1-C2-N2	2.78	119.39	116.56
32	1a	1519	MA6	N3-C4-N9	2.78	131.89	127.17
32	2a	1407	5MC	C5-C4-N3	-2.77	118.92	121.75
32	2a	1519	MA6	N3-C4-N9	2.77	131.87	127.17
32	1a	1207	2MG	C4-C5-N7	-2.74	106.32	110.67
1	2A	2503	2MA	N6-C6-N1	2.73	120.71	117.03
55	1y	37	MIA	N3-C2-N1	-2.70	122.07	127.00
1	1A	2503	2MA	C2-N1-C6	2.70	122.24	118.10
1	1A	1915	5MU	O2-C2-N1	-2.68	119.30	122.80
32	1a	1404	5MC	C5-C4-N3	-2.68	119.00	121.75
1	2A	2605	PSU	C5-C6-N1	-2.68	118.42	122.14
32	1a	1400	5MC	C5-C4-N3	-2.67	119.02	121.75
1	2A	2605	PSU	O2-C2-N1	-2.66	120.04	122.79
1	2A	2552	OMU	O4-C4-C5	-2.66	120.58	125.16
55	2x	46	G7M	O6-C6-C5	-2.63	122.14	128.01
55	1x	8	4SU	C5-C4-S4	-2.63	121.30	124.31
32	2a	1407	5MC	C5-C6-N1	-2.62	120.47	123.31
32	1a	1407	5MC	C5-C4-N3	-2.62	119.07	121.75
55	2x	37	MIA	C5-N7-C8	2.62	107.56	103.45
32	2a	966	M2G	C4-C5-N7	-2.61	106.54	110.67
1	2A	2503	2MA	C5-N7-C8	2.59	107.51	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1y	37	MIA	C4-N9-C8	2.57	108.44	105.74
1	1A	2251	OMG	C4-C5-N7	-2.57	106.60	110.67
1	2A	2503	2MA	C4-N9-C8	2.56	108.42	105.74
55	1y	37	MIA	C5-N7-C8	2.55	107.46	103.45
55	2x	37	MIA	C4-N9-C8	2.55	108.41	105.74
32	2a	1207	2MG	CM2-N2-C2	-2.53	118.22	123.65
32	1a	1207	2MG	N2-C2-N3	-2.53	117.29	120.51
32	1a	527	G7M	O6-C6-C5	-2.51	122.41	128.01
1	1A	2552	OMU	O2-C2-N1	-2.51	119.53	122.80
55	2x	8	4SU	C1'-N1-C2	2.50	122.08	117.59
1	2A	2251	OMG	C6-C5-N7	2.50	134.83	130.29
55	2y	37	MIA	C5-N7-C8	2.47	107.34	103.45
32	2a	967	5MC	C5-C4-N3	-2.46	119.23	121.75
1	2A	2552	OMU	O2-C2-N1	-2.46	119.60	122.80
55	1y	37	MIA	C2-N1-C6	2.44	122.18	117.54
1	1A	1920	OMC	O2-C2-N3	-2.44	118.49	122.33
32	1a	1519	MA6	C4-C5-C6	2.43	118.42	115.91
55	2x	39	PSU	O2-C2-N1	-2.43	120.28	122.79
55	1x	37	MIA	C5-N7-C8	2.42	107.26	103.45
1	1A	2503	2MA	N9-C8-N7	-2.42	110.50	113.94
32	2a	1518	MA6	N3-C4-N9	2.42	131.28	127.17
55	1x	46	G7M	O6-C6-C5	-2.41	122.64	128.01
1	2A	2503	2MA	C2-N1-C6	2.39	121.77	118.10
55	1y	54	5MU	O2-C2-N1	-2.39	119.69	122.80
55	2y	8	4SU	O2-C2-N1	-2.39	119.69	122.80
1	1A	1911	PSU	C5-C6-N1	-2.38	118.83	122.14
1	2A	2605	PSU	O2-C2-N3	-2.36	117.66	121.86
55	1y	54	5MU	C5M-C5-C4	2.36	121.30	118.78
55	1x	37	MIA	N6-C6-N1	2.36	121.49	118.33
32	1a	1402	4OC	CM4-N4-C4	-2.35	117.86	122.45
32	2a	527	G7M	O6-C6-C5	-2.35	122.77	128.01
55	2y	37	MIA	N3-C2-N1	-2.35	122.72	127.00
55	2x	39	PSU	C6-C5-C4	-2.34	116.59	118.17
55	1x	37	MIA	C4-N9-C8	2.34	108.19	105.74
55	2y	46	G7M	O6-C6-C5	-2.33	122.80	128.01
32	1a	1518	MA6	C4-N9-C8	2.33	108.18	105.74
1	1A	2503	2MA	C6-C5-N7	2.32	136.56	132.09
55	2y	37	MIA	C2-N1-C6	2.31	121.93	117.54
55	2x	37	MIA	C2-N1-C6	2.30	121.91	117.54
1	2A	2251	OMG	C4-C5-N7	-2.30	107.03	110.67
32	2a	1402	4OC	C6-C5-C4	2.30	119.77	117.00
1	2A	2251	OMG	O6-C6-C5	-2.29	120.49	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	1x	55	PSU	C5-C6-N1	-2.29	118.97	122.14
32	1a	966	M2G	O6-C6-C5	-2.28	120.52	126.53
55	2x	54	5MU	C5M-C5-C4	2.26	121.20	118.78
55	1x	37	MIA	C2-N1-C6	2.26	121.83	117.54
32	1a	527	G7M	C5-C6-N1	2.24	116.47	111.84
55	2x	37	MIA	N6-C6-N1	2.24	121.33	118.33
32	1a	516	PSU	O4'-C1'-C2'	2.23	108.24	105.15
55	2y	54	5MU	O2-C2-N1	-2.23	119.89	122.80
1	2A	1962	5MC	C5-C4-N3	-2.22	119.47	121.75
55	2x	46	G7M	C5-C6-N1	2.22	116.44	111.84
55	2x	32	PSU	C6-C5-C4	-2.22	116.68	118.17
32	2a	1400	5MC	C5-C4-N3	-2.22	119.48	121.75
32	2a	1519	MA6	C4-C5-C6	2.21	118.19	115.91
32	2a	1404	5MC	O2-C2-N3	-2.20	118.87	122.33
32	1a	1519	MA6	C4-N9-C8	2.19	108.04	105.74
55	1y	46	G7M	O6-C6-C5	-2.19	123.12	128.01
55	1y	37	MIA	N6-C6-N1	2.18	121.25	118.33
55	1x	37	MIA	N3-C2-N1	-2.18	123.03	127.00
32	1a	516	PSU	C5-C6-N1	-2.17	119.13	122.14
55	2x	55	PSU	C5-C6-N1	-2.17	119.14	122.14
55	2x	54	5MU	C5M-C5-C6	-2.16	119.92	122.85
55	1y	32	PSU	C6-C5-C4	-2.16	116.72	118.17
55	1x	39	PSU	O2-C2-N1	-2.15	120.57	122.79
55	2x	37	MIA	N3-C2-N1	-2.15	123.08	127.00
1	2A	1915	5MU	O2-C2-N1	-2.14	120.02	122.80
32	1a	1498	UR3	C3U-N3-C2	2.12	121.03	117.33
55	2y	46	G7M	C5-C6-N1	2.11	116.21	111.84
55	2y	54	5MU	C5M-C5-C4	2.11	121.04	118.78
32	2a	1407	5MC	O2-C2-N3	-2.11	119.00	122.33
55	1y	46	G7M	C5-C6-N1	2.10	116.18	111.84
32	2a	966	M2G	O6-C6-C5	-2.09	121.01	126.53
32	2a	527	G7M	C5-C6-N1	2.09	116.16	111.84
55	2y	37	MIA	N9-C8-N7	-2.07	111.00	113.94
1	1A	1962	5MC	C1'-N1-C6	-2.06	117.76	121.15
1	2A	1911	PSU	O4'-C1'-C2'	2.05	107.99	105.15
32	2a	516	PSU	O4'-C1'-C2'	2.05	107.98	105.15
1	1A	1962	5MC	C5-C4-N4	-2.04	118.52	121.39
1	1A	1962	5MC	C5-C4-N3	-2.04	119.67	121.75
55	1x	46	G7M	C5-C6-N1	2.03	116.05	111.84
32	1a	967	5MC	O2-C2-N3	-2.03	119.13	122.33
1	1A	2251	OMG	O6-C6-C5	-2.02	121.19	126.53
54	1w	230	MEQ	OE1-CD-CG	-2.02	118.37	122.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
55	2y	55	PSU	C5-C6-N1	-2.00	119.36	122.14
32	2a	1402	4OC	CM4-N4-C4	-2.00	118.54	122.45
32	1a	1402	4OC	C6-C5-C4	2.00	119.41	117.00

There are no chirality outliers.

All (73) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	CA-CB-SB-CSB
54	1w	230	MEQ	CG-CD-NE2-CE
55	1x	37	MIA	C5-C6-N6-C12
55	1x	37	MIA	C12-C13-C14-C15
55	1x	37	MIA	C12-C13-C14-C16
55	1x	46	G7M	C4'-C5'-O5'-P
55	1y	37	MIA	C5-C6-N6-C12
55	1y	37	MIA	C12-C13-C14-C15
55	1y	37	MIA	C12-C13-C14-C16
55	1y	46	G7M	C4'-C5'-O5'-P
55	1y	46	G7M	O4'-C4'-C5'-O5'
55	1y	46	G7M	C3'-C4'-C5'-O5'
32	2a	1207	2MG	N1-C2-N2-CM2
32	2a	1207	2MG	N3-C2-N2-CM2
32	2a	1519	MA6	O4'-C4'-C5'-O5'
55	2x	37	MIA	C5-C6-N6-C12
55	2x	37	MIA	N1-C2-S10-C11
55	2x	37	MIA	N3-C2-S10-C11
55	2x	37	MIA	C12-C13-C14-C15
55	2x	37	MIA	C12-C13-C14-C16
55	2y	37	MIA	C12-C13-C14-C15
55	2y	37	MIA	C12-C13-C14-C16
32	1a	1402	4OC	O4'-C4'-C5'-O5'
55	1x	46	G7M	C3'-C4'-C5'-O5'
55	1y	37	MIA	C3'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
55	2x	46	G7M	C3'-C4'-C5'-O5'
55	1y	37	MIA	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C3'-C4'-C5'-O5'
55	2x	46	G7M	O4'-C4'-C5'-O5'
54	1w	230	MEQ	OE1-CD-NE2-CE
32	1a	1519	MA6	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
32	2a	1519	MA6	C3'-C4'-C5'-O5'
55	2x	46	G7M	C4'-C5'-O5'-P
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1402	4OC	C3'-C4'-C5'-O5'
55	1x	46	G7M	O4'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
55	2x	37	MIA	N1-C6-N6-C12
55	2y	54	5MU	O4'-C4'-C5'-O5'
55	1x	37	MIA	N1-C6-N6-C12
55	1y	37	MIA	N1-C6-N6-C12
55	2y	54	5MU	C3'-C4'-C5'-O5'
43	2l	92	0TD	CG-CB-SB-CSB
43	1l	92	0TD	SB-CB-CG-OD1
43	2l	92	0TD	SB-CB-CG-OD1
55	2y	46	G7M	O4'-C1'-N9-C4
32	1a	527	G7M	O4'-C4'-C5'-O5'
55	2y	46	G7M	O4'-C4'-C5'-O5'
55	1y	55	PSU	O4'-C1'-C5-C4
54	1w	230	MEQ	OE1-CD-CG-CB
55	1x	37	MIA	N6-C12-C13-C14
1	2A	2503	2MA	C4'-C5'-O5'-P
54	1w	230	MEQ	NE2-CD-CG-CB
32	2a	967	5MC	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C4'-C5'-O5'-P
32	2a	1519	MA6	C4'-C5'-O5'-P
43	1l	92	0TD	SB-CB-CG-OD2
43	2l	92	0TD	SB-CB-CG-OD2
54	2w	230	MEQ	OE1-CD-CG-CB
55	1y	55	PSU	O4'-C1'-C5-C6
1	2A	1920	OMC	C3'-C2'-O2'-CM2
43	1l	92	0TD	CA-CB-CG-OD2
43	2l	92	0TD	CA-CB-CG-OD2
54	2w	230	MEQ	NE2-CD-CG-CB
43	1l	92	0TD	CG-CB-SB-CSB
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	1a	527	G7M	C4'-C5'-O5'-P
1	2A	2503	2MA	O4'-C1'-N9-C8
55	1y	8	4SU	C2'-C1'-N1-C2
1	2A	1962	5MC	O4'-C1'-N1-C6

There are no ring outliers.

30 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
43	1l	92	0TD	2	0
55	1y	8	4SU	1	0
1	2A	1920	OMC	1	0
32	1a	1519	MA6	2	0
1	2A	1939	5MU	2	0
1	1A	2552	OMU	1	0
55	2x	8	4SU	1	0
55	1y	39	PSU	1	0
32	2a	1402	4OC	3	0
55	1y	46	G7M	3	0
32	2a	1519	MA6	1	0
54	2w	230	MEQ	1	0
1	1A	1939	5MU	1	0
55	2x	32	PSU	1	0
55	1x	46	G7M	1	0
32	2a	1518	MA6	2	0
55	1x	8	4SU	1	0
32	2a	527	G7M	1	0
55	1x	37	MIA	2	0
55	2y	55	PSU	1	0
54	1w	230	MEQ	1	0
32	2a	966	M2G	1	0
55	2y	39	PSU	1	0
43	2l	92	0TD	2	0
1	2A	2503	2MA	2	0
32	1a	1402	4OC	3	0
55	2y	8	4SU	1	0
32	1a	1518	MA6	1	0
32	2a	1400	5MC	1	0
1	1A	1920	OMC	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2006 ligands modelled in this entry, 2004 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond

length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

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

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

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

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	1A	2860/2915 (98%)	-0.39	105 (3%) 45 35	12, 28, 89, 107	0
1	2A	2789/2915 (95%)	0.09	108 (3%) 43 34	25, 51, 91, 106	0
2	1B	120/121 (99%)	-0.32	0 100 100	23, 48, 63, 77	0
2	2B	120/121 (99%)	0.89	7 (5%) 29 21	57, 79, 92, 96	0
3	1D	275/276 (99%)	-0.28	0 100 100	13, 29, 46, 68	0
3	2D	275/276 (99%)	0.18	5 (1%) 67 61	26, 45, 59, 77	0
4	1E	204/206 (99%)	-0.34	1 (0%) 87 85	12, 28, 52, 67	0
4	2E	204/206 (99%)	0.15	1 (0%) 87 85	27, 48, 63, 72	0
5	1F	203/210 (96%)	-0.13	1 (0%) 87 85	13, 33, 60, 80	0
5	2F	203/210 (96%)	0.59	6 (2%) 52 44	28, 59, 73, 86	0
6	1G	181/182 (99%)	0.63	7 (3%) 43 34	45, 56, 69, 84	0
6	2G	181/182 (99%)	1.41	37 (20%) 3 2	63, 78, 84, 89	0
7	1H	174/180 (96%)	0.07	1 (0%) 85 82	32, 44, 58, 70	0
7	2H	174/180 (96%)	1.39	39 (22%) 2 2	62, 76, 85, 93	0
8	1I	146/148 (98%)	0.65	5 (3%) 48 38	37, 62, 74, 82	0
8	2I	146/148 (98%)	1.09	22 (15%) 5 4	48, 68, 76, 82	0
9	1N	140/140 (100%)	-0.19	2 (1%) 73 67	17, 28, 52, 67	0
9	2N	140/140 (100%)	0.43	0 100 100	41, 57, 71, 78	0
10	1O	122/122 (100%)	-0.14	0 100 100	18, 32, 49, 56	0
10	2O	122/122 (100%)	0.03	1 (0%) 82 78	33, 44, 60, 65	0
11	1P	149/150 (99%)	0.02	0 100 100	13, 35, 56, 64	0
11	2P	149/150 (99%)	0.70	11 (7%) 20 14	34, 60, 76, 83	0
12	1Q	141/141 (100%)	-0.01	0 100 100	20, 32, 46, 59	0
12	2Q	141/141 (100%)	0.67	7 (4%) 34 27	42, 60, 69, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.45	0 100 100	16, 26, 43, 54	0
13	2R	118/118 (100%)	0.39	0 100 100	33, 47, 57, 65	0
14	1S	110/112 (98%)	0.03	2 (1%) 67 61	35, 46, 59, 64	0
14	2S	110/112 (98%)	1.35	16 (14%) 6 4	63, 73, 80, 84	0
15	1T	131/146 (89%)	0.04	4 (3%) 51 43	24, 35, 63, 79	0
15	2T	131/146 (89%)	0.34	3 (2%) 61 52	36, 49, 69, 81	0
16	1U	116/118 (98%)	-0.44	0 100 100	13, 22, 33, 54	0
16	2U	116/118 (98%)	0.41	1 (0%) 81 76	36, 53, 68, 75	0
17	1V	101/101 (100%)	-0.33	0 100 100	15, 30, 46, 55	0
17	2V	101/101 (100%)	0.69	4 (3%) 42 33	40, 62, 72, 80	0
18	1W	112/113 (99%)	-0.44	1 (0%) 81 76	14, 22, 37, 76	0
18	2W	112/113 (99%)	0.20	0 100 100	33, 43, 59, 84	0
19	1X	95/96 (98%)	-0.10	1 (1%) 78 73	20, 31, 55, 71	0
19	2X	95/96 (98%)	0.68	6 (6%) 26 19	41, 59, 69, 74	0
20	1Y	107/110 (97%)	0.28	2 (1%) 66 59	28, 41, 63, 75	0
20	2Y	107/110 (97%)	1.12	16 (14%) 5 4	48, 65, 77, 83	0
21	1Z	183/206 (88%)	0.53	10 (5%) 30 23	35, 52, 66, 73	0
21	2Z	186/206 (90%)	1.09	15 (8%) 18 13	61, 72, 80, 87	0
22	10	76/85 (89%)	-0.15	2 (2%) 57 48	23, 31, 49, 64	0
22	20	77/85 (90%)	0.75	5 (6%) 25 18	42, 60, 68, 74	0
23	11	97/98 (98%)	0.03	3 (3%) 51 43	18, 37, 63, 72	0
23	21	97/98 (98%)	0.76	4 (4%) 41 32	38, 53, 72, 77	0
24	12	70/72 (97%)	0.33	4 (5%) 29 22	27, 44, 55, 76	0
24	22	70/72 (97%)	0.66	3 (4%) 40 31	55, 65, 73, 76	0
25	13	59/60 (98%)	-0.29	0 100 100	20, 28, 51, 68	0
25	23	59/60 (98%)	0.47	4 (6%) 23 17	45, 56, 70, 76	0
26	14	69/71 (97%)	1.20	18 (26%) 1 1	52, 73, 88, 93	0
26	24	68/71 (95%)	1.88	28 (41%) 0 0	72, 84, 91, 94	0
27	15	59/60 (98%)	-0.36	0 100 100	11, 23, 44, 54	0
27	25	59/60 (98%)	0.23	1 (1%) 69 63	30, 45, 63, 76	0
28	16	53/54 (98%)	-0.13	0 100 100	30, 37, 50, 56	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.56	2 (3%) 44 35	49, 60, 67, 73	0
29	17	48/49 (97%)	-0.04	2 (4%) 40 32	15, 22, 45, 65	0
29	27	48/49 (97%)	0.27	4 (8%) 17 13	27, 38, 63, 68	0
30	18	64/65 (98%)	-0.19	0 100 100	17, 27, 34, 41	0
30	28	64/65 (98%)	0.64	3 (4%) 36 28	41, 49, 57, 64	0
31	19	37/37 (100%)	-0.17	0 100 100	23, 30, 46, 50	0
31	29	37/37 (100%)	0.77	0 100 100	52, 61, 69, 75	0
32	1a	1488/1521 (97%)	0.56	83 (5%) 30 22	26, 68, 92, 106	0
32	2a	1491/1521 (98%)	0.69	94 (6%) 26 19	35, 69, 93, 105	0
33	1b	231/256 (90%)	1.08	27 (11%) 9 7	59, 73, 84, 90	0
33	2b	231/256 (90%)	1.51	62 (26%) 1 1	67, 78, 86, 90	0
34	1c	206/239 (86%)	1.45	42 (20%) 3 2	63, 75, 82, 85	0
34	2c	206/239 (86%)	1.36	36 (17%) 4 3	65, 77, 85, 89	0
35	1d	208/209 (99%)	1.10	24 (11%) 9 7	46, 67, 78, 83	0
35	2d	208/209 (99%)	0.76	7 (3%) 48 38	50, 61, 71, 75	0
36	1e	148/162 (91%)	0.51	2 (1%) 73 67	47, 58, 70, 80	0
36	2e	148/162 (91%)	0.84	8 (5%) 31 23	42, 65, 74, 88	0
37	1f	100/101 (99%)	0.47	1 (1%) 79 74	52, 63, 74, 77	0
37	2f	100/101 (99%)	0.74	3 (3%) 52 44	53, 69, 77, 81	0
38	1g	155/156 (99%)	0.93	12 (7%) 19 14	58, 70, 80, 84	0
38	2g	155/156 (99%)	1.37	30 (19%) 3 3	64, 77, 84, 88	0
39	1h	137/138 (99%)	0.51	2 (1%) 72 65	51, 60, 67, 72	0
39	2h	137/138 (99%)	0.86	8 (5%) 29 21	52, 66, 73, 78	0
40	1i	127/128 (99%)	1.43	23 (18%) 3 3	58, 76, 82, 87	0
40	2i	123/128 (96%)	1.87	49 (39%) 1 0	70, 81, 87, 91	0
41	1j	98/105 (93%)	1.99	47 (47%) 0 0	63, 79, 86, 92	0
41	2j	96/105 (91%)	2.27	56 (58%) 0 0	71, 81, 88, 93	0
42	1k	114/129 (88%)	0.49	2 (1%) 67 61	40, 60, 71, 76	0
42	2k	114/129 (88%)	0.77	5 (4%) 39 30	48, 68, 76, 83	0
43	1l	121/132 (91%)	0.71	5 (4%) 41 32	37, 55, 65, 70	0
43	2l	121/132 (91%)	0.63	3 (2%) 58 49	45, 54, 62, 68	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	118/126 (93%)	1.26	14 (11%) 9 7	63, 74, 80, 87	0
44	2m	115/126 (91%)	1.81	46 (40%) 1 0	70, 80, 86, 91	0
45	1n	60/61 (98%)	1.57	15 (25%) 2 1	61, 73, 82, 85	0
45	2n	60/61 (98%)	1.92	23 (38%) 1 0	70, 78, 83, 86	0
46	1o	88/89 (98%)	0.54	2 (2%) 61 52	42, 58, 72, 74	0
46	2o	88/89 (98%)	0.83	5 (5%) 29 22	49, 64, 76, 82	0
47	1p	82/88 (93%)	1.42	17 (20%) 2 2	54, 67, 78, 86	0
47	2p	82/88 (93%)	0.85	3 (3%) 45 35	49, 61, 68, 77	0
48	1q	99/105 (94%)	0.68	4 (4%) 42 33	47, 59, 70, 73	0
48	2q	99/105 (94%)	0.83	6 (6%) 27 20	50, 63, 72, 76	0
49	1r	68/88 (77%)	0.67	1 (1%) 72 65	48, 58, 76, 81	0
49	2r	68/88 (77%)	0.75	2 (2%) 53 45	56, 65, 73, 80	0
50	1s	83/93 (89%)	1.44	21 (25%) 1 1	69, 77, 85, 89	0
50	2s	83/93 (89%)	1.63	27 (32%) 1 1	72, 81, 88, 92	0
51	1t	96/106 (90%)	1.00	11 (11%) 9 7	55, 63, 73, 77	0
51	2t	96/106 (90%)	1.00	8 (8%) 17 13	51, 65, 77, 81	0
52	1u	23/27 (85%)	1.80	10 (43%) 0 0	65, 71, 76, 79	0
52	2u	23/27 (85%)	1.80	11 (47%) 0 0	72, 79, 83, 84	0
53	1v	13/24 (54%)	0.81	3 (23%) 2 2	45, 53, 91, 91	0
53	2v	13/24 (54%)	1.30	3 (23%) 2 2	59, 69, 99, 101	0
54	1w	248/354 (70%)	0.35	4 (1%) 70 64	26, 62, 77, 84	0
54	2w	252/354 (71%)	0.78	18 (7%) 22 16	44, 69, 83, 91	0
55	1x	68/76 (89%)	0.05	1 (1%) 72 65	23, 54, 69, 88	0
55	1y	67/76 (88%)	0.67	3 (4%) 38 29	32, 86, 95, 101	0
55	2x	68/76 (89%)	0.39	1 (1%) 72 65	42, 71, 82, 91	0
55	2y	67/76 (88%)	1.20	6 (8%) 15 12	55, 94, 100, 102	0
56	1z	14/18 (77%)	1.97	8 (57%) 0 0	29, 52, 72, 75	0
56	2z	14/18 (77%)	2.17	8 (57%) 0 0	52, 67, 76, 79	0
All	All	21290/22338 (95%)	0.43	1442 (6%) 23 17	11, 58, 85, 107	0

All (1442) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	2F	89	VAL	7.1
1	1A	1068	G	6.8
44	1m	2	ALA	6.7
38	2g	16	LEU	6.4
1	2A	2115	G	6.2
45	2n	2	ALA	6.2
1	2A	2146	C	6.1
1	2A	2147	G	6.0
23	21	2	SER	5.7
1	2A	2145	C	5.6
47	1p	82	GLN	5.6
32	2a	1030(B)	C	5.6
24	12	70	GLN	5.4
1	2A	2116	G	5.4
1	2A	2111	C	5.3
1	2A	2113	U	5.2
1	2A	2114	A	5.2
26	24	56	VAL	5.2
1	2A	2169	A	5.1
1	2A	2119	A	5.0
40	2i	126	SER	4.9
1	1A	1059	G	4.9
56	1z	6	VAL	4.8
1	1A	2115	G	4.8
8	2I	12	LEU	4.7
44	2m	4	ILE	4.7
38	2g	2	ALA	4.7
44	2m	100	GLY	4.7
1	2A	2170	A	4.7
44	2m	102	ARG	4.7
40	2i	6	GLY	4.6
50	2s	84	GLY	4.6
40	2i	15	ALA	4.6
51	2t	103	GLY	4.6
1	2A	2893	G	4.6
38	2g	83	ALA	4.6
6	2G	2	PRO	4.5
44	2m	98	VAL	4.5
35	2d	157	LEU	4.5
15	1T	131	ALA	4.5
38	2g	81	GLY	4.5
41	1j	64	GLU	4.5
29	17	47	ARG	4.5

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Mol	Chain	Res	Type	RSRZ
7	2H	96	ALA	4.4
56	2z	6	VAL	4.4
44	1m	102	ARG	4.4
1	2A	2117	A	4.4
1	2A	2319	G	4.4
32	1a	1353	G	4.4
1	2A	2120	G	4.3
41	1j	87	THR	4.3
29	17	48	LYS	4.3
7	2H	113	VAL	4.3
45	1n	2	ALA	4.3
45	1n	59	ALA	4.3
1	2A	1536	C	4.3
32	2a	1224	G	4.3
48	1q	100	LYS	4.3
40	1i	106	ALA	4.2
50	2s	13	ASP	4.2
1	1A	1088	A	4.2
1	2A	2118	U	4.2
1	2A	2110	G	4.2
32	1a	157	G	4.2
32	1a	1286	A	4.2
1	2A	2149	G	4.2
26	14	51	ASP	4.2
32	1a	1030(B)	C	4.1
33	2b	187	LEU	4.1
1	2A	2894	G	4.1
32	1a	1002	G	4.1
41	2j	59	SER	4.1
1	1A	2125	G	4.1
1	2A	2148	G	4.1
1	2A	2112	G	4.1
51	1t	14	LYS	4.0
50	2s	9	VAL	4.0
1	1A	2116	G	4.0
1	2A	2123	G	4.0
32	2a	1202	G	4.0
41	1j	59	SER	4.0
1	1A	2113	U	4.0
1	1A	1092	C	4.0
41	2j	52	GLY	4.0
44	1m	95	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
26	14	53	GLU	4.0
41	2j	47	PHE	4.0
8	2I	20	ASP	3.9
41	1j	45	ARG	3.9
7	2H	22	GLY	3.9
50	1s	84	GLY	3.9
54	2w	351	LEU	3.9
12	2Q	130	LYS	3.9
56	1z	8	ILE	3.9
26	14	54	GLY	3.9
44	1m	98	VAL	3.9
47	1p	17	TYR	3.9
35	1d	157	LEU	3.8
26	24	49	PHE	3.8
26	24	57	GLU	3.8
44	2m	101	GLN	3.8
33	2b	237	ALA	3.8
1	1A	1093	G	3.8
7	2H	100	GLY	3.8
1	2A	2164	C	3.8
50	1s	9	VAL	3.8
6	1G	25	TYR	3.8
40	2i	7	THR	3.8
52	2u	17	THR	3.8
1	1A	2793	G	3.8
45	2n	42	ILE	3.8
1	1A	1067	A	3.8
1	1A	2170	A	3.8
26	14	63	TYR	3.8
33	1b	237	ALA	3.8
44	2m	73	GLU	3.8
15	1T	111	ARG	3.8
7	2H	111	HIS	3.8
7	2H	102	ALA	3.8
32	2a	1286	A	3.8
33	2b	134	GLU	3.7
1	1A	2189	U	3.7
1	2A	2122	U	3.7
51	1t	9	ASN	3.7
32	1a	630	G	3.7
51	1t	103	GLY	3.7
33	2b	7	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
44	2m	87	TYR	3.7
1	2A	2179	C	3.7
7	2H	2	SER	3.7
22	10	9	SER	3.7
56	2z	9	PRO	3.7
41	2j	35	SER	3.7
51	2t	11	SER	3.7
6	2G	139	LEU	3.7
34	2c	187	ALA	3.7
26	24	32	TYR	3.7
41	1j	47	PHE	3.7
26	24	53	GLU	3.7
44	2m	9	ILE	3.7
53	1v	11	U	3.7
1	1A	1100	C	3.6
32	2a	1033	G	3.6
44	2m	65	LYS	3.6
34	1c	189	ALA	3.6
3	2D	276	LYS	3.6
1	1A	1063	G	3.6
32	1a	1186	G	3.6
15	1T	130	ALA	3.6
12	2Q	33	GLY	3.6
26	24	51	ASP	3.6
33	2b	200	ILE	3.6
41	2j	48	THR	3.6
33	2b	215	LEU	3.6
40	2i	96	LEU	3.6
17	2V	73	SER	3.6
38	2g	26	PHE	3.6
32	2a	1234	C	3.6
45	2n	3	ARG	3.5
1	1A	2120	G	3.5
33	2b	163	PHE	3.5
5	1F	208	GLY	3.5
41	1j	34	VAL	3.5
38	2g	24	THR	3.5
41	2j	76	ASN	3.5
32	2a	1249	C	3.5
29	27	47	ARG	3.5
1	2A	2897	U	3.5
45	2n	33	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
20	1Y	1	MET	3.5
32	1a	348	G	3.5
32	1a	1224	G	3.5
33	2b	121	LEU	3.5
37	2f	59	TYR	3.5
38	2g	84	ASN	3.5
24	12	69	ARG	3.5
42	2k	126	ARG	3.5
32	1a	1354	C	3.5
26	24	59	PHE	3.5
41	2j	41	PRO	3.5
41	1j	62	HIS	3.5
51	1t	18	GLN	3.5
1	1A	2178	C	3.5
1	2A	2896	C	3.5
5	2F	208	GLY	3.5
1	2A	1026	U	3.5
7	1H	2	SER	3.5
26	24	66	SER	3.5
40	2i	10	ARG	3.5
34	1c	62	ASP	3.5
41	1j	100	THR	3.5
1	1A	1058	G	3.4
32	2a	1002	G	3.4
3	2D	275	LYS	3.4
1	2A	652(B)	A	3.4
32	1a	345	C	3.4
26	14	69	LYS	3.4
26	24	54	GLY	3.4
19	1X	95	LEU	3.4
40	2i	86	VAL	3.4
40	2i	102	LEU	3.4
41	2j	49	VAL	3.4
1	1A	2792	G	3.4
1	1A	1077	A	3.4
1	2A	2173	A	3.4
33	2b	120	ALA	3.4
14	2S	7	TYR	3.4
41	2j	61	GLU	3.4
1	1A	2112	G	3.4
1	2A	2157	G	3.4
1	2A	2166	G	3.4

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Mol	Chain	Res	Type	RSRZ
33	2b	236	TYR	3.4
40	2i	42	ARG	3.4
32	2a	1219	U	3.4
7	2H	105	LEU	3.3
32	2a	1225	A	3.4
40	2i	109	VAL	3.3
32	1a	1029	C	3.3
32	1a	1397	C	3.3
38	1g	83	ALA	3.3
50	2s	35	SER	3.3
14	2S	56	LEU	3.3
38	2g	80	VAL	3.3
38	2g	4	ARG	3.3
1	2A	1171	G	3.3
7	2H	39	PRO	3.3
32	2a	973	G	3.3
33	2b	140	HIS	3.3
34	1c	8	ILE	3.3
41	1j	88	LEU	3.3
44	1m	119	GLY	3.3
1	1A	2114	A	3.3
32	1a	344	A	3.3
1	2A	2136	C	3.3
7	2H	89	ILE	3.3
34	2c	61	ALA	3.3
1	1A	2190	G	3.3
32	1a	347	G	3.3
33	2b	165	VAL	3.3
20	2Y	59	GLY	3.3
40	1i	67	GLY	3.3
32	1a	1532	U	3.3
41	2j	57	LYS	3.3
1	1A	1069	A	3.3
8	2I	146	ALA	3.3
32	1a	1001(A)	G	3.3
35	2d	2	GLY	3.3
45	1n	51	GLY	3.3
56	2z	5	PRO	3.2
45	2n	7	ILE	3.2
41	2j	40	LEU	3.2
50	1s	16	LEU	3.2
1	1A	1073	A	3.2

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Mol	Chain	Res	Type	RSRZ
1	1A	1098	A	3.2
41	1j	46	ARG	3.2
33	2b	71	VAL	3.2
48	2q	77	VAL	3.2
40	2i	67	GLY	3.2
7	2H	38	SER	3.2
1	2A	2144	U	3.2
1	2A	2159	G	3.2
1	2A	2805	G	3.2
20	2Y	1	MET	3.2
34	2c	62	ASP	3.2
32	2a	1532	U	3.2
41	1j	78	ASN	3.2
51	2t	9	ASN	3.2
38	2g	42	ILE	3.2
34	2c	129	ALA	3.2
34	1c	76	VAL	3.2
1	2A	2134	A	3.2
24	12	15	LYS	3.2
32	1a	1287	A	3.2
34	2c	185	GLY	3.2
21	1Z	1	MET	3.2
14	2S	58	LEU	3.2
1	1A	1071	G	3.2
32	1a	1026	G	3.2
33	2b	55	PHE	3.2
33	1b	165	VAL	3.2
41	1j	10	GLY	3.2
1	2A	2158	A	3.2
32	2a	977	A	3.2
6	2G	52	ILE	3.2
1	2A	2139	C	3.2
32	1a	1137	C	3.2
32	2a	1354	C	3.2
38	1g	2	ALA	3.2
41	2j	5	ARG	3.2
7	2H	44	VAL	3.2
26	14	45	GLY	3.2
32	1a	346	G	3.2
50	2s	8	GLY	3.2
53	2v	10	G	3.2
41	1j	96	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
43	2l	7	ILE	3.2
1	2A	2126	A	3.1
1	2A	2176	A	3.1
36	2e	27	ARG	3.1
51	1t	22	ARG	3.1
52	1u	24	ARG	3.1
41	1j	26	ALA	3.1
47	1p	16	HIS	3.1
1	2A	34	C	3.1
1	2A	2178	C	3.1
20	2Y	45	VAL	3.1
42	2k	13	GLN	3.1
41	2j	74	ILE	3.1
19	2X	92	LEU	3.1
40	2i	66	ARG	3.1
33	1b	233	SER	3.1
32	2a	1503	A	3.1
7	2H	99	VAL	3.1
36	2e	41	VAL	3.1
1	1A	1064	C	3.1
1	2A	2174	C	3.1
26	24	52	THR	3.1
40	1i	2	GLU	3.1
7	2H	64	LEU	3.1
26	24	55	ARG	3.1
41	2j	71	LEU	3.1
33	2b	133	LYS	3.1
43	1l	126	LYS	3.1
14	2S	92	TYR	3.1
1	1A	2131	G	3.1
1	2A	2125	G	3.1
55	2x	44	G	3.1
32	2a	1363(A)	A	3.1
1	1A	1060	U	3.1
41	1j	31	GLY	3.1
41	2j	23	ILE	3.1
38	1g	79	ARG	3.1
45	2n	17	LYS	3.1
50	2s	69	HIS	3.1
23	11	2	SER	3.1
50	2s	38	SER	3.1
1	1A	2790	A	3.1

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Mol	Chain	Res	Type	RSRZ
1	2A	2121	G	3.1
32	1a	1033	G	3.1
32	2a	1253	G	3.1
26	24	58	ARG	3.1
34	1c	52	LEU	3.1
1	2A	2789	C	3.1
32	2a	979	C	3.1
33	2b	218	ALA	3.0
4	2E	151	TYR	3.0
34	1c	103	VAL	3.0
22	20	8	GLY	3.0
41	2j	31	GLY	3.0
11	2P	15	ARG	3.0
44	2m	22	ILE	3.0
33	2b	138	LEU	3.0
41	2j	42	THR	3.0
1	1A	2166	G	3.0
1	2A	1533	G	3.0
32	2a	1030(A)	G	3.0
40	2i	14	VAL	3.0
1	1A	1075	C	3.0
1	2A	2138	C	3.0
32	1a	1028	C	3.0
26	24	5	ILE	3.0
33	2b	214	ILE	3.0
56	2z	8	ILE	3.0
25	23	2	PRO	3.0
34	2c	186	PHE	3.0
54	2w	327	VAL	3.0
1	1A	1087	G	3.0
32	2a	1353	G	3.0
45	2n	21	TYR	3.0
26	24	31	ILE	3.0
41	2j	36	GLY	3.0
51	2t	74	LYS	3.0
26	24	65	ASP	3.0
33	1b	11	LEU	3.0
41	2j	67	THR	3.0
47	1p	7	ALA	3.0
40	2i	65	VAL	3.0
45	2n	25	VAL	3.0
33	2b	201	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
35	1d	3	ARG	3.0
52	2u	15	ARG	3.0
40	2i	99	LEU	3.0
56	1z	10	GLN	3.0
1	1A	2168	G	3.0
32	1a	1034	G	3.0
32	1a	1030	C	3.0
49	2r	24	ALA	3.0
52	1u	17	THR	3.0
8	2I	3	VAL	3.0
47	1p	81	ARG	2.9
8	2I	35	LEU	2.9
34	1c	185	GLY	2.9
50	1s	5	LEU	2.9
1	1A	1074	G	2.9
1	1A	1091	G	2.9
1	1A	2165	G	2.9
1	2A	2127	G	2.9
40	2i	76	ALA	2.9
40	2i	106	ALA	2.9
40	2i	122	ALA	2.9
5	2F	90	PHE	2.9
14	2S	98	VAL	2.9
34	1c	207	VAL	2.9
41	2j	100	THR	2.9
54	2w	183	VAL	2.9
33	1b	19	HIS	2.9
41	2j	55	LYS	2.9
32	1a	1257	U	2.9
50	1s	71	LEU	2.9
6	2G	146	TYR	2.9
21	2Z	99	TYR	2.9
40	2i	88	TYR	2.9
39	2h	72	PRO	2.9
34	2c	106	VAL	2.9
44	2m	5	ALA	2.9
44	2m	15	VAL	2.9
33	2b	22	LYS	2.9
1	1A	1072	C	2.9
1	1A	2164	C	2.9
32	1a	1115	C	2.9
51	1t	25	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	1A	2805	G	2.9
1	2A	2133	G	2.9
32	1a	1003	G	2.9
32	2a	1186	G	2.9
44	2m	25	ILE	2.9
50	2s	31	ILE	2.9
34	1c	12	LEU	2.9
51	1t	10	LEU	2.9
40	1i	30	GLY	2.9
41	1j	93	GLY	2.9
50	2s	34	TRP	2.9
52	2u	4	GLY	2.9
14	2S	36	TYR	2.9
33	1b	236	TYR	2.9
38	2g	85	TYR	2.9
41	1j	76	ASN	2.9
43	1l	18	VAL	2.9
52	2u	24	ARG	2.9
1	1A	2803	C	2.9
1	2A	2140	C	2.9
1	2A	2177	C	2.9
1	1A	1078	U	2.9
1	1A	1090	U	2.9
1	1A	2150	U	2.9
1	2A	2168	G	2.9
32	1a	158	G	2.9
47	2p	82	GLN	2.9
41	2j	80	LYS	2.9
8	1I	146	ALA	2.9
26	14	56	VAL	2.9
40	1i	91	ASP	2.9
32	1a	975	A	2.9
33	1b	127	ILE	2.9
44	2m	66	LEU	2.9
11	2P	20	GLY	2.8
41	2j	37	PRO	2.8
1	1A	2111	C	2.8
1	1A	2129	C	2.8
53	2v	11	U	2.8
21	1Z	11	GLU	2.8
26	24	63	TYR	2.8
34	1c	23	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
26	14	50	VAL	2.8
32	2a	1024	G	2.8
32	2a	1032	G	2.8
37	2f	55	ASP	2.8
44	2m	92	HIS	2.8
44	2m	103	THR	2.8
7	2H	21	PRO	2.8
45	1n	61	TRP	2.8
45	2n	50	LYS	2.8
25	23	60	GLU	2.8
1	1A	2172	U	2.8
1	2A	2895	U	2.8
38	1g	85	TYR	2.8
40	2i	36	TYR	2.8
1	1A	2794	C	2.8
14	2S	69	VAL	2.8
38	2g	17	VAL	2.8
41	2j	72	VAL	2.8
6	2G	62	LEU	2.8
8	2I	96	ASP	2.8
33	2b	222	ILE	2.8
41	1j	40	LEU	2.8
44	1m	96	LEU	2.8
1	1A	1062	G	2.8
1	2A	2318	G	2.8
1	2A	2793	G	2.8
1	1A	1177	A	2.8
32	2a	1285	A	2.8
35	1d	23	GLY	2.8
40	2i	11	LYS	2.8
41	2j	77	PRO	2.8
1	2A	2189	U	2.8
26	24	50	VAL	2.8
34	2c	207	VAL	2.8
26	14	59	PHE	2.8
33	2b	207	ALA	2.8
38	1g	62	PHE	2.8
41	2j	26	ALA	2.8
6	1G	53	LEU	2.8
20	2Y	43	ASN	2.8
35	1d	154	ASN	2.8
41	1j	65	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
50	1s	20	LEU	2.8
32	1a	1363	C	2.8
39	2h	3	THR	2.8
54	2w	320	THR	2.8
41	2j	14	LYS	2.8
1	1A	1176	G	2.8
1	1A	2147	G	2.8
1	2A	2153	G	2.8
32	1a	1032	G	2.8
33	1b	232	PRO	2.8
6	2G	35	GLU	2.8
32	2a	1236	A	2.8
41	2j	46	ARG	2.8
8	2I	37	VAL	2.8
44	2m	45	VAL	2.8
20	2Y	90	LEU	2.8
41	2j	65	LEU	2.8
50	2s	40	ILE	2.8
34	2c	3	ASN	2.8
29	27	48	LYS	2.8
11	2P	23	PRO	2.8
40	2i	123	PRO	2.8
56	1z	5	PRO	2.8
34	2c	38	ARG	2.7
40	2i	12	GLU	2.7
1	1A	2110	G	2.7
1	2A	1847	A	2.7
34	1c	137	ALA	2.7
49	1r	20	ALA	2.7
1	2A	2155	G	2.7
32	2a	630	G	2.7
32	2a	1030(C)	G	2.7
32	2a	1220	G	2.7
41	1j	82	ILE	2.7
41	2j	8	LEU	2.7
41	2j	56	HIS	2.7
1	1A	271(K)	U	2.7
32	2a	1235	U	2.7
53	1v	22	U	2.7
40	2i	71	SER	2.7
7	2H	97	ARG	2.7
8	1I	41	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
6	2G	43	LEU	2.7
7	2H	136	ILE	2.7
34	1c	84	ILE	2.7
19	2X	69	TYR	2.7
54	2w	305	TYR	2.7
21	2Z	98	MET	2.7
32	2a	1250	A	2.7
42	1k	123	LYS	2.7
32	1a	104	G	2.7
54	2w	186	THR	2.7
6	2G	147	ASP	2.7
22	10	11	ARG	2.7
45	2n	41	ARG	2.7
11	2P	98	GLU	2.7
33	2b	129	GLU	2.7
33	1b	136	VAL	2.7
33	1b	229	VAL	2.7
8	2I	109	ILE	2.7
19	2X	46	ALA	2.7
21	2Z	48	PHE	2.7
35	1d	135	LEU	2.7
45	2n	11	LYS	2.7
43	1l	64	TYR	2.7
54	2w	322	HIS	2.7
42	2k	49	GLY	2.7
44	2m	24	GLY	2.7
51	2t	25	ARG	2.7
39	2h	4	ASP	2.7
56	1z	11	PRO	2.7
1	2A	2160	G	2.7
32	1a	1356	G	2.7
32	2a	1373	G	2.7
7	2H	50	VAL	2.7
6	1G	50	ALA	2.7
39	2h	31	PHE	2.7
40	1i	94	ALA	2.7
40	2i	13	ALA	2.7
41	2j	54	PHE	2.7
50	1s	74	PHE	2.7
51	2t	30	LYS	2.7
52	1u	3	LYS	2.7
7	2H	94	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
32	1a	1367	C	2.7
42	2k	50	TYR	2.7
25	23	29	ARG	2.7
44	2m	80	ARG	2.7
50	2s	37	ARG	2.7
39	2h	15	ASN	2.7
41	2j	87	THR	2.7
50	2s	33	THR	2.7
54	2w	150	THR	2.7
1	1A	1082	U	2.7
32	1a	1251	A	2.7
33	2b	221	LEU	2.7
41	1j	74	ILE	2.6
34	2c	53	ALA	2.6
40	2i	61	ALA	2.6
44	2m	107	ALA	2.6
1	2A	2141	G	2.6
1	2A	2802	G	2.6
32	2a	1117	G	2.6
53	1v	10	G	2.6
34	1c	6	HIS	2.6
38	2g	156	TRP	2.6
26	24	43	TYR	2.6
34	1c	184	TYR	2.6
7	2H	42	ARG	2.6
23	11	26	ARG	2.6
41	1j	60	ARG	2.6
41	1j	66	ARG	2.6
32	2a	1397	C	2.6
33	1b	234	PRO	2.6
41	1j	37	PRO	2.6
1	2A	2808	U	2.6
34	1c	195	VAL	2.6
36	2e	34	VAL	2.6
38	2g	12	LEU	2.6
39	2h	2	LEU	2.6
40	1i	19	LEU	2.6
41	1j	33	GLN	2.6
46	2o	60	VAL	2.6
47	1p	47	ASP	2.6
32	2a	1252	A	2.6
52	1u	13	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
34	1c	117	ALA	2.6
45	1n	5	ALA	2.6
45	2n	5	ALA	2.6
38	1g	156	TRP	2.6
1	2A	2124	G	2.6
1	2A	2156	G	2.6
1	2A	2165	G	2.6
30	28	64	TYR	2.6
32	1a	1024	G	2.6
50	1s	80	TYR	2.6
52	1u	9	ARG	2.6
55	1x	44	G	2.6
15	1T	37	GLY	2.6
34	1c	171	GLY	2.6
52	2u	23	PRO	2.6
21	2Z	150	LEU	2.6
26	24	33	VAL	2.6
32	2a	1223	C	2.6
40	2i	19	LEU	2.6
56	2z	18	LEU	2.6
33	2b	170	GLU	2.6
39	2h	99	GLU	2.6
44	2m	8	GLU	2.6
6	2G	148	MET	2.6
50	1s	12	ASP	2.6
40	1i	15	ALA	2.6
1	1A	2119	A	2.6
40	1i	66	ARG	2.6
44	2m	88	ARG	2.6
45	2n	45	ARG	2.6
26	14	67	TYR	2.6
42	2k	75	TYR	2.6
14	2S	90	GLY	2.6
26	24	29	PRO	2.6
1	1A	11	G	2.6
7	2H	148	ILE	2.6
32	1a	1021	G	2.6
40	2i	56	LEU	2.6
44	2m	19	LEU	2.6
8	2I	11	ASN	2.6
33	1b	129	GLU	2.6
7	2H	20	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
15	2T	131	ALA	2.6
33	2b	171	ALA	2.6
41	1j	11	PHE	2.6
44	2m	118	ALA	2.6
1	1A	2804	C	2.6
1	2A	2803	C	2.6
21	1Z	31	ARG	2.6
38	1g	5	ARG	2.6
1	1A	1070	A	2.6
32	1a	1531	A	2.6
6	2G	25	TYR	2.6
23	21	71	TYR	2.6
44	2m	31	LYS	2.6
35	1d	2	GLY	2.6
40	2i	57	GLY	2.6
44	2m	41	PRO	2.6
44	2m	113	PRO	2.6
8	2I	5	LEU	2.6
33	2b	80	ILE	2.6
41	1j	42	THR	2.6
45	1n	7	ILE	2.6
6	2G	30	GLU	2.6
41	2j	83	GLU	2.6
6	2G	50	ALA	2.6
33	1b	13	ALA	2.6
32	2a	951	G	2.5
32	2a	1356	G	2.5
55	2y	18	G	2.5
1	1A	1065	U	2.5
33	2b	82	ARG	2.5
34	1c	88	ARG	2.5
45	1n	57	ARG	2.5
45	2n	31	ARG	2.5
1	1A	888	C	2.5
1	1A	2179	C	2.5
1	2A	2142	C	2.5
1	2A	2135	A	2.5
7	2H	112	PRO	2.5
32	1a	1005	A	2.5
32	1a	1447	A	2.5
32	2a	1248	A	2.5
50	1s	76	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
52	2u	14	TRP	2.5
24	22	60	LEU	2.5
33	2b	196	LEU	2.5
6	2G	155	MET	2.5
26	24	35	VAL	2.5
29	27	46	VAL	2.5
41	2j	6	ILE	2.5
47	1p	2	VAL	2.5
54	2w	158	VAL	2.5
7	2H	58	GLU	2.5
12	2Q	139	GLU	2.5
27	25	59	GLU	2.5
56	2z	10	GLN	2.5
21	2Z	51	ALA	2.5
14	2S	20	ARG	2.5
41	2j	73	ASP	2.5
17	2V	78	LYS	2.5
20	2Y	94	LYS	2.5
40	1i	95	LYS	2.5
1	1A	2127	G	2.5
32	2a	963	G	2.5
55	1y	19	G	2.5
1	1A	2145	C	2.5
1	2A	2143	C	2.5
33	2b	232	PRO	2.5
34	2c	2	GLY	2.5
8	1I	19	VAL	2.5
38	2g	141	VAL	2.5
41	1j	4	ILE	2.5
34	1c	201	TYR	2.5
44	1m	87	TYR	2.5
1	1A	548	A	2.5
6	1G	48	GLU	2.5
8	1I	10	GLU	2.5
33	2b	70	PHE	2.5
34	1c	67	THR	2.5
46	2o	25	THR	2.5
50	2s	74	PHE	2.5
51	2t	8	ARG	2.5
47	1p	68	ASP	2.5
1	1A	1094	U	2.5
1	1A	1097	U	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2167	U	2.5
34	2c	109	PRO	2.5
52	1u	23	PRO	2.5
6	2G	101	ILE	2.5
11	2P	28	GLY	2.5
33	1b	172	ILE	2.5
33	2b	39	ILE	2.5
20	2Y	42	VAL	2.5
33	1b	97	TRP	2.5
33	2b	136	VAL	2.5
33	2b	164	VAL	2.5
44	2m	7	VAL	2.5
1	1A	2896	C	2.5
1	2A	2131	G	2.5
1	2A	2807	G	2.5
5	2F	145	GLU	2.5
33	2b	95	GLN	2.5
40	2i	18	PHE	2.5
54	2w	307	PHE	2.5
41	2j	27	ALA	2.5
44	2m	18	ALA	2.5
1	1A	2173	A	2.5
26	14	55	ARG	2.5
34	1c	11	ARG	2.5
23	21	48	LYS	2.5
40	2i	95	LYS	2.5
33	2b	48	MET	2.5
33	2b	149	LEU	2.5
21	1Z	129	SER	2.5
50	1s	2	PRO	2.5
34	2c	155	GLY	2.5
41	2j	38	ILE	2.5
33	2b	81	VAL	2.5
38	1g	80	VAL	2.5
47	2p	2	VAL	2.5
33	2b	88	ALA	2.5
44	2m	75	ALA	2.5
20	2Y	46	LYS	2.5
32	1a	1352	C	2.5
41	1j	3	LYS	2.5
32	2a	1222	G	2.5
32	1a	1001	A	2.5

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Mol	Chain	Res	Type	RSRZ
38	1g	84	ASN	2.5
47	1p	60	LEU	2.4
7	2H	151	ILE	2.4
41	2j	39	PRO	2.4
52	2u	13	ILE	2.4
6	2G	149	VAL	2.4
33	1b	71	VAL	2.4
38	2g	21	VAL	2.4
41	1j	35	SER	2.4
12	2Q	29	PHE	2.4
34	1c	122	GLU	2.4
46	2o	88	ARG	2.4
48	2q	91	ARG	2.4
54	2w	325	GLU	2.4
56	2z	12	ARG	2.4
6	1G	26	GLN	2.4
6	2G	12	TYR	2.4
47	1p	22	THR	2.4
32	1a	1007	C	2.4
38	2g	109	ASN	2.4
40	1i	102	LEU	2.4
32	1a	532	A	2.4
32	2a	1349	A	2.4
1	2A	879	G	2.4
2	2B	103	G	2.4
32	1a	378	G	2.4
32	1a	1023	G	2.4
32	2a	1355	G	2.4
36	2e	109	ILE	2.4
41	1j	73	ASP	2.4
44	2m	78	ILE	2.4
6	2G	109	VAL	2.4
33	1b	227	GLY	2.4
33	2b	38	GLY	2.4
6	1G	21	ARG	2.4
6	2G	48	GLU	2.4
11	2P	74	GLU	2.4
17	2V	75	PHE	2.4
26	14	49	PHE	2.4
32	1a	950	U	2.4
34	1c	90	GLU	2.4
33	1b	173	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
40	1i	43	ALA	2.4
47	2p	19	ILE	2.4
21	2Z	179	ASP	2.4
35	1d	17	VAL	2.4
41	2j	44	VAL	2.4
1	1A	2158	A	2.4
2	2B	26	A	2.4
14	2S	93	LYS	2.4
26	24	61	ARG	2.4
30	28	15	LYS	2.4
34	1c	4	LYS	2.4
40	2i	127	LYS	2.4
41	2j	45	ARG	2.4
45	1n	41	ARG	2.4
1	1A	2151	G	2.4
1	1A	2159	G	2.4
1	1A	2181	G	2.4
32	1a	1187	G	2.4
32	2a	1034	G	2.4
32	2a	1311	G	2.4
34	1c	10	PHE	2.4
34	1c	186	PHE	2.4
50	2s	73	GLU	2.4
34	1c	187	ALA	2.4
34	2c	160	ALA	2.4
32	1a	204	U	2.4
33	2b	148	TYR	2.4
47	1p	58	TYR	2.4
41	1j	81	THR	2.4
50	2s	14	HIS	2.4
24	22	61	LEU	2.4
34	1c	47	LEU	2.4
44	2m	81	LEU	2.4
44	2m	39	ILE	2.4
33	2b	234	PRO	2.4
8	2I	21	VAL	2.4
9	1N	9	VAL	2.4
35	1d	8	VAL	2.4
45	2n	55	GLY	2.4
50	2s	67	VAL	2.4
20	2Y	23	ARG	2.4
22	20	11	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
41	2j	60	ARG	2.4
1	1A	34	C	2.4
32	2a	1369	C	2.4
1	2A	2171	A	2.4
6	2G	102	PHE	2.4
8	2I	60	GLU	2.4
26	24	30	GLU	2.4
34	2c	189	ALA	2.4
22	20	9	SER	2.4
51	1t	11	SER	2.4
1	1A	1066	U	2.4
1	1A	2121	G	2.4
2	2B	1	U	2.4
32	2a	1001(A)	G	2.4
32	2a	1190	G	2.4
32	2a	1233	G	2.4
48	2q	95	TYR	2.4
50	1s	39	THR	2.4
33	2b	40	HIS	2.4
45	2n	6	LEU	2.4
33	2b	208	ILE	2.4
20	1Y	53	PRO	2.4
41	2j	91	PRO	2.4
34	1c	130	VAL	2.3
34	2c	70	VAL	2.3
34	2c	199	LYS	2.3
40	1i	109	VAL	2.3
46	1o	89	GLY	2.3
45	1n	16	PHE	2.3
46	2o	15	PHE	2.3
33	2b	123	ALA	2.3
34	1c	200	ALA	2.3
1	1A	1076	C	2.3
1	2A	2129	C	2.3
6	2G	76	SER	2.3
32	2a	1251	A	2.3
8	2I	133	HIS	2.3
33	2b	115	LEU	2.3
35	1d	155	LEU	2.3
41	1j	85	LEU	2.3
41	2j	13	HIS	2.3
51	1t	71	THR	2.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1446	U	2.3
40	2i	63	ILE	2.3
6	2G	17	PRO	2.3
14	2S	33	LYS	2.3
45	2n	14	PRO	2.3
1	1A	1089	G	2.3
8	2I	33	ARG	2.3
32	1a	1009	G	2.3
32	2a	1124	G	2.3
44	2m	53	VAL	2.3
44	2m	114	ARG	2.3
11	2P	109	GLY	2.3
41	1j	86	MET	2.3
12	2Q	37	LEU	2.3
33	1b	10	LEU	2.3
35	1d	152	SER	2.3
38	2g	99	LEU	2.3
41	2j	16	LEU	2.3
44	2m	48	LEU	2.3
1	1A	1509	C	2.3
1	2A	2804	C	2.3
32	2a	1149	C	2.3
1	1A	1046	A	2.3
1	2A	2320	A	2.3
21	2Z	171	ILE	2.3
38	2g	151	TYR	2.3
40	1i	64	THR	2.3
12	2Q	22	LYS	2.3
26	24	28	LYS	2.3
1	2A	2172	U	2.3
15	2T	111	ARG	2.3
26	14	62	ARG	2.3
35	2d	132	ARG	2.3
38	2g	93	PRO	2.3
41	1j	77	PRO	2.3
50	2s	36	ARG	2.3
50	2s	51	VAL	2.3
11	2P	73	GLY	2.3
45	2n	28	GLY	2.3
1	1A	1099	G	2.3
1	1A	2162	G	2.3
1	2A	2101	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2104	G	2.3
7	2H	159	GLU	2.3
28	26	2	ALA	2.3
32	1a	159	G	2.3
32	1a	1030(C)	G	2.3
32	1a	1368	G	2.3
32	2a	1310	G	2.3
39	1h	4	ASP	2.3
21	1Z	70	LEU	2.3
26	24	9	LEU	2.3
34	2c	12	LEU	2.3
35	1d	26	CYS	2.3
33	2b	19	HIS	2.3
41	2j	30	SER	2.3
26	24	44	THR	2.3
26	14	48	ARG	2.3
40	1i	10	ARG	2.3
1	1A	1057	A	2.3
1	2A	2188	C	2.3
7	2H	45	VAL	2.3
1	2A	2150	U	2.3
32	1a	160	A	2.3
34	2c	120	VAL	2.3
40	2i	108	VAL	2.3
55	1y	4	C	2.3
6	2G	65	GLY	2.3
7	2H	14	GLY	2.3
35	1d	180	GLY	2.3
45	2n	51	GLY	2.3
6	2G	158	ALA	2.3
7	2H	41	MET	2.3
34	1c	19	GLU	2.3
41	1j	83	GLU	2.3
44	2m	82	MET	2.3
33	2b	10	LEU	2.3
37	1f	55	ASP	2.3
40	1i	116	LYS	2.3
1	2A	11	G	2.3
1	2A	2792	G	2.3
14	2S	35	ILE	2.3
32	1a	107	G	2.3
32	1a	629	G	2.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1370	G	2.3
36	1e	13	ILE	2.3
33	2b	97	TRP	2.3
34	1c	127	ARG	2.3
48	1q	7	THR	2.3
48	1q	97	SER	2.3
50	1s	35	SER	2.3
52	1u	10	ARG	2.3
52	1u	15	ARG	2.3
7	2H	128	PRO	2.3
34	2c	184	TYR	2.3
40	2i	53	VAL	2.3
40	2i	80	GLY	2.3
32	1a	202	U	2.3
55	2y	33	U	2.3
1	1A	2136	C	2.2
1	1A	2137	C	2.2
32	2a	1098	C	2.2
6	2G	13	GLU	2.2
7	2H	103	LEU	2.2
54	1w	348	LEU	2.2
41	1j	99	LYS	2.2
41	2j	22	LYS	2.2
41	2j	96	ILE	2.2
35	1d	43	HIS	2.2
44	1m	108	ARG	2.2
50	1s	78	ARG	2.2
34	2c	191	THR	2.2
21	1Z	66	SER	2.2
34	1c	66	VAL	2.2
36	2e	133	TYR	2.2
32	1a	216	G	2.2
21	1Z	143	GLY	2.2
12	2Q	65	PHE	2.2
21	1Z	136	PHE	2.2
1	1A	1175	U	2.2
4	1E	73	GLU	2.2
8	2I	36	ALA	2.2
20	2Y	29	GLU	2.2
33	1b	134	GLU	2.2
1	2A	887	A	2.2
1	2A	2801(A)	A	2.2

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Mol	Chain	Res	Type	RSRZ
35	1d	120	LEU	2.2
41	1j	71	LEU	2.2
32	1a	1362	C	2.2
32	2a	1322	C	2.2
33	2b	127	ILE	2.2
7	2H	101	ARG	2.2
34	2c	79	ARG	2.2
50	1s	13	ASP	2.2
6	2G	28	VAL	2.2
20	2Y	85	VAL	2.2
21	2Z	71	VAL	2.2
34	1c	167	TRP	2.2
34	2c	73	PRO	2.2
50	2s	11	VAL	2.2
50	2s	4	SER	2.2
3	2D	180	GLY	2.2
14	1S	60	GLY	2.2
16	2U	7	GLY	2.2
26	14	64	GLY	2.2
6	2G	117	PHE	2.2
7	2H	25	LYS	2.2
35	1d	46	LYS	2.2
10	2O	108	GLU	2.2
32	2a	1017	G	2.2
38	1g	101	LEU	2.2
40	1i	12	GLU	2.2
40	1i	110	GLU	2.2
40	2i	46	ALA	2.2
40	2i	94	ALA	2.2
44	2m	33	ALA	2.2
1	1A	2130	U	2.2
51	2t	75	ASN	2.2
7	2H	95	ARG	2.2
9	1N	8	GLN	2.2
39	2h	35	ILE	2.2
41	1j	84	GLN	2.2
41	2j	75	ILE	2.2
45	1n	3	ARG	2.2
54	1w	192	ILE	2.2
32	1a	977	A	2.2
32	2a	974	A	2.2
32	2a	1015	A	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1280	A	2.2
1	2A	2161	C	2.2
1	2A	2175	C	2.2
32	1a	1006	C	2.2
32	1a	1027	C	2.2
38	2g	66	VAL	2.2
41	1j	91	PRO	2.2
50	1s	67	VAL	2.2
40	2i	103	THR	2.2
17	2V	81	TYR	2.2
20	2Y	22	GLY	2.2
34	1c	13	GLY	2.2
35	1d	113	SER	2.2
35	2d	41	GLY	2.2
40	1i	126	SER	2.2
44	2m	6	GLY	2.2
45	1n	60	SER	2.2
6	2G	182	LYS	2.2
38	2g	29	LYS	2.2
41	1j	55	LYS	2.2
41	1j	63	PHE	2.2
43	1l	32	PHE	2.2
8	1I	5	LEU	2.2
24	12	16	LEU	2.2
40	1i	96	LEU	2.2
6	2G	144	ILE	2.2
8	2I	97	ILE	2.2
21	1Z	80	ARG	2.2
21	2Z	146	ILE	2.2
26	14	68	ARG	2.2
33	2b	30	ARG	2.2
34	2c	134	ILE	2.2
40	2i	121	ARG	2.2
42	1k	54	ARG	2.2
50	2s	3	ARG	2.2
40	2i	73	GLN	2.2
1	1A	1173	G	2.2
21	2Z	121	HIS	2.2
32	2a	1061	G	2.2
32	2a	1337	G	2.2
1	1A	2801(A)	A	2.2
7	2H	114	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
41	1j	72	VAL	2.2
32	2a	931	C	2.2
32	2a	934	C	2.2
32	2a	1282	C	2.2
55	2y	61	C	2.2
34	2c	192	THR	2.2
40	2i	27	THR	2.2
3	2D	38	LYS	2.2
6	2G	55	LYS	2.2
14	2S	60	GLY	2.2
52	1u	14	TRP	2.2
43	2l	17	LYS	2.2
45	1n	4	LYS	2.2
20	2Y	60	PHE	2.2
33	2b	92	TYR	2.2
34	2c	10	PHE	2.2
45	2n	34	TYR	2.2
8	2I	38	LEU	2.2
35	1d	186	LEU	2.2
50	2s	71	LEU	2.2
54	2w	152	LEU	2.2
6	2G	163	ALA	2.2
34	1c	61	ALA	2.2
6	1G	52	ILE	2.1
29	27	23	ARG	2.1
41	1j	23	ILE	2.1
41	2j	66	ARG	2.1
46	1o	88	ARG	2.1
49	2r	32	ARG	2.1
33	1b	95	GLN	2.1
1	1A	2897	U	2.1
32	1a	1000	U	2.1
32	1a	1136	U	2.1
32	2a	1126	U	2.1
32	2a	1522	U	2.1
54	2w	306	ASN	2.1
55	2y	47	U	2.1
7	2H	144	VAL	2.1
14	2S	49	VAL	2.1
33	1b	15	VAL	2.1
38	2g	144	MET	2.1
1	2A	2751	G	2.1

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Mol	Chain	Res	Type	RSRZ
2	2B	51	G	2.1
7	2H	106	THR	2.1
11	2P	76	LYS	2.1
23	11	81	LYS	2.1
1	1A	1095	A	2.1
32	1a	1035	A	2.1
32	1a	1355	G	2.1
32	1a	1357	A	2.1
32	2a	485	G	2.1
32	2a	971	G	2.1
32	2a	1131	G	2.1
43	1l	28	LYS	2.1
46	2o	20	GLY	2.1
1	1A	1079	C	2.1
32	2a	1027	C	2.1
35	1d	21	LEU	2.1
37	2f	45	LEU	2.1
45	1n	36	PHE	2.1
50	2s	15	LEU	2.1
55	2y	56	C	2.1
36	2e	21	ALA	2.1
41	2j	20	ALA	2.1
44	2m	30	ALA	2.1
14	2S	3	ARG	2.1
19	2X	90	GLU	2.1
50	1s	37	ARG	2.1
52	2u	6	ARG	2.1
56	1z	12	ARG	2.1
35	2d	67	ILE	2.1
41	2j	33	GLN	2.1
19	2X	31	HIS	2.1
1	2A	2109	U	2.1
7	2H	37	VAL	2.1
32	2a	1257	U	2.1
38	2g	75	VAL	2.1
40	2i	17	VAL	2.1
44	2m	10	PRO	2.1
44	2m	54	VAL	2.1
56	2z	11	PRO	2.1
20	2Y	63	LYS	2.1
33	2b	169	LYS	2.1
33	2b	107	THR	2.1

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Mol	Chain	Res	Type	RSRZ
38	1g	34	GLY	2.1
38	2g	82	GLY	2.1
50	1s	68	GLY	2.1
54	2w	234	THR	2.1
40	2i	37	PHE	2.1
40	2i	101	PHE	2.1
45	2n	36	PHE	2.1
1	1A	2135	A	2.1
1	1A	2169	A	2.1
21	2Z	131	ARG	2.1
22	20	18	ALA	2.1
32	2a	1180	A	2.1
32	2a	1357	A	2.1
33	2b	199	TYR	2.1
34	1c	53	ALA	2.1
34	2c	60	ALA	2.1
34	2c	71	ALA	2.1
34	2c	190	ARG	2.1
54	2w	205	ALA	2.1
1	1A	2152	G	2.1
1	2A	2152	G	2.1
1	2A	2182	G	2.1
21	2Z	153	SER	2.1
32	1a	1030(A)	G	2.1
41	1j	98	ILE	2.1
1	1A	645	C	2.1
32	1a	381	C	2.1
32	2a	1029	C	2.1
32	2a	1129	C	2.1
32	2a	1141	C	2.1
45	2n	40	CYS	2.1
51	1t	70	SER	2.1
54	2w	189	GLN	2.1
50	1s	14	HIS	2.1
7	2H	12	PRO	2.1
14	1S	16	ASN	2.1
24	22	8	LYS	2.1
33	2b	147	LYS	2.1
40	1i	53	VAL	2.1
50	1s	11	VAL	2.1
54	2w	260	LYS	2.1
32	2a	1150	U	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	107	LEU	2.1
34	2c	96	GLY	2.1
35	1d	194	LEU	2.1
36	2e	97	GLY	2.1
40	2i	115	GLY	2.1
43	2l	93	LEU	2.1
44	2m	68	GLY	2.1
52	2u	11	GLY	2.1
44	1m	49	THR	2.1
47	1p	80	PHE	2.1
15	2T	115	ARG	2.1
34	1c	18	TRP	2.1
44	1m	104	ARG	2.1
45	2n	61	TRP	2.1
47	1p	72	ARG	2.1
52	1u	6	ARG	2.1
3	2D	2	ALA	2.1
20	2Y	100	ALA	2.1
38	2g	7	ALA	2.1
33	2b	31	TYR	2.1
39	1h	80	ILE	2.1
1	1A	2126	A	2.1
1	2A	2629	A	2.1
30	28	37	SER	2.1
32	1a	1183	A	2.1
32	2a	1447	A	2.1
21	2Z	118	GLN	2.1
36	2e	20	GLN	2.1
44	1m	101	GLN	2.1
1	1A	614(B)	G	2.1
1	1A	886	C	2.1
1	1A	2894	G	2.1
1	2A	1537	G	2.1
1	2A	2128	C	2.1
2	2B	88	C	2.1
32	1a	105	G	2.1
32	1a	306	G	2.1
32	1a	1116	C	2.1
32	1a	1370	G	2.1
32	2a	1003	G	2.1
32	2a	1007	C	2.1
33	2b	184	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
34	2c	151	VAL	2.1
44	2m	46	LYS	2.1
50	2s	70	LYS	2.1
44	1m	106	ASN	2.1
33	1b	215	LEU	2.1
34	1c	188	LEU	2.1
1	2A	2132	U	2.1
32	1a	90	U	2.1
32	2a	950	U	2.1
32	2a	1085	U	2.1
34	2c	158	GLY	2.1
38	1g	82	GLY	2.1
38	2g	133	GLY	2.1
50	2s	68	GLY	2.1
53	2v	22	U	2.1
54	2w	117	GLY	2.1
35	2d	122	ARG	2.1
38	2g	5	ARG	2.1
41	1j	29	ARG	2.1
21	2Z	184	ALA	2.1
25	23	51	ALA	2.1
38	2g	25	ALA	2.1
8	2I	7	GLU	2.1
21	1Z	2	GLU	2.1
34	2c	161	GLU	2.1
35	1d	192	GLU	2.1
44	2m	69	GLU	2.1
5	2F	7	TYR	2.1
40	2i	62	TYR	2.1
56	1z	7	TYR	2.1
33	2b	101	MET	2.0
35	1d	201	GLN	2.0
40	2i	78	LYS	2.0
48	1q	99	SER	2.0
48	2q	97	SER	2.0
1	2A	229	A	2.0
2	2B	57	A	2.0
5	2F	126	VAL	2.0
6	2G	5	VAL	2.0
26	14	33	VAL	2.0
32	1a	994	A	2.0
32	2a	1014	A	2.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1289	A	2.0
34	2c	153	VAL	2.0
26	24	7	PRO	2.0
51	1t	98	PRO	2.0
1	2A	277	C	2.0
1	2A	1532	C	2.0
6	2G	34	LEU	2.0
32	1a	1533	C	2.0
33	1b	118	LEU	2.0
35	2d	154	ASN	2.0
41	2j	90	LEU	2.0
50	2s	53	ASN	2.0
1	1A	2123	G	2.0
1	2A	2151	G	2.0
19	2X	68	ARG	2.0
26	24	45	GLY	2.0
32	1a	973	G	2.0
32	1a	1036	G	2.0
32	1a	1166	G	2.0
32	2a	1011	G	2.0
32	2a	1036	G	2.0
32	2a	1088	G	2.0
33	1b	38	GLY	2.0
54	1w	190	GLY	2.0
1	1A	1026	U	2.0
33	1b	162	ILE	2.0
44	1m	105	THR	2.0
55	2y	20	U	2.0
14	2S	6	ALA	2.0
33	2b	166	ASP	2.0
38	2g	65	ALA	2.0
40	1i	61	ALA	2.0
6	2G	29	TRP	2.0
6	2G	137	GLU	2.0
8	2I	41	GLU	2.0
41	2j	64	GLU	2.0
48	2q	24	GLU	2.0
20	2Y	19	LYS	2.0
26	14	32	TYR	2.0
35	1d	138	TYR	2.0
45	1n	17	LYS	2.0
8	2I	42	SER	2.0

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Mol	Chain	Res	Type	RSRZ
33	1b	7	VAL	2.0
33	2b	15	VAL	2.0
34	1c	70	VAL	2.0
34	1c	136	GLN	2.0
34	2c	68	VAL	2.0
41	2j	34	VAL	2.0
47	1p	13	HIS	2.0
47	1p	65	GLN	2.0
50	2s	41	VAL	2.0
56	1z	15	HIS	2.0
11	2P	97	PRO	2.0
35	1d	136	PRO	2.0
8	2I	47	LEU	2.0
32	1a	349	A	2.0
32	2a	1035	A	2.0
22	20	74	ARG	2.0
28	26	50	ARG	2.0
35	1d	131	ARG	2.0
41	1j	9	ARG	2.0
44	2m	106	ASN	2.0
45	1n	12	ARG	2.0
48	2q	92	ARG	2.0
52	2u	10	ARG	2.0
18	1W	112	GLY	2.0
34	1c	128	PHE	2.0
36	1e	85	GLY	2.0
44	1m	6	GLY	2.0
52	2u	16	GLY	2.0
1	1A	271(J)	C	2.0
1	1A	2128	C	2.0
1	2A	2788	C	2.0
8	2I	4	ILE	2.0
11	2P	75	ILE	2.0
32	2a	972	C	2.0
32	2a	1030	C	2.0
41	2j	50	ILE	2.0
40	2i	84	ALA	2.0
54	1w	188	THR	2.0
1	2A	895	U	2.0
1	2A	958	U	2.0
2	2B	89	G	2.0
6	2G	54	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
6	2G	81	LYS	2.0
23	21	75	GLU	2.0
32	2a	1381	U	2.0
33	2b	79	ASP	2.0
32	1a	1365	G	2.0
32	2a	945	G	2.0
32	2a	1031	G	2.0
47	1p	35	LYS	2.0
50	1s	6	LYS	2.0
55	1y	15	G	2.0
47	1p	1	MET	2.0
40	1i	114	TYR	2.0
21	2Z	161	VAL	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
55	G7M	1y	46	24/25	0.58	0.16	85,90,107,120	0
55	4SU	2y	8	20/21	0.61	0.14	89,97,111,122	0
55	5MU	2y	54	21/22	0.63	0.16	88,98,108,120	0
55	G7M	2y	46	24/25	0.64	0.13	85,96,105,129	0
55	PSU	2y	55	20/21	0.67	0.17	88,98,106,116	0
55	PSU	2y	32	20/21	0.69	0.14	83,87,93,96	0
55	PSU	1y	55	20/21	0.72	0.12	82,92,101,109	0
55	PSU	2y	39	20/21	0.75	0.14	75,87,90,93	0
55	5MU	1y	54	21/22	0.77	0.11	81,86,98,113	0
55	PSU	1y	32	20/21	0.78	0.15	67,82,88,89	0
55	4SU	1y	8	20/21	0.79	0.12	86,91,99,99	0
55	MIA	2y	37	29/30	0.79	0.16	76,82,95,106	0
55	PSU	1y	39	20/21	0.80	0.14	64,74,79,82	0
55	G7M	2x	46	24/25	0.81	0.14	68,74,79,100	0
32	2MG	1a	1207	24/25	0.83	0.13	75,79,83,90	0
32	2MG	2a	1207	24/25	0.85	0.12	62,78,83,85	0
55	MIA	1y	37	29/30	0.87	0.14	62,73,78,78	0
43	0TD	1l	92	10/11	0.88	0.14	45,55,58,59	0
55	PSU	2x	55	20/21	0.88	0.10	63,72,79,81	0
55	G7M	1x	46	24/25	0.88	0.10	44,54,82,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	PSU	2x	32	20/21	0.89	0.11	52,69,82,83	0
32	5MC	2a	967	21/22	0.89	0.12	59,66,76,82	0
1	5MU	2A	1915	21/22	0.91	0.11	52,62,73,78	0
55	5MU	2x	54	21/22	0.91	0.10	60,69,77,80	0
32	PSU	2a	516	20/21	0.91	0.10	61,67,70,70	0
32	G7M	2a	527	24/25	0.91	0.12	56,63,68,79	0
1	5MU	1A	1915	21/22	0.91	0.11	37,51,62,63	0
55	5MU	1x	54	21/22	0.91	0.11	50,58,62,69	0
32	5MC	2a	1400	21/22	0.91	0.12	52,65,70,72	0
43	0TD	2l	92	10/11	0.91	0.14	50,55,63,64	0
55	4SU	2x	8	20/21	0.91	0.11	63,68,71,72	0
32	PSU	1a	516	20/21	0.91	0.12	45,67,73,73	0
32	M2G	2a	966	25/26	0.92	0.11	56,62,73,78	0
55	PSU	2x	39	20/21	0.92	0.10	41,65,71,71	0
1	PSU	2A	1911	20/21	0.92	0.10	52,56,59,67	0
32	M2G	1a	966	25/26	0.92	0.13	47,53,65,72	0
32	5MC	2a	1404	21/22	0.93	0.12	43,50,55,56	0
32	5MC	1a	967	21/22	0.93	0.12	49,55,64,66	0
55	PSU	1x	32	20/21	0.93	0.11	53,59,66,73	0
55	PSU	1x	55	20/21	0.93	0.09	53,59,62,64	0
32	4OC	2a	1402	22/23	0.93	0.12	44,52,58,62	0
32	MA6	2a	1518	24/25	0.94	0.12	42,57,62,66	0
32	G7M	1a	527	24/25	0.94	0.11	48,58,65,66	0
1	PSU	1A	1917	20/21	0.94	0.08	38,47,60,61	0
1	PSU	2A	1917	20/21	0.95	0.08	45,53,56,59	0
32	MA6	2a	1519	24/25	0.95	0.13	43,52,59,60	0
1	OMC	2A	1920	21/22	0.95	0.10	51,53,59,62	0
54	MEQ	2w	230	10/11	0.95	0.12	47,51,53,54	0
32	5MC	1a	1400	21/22	0.95	0.11	45,56,61,62	0
55	MIA	1x	37	29/30	0.95	0.11	36,51,59,67	0
55	MIA	2x	37	29/30	0.95	0.12	60,66,71,71	0
55	PSU	1x	39	20/21	0.95	0.10	44,54,60,61	0
32	5MC	2a	1407	21/22	0.95	0.09	39,47,54,60	0
32	5MC	1a	1404	21/22	0.96	0.09	34,39,42,46	0
32	5MC	1a	1407	21/22	0.96	0.09	27,38,42,43	0
1	5MC	2A	1962	21/22	0.96	0.10	25,32,38,41	0
1	PSU	1A	1911	20/21	0.96	0.09	37,46,55,55	0
1	OMC	1A	1920	21/22	0.96	0.09	32,40,45,48	0
32	UR3	2a	1498	21/22	0.96	0.10	42,49,54,56	0
1	5MC	1A	1942	21/22	0.96	0.07	20,26,30,36	0
32	4OC	1a	1402	22/23	0.96	0.09	30,38,46,53	0
55	4SU	1x	8	20/21	0.97	0.08	36,44,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	MA6	1a	1518	24/25	0.97	0.09	31,35,38,38	0
32	MA6	1a	1519	24/25	0.97	0.09	28,33,37,38	0
1	5MU	2A	1939	21/22	0.97	0.09	28,32,36,37	0
1	5MC	2A	1942	21/22	0.97	0.09	37,46,48,50	0
1	5MC	1A	1962	21/22	0.97	0.07	22,27,30,37	0
1	OMG	2A	2251	24/25	0.97	0.09	30,36,39,44	0
1	2MA	2A	2503	23/24	0.97	0.07	25,29,31,33	0
54	MEQ	1w	230	10/11	0.97	0.09	20,29,32,32	0
1	5MU	1A	1939	21/22	0.98	0.06	15,19,23,26	0
1	OMG	1A	2251	24/25	0.98	0.06	14,18,21,23	0
1	OMU	2A	2552	21/22	0.98	0.07	23,30,34,38	0
1	PSU	2A	2605	20/21	0.98	0.07	23,30,35,36	0
1	2MA	1A	2503	23/24	0.98	0.06	11,14,17,19	0
1	OMU	1A	2552	21/22	0.98	0.07	14,19,25,26	0
32	UR3	1a	1498	21/22	0.98	0.07	29,35,41,44	0
1	PSU	1A	2605	20/21	0.98	0.07	14,18,23,23	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
57	MG	1A	3636	1/1	0.46	0.26	56,56,56,56	0
57	MG	2a	1764	1/1	0.46	0.18	77,77,77,77	0
57	MG	1a	1662	1/1	0.48	0.40	73,73,73,73	0
57	MG	2A	3631	1/1	0.59	0.30	79,79,79,79	0
57	MG	1A	3649	1/1	0.60	0.17	49,49,49,49	0
57	MG	2a	1732	1/1	0.61	0.19	58,58,58,58	0
57	MG	2A	3491	1/1	0.61	0.19	65,65,65,65	0
57	MG	2A	3569	1/1	0.62	0.21	54,54,54,54	0
57	MG	2A	3340	1/1	0.62	0.29	77,77,77,77	0
57	MG	2A	3100	1/1	0.63	0.15	79,79,79,79	0
57	MG	2A	3632	1/1	0.63	0.29	70,70,70,70	0
57	MG	2A	3510	1/1	0.66	0.20	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3749	1/1	0.66	0.37	34,34,34,34	0
57	MG	2A	3236	1/1	0.66	0.17	73,73,73,73	0
57	MG	1A	3480	1/1	0.66	0.16	62,62,62,62	0
57	MG	2A	3345	1/1	0.66	0.13	79,79,79,79	0
57	MG	1a	1763	1/1	0.66	0.22	64,64,64,64	0
57	MG	1a	1751	1/1	0.67	0.17	71,71,71,71	0
57	MG	2A	3591	1/1	0.67	0.20	69,69,69,69	0
57	MG	2A	3271	1/1	0.68	0.21	59,59,59,59	0
57	MG	2A	3070	1/1	0.69	0.15	63,63,63,63	0
57	MG	2A	3112	1/1	0.69	0.21	61,61,61,61	0
57	MG	2A	3460	1/1	0.70	0.17	59,59,59,59	0
57	MG	1A	3793	1/1	0.70	0.13	67,67,67,67	0
57	MG	2a	1762	1/1	0.70	0.26	76,76,76,76	0
57	MG	2A	3451	1/1	0.70	0.15	56,56,56,56	0
57	MG	2A	3026	1/1	0.71	0.14	62,62,62,62	0
57	MG	2A	3111	1/1	0.71	0.37	69,69,69,69	0
57	MG	1A	3740	1/1	0.71	0.18	40,40,40,40	0
57	MG	1A	3363	1/1	0.72	0.15	58,58,58,58	0
57	MG	1Q	204	1/1	0.72	0.17	58,58,58,58	0
57	MG	2A	3471	1/1	0.72	0.23	68,68,68,68	0
57	MG	2A	3091	1/1	0.73	0.20	62,62,62,62	0
57	MG	1A	3154	1/1	0.73	0.08	70,70,70,70	0
57	MG	1A	3707	1/1	0.74	0.16	43,43,43,43	0
57	MG	2A	3594	1/1	0.74	0.22	82,82,82,82	0
57	MG	2A	3605	1/1	0.74	0.21	56,56,56,56	0
57	MG	1a	1704	1/1	0.74	0.26	68,68,68,68	0
57	MG	2v	102	1/1	0.74	0.22	67,67,67,67	0
57	MG	2x	108	1/1	0.74	0.27	67,67,67,67	0
57	MG	2a	1605	1/1	0.75	0.18	57,57,57,57	0
57	MG	2a	1676	1/1	0.75	0.35	66,66,66,66	0
57	MG	2A	3463	1/1	0.75	0.13	65,65,65,65	0
57	MG	2a	1750	1/1	0.75	0.16	48,48,48,48	0
57	MG	1a	1697	1/1	0.75	0.32	59,59,59,59	0
57	MG	1A	3592	1/1	0.75	0.33	51,51,51,51	0
57	MG	1A	3437	1/1	0.75	0.25	63,63,63,63	0
57	MG	1A	3540	1/1	0.75	0.16	16,16,16,16	0
57	MG	2a	1705	1/1	0.76	0.22	77,77,77,77	0
57	MG	2A	3110	1/1	0.76	0.34	68,68,68,68	0
57	MG	2a	1737	1/1	0.76	0.21	62,62,62,62	0
57	MG	2A	3566	1/1	0.76	0.18	56,56,56,56	0
57	MG	1a	1735	1/1	0.76	0.15	60,60,60,60	0
57	MG	2F	304	1/1	0.76	0.18	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1609	1/1	0.76	0.25	64,64,64,64	0
57	MG	2A	3034	1/1	0.76	0.31	52,52,52,52	0
57	MG	2A	3472	1/1	0.77	0.15	41,41,41,41	0
57	MG	1A	3725	1/1	0.77	0.13	15,15,15,15	0
57	MG	2A	3425	1/1	0.77	0.15	61,61,61,61	0
57	MG	1a	1674	1/1	0.77	0.39	70,70,70,70	0
57	MG	2A	3306	1/1	0.77	0.24	60,60,60,60	0
57	MG	2A	3327	1/1	0.77	0.17	66,66,66,66	0
57	MG	1A	3340	1/1	0.77	0.17	57,57,57,57	0
57	MG	1v	103	1/1	0.78	0.21	68,68,68,68	0
57	MG	2A	3488	1/1	0.78	0.16	58,58,58,58	0
57	MG	1x	104	1/1	0.78	0.28	63,63,63,63	0
57	MG	2a	1609	1/1	0.78	0.23	70,70,70,70	0
57	MG	2A	3346	1/1	0.78	0.18	67,67,67,67	0
57	MG	2a	1681	1/1	0.78	0.15	66,66,66,66	0
57	MG	2A	3540	1/1	0.78	0.19	66,66,66,66	0
57	MG	2a	1723	1/1	0.78	0.20	64,64,64,64	0
57	MG	1A	3431	1/1	0.78	0.10	53,53,53,53	0
57	MG	2A	3434	1/1	0.78	0.16	67,67,67,67	0
57	MG	2A	3576	1/1	0.78	0.15	69,69,69,69	0
57	MG	1a	1721	1/1	0.78	0.23	52,52,52,52	0
57	MG	1A	3510	1/1	0.78	0.13	45,45,45,45	0
57	MG	1A	3462	1/1	0.78	0.17	55,55,55,55	0
57	MG	1A	3465	1/1	0.78	0.13	31,31,31,31	0
57	MG	1A	3350	1/1	0.79	0.19	49,49,49,49	0
57	MG	2A	3646	1/1	0.79	0.28	56,56,56,56	0
57	MG	2F	301	1/1	0.79	0.19	47,47,47,47	0
57	MG	1A	3506	1/1	0.79	0.15	30,30,30,30	0
57	MG	1a	1666	1/1	0.79	0.36	65,65,65,65	0
57	MG	1a	1767	1/1	0.79	0.18	58,58,58,58	0
57	MG	2A	3492	1/1	0.79	0.17	59,59,59,59	0
57	MG	1A	3746	1/1	0.79	0.33	32,32,32,32	0
57	MG	2A	3371	1/1	0.79	0.17	70,70,70,70	0
57	MG	2A	3555	1/1	0.79	0.30	66,66,66,66	0
57	MG	2A	3403	1/1	0.79	0.16	45,45,45,45	0
57	MG	1A	3424	1/1	0.79	0.19	61,61,61,61	0
57	MG	2A	3144	1/1	0.79	0.11	61,61,61,61	0
57	MG	2A	3445	1/1	0.79	0.14	55,55,55,55	0
57	MG	2A	3148	1/1	0.79	0.28	69,69,69,69	0
57	MG	1A	3670	1/1	0.79	0.20	55,55,55,55	0
57	MG	1A	3476	1/1	0.79	0.24	75,75,75,75	0
57	MG	1a	1646	1/1	0.80	0.24	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3326	1/1	0.80	0.15	32,32,32,32	0
57	MG	2a	1654	1/1	0.80	0.27	70,70,70,70	0
57	MG	1B	211	1/1	0.80	0.15	52,52,52,52	0
57	MG	1A	3600	1/1	0.80	0.52	37,37,37,37	0
57	MG	1a	1682	1/1	0.80	0.23	64,64,64,64	0
57	MG	1A	3784	1/1	0.80	0.13	68,68,68,68	0
57	MG	2A	3486	1/1	0.80	0.11	65,65,65,65	0
57	MG	1a	1634	1/1	0.80	0.22	64,64,64,64	0
57	MG	2A	3391	1/1	0.80	0.21	53,53,53,53	0
57	MG	2a	1752	1/1	0.80	0.17	58,58,58,58	0
57	MG	1a	1635	1/1	0.80	0.28	65,65,65,65	0
57	MG	2A	3055	1/1	0.80	0.23	63,63,63,63	0
57	MG	2A	3261	1/1	0.80	0.25	53,53,53,53	0
57	MG	21	101	1/1	0.80	0.23	58,58,58,58	0
57	MG	2A	3559	1/1	0.81	0.12	61,61,61,61	0
57	MG	2A	3190	1/1	0.81	0.16	59,59,59,59	0
57	MG	2a	1653	1/1	0.81	0.36	52,52,52,52	0
57	MG	2A	3228	1/1	0.81	0.14	46,46,46,46	0
57	MG	2A	3348	1/1	0.81	0.15	67,67,67,67	0
57	MG	2A	3589	1/1	0.81	0.12	58,58,58,58	0
57	MG	2A	3360	1/1	0.81	0.14	53,53,53,53	0
57	MG	2A	3039	1/1	0.81	0.15	54,54,54,54	0
57	MG	2A	3598	1/1	0.81	0.11	60,60,60,60	0
57	MG	1A	3582	1/1	0.81	0.12	30,30,30,30	0
57	MG	2A	3398	1/1	0.81	0.16	53,53,53,53	0
57	MG	2A	3068	1/1	0.81	0.23	47,47,47,47	0
57	MG	1a	1618	1/1	0.81	0.25	60,60,60,60	0
57	MG	2A	3084	1/1	0.81	0.14	49,49,49,49	0
57	MG	2A	3444	1/1	0.81	0.18	49,49,49,49	0
57	MG	1a	1619	1/1	0.81	0.14	51,51,51,51	0
57	MG	10	104	1/1	0.82	0.09	42,42,42,42	0
57	MG	2Q	201	1/1	0.82	0.22	58,58,58,58	0
57	MG	2A	3195	1/1	0.82	0.17	56,56,56,56	0
57	MG	1a	1621	1/1	0.82	0.16	59,59,59,59	0
57	MG	2A	3453	1/1	0.82	0.40	52,52,52,52	0
57	MG	2a	1646	1/1	0.82	0.19	54,54,54,54	0
57	MG	1A	3696	1/1	0.82	0.15	40,40,40,40	0
57	MG	2A	3578	1/1	0.82	0.24	55,55,55,55	0
57	MG	2A	3583	1/1	0.82	0.16	71,71,71,71	0
57	MG	2A	3118	1/1	0.82	0.14	51,51,51,51	0
57	MG	1a	1717	1/1	0.82	0.26	48,48,48,48	0
57	MG	2a	1713	1/1	0.82	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
57	MG	2A	3275	1/1	0.82	0.16	39,39,39,39	0
57	MG	2A	3279	1/1	0.82	0.14	57,57,57,57	0
57	MG	2A	3602	1/1	0.82	0.30	42,42,42,42	0
57	MG	2A	3402	1/1	0.82	0.18	50,50,50,50	0
57	MG	2a	1751	1/1	0.82	0.18	72,72,72,72	0
57	MG	2A	3612	1/1	0.82	0.11	61,61,61,61	0
57	MG	2a	1757	1/1	0.82	0.17	78,78,78,78	0
57	MG	2A	3293	1/1	0.82	0.11	40,40,40,40	0
57	MG	2A	3409	1/1	0.82	0.18	51,51,51,51	0
57	MG	2k	201	1/1	0.82	0.16	58,58,58,58	0
57	MG	1A	3667	1/1	0.82	0.20	59,59,59,59	0
57	MG	2A	3184	1/1	0.82	0.22	53,53,53,53	0
57	MG	2A	3062	1/1	0.83	0.19	59,59,59,59	0
57	MG	2A	3367	1/1	0.83	0.15	44,44,44,44	0
57	MG	1A	3353	1/1	0.83	0.12	31,31,31,31	0
57	MG	23	102	1/1	0.83	0.26	63,63,63,63	0
57	MG	1a	1615	1/1	0.83	0.12	51,51,51,51	0
57	MG	1A	3574	1/1	0.83	0.13	59,59,59,59	0
57	MG	2a	1645	1/1	0.83	0.20	51,51,51,51	0
57	MG	2A	3401	1/1	0.83	0.16	55,55,55,55	0
57	MG	2a	1649	1/1	0.83	0.22	62,62,62,62	0
57	MG	2A	3090	1/1	0.83	0.15	50,50,50,50	0
57	MG	1A	3626	1/1	0.83	0.08	38,38,38,38	0
57	MG	2A	3269	1/1	0.83	0.14	47,47,47,47	0
57	MG	1A	3504	1/1	0.83	0.19	54,54,54,54	0
57	MG	2A	3107	1/1	0.83	0.21	69,69,69,69	0
57	MG	1x	106	1/1	0.83	0.20	59,59,59,59	0
57	MG	2A	3290	1/1	0.83	0.17	56,56,56,56	0
57	MG	2A	3450	1/1	0.83	0.17	46,46,46,46	0
57	MG	2A	3024	1/1	0.83	0.20	66,66,66,66	0
57	MG	2A	3297	1/1	0.83	0.11	41,41,41,41	0
57	MG	1a	1622	1/1	0.83	0.31	66,66,66,66	0
57	MG	1A	3718	1/1	0.83	0.14	51,51,51,51	0
57	MG	2A	3619	1/1	0.83	0.10	66,66,66,66	0
57	MG	2A	3629	1/1	0.83	0.21	60,60,60,60	0
57	MG	2A	3134	1/1	0.83	0.23	59,59,59,59	0
57	MG	2A	3143	1/1	0.83	0.12	50,50,50,50	0
57	MG	1A	3591	1/1	0.83	0.12	29,29,29,29	0
57	MG	1A	3663	1/1	0.83	0.11	39,39,39,39	0
57	MG	2A	3509	1/1	0.84	0.12	48,48,48,48	0
57	MG	2A	3399	1/1	0.84	0.14	43,43,43,43	0
57	MG	2A	3526	1/1	0.84	0.17	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3076	1/1	0.84	0.17	53,53,53,53	0
57	MG	1a	1747	1/1	0.84	0.11	48,48,48,48	0
57	MG	1A	3396	1/1	0.84	0.12	20,20,20,20	0
57	MG	1a	1756	1/1	0.84	0.19	57,57,57,57	0
57	MG	1A	3206	1/1	0.84	0.08	15,15,15,15	0
57	MG	1a	1651	1/1	0.84	0.28	67,67,67,67	0
57	MG	1A	3553	1/1	0.84	0.13	38,38,38,38	0
57	MG	11	102	1/1	0.84	0.23	64,64,64,64	0
57	MG	1A	3638	1/1	0.84	0.21	55,55,55,55	0
57	MG	2a	1668	1/1	0.84	0.20	60,60,60,60	0
57	MG	1y	103	1/1	0.84	0.29	81,81,81,81	0
57	MG	2a	1677	1/1	0.84	0.18	59,59,59,59	0
57	MG	1A	3644	1/1	0.84	0.11	54,54,54,54	0
57	MG	1A	3120	1/1	0.84	0.17	68,68,68,68	0
57	MG	1A	3436	1/1	0.84	0.05	9,9,9,9	0
57	MG	1A	3780	1/1	0.84	0.17	43,43,43,43	0
57	MG	2A	3047	1/1	0.84	0.12	48,48,48,48	0
57	MG	1A	3044	1/1	0.84	0.11	57,57,57,57	0
57	MG	2a	1739	1/1	0.84	0.20	58,58,58,58	0
57	MG	1a	1726	1/1	0.84	0.21	70,70,70,70	0
57	MG	1a	1734	1/1	0.84	0.23	54,54,54,54	0
57	MG	1A	3456	1/1	0.84	0.13	36,36,36,36	0
57	MG	2A	3643	1/1	0.84	0.12	45,45,45,45	0
57	MG	2A	3500	1/1	0.84	0.12	47,47,47,47	0
57	MG	2A	3656	1/1	0.84	0.27	49,49,49,49	0
57	MG	2B	206	1/1	0.84	0.35	54,54,54,54	0
57	MG	2D	306	1/1	0.84	0.19	62,62,62,62	0
57	MG	2D	307	1/1	0.84	0.16	56,56,56,56	0
57	MG	1a	1714	1/1	0.85	0.28	61,61,61,61	0
57	MG	1A	3007	1/1	0.85	0.08	30,30,30,30	0
57	MG	2A	3249	1/1	0.85	0.26	52,52,52,52	0
57	MG	2A	3254	1/1	0.85	0.17	63,63,63,63	0
57	MG	1A	3123	1/1	0.85	0.18	21,21,21,21	0
57	MG	1A	3634	1/1	0.85	0.18	56,56,56,56	0
57	MG	1A	3447	1/1	0.85	0.14	37,37,37,37	0
57	MG	1A	3221	1/1	0.85	0.18	49,49,49,49	0
57	MG	1a	1744	1/1	0.85	0.22	70,70,70,70	0
57	MG	1A	3266	1/1	0.85	0.12	59,59,59,59	0
57	MG	2A	3476	1/1	0.85	0.20	49,49,49,49	0
57	MG	2F	303	1/1	0.85	0.16	57,57,57,57	0
57	MG	1A	3307	1/1	0.85	0.20	54,54,54,54	0
57	MG	1a	1755	1/1	0.85	0.25	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1640	1/1	0.85	0.17	61,61,61,61	0
57	MG	1A	3318	1/1	0.85	0.28	51,51,51,51	0
57	MG	2A	3496	1/1	0.85	0.30	57,57,57,57	0
57	MG	1A	3585	1/1	0.85	0.15	24,24,24,24	0
57	MG	2a	1633	1/1	0.85	0.18	60,60,60,60	0
57	MG	2A	3508	1/1	0.85	0.20	55,55,55,55	0
57	MG	1A	3149	1/1	0.85	0.23	47,47,47,47	0
57	MG	2a	1648	1/1	0.85	0.19	53,53,53,53	0
57	MG	1A	3673	1/1	0.85	0.17	45,45,45,45	0
57	MG	2A	3516	1/1	0.85	0.17	51,51,51,51	0
57	MG	1A	3684	1/1	0.85	0.12	42,42,42,42	0
57	MG	2a	1658	1/1	0.85	0.20	54,54,54,54	0
57	MG	2a	1661	1/1	0.85	0.29	66,66,66,66	0
57	MG	2a	1666	1/1	0.85	0.30	70,70,70,70	0
57	MG	1a	1675	1/1	0.85	0.22	57,57,57,57	0
57	MG	2A	3546	1/1	0.85	0.24	59,59,59,59	0
57	MG	2A	3365	1/1	0.85	0.17	64,64,64,64	0
57	MG	2a	1678	1/1	0.85	0.14	65,65,65,65	0
57	MG	2A	3556	1/1	0.85	0.14	50,50,50,50	0
57	MG	2a	1698	1/1	0.85	0.14	71,71,71,71	0
57	MG	2A	3014	1/1	0.85	0.17	48,48,48,48	0
57	MG	2A	3370	1/1	0.85	0.15	53,53,53,53	0
57	MG	2a	1716	1/1	0.85	0.17	80,80,80,80	0
57	MG	1A	3502	1/1	0.85	0.14	30,30,30,30	0
57	MG	2a	1731	1/1	0.85	0.18	56,56,56,56	0
57	MG	2A	3573	1/1	0.85	0.12	82,82,82,82	0
57	MG	2A	3154	1/1	0.85	0.20	59,59,59,59	0
57	MG	2A	3176	1/1	0.85	0.26	53,53,53,53	0
57	MG	2a	1742	1/1	0.85	0.14	66,66,66,66	0
57	MG	1a	1684	1/1	0.85	0.14	57,57,57,57	0
57	MG	2A	3586	1/1	0.85	0.15	81,81,81,81	0
57	MG	1a	1603	1/1	0.85	0.19	54,54,54,54	0
57	MG	1A	3698	1/1	0.85	0.15	53,53,53,53	0
57	MG	2A	3197	1/1	0.85	0.14	62,62,62,62	0
57	MG	2A	3203	1/1	0.85	0.16	57,57,57,57	0
57	MG	2e	201	1/1	0.85	0.18	66,66,66,66	0
57	MG	2A	3411	1/1	0.85	0.13	26,26,26,26	0
57	MG	2A	3207	1/1	0.85	0.13	58,58,58,58	0
57	MG	2x	104	1/1	0.85	0.19	69,69,69,69	0
57	MG	2A	3429	1/1	0.85	0.14	33,33,33,33	0
57	MG	2A	3350	1/1	0.86	0.17	48,48,48,48	0
57	MG	2A	3167	1/1	0.86	0.23	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3174	1/1	0.86	0.20	58,58,58,58	0
57	MG	2a	1604	1/1	0.86	0.17	59,59,59,59	0
57	MG	1A	3575	1/1	0.86	0.11	17,17,17,17	0
57	MG	2A	3533	1/1	0.86	0.07	65,65,65,65	0
57	MG	1A	3113	1/1	0.86	0.16	32,32,32,32	0
57	MG	1A	3351	1/1	0.86	0.14	46,46,46,46	0
57	MG	2A	3389	1/1	0.86	0.15	50,50,50,50	0
57	MG	1a	1742	1/1	0.86	0.26	86,86,86,86	0
57	MG	1A	3650	1/1	0.86	0.11	44,44,44,44	0
57	MG	2a	1652	1/1	0.86	0.30	44,44,44,44	0
57	MG	2A	3199	1/1	0.86	0.15	55,55,55,55	0
57	MG	2A	3400	1/1	0.86	0.11	54,54,54,54	0
57	MG	2a	1655	1/1	0.86	0.24	56,56,56,56	0
57	MG	1a	1746	1/1	0.86	0.17	62,62,62,62	0
57	MG	1A	3066	1/1	0.86	0.32	51,51,51,51	0
57	MG	2A	3216	1/1	0.86	0.14	40,40,40,40	0
57	MG	2A	3581	1/1	0.86	0.10	52,52,52,52	0
57	MG	2A	3226	1/1	0.86	0.17	51,51,51,51	0
57	MG	1A	3073	1/1	0.86	0.51	62,62,62,62	0
57	MG	2A	3077	1/1	0.86	0.27	63,63,63,63	0
57	MG	2A	3248	1/1	0.86	0.18	39,39,39,39	0
57	MG	2a	1687	1/1	0.86	0.13	56,56,56,56	0
57	MG	1a	1677	1/1	0.86	0.23	58,58,58,58	0
57	MG	2A	3595	1/1	0.86	0.13	63,63,63,63	0
57	MG	2a	1709	1/1	0.86	0.13	47,47,47,47	0
57	MG	2A	3251	1/1	0.86	0.18	62,62,62,62	0
57	MG	1a	1678	1/1	0.86	0.20	57,57,57,57	0
57	MG	1a	1757	1/1	0.86	0.22	57,57,57,57	0
57	MG	1a	1681	1/1	0.86	0.39	74,74,74,74	0
57	MG	2A	3102	1/1	0.86	0.34	67,67,67,67	0
57	MG	1A	3334	1/1	0.86	0.12	39,39,39,39	0
57	MG	1i	201	1/1	0.86	0.23	70,70,70,70	0
57	MG	1a	1683	1/1	0.86	0.19	60,60,60,60	0
57	MG	1A	3768	1/1	0.86	0.10	15,15,15,15	0
57	MG	1A	3775	1/1	0.86	0.19	62,62,62,62	0
57	MG	2A	3650	1/1	0.86	0.17	61,61,61,61	0
57	MG	1A	3411	1/1	0.86	0.13	39,39,39,39	0
57	MG	2B	204	1/1	0.86	0.14	49,49,49,49	0
57	MG	2A	3314	1/1	0.86	0.18	47,47,47,47	0
57	MG	2A	3140	1/1	0.86	0.10	51,51,51,51	0
57	MG	1A	3681	1/1	0.86	0.27	20,20,20,20	0
57	MG	2v	101	1/1	0.86	0.23	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3015	1/1	0.86	0.20	42,42,42,42	0
57	MG	1A	3421	1/1	0.86	0.09	49,49,49,49	0
57	MG	1A	3106	1/1	0.86	0.14	45,45,45,45	0
57	MG	1B	209	1/1	0.87	0.15	59,59,59,59	0
57	MG	1a	1637	1/1	0.87	0.27	62,62,62,62	0
57	MG	2R	201	1/1	0.87	0.14	51,51,51,51	0
57	MG	2A	3069	1/1	0.87	0.24	61,61,61,61	0
57	MG	2A	3522	1/1	0.87	0.26	64,64,64,64	0
57	MG	1A	3714	1/1	0.87	0.26	25,25,25,25	0
57	MG	2A	3532	1/1	0.87	0.19	54,54,54,54	0
57	MG	2A	3205	1/1	0.87	0.12	39,39,39,39	0
57	MG	2a	1625	1/1	0.87	0.29	61,61,61,61	0
57	MG	2A	3373	1/1	0.87	0.09	33,33,33,33	0
57	MG	1B	220	1/1	0.87	0.14	44,44,44,44	0
57	MG	1a	1647	1/1	0.87	0.14	53,53,53,53	0
57	MG	2A	3392	1/1	0.87	0.18	59,59,59,59	0
57	MG	2A	3397	1/1	0.87	0.17	45,45,45,45	0
57	MG	2A	3221	1/1	0.87	0.32	56,56,56,56	0
57	MG	2A	3568	1/1	0.87	0.10	39,39,39,39	0
57	MG	1E	307	1/1	0.87	0.18	42,42,42,42	0
57	MG	1a	1658	1/1	0.87	0.19	54,54,54,54	0
57	MG	2A	3230	1/1	0.87	0.12	50,50,50,50	0
57	MG	1P	204	1/1	0.87	0.11	43,43,43,43	0
57	MG	1A	3402	1/1	0.87	0.11	24,24,24,24	0
57	MG	2a	1667	1/1	0.87	0.15	55,55,55,55	0
57	MG	1a	1667	1/1	0.87	0.27	59,59,59,59	0
57	MG	1V	204	1/1	0.87	0.14	30,30,30,30	0
57	MG	1A	3580	1/1	0.87	0.14	16,16,16,16	0
57	MG	1A	3646	1/1	0.87	0.10	36,36,36,36	0
57	MG	2A	3593	1/1	0.87	0.17	57,57,57,57	0
57	MG	18	101	1/1	0.87	0.21	44,44,44,44	0
57	MG	1A	3359	1/1	0.87	0.12	12,12,12,12	0
57	MG	2A	3124	1/1	0.87	0.27	49,49,49,49	0
57	MG	1A	3685	1/1	0.87	0.10	59,59,59,59	0
57	MG	1a	1613	1/1	0.87	0.15	41,41,41,41	0
57	MG	2A	3607	1/1	0.87	0.18	31,31,31,31	0
57	MG	2a	1719	1/1	0.87	0.14	61,61,61,61	0
57	MG	1A	3694	1/1	0.87	0.16	45,45,45,45	0
57	MG	1a	1687	1/1	0.87	0.12	38,38,38,38	0
57	MG	2A	3299	1/1	0.87	0.12	45,45,45,45	0
57	MG	1A	3631	1/1	0.87	0.13	33,33,33,33	0
57	MG	1A	3096	1/1	0.87	0.14	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1741	1/1	0.87	0.18	62,62,62,62	0
57	MG	1a	1708	1/1	0.87	0.15	64,64,64,64	0
57	MG	2A	3645	1/1	0.87	0.14	65,65,65,65	0
57	MG	2A	3479	1/1	0.87	0.20	42,42,42,42	0
57	MG	2A	3481	1/1	0.87	0.13	40,40,40,40	0
57	MG	1A	3705	1/1	0.87	0.17	27,27,27,27	0
57	MG	2A	3657	1/1	0.87	0.27	68,68,68,68	0
57	MG	2B	202	1/1	0.87	0.17	64,64,64,64	0
57	MG	1A	3006	1/1	0.87	0.14	53,53,53,53	0
57	MG	2f	201	1/1	0.87	0.18	53,53,53,53	0
57	MG	1B	208	1/1	0.87	0.18	52,52,52,52	0
57	MG	1a	1723	1/1	0.87	0.11	53,53,53,53	0
57	MG	2A	3191	1/1	0.87	0.26	55,55,55,55	0
57	MG	2A	3351	1/1	0.87	0.12	45,45,45,45	0
57	MG	2A	3359	1/1	0.87	0.09	63,63,63,63	0
57	MG	2A	3394	1/1	0.88	0.13	39,39,39,39	0
57	MG	1A	3011	1/1	0.88	0.11	47,47,47,47	0
57	MG	2A	3123	1/1	0.88	0.12	52,52,52,52	0
57	MG	1a	1730	1/1	0.88	0.15	46,46,46,46	0
57	MG	1a	1670	1/1	0.88	0.22	53,53,53,53	0
57	MG	2a	1614	1/1	0.88	0.15	49,49,49,49	0
57	MG	1G	203	1/1	0.88	0.09	39,39,39,39	0
57	MG	2a	1626	1/1	0.88	0.17	47,47,47,47	0
57	MG	2A	3562	1/1	0.88	0.16	68,68,68,68	0
57	MG	2a	1644	1/1	0.88	0.24	58,58,58,58	0
57	MG	1A	3770	1/1	0.88	0.11	45,45,45,45	0
57	MG	1A	3060	1/1	0.88	0.12	41,41,41,41	0
57	MG	1a	1626	1/1	0.88	0.14	45,45,45,45	0
57	MG	2A	3277	1/1	0.88	0.11	67,67,67,67	0
57	MG	2A	3413	1/1	0.88	0.23	45,45,45,45	0
57	MG	2A	3417	1/1	0.88	0.19	74,74,74,74	0
57	MG	2A	3150	1/1	0.88	0.22	52,52,52,52	0
57	MG	1a	1628	1/1	0.88	0.26	55,55,55,55	0
57	MG	1a	1750	1/1	0.88	0.24	66,66,66,66	0
57	MG	2A	3171	1/1	0.88	0.12	37,37,37,37	0
57	MG	2A	3064	1/1	0.88	0.13	47,47,47,47	0
57	MG	1A	3322	1/1	0.88	0.28	13,13,13,13	0
57	MG	1Z	301	1/1	0.88	0.11	48,48,48,48	0
57	MG	1A	3482	1/1	0.88	0.17	51,51,51,51	0
57	MG	1a	1638	1/1	0.88	0.08	56,56,56,56	0
57	MG	2A	3462	1/1	0.88	0.20	38,38,38,38	0
57	MG	2A	3193	1/1	0.88	0.15	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1686	1/1	0.88	0.18	43,43,43,43	0
57	MG	1A	3134	1/1	0.88	0.09	36,36,36,36	0
57	MG	2A	3080	1/1	0.88	0.29	61,61,61,61	0
57	MG	2A	3617	1/1	0.88	0.10	53,53,53,53	0
57	MG	1A	3373	1/1	0.88	0.16	42,42,42,42	0
57	MG	2A	3478	1/1	0.88	0.17	65,65,65,65	0
57	MG	1a	1601	1/1	0.88	0.12	53,53,53,53	0
57	MG	2A	3357	1/1	0.88	0.09	53,53,53,53	0
57	MG	2A	3641	1/1	0.88	0.24	52,52,52,52	0
57	MG	2A	3482	1/1	0.88	0.12	45,45,45,45	0
57	MG	2A	3485	1/1	0.88	0.19	64,64,64,64	0
57	MG	1A	3226	1/1	0.88	0.09	37,37,37,37	0
57	MG	1x	103	1/1	0.88	0.17	51,51,51,51	0
57	MG	2A	3361	1/1	0.88	0.16	47,47,47,47	0
57	MG	1A	3090	1/1	0.88	0.34	38,38,38,38	0
57	MG	2a	1749	1/1	0.88	0.21	57,57,57,57	0
57	MG	2A	3105	1/1	0.88	0.11	43,43,43,43	0
57	MG	2A	3223	1/1	0.88	0.11	68,68,68,68	0
57	MG	1A	3276	1/1	0.88	0.26	44,44,44,44	0
57	MG	2B	207	1/1	0.88	0.23	60,60,60,60	0
57	MG	2a	1758	1/1	0.88	0.13	65,65,65,65	0
57	MG	2D	301	1/1	0.88	0.18	34,34,34,34	0
57	MG	1E	303	1/1	0.88	0.20	49,49,49,49	0
57	MG	2A	3376	1/1	0.88	0.18	52,52,52,52	0
57	MG	2A	3383	1/1	0.88	0.19	55,55,55,55	0
57	MG	2A	3001	1/1	0.88	0.23	50,50,50,50	0
57	MG	2A	3525	1/1	0.88	0.20	61,61,61,61	0
57	MG	2A	3010	1/1	0.88	0.10	55,55,55,55	0
57	MG	2A	3242	1/1	0.88	0.12	44,44,44,44	0
57	MG	2V	201	1/1	0.88	0.24	46,46,46,46	0
57	MG	2x	109	1/1	0.88	0.18	60,60,60,60	0
57	MG	1A	3622	1/1	0.89	0.17	60,60,60,60	0
57	MG	1y	102	1/1	0.89	0.24	63,63,63,63	0
57	MG	1A	3246	1/1	0.89	0.22	66,66,66,66	0
57	MG	1A	3629	1/1	0.89	0.15	29,29,29,29	0
57	MG	1A	3264	1/1	0.89	0.12	34,34,34,34	0
57	MG	1A	3027	1/1	0.89	0.09	40,40,40,40	0
57	MG	25	102	1/1	0.89	0.12	54,54,54,54	0
57	MG	1A	3270	1/1	0.89	0.34	56,56,56,56	0
57	MG	1A	3152	1/1	0.89	0.09	66,66,66,66	0
57	MG	2a	1606	1/1	0.89	0.22	50,50,50,50	0
57	MG	2a	1608	1/1	0.89	0.32	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3277	1/1	0.89	0.40	36,36,36,36	0
57	MG	2A	3536	1/1	0.89	0.14	49,49,49,49	0
57	MG	2a	1615	1/1	0.89	0.25	58,58,58,58	0
57	MG	2a	1624	1/1	0.89	0.14	54,54,54,54	0
57	MG	1a	1696	1/1	0.89	0.11	45,45,45,45	0
57	MG	2A	3544	1/1	0.89	0.16	56,56,56,56	0
57	MG	2a	1628	1/1	0.89	0.09	45,45,45,45	0
57	MG	1A	3443	1/1	0.89	0.10	22,22,22,22	0
57	MG	2a	1641	1/1	0.89	0.11	55,55,55,55	0
57	MG	2A	3553	1/1	0.89	0.10	26,26,26,26	0
57	MG	1A	3761	1/1	0.89	0.08	39,39,39,39	0
57	MG	2A	3048	1/1	0.89	0.19	64,64,64,64	0
57	MG	2A	3053	1/1	0.89	0.16	51,51,51,51	0
57	MG	2A	3054	1/1	0.89	0.20	33,33,33,33	0
57	MG	1A	3559	1/1	0.89	0.10	26,26,26,26	0
57	MG	1a	1713	1/1	0.89	0.14	46,46,46,46	0
57	MG	1A	3567	1/1	0.89	0.11	45,45,45,45	0
57	MG	1A	3652	1/1	0.89	0.15	43,43,43,43	0
57	MG	2A	3574	1/1	0.89	0.11	50,50,50,50	0
57	MG	1A	3658	1/1	0.89	0.13	39,39,39,39	0
57	MG	1a	1624	1/1	0.89	0.18	49,49,49,49	0
57	MG	1A	3445	1/1	0.89	0.14	33,33,33,33	0
57	MG	1a	1627	1/1	0.89	0.13	51,51,51,51	0
57	MG	2a	1670	1/1	0.89	0.28	58,58,58,58	0
57	MG	1A	3122	1/1	0.89	0.27	37,37,37,37	0
57	MG	2A	3081	1/1	0.89	0.21	49,49,49,49	0
57	MG	2A	3412	1/1	0.89	0.22	66,66,66,66	0
57	MG	1a	1629	1/1	0.89	0.11	37,37,37,37	0
57	MG	1A	3029	1/1	0.89	0.14	65,65,65,65	0
57	MG	1A	3378	1/1	0.89	0.14	45,45,45,45	0
57	MG	2A	3597	1/1	0.89	0.15	35,35,35,35	0
57	MG	2A	3098	1/1	0.89	0.16	46,46,46,46	0
57	MG	2A	3099	1/1	0.89	0.08	46,46,46,46	0
57	MG	2a	1710	1/1	0.89	0.17	56,56,56,56	0
57	MG	1A	3674	1/1	0.89	0.09	49,49,49,49	0
57	MG	1A	3380	1/1	0.89	0.19	46,46,46,46	0
57	MG	1E	302	1/1	0.89	0.10	16,16,16,16	0
57	MG	2a	1721	1/1	0.89	0.16	47,47,47,47	0
57	MG	1A	3683	1/1	0.89	0.11	55,55,55,55	0
57	MG	2A	3278	1/1	0.89	0.15	58,58,58,58	0
57	MG	2A	3622	1/1	0.89	0.27	58,58,58,58	0
57	MG	1A	3466	1/1	0.89	0.24	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3289	1/1	0.89	0.13	41,41,41,41	0
57	MG	1F	301	1/1	0.89	0.15	39,39,39,39	0
57	MG	2A	3468	1/1	0.89	0.16	58,58,58,58	0
57	MG	2a	1747	1/1	0.89	0.24	53,53,53,53	0
57	MG	2A	3292	1/1	0.89	0.09	30,30,30,30	0
57	MG	1F	305	1/1	0.89	0.33	31,31,31,31	0
57	MG	2A	3117	1/1	0.89	0.29	59,59,59,59	0
57	MG	1a	1761	1/1	0.89	0.10	45,45,45,45	0
57	MG	2A	3654	1/1	0.89	0.15	61,61,61,61	0
57	MG	1A	3064	1/1	0.89	0.19	45,45,45,45	0
57	MG	2A	3310	1/1	0.89	0.19	29,29,29,29	0
57	MG	1a	1664	1/1	0.89	0.25	53,53,53,53	0
57	MG	2A	3125	1/1	0.89	0.27	45,45,45,45	0
57	MG	2A	3333	1/1	0.89	0.21	61,61,61,61	0
57	MG	2A	3132	1/1	0.89	0.06	51,51,51,51	0
57	MG	2A	3490	1/1	0.89	0.16	55,55,55,55	0
57	MG	1N	203	1/1	0.89	0.12	41,41,41,41	0
57	MG	2x	103	1/1	0.89	0.18	47,47,47,47	0
57	MG	1A	3136	1/1	0.89	0.36	46,46,46,46	0
57	MG	1A	3621	1/1	0.89	0.16	60,60,60,60	0
57	MG	1V	202	1/1	0.89	0.39	30,30,30,30	0
57	MG	2A	3257	1/1	0.90	0.13	53,53,53,53	0
57	MG	2B	203	1/1	0.90	0.17	57,57,57,57	0
57	MG	1A	3699	1/1	0.90	0.23	51,51,51,51	0
57	MG	1A	3602	1/1	0.90	0.10	48,48,48,48	0
57	MG	1a	1719	1/1	0.90	0.15	48,48,48,48	0
57	MG	2B	210	1/1	0.90	0.08	60,60,60,60	0
57	MG	1A	3611	1/1	0.90	0.16	43,43,43,43	0
57	MG	1A	3618	1/1	0.90	0.15	38,38,38,38	0
57	MG	1A	3620	1/1	0.90	0.12	53,53,53,53	0
57	MG	2A	3093	1/1	0.90	0.19	48,48,48,48	0
57	MG	2A	3483	1/1	0.90	0.10	46,46,46,46	0
57	MG	2A	3484	1/1	0.90	0.40	39,39,39,39	0
57	MG	2A	3094	1/1	0.90	0.17	51,51,51,51	0
57	MG	1A	3720	1/1	0.90	0.14	51,51,51,51	0
57	MG	2A	3487	1/1	0.90	0.14	46,46,46,46	0
57	MG	1a	1732	1/1	0.90	0.10	50,50,50,50	0
57	MG	1A	3019	1/1	0.90	0.12	44,44,44,44	0
57	MG	1a	1617	1/1	0.90	0.28	48,48,48,48	0
57	MG	1a	1741	1/1	0.90	0.17	63,63,63,63	0
57	MG	2A	3106	1/1	0.90	0.18	58,58,58,58	0
57	MG	2A	3308	1/1	0.90	0.07	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1607	1/1	0.90	0.19	47,47,47,47	0
57	MG	2A	3505	1/1	0.90	0.16	39,39,39,39	0
57	MG	1A	3107	1/1	0.90	0.09	31,31,31,31	0
57	MG	2a	1612	1/1	0.90	0.23	60,60,60,60	0
57	MG	1A	3267	1/1	0.90	0.23	24,24,24,24	0
57	MG	1A	3747	1/1	0.90	0.19	16,16,16,16	0
57	MG	2A	3331	1/1	0.90	0.14	35,35,35,35	0
57	MG	1A	3627	1/1	0.90	0.09	14,14,14,14	0
57	MG	2A	3524	1/1	0.90	0.11	45,45,45,45	0
57	MG	1A	3757	1/1	0.90	0.13	39,39,39,39	0
57	MG	1A	3170	1/1	0.90	0.09	53,53,53,53	0
57	MG	2a	1635	1/1	0.90	0.12	65,65,65,65	0
57	MG	2a	1640	1/1	0.90	0.20	39,39,39,39	0
57	MG	1A	3467	1/1	0.90	0.12	28,28,28,28	0
57	MG	2a	1642	1/1	0.90	0.20	44,44,44,44	0
57	MG	1A	3471	1/1	0.90	0.15	32,32,32,32	0
57	MG	1A	3177	1/1	0.90	0.20	44,44,44,44	0
57	MG	1A	3384	1/1	0.90	0.14	40,40,40,40	0
57	MG	2A	3354	1/1	0.90	0.14	35,35,35,35	0
57	MG	1a	1762	1/1	0.90	0.14	50,50,50,50	0
57	MG	1A	3389	1/1	0.90	0.11	18,18,18,18	0
57	MG	2A	3554	1/1	0.90	0.20	50,50,50,50	0
57	MG	2A	3142	1/1	0.90	0.17	42,42,42,42	0
57	MG	1a	1766	1/1	0.90	0.13	54,54,54,54	0
57	MG	1A	3785	1/1	0.90	0.11	61,61,61,61	0
57	MG	1A	3786	1/1	0.90	0.08	19,19,19,19	0
57	MG	2a	1662	1/1	0.90	0.10	54,54,54,54	0
57	MG	2A	3563	1/1	0.90	0.23	57,57,57,57	0
57	MG	1v	101	1/1	0.90	0.14	48,48,48,48	0
57	MG	1A	3790	1/1	0.90	0.22	45,45,45,45	0
57	MG	2A	3156	1/1	0.90	0.18	51,51,51,51	0
57	MG	2a	1674	1/1	0.90	0.16	60,60,60,60	0
57	MG	2a	1675	1/1	0.90	0.13	59,59,59,59	0
57	MG	2A	3572	1/1	0.90	0.16	56,56,56,56	0
57	MG	1a	1645	1/1	0.90	0.13	66,66,66,66	0
57	MG	2A	3382	1/1	0.90	0.17	47,47,47,47	0
57	MG	2a	1679	1/1	0.90	0.13	59,59,59,59	0
57	MG	2A	3575	1/1	0.90	0.25	53,53,53,53	0
57	MG	1A	3792	1/1	0.90	0.11	41,41,41,41	0
57	MG	1A	3393	1/1	0.90	0.10	20,20,20,20	0
57	MG	2a	1695	1/1	0.90	0.10	61,61,61,61	0
57	MG	2A	3580	1/1	0.90	0.13	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2a	1702	1/1	0.90	0.24	57,57,57,57	0
57	MG	1B	201	1/1	0.90	0.12	58,58,58,58	0
57	MG	2a	1707	1/1	0.90	0.16	49,49,49,49	0
57	MG	1B	202	1/1	0.90	0.22	43,43,43,43	0
57	MG	2A	3393	1/1	0.90	0.12	19,19,19,19	0
57	MG	1A	3179	1/1	0.90	0.11	38,38,38,38	0
57	MG	2A	3590	1/1	0.90	0.18	45,45,45,45	0
57	MG	2A	3396	1/1	0.90	0.13	56,56,56,56	0
57	MG	1A	3287	1/1	0.90	0.08	42,42,42,42	0
57	MG	1A	3190	1/1	0.90	0.12	29,29,29,29	0
57	MG	2a	1725	1/1	0.90	0.28	57,57,57,57	0
57	MG	2a	1726	1/1	0.90	0.22	58,58,58,58	0
57	MG	2a	1730	1/1	0.90	0.12	44,44,44,44	0
57	MG	1A	3520	1/1	0.90	0.14	23,23,23,23	0
57	MG	1D	302	1/1	0.90	0.37	36,36,36,36	0
57	MG	1A	3204	1/1	0.90	0.22	42,42,42,42	0
57	MG	2A	3200	1/1	0.90	0.15	55,55,55,55	0
57	MG	1A	3049	1/1	0.90	0.12	43,43,43,43	0
57	MG	1E	305	1/1	0.90	0.11	46,46,46,46	0
57	MG	2a	1745	1/1	0.90	0.13	59,59,59,59	0
57	MG	2A	3043	1/1	0.90	0.16	59,59,59,59	0
57	MG	1A	3213	1/1	0.90	0.14	41,41,41,41	0
57	MG	1A	3097	1/1	0.90	0.10	32,32,32,32	0
57	MG	1A	3144	1/1	0.90	0.19	28,28,28,28	0
57	MG	2A	3626	1/1	0.90	0.08	47,47,47,47	0
57	MG	2A	3627	1/1	0.90	0.12	54,54,54,54	0
57	MG	1A	3439	1/1	0.90	0.08	49,49,49,49	0
57	MG	2A	3227	1/1	0.90	0.19	46,46,46,46	0
57	MG	1A	3238	1/1	0.90	0.10	38,38,38,38	0
57	MG	2A	3640	1/1	0.90	0.17	37,37,37,37	0
57	MG	1A	3444	1/1	0.90	0.10	24,24,24,24	0
57	MG	1A	3121	1/1	0.90	0.09	34,34,34,34	0
57	MG	1A	3692	1/1	0.90	0.09	31,31,31,31	0
57	MG	1A	3446	1/1	0.90	0.09	23,23,23,23	0
57	MG	1A	3253	1/1	0.90	0.15	48,48,48,48	0
57	MG	2A	3072	1/1	0.90	0.16	53,53,53,53	0
57	MG	2x	106	1/1	0.90	0.24	68,68,68,68	0
57	MG	2A	3252	1/1	0.90	0.14	49,49,49,49	0
57	MG	1A	3454	1/1	0.90	0.10	19,19,19,19	0
57	MG	2A	3637	1/1	0.91	0.14	34,34,34,34	0
57	MG	2A	3188	1/1	0.91	0.10	51,51,51,51	0
57	MG	2A	3005	1/1	0.91	0.15	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3268	1/1	0.91	0.14	30,30,30,30	0
57	MG	2A	3192	1/1	0.91	0.16	47,47,47,47	0
57	MG	1A	3100	1/1	0.91	0.25	35,35,35,35	0
57	MG	2A	3416	1/1	0.91	0.07	34,34,34,34	0
57	MG	2A	3653	1/1	0.91	0.12	49,49,49,49	0
57	MG	1a	1676	1/1	0.91	0.10	41,41,41,41	0
57	MG	2A	3020	1/1	0.91	0.10	51,51,51,51	0
57	MG	2A	3428	1/1	0.91	0.22	50,50,50,50	0
57	MG	1P	203	1/1	0.91	0.15	26,26,26,26	0
57	MG	1A	3232	1/1	0.91	0.12	31,31,31,31	0
57	MG	2A	3201	1/1	0.91	0.14	45,45,45,45	0
57	MG	2B	205	1/1	0.91	0.14	53,53,53,53	0
57	MG	2A	3027	1/1	0.91	0.41	47,47,47,47	0
57	MG	2A	3448	1/1	0.91	0.22	55,55,55,55	0
57	MG	1a	1680	1/1	0.91	0.17	39,39,39,39	0
57	MG	2A	3036	1/1	0.91	0.10	49,49,49,49	0
57	MG	1A	3358	1/1	0.91	0.09	33,33,33,33	0
57	MG	2A	3220	1/1	0.91	0.17	50,50,50,50	0
57	MG	2E	302	1/1	0.91	0.28	40,40,40,40	0
57	MG	1U	207	1/1	0.91	0.11	31,31,31,31	0
57	MG	2A	3044	1/1	0.91	0.12	55,55,55,55	0
57	MG	2A	3464	1/1	0.91	0.10	52,52,52,52	0
57	MG	1A	3512	1/1	0.91	0.08	36,36,36,36	0
57	MG	2A	3469	1/1	0.91	0.14	63,63,63,63	0
57	MG	1A	3159	1/1	0.91	0.12	28,28,28,28	0
57	MG	1a	1686	1/1	0.91	0.23	44,44,44,44	0
57	MG	2A	3229	1/1	0.91	0.08	38,38,38,38	0
57	MG	25	101	1/1	0.91	0.30	42,42,42,42	0
57	MG	1A	3730	1/1	0.91	0.11	36,36,36,36	0
57	MG	1Z	302	1/1	0.91	0.17	44,44,44,44	0
57	MG	2A	3238	1/1	0.91	0.22	49,49,49,49	0
57	MG	2A	3241	1/1	0.91	0.16	60,60,60,60	0
57	MG	1A	3168	1/1	0.91	0.16	42,42,42,42	0
57	MG	2A	3063	1/1	0.91	0.09	55,55,55,55	0
57	MG	1A	3742	1/1	0.91	0.09	54,54,54,54	0
57	MG	2a	1610	1/1	0.91	0.11	51,51,51,51	0
57	MG	2a	1611	1/1	0.91	0.12	58,58,58,58	0
57	MG	2A	3067	1/1	0.91	0.07	44,44,44,44	0
57	MG	15	103	1/1	0.91	0.21	28,28,28,28	0
57	MG	1A	3745	1/1	0.91	0.12	34,34,34,34	0
57	MG	2a	1620	1/1	0.91	0.13	59,59,59,59	0
57	MG	2A	3489	1/1	0.91	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
57	MG	1A	3368	1/1	0.91	0.10	34,34,34,34	0
57	MG	1A	3036	1/1	0.91	0.39	39,39,39,39	0
57	MG	2A	3263	1/1	0.91	0.09	34,34,34,34	0
57	MG	2A	3073	1/1	0.91	0.17	48,48,48,48	0
57	MG	1A	3312	1/1	0.91	0.10	36,36,36,36	0
57	MG	2A	3272	1/1	0.91	0.12	46,46,46,46	0
57	MG	1A	3647	1/1	0.91	0.08	50,50,50,50	0
57	MG	1A	3568	1/1	0.91	0.07	33,33,33,33	0
57	MG	1A	3573	1/1	0.91	0.14	41,41,41,41	0
57	MG	1A	3452	1/1	0.91	0.11	42,42,42,42	0
57	MG	1a	1731	1/1	0.91	0.14	64,64,64,64	0
57	MG	1A	3771	1/1	0.91	0.09	33,33,33,33	0
57	MG	1A	3657	1/1	0.91	0.09	26,26,26,26	0
57	MG	1A	3314	1/1	0.91	0.10	14,14,14,14	0
57	MG	2A	3527	1/1	0.91	0.12	60,60,60,60	0
57	MG	1A	3577	1/1	0.91	0.11	11,11,11,11	0
57	MG	1a	1625	1/1	0.91	0.17	48,48,48,48	0
57	MG	2a	1656	1/1	0.91	0.11	50,50,50,50	0
57	MG	2A	3534	1/1	0.91	0.16	60,60,60,60	0
57	MG	2A	3301	1/1	0.91	0.10	30,30,30,30	0
57	MG	2A	3539	1/1	0.91	0.15	37,37,37,37	0
57	MG	1A	3666	1/1	0.91	0.13	38,38,38,38	0
57	MG	2A	3542	1/1	0.91	0.17	58,58,58,58	0
57	MG	1A	3256	1/1	0.91	0.27	35,35,35,35	0
57	MG	1A	3457	1/1	0.91	0.13	38,38,38,38	0
57	MG	2a	1671	1/1	0.91	0.29	57,57,57,57	0
57	MG	2a	1673	1/1	0.91	0.16	80,80,80,80	0
57	MG	1a	1749	1/1	0.91	0.08	55,55,55,55	0
57	MG	1A	3261	1/1	0.91	0.20	32,32,32,32	0
57	MG	1A	3172	1/1	0.91	0.11	32,32,32,32	0
57	MG	1a	1752	1/1	0.91	0.17	67,67,67,67	0
57	MG	1a	1753	1/1	0.91	0.17	64,64,64,64	0
57	MG	2A	3560	1/1	0.91	0.11	44,44,44,44	0
57	MG	1A	3677	1/1	0.91	0.13	38,38,38,38	0
57	MG	1A	3332	1/1	0.91	0.09	45,45,45,45	0
57	MG	2A	3565	1/1	0.91	0.09	59,59,59,59	0
57	MG	2a	1690	1/1	0.91	0.09	41,41,41,41	0
57	MG	2A	3347	1/1	0.91	0.10	22,22,22,22	0
57	MG	1A	3117	1/1	0.91	0.25	53,53,53,53	0
57	MG	2a	1700	1/1	0.91	0.17	36,36,36,36	0
57	MG	1a	1759	1/1	0.91	0.12	49,49,49,49	0
57	MG	1A	3406	1/1	0.91	0.09	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3126	1/1	0.91	0.12	49,49,49,49	0
57	MG	2a	1708	1/1	0.91	0.16	65,65,65,65	0
57	MG	2A	3356	1/1	0.91	0.17	67,67,67,67	0
57	MG	2A	3130	1/1	0.91	0.09	34,34,34,34	0
57	MG	1a	1644	1/1	0.91	0.27	55,55,55,55	0
57	MG	2A	3133	1/1	0.91	0.16	57,57,57,57	0
57	MG	2a	1718	1/1	0.91	0.21	52,52,52,52	0
57	MG	1A	3474	1/1	0.91	0.09	53,53,53,53	0
57	MG	2A	3139	1/1	0.91	0.17	56,56,56,56	0
57	MG	2A	3582	1/1	0.91	0.10	50,50,50,50	0
57	MG	1A	3689	1/1	0.91	0.10	39,39,39,39	0
57	MG	2A	3584	1/1	0.91	0.09	61,61,61,61	0
57	MG	2a	1729	1/1	0.91	0.13	57,57,57,57	0
57	MG	1A	3613	1/1	0.91	0.17	26,26,26,26	0
57	MG	1a	1648	1/1	0.91	0.16	53,53,53,53	0
57	MG	1A	3615	1/1	0.91	0.10	31,31,31,31	0
57	MG	2a	1734	1/1	0.91	0.26	56,56,56,56	0
57	MG	2A	3147	1/1	0.91	0.09	40,40,40,40	0
57	MG	2A	3377	1/1	0.91	0.09	36,36,36,36	0
57	MG	2A	3379	1/1	0.91	0.16	62,62,62,62	0
57	MG	2A	3381	1/1	0.91	0.14	54,54,54,54	0
57	MG	1A	3338	1/1	0.91	0.07	21,21,21,21	0
57	MG	1w	401	1/1	0.91	0.30	44,44,44,44	0
57	MG	2A	3599	1/1	0.91	0.16	44,44,44,44	0
57	MG	1w	403	1/1	0.91	0.10	43,43,43,43	0
57	MG	2A	3604	1/1	0.91	0.53	57,57,57,57	0
57	MG	1A	3225	1/1	0.91	0.14	33,33,33,33	0
57	MG	2a	1756	1/1	0.91	0.10	59,59,59,59	0
57	MG	2A	3158	1/1	0.91	0.20	47,47,47,47	0
57	MG	2A	3163	1/1	0.91	0.12	59,59,59,59	0
57	MG	2A	3613	1/1	0.91	0.12	62,62,62,62	0
57	MG	2A	3614	1/1	0.91	0.19	54,54,54,54	0
57	MG	1A	3343	1/1	0.91	0.13	29,29,29,29	0
57	MG	2A	3170	1/1	0.91	0.13	45,45,45,45	0
57	MG	2A	3620	1/1	0.91	0.12	48,48,48,48	0
57	MG	2t	201	1/1	0.91	0.12	50,50,50,50	0
57	MG	1A	3700	1/1	0.91	0.10	40,40,40,40	0
57	MG	2A	3172	1/1	0.91	0.17	50,50,50,50	0
57	MG	1A	3703	1/1	0.91	0.10	46,46,46,46	0
57	MG	1F	311	1/1	0.91	0.41	38,38,38,38	0
57	MG	2A	3180	1/1	0.91	0.33	59,59,59,59	0
57	MG	1a	1671	1/1	0.91	0.23	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3636	1/1	0.91	0.17	46,46,46,46	0
57	MG	1A	3563	1/1	0.92	0.11	44,44,44,44	0
57	MG	2A	3013	1/1	0.92	0.11	40,40,40,40	0
57	MG	1a	1650	1/1	0.92	0.24	36,36,36,36	0
57	MG	1A	3150	1/1	0.92	0.11	41,41,41,41	0
57	MG	2A	3414	1/1	0.92	0.22	42,42,42,42	0
57	MG	2A	3194	1/1	0.92	0.14	44,44,44,44	0
57	MG	1a	1654	1/1	0.92	0.23	53,53,53,53	0
57	MG	2A	3649	1/1	0.92	0.23	38,38,38,38	0
57	MG	1a	1655	1/1	0.92	0.13	38,38,38,38	0
57	MG	2A	3652	1/1	0.92	0.11	45,45,45,45	0
57	MG	1A	3050	1/1	0.92	0.22	40,40,40,40	0
57	MG	1a	1659	1/1	0.92	0.22	51,51,51,51	0
57	MG	2A	3433	1/1	0.92	0.08	29,29,29,29	0
57	MG	2A	3029	1/1	0.92	0.29	34,34,34,34	0
57	MG	2B	201	1/1	0.92	0.12	68,68,68,68	0
57	MG	2A	3438	1/1	0.92	0.07	33,33,33,33	0
57	MG	2A	3202	1/1	0.92	0.21	44,44,44,44	0
57	MG	1A	3212	1/1	0.92	0.14	26,26,26,26	0
57	MG	1B	205	1/1	0.92	0.07	55,55,55,55	0
57	MG	2A	3449	1/1	0.92	0.07	50,50,50,50	0
57	MG	2A	3206	1/1	0.92	0.17	43,43,43,43	0
57	MG	2B	208	1/1	0.92	0.48	59,59,59,59	0
57	MG	2A	3038	1/1	0.92	0.13	51,51,51,51	0
57	MG	2A	3208	1/1	0.92	0.19	45,45,45,45	0
57	MG	2D	303	1/1	0.92	0.15	38,38,38,38	0
57	MG	2A	3458	1/1	0.92	0.09	62,62,62,62	0
57	MG	2A	3209	1/1	0.92	0.32	67,67,67,67	0
57	MG	1A	3352	1/1	0.92	0.08	36,36,36,36	0
57	MG	2A	3219	1/1	0.92	0.21	38,38,38,38	0
57	MG	1A	3273	1/1	0.92	0.26	53,53,53,53	0
57	MG	2A	3466	1/1	0.92	0.18	40,40,40,40	0
57	MG	2O	201	1/1	0.92	0.16	51,51,51,51	0
57	MG	1A	3356	1/1	0.92	0.14	35,35,35,35	0
57	MG	1A	3058	1/1	0.92	0.10	25,25,25,25	0
57	MG	2U	201	1/1	0.92	0.14	50,50,50,50	0
57	MG	2A	3470	1/1	0.92	0.15	42,42,42,42	0
57	MG	2W	201	1/1	0.92	0.16	39,39,39,39	0
57	MG	1A	3581	1/1	0.92	0.09	19,19,19,19	0
57	MG	1A	3059	1/1	0.92	0.07	30,30,30,30	0
57	MG	2A	3475	1/1	0.92	0.17	68,68,68,68	0
57	MG	1A	3686	1/1	0.92	0.12	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3165	1/1	0.92	0.12	56,56,56,56	0
57	MG	2A	3057	1/1	0.92	0.24	62,62,62,62	0
57	MG	1A	3366	1/1	0.92	0.10	26,26,26,26	0
57	MG	1A	3693	1/1	0.92	0.12	43,43,43,43	0
57	MG	1A	3367	1/1	0.92	0.09	16,16,16,16	0
57	MG	2A	3066	1/1	0.92	0.13	46,46,46,46	0
57	MG	2A	3243	1/1	0.92	0.08	23,23,23,23	0
57	MG	1F	307	1/1	0.92	0.10	34,34,34,34	0
57	MG	1A	3458	1/1	0.92	0.12	47,47,47,47	0
57	MG	1A	3697	1/1	0.92	0.14	51,51,51,51	0
57	MG	1N	202	1/1	0.92	0.13	33,33,33,33	0
57	MG	1A	3304	1/1	0.92	0.09	24,24,24,24	0
57	MG	1A	3610	1/1	0.92	0.09	39,39,39,39	0
57	MG	1A	3010	1/1	0.92	0.09	25,25,25,25	0
57	MG	2A	3493	1/1	0.92	0.12	60,60,60,60	0
57	MG	2a	1627	1/1	0.92	0.27	51,51,51,51	0
57	MG	1A	3308	1/1	0.92	0.11	17,17,17,17	0
57	MG	1U	204	1/1	0.92	0.23	27,27,27,27	0
57	MG	2A	3501	1/1	0.92	0.11	54,54,54,54	0
57	MG	2a	1636	1/1	0.92	0.19	45,45,45,45	0
57	MG	2a	1637	1/1	0.92	0.19	39,39,39,39	0
57	MG	2a	1638	1/1	0.92	0.21	52,52,52,52	0
57	MG	2A	3504	1/1	0.92	0.19	51,51,51,51	0
57	MG	1a	1711	1/1	0.92	0.14	29,29,29,29	0
57	MG	2A	3082	1/1	0.92	0.10	41,41,41,41	0
57	MG	2a	1643	1/1	0.92	0.25	47,47,47,47	0
57	MG	1A	3309	1/1	0.92	0.09	40,40,40,40	0
57	MG	1A	3381	1/1	0.92	0.21	57,57,57,57	0
57	MG	1A	3708	1/1	0.92	0.35	29,29,29,29	0
57	MG	1W	202	1/1	0.92	0.07	25,25,25,25	0
57	MG	2A	3287	1/1	0.92	0.17	57,57,57,57	0
57	MG	1A	3230	1/1	0.92	0.37	28,28,28,28	0
57	MG	1A	3716	1/1	0.92	0.26	23,23,23,23	0
57	MG	1A	3313	1/1	0.92	0.10	45,45,45,45	0
57	MG	2A	3530	1/1	0.92	0.09	51,51,51,51	0
57	MG	1A	3478	1/1	0.92	0.18	46,46,46,46	0
57	MG	2A	3101	1/1	0.92	0.21	46,46,46,46	0
57	MG	2A	3298	1/1	0.92	0.11	58,58,58,58	0
57	MG	12	101	1/1	0.92	0.10	43,43,43,43	0
57	MG	2a	1664	1/1	0.92	0.23	54,54,54,54	0
57	MG	1A	3124	1/1	0.92	0.18	29,29,29,29	0
57	MG	15	107	1/1	0.92	0.07	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	17	106	1/1	0.92	0.13	51,51,51,51	0
57	MG	1a	1736	1/1	0.92	0.17	55,55,55,55	0
57	MG	2A	3312	1/1	0.92	0.10	35,35,35,35	0
57	MG	2A	3547	1/1	0.92	0.08	36,36,36,36	0
57	MG	2A	3552	1/1	0.92	0.22	28,28,28,28	0
57	MG	1A	3729	1/1	0.92	0.17	41,41,41,41	0
57	MG	2A	3315	1/1	0.92	0.08	32,32,32,32	0
57	MG	1A	3039	1/1	0.92	0.09	33,33,33,33	0
57	MG	2A	3113	1/1	0.92	0.18	25,25,25,25	0
57	MG	2A	3558	1/1	0.92	0.08	63,63,63,63	0
57	MG	1A	3732	1/1	0.92	0.10	36,36,36,36	0
57	MG	1A	3735	1/1	0.92	0.12	19,19,19,19	0
57	MG	2A	3343	1/1	0.92	0.08	35,35,35,35	0
57	MG	2A	3344	1/1	0.92	0.12	40,40,40,40	0
57	MG	2A	3121	1/1	0.92	0.26	59,59,59,59	0
57	MG	1a	1610	1/1	0.92	0.12	33,33,33,33	0
57	MG	1a	1612	1/1	0.92	0.12	33,33,33,33	0
57	MG	1A	3738	1/1	0.92	0.11	22,22,22,22	0
57	MG	2A	3349	1/1	0.92	0.17	47,47,47,47	0
57	MG	1A	3486	1/1	0.92	0.09	40,40,40,40	0
57	MG	1A	3500	1/1	0.92	0.10	10,10,10,10	0
57	MG	1A	3501	1/1	0.92	0.12	22,22,22,22	0
57	MG	1A	3635	1/1	0.92	0.09	35,35,35,35	0
57	MG	2a	1711	1/1	0.92	0.15	52,52,52,52	0
57	MG	1a	1620	1/1	0.92	0.15	43,43,43,43	0
57	MG	2a	1715	1/1	0.92	0.12	66,66,66,66	0
57	MG	2A	3135	1/1	0.92	0.17	30,30,30,30	0
57	MG	2A	3136	1/1	0.92	0.26	53,53,53,53	0
57	MG	1A	3400	1/1	0.92	0.10	37,37,37,37	0
57	MG	1A	3021	1/1	0.92	0.23	30,30,30,30	0
57	MG	2a	1722	1/1	0.92	0.10	56,56,56,56	0
57	MG	1a	1623	1/1	0.92	0.21	50,50,50,50	0
57	MG	2a	1724	1/1	0.92	0.24	57,57,57,57	0
57	MG	1A	3751	1/1	0.92	0.11	46,46,46,46	0
57	MG	1A	3753	1/1	0.92	0.09	43,43,43,43	0
57	MG	1A	3324	1/1	0.92	0.09	29,29,29,29	0
57	MG	1A	3758	1/1	0.92	0.11	35,35,35,35	0
57	MG	2A	3592	1/1	0.92	0.17	64,64,64,64	0
57	MG	1A	3067	1/1	0.92	0.10	43,43,43,43	0
57	MG	2A	3151	1/1	0.92	0.30	55,55,55,55	0
57	MG	2a	1735	1/1	0.92	0.17	55,55,55,55	0
57	MG	2a	1736	1/1	0.92	0.20	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3762	1/1	0.92	0.19	52,52,52,52	0
57	MG	1a	1632	1/1	0.92	0.15	48,48,48,48	0
57	MG	1A	3180	1/1	0.92	0.24	23,23,23,23	0
57	MG	2A	3384	1/1	0.92	0.07	45,45,45,45	0
57	MG	2A	3387	1/1	0.92	0.20	61,61,61,61	0
57	MG	1A	3648	1/1	0.92	0.10	27,27,27,27	0
57	MG	2A	3390	1/1	0.92	0.09	20,20,20,20	0
57	MG	1x	102	1/1	0.92	0.12	37,37,37,37	0
57	MG	2A	3168	1/1	0.92	0.15	31,31,31,31	0
57	MG	1A	3188	1/1	0.92	0.08	33,33,33,33	0
57	MG	2a	1754	1/1	0.92	0.18	63,63,63,63	0
57	MG	1A	3531	1/1	0.92	0.09	10,10,10,10	0
57	MG	2A	3616	1/1	0.92	0.09	48,48,48,48	0
57	MG	1A	3427	1/1	0.92	0.11	31,31,31,31	0
57	MG	2A	3618	1/1	0.92	0.22	38,38,38,38	0
57	MG	1A	3653	1/1	0.92	0.06	31,31,31,31	0
57	MG	2a	1765	1/1	0.92	0.15	75,75,75,75	0
57	MG	1A	3548	1/1	0.92	0.09	33,33,33,33	0
57	MG	2e	202	1/1	0.92	0.07	64,64,64,64	0
57	MG	2A	3621	1/1	0.92	0.08	47,47,47,47	0
57	MG	2A	3177	1/1	0.92	0.12	60,60,60,60	0
57	MG	2A	3624	1/1	0.92	0.12	48,48,48,48	0
57	MG	2A	3625	1/1	0.92	0.12	45,45,45,45	0
57	MG	1A	3031	1/1	0.92	0.07	34,34,34,34	0
57	MG	2x	101	1/1	0.92	0.24	71,71,71,71	0
57	MG	2x	102	1/1	0.92	0.42	64,64,64,64	0
57	MG	2A	3182	1/1	0.92	0.24	51,51,51,51	0
57	MG	1A	3193	1/1	0.92	0.17	51,51,51,51	0
57	MG	2A	3007	1/1	0.92	0.14	47,47,47,47	0
57	MG	2A	3404	1/1	0.92	0.09	50,50,50,50	0
57	MG	2A	3635	1/1	0.92	0.14	55,55,55,55	0
57	MG	2X	101	1/1	0.93	0.17	44,44,44,44	0
57	MG	20	101	1/1	0.93	0.15	62,62,62,62	0
57	MG	1X	101	1/1	0.93	0.18	37,37,37,37	0
57	MG	2A	3035	1/1	0.93	0.13	62,62,62,62	0
57	MG	1A	3479	1/1	0.93	0.09	41,41,41,41	0
57	MG	2A	3037	1/1	0.93	0.12	38,38,38,38	0
57	MG	26	101	1/1	0.93	0.11	62,62,62,62	0
57	MG	1A	3662	1/1	0.93	0.09	44,44,44,44	0
57	MG	1A	3228	1/1	0.93	0.10	25,25,25,25	0
57	MG	1A	3750	1/1	0.93	0.10	39,39,39,39	0
57	MG	1A	3433	1/1	0.93	0.06	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3183	1/1	0.93	0.12	36,36,36,36	0
57	MG	2A	3045	1/1	0.93	0.26	46,46,46,46	0
57	MG	2A	3186	1/1	0.93	0.18	50,50,50,50	0
57	MG	1A	3108	1/1	0.93	0.17	58,58,58,58	0
57	MG	2A	3372	1/1	0.93	0.11	59,59,59,59	0
57	MG	1a	1705	1/1	0.93	0.10	56,56,56,56	0
57	MG	2A	3549	1/1	0.93	0.08	48,48,48,48	0
57	MG	2a	1617	1/1	0.93	0.17	53,53,53,53	0
57	MG	2A	3551	1/1	0.93	0.18	23,23,23,23	0
57	MG	2a	1623	1/1	0.93	0.30	40,40,40,40	0
57	MG	2A	3375	1/1	0.93	0.18	39,39,39,39	0
57	MG	2A	3051	1/1	0.93	0.08	49,49,49,49	0
57	MG	15	104	1/1	0.93	0.23	28,28,28,28	0
57	MG	1A	3492	1/1	0.93	0.10	45,45,45,45	0
57	MG	17	103	1/1	0.93	0.17	33,33,33,33	0
57	MG	2A	3056	1/1	0.93	0.11	37,37,37,37	0
57	MG	2A	3196	1/1	0.93	0.10	58,58,58,58	0
57	MG	1A	3094	1/1	0.93	0.21	32,32,32,32	0
57	MG	2A	3385	1/1	0.93	0.13	62,62,62,62	0
57	MG	2A	3061	1/1	0.93	0.11	52,52,52,52	0
57	MG	2a	1639	1/1	0.93	0.20	56,56,56,56	0
57	MG	2A	3564	1/1	0.93	0.13	47,47,47,47	0
57	MG	2A	3388	1/1	0.93	0.17	45,45,45,45	0
57	MG	1A	3595	1/1	0.93	0.12	55,55,55,55	0
57	MG	1A	3676	1/1	0.93	0.13	14,14,14,14	0
57	MG	1A	3767	1/1	0.93	0.09	37,37,37,37	0
57	MG	1A	3327	1/1	0.93	0.15	32,32,32,32	0
57	MG	2A	3204	1/1	0.93	0.20	29,29,29,29	0
57	MG	1A	3769	1/1	0.93	0.09	14,14,14,14	0
57	MG	2A	3395	1/1	0.93	0.11	31,31,31,31	0
57	MG	2a	1650	1/1	0.93	0.12	48,48,48,48	0
57	MG	1A	3678	1/1	0.93	0.13	27,27,27,27	0
57	MG	1A	3200	1/1	0.93	0.13	40,40,40,40	0
57	MG	2A	3579	1/1	0.93	0.23	47,47,47,47	0
57	MG	1A	3773	1/1	0.93	0.14	53,53,53,53	0
57	MG	1A	3682	1/1	0.93	0.13	33,33,33,33	0
57	MG	1A	3777	1/1	0.93	0.14	38,38,38,38	0
57	MG	2A	3074	1/1	0.93	0.11	61,61,61,61	0
57	MG	1A	3503	1/1	0.93	0.07	11,11,11,11	0
57	MG	2a	1663	1/1	0.93	0.12	51,51,51,51	0
57	MG	1a	1737	1/1	0.93	0.20	46,46,46,46	0
57	MG	2A	3222	1/1	0.93	0.17	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3782	1/1	0.93	0.07	29,29,29,29	0
57	MG	2A	3224	1/1	0.93	0.18	62,62,62,62	0
57	MG	1A	3239	1/1	0.93	0.07	16,16,16,16	0
57	MG	1A	3283	1/1	0.93	0.33	44,44,44,44	0
57	MG	1A	3038	1/1	0.93	0.25	35,35,35,35	0
57	MG	2A	3415	1/1	0.93	0.15	32,32,32,32	0
57	MG	1A	3687	1/1	0.93	0.07	42,42,42,42	0
57	MG	1A	3791	1/1	0.93	0.12	43,43,43,43	0
57	MG	2A	3418	1/1	0.93	0.10	39,39,39,39	0
57	MG	2A	3422	1/1	0.93	0.10	39,39,39,39	0
57	MG	2A	3603	1/1	0.93	0.09	43,43,43,43	0
57	MG	1A	3616	1/1	0.93	0.08	43,43,43,43	0
57	MG	2a	1682	1/1	0.93	0.24	52,52,52,52	0
57	MG	1A	3617	1/1	0.93	0.13	47,47,47,47	0
57	MG	1A	3511	1/1	0.93	0.12	46,46,46,46	0
57	MG	2A	3608	1/1	0.93	0.09	37,37,37,37	0
57	MG	2A	3430	1/1	0.93	0.07	45,45,45,45	0
57	MG	2a	1697	1/1	0.93	0.11	48,48,48,48	0
57	MG	1A	3619	1/1	0.93	0.09	50,50,50,50	0
57	MG	1B	203	1/1	0.93	0.10	45,45,45,45	0
57	MG	2A	3245	1/1	0.93	0.16	25,25,25,25	0
57	MG	2a	1703	1/1	0.93	0.20	64,64,64,64	0
57	MG	2a	1704	1/1	0.93	0.18	53,53,53,53	0
57	MG	2A	3439	1/1	0.93	0.17	33,33,33,33	0
57	MG	2A	3443	1/1	0.93	0.16	45,45,45,45	0
57	MG	1A	3294	1/1	0.93	0.15	39,39,39,39	0
57	MG	1A	3391	1/1	0.93	0.08	25,25,25,25	0
57	MG	1A	3524	1/1	0.93	0.15	36,36,36,36	0
57	MG	1A	3623	1/1	0.93	0.48	25,25,25,25	0
57	MG	2A	3253	1/1	0.93	0.14	48,48,48,48	0
57	MG	2a	1714	1/1	0.93	0.16	43,43,43,43	0
57	MG	1B	212	1/1	0.93	0.06	46,46,46,46	0
57	MG	1A	3527	1/1	0.93	0.10	29,29,29,29	0
57	MG	1a	1764	1/1	0.93	0.20	70,70,70,70	0
57	MG	1A	3250	1/1	0.93	0.12	35,35,35,35	0
57	MG	2A	3461	1/1	0.93	0.15	48,48,48,48	0
57	MG	1D	308	1/1	0.93	0.10	41,41,41,41	0
57	MG	2A	3270	1/1	0.93	0.12	65,65,65,65	0
57	MG	1A	3533	1/1	0.93	0.11	16,16,16,16	0
57	MG	1A	3045	1/1	0.93	0.09	30,30,30,30	0
57	MG	1A	3543	1/1	0.93	0.10	43,43,43,43	0
57	MG	2a	1727	1/1	0.93	0.10	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3122	1/1	0.93	0.30	61,61,61,61	0
57	MG	1A	3711	1/1	0.93	0.18	23,23,23,23	0
57	MG	1A	3254	1/1	0.93	0.11	48,48,48,48	0
57	MG	2A	3284	1/1	0.93	0.13	55,55,55,55	0
57	MG	2a	1733	1/1	0.93	0.20	49,49,49,49	0
57	MG	1A	3551	1/1	0.93	0.07	25,25,25,25	0
57	MG	2A	3288	1/1	0.93	0.13	51,51,51,51	0
57	MG	1A	3173	1/1	0.93	0.41	36,36,36,36	0
57	MG	1A	3639	1/1	0.93	0.19	40,40,40,40	0
57	MG	1x	105	1/1	0.93	0.19	26,26,26,26	0
57	MG	1A	3723	1/1	0.93	0.09	32,32,32,32	0
57	MG	1A	3405	1/1	0.93	0.09	11,11,11,11	0
57	MG	1a	1665	1/1	0.93	0.23	49,49,49,49	0
57	MG	2a	1746	1/1	0.93	0.20	40,40,40,40	0
57	MG	1A	3074	1/1	0.93	0.25	46,46,46,46	0
57	MG	2A	3137	1/1	0.93	0.07	60,60,60,60	0
57	MG	1A	3565	1/1	0.93	0.10	31,31,31,31	0
57	MG	2A	3006	1/1	0.93	0.21	45,45,45,45	0
57	MG	1A	3731	1/1	0.93	0.11	45,45,45,45	0
57	MG	1A	3407	1/1	0.93	0.08	29,29,29,29	0
57	MG	1Q	205	1/1	0.93	0.16	30,30,30,30	0
57	MG	2B	209	1/1	0.93	0.21	58,58,58,58	0
57	MG	1R	201	1/1	0.93	0.11	27,27,27,27	0
57	MG	1A	3103	1/1	0.93	0.25	42,42,42,42	0
57	MG	2a	1763	1/1	0.93	0.20	71,71,71,71	0
57	MG	2A	3495	1/1	0.93	0.08	45,45,45,45	0
57	MG	2D	304	1/1	0.93	0.32	41,41,41,41	0
57	MG	2A	3017	1/1	0.93	0.14	52,52,52,52	0
57	MG	1A	3420	1/1	0.93	0.10	11,11,11,11	0
57	MG	2A	3334	1/1	0.93	0.09	27,27,27,27	0
57	MG	2E	305	1/1	0.93	0.13	30,30,30,30	0
57	MG	2E	306	1/1	0.93	0.12	55,55,55,55	0
57	MG	2A	3502	1/1	0.93	0.09	51,51,51,51	0
57	MG	1A	3089	1/1	0.93	0.12	46,46,46,46	0
57	MG	1A	3361	1/1	0.93	0.20	54,54,54,54	0
57	MG	1A	3030	1/1	0.93	0.21	27,27,27,27	0
57	MG	2A	3160	1/1	0.93	0.18	38,38,38,38	0
57	MG	2A	3162	1/1	0.93	0.21	36,36,36,36	0
57	MG	2A	3028	1/1	0.93	0.28	43,43,43,43	0
57	MG	1W	203	1/1	0.93	0.10	17,17,17,17	0
57	MG	2A	3033	1/1	0.93	0.18	55,55,55,55	0
58	ZN	14	501	1/1	0.93	0.16	119,119,119,119	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	15	106	1/1	0.94	0.25	28,28,28,28	0
57	MG	1A	3008	1/1	0.94	0.16	21,21,21,21	0
57	MG	2A	3149	1/1	0.94	0.17	54,54,54,54	0
57	MG	1A	3148	1/1	0.94	0.49	33,33,33,33	0
57	MG	17	105	1/1	0.94	0.20	31,31,31,31	0
57	MG	2A	3153	1/1	0.94	0.24	38,38,38,38	0
57	MG	1A	3734	1/1	0.94	0.09	17,17,17,17	0
57	MG	1A	3493	1/1	0.94	0.05	19,19,19,19	0
57	MG	1A	3395	1/1	0.94	0.10	16,16,16,16	0
57	MG	1A	3739	1/1	0.94	0.07	18,18,18,18	0
57	MG	1a	1607	1/1	0.94	0.10	68,68,68,68	0
57	MG	1A	3315	1/1	0.94	0.18	39,39,39,39	0
57	MG	2A	3164	1/1	0.94	0.12	56,56,56,56	0
57	MG	2A	3166	1/1	0.94	0.09	38,38,38,38	0
57	MG	1A	3397	1/1	0.94	0.06	35,35,35,35	0
57	MG	1k	201	1/1	0.94	0.17	55,55,55,55	0
57	MG	1A	3743	1/1	0.94	0.12	35,35,35,35	0
57	MG	1v	102	1/1	0.94	0.12	63,63,63,63	0
57	MG	1A	3628	1/1	0.94	0.08	20,20,20,20	0
57	MG	2A	3655	1/1	0.94	0.17	47,47,47,47	0
57	MG	1a	1614	1/1	0.94	0.20	48,48,48,48	0
57	MG	1A	3119	1/1	0.94	0.06	28,28,28,28	0
57	MG	1A	3241	1/1	0.94	0.10	55,55,55,55	0
57	MG	1A	3633	1/1	0.94	0.07	32,32,32,32	0
57	MG	1A	3244	1/1	0.94	0.11	35,35,35,35	0
57	MG	1A	3186	1/1	0.94	0.14	35,35,35,35	0
57	MG	1A	3249	1/1	0.94	0.15	34,34,34,34	0
57	MG	2A	3185	1/1	0.94	0.14	40,40,40,40	0
57	MG	1x	109	1/1	0.94	0.17	48,48,48,48	0
57	MG	1y	101	1/1	0.94	0.18	34,34,34,34	0
57	MG	2A	3419	1/1	0.94	0.07	24,24,24,24	0
57	MG	2A	3421	1/1	0.94	0.16	45,45,45,45	0
57	MG	1A	3754	1/1	0.94	0.15	34,34,34,34	0
57	MG	1A	3756	1/1	0.94	0.06	32,32,32,32	0
57	MG	1A	3637	1/1	0.94	0.15	36,36,36,36	0
57	MG	1A	3085	1/1	0.94	0.22	41,41,41,41	0
57	MG	1A	3759	1/1	0.94	0.12	44,44,44,44	0
57	MG	1A	3519	1/1	0.94	0.11	43,43,43,43	0
57	MG	1A	3412	1/1	0.94	0.06	13,13,13,13	0
57	MG	2A	3436	1/1	0.94	0.07	38,38,38,38	0
57	MG	2A	3011	1/1	0.94	0.15	41,41,41,41	0
57	MG	2A	3198	1/1	0.94	0.10	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3442	1/1	0.94	0.09	35,35,35,35	0
57	MG	2F	305	1/1	0.94	0.15	42,42,42,42	0
57	MG	2A	3012	1/1	0.94	0.06	35,35,35,35	0
57	MG	1A	3413	1/1	0.94	0.09	17,17,17,17	0
57	MG	2Q	203	1/1	0.94	0.23	53,53,53,53	0
57	MG	1A	3418	1/1	0.94	0.08	25,25,25,25	0
57	MG	2A	3447	1/1	0.94	0.18	36,36,36,36	0
57	MG	2U	202	1/1	0.94	0.05	52,52,52,52	0
57	MG	1A	3530	1/1	0.94	0.10	9,9,9,9	0
57	MG	2V	202	1/1	0.94	0.17	53,53,53,53	0
57	MG	1A	3040	1/1	0.94	0.16	24,24,24,24	0
57	MG	2A	3018	1/1	0.94	0.25	42,42,42,42	0
57	MG	2A	3019	1/1	0.94	0.11	31,31,31,31	0
57	MG	1A	3191	1/1	0.94	0.30	43,43,43,43	0
57	MG	2A	3454	1/1	0.94	0.27	64,64,64,64	0
57	MG	2A	3023	1/1	0.94	0.24	39,39,39,39	0
57	MG	2A	3459	1/1	0.94	0.20	61,61,61,61	0
57	MG	1A	3339	1/1	0.94	0.10	29,29,29,29	0
57	MG	28	101	1/1	0.94	0.09	52,52,52,52	0
57	MG	2a	1602	1/1	0.94	0.09	63,63,63,63	0
57	MG	1a	1639	1/1	0.94	0.08	47,47,47,47	0
57	MG	2A	3212	1/1	0.94	0.18	51,51,51,51	0
57	MG	2A	3213	1/1	0.94	0.26	50,50,50,50	0
57	MG	1A	3541	1/1	0.94	0.11	15,15,15,15	0
57	MG	2A	3465	1/1	0.94	0.17	65,65,65,65	0
57	MG	2A	3217	1/1	0.94	0.23	46,46,46,46	0
57	MG	1A	3654	1/1	0.94	0.23	47,47,47,47	0
57	MG	1A	3778	1/1	0.94	0.15	28,28,28,28	0
57	MG	1A	3542	1/1	0.94	0.10	56,56,56,56	0
57	MG	2a	1613	1/1	0.94	0.17	41,41,41,41	0
57	MG	1A	3192	1/1	0.94	0.18	27,27,27,27	0
57	MG	1A	3661	1/1	0.94	0.13	48,48,48,48	0
57	MG	1A	3428	1/1	0.94	0.09	39,39,39,39	0
57	MG	1A	3342	1/1	0.94	0.07	10,10,10,10	0
57	MG	2a	1622	1/1	0.94	0.22	57,57,57,57	0
57	MG	1a	1653	1/1	0.94	0.14	27,27,27,27	0
57	MG	1A	3054	1/1	0.94	0.16	33,33,33,33	0
57	MG	2A	3480	1/1	0.94	0.10	50,50,50,50	0
57	MG	2A	3041	1/1	0.94	0.26	38,38,38,38	0
57	MG	1A	3557	1/1	0.94	0.07	65,65,65,65	0
57	MG	2A	3234	1/1	0.94	0.13	51,51,51,51	0
57	MG	2a	1631	1/1	0.94	0.26	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3669	1/1	0.94	0.12	42,42,42,42	0
57	MG	2a	1634	1/1	0.94	0.17	48,48,48,48	0
57	MG	2A	3237	1/1	0.94	0.22	48,48,48,48	0
57	MG	1A	3155	1/1	0.94	0.10	23,23,23,23	0
57	MG	2A	3239	1/1	0.94	0.09	34,34,34,34	0
57	MG	1A	3561	1/1	0.94	0.10	48,48,48,48	0
57	MG	1a	1663	1/1	0.94	0.14	42,42,42,42	0
57	MG	1A	3201	1/1	0.94	0.22	28,28,28,28	0
57	MG	1A	3069	1/1	0.94	0.30	45,45,45,45	0
57	MG	1B	204	1/1	0.94	0.13	31,31,31,31	0
57	MG	1A	3160	1/1	0.94	0.13	29,29,29,29	0
57	MG	1a	1669	1/1	0.94	0.19	53,53,53,53	0
57	MG	1B	206	1/1	0.94	0.07	33,33,33,33	0
57	MG	2A	3499	1/1	0.94	0.16	52,52,52,52	0
57	MG	1A	3269	1/1	0.94	0.17	56,56,56,56	0
57	MG	1A	3570	1/1	0.94	0.12	51,51,51,51	0
57	MG	1A	3357	1/1	0.94	0.08	35,35,35,35	0
57	MG	2A	3259	1/1	0.94	0.09	51,51,51,51	0
57	MG	1A	3164	1/1	0.94	0.13	42,42,42,42	0
57	MG	2A	3506	1/1	0.94	0.09	44,44,44,44	0
57	MG	2A	3507	1/1	0.94	0.14	52,52,52,52	0
57	MG	1A	3095	1/1	0.94	0.20	33,33,33,33	0
57	MG	2A	3265	1/1	0.94	0.12	33,33,33,33	0
57	MG	2a	1659	1/1	0.94	0.08	52,52,52,52	0
57	MG	2A	3267	1/1	0.94	0.09	34,34,34,34	0
57	MG	1A	3214	1/1	0.94	0.18	39,39,39,39	0
57	MG	2A	3520	1/1	0.94	0.09	53,53,53,53	0
57	MG	2A	3521	1/1	0.94	0.12	55,55,55,55	0
57	MG	1a	1679	1/1	0.94	0.16	60,60,60,60	0
57	MG	1D	304	1/1	0.94	0.09	30,30,30,30	0
57	MG	1A	3579	1/1	0.94	0.10	15,15,15,15	0
57	MG	2a	1669	1/1	0.94	0.13	62,62,62,62	0
57	MG	2A	3273	1/1	0.94	0.20	51,51,51,51	0
57	MG	1A	3215	1/1	0.94	0.14	24,24,24,24	0
57	MG	2A	3276	1/1	0.94	0.14	27,27,27,27	0
57	MG	2A	3531	1/1	0.94	0.08	60,60,60,60	0
57	MG	1A	3688	1/1	0.94	0.22	47,47,47,47	0
57	MG	1A	3455	1/1	0.94	0.10	26,26,26,26	0
57	MG	1A	3364	1/1	0.94	0.13	24,24,24,24	0
57	MG	2A	3535	1/1	0.94	0.13	61,61,61,61	0
57	MG	1A	3216	1/1	0.94	0.15	52,52,52,52	0
57	MG	2A	3538	1/1	0.94	0.16	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3285	1/1	0.94	0.19	38,38,38,38	0
57	MG	2a	1685	1/1	0.94	0.18	56,56,56,56	0
57	MG	2A	3079	1/1	0.94	0.18	36,36,36,36	0
57	MG	1A	3587	1/1	0.94	0.10	26,26,26,26	0
57	MG	1A	3589	1/1	0.94	0.06	25,25,25,25	0
57	MG	2a	1691	1/1	0.94	0.10	41,41,41,41	0
57	MG	2a	1693	1/1	0.94	0.16	49,49,49,49	0
57	MG	2a	1694	1/1	0.94	0.11	48,48,48,48	0
57	MG	2A	3545	1/1	0.94	0.12	43,43,43,43	0
57	MG	2a	1696	1/1	0.94	0.09	42,42,42,42	0
57	MG	1a	1702	1/1	0.94	0.23	36,36,36,36	0
57	MG	1A	3590	1/1	0.94	0.07	43,43,43,43	0
57	MG	2a	1699	1/1	0.94	0.12	59,59,59,59	0
57	MG	1A	3218	1/1	0.94	0.12	28,28,28,28	0
57	MG	2A	3550	1/1	0.94	0.07	62,62,62,62	0
57	MG	1a	1706	1/1	0.94	0.14	48,48,48,48	0
57	MG	2A	3092	1/1	0.94	0.12	58,58,58,58	0
57	MG	1N	201	1/1	0.94	0.12	35,35,35,35	0
57	MG	1a	1710	1/1	0.94	0.12	47,47,47,47	0
57	MG	2A	3097	1/1	0.94	0.14	27,27,27,27	0
57	MG	1A	3459	1/1	0.94	0.07	38,38,38,38	0
57	MG	2A	3309	1/1	0.94	0.15	25,25,25,25	0
57	MG	1a	1712	1/1	0.94	0.22	57,57,57,57	0
57	MG	2A	3311	1/1	0.94	0.12	38,38,38,38	0
57	MG	1A	3594	1/1	0.94	0.08	40,40,40,40	0
57	MG	1A	3130	1/1	0.94	0.35	37,37,37,37	0
57	MG	1a	1715	1/1	0.94	0.19	52,52,52,52	0
57	MG	2A	3316	1/1	0.94	0.10	28,28,28,28	0
57	MG	2A	3320	1/1	0.94	0.09	60,60,60,60	0
57	MG	2a	1720	1/1	0.94	0.14	59,59,59,59	0
57	MG	2A	3567	1/1	0.94	0.10	28,28,28,28	0
57	MG	2A	3324	1/1	0.94	0.09	45,45,45,45	0
57	MG	2A	3326	1/1	0.94	0.09	24,24,24,24	0
57	MG	2A	3571	1/1	0.94	0.13	57,57,57,57	0
57	MG	1a	1716	1/1	0.94	0.17	41,41,41,41	0
57	MG	2A	3328	1/1	0.94	0.13	38,38,38,38	0
57	MG	2A	3329	1/1	0.94	0.07	28,28,28,28	0
57	MG	2A	3330	1/1	0.94	0.07	42,42,42,42	0
57	MG	1A	3596	1/1	0.94	0.06	30,30,30,30	0
57	MG	2A	3577	1/1	0.94	0.12	60,60,60,60	0
57	MG	1Q	202	1/1	0.94	0.16	30,30,30,30	0
57	MG	2A	3109	1/1	0.94	0.12	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3338	1/1	0.94	0.12	38,38,38,38	0
57	MG	1A	3706	1/1	0.94	0.10	30,30,30,30	0
57	MG	1a	1722	1/1	0.94	0.14	39,39,39,39	0
57	MG	1A	3371	1/1	0.94	0.11	29,29,29,29	0
57	MG	1a	1724	1/1	0.94	0.19	40,40,40,40	0
57	MG	2A	3114	1/1	0.94	0.10	51,51,51,51	0
57	MG	2A	3588	1/1	0.94	0.33	62,62,62,62	0
57	MG	1A	3303	1/1	0.94	0.09	13,13,13,13	0
57	MG	1a	1728	1/1	0.94	0.15	53,53,53,53	0
57	MG	1U	201	1/1	0.94	0.18	18,18,18,18	0
57	MG	1A	3710	1/1	0.94	0.09	43,43,43,43	0
57	MG	1A	3607	1/1	0.94	0.09	15,15,15,15	0
57	MG	2A	3353	1/1	0.94	0.11	39,39,39,39	0
57	MG	1A	3712	1/1	0.94	0.36	33,33,33,33	0
57	MG	1A	3713	1/1	0.94	0.36	23,23,23,23	0
57	MG	1W	201	1/1	0.94	0.15	23,23,23,23	0
57	MG	2A	3127	1/1	0.94	0.16	28,28,28,28	0
57	MG	2A	3600	1/1	0.94	0.10	37,37,37,37	0
57	MG	2a	1761	1/1	0.94	0.10	49,49,49,49	0
57	MG	2A	3129	1/1	0.94	0.09	42,42,42,42	0
57	MG	1A	3376	1/1	0.94	0.10	31,31,31,31	0
57	MG	2A	3131	1/1	0.94	0.11	65,65,65,65	0
57	MG	1A	3715	1/1	0.94	0.09	40,40,40,40	0
57	MG	2A	3368	1/1	0.94	0.08	51,51,51,51	0
57	MG	2A	3369	1/1	0.94	0.15	56,56,56,56	0
57	MG	2e	203	1/1	0.94	0.23	55,55,55,55	0
57	MG	1A	3061	1/1	0.94	0.07	40,40,40,40	0
57	MG	1A	3115	1/1	0.94	0.21	33,33,33,33	0
57	MG	1A	3227	1/1	0.94	0.23	46,46,46,46	0
57	MG	2A	3615	1/1	0.94	0.09	53,53,53,53	0
57	MG	1A	3722	1/1	0.94	0.09	31,31,31,31	0
57	MG	1a	1748	1/1	0.94	0.06	52,52,52,52	0
57	MG	1A	3137	1/1	0.94	0.23	29,29,29,29	0
57	MG	1A	3385	1/1	0.94	0.19	36,36,36,36	0
57	MG	15	101	1/1	0.94	0.17	34,34,34,34	0
57	MG	2x	105	1/1	0.94	0.20	40,40,40,40	0
57	MG	1A	3176	1/1	0.94	0.13	36,36,36,36	0
57	MG	1A	3390	1/1	0.94	0.14	36,36,36,36	0
57	MG	2A	3623	1/1	0.94	0.23	48,48,48,48	0
57	MG	2A	3145	1/1	0.94	0.21	44,44,44,44	0
57	MG	2A	3477	1/1	0.95	0.10	33,33,33,33	0
57	MG	2A	3274	1/1	0.95	0.08	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2E	307	1/1	0.95	0.17	27,27,27,27	0
57	MG	1a	1738	1/1	0.95	0.24	33,33,33,33	0
57	MG	1A	3333	1/1	0.95	0.10	35,35,35,35	0
57	MG	1A	3001	1/1	0.95	0.11	23,23,23,23	0
57	MG	1a	1743	1/1	0.95	0.13	54,54,54,54	0
57	MG	1A	3532	1/1	0.95	0.09	24,24,24,24	0
57	MG	2P	201	1/1	0.95	0.12	52,52,52,52	0
57	MG	2A	3281	1/1	0.95	0.13	51,51,51,51	0
57	MG	1A	3151	1/1	0.95	0.18	38,38,38,38	0
57	MG	1A	3194	1/1	0.95	0.22	34,34,34,34	0
57	MG	1A	3086	1/1	0.95	0.22	36,36,36,36	0
57	MG	2A	3115	1/1	0.95	0.19	47,47,47,47	0
57	MG	2A	3116	1/1	0.95	0.26	53,53,53,53	0
57	MG	1A	3257	1/1	0.95	0.16	34,34,34,34	0
57	MG	1A	3020	1/1	0.95	0.20	39,39,39,39	0
57	MG	1A	3015	1/1	0.95	0.12	36,36,36,36	0
57	MG	2Y	201	1/1	0.95	0.10	52,52,52,52	0
57	MG	2A	3295	1/1	0.95	0.07	35,35,35,35	0
57	MG	1A	3655	1/1	0.95	0.07	49,49,49,49	0
57	MG	1A	3656	1/1	0.95	0.08	30,30,30,30	0
57	MG	1a	1754	1/1	0.95	0.07	48,48,48,48	0
57	MG	2A	3300	1/1	0.95	0.10	46,46,46,46	0
57	MG	1a	1616	1/1	0.95	0.04	45,45,45,45	0
57	MG	2A	3302	1/1	0.95	0.11	58,58,58,58	0
57	MG	2A	3503	1/1	0.95	0.12	42,42,42,42	0
57	MG	2a	1603	1/1	0.95	0.09	62,62,62,62	0
57	MG	2A	3305	1/1	0.95	0.10	41,41,41,41	0
57	MG	1A	3430	1/1	0.95	0.05	14,14,14,14	0
57	MG	1A	3205	1/1	0.95	0.10	25,25,25,25	0
57	MG	1A	3556	1/1	0.95	0.10	15,15,15,15	0
57	MG	1a	1760	1/1	0.95	0.21	57,57,57,57	0
57	MG	1A	3063	1/1	0.95	0.05	19,19,19,19	0
57	MG	1A	3435	1/1	0.95	0.10	10,10,10,10	0
57	MG	2A	3514	1/1	0.95	0.05	35,35,35,35	0
57	MG	1A	3211	1/1	0.95	0.15	41,41,41,41	0
57	MG	2A	3519	1/1	0.95	0.13	38,38,38,38	0
57	MG	1A	3355	1/1	0.95	0.07	21,21,21,21	0
57	MG	1a	1765	1/1	0.95	0.06	45,45,45,45	0
57	MG	1A	3048	1/1	0.95	0.22	30,30,30,30	0
57	MG	2a	1618	1/1	0.95	0.18	57,57,57,57	0
57	MG	2A	3523	1/1	0.95	0.07	46,46,46,46	0
57	MG	1A	3781	1/1	0.95	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
57	MG	2A	3138	1/1	0.95	0.10	42,42,42,42	0
57	MG	1f	201	1/1	0.95	0.13	52,52,52,52	0
57	MG	1A	3440	1/1	0.95	0.10	21,21,21,21	0
57	MG	2A	3529	1/1	0.95	0.09	49,49,49,49	0
57	MG	2A	3141	1/1	0.95	0.13	39,39,39,39	0
57	MG	1A	3672	1/1	0.95	0.12	48,48,48,48	0
57	MG	1n	101	1/1	0.95	0.12	50,50,50,50	0
57	MG	2A	3332	1/1	0.95	0.15	34,34,34,34	0
57	MG	1A	3035	1/1	0.95	0.27	26,26,26,26	0
57	MG	1A	3271	1/1	0.95	0.12	29,29,29,29	0
57	MG	2A	3336	1/1	0.95	0.04	39,39,39,39	0
57	MG	1A	3787	1/1	0.95	0.06	31,31,31,31	0
57	MG	1A	3571	1/1	0.95	0.12	17,17,17,17	0
57	MG	1A	3572	1/1	0.95	0.10	55,55,55,55	0
57	MG	1A	3272	1/1	0.95	0.16	36,36,36,36	0
57	MG	1A	3026	1/1	0.95	0.19	36,36,36,36	0
57	MG	2A	3152	1/1	0.95	0.17	34,34,34,34	0
57	MG	1A	3362	1/1	0.95	0.15	51,51,51,51	0
57	MG	1A	3275	1/1	0.95	0.14	34,34,34,34	0
57	MG	1a	1641	1/1	0.95	0.29	46,46,46,46	0
57	MG	1a	1642	1/1	0.95	0.17	48,48,48,48	0
57	MG	2a	1647	1/1	0.95	0.15	43,43,43,43	0
57	MG	2A	3159	1/1	0.95	0.15	40,40,40,40	0
57	MG	1a	1643	1/1	0.95	0.14	47,47,47,47	0
57	MG	1A	3098	1/1	0.95	0.18	27,27,27,27	0
57	MG	1A	3365	1/1	0.95	0.07	26,26,26,26	0
57	MG	1A	3132	1/1	0.95	0.08	25,25,25,25	0
57	MG	2A	3165	1/1	0.95	0.18	52,52,52,52	0
57	MG	1A	3171	1/1	0.95	0.23	21,21,21,21	0
57	MG	1A	3219	1/1	0.95	0.08	38,38,38,38	0
57	MG	2a	1657	1/1	0.95	0.26	44,44,44,44	0
57	MG	1A	3293	1/1	0.95	0.15	32,32,32,32	0
57	MG	2A	3366	1/1	0.95	0.16	35,35,35,35	0
57	MG	2a	1660	1/1	0.95	0.10	44,44,44,44	0
57	MG	1A	3220	1/1	0.95	0.11	32,32,32,32	0
57	MG	1A	3464	1/1	0.95	0.07	18,18,18,18	0
57	MG	1B	214	1/1	0.95	0.06	29,29,29,29	0
57	MG	1B	218	1/1	0.95	0.14	44,44,44,44	0
57	MG	1a	1657	1/1	0.95	0.14	50,50,50,50	0
57	MG	1A	3296	1/1	0.95	0.06	24,24,24,24	0
57	MG	2A	3179	1/1	0.95	0.23	47,47,47,47	0
57	MG	1D	301	1/1	0.95	0.08	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3181	1/1	0.95	0.22	51,51,51,51	0
57	MG	1A	3377	1/1	0.95	0.07	49,49,49,49	0
57	MG	1D	303	1/1	0.95	0.15	29,29,29,29	0
57	MG	1A	3016	1/1	0.95	0.08	35,35,35,35	0
57	MG	1D	306	1/1	0.95	0.04	28,28,28,28	0
57	MG	1D	307	1/1	0.95	0.09	30,30,30,30	0
57	MG	1A	3379	1/1	0.95	0.06	30,30,30,30	0
57	MG	2A	3189	1/1	0.95	0.28	50,50,50,50	0
57	MG	1a	1668	1/1	0.95	0.08	35,35,35,35	0
57	MG	1D	309	1/1	0.95	0.06	16,16,16,16	0
57	MG	1A	3071	1/1	0.95	0.12	38,38,38,38	0
57	MG	2a	1683	1/1	0.95	0.26	48,48,48,48	0
57	MG	2A	3030	1/1	0.95	0.34	38,38,38,38	0
57	MG	1A	3597	1/1	0.95	0.08	43,43,43,43	0
57	MG	1a	1673	1/1	0.95	0.12	42,42,42,42	0
57	MG	2a	1688	1/1	0.95	0.20	56,56,56,56	0
57	MG	1A	3598	1/1	0.95	0.08	30,30,30,30	0
57	MG	1A	3704	1/1	0.95	0.10	51,51,51,51	0
57	MG	1A	3175	1/1	0.95	0.10	37,37,37,37	0
57	MG	1A	3601	1/1	0.95	0.12	54,54,54,54	0
57	MG	1A	3382	1/1	0.95	0.11	35,35,35,35	0
57	MG	1A	3383	1/1	0.95	0.11	46,46,46,46	0
57	MG	1G	202	1/1	0.95	0.09	60,60,60,60	0
57	MG	1A	3072	1/1	0.95	0.11	29,29,29,29	0
57	MG	2A	3596	1/1	0.95	0.09	36,36,36,36	0
57	MG	1A	3138	1/1	0.95	0.11	26,26,26,26	0
57	MG	1A	3612	1/1	0.95	0.11	27,27,27,27	0
57	MG	1A	3484	1/1	0.95	0.07	33,33,33,33	0
57	MG	1P	201	1/1	0.95	0.24	24,24,24,24	0
57	MG	2A	3405	1/1	0.95	0.09	31,31,31,31	0
57	MG	2A	3408	1/1	0.95	0.15	29,29,29,29	0
57	MG	2A	3052	1/1	0.95	0.23	49,49,49,49	0
57	MG	2A	3410	1/1	0.95	0.09	43,43,43,43	0
57	MG	2A	3606	1/1	0.95	0.14	48,48,48,48	0
57	MG	1P	202	1/1	0.95	0.06	15,15,15,15	0
57	MG	2A	3211	1/1	0.95	0.07	37,37,37,37	0
57	MG	2A	3609	1/1	0.95	0.12	40,40,40,40	0
57	MG	1a	1692	1/1	0.95	0.14	60,60,60,60	0
57	MG	1a	1695	1/1	0.95	0.15	70,70,70,70	0
57	MG	2a	1717	1/1	0.95	0.12	46,46,46,46	0
57	MG	1A	3485	1/1	0.95	0.16	37,37,37,37	0
57	MG	1A	3388	1/1	0.95	0.10	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3218	1/1	0.95	0.55	42,42,42,42	0
57	MG	1A	3490	1/1	0.95	0.06	37,37,37,37	0
57	MG	1A	3139	1/1	0.95	0.11	40,40,40,40	0
57	MG	1A	3719	1/1	0.95	0.13	29,29,29,29	0
57	MG	1A	3141	1/1	0.95	0.18	28,28,28,28	0
57	MG	2A	3423	1/1	0.95	0.31	52,52,52,52	0
57	MG	1A	3494	1/1	0.95	0.16	31,31,31,31	0
57	MG	1a	1709	1/1	0.95	0.11	37,37,37,37	0
57	MG	2a	1728	1/1	0.95	0.10	49,49,49,49	0
57	MG	2A	3225	1/1	0.95	0.32	48,48,48,48	0
57	MG	1A	3184	1/1	0.95	0.18	25,25,25,25	0
57	MG	1A	3392	1/1	0.95	0.09	13,13,13,13	0
57	MG	1A	3728	1/1	0.95	0.10	16,16,16,16	0
57	MG	2A	3628	1/1	0.95	0.07	54,54,54,54	0
57	MG	1A	3185	1/1	0.95	0.17	40,40,40,40	0
57	MG	2A	3630	1/1	0.95	0.09	37,37,37,37	0
57	MG	2A	3437	1/1	0.95	0.08	45,45,45,45	0
57	MG	1A	3625	1/1	0.95	0.08	31,31,31,31	0
57	MG	1A	3317	1/1	0.95	0.12	36,36,36,36	0
57	MG	2A	3440	1/1	0.95	0.14	66,66,66,66	0
57	MG	2A	3441	1/1	0.95	0.12	29,29,29,29	0
57	MG	2A	3638	1/1	0.95	0.16	29,29,29,29	0
57	MG	2A	3235	1/1	0.95	0.09	56,56,56,56	0
57	MG	2A	3075	1/1	0.95	0.10	25,25,25,25	0
57	MG	1A	3055	1/1	0.95	0.16	11,11,11,11	0
57	MG	2A	3644	1/1	0.95	0.17	45,45,45,45	0
57	MG	1A	3505	1/1	0.95	0.11	49,49,49,49	0
57	MG	1a	1718	1/1	0.95	0.19	39,39,39,39	0
57	MG	2a	1753	1/1	0.95	0.11	44,44,44,44	0
57	MG	1A	3146	1/1	0.95	0.28	32,32,32,32	0
57	MG	1a	1720	1/1	0.95	0.08	53,53,53,53	0
57	MG	2A	3651	1/1	0.95	0.17	41,41,41,41	0
57	MG	1A	3028	1/1	0.95	0.19	33,33,33,33	0
57	MG	2a	1760	1/1	0.95	0.11	33,33,33,33	0
57	MG	2A	3083	1/1	0.95	0.07	52,52,52,52	0
57	MG	1A	3632	1/1	0.95	0.08	44,44,44,44	0
57	MG	2A	3086	1/1	0.95	0.07	58,58,58,58	0
57	MG	2A	3456	1/1	0.95	0.19	49,49,49,49	0
57	MG	2A	3087	1/1	0.95	0.17	38,38,38,38	0
57	MG	1A	3247	1/1	0.95	0.19	47,47,47,47	0
57	MG	1A	3403	1/1	0.95	0.07	18,18,18,18	0
57	MG	1A	3248	1/1	0.95	0.12	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3256	1/1	0.95	0.12	42,42,42,42	0
57	MG	15	102	1/1	0.95	0.44	36,36,36,36	0
57	MG	1A	3744	1/1	0.95	0.25	51,51,51,51	0
57	MG	2A	3096	1/1	0.95	0.14	46,46,46,46	0
57	MG	1A	3329	1/1	0.95	0.09	20,20,20,20	0
57	MG	15	105	1/1	0.95	0.15	39,39,39,39	0
57	MG	1a	1733	1/1	0.95	0.09	50,50,50,50	0
57	MG	1A	3330	1/1	0.95	0.06	34,34,34,34	0
57	MG	1A	3525	1/1	0.95	0.09	12,12,12,12	0
57	MG	1A	3076	1/1	0.95	0.08	39,39,39,39	0
57	MG	2D	305	1/1	0.95	0.08	34,34,34,34	0
57	MG	2x	107	1/1	0.95	0.06	74,74,74,74	0
57	MG	2A	3474	1/1	0.95	0.08	45,45,45,45	0
57	MG	2A	3103	1/1	0.95	0.11	52,52,52,52	0
57	MG	1A	3641	1/1	0.95	0.07	47,47,47,47	0
57	MG	1a	1604	1/1	0.96	0.15	68,68,68,68	0
57	MG	1a	1606	1/1	0.96	0.11	25,25,25,25	0
57	MG	1A	3408	1/1	0.96	0.06	26,26,26,26	0
57	MG	1a	1608	1/1	0.96	0.17	55,55,55,55	0
57	MG	2A	3304	1/1	0.96	0.14	34,34,34,34	0
57	MG	1A	3513	1/1	0.96	0.07	39,39,39,39	0
57	MG	1A	3518	1/1	0.96	0.09	37,37,37,37	0
57	MG	2A	3497	1/1	0.96	0.13	34,34,34,34	0
57	MG	1A	3337	1/1	0.96	0.06	36,36,36,36	0
57	MG	1A	3258	1/1	0.96	0.14	16,16,16,16	0
57	MG	1A	3521	1/1	0.96	0.11	11,11,11,11	0
57	MG	1A	3522	1/1	0.96	0.09	39,39,39,39	0
57	MG	1A	3760	1/1	0.96	0.15	61,61,61,61	0
57	MG	1A	3259	1/1	0.96	0.15	32,32,32,32	0
57	MG	1A	3416	1/1	0.96	0.07	23,23,23,23	0
57	MG	23	101	1/1	0.96	0.13	40,40,40,40	0
57	MG	1A	3643	1/1	0.96	0.07	44,44,44,44	0
57	MG	1A	3417	1/1	0.96	0.07	18,18,18,18	0
57	MG	2A	3321	1/1	0.96	0.08	28,28,28,28	0
57	MG	1A	3260	1/1	0.96	0.22	40,40,40,40	0
57	MG	1A	3210	1/1	0.96	0.10	40,40,40,40	0
57	MG	2a	1601	1/1	0.96	0.18	33,33,33,33	0
57	MG	2A	3512	1/1	0.96	0.16	50,50,50,50	0
57	MG	2A	3513	1/1	0.96	0.18	54,54,54,54	0
57	MG	1A	3116	1/1	0.96	0.06	34,34,34,34	0
57	MG	1A	3422	1/1	0.96	0.12	35,35,35,35	0
57	MG	2A	3518	1/1	0.96	0.08	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3774	1/1	0.96	0.13	35,35,35,35	0
57	MG	1A	3534	1/1	0.96	0.08	26,26,26,26	0
57	MG	1A	3776	1/1	0.96	0.08	46,46,46,46	0
57	MG	1A	3537	1/1	0.96	0.11	15,15,15,15	0
57	MG	1A	3423	1/1	0.96	0.10	15,15,15,15	0
57	MG	1a	1630	1/1	0.96	0.21	49,49,49,49	0
57	MG	1A	3779	1/1	0.96	0.12	38,38,38,38	0
57	MG	1a	1633	1/1	0.96	0.18	52,52,52,52	0
57	MG	1A	3345	1/1	0.96	0.09	51,51,51,51	0
57	MG	2a	1616	1/1	0.96	0.10	38,38,38,38	0
57	MG	2A	3528	1/1	0.96	0.09	42,42,42,42	0
57	MG	2A	3341	1/1	0.96	0.19	30,30,30,30	0
57	MG	2A	3342	1/1	0.96	0.08	33,33,33,33	0
57	MG	1A	3140	1/1	0.96	0.16	26,26,26,26	0
57	MG	2A	3155	1/1	0.96	0.12	29,29,29,29	0
57	MG	1A	3080	1/1	0.96	0.08	22,22,22,22	0
57	MG	2A	3157	1/1	0.96	0.14	25,25,25,25	0
57	MG	1A	3544	1/1	0.96	0.10	13,13,13,13	0
57	MG	1x	108	1/1	0.96	0.05	60,60,60,60	0
57	MG	1A	3547	1/1	0.96	0.04	15,15,15,15	0
57	MG	2a	1629	1/1	0.96	0.12	50,50,50,50	0
57	MG	2A	3161	1/1	0.96	0.14	37,37,37,37	0
57	MG	1A	3660	1/1	0.96	0.06	39,39,39,39	0
57	MG	1A	3142	1/1	0.96	0.07	22,22,22,22	0
57	MG	1A	3788	1/1	0.96	0.10	17,17,17,17	0
57	MG	1A	3118	1/1	0.96	0.27	51,51,51,51	0
57	MG	2A	3002	1/1	0.96	0.14	46,46,46,46	0
57	MG	1A	3552	1/1	0.96	0.10	16,16,16,16	0
57	MG	1A	3665	1/1	0.96	0.06	41,41,41,41	0
57	MG	1A	3034	1/1	0.96	0.21	25,25,25,25	0
57	MG	1A	3217	1/1	0.96	0.13	53,53,53,53	0
57	MG	1A	3099	1/1	0.96	0.29	24,24,24,24	0
57	MG	1A	3558	1/1	0.96	0.11	31,31,31,31	0
57	MG	1A	3671	1/1	0.96	0.15	28,28,28,28	0
57	MG	1a	1652	1/1	0.96	0.10	41,41,41,41	0
57	MG	1A	3062	1/1	0.96	0.06	33,33,33,33	0
57	MG	1A	3560	1/1	0.96	0.09	50,50,50,50	0
57	MG	1A	3438	1/1	0.96	0.06	15,15,15,15	0
57	MG	1a	1656	1/1	0.96	0.07	53,53,53,53	0
57	MG	2A	3561	1/1	0.96	0.06	33,33,33,33	0
57	MG	2A	3374	1/1	0.96	0.12	65,65,65,65	0
57	MG	1A	3057	1/1	0.96	0.08	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3021	1/1	0.96	0.11	20,20,20,20	0
57	MG	1B	210	1/1	0.96	0.19	48,48,48,48	0
57	MG	1A	3360	1/1	0.96	0.13	11,11,11,11	0
57	MG	2A	3380	1/1	0.96	0.09	46,46,46,46	0
57	MG	2A	3187	1/1	0.96	0.21	48,48,48,48	0
57	MG	1a	1661	1/1	0.96	0.08	56,56,56,56	0
57	MG	1A	3104	1/1	0.96	0.17	48,48,48,48	0
57	MG	1A	3679	1/1	0.96	0.08	22,22,22,22	0
57	MG	1A	3222	1/1	0.96	0.11	29,29,29,29	0
57	MG	2A	3386	1/1	0.96	0.11	48,48,48,48	0
57	MG	1B	219	1/1	0.96	0.08	28,28,28,28	0
57	MG	1A	3281	1/1	0.96	0.15	30,30,30,30	0
57	MG	1A	3282	1/1	0.96	0.06	33,33,33,33	0
57	MG	1A	3224	1/1	0.96	0.24	38,38,38,38	0
57	MG	1A	3448	1/1	0.96	0.07	17,17,17,17	0
57	MG	1A	3451	1/1	0.96	0.12	17,17,17,17	0
57	MG	1A	3284	1/1	0.96	0.18	29,29,29,29	0
57	MG	1A	3453	1/1	0.96	0.08	47,47,47,47	0
57	MG	2A	3040	1/1	0.96	0.07	48,48,48,48	0
57	MG	1A	3285	1/1	0.96	0.05	24,24,24,24	0
57	MG	2A	3585	1/1	0.96	0.10	42,42,42,42	0
57	MG	1A	3051	1/1	0.96	0.08	22,22,22,22	0
57	MG	2A	3587	1/1	0.96	0.13	52,52,52,52	0
57	MG	1A	3370	1/1	0.96	0.05	32,32,32,32	0
57	MG	2a	1680	1/1	0.96	0.11	57,57,57,57	0
57	MG	1A	3290	1/1	0.96	0.07	29,29,29,29	0
57	MG	1A	3583	1/1	0.96	0.08	31,31,31,31	0
57	MG	1E	306	1/1	0.96	0.09	11,11,11,11	0
57	MG	2a	1684	1/1	0.96	0.17	38,38,38,38	0
57	MG	2A	3049	1/1	0.96	0.07	40,40,40,40	0
57	MG	2A	3050	1/1	0.96	0.10	48,48,48,48	0
57	MG	1A	3584	1/1	0.96	0.09	63,63,63,63	0
57	MG	1A	3291	1/1	0.96	0.12	40,40,40,40	0
57	MG	2A	3406	1/1	0.96	0.17	35,35,35,35	0
57	MG	2A	3407	1/1	0.96	0.07	25,25,25,25	0
57	MG	1A	3586	1/1	0.96	0.09	46,46,46,46	0
57	MG	1A	3374	1/1	0.96	0.05	37,37,37,37	0
57	MG	1F	308	1/1	0.96	0.11	20,20,20,20	0
57	MG	1A	3702	1/1	0.96	0.11	43,43,43,43	0
57	MG	1G	201	1/1	0.96	0.11	60,60,60,60	0
57	MG	2A	3058	1/1	0.96	0.07	51,51,51,51	0
57	MG	1a	1688	1/1	0.96	0.06	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1689	1/1	0.96	0.07	32,32,32,32	0
57	MG	1A	3187	1/1	0.96	0.27	44,44,44,44	0
57	MG	1A	3463	1/1	0.96	0.18	32,32,32,32	0
57	MG	2A	3065	1/1	0.96	0.14	29,29,29,29	0
57	MG	2A	3610	1/1	0.96	0.10	61,61,61,61	0
57	MG	1A	3126	1/1	0.96	0.16	27,27,27,27	0
57	MG	2A	3420	1/1	0.96	0.06	23,23,23,23	0
57	MG	1A	3129	1/1	0.96	0.07	25,25,25,25	0
57	MG	1a	1699	1/1	0.96	0.09	51,51,51,51	0
57	MG	1a	1700	1/1	0.96	0.15	60,60,60,60	0
57	MG	2a	1712	1/1	0.96	0.05	58,58,58,58	0
57	MG	1A	3156	1/1	0.96	0.09	22,22,22,22	0
57	MG	2A	3426	1/1	0.96	0.17	22,22,22,22	0
57	MG	1a	1703	1/1	0.96	0.06	33,33,33,33	0
57	MG	2A	3232	1/1	0.96	0.09	41,41,41,41	0
57	MG	1A	3093	1/1	0.96	0.12	41,41,41,41	0
57	MG	2A	3431	1/1	0.96	0.07	45,45,45,45	0
57	MG	1A	3233	1/1	0.96	0.33	37,37,37,37	0
57	MG	1A	3234	1/1	0.96	0.06	24,24,24,24	0
57	MG	2A	3435	1/1	0.96	0.12	34,34,34,34	0
57	MG	1A	3235	1/1	0.96	0.14	15,15,15,15	0
57	MG	1A	3311	1/1	0.96	0.06	16,16,16,16	0
57	MG	2A	3078	1/1	0.96	0.14	44,44,44,44	0
57	MG	1A	3237	1/1	0.96	0.12	23,23,23,23	0
57	MG	1A	3387	1/1	0.96	0.10	41,41,41,41	0
57	MG	1A	3603	1/1	0.96	0.07	57,57,57,57	0
57	MG	1A	3604	1/1	0.96	0.12	34,34,34,34	0
57	MG	2A	3634	1/1	0.96	0.19	51,51,51,51	0
57	MG	2A	3246	1/1	0.96	0.13	54,54,54,54	0
57	MG	1U	203	1/1	0.96	0.10	24,24,24,24	0
57	MG	1A	3605	1/1	0.96	0.14	37,37,37,37	0
57	MG	1U	205	1/1	0.96	0.07	32,32,32,32	0
57	MG	2A	3639	1/1	0.96	0.16	22,22,22,22	0
57	MG	1A	3052	1/1	0.96	0.15	36,36,36,36	0
57	MG	2A	3089	1/1	0.96	0.11	27,27,27,27	0
57	MG	2A	3642	1/1	0.96	0.13	43,43,43,43	0
57	MG	2a	1738	1/1	0.96	0.14	36,36,36,36	0
57	MG	1V	201	1/1	0.96	0.21	18,18,18,18	0
57	MG	2a	1740	1/1	0.96	0.15	40,40,40,40	0
57	MG	1A	3721	1/1	0.96	0.07	31,31,31,31	0
57	MG	1A	3609	1/1	0.96	0.14	30,30,30,30	0
57	MG	2a	1743	1/1	0.96	0.11	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3161	1/1	0.96	0.22	42,42,42,42	0
57	MG	2A	3648	1/1	0.96	0.06	25,25,25,25	0
57	MG	2A	3455	1/1	0.96	0.06	40,40,40,40	0
57	MG	2a	1748	1/1	0.96	0.17	50,50,50,50	0
57	MG	2A	3260	1/1	0.96	0.06	24,24,24,24	0
57	MG	2A	3457	1/1	0.96	0.21	47,47,47,47	0
57	MG	1A	3724	1/1	0.96	0.09	34,34,34,34	0
57	MG	1A	3195	1/1	0.96	0.08	28,28,28,28	0
57	MG	1A	3196	1/1	0.96	0.05	38,38,38,38	0
57	MG	1a	1725	1/1	0.96	0.19	49,49,49,49	0
57	MG	2a	1755	1/1	0.96	0.08	46,46,46,46	0
57	MG	1A	3197	1/1	0.96	0.17	45,45,45,45	0
57	MG	1A	3614	1/1	0.96	0.06	35,35,35,35	0
57	MG	1A	3198	1/1	0.96	0.17	38,38,38,38	0
57	MG	2a	1759	1/1	0.96	0.08	61,61,61,61	0
57	MG	1A	3394	1/1	0.96	0.08	23,23,23,23	0
57	MG	1A	3110	1/1	0.96	0.18	49,49,49,49	0
57	MG	1A	3497	1/1	0.96	0.07	54,54,54,54	0
57	MG	1A	3736	1/1	0.96	0.06	37,37,37,37	0
57	MG	1A	3499	1/1	0.96	0.09	32,32,32,32	0
57	MG	2A	3108	1/1	0.96	0.14	45,45,45,45	0
57	MG	1A	3111	1/1	0.96	0.09	29,29,29,29	0
57	MG	1A	3203	1/1	0.96	0.15	26,26,26,26	0
57	MG	1A	3399	1/1	0.96	0.11	31,31,31,31	0
57	MG	1a	1739	1/1	0.96	0.06	23,23,23,23	0
57	MG	1a	1740	1/1	0.96	0.07	40,40,40,40	0
57	MG	2k	202	1/1	0.96	0.07	61,61,61,61	0
57	MG	1A	3252	1/1	0.96	0.06	39,39,39,39	0
57	MG	1A	3167	1/1	0.96	0.21	46,46,46,46	0
57	MG	1A	3331	1/1	0.96	0.06	33,33,33,33	0
57	MG	1A	3022	1/1	0.96	0.10	16,16,16,16	0
57	MG	2E	301	1/1	0.96	0.13	36,36,36,36	0
57	MG	1A	3508	1/1	0.96	0.10	35,35,35,35	0
57	MG	2E	303	1/1	0.96	0.29	49,49,49,49	0
57	MG	2A	3120	1/1	0.96	0.18	38,38,38,38	0
57	MG	2A	3294	1/1	0.96	0.08	43,43,43,43	0
57	MG	19	101	1/1	0.96	0.11	33,33,33,33	0
57	MG	2A	3296	1/1	0.96	0.07	37,37,37,37	0
57	MG	1A	3078	1/1	0.96	0.06	34,34,34,34	0
57	MG	1A	3209	1/1	0.96	0.19	35,35,35,35	0
58	ZN	24	501	1/1	0.96	0.09	140,140,140,140	0
58	ZN	2n	501	1/1	0.96	0.07	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2A	3016	1/1	0.97	0.14	48,48,48,48	0
57	MG	2A	3335	1/1	0.97	0.10	62,62,62,62	0
57	MG	1A	3003	1/1	0.97	0.12	17,17,17,17	0
57	MG	2A	3337	1/1	0.97	0.05	35,35,35,35	0
57	MG	1A	3145	1/1	0.97	0.18	30,30,30,30	0
57	MG	2A	3339	1/1	0.97	0.07	27,27,27,27	0
57	MG	1a	1672	1/1	0.97	0.31	55,55,55,55	0
57	MG	1A	3640	1/1	0.97	0.09	39,39,39,39	0
57	MG	1A	3316	1/1	0.97	0.06	27,27,27,27	0
57	MG	1Q	201	1/1	0.97	0.16	41,41,41,41	0
57	MG	1A	3642	1/1	0.97	0.04	44,44,44,44	0
57	MG	2A	3025	1/1	0.97	0.11	39,39,39,39	0
57	MG	2A	3169	1/1	0.97	0.12	43,43,43,43	0
57	MG	1Q	203	1/1	0.97	0.09	16,16,16,16	0
57	MG	1A	3554	1/1	0.97	0.06	40,40,40,40	0
57	MG	1A	3555	1/1	0.97	0.18	46,46,46,46	0
57	MG	2A	3173	1/1	0.97	0.17	43,43,43,43	0
57	MG	1A	3645	1/1	0.97	0.13	33,33,33,33	0
57	MG	2A	3352	1/1	0.97	0.11	40,40,40,40	0
57	MG	1R	202	1/1	0.97	0.30	28,28,28,28	0
57	MG	2A	3031	1/1	0.97	0.07	34,34,34,34	0
57	MG	2a	1619	1/1	0.97	0.16	33,33,33,33	0
57	MG	2A	3178	1/1	0.97	0.07	51,51,51,51	0
57	MG	2a	1621	1/1	0.97	0.11	43,43,43,43	0
57	MG	2A	3541	1/1	0.97	0.06	61,61,61,61	0
57	MG	1A	3178	1/1	0.97	0.07	27,27,27,27	0
57	MG	2A	3358	1/1	0.97	0.10	50,50,50,50	0
57	MG	1U	202	1/1	0.97	0.23	19,19,19,19	0
57	MG	1A	3056	1/1	0.97	0.11	19,19,19,19	0
57	MG	1a	1685	1/1	0.97	0.12	37,37,37,37	0
57	MG	1A	3320	1/1	0.97	0.07	42,42,42,42	0
57	MG	1A	3460	1/1	0.97	0.12	40,40,40,40	0
57	MG	2a	1630	1/1	0.97	0.22	51,51,51,51	0
57	MG	1U	206	1/1	0.97	0.17	32,32,32,32	0
57	MG	1A	3461	1/1	0.97	0.24	41,41,41,41	0
57	MG	1a	1690	1/1	0.97	0.11	39,39,39,39	0
57	MG	2A	3042	1/1	0.97	0.15	41,41,41,41	0
57	MG	1A	3041	1/1	0.97	0.10	16,16,16,16	0
57	MG	1A	3752	1/1	0.97	0.22	26,26,26,26	0
57	MG	2A	3557	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3183	1/1	0.97	0.17	23,23,23,23	0
57	MG	1V	205	1/1	0.97	0.21	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1a	1698	1/1	0.97	0.14	54,54,54,54	0
57	MG	1A	3325	1/1	0.97	0.09	41,41,41,41	0
57	MG	1A	3755	1/1	0.97	0.12	38,38,38,38	0
57	MG	1A	3262	1/1	0.97	0.10	39,39,39,39	0
57	MG	1A	3042	1/1	0.97	0.23	33,33,33,33	0
57	MG	1X	103	1/1	0.97	0.10	25,25,25,25	0
57	MG	1A	3004	1/1	0.97	0.10	17,17,17,17	0
57	MG	1A	3012	1/1	0.97	0.05	18,18,18,18	0
57	MG	1a	1707	1/1	0.97	0.18	57,57,57,57	0
57	MG	10	102	1/1	0.97	0.17	40,40,40,40	0
57	MG	2a	1651	1/1	0.97	0.14	48,48,48,48	0
57	MG	1A	3473	1/1	0.97	0.13	41,41,41,41	0
57	MG	2A	3059	1/1	0.97	0.17	49,49,49,49	0
57	MG	2A	3060	1/1	0.97	0.06	45,45,45,45	0
57	MG	11	101	1/1	0.97	0.26	31,31,31,31	0
57	MG	1A	3033	1/1	0.97	0.23	19,19,19,19	0
57	MG	1A	3153	1/1	0.97	0.14	34,34,34,34	0
57	MG	1A	3763	1/1	0.97	0.06	40,40,40,40	0
57	MG	1A	3223	1/1	0.97	0.10	35,35,35,35	0
57	MG	1A	3664	1/1	0.97	0.06	41,41,41,41	0
57	MG	1A	3189	1/1	0.97	0.22	30,30,30,30	0
57	MG	2A	3214	1/1	0.97	0.17	28,28,28,28	0
57	MG	1A	3578	1/1	0.97	0.06	36,36,36,36	0
57	MG	1A	3335	1/1	0.97	0.05	15,15,15,15	0
57	MG	2a	1665	1/1	0.97	0.17	43,43,43,43	0
57	MG	1A	3772	1/1	0.97	0.04	34,34,34,34	0
57	MG	2A	3071	1/1	0.97	0.13	43,43,43,43	0
57	MG	16	101	1/1	0.97	0.13	44,44,44,44	0
57	MG	1A	3668	1/1	0.97	0.10	10,10,10,10	0
57	MG	1A	3398	1/1	0.97	0.07	45,45,45,45	0
57	MG	1A	3336	1/1	0.97	0.10	38,38,38,38	0
57	MG	2a	1672	1/1	0.97	0.16	30,30,30,30	0
57	MG	1A	3102	1/1	0.97	0.16	34,34,34,34	0
57	MG	1A	3013	1/1	0.97	0.15	24,24,24,24	0
57	MG	1A	3274	1/1	0.97	0.04	18,18,18,18	0
57	MG	1a	1602	1/1	0.97	0.08	45,45,45,45	0
57	MG	1A	3491	1/1	0.97	0.08	48,48,48,48	0
57	MG	1A	3128	1/1	0.97	0.46	23,23,23,23	0
57	MG	1a	1605	1/1	0.97	0.21	37,37,37,37	0
57	MG	2A	3231	1/1	0.97	0.11	50,50,50,50	0
57	MG	1A	3341	1/1	0.97	0.06	22,22,22,22	0
57	MG	2A	3233	1/1	0.97	0.12	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3157	1/1	0.97	0.15	35,35,35,35	0
57	MG	2A	3085	1/1	0.97	0.17	39,39,39,39	0
57	MG	1A	3496	1/1	0.97	0.05	24,24,24,24	0
57	MG	1A	3083	1/1	0.97	0.32	30,30,30,30	0
57	MG	2A	3088	1/1	0.97	0.07	31,31,31,31	0
57	MG	1A	3344	1/1	0.97	0.06	13,13,13,13	0
57	MG	2a	1689	1/1	0.97	0.09	43,43,43,43	0
57	MG	1a	1611	1/1	0.97	0.14	37,37,37,37	0
57	MG	1A	3593	1/1	0.97	0.07	18,18,18,18	0
57	MG	2a	1692	1/1	0.97	0.07	36,36,36,36	0
57	MG	1A	3231	1/1	0.97	0.10	34,34,34,34	0
57	MG	2A	3424	1/1	0.97	0.09	26,26,26,26	0
57	MG	2A	3244	1/1	0.97	0.08	43,43,43,43	0
57	MG	1A	3346	1/1	0.97	0.10	22,22,22,22	0
57	MG	2A	3427	1/1	0.97	0.14	46,46,46,46	0
57	MG	1A	3349	1/1	0.97	0.05	29,29,29,29	0
57	MG	2A	3247	1/1	0.97	0.06	41,41,41,41	0
57	MG	2A	3095	1/1	0.97	0.10	33,33,33,33	0
57	MG	1A	3023	1/1	0.97	0.16	32,32,32,32	0
57	MG	1A	3005	1/1	0.97	0.05	37,37,37,37	0
57	MG	1a	1745	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3162	1/1	0.97	0.14	30,30,30,30	0
57	MG	1A	3691	1/1	0.97	0.10	50,50,50,50	0
57	MG	1A	3087	1/1	0.97	0.09	15,15,15,15	0
57	MG	1A	3286	1/1	0.97	0.13	22,22,22,22	0
57	MG	1A	3236	1/1	0.97	0.07	22,22,22,22	0
57	MG	2A	3104	1/1	0.97	0.13	33,33,33,33	0
57	MG	1A	3288	1/1	0.97	0.07	40,40,40,40	0
57	MG	1A	3289	1/1	0.97	0.28	36,36,36,36	0
57	MG	2A	3264	1/1	0.97	0.07	30,30,30,30	0
57	MG	1A	3199	1/1	0.97	0.07	40,40,40,40	0
57	MG	2A	3266	1/1	0.97	0.15	32,32,32,32	0
57	MG	1A	3608	1/1	0.97	0.08	26,26,26,26	0
57	MG	2A	3268	1/1	0.97	0.18	56,56,56,56	0
57	MG	1A	3135	1/1	0.97	0.12	32,32,32,32	0
57	MG	1A	3292	1/1	0.97	0.14	30,30,30,30	0
57	MG	1A	3432	1/1	0.97	0.05	26,26,26,26	0
57	MG	1A	3109	1/1	0.97	0.09	24,24,24,24	0
57	MG	1a	1631	1/1	0.97	0.08	23,23,23,23	0
57	MG	1A	3202	1/1	0.97	0.29	20,20,20,20	0
57	MG	1A	3088	1/1	0.97	0.04	11,11,11,11	0
57	MG	1A	3299	1/1	0.97	0.16	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3300	1/1	0.97	0.07	46,46,46,46	0
57	MG	1A	3065	1/1	0.97	0.21	21,21,21,21	0
57	MG	2A	3119	1/1	0.97	0.07	44,44,44,44	0
57	MG	2A	3280	1/1	0.97	0.14	32,32,32,32	0
57	MG	1A	3009	1/1	0.97	0.04	11,11,11,11	0
57	MG	2A	3282	1/1	0.97	0.09	43,43,43,43	0
57	MG	1D	305	1/1	0.97	0.05	24,24,24,24	0
57	MG	1A	3442	1/1	0.97	0.04	20,20,20,20	0
57	MG	2A	3286	1/1	0.97	0.10	37,37,37,37	0
57	MG	2A	3467	1/1	0.97	0.10	50,50,50,50	0
57	MG	1A	3369	1/1	0.97	0.07	18,18,18,18	0
57	MG	1A	3305	1/1	0.97	0.11	25,25,25,25	0
57	MG	1A	3535	1/1	0.97	0.06	17,17,17,17	0
57	MG	1E	301	1/1	0.97	0.19	28,28,28,28	0
57	MG	2A	3291	1/1	0.97	0.05	47,47,47,47	0
57	MG	2A	3473	1/1	0.97	0.04	40,40,40,40	0
57	MG	1A	3536	1/1	0.97	0.07	29,29,29,29	0
57	MG	2A	3128	1/1	0.97	0.11	48,48,48,48	0
57	MG	1A	3624	1/1	0.97	0.06	43,43,43,43	0
57	MG	1A	3114	1/1	0.97	0.16	11,11,11,11	0
57	MG	1A	3538	1/1	0.97	0.07	14,14,14,14	0
57	MG	1x	101	1/1	0.97	0.20	44,44,44,44	0
57	MG	1a	1649	1/1	0.97	0.21	47,47,47,47	0
57	MG	1A	3539	1/1	0.97	0.13	18,18,18,18	0
57	MG	1A	3207	1/1	0.97	0.04	25,25,25,25	0
57	MG	2D	302	1/1	0.97	0.12	22,22,22,22	0
57	MG	1F	302	1/1	0.97	0.15	24,24,24,24	0
57	MG	1F	304	1/1	0.97	0.26	37,37,37,37	0
57	MG	2A	3303	1/1	0.97	0.10	25,25,25,25	0
57	MG	1x	107	1/1	0.97	0.09	47,47,47,47	0
57	MG	1A	3208	1/1	0.97	0.16	21,21,21,21	0
57	MG	1F	306	1/1	0.97	0.10	29,29,29,29	0
57	MG	2A	3307	1/1	0.97	0.05	33,33,33,33	0
57	MG	1x	110	1/1	0.97	0.10	36,36,36,36	0
57	MG	2E	304	1/1	0.97	0.05	46,46,46,46	0
57	MG	1A	3630	1/1	0.97	0.07	48,48,48,48	0
57	MG	1A	3375	1/1	0.97	0.10	20,20,20,20	0
57	MG	1F	309	1/1	0.97	0.14	28,28,28,28	0
57	MG	2A	3494	1/1	0.97	0.09	42,42,42,42	0
57	MG	1F	310	1/1	0.97	0.08	15,15,15,15	0
57	MG	2A	3313	1/1	0.97	0.11	23,23,23,23	0
57	MG	2A	3146	1/1	0.97	0.21	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	2j	201	1/1	0.97	0.15	58,58,58,58	0
57	MG	2A	3498	1/1	0.97	0.08	34,34,34,34	0
57	MG	1a	1660	1/1	0.97	0.10	40,40,40,40	0
57	MG	2A	3004	1/1	0.97	0.17	27,27,27,27	0
57	MG	2A	3317	1/1	0.97	0.10	35,35,35,35	0
57	MG	2A	3318	1/1	0.97	0.07	54,54,54,54	0
57	MG	2A	3319	1/1	0.97	0.09	42,42,42,42	0
57	MG	1A	3449	1/1	0.97	0.06	16,16,16,16	0
57	MG	1F	312	1/1	0.97	0.04	43,43,43,43	0
57	MG	1F	314	1/1	0.97	0.09	27,27,27,27	0
57	MG	2A	3008	1/1	0.97	0.05	30,30,30,30	0
57	MG	2A	3009	1/1	0.97	0.10	47,47,47,47	0
57	MG	1A	3092	1/1	0.97	0.18	31,31,31,31	0
57	MG	1A	3545	1/1	0.97	0.07	13,13,13,13	0
57	MG	1A	3174	1/1	0.97	0.37	28,28,28,28	0
57	MG	1A	3017	1/1	0.97	0.12	22,22,22,22	0
57	MG	1A	3733	1/1	0.97	0.04	35,35,35,35	0
57	MG	1A	3549	1/1	0.97	0.05	56,56,56,56	0
57	MG	1A	3328	1/1	0.98	0.03	16,16,16,16	0
57	MG	2A	3517	1/1	0.98	0.04	57,57,57,57	0
57	MG	1T	201	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3131	1/1	0.98	0.17	25,25,25,25	0
57	MG	1A	3483	1/1	0.98	0.12	28,28,28,28	0
57	MG	2A	3647	1/1	0.98	0.10	32,32,32,32	0
57	MG	1A	3695	1/1	0.98	0.05	29,29,29,29	0
57	MG	1A	3372	1/1	0.98	0.05	48,48,48,48	0
57	MG	1A	3101	1/1	0.98	0.07	35,35,35,35	0
57	MG	1A	3255	1/1	0.98	0.23	31,31,31,31	0
57	MG	1A	3487	1/1	0.98	0.06	22,22,22,22	0
57	MG	1U	208	1/1	0.98	0.04	26,26,26,26	0
57	MG	2A	3175	1/1	0.98	0.05	34,34,34,34	0
57	MG	1a	1758	1/1	0.98	0.06	47,47,47,47	0
57	MG	1A	3133	1/1	0.98	0.06	28,28,28,28	0
57	MG	1A	3701	1/1	0.98	0.04	21,21,21,21	0
57	MG	1V	203	1/1	0.98	0.10	18,18,18,18	0
57	MG	1A	3046	1/1	0.98	0.15	19,19,19,19	0
57	MG	1A	3091	1/1	0.98	0.16	30,30,30,30	0
57	MG	1A	3079	1/1	0.98	0.10	22,22,22,22	0
57	MG	1A	3564	1/1	0.98	0.07	32,32,32,32	0
57	MG	1A	3229	1/1	0.98	0.53	24,24,24,24	0
57	MG	1A	3789	1/1	0.98	0.08	18,18,18,18	0
57	MG	1A	3434	1/1	0.98	0.04	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3295	1/1	0.98	0.10	22,22,22,22	0
57	MG	1A	3709	1/1	0.98	0.08	50,50,50,50	0
57	MG	1m	3001	1/1	0.98	0.04	62,62,62,62	0
57	MG	10	101	1/1	0.98	0.22	36,36,36,36	0
57	MG	1A	3569	1/1	0.98	0.08	14,14,14,14	0
57	MG	10	103	1/1	0.98	0.07	36,36,36,36	0
57	MG	1A	3181	1/1	0.98	0.16	25,25,25,25	0
57	MG	2A	3548	1/1	0.98	0.06	24,24,24,24	0
57	MG	1A	3298	1/1	0.98	0.16	45,45,45,45	0
57	MG	1w	402	1/1	0.98	0.18	36,36,36,36	0
57	MG	1A	3182	1/1	0.98	0.05	20,20,20,20	0
57	MG	11	103	1/1	0.98	0.06	29,29,29,29	0
57	MG	1A	3105	1/1	0.98	0.10	17,17,17,17	0
57	MG	1A	3302	1/1	0.98	0.05	30,30,30,30	0
57	MG	2A	3432	1/1	0.98	0.06	42,42,42,42	0
57	MG	1A	3441	1/1	0.98	0.05	28,28,28,28	0
57	MG	1B	207	1/1	0.98	0.07	42,42,42,42	0
57	MG	2F	302	1/1	0.98	0.04	34,34,34,34	0
57	MG	1A	3717	1/1	0.98	0.14	32,32,32,32	0
57	MG	1A	3576	1/1	0.98	0.09	15,15,15,15	0
57	MG	1A	3386	1/1	0.98	0.04	35,35,35,35	0
57	MG	2a	1706	1/1	0.98	0.08	46,46,46,46	0
57	MG	1A	3158	1/1	0.98	0.05	38,38,38,38	0
57	MG	1A	3507	1/1	0.98	0.17	27,27,27,27	0
57	MG	17	101	1/1	0.98	0.13	26,26,26,26	0
57	MG	2Q	202	1/1	0.98	0.05	42,42,42,42	0
57	MG	17	102	1/1	0.98	0.12	34,34,34,34	0
57	MG	2A	3322	1/1	0.98	0.11	45,45,45,45	0
57	MG	1B	213	1/1	0.98	0.05	30,30,30,30	0
57	MG	2A	3325	1/1	0.98	0.04	39,39,39,39	0
57	MG	2A	3210	1/1	0.98	0.05	31,31,31,31	0
57	MG	2A	3446	1/1	0.98	0.06	45,45,45,45	0
57	MG	17	104	1/1	0.98	0.08	20,20,20,20	0
57	MG	1A	3070	1/1	0.98	0.06	27,27,27,27	0
57	MG	2A	3003	1/1	0.98	0.10	18,18,18,18	0
57	MG	1a	1691	1/1	0.98	0.06	42,42,42,42	0
57	MG	2A	3215	1/1	0.98	0.13	46,46,46,46	0
57	MG	2A	3452	1/1	0.98	0.08	30,30,30,30	0
57	MG	1B	216	1/1	0.98	0.08	39,39,39,39	0
57	MG	1a	1694	1/1	0.98	0.09	45,45,45,45	0
57	MG	1A	3025	1/1	0.98	0.17	30,30,30,30	0
57	MG	18	102	1/1	0.98	0.07	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3306	1/1	0.98	0.11	50,50,50,50	0
57	MG	1A	3347	1/1	0.98	0.04	17,17,17,17	0
57	MG	1A	3726	1/1	0.98	0.06	14,14,14,14	0
57	MG	1A	3348	1/1	0.98	0.10	35,35,35,35	0
57	MG	1A	3514	1/1	0.98	0.08	45,45,45,45	0
57	MG	1A	3516	1/1	0.98	0.07	17,17,17,17	0
57	MG	1A	3084	1/1	0.98	0.09	5,5,5,5	0
57	MG	1A	3588	1/1	0.98	0.04	21,21,21,21	0
57	MG	1A	3450	1/1	0.98	0.06	11,11,11,11	0
57	MG	1A	3043	1/1	0.98	0.41	25,25,25,25	0
57	MG	1A	3659	1/1	0.98	0.07	67,67,67,67	0
57	MG	1A	3002	1/1	0.98	0.17	35,35,35,35	0
57	MG	1A	3310	1/1	0.98	0.08	33,33,33,33	0
57	MG	2A	3022	1/1	0.98	0.05	35,35,35,35	0
57	MG	1A	3143	1/1	0.98	0.05	23,23,23,23	0
57	MG	1A	3354	1/1	0.98	0.06	10,10,10,10	0
57	MG	1A	3741	1/1	0.98	0.10	22,22,22,22	0
57	MG	2a	1744	1/1	0.98	0.05	53,53,53,53	0
57	MG	1A	3526	1/1	0.98	0.15	35,35,35,35	0
57	MG	1A	3240	1/1	0.98	0.05	29,29,29,29	0
57	MG	1A	3125	1/1	0.98	0.12	19,19,19,19	0
57	MG	2A	3601	1/1	0.98	0.09	37,37,37,37	0
57	MG	2A	3240	1/1	0.98	0.18	38,38,38,38	0
57	MG	1A	3243	1/1	0.98	0.11	24,24,24,24	0
57	MG	1A	3014	1/1	0.98	0.11	19,19,19,19	0
57	MG	1A	3404	1/1	0.98	0.05	10,10,10,10	0
57	MG	2A	3032	1/1	0.98	0.21	39,39,39,39	0
57	MG	1A	3748	1/1	0.98	0.14	33,33,33,33	0
57	MG	1A	3245	1/1	0.98	0.07	32,32,32,32	0
57	MG	1A	3278	1/1	0.98	0.16	11,11,11,11	0
57	MG	1A	3279	1/1	0.98	0.04	17,17,17,17	0
57	MG	1A	3319	1/1	0.98	0.06	10,10,10,10	0
57	MG	2A	3250	1/1	0.98	0.09	33,33,33,33	0
57	MG	2a	1632	1/1	0.98	0.10	48,48,48,48	0
57	MG	1A	3606	1/1	0.98	0.06	37,37,37,37	0
57	MG	1F	313	1/1	0.98	0.08	27,27,27,27	0
57	MG	1a	1727	1/1	0.98	0.11	44,44,44,44	0
57	MG	1A	3675	1/1	0.98	0.07	53,53,53,53	0
57	MG	2A	3255	1/1	0.98	0.04	41,41,41,41	0
57	MG	1A	3409	1/1	0.98	0.11	8,8,8,8	0
57	MG	1A	3169	1/1	0.98	0.19	24,24,24,24	0
57	MG	2A	3378	1/1	0.98	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
57	MG	2A	3258	1/1	0.98	0.07	37,37,37,37	0
57	MG	1A	3321	1/1	0.98	0.07	25,25,25,25	0
57	MG	1A	3468	1/1	0.98	0.07	54,54,54,54	0
57	MG	2A	3046	1/1	0.98	0.24	59,59,59,59	0
57	MG	1A	3469	1/1	0.98	0.06	23,23,23,23	0
57	MG	1A	3127	1/1	0.98	0.19	28,28,28,28	0
57	MG	1a	1636	1/1	0.98	0.05	49,49,49,49	0
57	MG	1O	201	1/1	0.98	0.12	31,31,31,31	0
57	MG	1A	3147	1/1	0.98	0.20	25,25,25,25	0
57	MG	1A	3112	1/1	0.98	0.21	38,38,38,38	0
57	MG	1A	3546	1/1	0.98	0.07	24,24,24,24	0
57	MG	1A	3764	1/1	0.98	0.05	25,25,25,25	0
57	MG	1A	3068	1/1	0.98	0.11	26,26,26,26	0
57	MG	1A	3477	1/1	0.98	0.07	37,37,37,37	0
57	MG	1A	3419	1/1	0.98	0.03	18,18,18,18	0
57	MG	1A	3550	1/1	0.98	0.05	25,25,25,25	0
57	MG	1A	3690	1/1	0.98	0.12	27,27,27,27	0
58	ZN	1n	102	1/1	0.98	0.05	91,91,91,91	0
58	ZN	2Y	202	1/1	0.98	0.04	92,92,92,92	0
57	MG	1A	3077	1/1	0.98	0.07	32,32,32,32	0
57	MG	2A	3515	1/1	0.98	0.04	51,51,51,51	0
59	SF4	1d	501	8/8	0.98	0.05	54,70,79,79	0
57	MG	1F	303	1/1	0.99	0.12	23,23,23,23	0
57	MG	1A	3410	1/1	0.99	0.10	10,10,10,10	0
57	MG	1A	3783	1/1	0.99	0.08	23,23,23,23	0
57	MG	2A	3355	1/1	0.99	0.09	31,31,31,31	0
57	MG	1A	3737	1/1	0.99	0.07	29,29,29,29	0
57	MG	1A	3528	1/1	0.99	0.04	13,13,13,13	0
57	MG	1A	3651	1/1	0.99	0.06	30,30,30,30	0
57	MG	1A	3529	1/1	0.99	0.06	21,21,21,21	0
57	MG	1A	3081	1/1	0.99	0.05	13,13,13,13	0
57	MG	13	101	1/1	0.99	0.23	31,31,31,31	0
57	MG	2A	3362	1/1	0.99	0.07	24,24,24,24	0
57	MG	2A	3363	1/1	0.99	0.06	28,28,28,28	0
57	MG	2A	3364	1/1	0.99	0.04	33,33,33,33	0
57	MG	1A	3301	1/1	0.99	0.05	28,28,28,28	0
57	MG	1A	3163	1/1	0.99	0.10	11,11,11,11	0
57	MG	1a	1693	1/1	0.99	0.05	50,50,50,50	0
57	MG	1A	3495	1/1	0.99	0.05	38,38,38,38	0
57	MG	2A	3633	1/1	0.99	0.05	31,31,31,31	0
57	MG	1A	3414	1/1	0.99	0.03	19,19,19,19	0
57	MG	1A	3415	1/1	0.99	0.04	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1A	3498	1/1	0.99	0.03	46,46,46,46	0
57	MG	1A	3082	1/1	0.99	0.25	25,25,25,25	0
57	MG	1A	3242	1/1	0.99	0.04	22,22,22,22	0
57	MG	1A	3037	1/1	0.99	0.12	26,26,26,26	0
57	MG	2A	3570	1/1	0.99	0.03	38,38,38,38	0
57	MG	1a	1701	1/1	0.99	0.03	29,29,29,29	0
57	MG	1A	3166	1/1	0.99	0.05	27,27,27,27	0
57	MG	1A	3470	1/1	0.99	0.09	30,30,30,30	0
57	MG	1A	3075	1/1	0.99	0.13	21,21,21,21	0
57	MG	1A	3472	1/1	0.99	0.10	17,17,17,17	0
57	MG	1A	3018	1/1	0.99	0.09	31,31,31,31	0
57	MG	17	107	1/1	0.99	0.05	37,37,37,37	0
57	MG	1A	3047	1/1	0.99	0.13	22,22,22,22	0
57	MG	2A	3511	1/1	0.99	0.12	25,25,25,25	0
57	MG	1A	3475	1/1	0.99	0.04	19,19,19,19	0
57	MG	1A	3509	1/1	0.99	0.06	22,22,22,22	0
57	MG	2A	3262	1/1	0.99	0.08	34,34,34,34	0
57	MG	1A	3401	1/1	0.99	0.04	21,21,21,21	0
57	MG	2A	3323	1/1	0.99	0.07	18,18,18,18	0
57	MG	1A	3053	1/1	0.99	0.06	25,25,25,25	0
57	MG	1B	215	1/1	0.99	0.06	37,37,37,37	0
57	MG	1A	3425	1/1	0.99	0.07	31,31,31,31	0
57	MG	1B	217	1/1	0.99	0.05	35,35,35,35	0
57	MG	1A	3426	1/1	0.99	0.07	11,11,11,11	0
57	MG	1A	3032	1/1	0.99	0.05	21,21,21,21	0
57	MG	1A	3515	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3765	1/1	0.99	0.08	21,21,21,21	0
57	MG	1A	3766	1/1	0.99	0.06	32,32,32,32	0
57	MG	1A	3481	1/1	0.99	0.06	25,25,25,25	0
57	MG	1A	3517	1/1	0.99	0.07	32,32,32,32	0
57	MG	1A	3263	1/1	0.99	0.28	26,26,26,26	0
57	MG	1A	3680	1/1	0.99	0.04	42,42,42,42	0
57	MG	2a	1701	1/1	0.99	0.16	32,32,32,32	0
57	MG	1A	3429	1/1	0.99	0.05	18,18,18,18	0
57	MG	1A	3024	1/1	0.99	0.14	11,11,11,11	0
57	MG	1A	3599	1/1	0.99	0.06	16,16,16,16	0
57	MG	1A	3280	1/1	0.99	0.07	17,17,17,17	0
57	MG	1a	1729	1/1	0.99	0.07	33,33,33,33	0
57	MG	1A	3297	1/1	0.99	0.12	17,17,17,17	0
57	MG	2A	3283	1/1	0.99	0.03	43,43,43,43	0
57	MG	2A	3537	1/1	0.99	0.04	42,42,42,42	0
57	MG	1A	3523	1/1	0.99	0.06	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
57	MG	1E	304	1/1	0.99	0.07	11,11,11,11	0
57	MG	1A	3562	1/1	0.99	0.07	30,30,30,30	0
57	MG	1A	3265	1/1	0.99	0.07	42,42,42,42	0
58	ZN	1Y	501	1/1	0.99	0.03	58,58,58,58	0
57	MG	1X	102	1/1	0.99	0.07	33,33,33,33	0
58	ZN	15	108	1/1	0.99	0.04	35,35,35,35	0
58	ZN	16	102	1/1	0.99	0.04	37,37,37,37	0
58	ZN	19	102	1/1	0.99	0.04	39,39,39,39	0
57	MG	2A	3611	1/1	0.99	0.07	46,46,46,46	0
57	MG	2A	3543	1/1	0.99	0.15	32,32,32,32	0
57	MG	1A	3489	1/1	0.99	0.04	9,9,9,9	0
58	ZN	26	102	1/1	0.99	0.05	64,64,64,64	0
58	ZN	29	501	1/1	0.99	0.04	64,64,64,64	0
57	MG	1A	3251	1/1	0.99	0.25	24,24,24,24	0
57	MG	1A	3566	1/1	0.99	0.07	21,21,21,21	0
59	SF4	2d	501	8/8	0.99	0.04	46,66,70,70	0
57	MG	1A	3727	1/1	1.00	0.07	14,14,14,14	0
57	MG	1A	3323	1/1	1.00	0.02	19,19,19,19	0
58	ZN	25	103	1/1	1.00	0.05	52,52,52,52	0
57	MG	1A	3488	1/1	1.00	0.05	9,9,9,9	0

6.5 Other polymers (i)

There are no such residues in this entry.