Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:14 PM UTC

PDB ID	:	5HCQ / pdb_00005hcq
Title	:	Crystal structure of antimicrobial peptide Oncocin d15-19 bound to the Thermus thermophilus 70S ribosome
Authors	:	Gagnon, M.G.; Roy, R.N.; Lomakin, I.B.; Florin, T.; Mankin, A.S.; Steitz, T.A.
Deposited on	:	2016-01-04
Resolution	:	2.80 Å(reported)

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

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

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

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

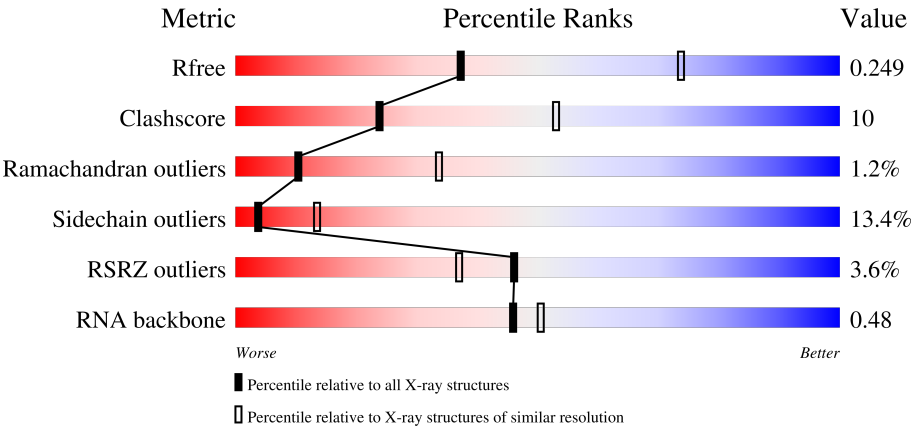
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)
RNA backbone	3983	1114 (3.00-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	64% 25% 5% 6%
1	2A	2915	54% 35% 7% .
2	1B	121	66% 31% ..
2	2B	121	3% 32% 49% 18% .

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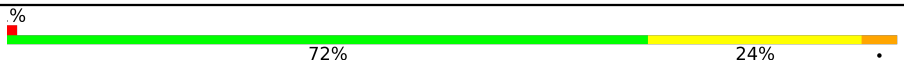
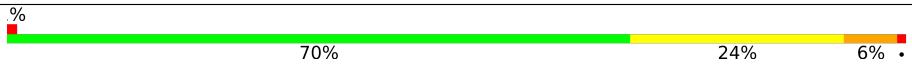
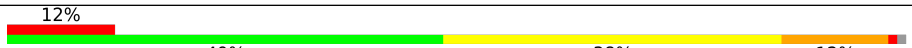
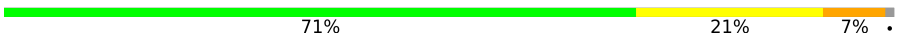
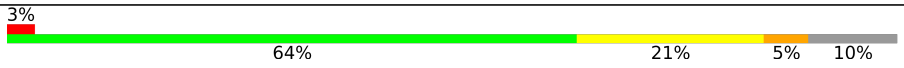
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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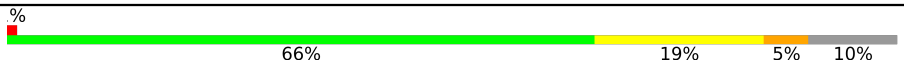
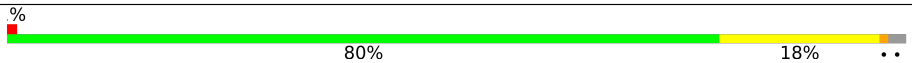
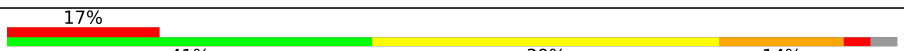
Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	
27	25	60	

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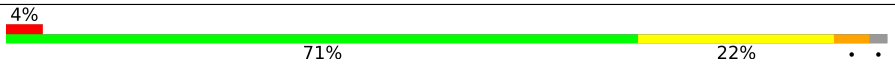
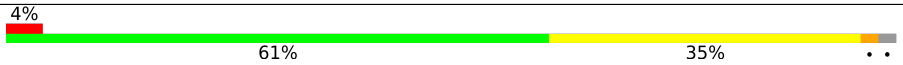
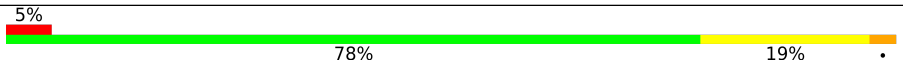
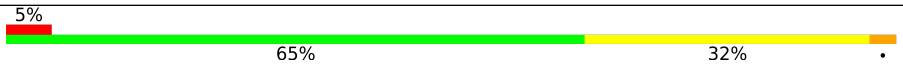
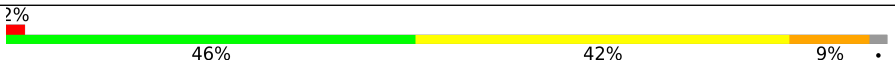
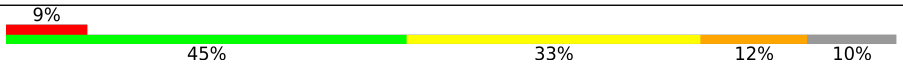
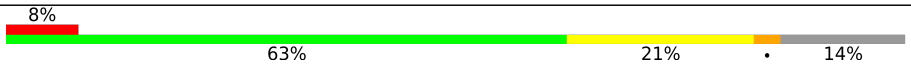
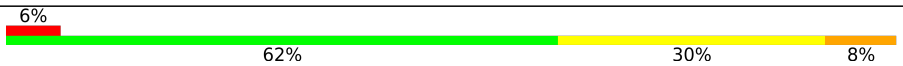
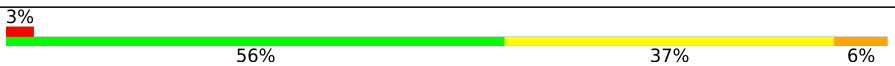
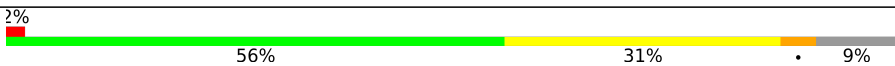
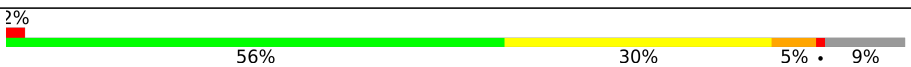
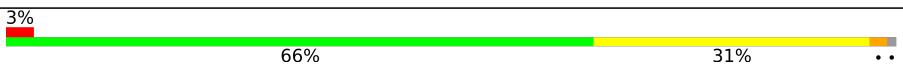
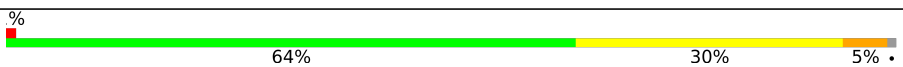
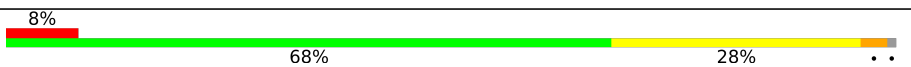
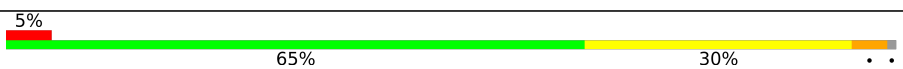
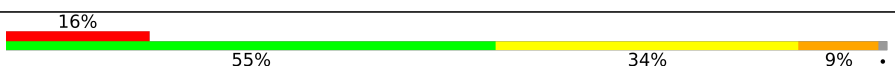
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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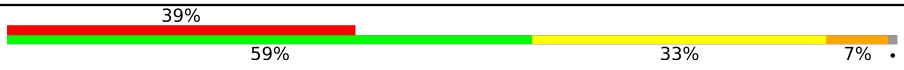
Mol	Chain	Length	Quality of chain
40	2i	128	
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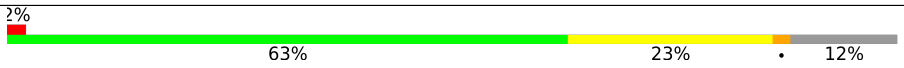
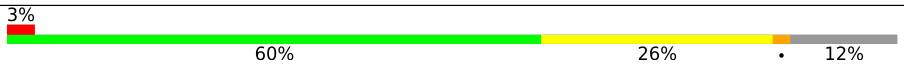
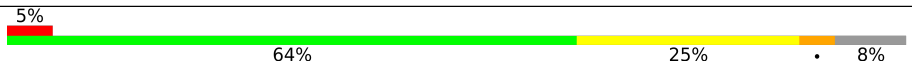
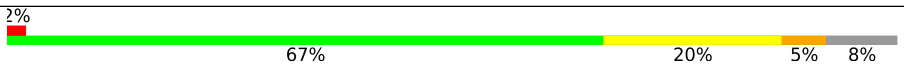
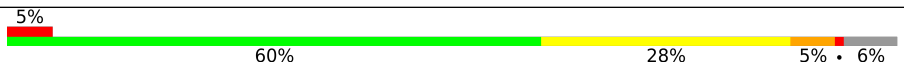
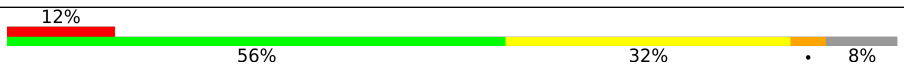
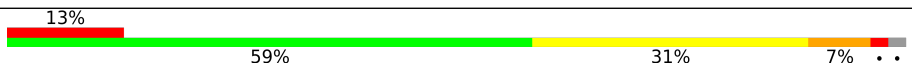
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
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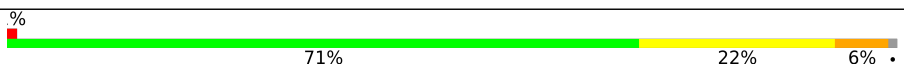
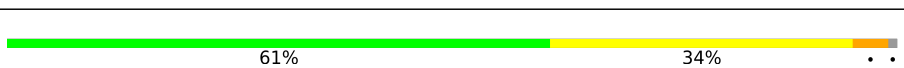
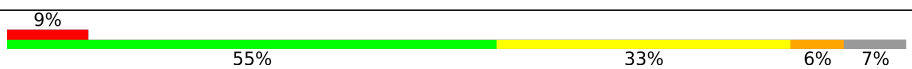
46	1o	89	
46	2o	89	
47	1p	88	
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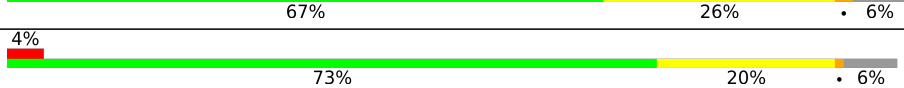
48	1q	105	
48	2q	105	
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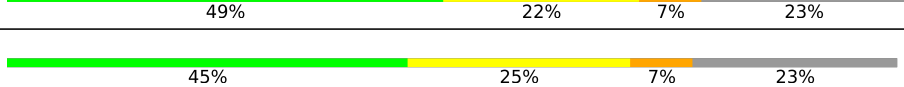
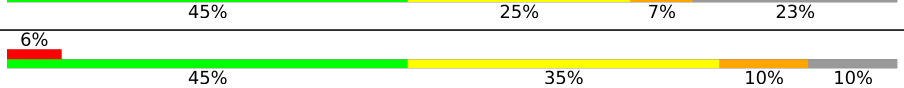
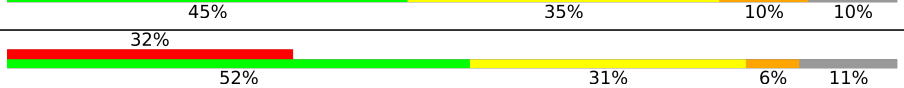
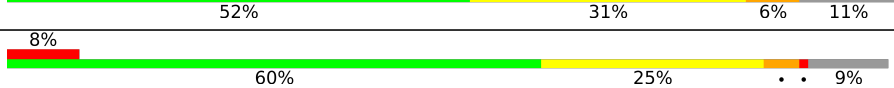
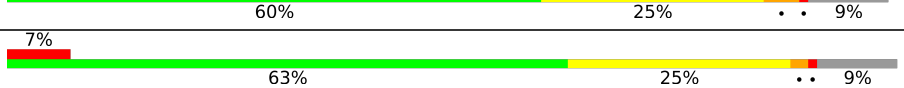
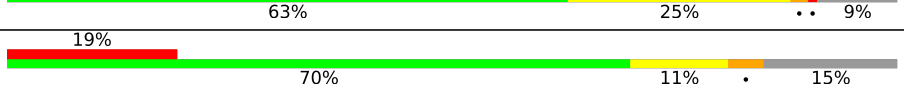
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	
52	1u	27	
52	2u	27	

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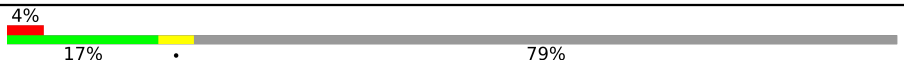
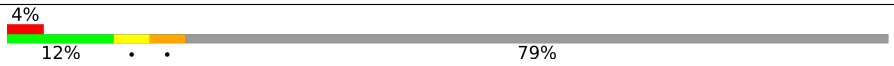
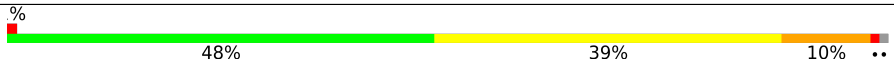
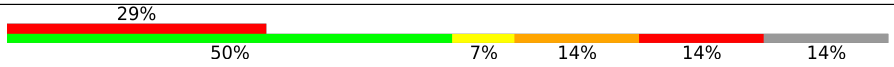
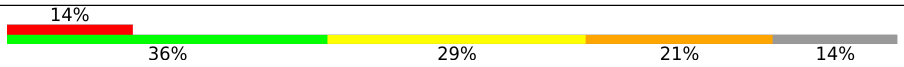
Mol	Chain	Length	Quality of chain
53	1v	24	
53	2v	24	
54	1x	77	
54	2x	77	
55	1z	14	
55	2z	14	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1a	1667	-	-	-	X
56	MG	2a	3034	-	-	-	X
56	MG	2a	3056	-	-	-	X
56	MG	2a	3220	-	-	-	X

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 288518 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	2746	Total	C	N	O	P	0	0	0
			59154	26327	11077	19005	2745			
1	2A	2790	Total	C	N	O	P	0	0	0
			60091	26746	11243	19313	2789			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1146	476	831	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2142	1352	426	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	C	N	O	S	0	0	0
			933	588	171	170	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total	C	N	O	S	0	0	0
			1139	709	231	196	3			
11	2P	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			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
			750	488	135	126	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	186	Total	C	N	O	S	0	0	0
			1470	937	262	269	2			
21	2Z	186	Total	C	N	O	S	0	0	0
			1454	929	256	267	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			
22	20	75	Total	C	N	O	S	0	0	0
			598	370	127	100	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
			558	352	102	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			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
			517	331	102	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1477	Total	C	N	O	P	0	0	0
			31750	14131	5883	10259	1477			
32	2a	1483	Total	C	N	O	P	0	0	0
			31877	14188	5905	10301	1483			

- 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
			1786	1136	321	325	4			
33	2b	231	Total	C	N	O	S	0	0	0
			1697	1079	292	321	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
			1480	932	281	266	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1412	883	269	259	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
			1618	1013	312	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1630	1022	321	280	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
			1095	695	203	193	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			817	516	146	152	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
			1183	732	232	213	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1167	728	220	213	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
			1074	681	202	189	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
			976	620	189	167			
40	2i	127	Total	C	N	O	0	0	0
			932	589	177	166			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			682	424	130	128			
41	2j	96	Total	C	N	O	0	0	0
			678	424	126	128			

- 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
			826	513	156	154	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			829	516	155	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
			920	579	181	159	1			
43	2l	122	Total	C	N	O	S	0	0	0
			918	576	182	159	1			

- 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	116	Total	C	N	O	S	0	0	0
			903	555	187	159	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
			482	306	100	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			459	291	93	71	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
			715	447	140	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
			671	424	133	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
			811	519	148	142	2			
48	2q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	1r	68	Total	C	N	O	0	0	0
			555	355	108	92			
49	2r	68	Total	C	N	O	0	0	0
			555	355	108	92			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	84	Total	C	N	O	S	0	0	0
			642	409	119	112	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
			712	435	152	123	2			
51	2t	96	Total	C	N	O	S	0	0	0
			731	449	156	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
			187	116	42	29			
52	2u	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			
53	2v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

- Molecule 54 is a RNA chain called P-site tRNA.

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

- Molecule 55 is a protein called Oncocin d15-19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	1z	12	Total	C	N	O	0	0	0
			101	67	19	15			
55	2z	12	Total	C	N	O	0	0	0
			101	67	19	15			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	1051	Total	Mg	0	0
			1051	1051		
56	1B	26	Total	Mg	0	0
			26	26		
56	1D	17	Total	Mg	0	0
			17	17		
56	1E	10	Total	Mg	0	0
			10	10		
56	1F	7	Total	Mg	0	0
			7	7		
56	1G	3	Total	Mg	0	0
			3	3		
56	1H	4	Total	Mg	0	0
			4	4		
56	1N	8	Total	Mg	0	0
			8	8		
56	1O	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1P	5	Total Mg 5 5	0	0
56	1Q	6	Total Mg 6 6	0	0
56	1R	6	Total Mg 6 6	0	0
56	1T	5	Total Mg 5 5	0	0
56	1U	5	Total Mg 5 5	0	0
56	1V	1	Total Mg 1 1	0	0
56	1W	6	Total Mg 6 6	0	0
56	1X	2	Total Mg 2 2	0	0
56	1Y	1	Total Mg 1 1	0	0
56	1Z	3	Total Mg 3 3	0	0
56	10	7	Total Mg 7 7	0	0
56	11	1	Total Mg 1 1	0	0
56	13	2	Total Mg 2 2	0	0
56	14	1	Total Mg 1 1	0	0
56	15	4	Total Mg 4 4	0	0
56	16	2	Total Mg 2 2	0	0
56	17	4	Total Mg 4 4	0	0
56	18	5	Total Mg 5 5	0	0
56	19	3	Total Mg 3 3	0	0
56	1a	306	Total Mg 306 306	0	0
56	1b	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1c	1	Total Mg 1 1	0	0
56	1d	2	Total Mg 2 2	0	0
56	1e	4	Total Mg 4 4	0	0
56	1f	1	Total Mg 1 1	0	0
56	1h	3	Total Mg 3 3	0	0
56	1k	1	Total Mg 1 1	0	0
56	1l	1	Total Mg 1 1	0	0
56	1n	1	Total Mg 1 1	0	0
56	1o	2	Total Mg 2 2	0	0
56	1q	4	Total Mg 4 4	0	0
56	1r	3	Total Mg 3 3	0	0
56	1t	1	Total Mg 1 1	0	0
56	1x	11	Total Mg 11 11	0	0
56	2A	583	Total Mg 583 583	0	0
56	2B	10	Total Mg 10 10	0	0
56	2D	4	Total Mg 4 4	0	0
56	2E	7	Total Mg 7 7	0	0
56	2F	2	Total Mg 2 2	0	0
56	2G	1	Total Mg 1 1	0	0
56	2N	1	Total Mg 1 1	0	0
56	2O	3	Total Mg 3 3	0	0

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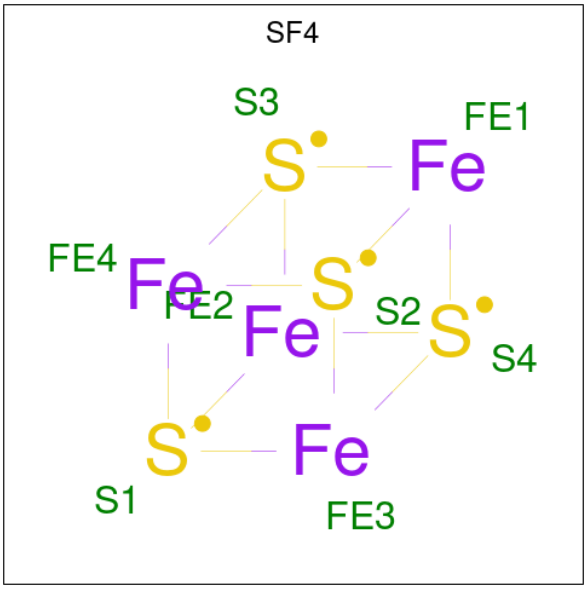
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	2P	1	Total Mg 1 1	0	0
56	2Q	5	Total Mg 5 5	0	0
56	2R	1	Total Mg 1 1	0	0
56	2U	2	Total Mg 2 2	0	0
56	2V	1	Total Mg 1 1	0	0
56	2Y	1	Total Mg 1 1	0	0
56	20	1	Total Mg 1 1	0	0
56	25	1	Total Mg 1 1	0	0
56	26	1	Total Mg 1 1	0	0
56	28	1	Total Mg 1 1	0	0
56	2a	244	Total Mg 244 244	0	0
56	2d	2	Total Mg 2 2	0	0
56	2e	1	Total Mg 1 1	0	0
56	2f	1	Total Mg 1 1	0	0
56	2k	2	Total Mg 2 2	0	0
56	2l	3	Total Mg 3 3	0	0
56	2n	2	Total Mg 2 2	0	0
56	2p	1	Total Mg 1 1	0	0
56	2q	1	Total Mg 1 1	0	0
56	2t	1	Total Mg 1 1	0	0
56	2x	6	Total Mg 6 6	0	0

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

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

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



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

- Molecule 59 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	2110	Total O 2110 2110	0	0
59	1B	42	Total O 42 42	0	0
59	1D	24	Total O 24 24	0	0
59	1E	30	Total O 30 30	0	0
59	1F	16	Total O 16 16	0	0
59	1G	6	Total O 6 6	0	0
59	1H	3	Total O 3 3	0	0
59	1I	1	Total O 1 1	0	0
59	1N	7	Total O 7 7	0	0
59	1O	4	Total O 4 4	0	0
59	1P	21	Total O 21 21	0	0
59	1Q	11	Total O 11 11	0	0
59	1R	16	Total O 16 16	0	0
59	1S	2	Total O 2 2	0	0
59	1T	7	Total O 7 7	0	0
59	1U	14	Total O 14 14	0	0
59	1V	4	Total O 4 4	0	0
59	1W	5	Total O 5 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1X	4	Total O 4 4	0	0
59	1Y	1	Total O 1 1	0	0
59	1Z	4	Total O 4 4	0	0
59	10	8	Total O 8 8	0	0
59	11	7	Total O 7 7	0	0
59	12	2	Total O 2 2	0	0
59	13	4	Total O 4 4	0	0
59	15	7	Total O 7 7	0	0
59	16	5	Total O 5 5	0	0
59	17	8	Total O 8 8	0	0
59	18	9	Total O 9 9	0	0
59	19	4	Total O 4 4	0	0
59	1a	393	Total O 393 393	0	0
59	1b	1	Total O 1 1	0	0
59	1c	1	Total O 1 1	0	0
59	1d	5	Total O 5 5	0	0
59	1e	3	Total O 3 3	0	0
59	1f	1	Total O 1 1	0	0
59	1h	3	Total O 3 3	0	0
59	1i	1	Total O 1 1	0	0
59	1j	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1k	1	Total O 1 1	0	0
59	1l	3	Total O 3 3	0	0
59	1m	1	Total O 1 1	0	0
59	1o	1	Total O 1 1	0	0
59	1p	1	Total O 1 1	0	0
59	1q	1	Total O 1 1	0	0
59	1s	1	Total O 1 1	0	0
59	1v	1	Total O 1 1	0	0
59	1x	8	Total O 8 8	0	0
59	1z	1	Total O 1 1	0	0
59	2A	813	Total O 813 813	0	0
59	2B	10	Total O 10 10	0	0
59	2D	16	Total O 16 16	0	0
59	2E	9	Total O 9 9	0	0
59	2F	5	Total O 5 5	0	0
59	2N	1	Total O 1 1	0	0
59	2O	3	Total O 3 3	0	0
59	2P	9	Total O 9 9	0	0
59	2Q	2	Total O 2 2	0	0
59	2R	3	Total O 3 3	0	0
59	2T	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	2U	3	Total O 3 3	0	0
59	2W	1	Total O 1 1	0	0
59	2X	2	Total O 2 2	0	0
59	2Y	1	Total O 1 1	0	0
59	2Z	4	Total O 4 4	0	0
59	20	3	Total O 3 3	0	0
59	21	1	Total O 1 1	0	0
59	23	2	Total O 2 2	0	0
59	26	1	Total O 1 1	0	0
59	27	2	Total O 2 2	0	0
59	28	2	Total O 2 2	0	0
59	2a	321	Total O 321 321	0	0
59	2d	1	Total O 1 1	0	0
59	2e	1	Total O 1 1	0	0
59	2i	2	Total O 2 2	0	0
59	2j	1	Total O 1 1	0	0
59	2l	1	Total O 1 1	0	0
59	2m	3	Total O 3 3	0	0
59	2p	1	Total O 1 1	0	0
59	2q	1	Total O 1 1	0	0
59	2t	4	Total O 4 4	0	0

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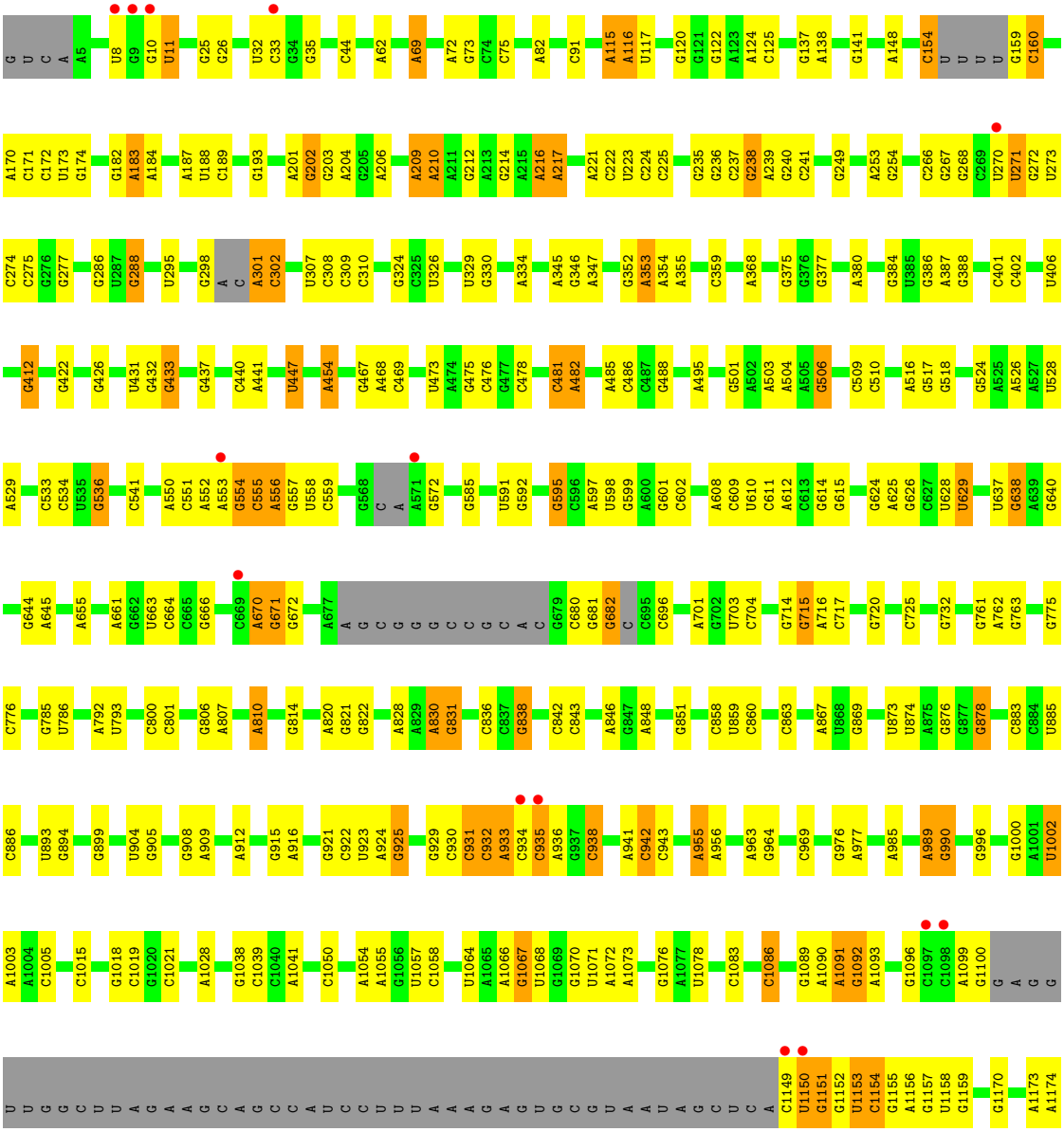
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	2x	7	Total O 7 7	0	0
59	2z	1	Total O 1 1	0	0

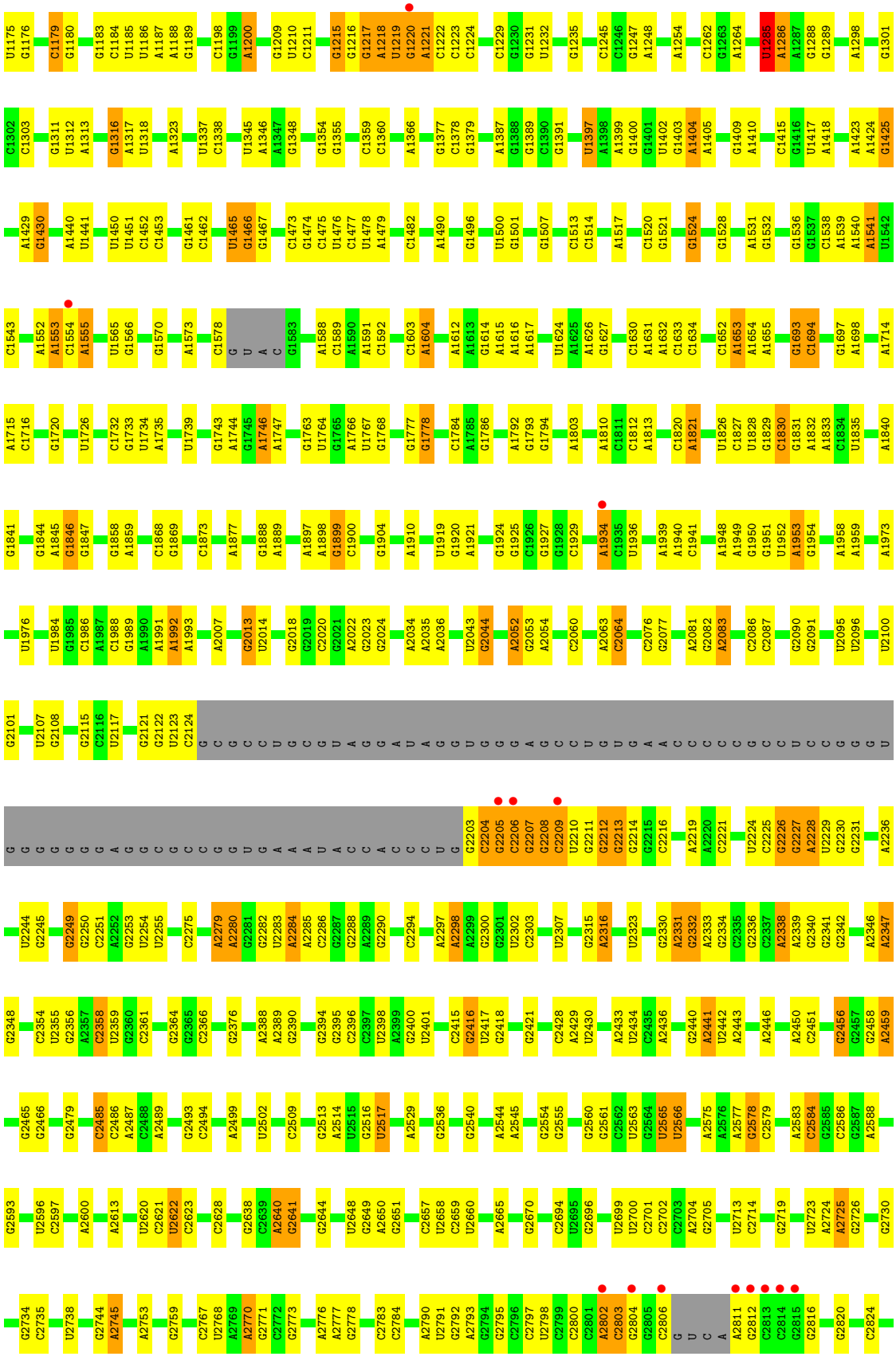
3 Residue-property plots (i)

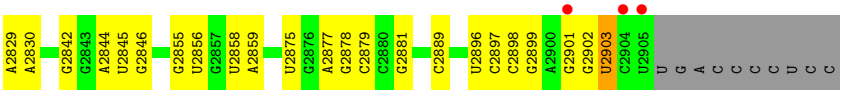
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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:

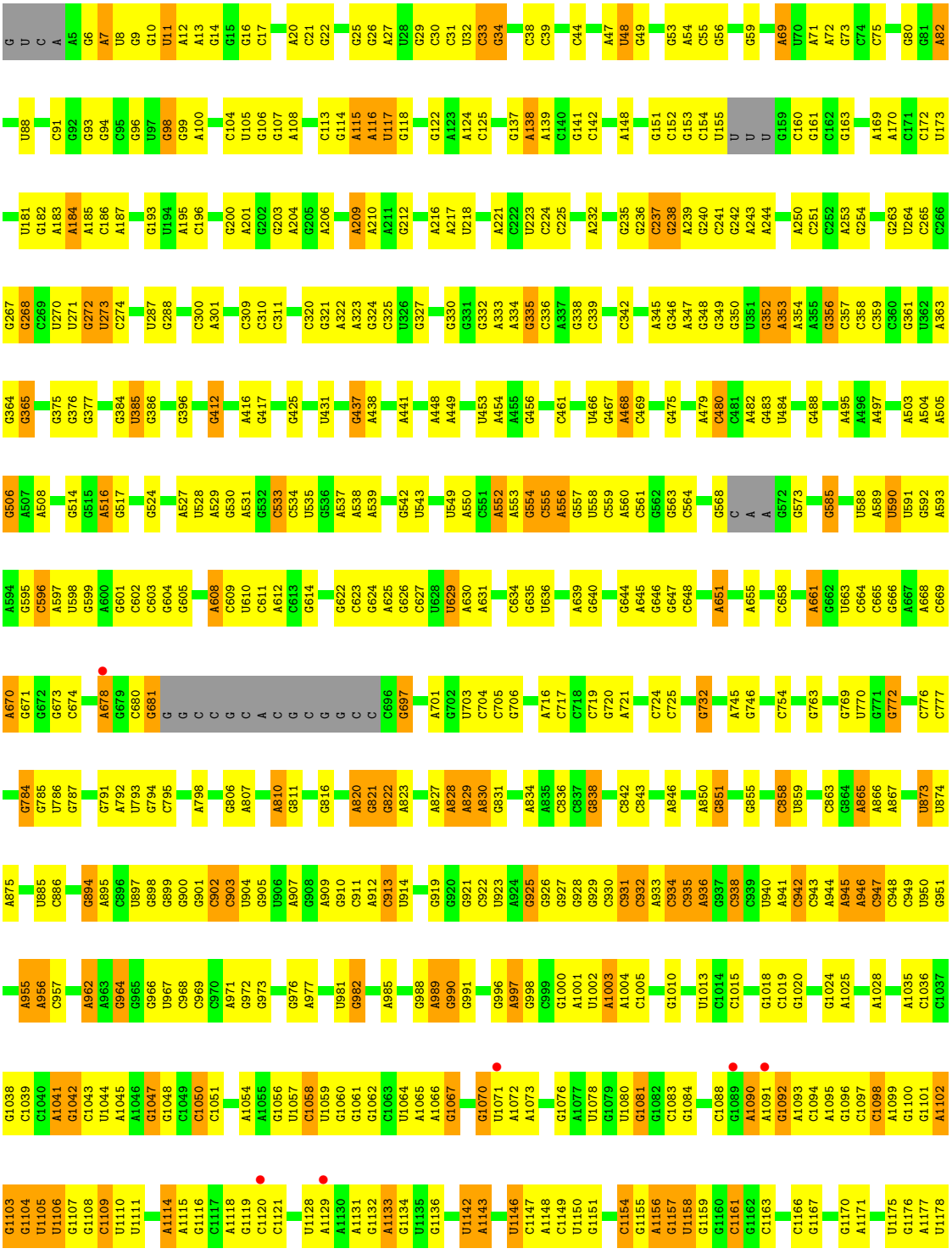


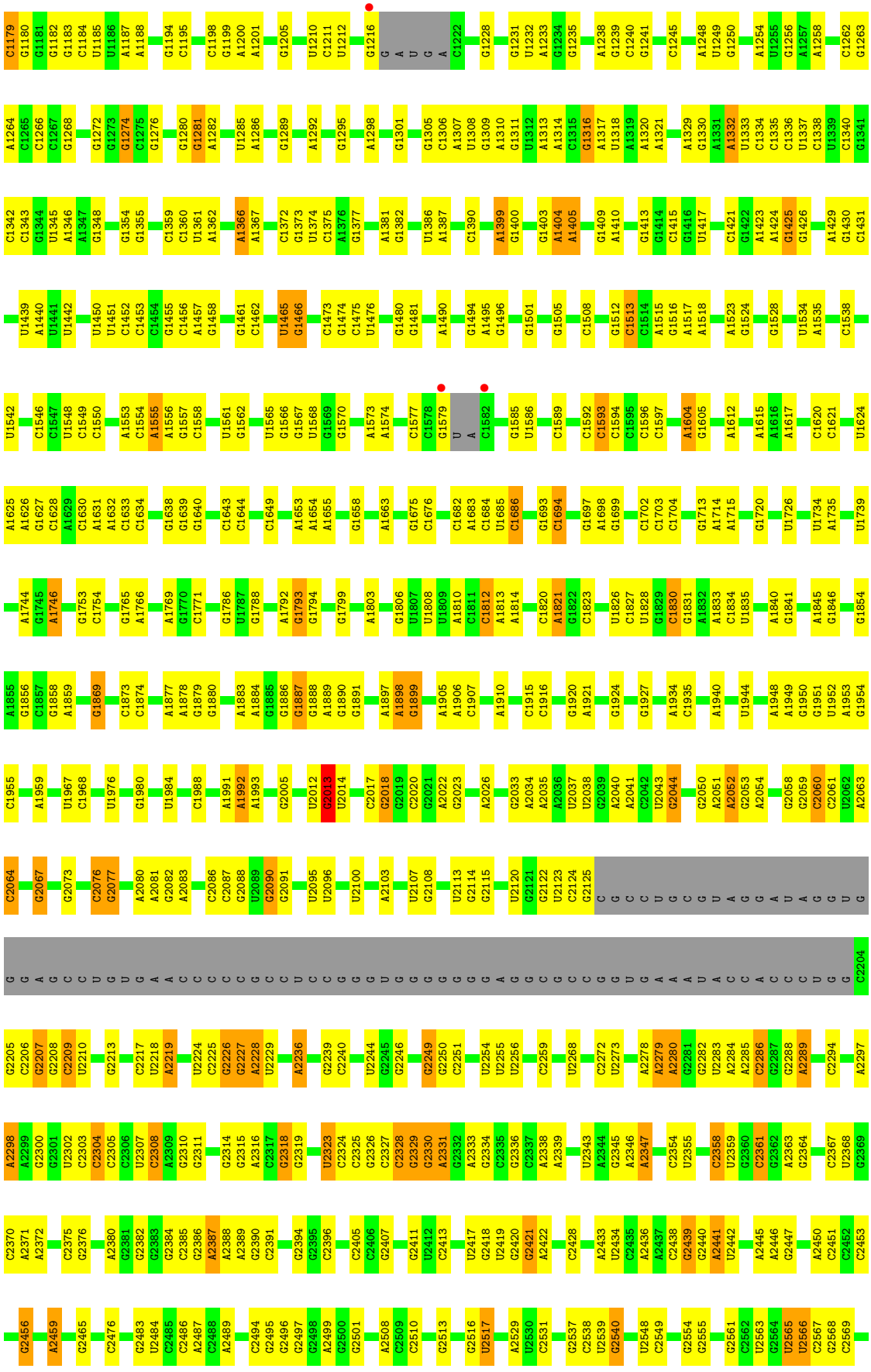


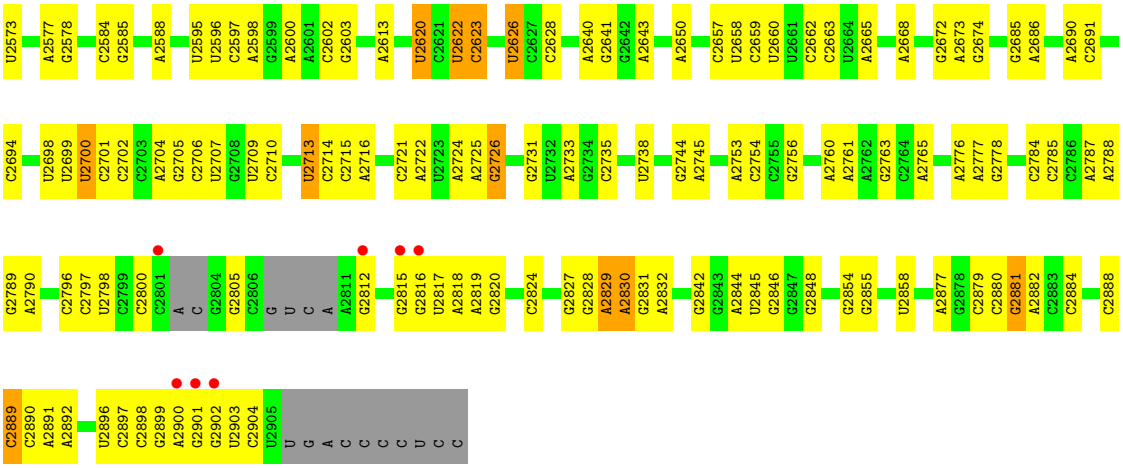


• Molecule 1: 23S Ribosomal RNA

Chain 2A:

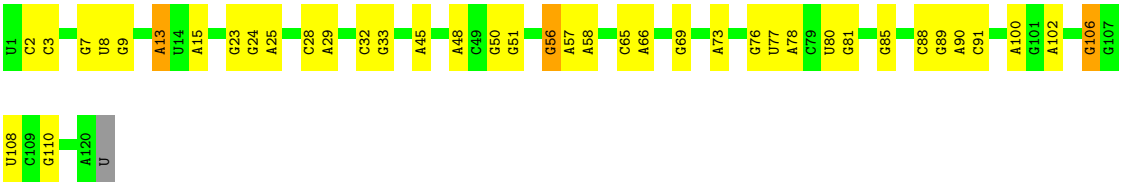






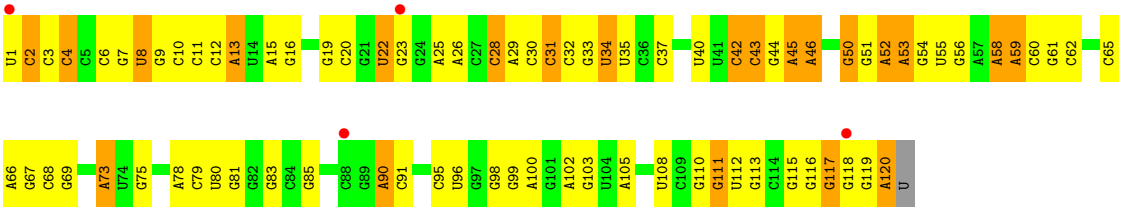
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



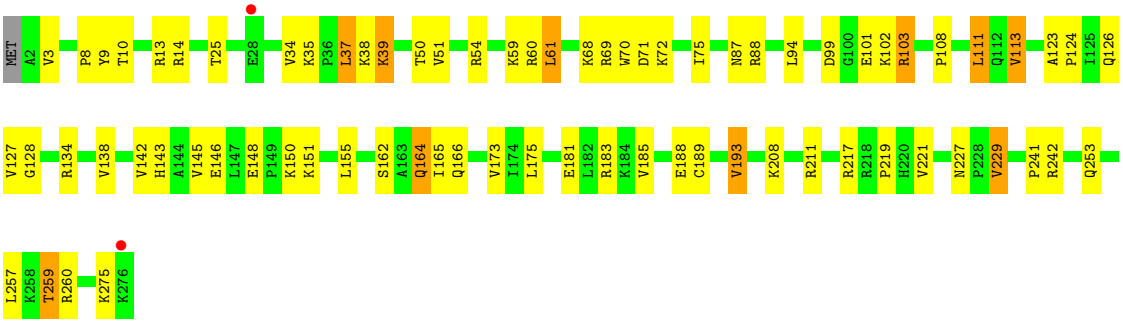
• Molecule 2: 5S Ribosomal RNA

Chain 2B:



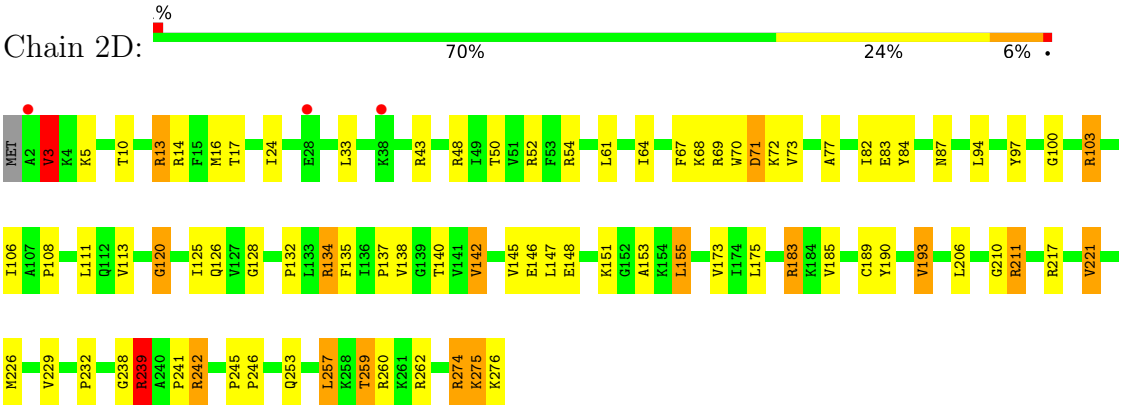
• Molecule 3: 50S ribosomal protein L2

Chain 1D:



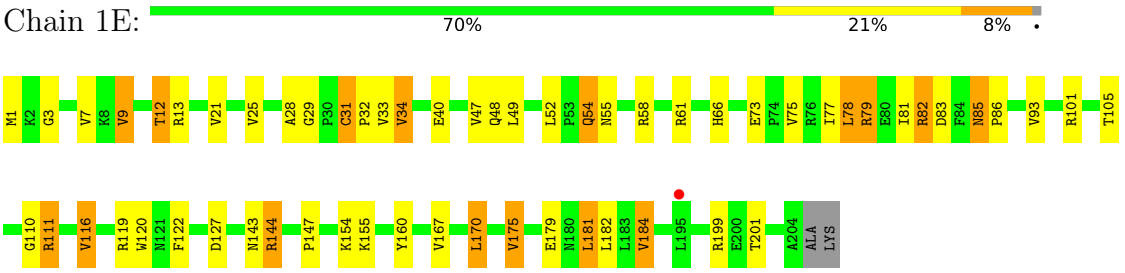
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



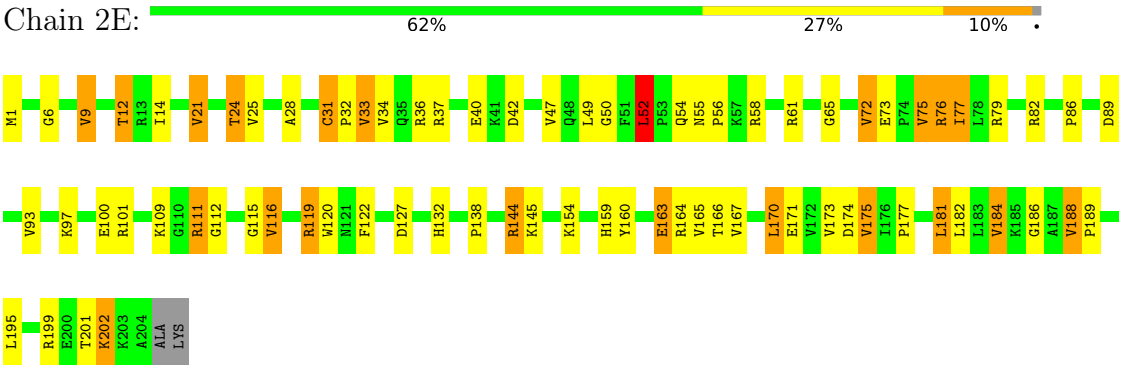
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



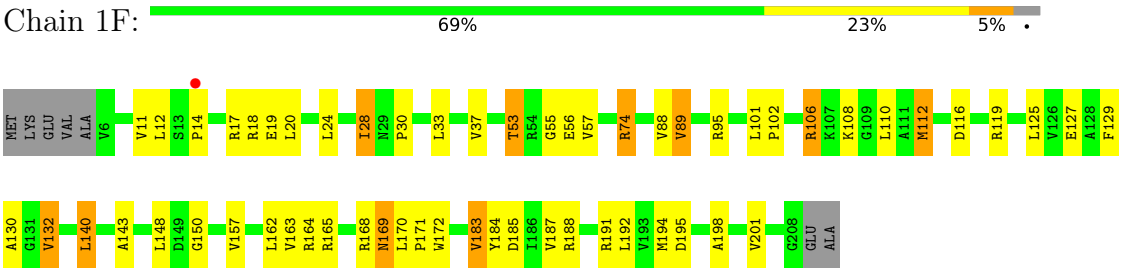
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



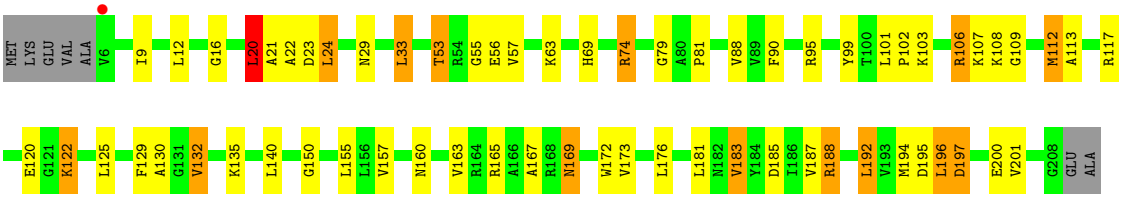
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



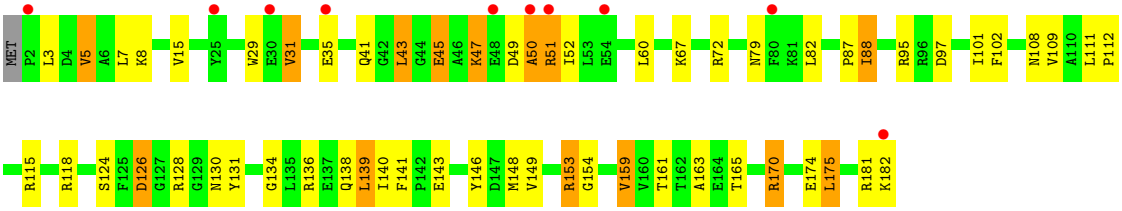
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



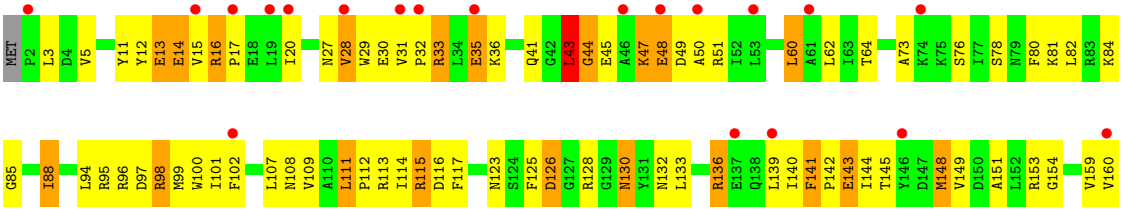
• Molecule 6: 50S ribosomal protein L5

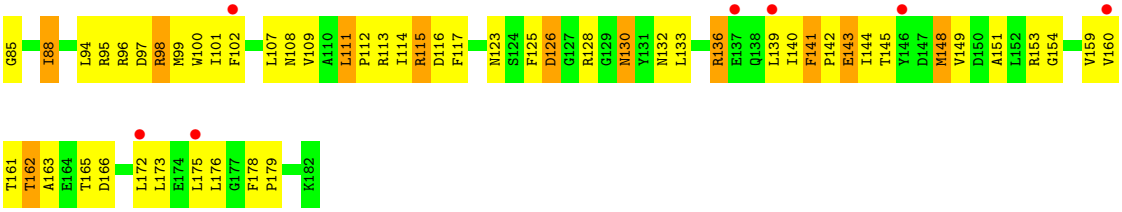
Chain 1G:



• Molecule 6: 50S ribosomal protein L5

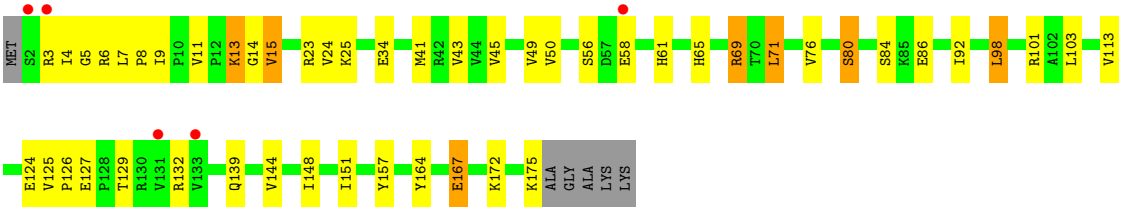
Chain 2G:





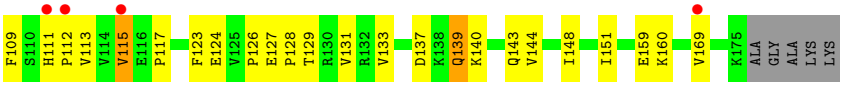
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



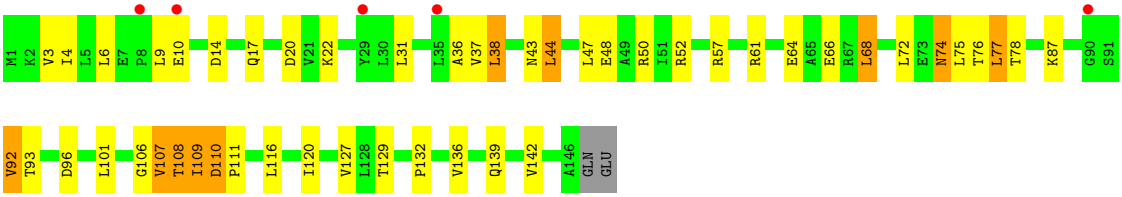
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



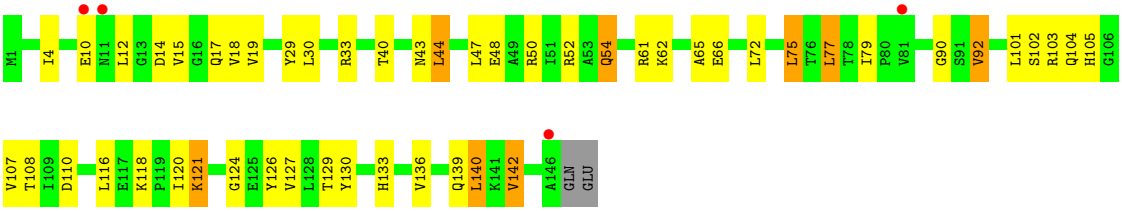
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



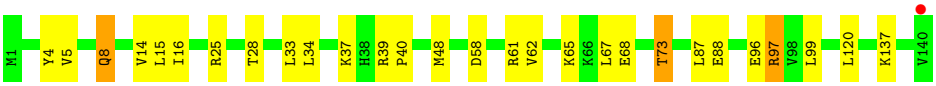
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



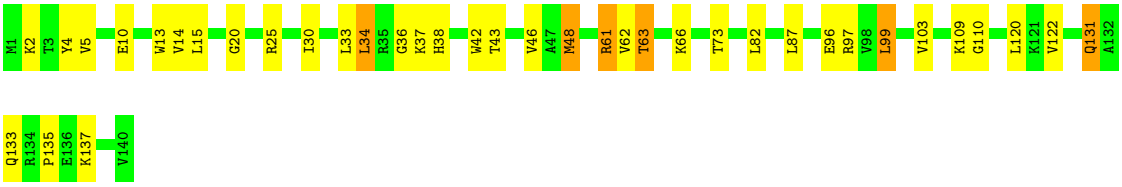
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



• Molecule 9: 50S ribosomal protein L13

Chain 2N:

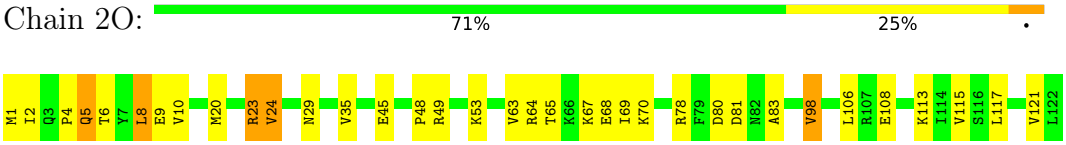


• Molecule 10: 50S ribosomal protein L14

Chain 1O:

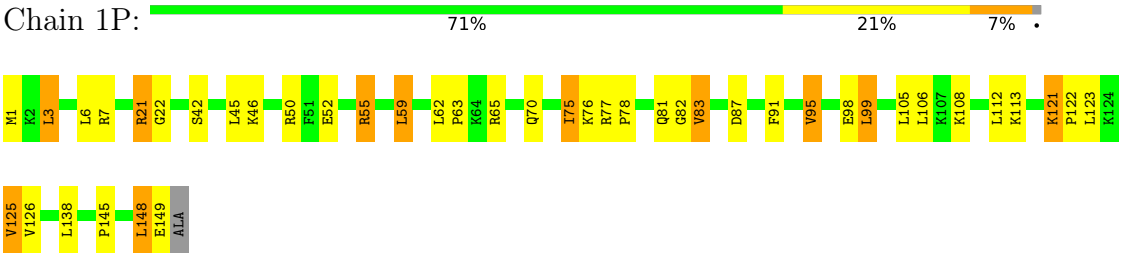
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



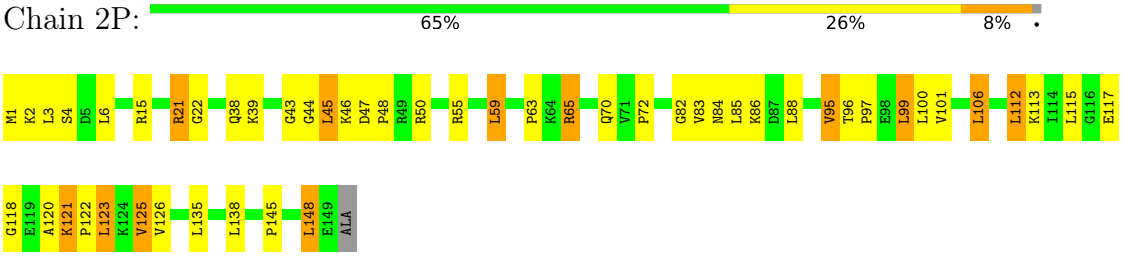
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



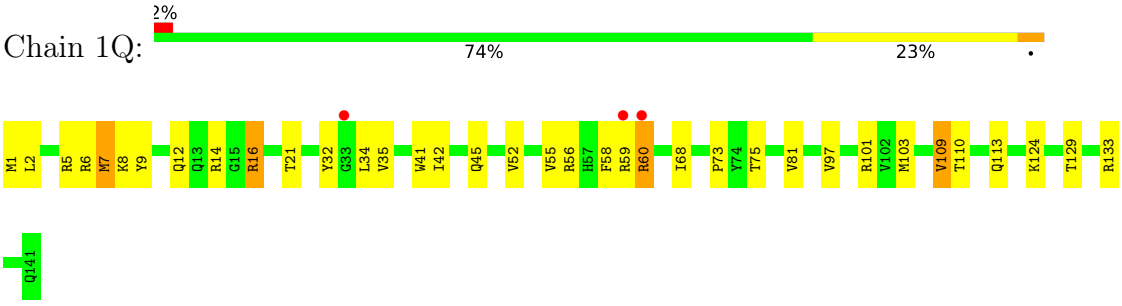
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



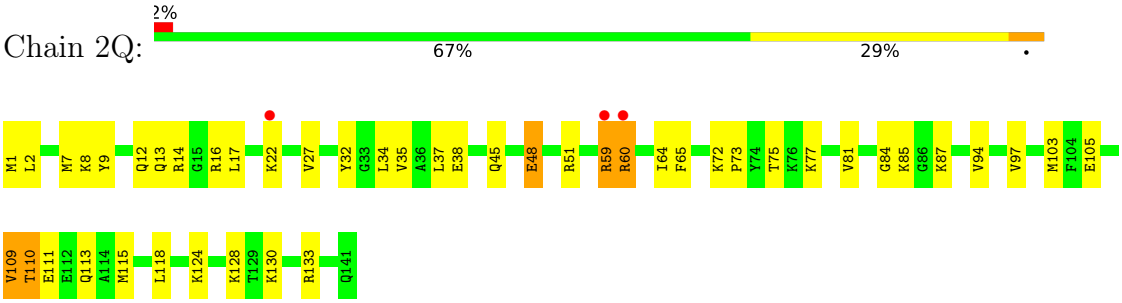
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



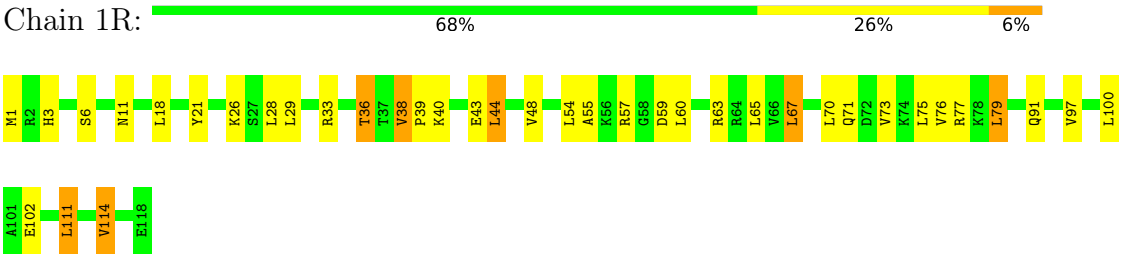
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



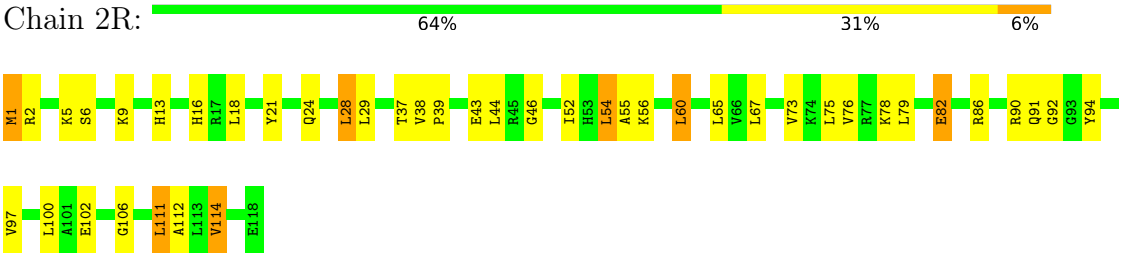
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



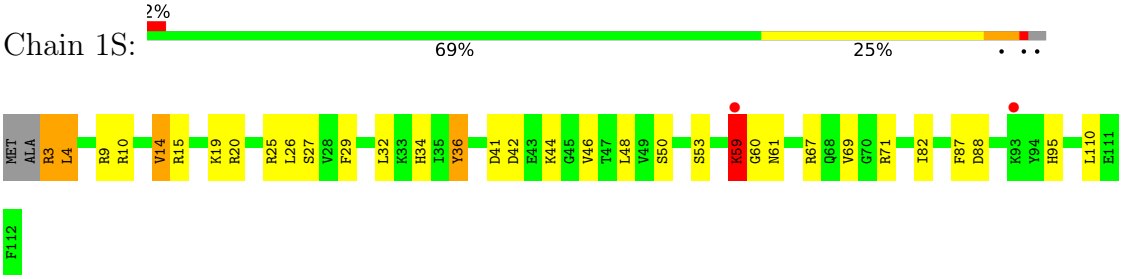
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



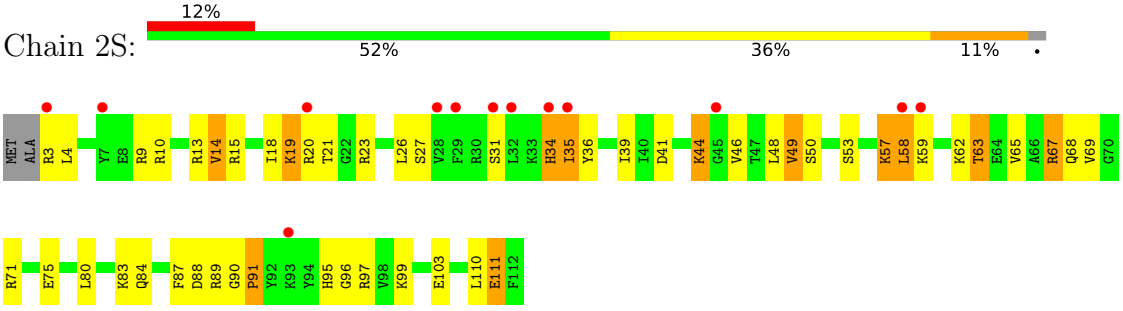
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



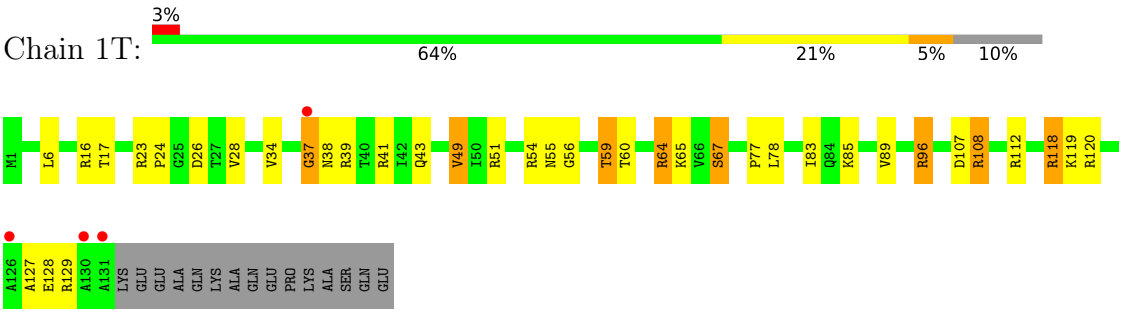
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



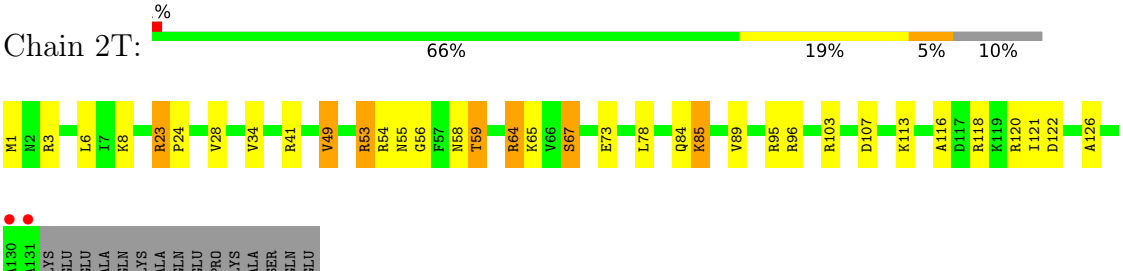
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



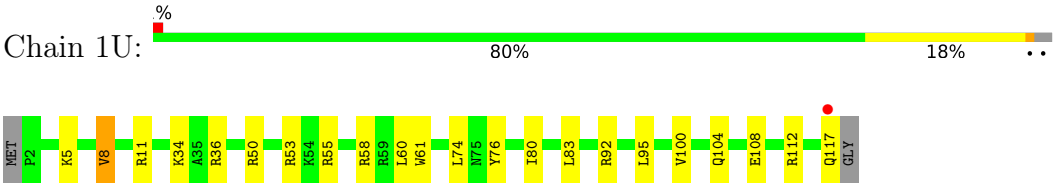
• Molecule 15: 50S ribosomal protein L19

Chain 2T:



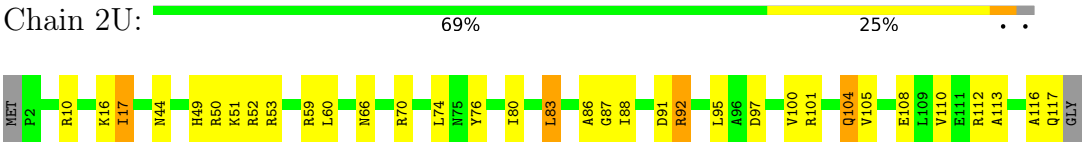
• Molecule 16: 50S ribosomal protein L20

Chain 1U:



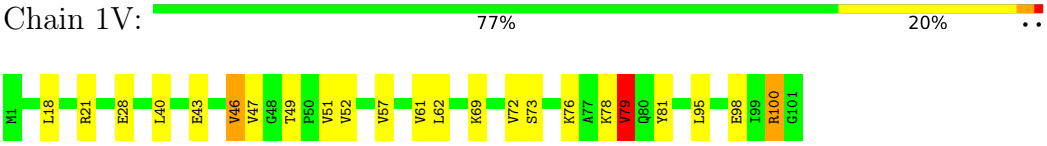
• Molecule 16: 50S ribosomal protein L20

Chain 2U:



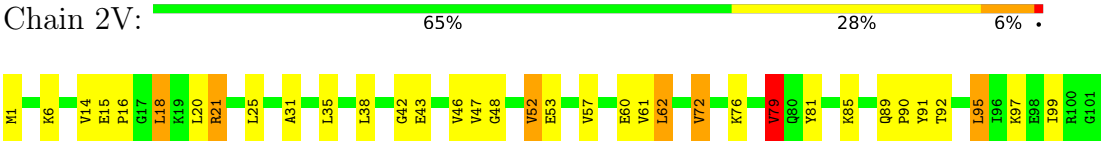
• Molecule 17: 50S ribosomal protein L21

Chain 1V:



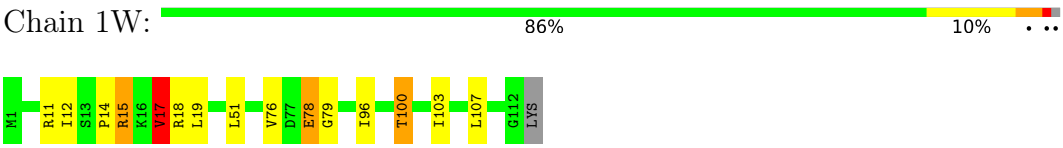
• Molecule 17: 50S ribosomal protein L21

Chain 2V:



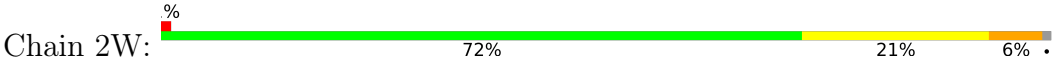
• Molecule 18: 50S ribosomal protein L22

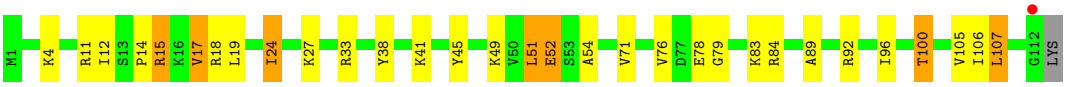
Chain 1W:



• Molecule 18: 50S ribosomal protein L22

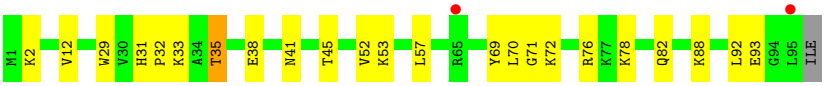
Chain 2W:





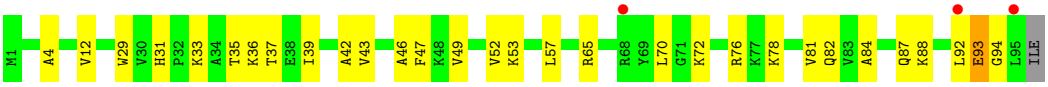
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



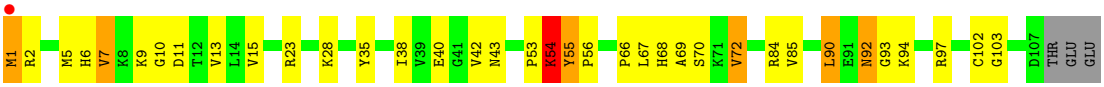
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



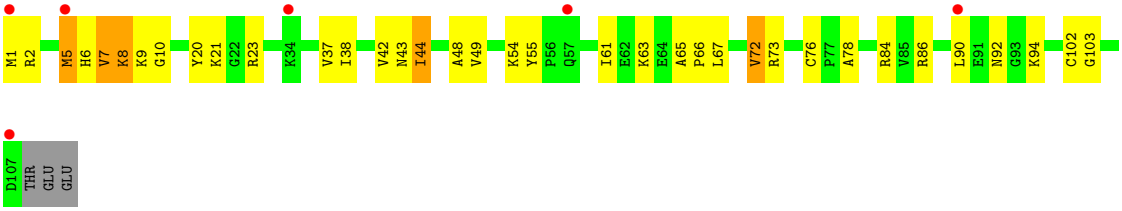
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



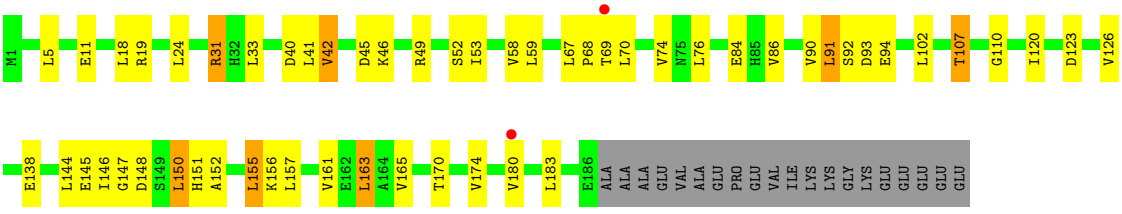
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



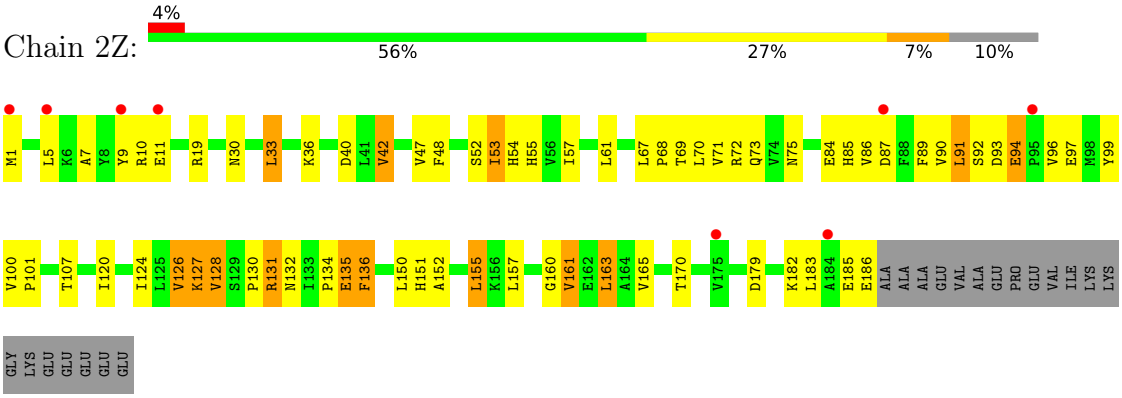
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



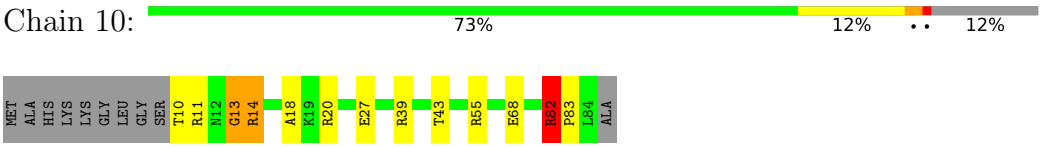
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



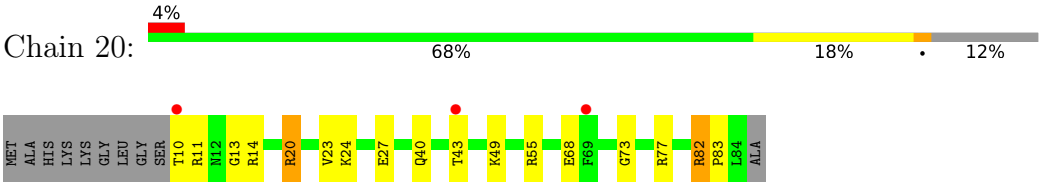
• Molecule 22: 50S ribosomal protein L27

Chain 10:



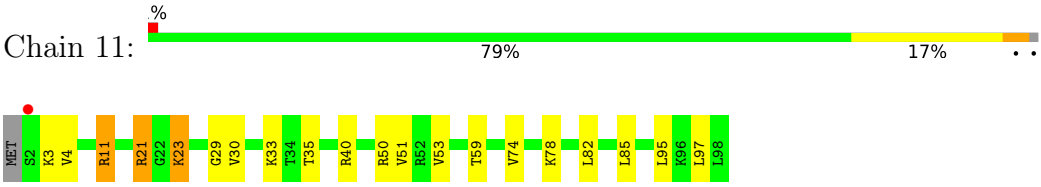
• Molecule 22: 50S ribosomal protein L27

Chain 20:



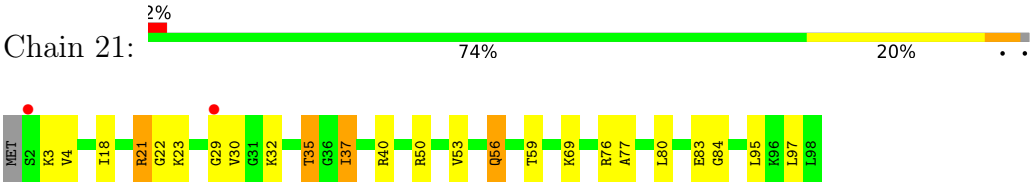
• Molecule 23: 50S ribosomal protein L28

Chain 11:



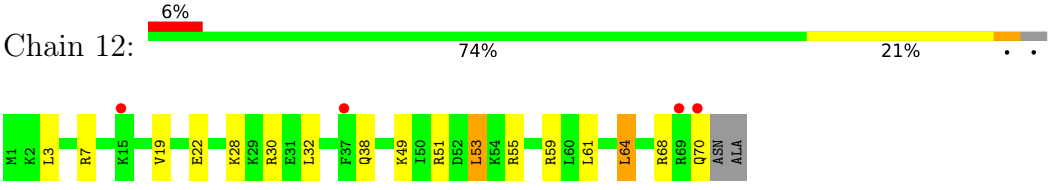
• Molecule 23: 50S ribosomal protein L28

Chain 21:



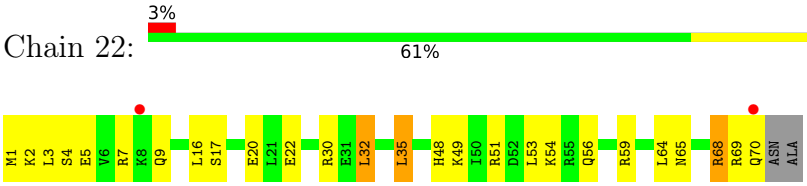
• Molecule 24: 50S ribosomal protein L29

Chain 12:



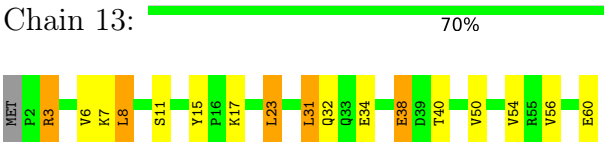
• Molecule 24: 50S ribosomal protein L29

Chain 22:



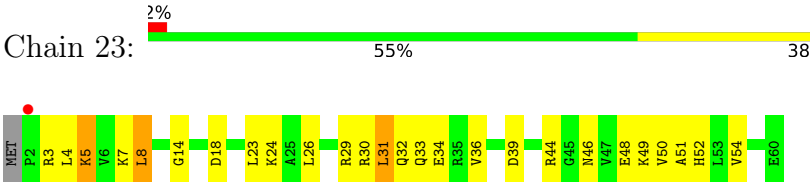
• Molecule 25: 50S ribosomal protein L30

Chain 13:



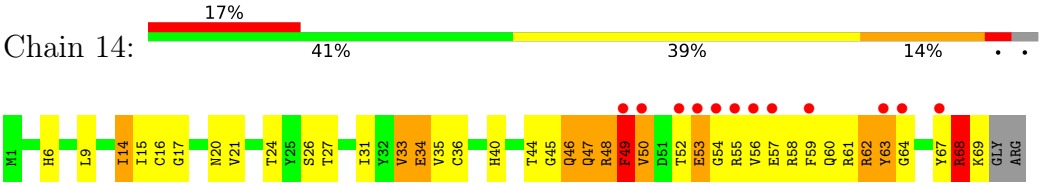
• Molecule 25: 50S ribosomal protein L30

Chain 23:



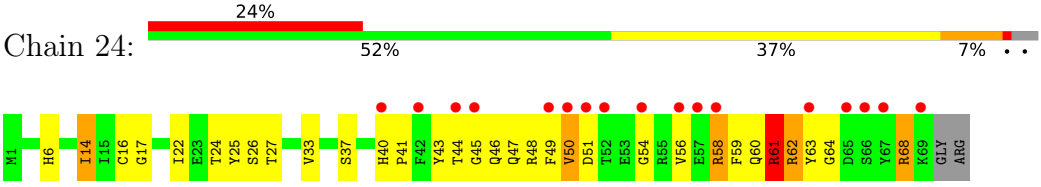
• Molecule 26: 50S ribosomal protein L31

Chain 14:



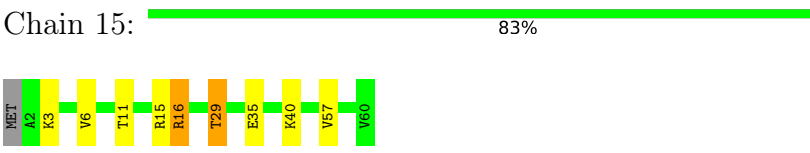
• Molecule 26: 50S ribosomal protein L31

Chain 24:



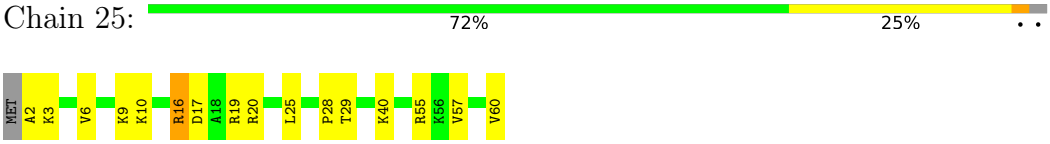
• Molecule 27: 50S ribosomal protein L32

Chain 15:



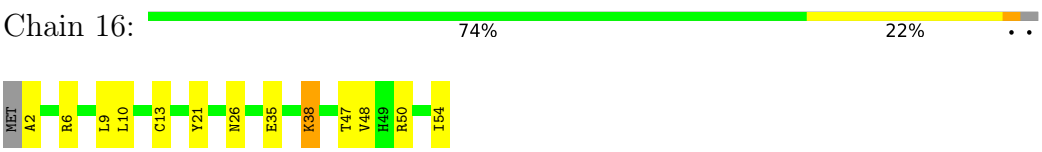
• Molecule 27: 50S ribosomal protein L32

Chain 25:



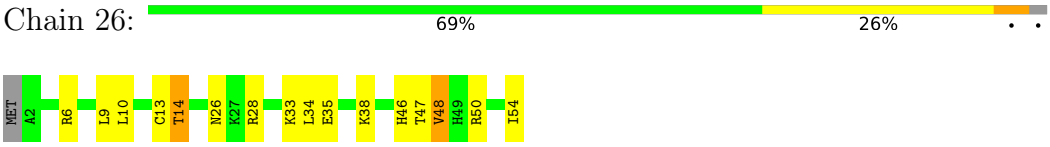
• Molecule 28: 50S ribosomal protein L33

Chain 16:



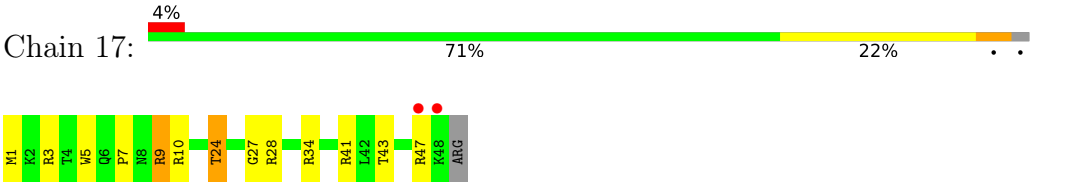
• Molecule 28: 50S ribosomal protein L33

Chain 26:



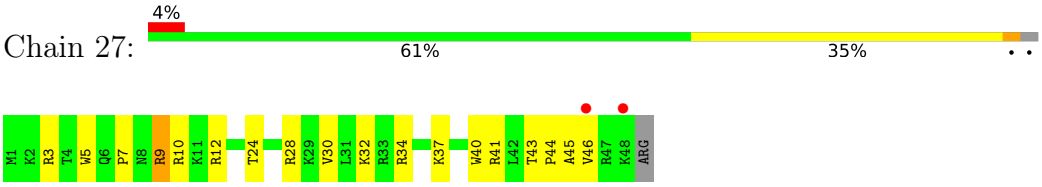
• Molecule 29: 50S ribosomal protein L34

Chain 17:



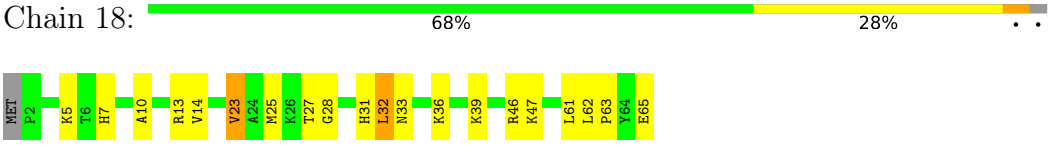
• Molecule 29: 50S ribosomal protein L34

Chain 27:



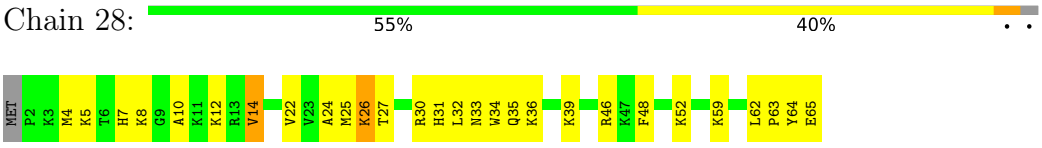
• Molecule 30: 50S ribosomal protein L35

Chain 18:



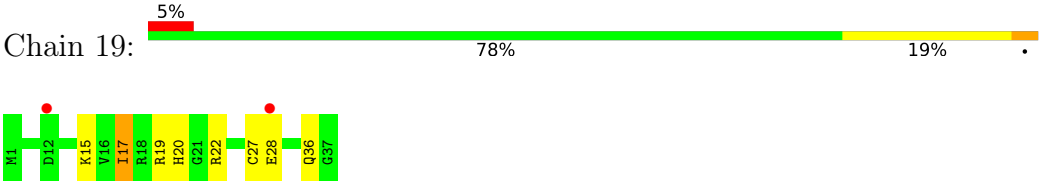
• Molecule 30: 50S ribosomal protein L35

Chain 28:



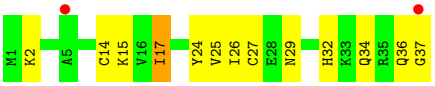
• Molecule 31: 50S ribosomal protein L36

Chain 19:



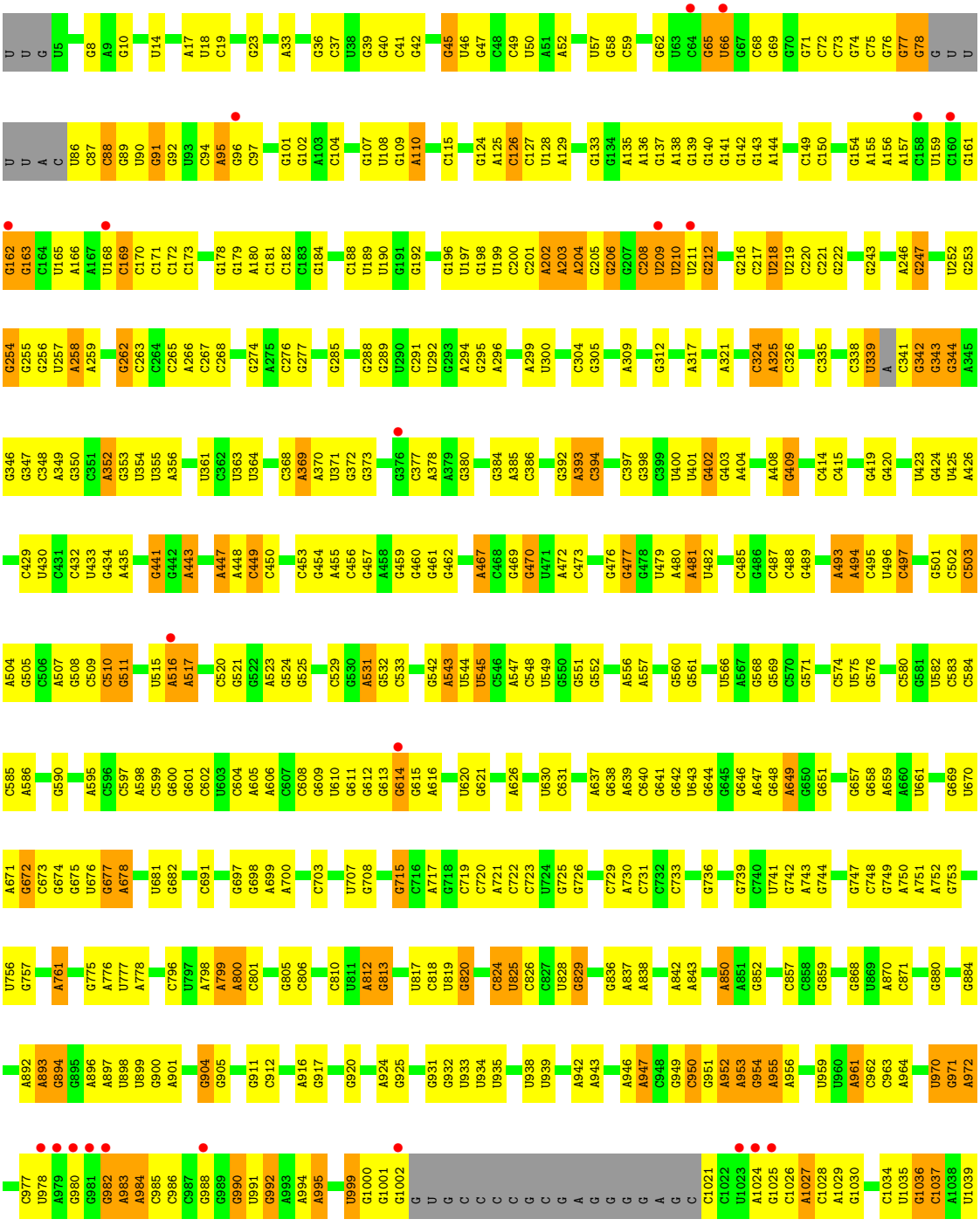
• Molecule 31: 50S ribosomal protein L36

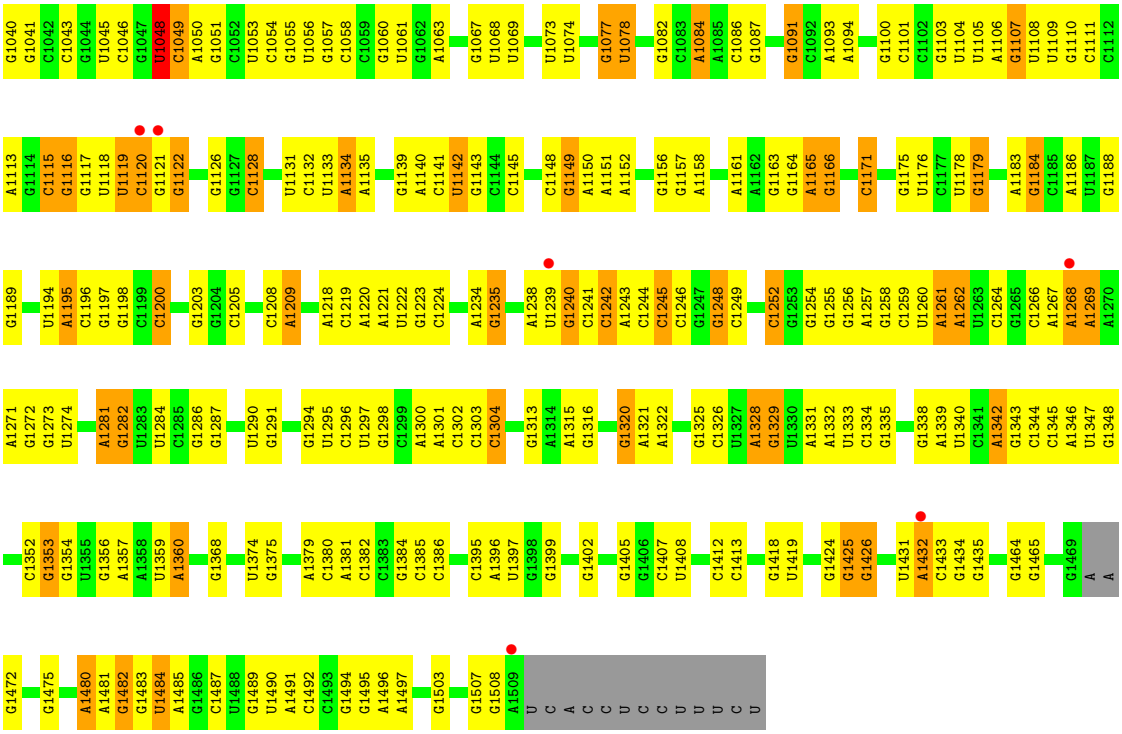
Chain 29:



• Molecule 32: 16S Ribosomal RNA

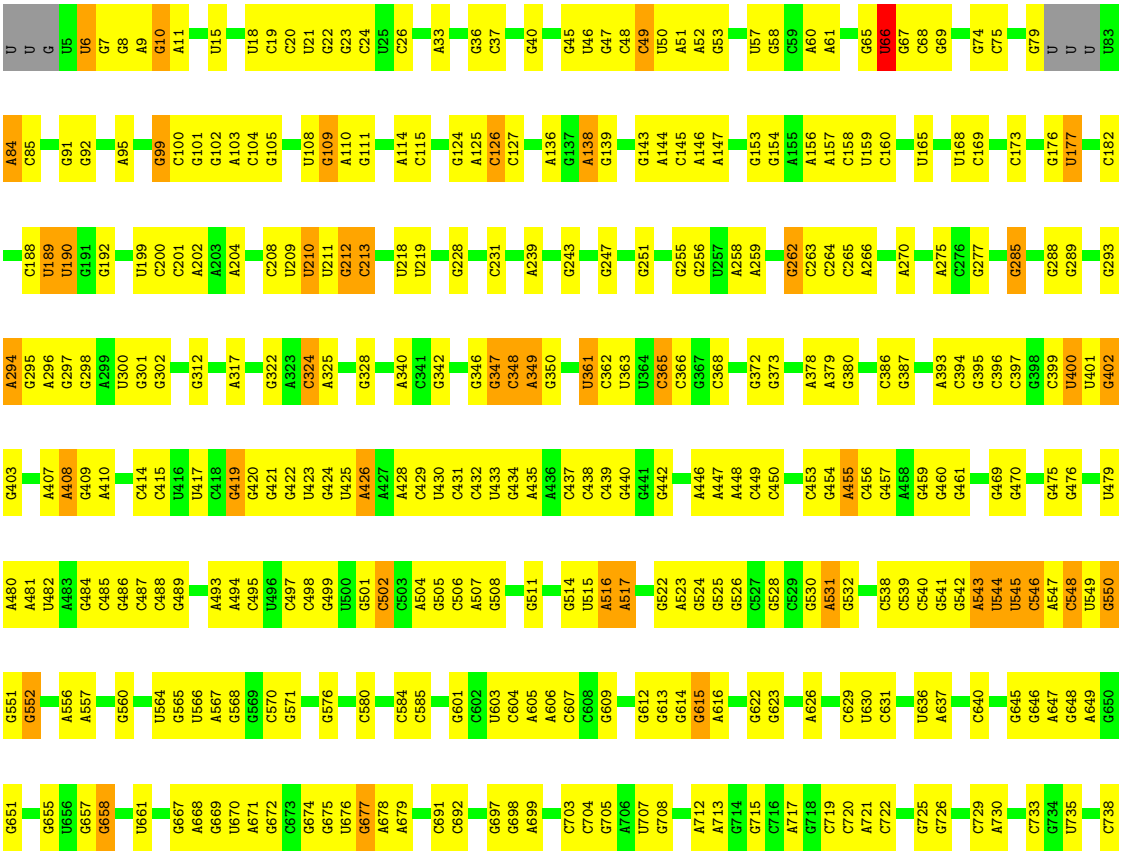
Chain 1a:

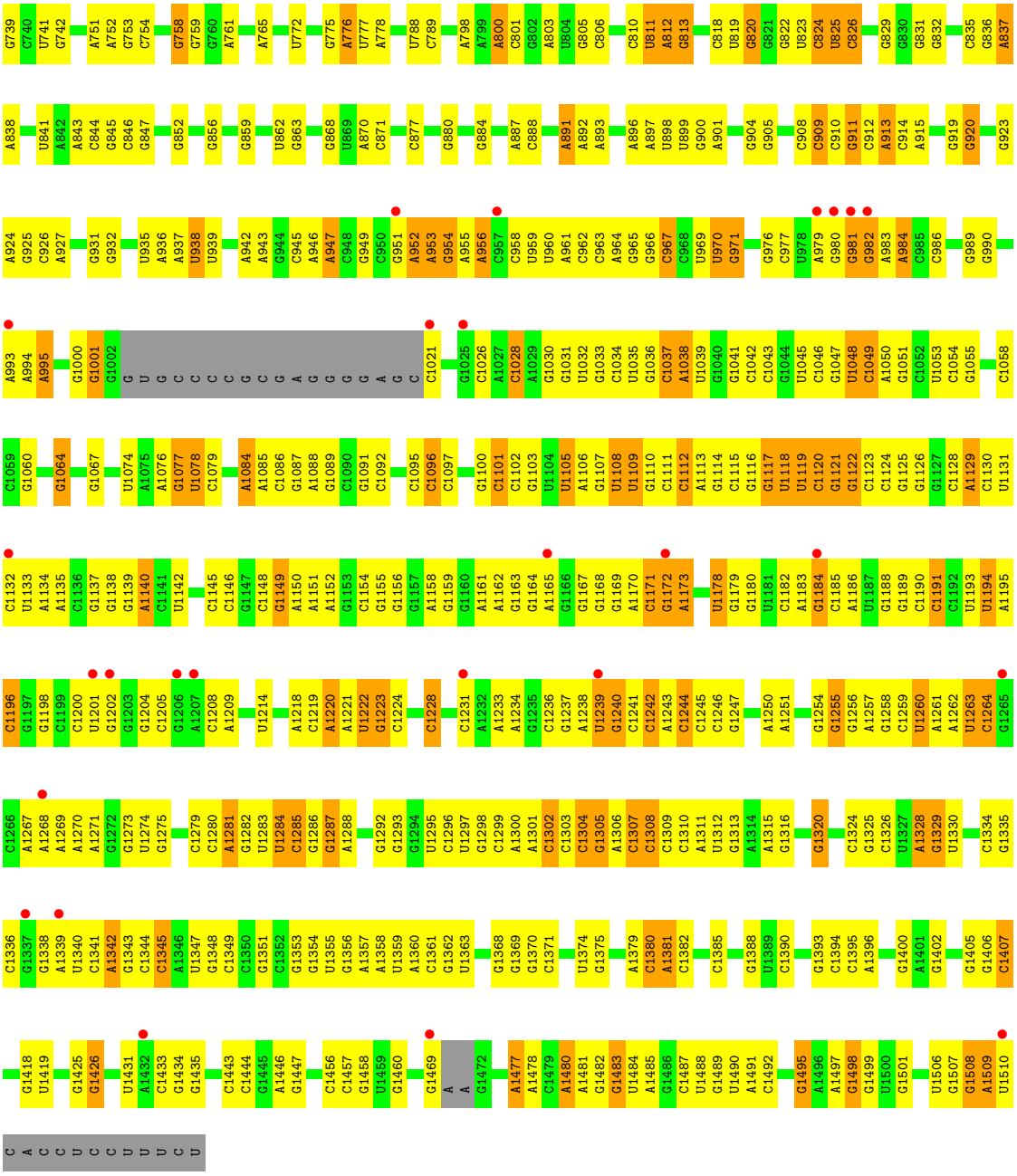




• Molecule 32: 16S Ribosomal RNA

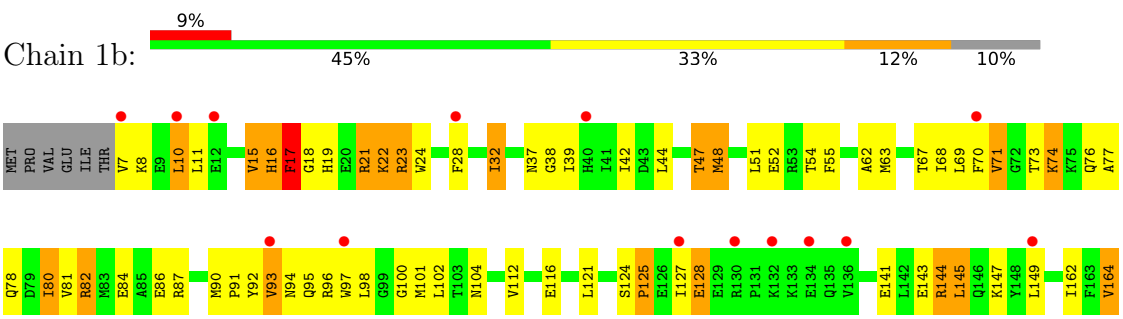
Chain 2a:

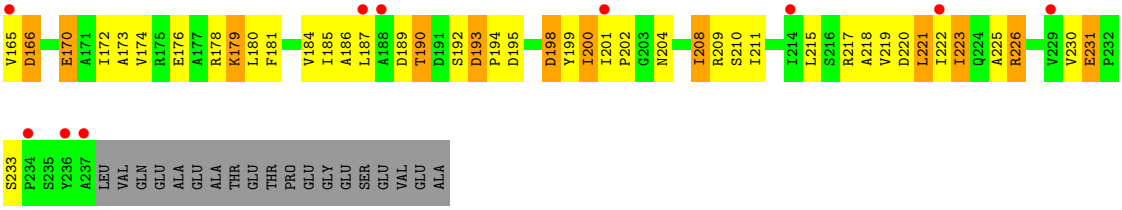




• Molecule 33: 30S ribosomal protein S2

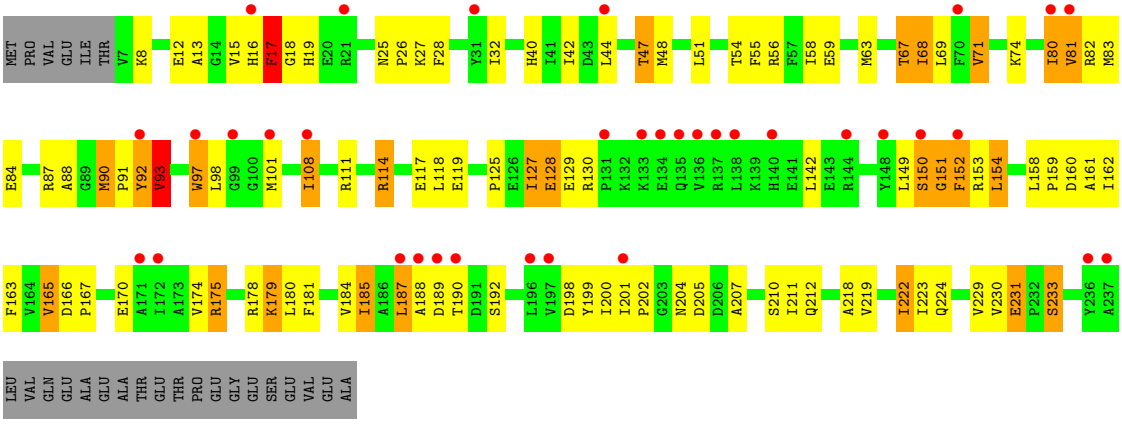
Chain 1b:





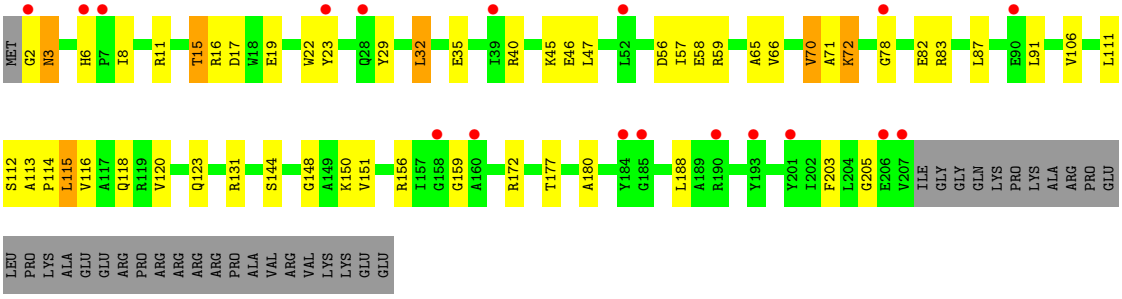
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



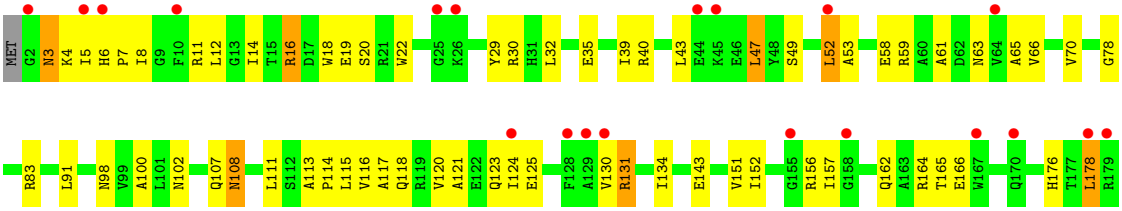
• Molecule 34: 30S ribosomal protein S3

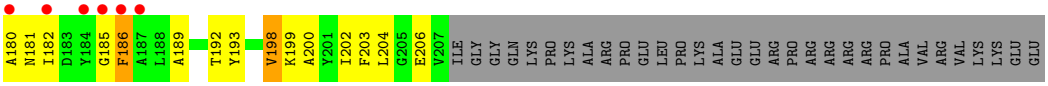
Chain 1c:



• Molecule 34: 30S ribosomal protein S3

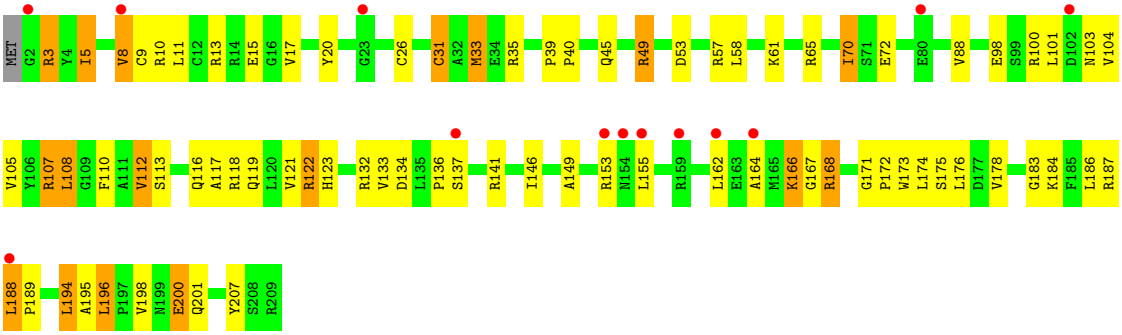
Chain 2c:





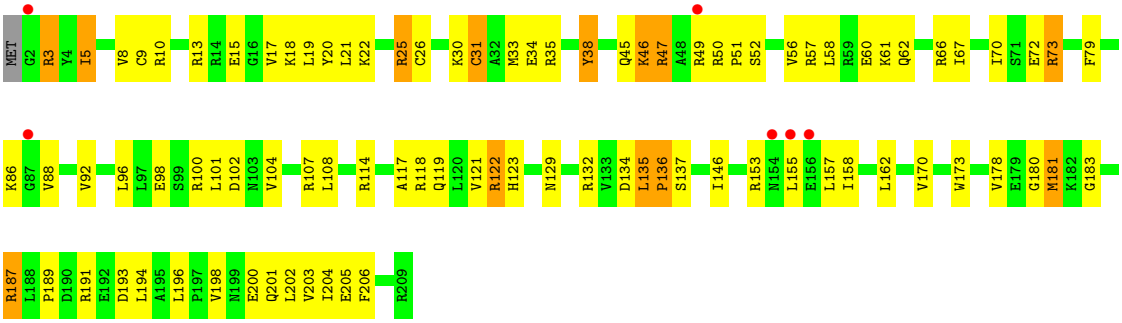
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



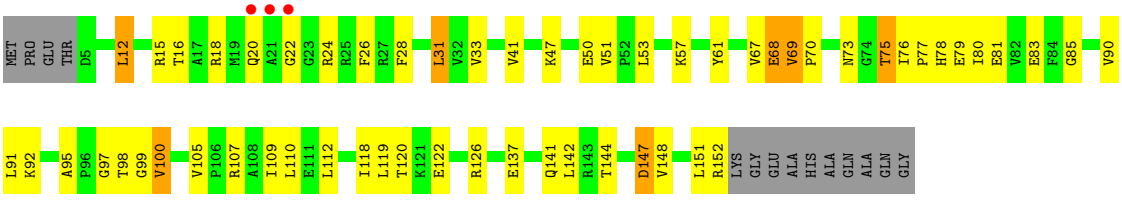
• Molecule 35: 30S ribosomal protein S4

Chain 2d:



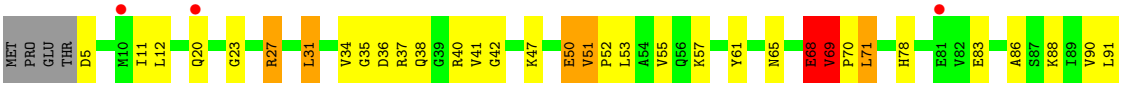
• Molecule 36: 30S ribosomal protein S5

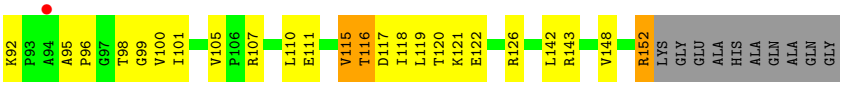
Chain 1e:



• Molecule 36: 30S ribosomal protein S5

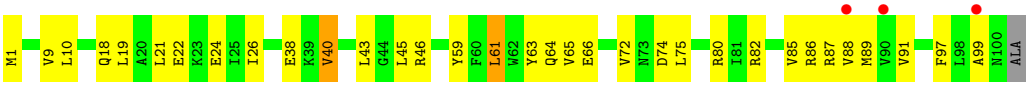
Chain 2e:





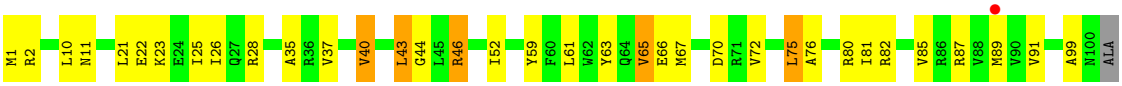
• Molecule 37: 30S ribosomal protein S6

Chain 1f:



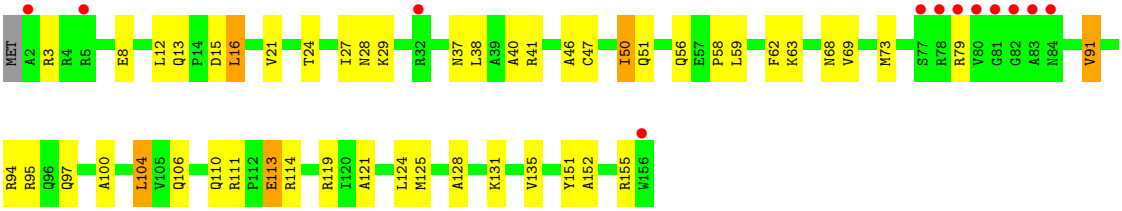
• Molecule 37: 30S ribosomal protein S6

Chain 2f:



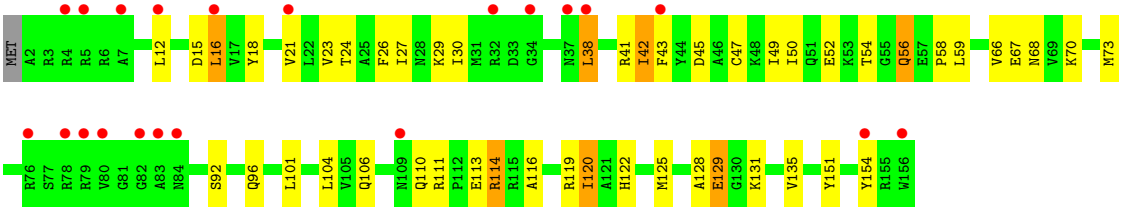
• Molecule 38: 30S ribosomal protein S7

Chain 1g:



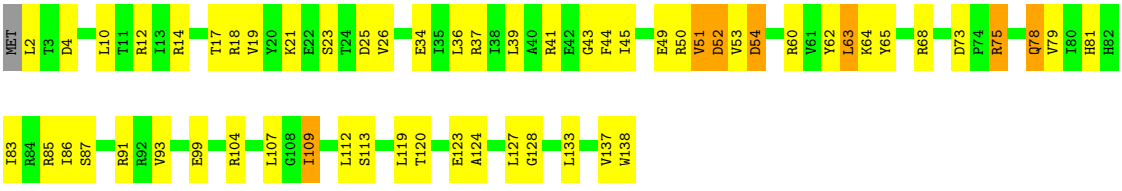
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



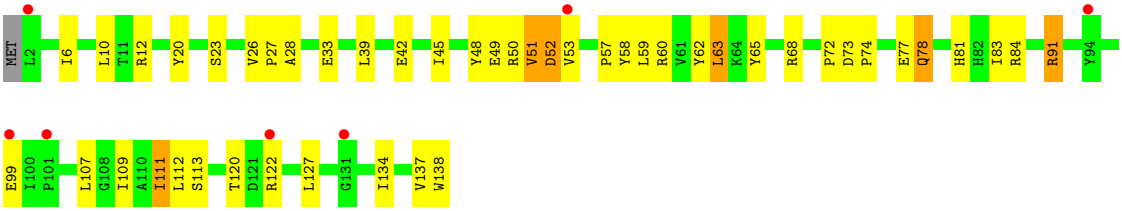
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



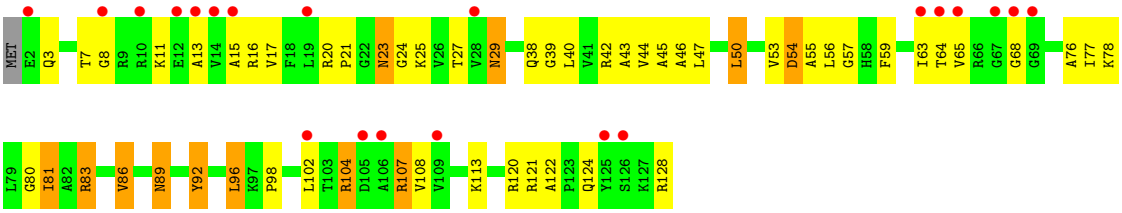
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



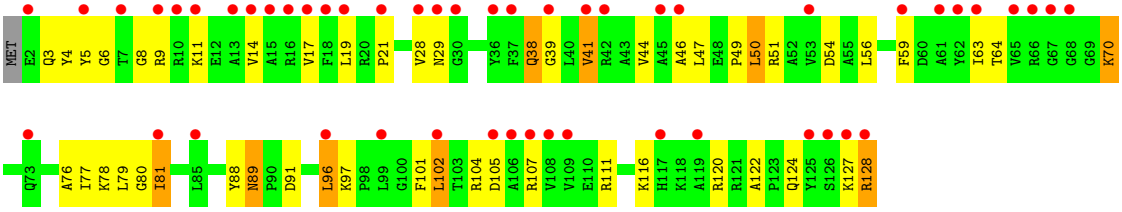
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



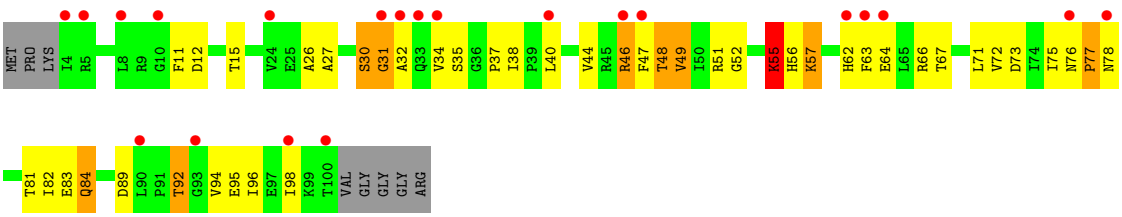
• Molecule 40: 30S ribosomal protein S9

Chain 2i:



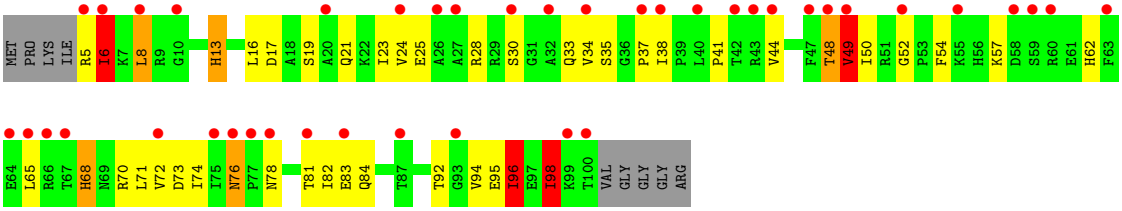
• Molecule 41: 30S ribosomal protein S10

Chain 1j:



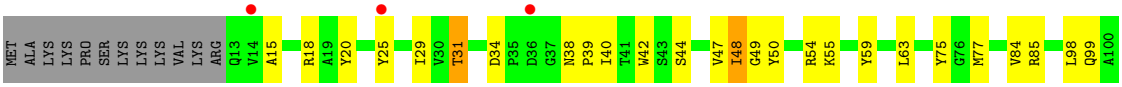
• Molecule 41: 30S ribosomal protein S10

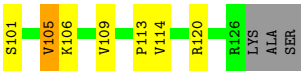
Chain 2j:



• Molecule 42: 30S ribosomal protein S11

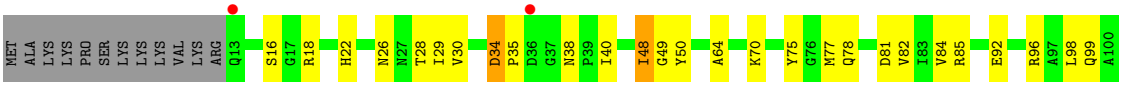
Chain 1k:

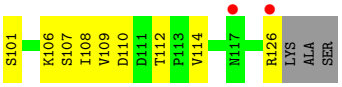




• Molecule 42: 30S ribosomal protein S11

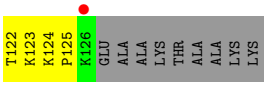
Chain 2k:





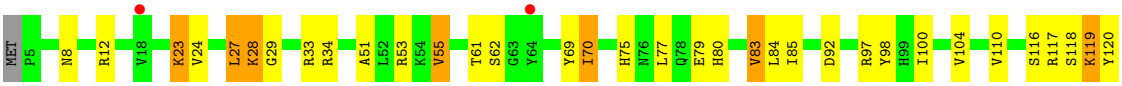
• Molecule 43: 30S ribosomal protein S12

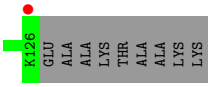
Chain 1l:



• Molecule 43: 30S ribosomal protein S12

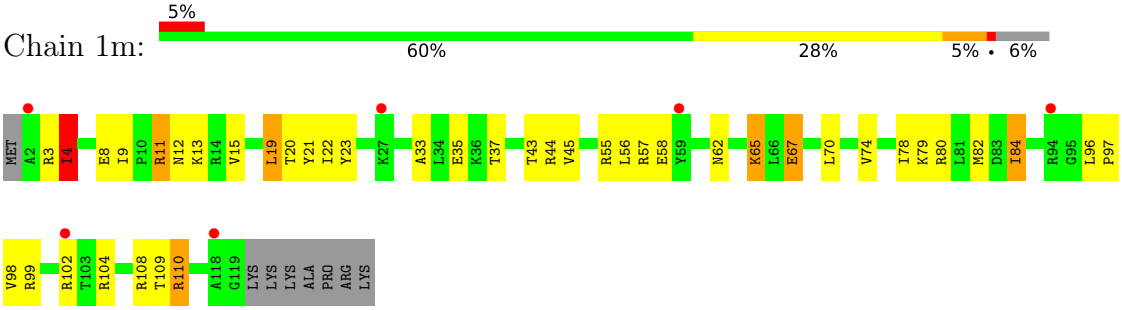
Chain 2l:





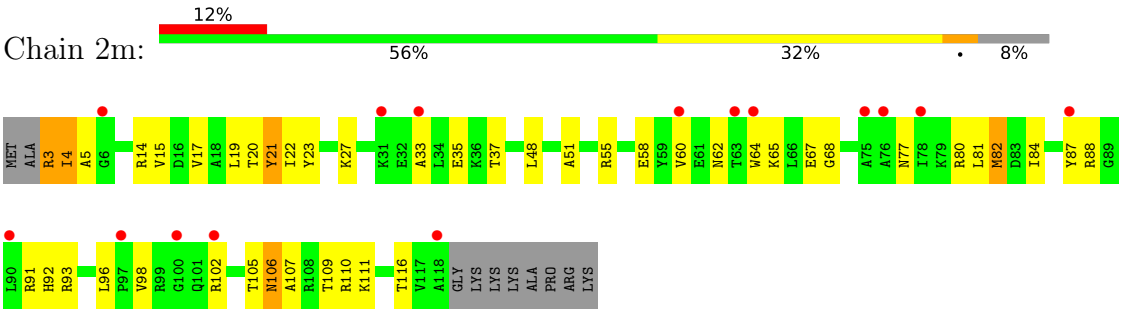
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



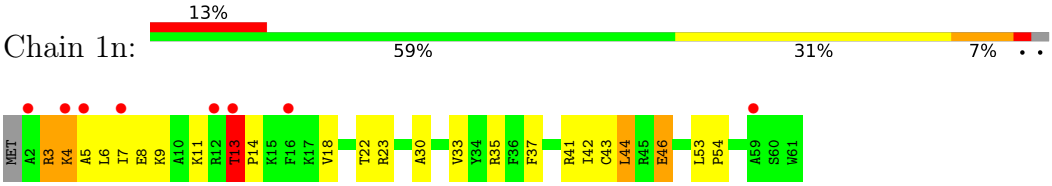
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



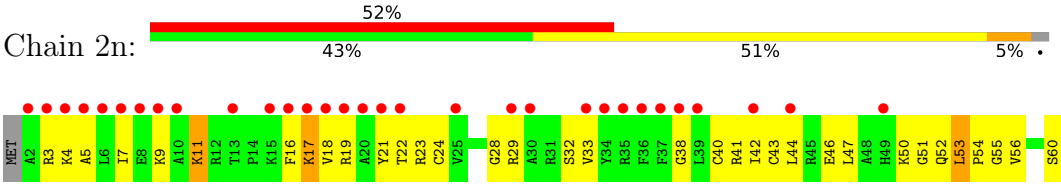
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



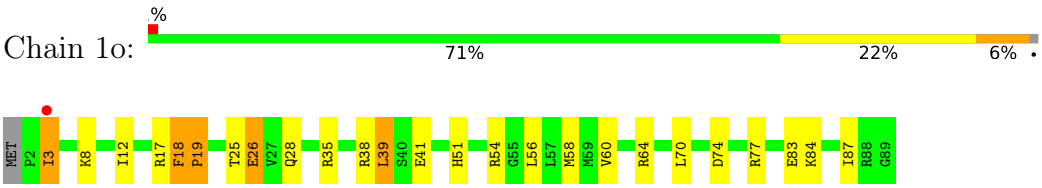
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:



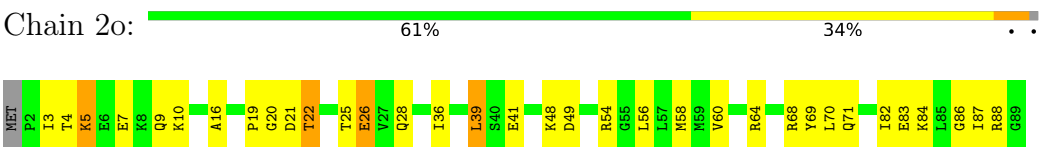
• Molecule 46: 30S ribosomal protein S15

Chain 1o:



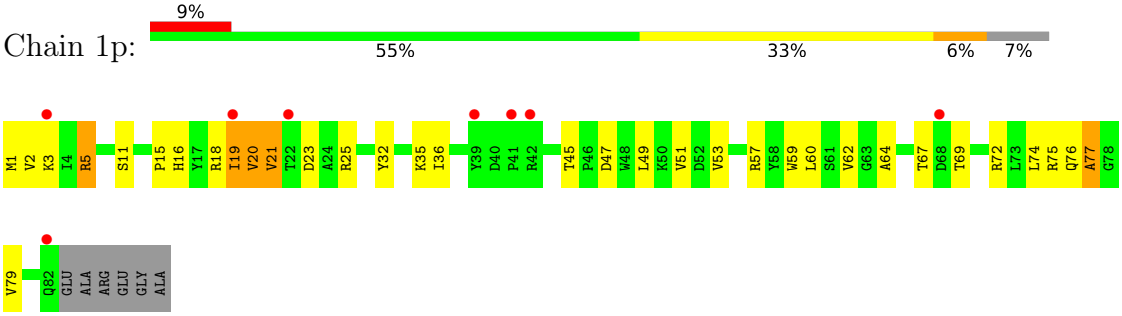
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



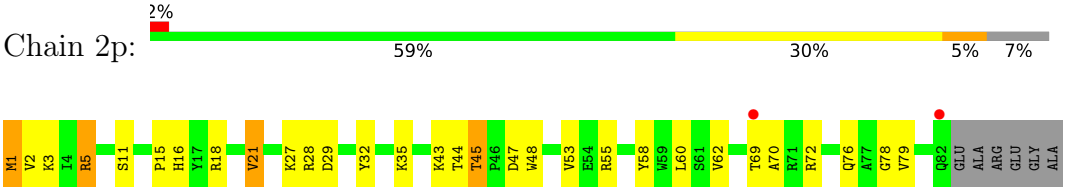
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



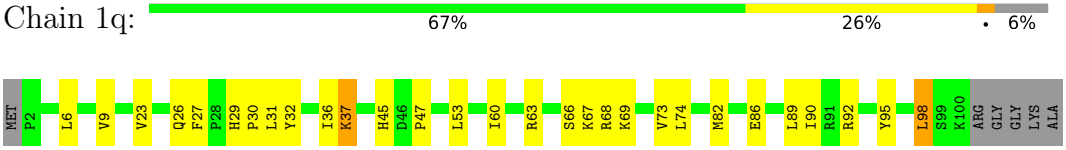
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



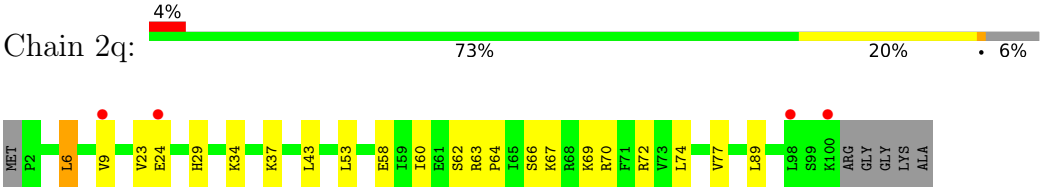
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



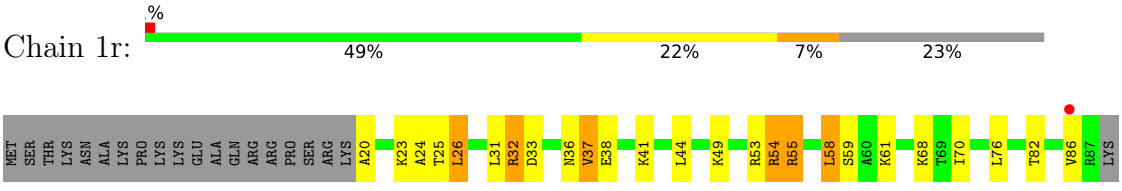
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



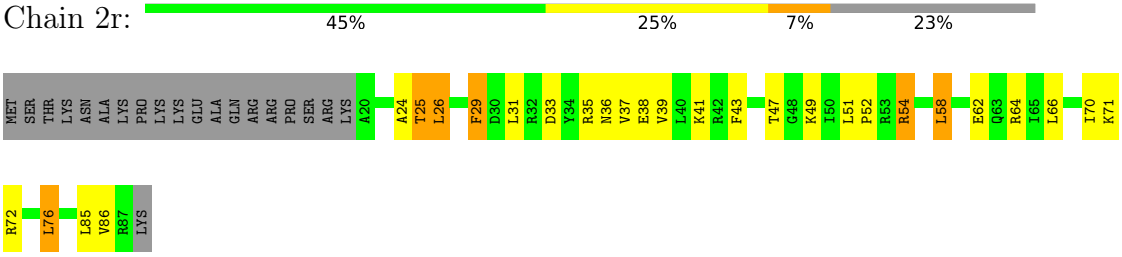
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



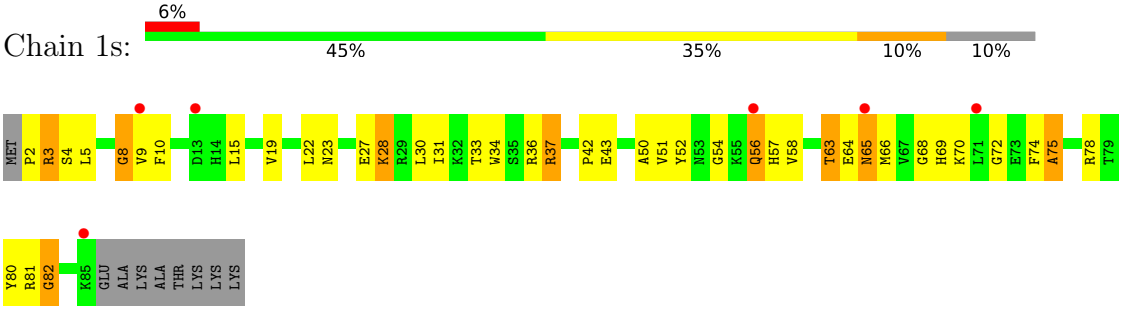
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



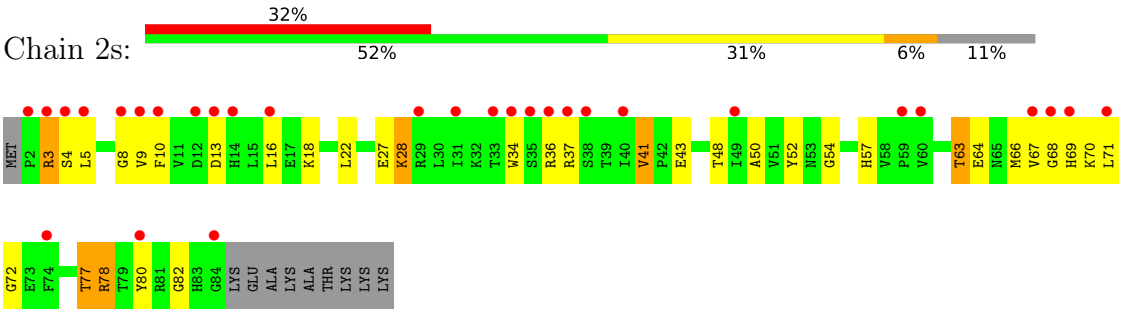
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



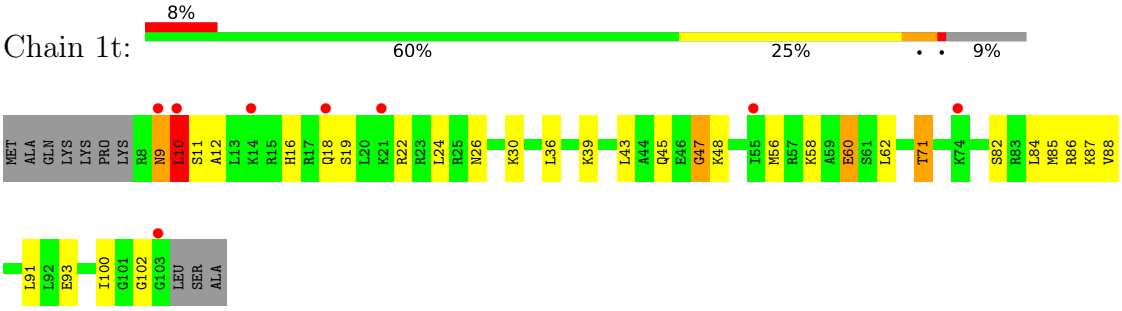
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



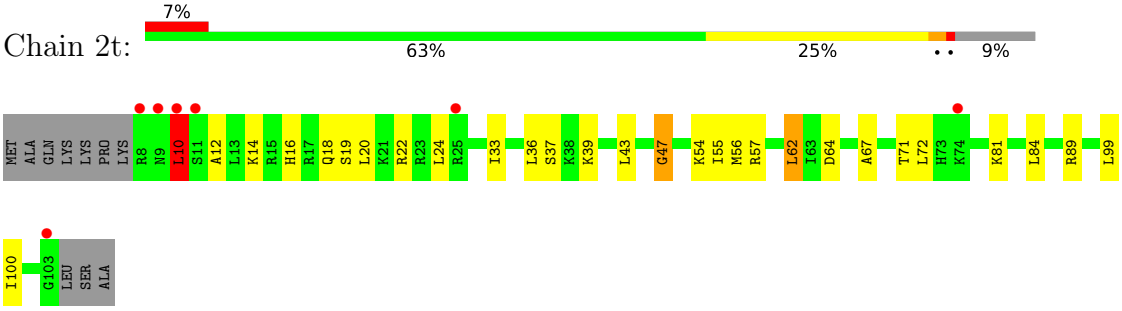
• Molecule 51: 30S ribosomal protein S20

Chain 1t:



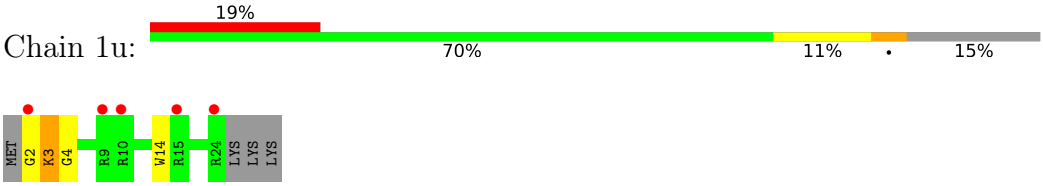
• Molecule 51: 30S ribosomal protein S20

Chain 2t:



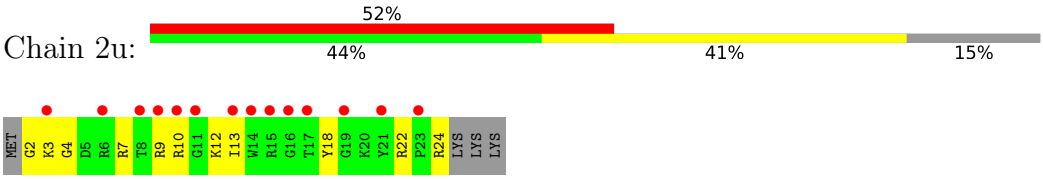
• Molecule 52: 30S ribosomal protein Thx

Chain 1u:



• Molecule 52: 30S ribosomal protein Thx

Chain 2u:

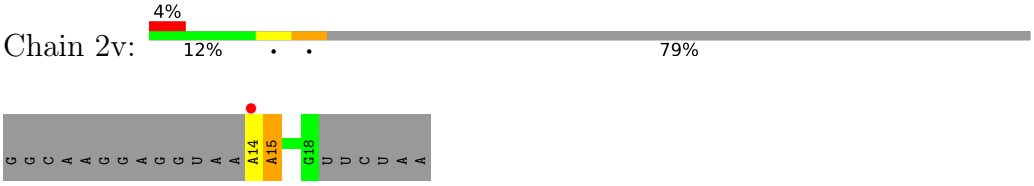


• Molecule 53: mRNA

Chain 1v:

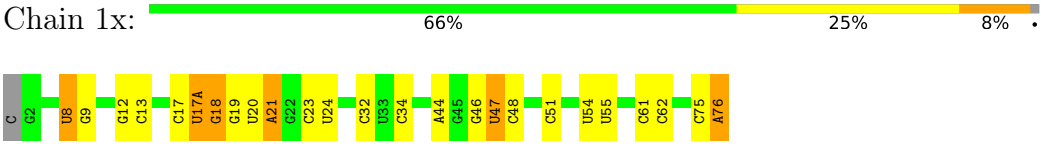
• Molecule 53: mRNA

Chain 2v:



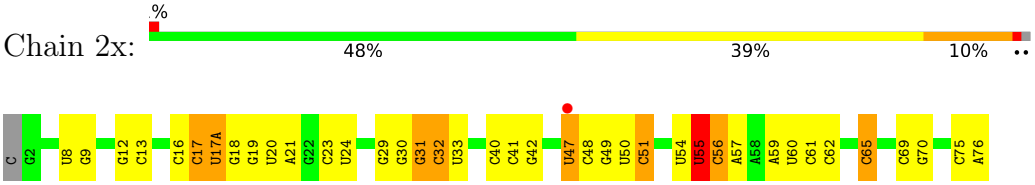
• Molecule 54: P-site tRNA

Chain 1x:



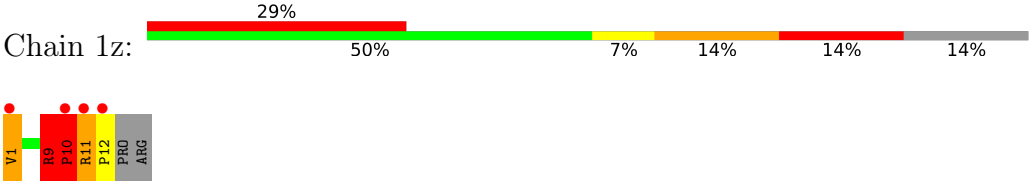
• Molecule 54: P-site tRNA

Chain 2x:



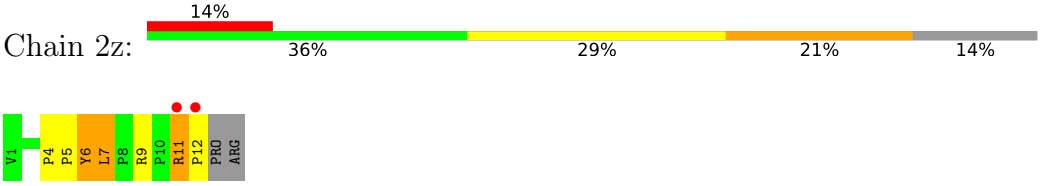
• Molecule 55: Oncocin d15-19

Chain 1z:



• Molecule 55: Oncocin d15-19

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	210.05Å 450.75Å 623.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.92 – 2.80 49.92 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.92-2.80) 99.6 (49.92-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 2.81Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.200 , 0.251 0.200 , 0.249	Depositor DCC
R_{free} test set	71597 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	57.7	Xtriage
Anisotropy	0.179	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 53.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	288518	wwPDB-VP
Average B, all atoms (Å^2)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, 4SU, ZN, MG, SF4, 5MC, 5MU

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	0.47	0/66249	0.58	4/103407 (0.0%)
1	2A	0.35	0/67298	0.56	1/105044 (0.0%)
2	1B	0.35	0/2877	0.50	0/4488
2	2B	0.42	0/2878	0.57	0/4490
3	1D	0.70	0/2186	0.96	0/2944
3	2D	0.58	0/2192	0.97	4/2951 (0.1%)
4	1E	0.72	0/1592	1.01	4/2149 (0.2%)
4	2E	0.60	0/1592	1.01	8/2149 (0.4%)
5	1F	0.70	0/1619	0.99	3/2193 (0.1%)
5	2F	0.51	0/1615	1.01	2/2188 (0.1%)
6	1G	0.55	0/1450	0.94	4/1959 (0.2%)
6	2G	0.56	0/1449	1.09	6/1958 (0.3%)
7	1H	0.63	0/1356	0.94	4/1834 (0.2%)
7	2H	0.55	0/1356	1.02	1/1834 (0.1%)
8	1I	0.53	0/1100	0.99	2/1501 (0.1%)
8	2I	0.50	0/1076	1.02	5/1471 (0.3%)
9	1N	0.69	0/1144	0.84	0/1543
9	2N	0.50	0/1144	0.92	2/1543 (0.1%)
10	1O	0.72	0/943	0.94	0/1269
10	2O	0.57	0/943	0.98	0/1269
11	1P	0.65	0/1156	0.93	2/1537 (0.1%)
11	2P	0.52	0/1152	1.03	5/1533 (0.3%)
12	1Q	0.70	0/1143	0.93	0/1527
12	2Q	0.55	0/1143	0.95	1/1527 (0.1%)
13	1R	0.77	1/982 (0.1%)	0.86	0/1312
13	2R	0.52	0/982	0.85	0/1312
14	1S	0.57	0/887	0.91	1/1180 (0.1%)
14	2S	0.61	0/880	1.05	5/1172 (0.4%)
15	1T	0.64	0/1105	0.94	0/1477
15	2T	0.50	0/1097	0.90	0/1468
16	1U	0.81	0/977	0.92	0/1301
16	2U	0.56	0/977	0.89	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	1V	0.68	0/782	0.91	0/1049
17	2V	0.58	0/782	0.91	1/1049 (0.1%)
18	1W	0.80	0/897	0.92	1/1205 (0.1%)
18	2W	0.62	0/897	0.94	1/1205 (0.1%)
19	1X	0.68	0/764	0.91	1/1025 (0.1%)
19	2X	0.57	0/764	0.95	1/1025 (0.1%)
20	1Y	0.66	0/819	0.97	2/1095 (0.2%)
20	2Y	0.51	0/819	0.98	0/1095
21	1Z	0.56	0/1502	0.98	3/2041 (0.1%)
21	2Z	0.54	0/1486	1.00	2/2022 (0.1%)
22	10	0.65	0/606	1.02	4/808 (0.5%)
22	20	0.47	0/606	0.97	4/808 (0.5%)
23	11	0.66	0/762	0.90	0/1014
23	21	0.58	0/762	0.91	0/1014
24	12	0.65	0/590	0.85	0/781
24	22	0.50	0/590	0.85	0/781
25	13	0.72	0/474	1.01	4/635 (0.6%)
25	23	0.50	0/469	0.93	0/630
26	14	0.52	0/571	1.03	3/768 (0.4%)
26	24	0.63	0/545	1.20	2/737 (0.3%)
27	15	0.76	0/469	0.95	0/635
27	25	0.59	0/469	0.93	0/635
28	16	0.63	0/460	0.82	0/613
28	26	0.57	0/456	0.87	0/608
29	17	0.76	0/426	0.89	1/561 (0.2%)
29	27	0.63	0/426	0.92	1/561 (0.2%)
30	18	0.71	0/525	0.91	1/691 (0.1%)
30	28	0.56	0/525	0.96	0/691
31	19	0.74	0/310	0.91	0/407
31	29	0.51	0/310	0.99	0/407
32	1a	0.31	0/35537	0.50	2/55456 (0.0%)
32	2a	0.28	0/35680	0.48	1/55681 (0.0%)
33	1b	0.51	0/1820	1.02	7/2468 (0.3%)
33	2b	1.65	8/1728 (0.5%)	1.17	12/2352 (0.5%)
34	1c	0.50	0/1504	0.90	2/2047 (0.1%)
34	2c	0.55	0/1435	0.99	0/1960
35	1d	0.52	0/1648	0.94	2/2222 (0.1%)
35	2d	0.48	0/1659	0.94	0/2230
36	1e	0.53	0/1145	1.02	6/1543 (0.4%)
36	2e	0.50	0/1111	1.09	10/1504 (0.7%)
37	1f	0.48	0/819	0.86	0/1111
37	2f	0.47	0/830	0.86	2/1125 (0.2%)
38	1g	0.46	0/1198	0.94	1/1613 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	2g	0.47	0/1185	0.91	0/1602
39	1h	0.46	0/1108	0.92	0/1494
39	2h	0.43	0/1094	0.91	2/1478 (0.1%)
40	1i	0.46	0/995	0.93	2/1339 (0.1%)
40	2i	0.54	0/949	0.94	1/1284 (0.1%)
41	1j	0.59	0/695	1.13	7/950 (0.7%)
41	2j	0.59	0/690	1.15	10/943 (1.1%)
42	1k	0.50	0/840	0.95	1/1138 (0.1%)
42	2k	0.46	0/844	0.93	4/1145 (0.3%)
43	1l	0.53	0/936	0.93	0/1263
43	2l	0.51	0/934	0.97	4/1262 (0.3%)
44	1m	0.46	0/933	0.93	1/1254 (0.1%)
44	2m	0.54	0/913	0.93	0/1230
45	1n	0.50	0/491	1.08	3/653 (0.5%)
45	2n	0.48	0/467	0.92	0/624
46	1o	0.49	0/726	0.94	2/970 (0.2%)
46	2o	0.44	0/739	0.89	0/985
47	1p	0.49	0/686	0.96	2/926 (0.2%)
47	2p	0.51	0/693	0.91	3/935 (0.3%)
48	1q	0.46	0/824	0.85	0/1105
48	2q	0.44	0/836	0.85	2/1117 (0.2%)
49	1r	0.49	0/560	0.89	0/746
49	2r	0.44	0/560	0.84	0/746
50	1s	0.49	0/657	1.04	6/890 (0.7%)
50	2s	0.52	0/661	1.02	1/893 (0.1%)
51	1t	0.46	0/714	1.04	1/948 (0.1%)
51	2t	0.47	0/733	0.93	0/969
52	1u	0.41	0/191	0.79	0/252
52	2u	0.49	0/203	1.03	2/266 (0.8%)
53	1v	0.42	0/122	0.76	0/188
53	2v	0.47	0/122	0.61	0/188
54	1x	0.37	0/1725	0.55	0/2689
54	2x	0.34	0/1725	0.54	0/2689
55	1z	1.16	1/106 (0.9%)	1.36	2/146 (1.4%)
55	2z	0.78	0/106	1.65	4/146 (2.7%)
All	All	0.46	10/306280 (0.0%)	0.68	201/458192 (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
5	2F	0	1
19	1X	0	1
19	2X	0	1
20	1Y	0	1
34	2c	0	1
All	All	0	5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	2b	92	TYR	CD1-CE1	30.24	2.29	1.38
33	2b	92	TYR	CD2-CE2	26.56	2.18	1.38
33	2b	151	GLY	N-CA	23.94	1.80	1.45
33	2b	92	TYR	CE1-CZ	22.82	1.93	1.38
33	2b	92	TYR	CE2-CZ	22.55	1.92	1.38
33	2b	92	TYR	CG-CD1	20.85	1.83	1.39
33	2b	92	TYR	CG-CD2	19.84	1.81	1.39
33	2b	150	SER	C-N	12.48	1.51	1.33
55	1z	9	ARG	CA-C	7.44	1.62	1.52
13	1R	38	VAL	CA-CB	-5.61	1.51	1.54

All (201) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	2b	150	SER	CA-C-N	17.99	156.68	121.41
33	2b	150	SER	C-N-CA	17.99	156.68	121.41
33	2b	151	GLY	N-CA-C	9.45	135.57	113.18
1	1A	2013	G	C2'-C3'-O3'	9.33	123.50	109.50
36	1e	105	VAL	CA-C-N	-9.12	110.42	119.64
36	1e	105	VAL	C-N-CA	-9.12	110.42	119.64
26	24	61	ARG	N-CA-C	-9.05	102.24	113.28
7	2H	9	ILE	N-CA-C	8.56	115.35	107.56
55	2z	9	ARG	CA-C-N	8.46	128.52	119.89
55	2z	9	ARG	C-N-CA	8.46	128.52	119.89
11	2P	43	GLY	N-CA-C	8.41	123.63	113.79
6	2G	44	GLY	N-CA-C	-7.82	104.97	115.36
22	20	82	ARG	CA-C-N	7.77	128.24	119.92
22	20	82	ARG	C-N-CA	7.77	128.24	119.92
11	2P	44	GLY	CA-C-N	7.46	135.13	121.70
11	2P	44	GLY	C-N-CA	7.46	135.13	121.70
1	2A	2013	G	C2'-C3'-O3'	7.42	120.62	109.50
21	1Z	107	THR	CA-C-N	7.40	127.43	119.89
21	1Z	107	THR	C-N-CA	7.40	127.43	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	24	51	ASP	N-CA-C	7.39	119.85	110.61
36	1e	99	GLY	N-CA-C	-7.22	104.13	112.79
41	2j	98	ILE	N-CA-C	7.21	117.29	108.06
36	2e	23	GLY	N-CA-C	7.10	119.67	110.45
8	1I	110	ASP	CA-C-N	7.09	126.62	119.24
8	1I	110	ASP	C-N-CA	7.09	126.62	119.24
43	2l	119	LYS	N-CA-C	-7.04	100.57	110.50
55	2z	9	ARG	N-CA-C	-7.04	101.21	109.93
45	1n	13	THR	CA-C-N	7.03	129.37	120.51
45	1n	13	THR	C-N-CA	7.03	129.37	120.51
36	2e	105	VAL	CA-C-N	-6.95	112.62	119.64
36	2e	105	VAL	C-N-CA	-6.95	112.62	119.64
14	2S	34	HIS	N-CA-C	6.91	119.00	109.18
21	2Z	120	ILE	N-CA-C	6.88	117.64	110.62
33	2b	130	ARG	CA-C-N	6.87	128.43	119.84
33	2b	130	ARG	C-N-CA	6.87	128.43	119.84
35	1d	33	MET	N-CA-C	-6.85	103.89	111.36
26	14	40	HIS	CA-C-N	6.80	127.35	119.47
26	14	40	HIS	C-N-CA	6.80	127.35	119.47
26	14	52	THR	N-CA-C	-6.79	105.00	113.28
44	1m	84	ILE	N-CA-C	6.74	120.47	111.44
8	2I	79	ILE	CA-C-N	6.71	128.22	119.84
8	2I	79	ILE	C-N-CA	6.71	128.22	119.84
33	1b	166	ASP	CA-C-N	6.70	126.15	118.85
33	1b	166	ASP	C-N-CA	6.70	126.15	118.85
4	1E	31	CYS	CA-C-N	6.65	126.41	119.76
4	1E	31	CYS	C-N-CA	6.65	126.41	119.76
33	2b	233	SER	N-CA-C	6.64	119.46	110.29
25	13	11	SER	CA-C-N	6.60	127.17	120.04
25	13	11	SER	C-N-CA	6.60	127.17	120.04
41	2j	83	GLU	N-CA-C	-6.45	106.62	114.75
5	1F	89	VAL	N-CA-C	6.42	116.58	110.74
6	2G	141	PHE	CA-C-N	6.41	125.84	118.85
6	2G	141	PHE	C-N-CA	6.41	125.84	118.85
36	2e	95	ALA	CA-C-N	6.38	127.82	119.84
36	2e	95	ALA	C-N-CA	6.38	127.82	119.84
14	2S	63	THR	N-CA-C	6.32	117.96	111.14
6	1G	45	GLU	N-CA-C	-6.16	105.61	113.01
41	1j	57	LYS	N-CA-C	6.15	117.98	111.28
4	2E	21	VAL	CA-C-N	6.15	126.36	119.90
4	2E	21	VAL	C-N-CA	6.15	126.36	119.90
33	2b	231	GLU	CA-C-N	6.12	126.44	119.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	2b	231	GLU	C-N-CA	6.12	126.44	119.83
29	17	47	ARG	N-CA-C	6.11	120.81	113.23
6	1G	31	VAL	CA-C-N	6.11	127.47	119.84
6	1G	31	VAL	C-N-CA	6.11	127.47	119.84
41	2j	76	ASN	CA-C-N	6.05	127.40	119.84
41	2j	76	ASN	C-N-CA	6.05	127.40	119.84
36	2e	98	THR	N-CA-C	6.03	123.63	110.80
42	2k	34	ASP	CA-C-N	-6.02	112.81	119.19
42	2k	34	ASP	C-N-CA	-6.02	112.81	119.19
39	2h	73	ASP	CA-C-N	5.98	126.93	120.83
39	2h	73	ASP	C-N-CA	5.98	126.93	120.83
1	1A	2013	G	P-O3'-C3'	5.97	129.16	120.20
37	2f	11	ASN	CA-C-N	5.97	125.36	118.85
37	2f	11	ASN	C-N-CA	5.97	125.36	118.85
50	2s	82	GLY	N-CA-C	5.96	119.30	110.60
7	1H	9	ILE	N-CA-C	5.95	113.44	107.55
40	1i	89	ASN	CA-C-N	5.93	125.81	119.28
40	1i	89	ASN	C-N-CA	5.93	125.81	119.28
30	18	33	ASN	N-CA-C	5.90	120.48	113.28
1	1A	1285	U	C4'-C3'-O3'	5.89	121.84	113.00
4	1E	85	ASN	CA-C-N	5.89	125.65	119.76
4	1E	85	ASN	C-N-CA	5.89	125.65	119.76
11	1P	22	GLY	CA-C-N	5.88	125.27	118.85
11	1P	22	GLY	C-N-CA	5.88	125.27	118.85
33	1b	15	VAL	N-CA-C	5.87	116.73	108.17
18	2W	24	ILE	CB-CA-C	-5.86	104.30	110.62
6	2G	43	LEU	CB-CA-C	-5.85	109.85	116.63
7	1H	92	ILE	N-CA-C	5.84	115.97	110.30
14	2S	91	PRO	N-CA-C	-5.83	108.61	114.68
43	2l	28	LYS	N-CA-C	5.82	119.28	111.24
12	2Q	27	VAL	N-CA-C	5.79	115.91	110.30
41	2j	52	GLY	CA-C-N	5.78	125.32	119.19
41	2j	52	GLY	C-N-CA	5.78	125.32	119.19
3	2D	83	GLU	N-CA-C	5.77	118.63	109.81
4	2E	72	VAL	N-CA-C	5.74	116.38	108.12
25	13	15	TYR	CA-C-N	5.73	125.74	119.89
25	13	15	TYR	C-N-CA	5.73	125.74	119.89
51	1t	10	LEU	N-CA-C	5.73	123.00	110.80
32	1a	262	G	C2'-C3'-O3'	5.73	118.09	109.50
41	2j	28	ARG	N-CA-C	-5.71	104.67	111.69
36	2e	35	GLY	N-CA-C	5.71	119.08	110.18
55	1z	10	PRO	CA-N-CD	-5.66	104.08	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
14	1S	59	LYS	N-CA-C	5.63	120.66	113.18
55	1z	9	ARG	N-CA-C	5.62	122.24	109.81
41	1j	89	ASP	N-CA-C	5.62	117.88	107.99
38	1g	79	ARG	N-CA-C	-5.61	106.60	113.50
42	2k	38	ASN	CA-C-N	5.61	125.62	119.90
42	2k	38	ASN	C-N-CA	5.61	125.62	119.90
41	1j	52	GLY	CA-C-N	5.59	125.12	119.19
41	1j	52	GLY	C-N-CA	5.59	125.12	119.19
8	2I	124	GLY	N-CA-C	5.56	118.41	110.46
3	2D	275	LYS	N-CA-C	-5.55	98.99	110.80
5	2F	16	GLY	N-CA-C	5.54	118.68	110.60
32	1a	1048	U	C2'-C3'-O3'	5.52	117.78	109.50
3	2D	120	GLY	CA-C-N	5.51	125.60	119.32
3	2D	120	GLY	C-N-CA	5.51	125.60	119.32
52	2u	22	ARG	CA-C-N	5.51	126.73	119.84
52	2u	22	ARG	C-N-CA	5.51	126.73	119.84
41	2j	96	ILE	N-CA-C	5.50	116.82	108.80
46	1o	18	PHE	CA-C-N	5.46	126.67	119.84
46	1o	18	PHE	C-N-CA	5.46	126.67	119.84
41	1j	76	ASN	CA-C-N	5.45	126.65	119.84
41	1j	76	ASN	C-N-CA	5.45	126.65	119.84
36	2e	69	VAL	CA-C-N	5.44	126.64	119.84
36	2e	69	VAL	C-N-CA	5.44	126.64	119.84
9	2N	110	GLY	CA-C-N	5.42	125.06	119.05
9	2N	110	GLY	C-N-CA	5.42	125.06	119.05
14	2S	59	LYS	N-CA-C	5.41	115.43	108.34
17	2V	53	GLU	N-CA-C	5.41	116.87	110.97
47	2p	70	ALA	N-CA-C	-5.40	107.06	113.97
33	1b	200	ILE	N-CA-C	5.38	115.86	108.12
22	10	13	GLY	N-CA-C	5.37	125.91	113.18
50	1s	56	GLN	N-CA-C	5.37	115.38	108.34
47	1p	45	THR	CA-C-N	5.37	126.55	119.84
47	1p	45	THR	C-N-CA	5.37	126.55	119.84
33	1b	193	ASP	CA-C-N	5.37	125.01	119.05
33	1b	193	ASP	C-N-CA	5.37	125.01	119.05
5	2F	79	GLY	N-CA-C	-5.36	107.30	115.66
32	2a	66	U	C2'-C3'-O3'	5.36	117.54	109.50
36	1e	95	ALA	CA-C-N	5.36	126.53	119.84
36	1e	95	ALA	C-N-CA	5.36	126.53	119.84
36	1e	68	GLU	N-CA-C	5.35	116.80	111.07
33	2b	150	SER	CA-C-O	-5.35	112.86	120.51
50	1s	8	GLY	N-CA-C	5.34	120.03	111.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	10	14	ARG	N-CA-C	5.32	118.40	110.52
6	2G	78	SER	N-CA-C	5.31	117.15	111.36
4	2E	188	VAL	CA-C-N	5.28	125.22	119.78
4	2E	188	VAL	C-N-CA	5.28	125.22	119.78
6	2G	48	GLU	N-CA-C	-5.27	107.01	113.50
36	2e	68	GLU	N-CA-C	5.27	116.71	111.07
8	2I	118	LYS	CA-C-N	5.26	126.42	119.84
8	2I	118	LYS	C-N-CA	5.26	126.42	119.84
33	2b	152	PHE	N-CA-C	-5.24	106.94	113.38
50	1s	31	ILE	N-CA-C	5.22	113.89	106.53
41	2j	49	VAL	N-CA-C	5.22	115.08	107.88
21	1Z	120	ILE	N-CA-C	5.20	115.93	110.62
41	2j	6	ILE	N-CA-C	5.19	115.33	107.80
4	2E	6	GLY	N-CA-C	5.19	118.27	110.18
19	2X	46	ALA	N-CA-C	-5.19	107.97	114.56
19	1X	69	TYR	N-CA-C	5.18	117.05	108.20
22	10	82	ARG	CA-C-N	5.17	125.45	119.92
22	10	82	ARG	C-N-CA	5.17	125.45	119.92
48	2q	29	HIS	CA-C-N	5.16	125.45	119.47
48	2q	29	HIS	C-N-CA	5.16	125.45	119.47
41	1j	55	LYS	N-CA-C	5.14	121.76	110.80
14	2S	57	LYS	N-CA-C	5.14	121.75	110.80
22	20	13	GLY	N-CA-C	5.14	121.89	115.21
33	2b	114	ARG	N-CA-C	-5.13	107.09	113.55
43	2l	29	GLY	N-CA-C	-5.13	98.43	113.30
5	1F	89	VAL	CA-C-N	-5.11	114.15	123.34
5	1F	89	VAL	C-N-CA	-5.11	114.15	123.34
21	2Z	53	ILE	N-CA-C	-5.10	107.78	112.83
42	1k	75	TYR	N-CA-C	-5.10	106.84	113.16
29	27	45	ALA	N-CA-C	5.09	119.12	113.01
40	2i	70	LYS	N-CA-C	5.09	117.22	111.11
11	2P	22	GLY	CA-C-N	5.09	124.70	119.05
11	2P	22	GLY	C-N-CA	5.09	124.70	119.05
18	1W	17	VAL	CB-CA-C	-5.09	105.27	112.14
55	2z	6	TYR	N-CA-C	-5.09	107.11	113.72
20	1Y	55	TYR	CA-C-N	-5.08	115.49	120.52
20	1Y	55	TYR	C-N-CA	-5.08	115.49	120.52
4	2E	31	CYS	CA-C-N	5.08	124.84	119.76
4	2E	31	CYS	C-N-CA	5.08	124.84	119.76
35	1d	166	LYS	N-CA-C	5.08	116.51	111.07
45	1n	4	LYS	N-CA-C	5.06	116.49	111.07
43	2l	23	LYS	N-CA-C	-5.06	106.41	112.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	536	G	O4'-C1'-N9	5.05	115.78	108.20
6	1G	108	ASN	N-CA-C	5.05	116.86	111.36
33	1b	186	ALA	N-CA-C	5.04	116.72	108.76
47	2p	45	THR	CA-C-N	5.03	126.13	119.84
47	2p	45	THR	C-N-CA	5.03	126.13	119.84
50	1s	82	GLY	N-CA-C	5.03	117.22	110.43
7	1H	167	GLU	CA-C-N	5.03	124.96	119.78
7	1H	167	GLU	C-N-CA	5.03	124.96	119.78
33	2b	27	LYS	N-CA-C	-5.02	106.67	112.89
34	1c	72	LYS	CA-C-N	5.02	124.68	119.56
34	1c	72	LYS	C-N-CA	5.02	124.68	119.56
50	1s	75	ALA	CA-C-N	5.01	125.24	119.83
50	1s	75	ALA	C-N-CA	5.01	125.24	119.83
22	20	40	GLN	N-CA-C	5.00	116.45	108.79

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
19	1X	93	GLU	Peptide
20	1Y	54	LYS	Peptide
5	2F	20	LEU	Peptide
19	2X	93	GLU	Peptide
34	2c	186	PHE	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	59154	0	29828	522	0
1	2A	60091	0	30300	810	0
2	1B	2572	0	1306	31	0
2	2B	2573	0	1306	61	0
3	1D	2136	0	2218	51	0
3	2D	2142	0	2229	61	0
4	1E	1559	0	1618	35	0
4	2E	1559	0	1618	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	1F	1584	0	1625	33	0
5	2F	1580	0	1619	49	0
6	1G	1425	0	1443	35	0
6	2G	1424	0	1434	75	0
7	1H	1330	0	1407	26	0
7	2H	1330	0	1407	38	0
8	1I	1085	0	1114	25	0
8	2I	1061	0	1080	28	0
9	1N	1117	0	1184	14	0
9	2N	1117	0	1184	21	0
10	1O	933	0	996	16	0
10	2O	933	0	996	21	0
11	1P	1139	0	1223	32	0
11	2P	1135	0	1212	40	0
12	1Q	1122	0	1179	23	0
12	2Q	1122	0	1179	28	0
13	1R	968	0	1033	16	0
13	2R	968	0	1033	22	0
14	1S	877	0	938	28	0
14	2S	870	0	923	31	0
15	1T	1091	0	1151	25	0
15	2T	1083	0	1136	22	0
16	1U	959	0	1019	11	0
16	2U	959	0	1018	24	0
17	1V	771	0	830	9	0
17	2V	771	0	830	18	0
18	1W	886	0	940	8	0
18	2W	886	0	940	19	0
19	1X	750	0	814	16	0
19	2X	750	0	814	16	0
20	1Y	806	0	881	26	0
20	2Y	806	0	881	27	0
21	1Z	1470	0	1478	24	0
21	2Z	1454	0	1452	49	0
22	10	598	0	614	11	0
22	20	598	0	614	12	0
23	11	755	0	826	12	0
23	21	755	0	826	12	0
24	12	588	0	643	7	0
24	22	588	0	643	16	0
25	13	469	0	518	6	0
25	23	464	0	514	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	14	558	0	544	40	0
26	24	532	0	503	26	0
27	15	455	0	465	7	0
27	25	455	0	465	13	0
28	16	453	0	472	7	0
28	26	449	0	469	6	0
29	17	418	0	467	8	0
29	27	418	0	467	11	0
30	18	517	0	582	18	0
30	28	517	0	582	27	0
31	19	307	0	335	7	0
31	29	307	0	335	8	0
32	1a	31750	0	16028	528	0
32	2a	31877	0	16090	618	0
33	1b	1786	0	1744	81	0
33	2b	1697	0	1574	112	0
34	1c	1480	0	1400	39	0
34	2c	1412	0	1246	67	0
35	1d	1618	0	1579	60	0
35	2d	1630	0	1633	62	0
36	1e	1129	0	1184	33	0
36	2e	1095	0	1124	40	0
37	1f	806	0	793	18	0
37	2f	817	0	808	22	0
38	1g	1183	0	1165	26	0
38	2g	1167	0	1119	31	0
39	1h	1088	0	1126	34	0
39	2h	1074	0	1100	28	0
40	1i	976	0	973	39	0
40	2i	932	0	891	39	0
41	1j	682	0	598	32	0
41	2j	678	0	612	24	0
42	1k	826	0	829	21	0
42	2k	829	0	825	16	0
43	1l	920	0	958	22	0
43	2l	918	0	947	31	0
44	1m	923	0	962	32	0
44	2m	903	0	923	41	0
45	1n	482	0	507	24	0
45	2n	459	0	467	40	0
46	1o	715	0	729	14	0
46	2o	728	0	760	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	1p	671	0	679	23	0
47	2p	677	0	686	21	0
48	1q	811	0	858	16	0
48	2q	823	0	891	14	0
49	1r	555	0	618	13	0
49	2r	555	0	618	21	0
50	1s	642	0	629	39	0
50	2s	646	0	644	31	0
51	1t	712	0	759	20	0
51	2t	731	0	807	18	0
52	1u	187	0	186	5	0
52	2u	199	0	208	9	0
53	1v	109	0	55	0	0
53	2v	109	0	55	2	0
54	1x	1625	0	829	12	0
54	2x	1625	0	829	20	0
55	1z	101	0	109	7	0
55	2z	101	0	109	4	0
56	10	7	0	0	0	0
56	11	1	0	0	0	0
56	13	2	0	0	0	0
56	14	1	0	0	0	0
56	15	4	0	0	0	0
56	16	2	0	0	0	0
56	17	4	0	0	0	0
56	18	5	0	0	0	0
56	19	3	0	0	0	0
56	1A	1051	0	0	0	0
56	1B	26	0	0	0	0
56	1D	17	0	0	0	0
56	1E	10	0	0	0	0
56	1F	7	0	0	0	0
56	1G	3	0	0	0	0
56	1H	4	0	0	0	0
56	1N	8	0	0	0	0
56	1O	2	0	0	0	0
56	1P	5	0	0	0	0
56	1Q	6	0	0	0	0
56	1R	6	0	0	0	0
56	1T	5	0	0	0	0
56	1U	5	0	0	0	0
56	1V	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1W	6	0	0	0	0
56	1X	2	0	0	0	0
56	1Y	1	0	0	0	0
56	1Z	3	0	0	0	0
56	1a	306	0	0	0	0
56	1b	2	0	0	0	0
56	1c	1	0	0	0	0
56	1d	2	0	0	0	0
56	1e	4	0	0	0	0
56	1f	1	0	0	0	0
56	1h	3	0	0	0	0
56	1k	1	0	0	0	0
56	1l	1	0	0	0	0
56	1n	1	0	0	0	0
56	1o	2	0	0	0	0
56	1q	4	0	0	0	0
56	1r	3	0	0	0	0
56	1t	1	0	0	0	0
56	1x	11	0	0	0	0
56	20	1	0	0	0	0
56	25	1	0	0	0	0
56	26	1	0	0	0	0
56	28	1	0	0	0	0
56	2A	583	0	0	0	0
56	2B	10	0	0	0	0
56	2D	4	0	0	0	0
56	2E	7	0	0	0	0
56	2F	2	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	3	0	0	0	0
56	2P	1	0	0	0	0
56	2Q	5	0	0	0	0
56	2R	1	0	0	0	0
56	2U	2	0	0	0	0
56	2V	1	0	0	0	0
56	2Y	1	0	0	0	0
56	2a	244	0	0	0	0
56	2d	2	0	0	0	0
56	2e	1	0	0	0	0
56	2f	1	0	0	0	0
56	2k	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2l	3	0	0	0	0
56	2n	2	0	0	0	0
56	2p	1	0	0	0	0
56	2q	1	0	0	0	0
56	2t	1	0	0	0	0
56	2x	6	0	0	0	0
57	14	1	0	0	0	0
57	15	1	0	0	0	0
57	16	1	0	0	0	0
57	19	1	0	0	0	0
57	1Y	1	0	0	0	0
57	1n	1	0	0	0	0
57	24	1	0	0	0	0
57	25	1	0	0	0	0
57	26	1	0	0	0	0
57	29	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2n	1	0	0	0	0
58	1d	8	0	0	0	0
58	2d	8	0	0	0	0
59	10	8	0	0	0	0
59	11	7	0	0	0	0
59	12	2	0	0	0	0
59	13	4	0	0	0	0
59	15	7	0	0	1	0
59	16	5	0	0	1	0
59	17	8	0	0	0	0
59	18	9	0	0	0	0
59	19	4	0	0	2	0
59	1A	2110	0	0	85	0
59	1B	42	0	0	4	0
59	1D	24	0	0	0	0
59	1E	30	0	0	4	0
59	1F	16	0	0	1	0
59	1G	6	0	0	0	0
59	1H	3	0	0	1	0
59	1I	1	0	0	0	0
59	1N	7	0	0	0	0
59	1O	4	0	0	0	0
59	1P	21	0	0	1	0
59	1Q	11	0	0	0	0
59	1R	16	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	1S	2	0	0	0	0
59	1T	7	0	0	1	0
59	1U	14	0	0	0	0
59	1V	4	0	0	1	0
59	1W	5	0	0	0	0
59	1X	4	0	0	0	0
59	1Y	1	0	0	0	0
59	1Z	4	0	0	0	0
59	1a	393	0	0	32	0
59	1b	1	0	0	0	0
59	1c	1	0	0	0	0
59	1d	5	0	0	0	0
59	1e	3	0	0	0	0
59	1f	1	0	0	0	0
59	1h	3	0	0	0	0
59	1i	1	0	0	0	0
59	1j	1	0	0	0	0
59	1k	1	0	0	1	0
59	1l	3	0	0	0	0
59	1m	1	0	0	0	0
59	1o	1	0	0	0	0
59	1p	1	0	0	0	0
59	1q	1	0	0	0	0
59	1s	1	0	0	1	0
59	1v	1	0	0	0	0
59	1x	8	0	0	1	0
59	1z	1	0	0	0	0
59	20	3	0	0	0	0
59	21	1	0	0	0	0
59	23	2	0	0	0	0
59	26	1	0	0	0	0
59	27	2	0	0	0	0
59	28	2	0	0	0	0
59	2A	813	0	0	62	0
59	2B	10	0	0	0	0
59	2D	16	0	0	1	0
59	2E	9	0	0	2	0
59	2F	5	0	0	0	0
59	2N	1	0	0	0	0
59	2O	3	0	0	0	0
59	2P	9	0	0	0	0
59	2Q	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	2R	3	0	0	0	0
59	2T	1	0	0	0	0
59	2U	3	0	0	0	0
59	2W	1	0	0	0	0
59	2X	2	0	0	0	0
59	2Y	1	0	0	1	0
59	2Z	4	0	0	2	0
59	2a	321	0	0	52	0
59	2d	1	0	0	0	0
59	2e	1	0	0	0	0
59	2i	2	0	0	0	0
59	2j	1	0	0	0	0
59	2l	1	0	0	0	0
59	2m	3	0	0	0	0
59	2p	1	0	0	0	0
59	2q	1	0	0	0	0
59	2t	4	0	0	0	0
59	2x	7	0	0	1	0
59	2z	1	0	0	0	0
All	All	288518	0	189963	4624	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 10.

All (4624) 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)
33:2b:92:TYR:CD1	33:2b:92:TYR:CG	1.83	1.60
33:2b:92:TYR:CG	33:2b:92:TYR:CD2	1.81	1.60
33:2b:92:TYR:CZ	33:2b:92:TYR:CE2	1.92	1.56
33:2b:92:TYR:CZ	33:2b:92:TYR:CE1	1.93	1.52
33:2b:151:GLY:N	33:2b:151:GLY:CA	1.80	1.45
33:2b:92:TYR:CZ	33:2b:151:GLY:N	1.88	1.37
33:2b:92:TYR:CE2	33:2b:151:GLY:N	1.92	1.37
33:2b:92:TYR:CE1	33:2b:151:GLY:N	1.94	1.36
33:2b:92:TYR:CD2	33:2b:92:TYR:CE2	2.18	1.32
33:2b:92:TYR:CD2	33:2b:151:GLY:N	2.05	1.25
33:2b:92:TYR:CD1	33:2b:151:GLY:N	2.10	1.20
33:2b:92:TYR:CD1	33:2b:92:TYR:CE1	2.29	1.19
33:2b:92:TYR:CG	33:2b:151:GLY:HA3	1.82	1.14
33:2b:92:TYR:CG	33:2b:151:GLY:N	2.20	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:92:TYR:CD1	33:2b:151:GLY:CA	2.35	1.08
33:2b:92:TYR:CG	33:2b:151:GLY:CA	2.41	1.03
32:2a:1145:C:H42	32:2a:1156:G:H1	1.05	0.99
32:1a:1480:A:H2	32:1a:1483:G:H1	1.11	0.97
1:2A:1828:U:H5'	3:2D:259:THR:HG22	1.47	0.96
33:2b:92:TYR:CD2	33:2b:151:GLY:CA	2.49	0.96
32:2a:976:G:H1	32:2a:1026:C:H42	1.06	0.94
32:2a:1480:A:H2	32:2a:1483:G:H1	1.11	0.94
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.49	0.94
38:1g:50:ILE:HD11	38:1g:58:PRO:HA	1.48	0.93
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.33	0.93
33:2b:92:TYR:CE1	33:2b:151:GLY:CA	2.52	0.93
44:2m:37:THR:HB	44:2m:55:ARG:HH12	1.33	0.92
1:2A:1098:C:H42	1:2A:1151:G:H1	1.12	0.92
55:1z:9:ARG:HB3	55:1z:10:PRO:HD3	1.51	0.92
32:2a:1145:C:N4	32:2a:1156:G:H1	1.67	0.91
32:2a:976:G:H1	32:2a:1026:C:N4	1.68	0.91
1:1A:353:A:H2	1:1A:1254:A:HO2'	0.94	0.90
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.36	0.90
33:1b:16:HIS:O	33:1b:18:GLY:N	2.04	0.90
33:2b:178:ARG:HH12	39:2h:68:ARG:HH22	1.16	0.90
1:1A:1735:A:H62	1:1A:1744:A:H2	1.15	0.90
1:1A:1828:U:H5'	3:1D:259:THR:HG22	1.52	0.90
33:2b:13:ALA:HA	33:2b:15:VAL:H	1.34	0.90
1:1A:786:U:OP2	59:1A:4101:HOH:O	1.90	0.89
33:2b:92:TYR:CD1	33:2b:150:SER:C	2.50	0.89
1:2A:2226:G:H3'	1:2A:2227:G:C8	2.07	0.89
1:2A:1248:A:H2	1:2A:1286:A:H62	1.20	0.89
1:1A:2465:G:OP1	59:1A:4102:HOH:O	1.91	0.89
1:1A:1000:G:OP2	12:1Q:14:ARG:NH2	2.06	0.88
36:1e:78:HIS:HD1	39:1h:104:ARG:HD2	1.37	0.88
54:2x:49:G:H1	54:2x:65:C:H42	1.18	0.88
1:1A:1355:G:OP2	29:17:9:ARG:NH1	2.07	0.88
1:1A:1316:G:OP2	59:1A:4103:HOH:O	1.92	0.87
1:2A:1735:A:H62	1:2A:1744:A:H2	1.23	0.87
29:17:24:THR:HG22	29:17:27:GLY:H	1.40	0.87
54:1x:47:U:H4'	54:1x:48:C:H5'	1.58	0.86
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.06	0.86
32:1a:543:A:OP1	36:1e:126:ARG:NH2	2.07	0.86
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.57	0.86
1:1A:2502:U:OP2	59:1A:4104:HOH:O	1.93	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:53:GLU:HB3	26:14:54:GLY:HA2	1.57	0.86
1:2A:267:G:HO2'	1:2A:268:G:H8	1.24	0.86
32:2a:953:A:H4'	32:2a:954:G:H5"	1.57	0.86
35:1d:53:ASP:HB3	35:1d:57:ARG:HH12	1.42	0.85
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.56	0.85
7:1H:3:ARG:HG2	7:1H:6:ARG:HG2	1.58	0.85
1:2A:655:A:OP1	11:2P:65:ARG:NH1	2.09	0.85
15:1T:54:ARG:HA	15:1T:59:THR:HB	1.60	0.84
1:1A:536:G:N7	59:1A:4108:HOH:O	2.08	0.84
33:2b:92:TYR:CG	33:2b:150:SER:C	2.55	0.84
1:1A:2100:U:OP1	23:11:21:ARG:NH2	2.11	0.84
23:11:21:ARG:HG2	23:11:21:ARG:HH11	1.42	0.83
33:2b:92:TYR:CD1	33:2b:151:GLY:HA2	2.12	0.83
1:1A:2330:G:N7	59:1A:4123:HOH:O	2.10	0.83
1:2A:2816:G:N1	1:2A:2901:G:O6	2.10	0.83
32:2a:981:G:H2'	32:2a:982:G:H8	1.44	0.83
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.60	0.83
32:2a:932:G:H21	32:2a:1209:A:H62	1.25	0.83
6:2G:80:PHE:O	6:2G:82:LEU:N	2.11	0.82
32:1a:1141:C:H5	32:1a:1163:G:H1	1.24	0.82
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.41	0.82
1:2A:1067:G:H22	1:2A:1187:A:H2	1.27	0.82
1:1A:1303:C:OP1	59:1A:4105:HOH:O	1.97	0.82
33:2b:92:TYR:CE1	33:2b:151:GLY:HA2	2.14	0.82
32:2a:386:C:O3'	47:2p:28:ARG:NH2	2.13	0.81
15:2T:54:ARG:HA	15:2T:59:THR:HB	1.62	0.81
32:2a:488:C:OP1	59:2a:3301:HOH:O	1.98	0.81
42:2k:48:ILE:O	42:2k:50:TYR:N	2.12	0.81
1:2A:1355:G:OP2	29:27:9:ARG:NH1	2.14	0.81
3:2D:276:LYS:HD3	3:2D:276:LYS:H	1.44	0.81
41:2j:5:ARG:N	41:2j:73:ASP:OD1	2.14	0.81
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.61	0.81
1:1A:550:A:OP1	59:1A:4106:HOH:O	1.98	0.81
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.13	0.81
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.43	0.81
1:2A:2226:G:H3'	1:2A:2227:G:H8	1.40	0.81
32:1a:953:A:H4'	32:1a:954:G:H5"	1.63	0.81
32:2a:1435:G:OP1	51:2t:39:LYS:NZ	2.14	0.81
1:1A:534:C:OP1	59:1A:4108:HOH:O	1.98	0.80
18:1W:14:PRO:HG2	18:1W:78:GLU:HG2	1.63	0.80
33:2b:92:TYR:CZ	33:2b:151:GLY:CA	2.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2815:G:H2'	1:2A:2816:G:H8	1.46	0.80
32:2a:548:C:O2'	39:2h:91:ARG:NH2	2.14	0.80
1:1A:475:G:O6	59:1A:4107:HOH:O	1.98	0.80
32:2a:900:G:H4'	36:2e:20:GLN:HA	1.62	0.80
33:2b:92:TYR:CE2	33:2b:151:GLY:CA	2.64	0.80
1:2A:141:G:H4'	19:2X:35:THR:HG21	1.61	0.80
1:2A:1188:A:OP1	9:2N:25:ARG:NH2	2.15	0.80
32:1a:951:G:OP1	41:1j:57:LYS:NZ	2.15	0.80
1:2A:786:U:OP2	59:2A:3602:HOH:O	1.99	0.80
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.62	0.80
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.64	0.80
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.64	0.80
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.14	0.80
6:1G:49:ASP:O	6:1G:51:ARG:N	2.15	0.79
35:2d:100:ARG:NH1	35:2d:137:SER:OG	2.15	0.79
1:1A:1000:G:O6	59:1A:4109:HOH:O	1.99	0.79
26:14:57:GLU:HB3	26:14:58:ARG:HG2	1.63	0.79
2:2B:4:C:H42	2:2B:117:G:H1	1.28	0.79
1:1A:1693:G:OP1	59:1A:4103:HOH:O	2.00	0.79
1:2A:673:G:H4'	30:28:46:ARG:HH22	1.48	0.79
33:2b:92:TYR:CD2	33:2b:150:SER:C	2.59	0.79
32:2a:951:G:OP1	41:2j:57:LYS:NZ	2.15	0.79
1:2A:1316:G:OP2	59:2A:3601:HOH:O	1.98	0.79
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.65	0.79
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.28	0.79
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.16	0.78
1:2A:1404:A:N6	1:2A:1417:U:O4	2.16	0.78
1:1A:1813:A:OP1	59:1A:4101:HOH:O	2.01	0.78
4:1E:54:GLN:HE21	4:1E:55:ASN:H	1.30	0.78
1:1A:2221:C:OP1	59:1A:4110:HOH:O	2.02	0.78
34:2c:151:VAL:HG13	34:2c:200:ALA:HB2	1.63	0.78
1:2A:1310:A:OP2	59:2A:3603:HOH:O	2.01	0.78
2:2B:22:U:H3	2:2B:61:G:H1	1.31	0.78
1:1A:1694:C:OP1	59:1A:4103:HOH:O	2.02	0.78
6:2G:41:GLN:HE22	6:2G:153:ARG:HB3	1.48	0.78
1:2A:8:U:H3	1:2A:2640:A:H2	1.28	0.78
1:2A:1813:A:OP1	59:2A:3602:HOH:O	2.01	0.78
6:2G:13:GLU:O	6:2G:15:VAL:N	2.17	0.78
15:1T:41:ARG:NH2	32:1a:342:G:OP1	2.17	0.78
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.66	0.78
1:2A:1649:C:OP2	59:2A:3605:HOH:O	2.02	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2441:A:OP2	59:2A:3604:HOH:O	2.02	0.77
1:2A:2588:A:H5'	27:25:3:LYS:HD2	1.67	0.77
5:1F:30:PRO:HB3	11:1P:1:MET:HE1	1.67	0.77
32:2a:1128:C:H4'	32:2a:1129:A:H5'	1.64	0.77
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.66	0.77
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.47	0.77
8:2I:65:ALA:HB1	8:2I:136:VAL:HG11	1.66	0.77
32:2a:1499:G:N3	59:2a:3328:HOH:O	2.18	0.77
1:1A:2466:G:OP2	59:1A:4111:HOH:O	2.03	0.77
1:1A:1248:A:H2	1:1A:1286:A:H62	1.31	0.77
32:1a:188:C:O2	32:1a:192:G:N1	2.18	0.77
1:2A:1064:U:H3	1:2A:1187:A:H62	1.32	0.77
1:2A:2310:G:H2'	1:2A:2311:G:H8	1.50	0.77
37:1f:18:GLN:HA	37:1f:21:LEU:HD12	1.67	0.76
1:1A:2456:G:OP1	5:1F:74:ARG:NH2	2.18	0.76
1:2A:117:U:OP2	59:2A:3607:HOH:O	2.03	0.76
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.18	0.76
34:2c:30:ARG:HH21	45:2n:38:GLY:HA2	1.51	0.76
1:1A:893:U:O4	1:1A:977:A:N6	2.19	0.76
36:2e:100:VAL:HG13	36:2e:107:ARG:HH21	1.51	0.76
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.68	0.75
32:2a:507:A:H61	43:2l:92:ASP:HB2	1.49	0.75
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.65	0.75
32:2a:1101:C:OP1	40:2i:104:ARG:NH1	2.19	0.75
2:1B:58:A:OP2	59:1B:301:HOH:O	2.03	0.75
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.68	0.75
1:1A:2795:G:N7	59:1A:4142:HOH:O	2.18	0.75
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.20	0.75
5:2F:20:LEU:HD13	5:2F:21:ALA:H	1.52	0.75
10:2O:1:MET:HE3	10:2O:67:LYS:HG2	1.68	0.75
44:2m:37:THR:O	44:2m:55:ARG:NH2	2.19	0.75
1:2A:957:C:OP1	12:2Q:8:LYS:NZ	2.20	0.75
1:2A:2815:G:H2'	1:2A:2816:G:C8	2.21	0.75
1:1A:2768:U:O4	1:1A:2770:A:N6	2.20	0.74
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.20	0.74
32:1a:648:G:H22	32:1a:725:G:H1	1.35	0.74
1:1A:2586:C:OP2	59:1A:4112:HOH:O	2.04	0.74
1:2A:1377:G:OP1	59:2A:3606:HOH:O	2.03	0.74
11:2P:65:ARG:HG3	30:28:25:MET:HG3	1.69	0.74
31:19:20:HIS:O	59:19:5001:HOH:O	2.05	0.74
1:2A:1039:C:OP1	16:2U:53:ARG:NH2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:516:A:O2'	32:2a:517:A:OP1	2.05	0.74
1:2A:1694:C:OP1	59:2A:3601:HOH:O	2.06	0.74
32:2a:428:A:OP2	59:2a:3303:HOH:O	2.06	0.74
33:2b:92:TYR:CE1	33:2b:150:SER:C	2.65	0.74
33:2b:92:TYR:CG	33:2b:150:SER:O	2.41	0.74
40:1i:3:GLN:HG2	40:1i:20:ARG:HE	1.52	0.74
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.70	0.74
32:2a:1202:G:H21	50:2s:54:GLY:HA2	1.52	0.74
1:2A:900:G:H2'	1:2A:901:G:H8	1.53	0.74
15:2T:41:ARG:NH2	32:2a:342:G:OP1	2.18	0.73
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.70	0.73
1:1A:2458:G:OP2	59:1A:4114:HOH:O	2.05	0.73
22:10:11:ARG:O	22:10:14:ARG:NH2	2.21	0.73
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.71	0.73
34:2c:124:ILE:HD11	34:2c:189:ALA:HB1	1.68	0.73
1:1A:2753:A:OP1	31:19:22:ARG:NH2	2.20	0.73
1:2A:777:C:OP1	59:2A:3609:HOH:O	2.06	0.73
32:2a:891:A:OP2	59:2a:3302:HOH:O	2.06	0.73
32:1a:423:U:OP1	35:1d:13:ARG:NH2	2.21	0.73
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.70	0.73
1:2A:10:G:H2'	1:2A:11:U:H5"	1.70	0.73
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	1.71	0.73
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.70	0.73
1:2A:2643:A:HO2'	1:2A:2820:G:HO2'	1.33	0.73
14:2S:10:ARG:NH2	14:2S:91:PRO:O	2.20	0.73
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.71	0.73
1:1A:1479:A:H61	1:1A:1604:A:H62	1.34	0.73
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.71	0.73
1:2A:183:A:N7	59:2A:3636:HOH:O	2.19	0.73
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.22	0.73
32:2a:36:G:O2'	43:2l:118:SER:O	2.05	0.73
1:1A:1552:A:HO2'	1:1A:1553:A:H8	1.37	0.73
32:1a:338:C:H2'	32:1a:339:U:H5"	1.71	0.73
1:2A:2600:A:OP1	59:2A:3608:HOH:O	2.06	0.73
33:2b:92:TYR:CD2	33:2b:151:GLY:HA3	2.21	0.73
32:1a:532:G:OP1	59:1a:2001:HOH:O	2.05	0.73
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	1.71	0.73
1:1A:1188:A:OP1	9:1N:25:ARG:NH2	2.22	0.72
32:1a:372:G:H5"	47:1p:5:ARG:HD3	1.71	0.72
41:1j:38:ILE:HD11	41:1j:71:LEU:HD23	1.71	0.72
22:20:11:ARG:O	22:20:14:ARG:NH2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1385:C:OP2	59:2a:3304:HOH:O	2.07	0.72
1:1A:1038:G:OP1	16:1U:50:ARG:NH2	2.20	0.72
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.70	0.72
1:1A:1514:C:OP1	59:1A:4116:HOH:O	2.08	0.72
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.69	0.72
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.71	0.72
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.72	0.72
1:2A:2067:G:H5'	27:25:19:ARG:HA	1.69	0.72
7:2H:3:ARG:HB3	7:2H:3:ARG:HH11	1.55	0.72
33:2b:13:ALA:HA	33:2b:15:VAL:N	2.05	0.72
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.71	0.72
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.55	0.72
26:24:46:GLN:O	26:24:48:ARG:N	2.22	0.72
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.71	0.72
40:1i:104:ARG:HH11	40:1i:104:ARG:HG3	1.54	0.72
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.69	0.72
40:1i:7:THR:O	40:1i:83:ARG:NH1	2.22	0.72
1:2A:1104:G:H3'	1:2A:1105:U:H6	1.55	0.72
1:2A:1360:C:OP2	59:2A:3606:HOH:O	2.08	0.72
32:1a:516:A:O2'	32:1a:517:A:OP1	2.08	0.72
41:1j:55:LYS:O	41:1j:57:LYS:N	2.23	0.71
1:2A:2328:C:H2'	1:2A:2329:G:H8	1.55	0.71
1:2A:2800:C:OP1	4:2E:61:ARG:NH2	2.23	0.71
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.55	0.71
1:2A:680:C:N4	1:2A:697:G:O6	2.17	0.71
1:2A:1185:U:OP2	9:2N:63:THR:OG1	2.08	0.71
1:2A:2694:C:OP1	15:2T:53:ARG:NH2	2.22	0.71
32:2a:66:U:O2'	59:2a:3306:HOH:O	2.08	0.71
32:2a:640:C:O2'	46:2o:28:GLN:NE2	2.22	0.71
43:2l:70:ILE:HD13	43:2l:77:LEU:HD12	1.71	0.71
1:1A:2561:G:OP1	59:1A:4117:HOH:O	2.08	0.71
41:1j:49:VAL:HG23	45:1n:41:ARG:HD2	1.73	0.71
43:1l:33:ARG:HD3	43:1l:62:SER:HB3	1.71	0.71
1:2A:552:A:O2'	1:2A:553:A:H5'	1.91	0.71
18:2W:14:PRO:HG2	18:2W:78:GLU:HG2	1.71	0.71
32:2a:1038:A:N7	32:2a:1182:C:N4	2.35	0.71
32:2a:1112:C:H42	32:2a:1126:G:H1	1.38	0.71
47:1p:53:VAL:HG13	47:1p:79:VAL:HG22	1.73	0.71
1:2A:1035:A:OP2	59:2A:3610:HOH:O	2.09	0.71
32:1a:460:G:H2'	32:1a:461:G:C8	2.25	0.71
32:1a:1397:U:H3	32:1a:1464:G:H1	1.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1154:C:H3'	1:2A:1155:G:C8	2.26	0.71
32:2a:506:C:H41	43:2l:53:ARG:HH22	1.36	0.71
32:2a:752:A:OP2	59:2a:3307:HOH:O	2.08	0.71
54:2x:49:G:H1	54:2x:65:C:N4	1.88	0.71
1:1A:725:C:OP1	59:1A:4115:HOH:O	2.08	0.71
1:1A:894:G:OP1	59:1A:4119:HOH:O	2.08	0.71
1:1A:2824:C:H5'	27:15:29:THR:HG21	1.73	0.71
32:2a:208:C:H42	32:2a:212:G:H1	1.38	0.71
1:1A:655:A:OP1	11:1P:65:ARG:NH1	2.21	0.71
32:2a:442:G:OP2	59:2a:3305:HOH:O	2.07	0.71
39:2h:113:SER:H	39:2h:134:ILE:HD13	1.56	0.71
1:2A:2053:G:N7	59:2A:3654:HOH:O	2.24	0.70
4:2E:132:HIS:NE2	59:2E:402:HOH:O	2.23	0.70
1:1A:1015:C:OP2	59:1A:4121:HOH:O	2.09	0.70
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.24	0.70
2:1B:23:G:O6	59:1B:302:HOH:O	2.07	0.70
59:1E:402:HOH:O	13:1R:3:HIS:NE2	2.24	0.70
23:11:23:LYS:HB3	23:11:29:GLY:HA3	1.73	0.70
2:2B:11:C:OP2	2:2B:12:C:N4	2.17	0.70
1:1A:138:A:H8	1:1A:1453:C:HO2'	1.40	0.70
1:1A:869:G:OP1	59:1A:4120:HOH:O	2.08	0.70
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.10	0.70
32:2a:648:G:H22	32:2a:725:G:H1	1.36	0.70
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.88	0.70
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.73	0.70
6:2G:33:ARG:NH1	6:2G:33:ARG:HB2	2.07	0.70
32:2a:1292:G:H5'	44:2m:77:ASN:HD21	1.56	0.70
32:2a:1298:G:N2	32:2a:1301:A:OP2	2.25	0.70
1:2A:2517:U:OP1	4:2E:144:ARG:NH2	2.25	0.70
32:2a:1116:G:H1	32:2a:1124:C:H42	1.38	0.70
1:1A:893:U:OP2	59:1A:4122:HOH:O	2.09	0.70
1:1A:1218:A:H4'	1:1A:1219:U:OP1	1.92	0.70
1:1A:2024:G:OP2	59:1A:4124:HOH:O	2.10	0.70
4:1E:127:ASP:OD2	59:1E:401:HOH:O	2.10	0.70
51:2t:16:HIS:O	51:2t:19:SER:OG	2.09	0.70
1:1A:553:A:N1	59:1A:4190:HOH:O	2.25	0.70
1:1A:1354:G:H4'	29:17:7:PRO:HB2	1.72	0.70
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.73	0.70
33:1b:15:VAL:HG21	33:1b:209:ARG:HB3	1.73	0.70
1:1A:1021:C:OP1	59:1A:4118:HOH:O	2.08	0.70
34:1c:35:GLU:OE2	34:1c:59:ARG:NH2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1070:G:O2'	59:2A:3612:HOH:O	2.10	0.70
1:1A:271:U:OP1	8:1I:50:ARG:NH2	2.25	0.69
32:1a:135:A:OP2	59:1a:2002:HOH:O	2.09	0.69
32:1a:582:U:H2'	32:1a:583:C:H6	1.55	0.69
35:1d:188:LEU:HD23	35:1d:188:LEU:H	1.57	0.69
14:2S:35:ILE:HD13	14:2S:97:ARG:HH21	1.57	0.69
32:2a:348:C:OP2	59:2a:3309:HOH:O	2.10	0.69
6:2G:43:LEU:HD12	6:2G:45:GLU:HG3	1.73	0.69
8:2I:129:THR:HG22	8:2I:139:GLN:HE22	1.56	0.69
1:1A:2298:A:H62	1:1A:2355:U:H3	1.38	0.69
32:1a:516:A:H2	32:1a:1188:G:H21	1.40	0.69
55:1z:11:ARG:HB3	55:1z:12:PRO:HD2	1.74	0.69
1:1A:2816:G:N1	1:1A:2901:G:O6	2.18	0.69
5:1F:89:VAL:O	59:1F:401:HOH:O	2.11	0.69
26:24:59:PHE:HA	26:24:61:ARG:N	2.07	0.69
1:1A:426:G:N7	59:1A:4181:HOH:O	2.24	0.69
32:1a:1093:A:OP2	59:1a:2003:HOH:O	2.10	0.69
1:2A:934:C:OP1	44:2m:93:ARG:NH1	2.24	0.69
32:2a:1109:U:O2'	59:2a:3311:HOH:O	2.11	0.69
1:1A:929:G:O6	1:1A:938:C:N4	2.25	0.69
26:14:53:GLU:OE2	44:1m:65:LYS:NZ	2.25	0.69
33:1b:63:MET:HG3	33:1b:225:ALA:HB1	1.72	0.69
32:2a:192:G:OP2	59:2a:3310:HOH:O	2.10	0.69
32:2a:1220:A:OP2	59:2a:3308:HOH:O	2.09	0.69
32:2a:1117:G:N2	32:2a:1119:U:O4	2.24	0.69
4:1E:110:GLY:O	59:1E:402:HOH:O	2.11	0.69
32:1a:1338:G:H2'	32:1a:1339:A:C8	2.27	0.69
36:1e:100:VAL:HG22	36:1e:118:ILE:HG22	1.75	0.69
32:2a:976:G:N2	32:2a:1026:C:N3	2.32	0.69
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	1.74	0.69
1:2A:1066:A:H62	1:2A:1185:U:H3	1.38	0.69
17:2V:6:LYS:HB2	17:2V:38:LEU:HD21	1.74	0.69
34:2c:43:LEU:HD22	34:2c:47:LEU:HD13	1.73	0.69
51:2t:14:LYS:HG2	51:2t:18:GLN:HE21	1.58	0.69
32:1a:1069:U:H3	32:1a:1082:G:H22	1.38	0.69
32:1a:1171:C:OP1	41:1j:51:ARG:NH2	2.23	0.69
38:1g:152:ALA:HB1	38:1g:155:ARG:HH21	1.57	0.69
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.75	0.69
1:2A:816:G:OP2	59:2A:3614:HOH:O	2.11	0.69
1:2A:2456:G:OP1	5:2F:74:ARG:NH2	2.24	0.69
32:2a:981:G:H2'	32:2a:982:G:C8	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:92:TYR:H	33:2b:151:GLY:HA3	1.58	0.69
1:1A:2007:A:OP1	59:1A:4125:HOH:O	2.11	0.68
32:1a:258:A:H2'	32:1a:259:A:C8	2.28	0.68
32:1a:900:G:H4'	36:1e:20:GLN:HA	1.75	0.68
1:2A:2595:U:O4	59:2A:3613:HOH:O	2.11	0.68
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.11	0.68
32:2a:859:G:P	43:2l:12:ARG:HH22	2.16	0.68
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.76	0.68
32:1a:1164:G:H4'	32:1a:1165:A:H5'	1.73	0.68
40:1i:23:ASN:HD21	40:1i:25:LYS:HG2	1.58	0.68
2:2B:8:U:H3	2:2B:113:G:H1	1.41	0.68
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.26	0.68
12:1Q:59:ARG:HA	12:1Q:60:ARG:NH2	2.07	0.68
36:1e:75:THR:OG1	36:1e:76:ILE:N	2.25	0.68
1:2A:163:G:O6	59:2A:3611:HOH:O	2.09	0.68
1:2A:829:A:OP2	59:2A:3608:HOH:O	2.10	0.68
33:1b:21:ARG:O	33:1b:23:ARG:N	2.25	0.68
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.26	0.68
1:2A:2405:C:OP2	30:28:30:ARG:NH1	2.25	0.68
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.75	0.68
24:22:35:LEU:HD11	24:22:49:LYS:HB3	1.75	0.68
32:2a:1300:A:OP1	50:2s:3:ARG:NH1	2.26	0.68
37:1f:99:ALA:HB1	49:1r:23:LYS:HE3	1.76	0.68
1:1A:2395:G:OP2	22:10:55:ARG:NH1	2.27	0.68
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.58	0.68
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.75	0.68
21:2Z:94:GLU:OE2	59:2Z:5001:HOH:O	2.11	0.68
6:1G:50:ALA:O	6:1G:52:ILE:N	2.26	0.68
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.42	0.68
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.25	0.68
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.27	0.68
1:2A:1092:G:H1'	1:2A:1155:G:H22	1.59	0.68
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.56	0.68
1:1A:1229:C:OP2	59:1A:4126:HOH:O	2.11	0.68
1:2A:2058:G:O6	59:2A:3615:HOH:O	2.12	0.68
6:2G:108:ASN:HA	26:24:37:SER:HB2	1.76	0.68
32:2a:657:G:O3'	37:2f:87:ARG:NH2	2.27	0.68
39:2h:51:VAL:HG21	39:2h:60:ARG:HB2	1.76	0.68
38:1g:16:LEU:HD21	40:1i:45:ALA:HB2	1.76	0.68
21:2Z:90:VAL:O	59:2Z:5002:HOH:O	2.11	0.68
32:2a:657:G:H2'	32:2a:658:G:C8	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.23	0.67
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.77	0.67
32:2a:1480:A:H2	32:2a:1483:G:N1	1.89	0.67
2:2B:43:C:O2	6:2G:95:ARG:NH1	2.25	0.67
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.26	0.67
1:1A:8:U:N3	1:1A:2640:A:H2	1.92	0.67
7:1H:175:LYS:O	59:1H:301:HOH:O	2.11	0.67
32:1a:661:U:H3	32:1a:697:G:H22	1.43	0.67
32:1a:1374:U:H2'	32:1a:1375:G:C8	2.29	0.67
1:2A:330:G:H21	1:2A:353:A:H62	1.41	0.67
1:2A:1494:G:O2'	1:2A:1574:A:N1	2.26	0.67
42:2k:98:LEU:O	42:2k:101:SER:OG	2.12	0.67
1:1A:481:C:H4'	59:1A:4893:HOH:O	1.93	0.67
26:14:44:THR:O	26:14:46:GLN:N	2.27	0.67
32:1a:626:A:N3	39:1h:113:SER:OG	2.26	0.67
32:1a:1480:A:H2	32:1a:1483:G:N1	1.88	0.67
32:2a:544:U:O2'	32:2a:545:U:OP2	2.10	0.67
1:1A:8:U:H3	1:1A:2640:A:H2	1.43	0.67
2:1B:102:A:N7	59:1B:305:HOH:O	2.27	0.67
8:1I:48:GLU:HG2	8:1I:52:ARG:HH22	1.59	0.67
26:14:46:GLN:O	26:14:48:ARG:N	2.27	0.67
32:1a:584:C:H2'	32:1a:585:C:C6	2.29	0.67
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.12	0.67
42:1k:59:TYR:CZ	42:1k:63:LEU:HD11	2.28	0.67
32:2a:460:G:H2'	32:2a:461:G:H8	1.59	0.67
40:2i:116:LYS:HD2	40:2i:122:ALA:HA	1.76	0.67
14:1S:59:LYS:HD2	14:1S:60:GLY:N	2.09	0.67
32:1a:571:G:N7	59:1a:2031:HOH:O	2.27	0.67
1:2A:721:A:OP1	5:2F:63:LYS:NZ	2.26	0.67
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	1.76	0.67
33:2b:92:TYR:CD1	33:2b:151:GLY:HA3	2.28	0.67
34:2c:12:LEU:HD23	34:2c:16:ARG:HB3	1.76	0.67
33:1b:15:VAL:HG11	33:1b:209:ARG:HG2	1.76	0.67
50:1s:3:ARG:NH1	50:1s:8:GLY:O	2.28	0.67
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.77	0.67
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.75	0.67
1:2A:894:G:H2'	1:2A:895:A:C8	2.30	0.67
15:2T:65:LYS:HE2	15:2T:67:SER:HB2	1.75	0.67
48:1q:95:TYR:HA	48:1q:98:LEU:HD22	1.77	0.67
1:1A:1989:G:OP1	59:1A:4130:HOH:O	2.13	0.66
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:29:GLY:HA3	59:1E:410:HOH:O	1.94	0.66
28:16:13:CYS:SG	28:16:47:THR:HG21	2.35	0.66
32:1a:971:G:H1	32:1a:1028:C:H42	1.43	0.66
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.42	0.66
34:2c:186:PHE:CZ	34:2c:200:ALA:HB3	2.30	0.66
44:2m:22:ILE:HG23	44:2m:67:GLU:HG2	1.75	0.66
2:1B:76:G:O6	59:1B:303:HOH:O	2.12	0.66
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.76	0.66
32:2a:1204:G:O6	59:2a:3312:HOH:O	2.11	0.66
38:2g:122:HIS:HA	38:2g:125:MET:HE2	1.76	0.66
32:2a:898:U:OP2	59:2a:3313:HOH:O	2.14	0.66
47:2p:1:MET:SD	47:2p:3:LYS:NZ	2.68	0.66
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.60	0.66
32:2a:1173:A:OP1	34:2c:3:ASN:ND2	2.28	0.66
43:2l:75:HIS:HD2	43:2l:77:LEU:H	1.41	0.66
32:1a:1043:C:C5	34:1c:2:GLY:HA3	2.30	0.66
1:2A:2284:A:H2'	1:2A:2285:A:C8	2.31	0.66
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.78	0.66
1:1A:638:G:OP1	59:1A:4129:HOH:O	2.13	0.66
12:1Q:32:TYR:CE1	12:1Q:133:ARG:HG3	2.30	0.66
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.59	0.66
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.78	0.66
15:2T:55:ASN:H	15:2T:59:THR:HG22	1.60	0.66
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.77	0.66
33:2b:92:TYR:CE2	33:2b:152:PHE:N	2.64	0.66
1:1A:1543:C:OP1	59:1A:4131:HOH:O	2.14	0.66
1:1A:2364:G:N7	59:1A:4209:HOH:O	2.27	0.66
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.76	0.66
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.77	0.66
32:1a:141:G:N2	32:1a:172:C:N3	2.44	0.66
1:2A:2626:U:OP1	59:2A:3603:HOH:O	2.12	0.66
32:2a:1112:C:N4	32:2a:1126:G:H1	1.94	0.66
20:2Y:94:LYS:NZ	59:2Y:601:HOH:O	2.28	0.66
32:2a:57:U:H2'	32:2a:58:G:H8	1.61	0.66
32:2a:868:G:O2'	32:2a:884:G:O6	2.13	0.66
32:2a:1311:A:OP2	52:2u:7:ARG:NH2	2.26	0.66
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.43	0.66
1:1A:932:C:H2'	1:1A:933:A:H5"	1.78	0.66
1:1A:1312:U:OP1	59:1A:4128:HOH:O	2.12	0.66
35:2d:100:ARG:HH22	35:2d:118:ARG:HH12	1.43	0.66
45:2n:17:LYS:H	45:2n:17:LYS:HE2	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:69:LYS:NZ	59:1V:301:HOH:O	2.29	0.65
32:1a:796:C:N3	59:1a:2036:HOH:O	2.29	0.65
1:2A:1198:C:OP1	16:2U:92:ARG:NH1	2.29	0.65
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.11	0.65
34:2c:181:ASN:HD21	34:2c:204:LEU:HD12	1.60	0.65
44:2m:60:VAL:HG23	44:2m:64:TRP:HE3	1.59	0.65
1:1A:1377:G:OP1	59:1A:4132:HOH:O	2.14	0.65
32:1a:110:A:H61	32:1a:309:A:H1'	1.61	0.65
32:1a:343:G:C2	32:1a:344:G:H1'	2.31	0.65
51:1t:60:GLU:HG3	51:1t:85:MET:HE3	1.78	0.65
1:2A:1421:C:OP2	59:2A:3616:HOH:O	2.13	0.65
4:2E:9:VAL:HG13	4:2E:25:VAL:O	1.96	0.65
7:2H:144:VAL:O	7:2H:148:ILE:HG12	1.97	0.65
32:2a:891:A:OP1	59:2a:3314:HOH:O	2.14	0.65
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.24	0.65
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.31	0.65
33:1b:178:ARG:HH22	39:1h:68:ARG:HH12	1.43	0.65
51:1t:10:LEU:HD23	51:1t:11:SER:H	1.61	0.65
21:2Z:70:LEU:HG	21:2Z:91:LEU:HD21	1.77	0.65
1:1A:2649:G:P	4:1E:82:ARG:HH22	2.19	0.65
32:1a:460:G:H2'	32:1a:461:G:H8	1.60	0.65
32:1a:611:G:H2'	32:1a:612:G:H8	1.62	0.65
32:2a:571:G:OP2	59:2a:3315:HOH:O	2.14	0.65
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.30	0.65
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.22	0.65
24:22:32:LEU:HD11	24:22:54:LYS:HG3	1.79	0.65
32:2a:109:G:OP1	59:2a:3316:HOH:O	2.15	0.65
36:2e:36:ASP:O	36:2e:38:GLN:N	2.27	0.65
1:1A:1089:G:OP2	59:1A:4133:HOH:O	2.14	0.65
1:1A:2493:G:OP1	59:1A:4134:HOH:O	2.14	0.65
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.61	0.65
1:2A:1042:G:OP1	16:2U:92:ARG:HG2	1.97	0.65
12:2Q:32:TYR:CE1	12:2Q:133:ARG:HG3	2.32	0.65
23:21:21:ARG:HD3	23:21:35:THR:HG21	1.78	0.65
32:2a:1112:C:H2'	32:2a:1122:G:N7	2.11	0.65
36:2e:36:ASP:C	36:2e:38:GLN:H	2.05	0.65
38:2g:47:CYS:HB3	38:2g:58:PRO:HB3	1.79	0.65
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.78	0.65
1:2A:2125:G:H22	1:2A:2207:G:H1'	1.62	0.65
32:2a:1134:A:HO2'	32:2a:1135:A:H8	1.44	0.65
1:1A:2253:G:OP1	59:1A:4115:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:6:C:H42	2:2B:115:G:H1	1.43	0.65
32:2a:1154:C:H2'	32:2a:1155:G:C8	2.32	0.65
26:14:46:GLN:HB2	26:14:48:ARG:HE	1.61	0.65
32:1a:459:G:H2'	32:1a:460:G:H8	1.62	0.65
32:1a:1296:C:OP2	50:1s:4:SER:OG	2.14	0.65
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.78	0.65
1:2A:181:U:OP2	59:2A:3621:HOH:O	2.15	0.65
1:2A:1828:U:OP2	3:2D:274:ARG:NH2	2.29	0.65
1:2A:2726:G:OP2	59:2A:3619:HOH:O	2.14	0.65
4:2E:111:ARG:HG3	4:2E:160:TYR:CD2	2.31	0.65
32:2a:1485:A:N6	32:2a:1506:U:O4	2.17	0.65
36:2e:52:PRO:HG2	36:2e:53:LEU:HD12	1.79	0.65
41:2j:38:ILE:HG12	41:2j:71:LEU:O	1.97	0.65
1:2A:1280:G:OP1	59:2A:3617:HOH:O	2.13	0.64
32:2a:898:U:H2'	32:2a:899:U:C6	2.32	0.64
32:2a:1145:C:N3	32:2a:1156:G:N2	2.38	0.64
32:1a:810:C:H4'	39:1h:12:ARG:HD3	1.79	0.64
1:2A:241:C:OP2	30:28:5:LYS:NZ	2.24	0.64
1:2A:533:C:OP1	59:2A:3618:HOH:O	2.14	0.64
1:2A:1111:U:N3	1:2A:1114:A:OP2	2.25	0.64
1:2A:2622:U:C4	27:25:3:LYS:HG2	2.32	0.64
7:2H:11:VAL:HG13	7:2H:15:VAL:HG22	1.80	0.64
21:2Z:134:PRO:HG3	21:2Z:161:VAL:HG21	1.78	0.64
1:1A:1379:G:N7	59:1A:4221:HOH:O	2.30	0.64
1:1A:1698:A:N6	59:1R:301:HOH:O	2.31	0.64
42:1k:99:GLN:O	59:1k:5001:HOH:O	2.15	0.64
48:1q:67:LYS:O	48:1q:69:LYS:N	2.30	0.64
1:2A:1455:G:H2'	1:2A:1456:C:C6	2.32	0.64
32:2a:46:U:H2'	32:2a:47:G:C8	2.32	0.64
32:2a:980:G:H3'	32:2a:981:G:H4'	1.80	0.64
54:2x:40:C:H2'	54:2x:41:C:H6	1.63	0.64
1:1A:288:G:N3	59:1A:4136:HOH:O	2.30	0.64
32:1a:584:C:H2'	32:1a:585:C:H6	1.61	0.64
32:1a:638:G:OP2	59:1a:2004:HOH:O	2.13	0.64
1:2A:2043:U:OP1	59:2A:3620:HOH:O	2.15	0.64
32:2a:1359:U:H2'	32:2a:1360:A:H8	1.61	0.64
38:2g:113:GLU:HB2	38:2g:119:ARG:HG2	1.79	0.64
4:1E:181:LEU:HD21	15:1T:6:LEU:HD12	1.79	0.64
11:2P:95:VAL:HG12	11:2P:123:LEU:HD22	1.78	0.64
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.78	0.64
32:1a:265:C:H2'	32:1a:266:A:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:459:G:H2'	32:1a:460:G:C8	2.33	0.64
32:1a:1259:C:O2'	32:1a:1261:A:H1'	1.96	0.64
54:1x:8:4SU:O5'	54:1x:8:4SU:H6	1.98	0.64
6:2G:115:ARG:HG2	6:2G:115:ARG:HH11	1.63	0.64
1:1A:1360:C:OP2	59:1A:4132:HOH:O	2.14	0.64
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.80	0.64
32:1a:59:C:O2'	32:1a:384:G:N7	2.29	0.64
31:19:19:ARG:NH2	59:19:5002:HOH:O	2.08	0.64
32:1a:544:U:O2'	32:1a:545:U:OP2	2.14	0.64
32:1a:952:A:OP2	45:1n:41:ARG:NH1	2.30	0.64
1:2A:1638:G:H2'	1:2A:1639:G:C8	2.33	0.64
7:2H:103:LEU:HB3	7:2H:115:VAL:HG13	1.78	0.64
32:2a:57:U:H2'	32:2a:58:G:C8	2.32	0.64
33:2b:108:ILE:H	33:2b:108:ILE:HD13	1.61	0.64
47:1p:75:ARG:O	47:1p:77:ALA:N	2.23	0.64
1:2A:2368:U:OP1	22:20:20:ARG:NH1	2.29	0.64
3:2D:238:GLY:O	3:2D:239:ARG:HB2	1.96	0.64
32:2a:1130:C:HO2'	40:2i:5:TYR:HH	1.44	0.64
32:1a:859:G:P	43:1l:12:ARG:HH22	2.21	0.64
32:1a:1418:G:H2'	32:1a:1419:U:C6	2.32	0.64
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.79	0.64
1:2A:1450:U:H2'	1:2A:1451:U:C6	2.32	0.64
1:2A:2489:A:OP2	31:29:2:LYS:NZ	2.24	0.64
1:1A:1934:A:N6	32:1a:1472:G:OP1	2.31	0.63
1:1A:2210:U:H2'	1:1A:2211:G:H8	1.62	0.63
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.81	0.63
10:1O:48:PRO:HB3	32:1a:1405:G:H5'	1.80	0.63
32:1a:78:G:H1	32:1a:86:U:H3	1.46	0.63
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.80	0.63
35:1d:100:ARG:HH22	35:1d:118:ARG:HH12	1.46	0.63
21:2Z:157:LEU:HD11	21:2Z:163:LEU:HD13	1.80	0.63
1:1A:2206:C:H2'	1:1A:2207:G:C8	2.34	0.63
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.80	0.63
51:1t:26:ASN:ND2	51:1t:71:THR:OG1	2.31	0.63
6:2G:107:LEU:HA	6:2G:111:LEU:HD22	1.80	0.63
6:2G:151:ALA:HB3	6:2G:153:ARG:HH11	1.62	0.63
32:2a:49:C:OP2	59:2a:3316:HOH:O	2.14	0.63
32:1a:37:C:OP1	43:1l:123:LYS:NZ	2.31	0.63
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.32	0.63
32:2a:566:U:OP1	46:2o:64:ARG:NH1	2.31	0.63
44:2m:107:ALA:HB3	44:2m:111:LYS:HE3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:7:VAL:HG11	33:1b:221:LEU:HD23	1.81	0.63
1:2A:935:C:O2'	1:2A:936:A:O5'	2.16	0.63
11:2P:95:VAL:HA	11:2P:99:LEU:HD21	1.79	0.63
21:2Z:134:PRO:O	21:2Z:136:PHE:N	2.31	0.63
32:2a:735:U:OP2	59:2a:3317:HOH:O	2.15	0.63
1:1A:2330:G:N2	14:1S:3:ARG:HA	2.12	0.63
32:1a:741:U:H2'	32:1a:742:G:O4'	1.98	0.63
26:24:14:ILE:HG22	26:24:22:ILE:HD13	1.81	0.63
32:2a:1261:A:O2'	32:2a:1263:U:OP2	2.15	0.63
34:2c:6:HIS:HD2	34:2c:7:PRO:HD2	1.64	0.63
42:2k:16:SER:OG	42:2k:106:LYS:NZ	2.31	0.63
44:2m:15:VAL:HG11	44:2m:48:LEU:HD21	1.81	0.63
1:1A:1846:G:O6	3:1D:35:LYS:NZ	2.31	0.63
1:1A:2123:U:O2	1:1A:2208:G:O6	2.17	0.63
1:2A:663:U:H2'	1:2A:664:C:C6	2.34	0.63
32:2a:954:G:H5'	32:2a:1340:U:O2'	1.98	0.63
32:2a:1053:U:H2'	32:2a:1054:C:H6	1.64	0.63
33:2b:92:TYR:CE2	33:2b:150:SER:C	2.76	0.63
40:2i:4:TYR:CE2	40:2i:88:TYR:HA	2.33	0.63
1:1A:267:G:OP2	59:1A:4135:HOH:O	2.16	0.63
44:1m:78:ILE:HG22	44:1m:82:MET:HE2	1.81	0.63
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.31	0.63
38:2g:24:THR:HA	38:2g:27:ILE:HD12	1.81	0.63
40:2i:17:VAL:HG21	40:2i:81:ILE:HG22	1.80	0.63
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.79	0.62
25:13:3:ARG:NH1	25:13:60:GLU:OE1	2.28	0.62
32:1a:142:G:H2'	32:1a:143:G:H8	1.64	0.62
32:1a:986:C:N3	32:1a:1001:G:O6	2.32	0.62
32:1a:1424:G:H5"	32:1a:1425:G:H5'	1.81	0.62
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.14	0.62
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.81	0.62
44:1m:11:ARG:HB3	44:1m:11:ARG:HH11	1.63	0.62
1:2A:1361:U:H2'	1:2A:1362:A:H8	1.64	0.62
1:2A:2022:A:H2'	1:2A:2023:G:C8	2.34	0.62
39:2h:51:VAL:HG12	39:2h:52:ASP:H	1.64	0.62
1:1A:2122:G:H2'	1:1A:2123:U:O4'	1.99	0.62
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.82	0.62
14:1S:15:ARG:O	14:1S:19:LYS:HG2	1.98	0.62
32:1a:920:G:H21	40:1i:124:GLN:NE2	1.97	0.62
51:1t:9:ASN:HD22	51:1t:10:LEU:H	1.46	0.62
1:2A:267:G:O2'	1:2A:268:G:H8	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2226:G:H5"	1:2A:2227:G:N7	2.14	0.62
21:2Z:53:ILE:HD11	21:2Z:99:TYR:HB2	1.80	0.62
1:1A:1739:U:O2'	3:1D:14:ARG:NH2	2.33	0.62
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.33	0.62
32:1a:1060:G:N2	32:1a:1063:A:OP2	2.32	0.62
37:1f:80:ARG:NH1	37:1f:88:VAL:O	2.32	0.62
1:2A:508:A:O2'	20:2Y:49:VAL:O	2.16	0.62
1:2A:842:C:H2'	1:2A:843:C:C6	2.35	0.62
7:2H:44:VAL:HB	7:2H:51:ARG:H	1.64	0.62
8:2I:14:ASP:N	8:2I:17:GLN:OE1	2.30	0.62
32:1a:453:C:H2'	32:1a:454:G:O4'	1.99	0.62
32:1a:1106:A:O2'	41:1j:37:PRO:O	2.16	0.62
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.00	0.62
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.81	0.62
45:2n:17:LYS:H	45:2n:17:LYS:CD	2.12	0.62
1:1A:1826:U:H2'	1:1A:1827:C:C6	2.34	0.62
6:2G:48:GLU:HA	6:2G:51:ARG:HE	1.65	0.62
33:2b:118:LEU:HG	33:2b:142:LEU:HD13	1.82	0.62
1:1A:846:A:H8	1:1A:846:A:OP1	1.82	0.62
12:1Q:58:PHE:O	12:1Q:60:ARG:NH2	2.33	0.62
26:14:63:TYR:N	26:14:64:GLY:HA2	2.14	0.62
33:1b:71:VAL:HB	33:1b:164:VAL:HG13	1.82	0.62
4:2E:1:MET:HE3	4:2E:199:ARG:HD2	1.81	0.62
16:2U:104:GLN:OE1	16:2U:105:VAL:N	2.27	0.62
32:2a:361:U:H5"	32:2a:362:C:OP1	2.00	0.62
32:2a:415:C:OP1	32:2a:497:C:O2'	2.15	0.62
32:2a:1241:C:N4	32:2a:1242:C:O2	2.33	0.62
35:2d:173:TRP:HB3	35:2d:187:ARG:HE	1.63	0.62
1:1A:214:G:H21	1:1A:216:A:H62	1.48	0.62
32:1a:179:G:H2'	32:1a:180:A:H8	1.65	0.62
1:2A:1064:U:OP1	1:2A:1080:U:O2'	2.15	0.62
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.82	0.62
23:21:22:GLY:O	23:21:32:LYS:NZ	2.32	0.62
44:2m:102:ARG:NH1	44:2m:105:THR:OG1	2.33	0.62
34:1c:115:LEU:HD22	34:1c:115:LEU:H	1.65	0.62
36:1e:147:ASP:OD1	36:1e:147:ASP:N	2.25	0.62
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.27	0.62
1:2A:629:U:OP1	5:2F:102:PRO:HA	1.99	0.62
32:2a:1316:G:OP2	59:2a:3319:HOH:O	2.16	0.62
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.82	0.62
3:1D:146:GLU:HB2	3:1D:189:CYS:HB3	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:402:G:H5'	35:1d:5:ILE:HD11	1.81	0.61
34:1c:6:HIS:CD2	34:1c:8:ILE:HB	2.35	0.61
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.82	0.61
1:2A:172:C:H2'	1:2A:173:U:C6	2.35	0.61
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.82	0.61
33:1b:198:ASP:OD2	33:1b:198:ASP:N	2.33	0.61
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.32	0.61
1:1A:2121:G:H1	1:1A:2210:U:H3	1.48	0.61
20:1Y:68:HIS:ND1	20:1Y:70:SER:HB3	2.16	0.61
32:1a:217:C:H2'	32:1a:218:U:H6	1.66	0.61
32:1a:1156:G:H2'	32:1a:1157:G:H8	1.65	0.61
45:2n:7:ILE:HG22	45:2n:23:ARG:HD3	1.82	0.61
46:2o:5:LYS:HZ3	46:2o:5:LYS:HB2	1.64	0.61
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.34	0.61
15:1T:51:ARG:NH1	59:1T:3101:HOH:O	2.20	0.61
26:24:50:VAL:HG11	44:2m:65:LYS:HB3	1.83	0.61
32:2a:1158:A:H2'	32:2a:1159:G:C8	2.35	0.61
52:2u:2:GLY:O	52:2u:4:GLY:N	2.33	0.61
1:1A:2657:C:OP2	1:1A:2744:G:O2'	2.16	0.61
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.82	0.61
1:2A:1845:A:OP2	3:2D:54:ARG:NH2	2.33	0.61
32:1a:208:C:H42	32:1a:212:G:H1	1.48	0.61
40:1i:21:PRO:HA	40:1i:59:PHE:HA	1.82	0.61
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.32	0.61
32:2a:188:C:O2	32:2a:192:G:N1	2.34	0.61
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.34	0.61
15:1T:118:ARG:HG3	15:1T:118:ARG:HH11	1.66	0.61
32:1a:819:U:O2'	59:1a:2006:HOH:O	2.16	0.61
1:2A:98:G:O2'	24:22:7:ARG:NH2	2.33	0.61
2:2B:90:A:C5	2:2B:91:C:H1'	2.35	0.61
32:2a:945:C:N3	59:2a:3364:HOH:O	2.31	0.61
41:2j:8:LEU:HB3	41:2j:96:ILE:HG23	1.82	0.61
1:1A:69:A:N7	19:1X:31:HIS:HE1	1.98	0.61
32:1a:156:A:H2'	32:1a:157:A:C8	2.36	0.61
38:1g:24:THR:O	38:1g:28:ASN:ND2	2.33	0.61
39:1h:73:ASP:OD1	39:1h:75:ARG:HD3	2.01	0.61
1:2A:1311:G:O5'	18:2W:15:ARG:NH2	2.33	0.61
1:2A:1823:C:OP1	59:2A:3623:HOH:O	2.16	0.61
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.83	0.61
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.82	0.61
39:2h:77:GLU:HG3	39:2h:78:GLN:N	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1465:U:O2'	1:1A:1466:G:OP1	2.19	0.61
32:1a:142:G:H2'	32:1a:143:G:C8	2.36	0.61
32:1a:507:A:H61	43:1l:92:ASP:HB2	1.65	0.61
32:1a:657:G:H2'	32:1a:658:G:C8	2.35	0.61
33:1b:15:VAL:HB	33:1b:209:ARG:HD3	1.81	0.61
36:2e:71:LEU:H	36:2e:71:LEU:HD22	1.66	0.61
1:1A:1091:A:H3'	1:1A:1092:G:H5'	1.81	0.61
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.81	0.61
14:1S:3:ARG:HD3	14:1S:4:LEU:N	2.16	0.61
1:1A:916:A:OP1	12:1Q:6:ARG:NH1	2.34	0.60
1:2A:554:G:N1	59:2A:3625:HOH:O	2.26	0.60
1:2A:1354:G:H4'	29:27:7:PRO:HB2	1.83	0.60
32:2a:915:A:O2'	59:2a:3321:HOH:O	2.16	0.60
38:2g:18:TYR:HB3	38:2g:59:LEU:HD12	1.83	0.60
42:2k:81:ASP:OD1	42:2k:107:SER:OG	2.18	0.60
16:1U:76:TYR:OH	16:1U:92:ARG:NH1	2.32	0.60
1:2A:2325:C:H2'	1:2A:2326:G:C8	2.36	0.60
1:1A:1221:A:O2'	1:1A:1222:C:O4'	2.16	0.60
1:2A:585:G:OP2	59:2A:3624:HOH:O	2.16	0.60
7:2H:3:ARG:HB3	7:2H:3:ARG:NH1	2.16	0.60
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.82	0.60
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.82	0.60
32:2a:1359:U:H2'	32:2a:1360:A:C8	2.36	0.60
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.33	0.60
40:2i:47:LEU:HB3	40:2i:50:LEU:HD22	1.83	0.60
50:2s:77:THR:HG23	50:2s:78:ARG:HG2	1.82	0.60
1:1A:629:U:OP1	5:1F:102:PRO:HA	2.01	0.60
32:1a:181:C:H2'	32:1a:182:C:C6	2.36	0.60
1:2A:2375:C:OP1	22:20:55:ARG:NH1	2.33	0.60
29:27:34:ARG:NH1	29:27:41:ARG:O	2.35	0.60
32:2a:208:C:OP1	59:2a:3322:HOH:O	2.17	0.60
32:2a:524:G:H2'	32:2a:525:G:H8	1.66	0.60
33:2b:92:TYR:CZ	33:2b:150:SER:C	2.79	0.60
32:1a:205:G:H2'	32:1a:206:G:H8	1.65	0.60
32:1a:1316:G:OP2	59:1a:2009:HOH:O	2.17	0.60
1:2A:2735:C:H5"	13:2R:1:MET:HE2	1.82	0.60
2:2B:40:U:N3	2:2B:43:C:OP2	2.34	0.60
14:2S:49:VAL:HG12	14:2S:80:LEU:HD22	1.82	0.60
32:2a:1149:G:N2	32:2a:1152:A:OP2	2.35	0.60
32:2a:1329:G:O2'	32:2a:1356:G:O6	2.19	0.60
32:2a:1418:G:H2'	32:2a:1419:U:C6	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2901:G:N2	59:1A:4151:HOH:O	2.19	0.60
2:1B:66:A:H61	2:1B:108:U:H2'	1.66	0.60
32:1a:1223:G:H2'	32:1a:1224:C:C6	2.37	0.60
32:1a:1274:U:P	38:1g:41:ARG:HH22	2.25	0.60
1:2A:1826:U:H2'	1:2A:1827:C:C6	2.36	0.60
1:2A:2100:U:OP1	23:21:21:ARG:NH2	2.34	0.60
32:2a:603:U:N3	35:2d:134:ASP:OD1	2.28	0.60
34:2c:114:PRO:HG3	34:2c:185:GLY:HA3	1.82	0.60
35:2d:46:LYS:O	35:2d:47:ARG:HB3	2.01	0.60
36:2e:152:ARG:HG2	39:2h:42:GLU:O	2.02	0.60
48:1q:26:GLN:HE21	48:1q:37:LYS:HE3	1.66	0.60
1:2A:346:G:HO2'	1:2A:1249:U:H3	1.50	0.60
1:2A:2298:A:H62	1:2A:2355:U:H3	1.48	0.60
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.67	0.60
32:2a:65:G:H4'	32:2a:66:U:H3'	1.84	0.60
32:2a:1303:C:H5"	32:2a:1304:C:H2'	1.83	0.60
1:1A:324:G:OP2	20:1Y:84:ARG:NH2	2.34	0.60
32:1a:137:G:H2'	32:1a:138:A:H8	1.67	0.60
32:1a:487:C:H2'	32:1a:488:C:H6	1.67	0.60
32:2a:1219:C:O2'	32:2a:1282:G:N1	2.31	0.60
1:1A:330:G:H21	1:1A:353:A:H62	1.50	0.60
1:2A:1337:U:H2'	1:2A:1338:C:C6	2.37	0.60
1:2A:2733:A:OP1	59:2A:3622:HOH:O	2.16	0.60
30:28:14:VAL:HG23	30:28:24:ALA:HB2	1.83	0.60
32:2a:50:U:O4	32:2a:361:U:H5	1.85	0.60
32:2a:393:A:OP2	59:2a:3318:HOH:O	2.15	0.60
32:2a:1114:G:H2'	32:2a:1115:C:C6	2.36	0.60
1:1A:996:G:OP1	12:1Q:16:ARG:NH2	2.34	0.60
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.34	0.60
4:2E:199:ARG:HH12	4:2E:202:LYS:HE3	1.67	0.60
32:2a:1158:A:H2'	32:2a:1159:G:H8	1.67	0.60
45:2n:16:PHE:HB3	45:2n:17:LYS:HE2	1.84	0.60
1:1A:2230:G:N7	59:1A:4224:HOH:O	2.30	0.59
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.84	0.59
32:2a:18:U:H2'	32:2a:19:C:C6	2.37	0.59
32:2a:549:U:OP2	32:2a:550:G:O2'	2.14	0.59
32:2a:806:C:OP2	59:2a:3320:HOH:O	2.16	0.59
4:1E:54:GLN:HE21	4:1E:55:ASN:N	1.97	0.59
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.83	0.59
41:1j:35:SER:N	41:1j:73:ASP:O	2.30	0.59
1:2A:1104:G:H3'	1:2A:1105:U:C6	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.82	0.59
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.01	0.59
25:23:8:LEU:HD13	25:23:31:LEU:HD23	1.85	0.59
32:2a:721:A:H2'	32:2a:722:C:C6	2.37	0.59
47:2p:18:ARG:HD3	47:2p:35:LYS:HE2	1.84	0.59
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.85	0.59
14:1S:59:LYS:HD2	14:1S:60:GLY:H	1.66	0.59
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.17	0.59
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD21	1.84	0.59
32:1a:295:G:O6	59:1a:2005:HOH:O	2.14	0.59
34:1c:58:GLU:HB2	34:1c:65:ALA:HB3	1.85	0.59
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.67	0.59
42:1k:48:ILE:O	42:1k:50:TYR:N	2.32	0.59
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.17	0.59
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.67	0.59
1:1A:2803:C:H2'	1:1A:2804:G:H8	1.65	0.59
1:2A:873:U:OP1	59:2A:3604:HOH:O	2.17	0.59
1:2A:1041:A:H2'	1:2A:1042:G:H8	1.66	0.59
1:2A:2879:C:H2'	1:2A:2880:C:O4'	2.02	0.59
32:2a:712:A:H2'	32:2a:713:A:C8	2.38	0.59
6:1G:49:ASP:C	6:1G:51:ARG:H	2.06	0.59
36:1e:122:GLU:O	36:1e:126:ARG:NH1	2.35	0.59
54:1x:23:C:H2'	54:1x:24:U:C6	2.38	0.59
1:1A:2366:C:H1'	22:10:39:ARG:HH21	1.67	0.59
44:1m:80:ARG:NH2	50:1s:69:HIS:HE1	2.00	0.59
1:2A:1833:A:H4'	3:2D:259:THR:HG23	1.83	0.59
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.84	0.59
1:1A:1847:G:OP1	3:1D:88:ARG:NH2	2.35	0.59
32:1a:401:U:OP2	35:1d:3:ARG:NH2	2.36	0.59
54:1x:75:C:H2'	54:1x:76:A:C2	2.38	0.59
55:1z:11:ARG:HB3	55:1z:12:PRO:CD	2.32	0.59
1:2A:1101:G:H5"	1:2A:1102:A:H5'	1.84	0.59
4:2E:199:ARG:NH1	4:2E:202:LYS:HE3	2.17	0.59
7:2H:3:ARG:HH12	7:2H:5:GLY:N	2.00	0.59
11:2P:121:LYS:O	11:2P:123:LEU:N	2.36	0.59
32:2a:397:C:O2'	32:2a:605:A:N3	2.32	0.59
45:2n:43:CYS:HA	45:2n:46:GLU:HB2	1.84	0.59
32:1a:246:A:H4'	32:1a:247:G:O5'	2.02	0.59
49:1r:37:VAL:O	49:1r:41:LYS:HG2	2.01	0.59
1:2A:2302:U:H2'	1:2A:2303:C:C6	2.37	0.59
32:2a:84:A:OP1	59:2a:3325:HOH:O	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:185:ASP:OD1	5:1F:188:ARG:NH1	2.34	0.59
11:1P:62:LEU:O	30:18:13:ARG:HD3	2.02	0.59
32:2a:408:A:O4'	35:2d:35:ARG:NH2	2.36	0.59
32:2a:721:A:H2'	32:2a:722:C:H6	1.67	0.59
32:2a:1086:C:H5"	33:2b:98:LEU:HD13	1.84	0.59
1:1A:1565:U:H2'	1:1A:1566:G:O4'	2.03	0.59
1:1A:2566:U:O2	55:1z:1:VAL:HG21	2.03	0.59
6:1G:109:VAL:HG13	26:14:33:VAL:HG11	1.85	0.59
32:1a:88:C:H2'	32:1a:89:G:C8	2.38	0.59
32:1a:1399:G:N7	59:1a:2045:HOH:O	2.32	0.59
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.85	0.59
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.36	0.59
1:2A:524:G:N1	1:2A:527:A:OP2	2.35	0.59
1:2A:2338:A:H2'	1:2A:2339:A:C8	2.37	0.59
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.03	0.59
32:2a:1054:C:H2'	32:2a:1055:G:C8	2.38	0.59
1:1A:478:C:OP1	59:1A:4107:HOH:O	2.17	0.58
32:1a:1359:U:H2'	32:1a:1360:A:C8	2.38	0.58
35:1d:88:VAL:HA	36:1e:97:GLY:HA2	1.84	0.58
1:2A:1084:G:H1	1:2A:1161:C:H42	1.51	0.58
1:2A:2858:U:OP2	15:2T:95:ARG:NH1	2.32	0.58
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.18	0.58
32:2a:1121:G:C6	32:2a:1123:C:H1'	2.37	0.58
34:2c:117:ALA:HB2	34:2c:186:PHE:CG	2.38	0.58
36:2e:78:HIS:CD2	36:2e:142:LEU:HD23	2.37	0.58
1:1A:2226:G:OP2	1:1A:2226:G:H4'	2.02	0.58
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.85	0.58
1:2A:661:A:H2'	11:2P:117:GLU:OE2	2.03	0.58
1:2A:1361:U:H2'	1:2A:1362:A:C8	2.38	0.58
6:2G:41:GLN:NE2	6:2G:154:GLY:O	2.34	0.58
13:2R:78:LYS:HG3	13:2R:82:GLU:HG3	1.85	0.58
32:2a:9:A:H5'	36:2e:101:ILE:HG22	1.84	0.58
1:1A:1153:U:O2'	1:1A:1154:C:H6	1.86	0.58
1:1A:2044:G:H5'	1:1A:2628:C:H4'	1.86	0.58
1:1A:2298:A:OP1	59:1A:4138:HOH:O	2.17	0.58
3:1D:126:GLN:NE2	3:1D:127:VAL:H	2.02	0.58
1:2A:310:C:H2'	1:2A:311:C:H6	1.68	0.58
1:2A:2858:U:O4	15:2T:23:ARG:NH2	2.33	0.58
6:2G:115:ARG:HG2	6:2G:136:ARG:HH21	1.67	0.58
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.85	0.58
19:2X:36:LYS:HA	19:2X:39:ILE:HD12	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:100:ALA:O	34:2c:102:ASN:ND2	2.36	0.58
34:2c:157:ILE:HD12	34:2c:164:ARG:HB3	1.86	0.58
1:1A:541:C:OP1	27:15:16:ARG:NH2	2.37	0.58
1:1A:1430:G:O2'	1:1A:1441:U:O2	2.16	0.58
37:1f:38:GLU:HB2	37:1f:64:GLN:HG2	1.86	0.58
1:2A:1240:C:H2'	1:2A:1241:G:H8	1.67	0.58
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.34	0.58
32:2a:703:C:N4	49:2r:71:LYS:HE2	2.18	0.58
32:1a:1094:A:N1	34:1c:177:THR:OG1	2.30	0.58
33:1b:47:THR:O	33:1b:51:LEU:N	2.32	0.58
21:2Z:130:PRO:HB2	21:2Z:131:ARG:HH21	1.67	0.58
32:2a:420:G:H2'	32:2a:421:G:H8	1.69	0.58
32:2a:900:G:H2'	32:2a:901:A:C8	2.38	0.58
40:2i:97:LYS:HA	40:2i:102:LEU:HG	1.86	0.58
54:2x:31:G:C5	54:2x:32:5MC:HM53	2.38	0.58
1:1A:595:G:OP2	17:1V:78:LYS:NZ	2.32	0.58
32:1a:643:U:H2'	32:1a:644:G:C8	2.39	0.58
32:1a:1329:G:N2	32:1a:1356:G:H2'	2.19	0.58
1:2A:2328:C:H2'	1:2A:2329:G:C8	2.37	0.58
5:2F:29:ASN:H	5:2F:112:MET:HE1	1.69	0.58
25:23:30:ARG:H	25:23:33:GLN:NE2	2.02	0.58
32:2a:1274:U:H2'	32:2a:1275:G:O4'	2.03	0.58
35:2d:61:LYS:HA	35:2d:203:VAL:HG22	1.84	0.58
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.69	0.58
32:1a:143:G:H1	32:1a:169:C:H42	1.52	0.58
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.67	0.58
30:28:32:LEU:O	30:28:36:LYS:HE3	2.04	0.58
32:2a:1344:C:H2'	32:2a:1345:C:H5"	1.86	0.58
34:2c:131:ARG:NH1	36:2e:50:GLU:HG2	2.18	0.58
1:1A:2800:C:OP1	4:1E:61:ARG:NH2	2.37	0.58
18:1W:12:ILE:HD13	18:1W:17:VAL:HG13	1.85	0.58
32:1a:487:C:OP2	43:1l:116:SER:OG	2.15	0.58
34:1c:112:SER:OG	34:1c:115:LEU:HD21	2.04	0.58
1:2A:897:U:H5'	25:23:49:LYS:HD2	1.85	0.58
1:2A:1423:A:OP1	29:27:10:ARG:NH2	2.37	0.58
1:2A:2568:G:H2'	1:2A:2569:C:C6	2.39	0.58
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.86	0.58
32:2a:265:C:H2'	32:2a:266:A:C8	2.39	0.58
32:2a:453:C:H2'	32:2a:454:G:O4'	2.04	0.58
32:2a:1097:C:O2'	45:2n:60:SER:O	2.20	0.58
13:1R:63:ARG:NH2	59:1R:303:HOH:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:449:C:H5”	32:1a:450:C:C5	2.38	0.58
32:1a:1058:C:OP1	33:1b:179:LYS:NZ	2.37	0.58
32:1a:1375:G:H21	32:1a:1480:A:H8	1.52	0.58
34:1c:15:THR:HG22	34:1c:16:ARG:HG3	1.85	0.58
1:2A:475:G:N7	59:2A:3685:HOH:O	2.32	0.58
8:2I:126:TYR:HB2	8:2I:142:VAL:HG23	1.86	0.58
32:2a:1054:C:H2’	32:2a:1055:G:H8	1.69	0.58
35:2d:19:LEU:O	35:2d:21:LEU:N	2.37	0.58
50:2s:13:ASP:HA	50:2s:16:LEU:HB3	1.84	0.58
12:1Q:60:ARG:H	12:1Q:60:ARG:CZ	2.16	0.58
35:1d:49:ARG:HE	35:1d:49:ARG:H	1.50	0.58
47:1p:19:ILE:HD13	47:1p:36:ILE:HG13	1.85	0.58
24:22:17:SER:N	24:22:20:GLU:OE2	2.37	0.58
32:2a:1223:G:H2’	32:2a:1224:C:C6	2.39	0.58
37:2f:89:MET:HE3	37:2f:91:VAL:HG21	1.86	0.58
1:1A:1153:U:O2’	1:1A:1154:C:O5’	2.18	0.57
1:1A:1220:G:H21	1:1A:1221:A:H4’	1.69	0.57
8:1I:4:ILE:HD11	8:1I:44:LEU:HD12	1.86	0.57
14:1S:3:ARG:HD3	14:1S:3:ARG:C	2.29	0.57
32:1a:1245:C:H2’	32:1a:1246:C:C6	2.39	0.57
32:1a:1484:U:OP1	59:1a:2007:HOH:O	2.17	0.57
44:1m:80:ARG:HH21	50:1s:69:HIS:HE1	1.52	0.57
1:2A:1828:U:H5’	3:2D:259:THR:CG2	2.29	0.57
1:2A:2314:G:O2’	6:2G:132:ASN:HB2	2.04	0.57
32:2a:143:G:H2’	32:2a:144:A:H8	1.69	0.57
1:1A:1784:C:OP1	15:1T:96:ARG:NH1	2.36	0.57
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	1.86	0.57
1:1A:1054:A:OP2	9:1N:37:LYS:NZ	2.37	0.57
1:1A:2323:U:H5’	6:1G:88:ILE:HD11	1.85	0.57
32:1a:90:U:H2’	32:1a:91:G:H5’	1.86	0.57
32:1a:267:C:H2’	32:1a:268:C:H6	1.68	0.57
32:1a:324:C:H4’	32:1a:325:A:H5”	1.86	0.57
1:2A:645:A:OP2	59:2A:3626:HOH:O	2.17	0.57
1:2A:1232:U:H4’	17:2V:79:VAL:HG22	1.86	0.57
1:2A:1808:U:H2’	1:2A:1814:A:N6	2.19	0.57
1:2A:2465:G:H1’	59:2A:3654:HOH:O	2.03	0.57
2:2B:15:A:OP2	2:2B:69:G:N2	2.34	0.57
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.37	0.57
45:2n:17:LYS:H	45:2n:17:LYS:CE	2.16	0.57
36:1e:144:THR:OG1	36:1e:147:ASP:OD1	2.15	0.57
1:2A:1475:C:H2’	1:2A:1476:U:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2278:A:H5"	1:2A:2279:A:H5'	1.85	0.57
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.85	0.57
6:2G:35:GLU:HG2	6:2G:36:LYS:HE2	1.86	0.57
32:2a:285:G:OP2	59:2a:3323:HOH:O	2.18	0.57
32:2a:691:C:H2'	32:2a:692:C:C6	2.40	0.57
35:2d:31:CYS:SG	35:2d:33:MET:HB2	2.44	0.57
42:2k:92:GLU:HG2	42:2k:96:ARG:HH21	1.70	0.57
44:2m:20:THR:C	44:2m:22:ILE:H	2.11	0.57
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.86	0.57
41:1j:38:ILE:HG12	41:1j:71:LEU:O	2.05	0.57
47:1p:75:ARG:C	47:1p:77:ALA:H	2.11	0.57
32:2a:1491:A:H2'	32:2a:1492:C:C6	2.40	0.57
35:2d:108:LEU:HD21	35:2d:183:GLY:HA3	1.86	0.57
40:2i:78:LYS:HD3	40:2i:101:PHE:HD2	1.69	0.57
54:2x:23:C:H2'	54:2x:24:U:C6	2.39	0.57
1:1A:154:C:H42	1:1A:159:G:H1	1.52	0.57
32:1a:205:G:H2'	32:1a:206:G:C8	2.39	0.57
32:1a:1078:U:OP1	32:1a:1091:G:N2	2.32	0.57
32:1a:1131:U:H2'	32:1a:1132:C:O4'	2.04	0.57
33:1b:220:ASP:O	33:1b:223:ILE:HG12	2.04	0.57
47:1p:57:ARG:NH1	47:1p:79:VAL:O	2.37	0.57
1:2A:1451:U:H2'	1:2A:1452:C:C6	2.39	0.57
1:2A:2043:U:OP1	59:2A:3625:HOH:O	2.17	0.57
1:2A:2896:U:H2'	1:2A:2897:C:H6	1.69	0.57
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.04	0.57
17:2V:1:MET:HA	17:2V:42:GLY:HA3	1.86	0.57
26:24:61:ARG:HH22	50:2s:9:VAL:HG21	1.70	0.57
32:2a:10:G:H2'	32:2a:11:A:H8	1.69	0.57
32:2a:1305:G:H4'	32:2a:1345:C:N3	2.19	0.57
1:1A:2771:G:N7	59:1A:4240:HOH:O	2.33	0.57
32:1a:674:G:OP1	59:1a:2011:HOH:O	2.18	0.57
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.85	0.57
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.05	0.57
32:2a:531:A:H4'	32:2a:532:G:O5'	2.04	0.57
32:2a:1329:G:C8	40:2i:107:ARG:HB2	2.40	0.57
1:1A:1397:U:OP2	59:1A:4140:HOH:O	2.18	0.57
33:1b:44:LEU:HA	33:1b:47:THR:HG23	1.86	0.57
1:2A:703:U:H2'	1:2A:704:C:C6	2.40	0.57
1:2A:706:G:H5'	5:2F:99:TYR:CE2	2.39	0.57
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.85	0.57
8:2I:50:ARG:HB3	8:2I:54:GLN:HE22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:111:G:OP2	59:2a:3323:HOH:O	2.17	0.57
32:2a:812:A:H2'	32:2a:813:G:O4'	2.05	0.57
35:2d:57:ARG:NH2	35:2d:205:GLU:OE2	2.33	0.57
1:1A:309:C:H2'	1:1A:310:C:H6	1.69	0.57
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.20	0.57
32:1a:1078:U:P	32:1a:1091:G:H1	2.27	0.57
32:1a:1295:U:OP1	50:1s:5:LEU:HB3	2.05	0.57
1:2A:2896:U:H2'	1:2A:2897:C:C6	2.40	0.57
5:2F:120:GLU:HG3	5:2F:122:LYS:HG2	1.86	0.57
38:2g:111:ARG:HB2	38:2g:119:ARG:HD2	1.87	0.57
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.40	0.57
1:1A:159:G:O2'	1:1A:160:C:H5'	2.03	0.57
12:1Q:109:VAL:HG13	12:1Q:113:GLN:HB2	1.87	0.57
32:1a:932:G:H21	32:1a:1209:A:H62	1.52	0.57
35:1d:107:ARG:HH22	35:1d:194:LEU:HD11	1.70	0.57
36:1e:137:GLU:O	36:1e:141:GLN:HG3	2.05	0.57
2:2B:28:C:H5"	14:2S:31:SER:OG	2.05	0.57
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.04	0.57
11:2P:85:LEU:HA	11:2P:88:LEU:HD12	1.87	0.57
32:2a:812:A:N6	32:2a:836:G:O2'	2.38	0.57
32:2a:923:G:N7	59:2a:3366:HOH:O	2.32	0.57
32:2a:1053:U:H2'	32:2a:1054:C:C6	2.40	0.57
33:2b:92:TYR:CD1	33:2b:150:SER:O	2.58	0.57
13:1R:55:ALA:HB2	13:1R:79:LEU:HD13	1.86	0.56
18:1W:18:ARG:NH1	18:1W:76:VAL:O	2.38	0.56
32:1a:1482:G:OP1	32:1a:1485:A:H4'	2.04	0.56
1:2A:69:A:N7	19:2X:31:HIS:HE1	2.03	0.56
1:2A:2761:A:H1'	7:2H:63:SER:HB3	1.86	0.56
33:2b:165:VAL:HA	33:2b:187:LEU:HD13	1.87	0.56
40:2i:128:ARG:NH2	54:2x:33:U:OP2	2.38	0.56
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.87	0.56
1:1A:1219:U:OP1	1:1A:1221:A:N6	2.36	0.56
1:1A:1222:C:H2'	1:1A:1223:C:C6	2.40	0.56
32:1a:1286:G:OP2	59:1a:2010:HOH:O	2.17	0.56
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.87	0.56
37:1f:10:LEU:HD23	37:1f:61:LEU:HD23	1.87	0.56
15:2T:24:PRO:HA	15:2T:49:VAL:HG22	1.87	0.56
32:2a:349:A:H5'	32:2a:349:A:H8	1.69	0.56
32:2a:720:C:H2'	32:2a:721:A:C8	2.40	0.56
32:2a:1079:C:O2'	59:2a:3324:HOH:O	2.17	0.56
32:2a:1286:G:OP2	59:2a:3326:HOH:O	2.17	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1070:G:C4	1:1A:1179:C:H1'	2.40	0.56
1:1A:2376:G:O6	30:18:39:LYS:HE3	2.06	0.56
8:1I:37:VAL:HG13	8:1I:38:LEU:HD12	1.88	0.56
28:16:10:LEU:HG	28:16:54:ILE:HG13	1.87	0.56
32:1a:65:G:H4'	32:1a:66:U:H3'	1.88	0.56
32:1a:398:G:N7	59:1a:2049:HOH:O	2.33	0.56
32:1a:1063:A:H5"	36:1e:16:THR:HG21	1.87	0.56
35:1d:108:LEU:HB3	35:1d:110:PHE:CE1	2.40	0.56
39:1h:64:LYS:HB3	39:1h:79:VAL:HG21	1.87	0.56
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.86	0.56
1:2A:272:G:H4'	1:2A:273:U:OP1	2.05	0.56
1:2A:865:A:C4	1:2A:1233:A:C2	2.93	0.56
1:2A:1101:G:H4'	1:2A:1131:A:H8	1.70	0.56
1:2A:1512:G:O2'	1:2A:1592:C:O2'	2.18	0.56
1:2A:2310:G:H2'	1:2A:2311:G:C8	2.36	0.56
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.87	0.56
20:2Y:23:ARG:HG2	20:2Y:42:VAL:HG22	1.86	0.56
21:2Z:11:GLU:O	21:2Z:36:LYS:NZ	2.36	0.56
32:2a:37:C:O2'	43:2l:117:ARG:NH2	2.39	0.56
32:2a:758:G:O6	32:2a:789:C:N4	2.38	0.56
32:2a:964:A:H1'	50:2s:54:GLY:O	2.05	0.56
32:2a:971:G:H1	32:2a:1028:C:H42	1.51	0.56
32:2a:994:A:H2'	32:2a:995:A:C8	2.40	0.56
35:2d:196:LEU:O	35:2d:198:VAL:N	2.32	0.56
36:2e:110:LEU:O	36:2e:115:VAL:HG13	2.05	0.56
37:2f:1:MET:HE3	37:2f:66:GLU:HG2	1.86	0.56
1:1A:552:A:C2	1:1A:2064:C:H4'	2.39	0.56
1:1A:2441:A:N3	1:1A:2441:A:H2'	2.21	0.56
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.71	0.56
17:2V:31:ALA:O	17:2V:61:VAL:HG12	2.06	0.56
23:21:56:GLN:HA	23:21:56:GLN:HE21	1.69	0.56
1:1A:666:G:H21	1:1A:670:A:H2	1.54	0.56
8:1I:14:ASP:N	8:1I:17:GLN:OE1	2.33	0.56
20:1Y:92:ASN:CB	20:1Y:94:LYS:H	2.14	0.56
32:1a:643:U:H2'	32:1a:644:G:H8	1.70	0.56
32:1a:868:G:O2'	32:1a:884:G:O6	2.20	0.56
51:1t:43:LEU:O	51:1t:47:GLY:N	2.38	0.56
32:2a:1231:C:O4'	40:2i:70:LYS:NZ	2.39	0.56
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.70	0.56
35:2d:153:ARG:NH2	35:2d:180:GLY:O	2.38	0.56
1:1A:1450:U:H2'	1:1A:1451:U:C6	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2583:A:N7	4:1E:144:ARG:HD2	2.20	0.56
40:1i:23:ASN:ND2	40:1i:25:LYS:HG2	2.18	0.56
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.88	0.56
1:2A:1129:A:N3	1:2A:1150:U:O2'	2.37	0.56
1:2A:1992:A:OP1	59:2A:3627:HOH:O	2.18	0.56
1:2A:2763:G:C4	7:2H:2:SER:HA	2.41	0.56
1:2A:2785:C:OP1	4:2E:166:THR:OG1	2.21	0.56
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.88	0.56
8:2I:102:SER:OG	8:2I:103:ARG:N	2.39	0.56
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HG2	1.87	0.56
32:2a:626:A:N3	39:2h:113:SER:OG	2.38	0.56
32:2a:719:C:H2'	32:2a:720:C:H6	1.71	0.56
32:2a:931:G:H5'	32:2a:943:A:H61	1.69	0.56
48:2q:6:LEU:HG	48:2q:23:VAL:HG11	1.87	0.56
1:1A:555:C:H4'	1:1A:556:A:H5"	1.87	0.56
1:1A:1934:A:C5	32:1a:1472:G:H5"	2.40	0.56
1:1A:2859:A:OP2	1:1A:2875:U:H5	1.88	0.56
1:2A:2384:G:H2'	1:2A:2385:C:C6	2.41	0.56
28:26:14:THR:OG1	28:26:48:VAL:O	2.19	0.56
32:2a:108:U:O2'	32:2a:109:G:H5'	2.05	0.56
32:2a:1205:C:P	50:2s:78:ARG:HH22	2.28	0.56
1:1A:1039:C:OP1	16:1U:53:ARG:NH2	2.39	0.56
1:1A:1231:G:H5"	17:1V:81:TYR:CE1	2.40	0.56
1:1A:1474:G:H2'	1:1A:1475:C:C6	2.40	0.56
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.39	0.56
13:1R:21:TYR:OH	13:1R:43:GLU:HG2	2.06	0.56
15:1T:108:ARG:HH22	15:1T:112:ARG:HH11	1.53	0.56
32:1a:1245:C:H2'	32:1a:1246:C:H6	1.70	0.56
4:2E:24:THR:HG23	4:2E:184:VAL:HG12	1.88	0.56
40:2i:17:VAL:HG23	40:2i:63:ILE:HG12	1.88	0.56
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.06	0.56
21:1Z:157:LEU:HD11	21:1Z:163:LEU:HD13	1.87	0.56
32:1a:295:G:O6	59:1a:2008:HOH:O	2.17	0.56
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.41	0.56
1:2A:1992:A:OP2	3:2D:242:ARG:NH2	2.39	0.56
7:2H:9:ILE:N	7:2H:50:VAL:O	2.39	0.56
32:2a:526:G:OP1	35:2d:10:ARG:NH2	2.32	0.56
32:2a:1244:C:H2'	32:2a:1245:C:H6	1.71	0.56
38:2g:23:VAL:HG13	38:2g:43:PHE:CE2	2.41	0.56
55:2z:6:TYR:CZ	55:2z:7:LEU:HD22	2.40	0.56
1:1A:2588:A:H5'	27:15:3:LYS:HD2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:265:C:H2'	32:1a:266:A:H8	1.71	0.56
1:2A:624:G:O2'	1:2A:701:A:N6	2.39	0.56
1:2A:2389:A:H4'	14:2S:23:ARG:HH11	1.70	0.56
5:2F:117:ARG:HH12	11:2P:1:MET:N	2.04	0.56
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.87	0.56
1:1A:1833:A:O2'	3:1D:259:THR:HG21	2.06	0.55
7:1H:144:VAL:O	7:1H:148:ILE:HG12	2.06	0.55
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.38	0.55
32:1a:169:C:OP1	59:1a:2013:HOH:O	2.18	0.55
39:1h:39:LEU:HB3	39:1h:45:ILE:HG12	1.87	0.55
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.88	0.55
32:2a:403:G:O4'	35:2d:119:GLN:NE2	2.39	0.55
40:2i:89:ASN:HD22	40:2i:91:ASP:H	1.53	0.55
1:1A:238:G:OP2	30:18:13:ARG:NH2	2.39	0.55
1:1A:1064:U:H3	1:1A:1187:A:H62	1.54	0.55
26:14:59:PHE:CD1	50:1s:64:GLU:HB3	2.41	0.55
32:1a:57:U:H2'	32:1a:58:G:C8	2.41	0.55
32:1a:312:G:OP2	32:1a:347:G:O2'	2.24	0.55
32:1a:595:A:H61	32:1a:613:G:H1	1.53	0.55
1:2A:2347:A:H61	22:20:43:THR:HG22	1.71	0.55
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.87	0.55
32:2a:524:G:H2'	32:2a:525:G:C8	2.41	0.55
32:2a:1309:C:H2'	32:2a:1310:C:C6	2.41	0.55
39:2h:12:ARG:NH1	39:2h:27:PRO:HD3	2.21	0.55
51:2t:56:MET:HG3	51:2t:84:LEU:HD11	1.87	0.55
1:1A:2494:C:N3	12:1Q:124:LYS:NZ	2.53	0.55
32:1a:963:C:H2'	32:1a:964:A:H8	1.71	0.55
32:1a:1242:C:OP1	32:1a:1266:C:O2'	2.23	0.55
48:1q:6:LEU:HD23	48:1q:23:VAL:HG21	1.88	0.55
1:2A:927:G:H1	1:2A:940:U:H3	1.54	0.55
1:2A:1010:G:OP1	59:2A:3631:HOH:O	2.18	0.55
1:2A:1292:A:OP1	5:2F:95:ARG:NH2	2.40	0.55
1:2A:1638:G:H2'	1:2A:1639:G:H8	1.71	0.55
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.87	0.55
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	1.88	0.55
45:2n:24:CYS:O	45:2n:28:GLY:N	2.37	0.55
1:1A:1064:U:O2'	1:1A:1066:A:H2	1.89	0.55
1:1A:1066:A:H62	1:1A:1185:U:H3	1.52	0.55
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.07	0.55
32:1a:898:U:H2'	32:1a:899:U:C6	2.41	0.55
1:2A:1465:U:O2'	1:2A:1466:G:OP1	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.38	0.55
44:2m:60:VAL:HG23	44:2m:64:TRP:CE3	2.41	0.55
1:1A:2347:A:H61	22:10:43:THR:CG2	2.19	0.55
32:1a:672:G:H2'	32:1a:673:C:H6	1.71	0.55
36:1e:78:HIS:NE2	36:1e:142:LEU:HA	2.21	0.55
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.70	0.55
1:2A:2122:G:O6	1:2A:2209:C:N4	2.38	0.55
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.87	0.55
20:2Y:1:MET:HG2	20:2Y:2:ARG:H	1.70	0.55
32:2a:942:A:N3	32:2a:947:A:O2'	2.39	0.55
32:2a:1328:A:H5"	40:2i:120:ARG:HH12	1.72	0.55
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.89	0.55
1:1A:2208:G:H2'	1:1A:2209:C:C6	2.40	0.55
32:1a:1030:G:H5"	45:1n:4:LYS:HD2	1.88	0.55
1:2A:200:G:H2'	1:2A:201:A:O4'	2.07	0.55
1:2A:1494:G:H1'	1:2A:1573:A:N1	2.22	0.55
32:2a:517:A:OP1	59:2a:3327:HOH:O	2.18	0.55
32:2a:719:C:H2'	32:2a:720:C:C6	2.42	0.55
32:2a:911:G:N2	32:2a:913:A:O4'	2.40	0.55
32:2a:1133:U:O4	32:2a:1134:A:N6	2.40	0.55
59:2a:3438:HOH:O	34:2c:3:ASN:HB2	2.07	0.55
38:2g:38:LEU:O	38:2g:42:ILE:HG13	2.07	0.55
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.89	0.55
32:1a:501:G:N2	32:1a:517:A:OP2	2.31	0.55
32:1a:1334:C:OP1	52:1u:3:LYS:NZ	2.28	0.55
35:1d:100:ARG:NH1	35:1d:137:SER:HB3	2.21	0.55
1:2A:2330:G:N1	14:2S:3:ARG:HA	2.21	0.55
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.41	0.55
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.89	0.55
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.41	0.55
32:2a:651:G:O2'	46:2o:49:ASP:OD1	2.17	0.55
32:1a:574:C:H2'	32:1a:575:U:H6	1.72	0.55
1:2A:1041:A:H4'	16:2U:91:ASP:OD2	2.07	0.55
17:2V:25:LEU:H	17:2V:92:THR:HG1	1.53	0.55
1:1A:1076:G:H21	31:19:36:GLN:HE22	1.54	0.55
1:1A:2227:G:O2'	1:1A:2228:A:OP1	2.25	0.55
1:2A:1409:G:P	23:21:3:LYS:HG3	2.47	0.55
6:2G:144:ILE:HG23	6:2G:148:MET:HE1	1.89	0.55
28:26:13:CYS:SG	28:26:47:THR:HG21	2.47	0.55
32:2a:966:G:H2'	32:2a:967:C:O4'	2.06	0.55
32:2a:1038:A:N3	34:2c:156:ARG:NH1	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2332:G:H5"	1:1A:2333:A:OP2	2.07	0.55
32:1a:1134:A:H5"	41:1j:40:LEU:O	2.07	0.55
1:2A:412:G:OP1	59:2A:3629:HOH:O	2.18	0.55
1:2A:1753:G:H2'	1:2A:1754:C:C6	2.42	0.55
1:2A:2124:C:O2	1:2A:2207:G:N2	2.40	0.55
3:2D:68:LYS:HD2	3:2D:70:TRP:CZ2	2.42	0.55
32:2a:402:G:N2	35:2d:119:GLN:OE1	2.38	0.55
32:2a:1298:G:N2	32:2a:1300:A:H3'	2.22	0.55
32:2a:1305:G:H2'	32:2a:1306:A:C8	2.42	0.55
1:1A:610:U:H2'	1:1A:611:C:C6	2.42	0.54
1:1A:2803:C:H2'	1:1A:2804:G:C8	2.42	0.54
51:1t:16:HIS:O	51:1t:19:SER:OG	2.24	0.54
1:2A:1070:G:C4	1:2A:1179:C:H1'	2.43	0.54
1:2A:1524:G:HO2'	1:2A:1604:A:H2	1.53	0.54
2:2B:3:C:H2'	2:2B:4:C:C6	2.43	0.54
32:2a:691:C:H2'	32:2a:692:C:H6	1.72	0.54
1:1A:1093:A:OP2	1:1A:1154:C:N4	2.36	0.54
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.22	0.54
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.22	0.54
32:1a:715:G:H5'	32:1a:750:A:H4'	1.89	0.54
32:1a:741:U:OP1	32:1a:806:C:O2'	2.24	0.54
39:1h:4:ASP:OD2	39:1h:85:ARG:NH1	2.40	0.54
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	1.89	0.54
30:28:63:PRO:HG2	30:28:64:TYR:CD2	2.42	0.54
32:2a:989:G:H2'	32:2a:990:G:H8	1.72	0.54
52:2u:2:GLY:C	52:2u:4:GLY:H	2.15	0.54
1:1A:1845:A:OP2	3:1D:54:ARG:NH2	2.38	0.54
1:1A:2208:G:H4'	1:1A:2209:C:OP1	2.07	0.54
1:1A:2600:A:OP2	59:1A:4143:HOH:O	2.18	0.54
54:1x:17:C:H3'	54:1x:17(A):U:H5"	1.88	0.54
1:2A:118:G:H4'	1:2A:148:A:H5'	1.90	0.54
1:2A:945:A:H2'	1:2A:946:A:O4'	2.07	0.54
1:2A:2297:A:H4'	1:2A:2298:A:O4'	2.06	0.54
1:2A:2327:C:H2'	1:2A:2328:C:C6	2.42	0.54
32:2a:925:G:O3'	44:2m:109:THR:OG1	2.26	0.54
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.40	0.54
1:1A:1200:A:OP1	16:1U:55:ARG:HD3	2.07	0.54
1:1A:2648:U:H5"	4:1E:82:ARG:HH21	1.72	0.54
11:1P:121:LYS:O	11:1P:123:LEU:N	2.40	0.54
33:1b:230:VAL:HG12	33:1b:231:GLU:H	1.71	0.54
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.22	0.54
1:2A:1734:U:O2	1:2A:1746:A:H5'	2.08	0.54
4:2E:54:GLN:HE21	4:2E:58:ARG:HB2	1.72	0.54
16:2U:86:ALA:HB2	16:2U:116:ALA:HB2	1.89	0.54
35:2d:73:ARG:HH11	35:2d:73:ARG:HB2	1.73	0.54
38:2g:67:GLU:OE2	38:2g:70:LYS:NZ	2.39	0.54
1:1A:598:U:H2'	1:1A:599:G:C8	2.43	0.54
14:1S:15:ARG:NE	14:1S:88:ASP:OD2	2.39	0.54
25:13:7:LYS:HG3	25:13:34:GLU:HG2	1.88	0.54
32:1a:304:C:H2'	32:1a:305:G:C8	2.43	0.54
32:1a:415:C:OP1	32:1a:497:C:O2'	2.21	0.54
47:1p:49:LEU:HD11	47:1p:51:VAL:HG23	1.89	0.54
1:2A:1833:A:O2'	3:2D:259:THR:HG21	2.08	0.54
19:2X:35:THR:HG22	19:2X:37:THR:H	1.72	0.54
32:2a:1342:A:H8	32:2a:1342:A:OP1	1.90	0.54
33:2b:114:ARG:O	33:2b:118:LEU:HD23	2.08	0.54
34:2c:181:ASN:ND2	34:2c:204:LEU:HD12	2.22	0.54
35:2d:61:LYS:NZ	35:2d:72:GLU:OE2	2.41	0.54
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.88	0.54
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.89	0.54
32:1a:400:U:H5'	35:1d:122:ARG:HD3	1.89	0.54
35:1d:8:VAL:HG22	35:1d:9:CYS:H	1.72	0.54
40:1i:13:ALA:HB2	40:1i:68:GLY:HA3	1.89	0.54
1:2A:1812:C:H1'	1:2A:2620:U:H5"	1.90	0.54
32:2a:218:U:H2'	32:2a:219:U:C6	2.42	0.54
32:2a:753:G:H4'	32:2a:1491:A:H4'	1.90	0.54
32:2a:1034:C:H2'	32:2a:1035:U:C6	2.43	0.54
32:2a:1330:U:H4'	40:2i:120:ARG:HD2	1.90	0.54
37:2f:99:ALA:HB3	49:2r:29:PHE:HE1	1.71	0.54
41:2j:17:ASP:OD1	41:2j:70:ARG:NH1	2.32	0.54
1:1A:172:C:H2'	1:1A:173:U:C6	2.43	0.54
1:1A:1735:A:N6	1:1A:1744:A:H2	1.96	0.54
3:1D:10:THR:OG1	3:1D:13:ARG:HB2	2.08	0.54
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.08	0.54
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.89	0.54
32:1a:154:G:O2'	32:1a:156:A:N6	2.40	0.54
32:1a:274:G:OP2	48:1q:92:ARG:NH2	2.41	0.54
41:1j:75:ILE:O	41:1j:77:PRO:HD3	2.07	0.54
1:2A:425:G:OP2	59:2A:3630:HOH:O	2.18	0.54
1:2A:907:A:C2	1:2A:962:A:C4	2.96	0.54
4:2E:12:THR:HG22	15:2T:58:ASN:OD1	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:112:GLY:O	4:2E:159:HIS:HA	2.08	0.54
6:2G:116:ASP:OD2	44:2m:68:GLY:HA3	2.08	0.54
10:2O:48:PRO:HB3	32:2a:1405:G:H5'	1.90	0.54
32:2a:544:U:H5'	32:2a:550:G:N2	2.22	0.54
32:2a:932:G:H21	32:2a:1209:A:N6	2.02	0.54
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.90	0.54
40:2i:50:LEU:HD23	40:2i:51:ARG:HG3	1.90	0.54
1:1A:1100:G:N2	1:1A:1149:C:O2	2.23	0.54
1:1A:2339:A:H2'	1:1A:2340:G:C8	2.43	0.54
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.35	0.54
26:14:26:SER:OG	26:14:27:THR:N	2.38	0.54
32:1a:504:A:N1	32:1a:520:C:H1'	2.23	0.54
32:1a:1221:A:H62	32:1a:1281:A:N6	2.06	0.54
32:1a:1359:U:H2'	32:1a:1360:A:H8	1.73	0.54
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.73	0.54
33:1b:211:ILE:O	33:1b:215:LEU:HB2	2.08	0.54
1:2A:321:G:H5"	1:2A:322:A:OP1	2.08	0.54
1:2A:988:G:O3'	59:2A:3628:HOH:O	2.18	0.54
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	1.90	0.54
5:2F:197:ASP:O	5:2F:200:GLU:HB2	2.08	0.54
14:2S:41:ASP:OD2	14:2S:44:LYS:NZ	2.40	0.54
32:2a:373:G:OP1	47:2p:3:LYS:HD2	2.07	0.54
32:2a:400:U:H2'	32:2a:401:U:C6	2.42	0.54
32:2a:485:C:H2'	32:2a:486:G:H8	1.72	0.54
32:2a:630:U:H2'	32:2a:631:C:C6	2.42	0.54
32:2a:1202:G:H21	50:2s:54:GLY:CA	2.21	0.54
1:1A:309:C:H2'	1:1A:310:C:C6	2.43	0.54
1:1A:1540:A:H2'	1:1A:1541:A:C8	2.42	0.54
32:1a:14:U:OP1	59:1a:2012:HOH:O	2.18	0.54
32:1a:172:C:H2'	32:1a:173:C:H6	1.73	0.54
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.90	0.54
40:1i:23:ASN:HD22	40:1i:24:GLY:N	2.06	0.54
45:1n:4:LYS:HA	45:1n:7:ILE:HG12	1.89	0.54
1:2A:810:A:H5'	3:2D:210:GLY:HA2	1.90	0.54
32:2a:125:A:O2'	32:2a:126:C:O5'	2.23	0.54
32:2a:956:A:H4'	32:2a:1304:C:N3	2.23	0.54
37:2f:89:MET:HE1	49:2r:72:ARG:HB3	1.88	0.54
1:1A:552:A:N1	1:1A:2063:A:H2'	2.23	0.54
1:1A:2315:G:H22	1:1A:2323:U:H3	1.56	0.54
6:1G:146:TYR:O	6:1G:149:VAL:HG12	2.07	0.54
32:1a:673:C:OP2	42:1k:55:LYS:NZ	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1375:G:N2	32:1a:1480:A:H8	2.05	0.54
42:1k:48:ILE:HG13	42:1k:63:LEU:HD22	1.90	0.54
1:2A:82:A:N1	1:2A:96:G:O2'	2.37	0.54
1:2A:235:G:H4'	1:2A:412:G:C5	2.44	0.54
1:2A:601:G:H2'	1:2A:602:C:C6	2.43	0.54
1:2A:2548:U:H2'	1:2A:2549:C:C6	2.43	0.54
6:2G:33:ARG:NH1	6:2G:162:THR:OG1	2.40	0.54
7:2H:117:PRO:HG3	7:2H:123:PHE:CD2	2.43	0.54
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.90	0.54
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.40	0.54
32:2a:823:U:O2'	32:2a:824:C:OP1	2.24	0.54
32:2a:1105:U:C4	32:2a:1106:A:N7	2.76	0.54
32:2a:1488:U:H2'	32:2a:1489:G:C8	2.42	0.54
36:2e:51:VAL:HG23	36:2e:52:PRO:HD3	1.90	0.54
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.08	0.54
1:1A:554:G:O4'	1:1A:554:G:N3	2.39	0.53
15:1T:118:ARG:HG3	15:1T:118:ARG:NH1	2.23	0.53
32:1a:137:G:H1	32:1a:217:C:H42	1.56	0.53
32:1a:978:U:H3	32:1a:1024:A:H61	1.55	0.53
32:1a:1036:G:N2	59:1a:2063:HOH:O	2.40	0.53
38:1g:152:ALA:O	38:1g:155:ARG:HB2	2.07	0.53
54:1x:75:C:OP1	59:1x:201:HOH:O	2.19	0.53
1:2A:909:A:H2'	1:2A:910:G:C8	2.43	0.53
32:2a:1299:C:OP1	45:2n:17:LYS:HD2	2.08	0.53
32:2a:1393:G:H2'	32:2a:1394:C:C6	2.43	0.53
32:2a:1394:C:H2'	32:2a:1395:C:H6	1.73	0.53
33:2b:150:SER:O	33:2b:150:SER:OG	2.19	0.53
1:1A:1378:C:OP1	59:1A:4145:HOH:O	2.19	0.53
4:1E:1:MET:HE3	4:1E:199:ARG:HB3	1.90	0.53
32:1a:931:G:H5'	32:1a:943:A:H61	1.74	0.53
33:1b:172:ILE:H	33:1b:172:ILE:HD12	1.73	0.53
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.73	0.53
39:1h:54:ASP:N	39:1h:54:ASP:OD1	2.41	0.53
1:2A:863:C:O2'	1:2A:885:U:H5"	2.09	0.53
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.09	0.53
32:2a:1200:C:H2'	32:2a:1201:U:C6	2.44	0.53
32:2a:1221:A:H62	32:2a:1281:A:H62	1.56	0.53
48:2q:66:SER:OG	48:2q:67:LYS:N	2.41	0.53
1:1A:2517:U:OP1	4:1E:144:ARG:NH2	2.41	0.53
32:1a:542:G:OP1	59:1a:2015:HOH:O	2.19	0.53
32:1a:1110:G:H5'	32:1a:1262:A:O2'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:94:ARG:O	38:1g:97:GLN:HB3	2.08	0.53
1:2A:82:A:H5"	20:2Y:8:LYS:HE3	1.90	0.53
1:2A:2227:G:H3'	1:2A:2228:A:H5"	1.88	0.53
1:2A:2323:U:C5	1:2A:2324:C:H5	2.27	0.53
8:2I:14:ASP:O	8:2I:17:GLN:HB3	2.08	0.53
12:2Q:109:VAL:HG13	12:2Q:113:GLN:HB2	1.90	0.53
32:2a:312:G:OP2	32:2a:347:G:O2'	2.26	0.53
32:2a:831:G:H2'	32:2a:832:G:H8	1.73	0.53
32:2a:1257:A:H2'	32:2a:1258:G:O4'	2.09	0.53
1:1A:956:A:H2'	12:1Q:9:TYR:OH	2.08	0.53
1:1A:1153:U:H6	1:1A:1154:C:C6	2.27	0.53
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.44	0.53
32:1a:202:A:H2'	32:1a:203:A:C4	2.44	0.53
32:1a:1026:C:C2'	32:1a:1027:A:H5'	2.39	0.53
32:1a:1141:C:H5	32:1a:1163:G:N1	2.01	0.53
1:2A:2382:G:O2'	28:26:46:HIS:ND1	2.40	0.53
1:2A:2765:A:N3	31:29:15:LYS:NZ	2.55	0.53
32:2a:433:U:H5'	35:2d:155:LEU:HD21	1.89	0.53
32:2a:434:G:N1	32:2a:480:A:OP2	2.32	0.53
32:2a:703:C:O2'	49:2r:49:LYS:HB3	2.08	0.53
32:2a:962:C:H2'	32:2a:963:C:H6	1.72	0.53
38:2g:26:PHE:CE1	38:2g:30:ILE:HD11	2.43	0.53
44:2m:15:VAL:O	44:2m:19:LEU:HD23	2.08	0.53
1:1A:266:C:OP2	59:1A:4141:HOH:O	2.18	0.53
1:1A:717:C:N4	59:1A:4304:HOH:O	2.40	0.53
1:1A:1158:U:H2'	1:1A:1159:G:C8	2.44	0.53
1:1A:1844:G:H4'	3:1D:51:VAL:HG21	1.91	0.53
1:1A:2249:G:N3	1:1A:2249:G:H2'	2.23	0.53
32:1a:254:G:H2'	32:1a:255:G:H8	1.72	0.53
32:1a:369:A:H2'	32:1a:370:A:H8	1.74	0.53
32:1a:523:A:H2'	32:1a:524:G:C8	2.42	0.53
32:1a:985:C:H42	32:1a:1002:G:H1	1.57	0.53
32:1a:1037:C:OP2	59:1a:2016:HOH:O	2.19	0.53
34:1c:78:GLY:HA3	34:1c:83:ARG:H	1.72	0.53
47:1p:15:PRO:O	47:1p:16:HIS:ND1	2.41	0.53
1:2A:1105:U:H4'	1:2A:1106:U:H5'	1.90	0.53
1:2A:1233:A:OP2	59:2A:3633:HOH:O	2.19	0.53
3:2D:108:PRO:HD2	3:2D:111:LEU:HG	1.90	0.53
32:2a:1490:U:H2'	32:2a:1491:A:C8	2.44	0.53
41:2j:37:PRO:HA	41:2j:72:VAL:HG12	1.90	0.53
1:1A:1210:U:H2'	1:1A:1211:C:C6	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.38	0.53
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.44	0.53
28:16:35:GLU:OE2	28:16:50:ARG:NH1	2.41	0.53
32:1a:424:G:OP2	35:1d:10:ARG:NH1	2.42	0.53
44:1m:12:ASN:O	44:1m:44:ARG:NH1	2.41	0.53
32:2a:516:A:H61	34:2c:193:TYR:HB2	1.74	0.53
32:2a:841:U:O2'	32:2a:843:A:N7	2.34	0.53
32:2a:983:A:H2'	32:2a:984:A:H5'	1.89	0.53
32:2a:1287:G:N2	32:2a:1313:G:H1'	2.24	0.53
46:2o:5:LYS:NZ	46:2o:5:LYS:H	2.06	0.53
1:1A:552:A:O2'	1:1A:553:A:H5'	2.08	0.53
1:1A:2347:A:H61	22:10:43:THR:HG22	1.73	0.53
2:1B:89:G:H2'	2:1B:90:A:C8	2.43	0.53
8:1I:106:GLY:HA2	8:1I:107:VAL:HB	1.90	0.53
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.90	0.53
1:2A:22:G:O3'	59:2A:3632:HOH:O	2.18	0.53
1:2A:1194:G:H2'	1:2A:1195:C:C6	2.43	0.53
1:2A:2308:C:H5	1:2A:2329:G:H21	1.57	0.53
3:2D:276:LYS:H	3:2D:276:LYS:CD	2.19	0.53
11:2P:39:LYS:HA	11:2P:45:LEU:HG	1.91	0.53
32:2a:144:A:H2'	32:2a:145:C:C6	2.43	0.53
32:2a:293:G:N2	32:2a:296:A:OP2	2.42	0.53
33:2b:119:GLU:OE2	33:2b:153:ARG:NH2	2.41	0.53
44:2m:51:ALA:O	44:2m:55:ARG:HB2	2.09	0.53
47:2p:28:ARG:NH1	47:2p:29:ASP:OD2	2.42	0.53
1:1A:138:A:H8	1:1A:1453:C:O2'	1.92	0.53
33:1b:51:LEU:HD23	33:1b:201:ILE:HD12	1.91	0.53
1:2A:1457:A:H2'	1:2A:1458:G:C8	2.43	0.53
1:2A:2760:A:O2'	7:2H:63:SER:O	2.17	0.53
6:2G:33:ARG:HB2	6:2G:33:ARG:HH11	1.74	0.53
32:2a:896:A:H2'	32:2a:897:A:O4'	2.09	0.53
32:2a:1296:C:OP2	50:2s:4:SER:OG	2.22	0.53
51:2t:43:LEU:O	51:2t:47:GLY:N	2.42	0.53
1:1A:1697:G:OP1	13:1R:40:LYS:NZ	2.41	0.53
32:1a:404:A:OP1	35:1d:113:SER:OG	2.15	0.53
39:1h:17:THR:HG22	39:1h:63:LEU:HG	1.91	0.53
1:2A:2061:C:OP2	9:2N:109:LYS:NZ	2.42	0.53
6:2G:32:PRO:HB3	6:2G:172:LEU:HD22	1.91	0.53
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.16	0.53
32:2a:526:G:P	35:2d:10:ARG:HH22	2.32	0.53
32:2a:836:G:O6	32:2a:847:G:H3'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1169:G:H4'	40:2i:111:ARG:NH1	2.24	0.53
1:1A:274:C:H2'	1:1A:275:C:C6	2.44	0.53
1:1A:558:U:H2'	1:1A:559:C:C6	2.44	0.53
1:1A:1149:C:H2'	1:1A:1150:U:H5	1.74	0.53
1:1A:1465:U:HO2'	1:1A:1466:G:P	2.32	0.53
26:14:47:GLN:O	26:14:49:PHE:N	2.41	0.53
32:1a:181:C:H2'	32:1a:182:C:H6	1.72	0.53
38:1g:59:LEU:HD11	38:1g:63:LYS:HE2	1.91	0.53
1:2A:346:G:O2'	1:2A:1249:U:N3	2.40	0.53
1:2A:542:G:H2'	1:2A:543:U:C6	2.44	0.53
1:2A:1002:U:OP2	12:2Q:14:ARG:NH1	2.42	0.53
1:2A:2668:A:O3'	7:2H:160:LYS:NZ	2.42	0.53
1:2A:2713:U:H4'	1:2A:2714:C:OP1	2.08	0.53
2:2B:19:G:H2'	2:2B:20:C:O4'	2.08	0.53
3:2D:71:ASP:CB	3:2D:103:ARG:HH22	2.22	0.53
13:2R:37:THR:HA	13:2R:111:LEU:HD12	1.91	0.53
24:22:1:MET:HE3	24:22:5:GLU:HB3	1.91	0.53
26:24:58:ARG:HG2	50:2s:67:VAL:HB	1.90	0.53
32:2a:61:A:N6	32:2a:104:C:N3	2.51	0.53
32:2a:810:C:H2'	32:2a:811:U:C6	2.42	0.53
32:2a:822:G:H1	32:2a:826:C:N4	2.07	0.53
1:1A:62:A:O3'	19:1X:71:GLY:HA3	2.09	0.52
3:1D:71:ASP:HB3	3:1D:103:ARG:NH2	2.20	0.52
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.91	0.52
32:1a:199:U:H2'	32:1a:200:C:H6	1.75	0.52
1:2A:353:A:HO2'	1:2A:354:A:H8	1.54	0.52
1:2A:898:G:H2'	1:2A:899:G:C8	2.44	0.52
1:2A:2483:G:H2'	1:2A:2486:C:H42	1.74	0.52
21:2Z:40:ASP:OD1	21:2Z:42:VAL:HG13	2.09	0.52
32:2a:986:C:H42	32:2a:1001:G:H1	1.56	0.52
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.91	0.52
42:2k:82:VAL:HB	42:2k:108:ILE:HG12	1.90	0.52
4:1E:120:TRP:CE3	4:1E:155:LYS:HD3	2.44	0.52
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.90	0.52
8:1I:72:LEU:C	8:1I:74:ASN:H	2.18	0.52
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.91	0.52
26:14:53:GLU:HB3	26:14:54:GLY:CA	2.34	0.52
32:1a:508:G:H2'	32:1a:509:C:C6	2.43	0.52
1:2A:1094:C:H1'	1:2A:1158:U:O2'	2.09	0.52
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.09	0.52
32:2a:646:G:H2'	32:2a:647:A:C8	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:3:ARG:HD3	35:2d:118:ARG:HD2	1.91	0.52
37:2f:25:ILE:HD13	37:2f:82:ARG:HE	1.73	0.52
38:2g:68:ASN:ND2	38:2g:128:ALA:O	2.42	0.52
51:2t:36:LEU:HD12	51:2t:55:ILE:HG23	1.91	0.52
1:1A:224:C:H2'	1:1A:225:C:C6	2.44	0.52
1:1A:354:A:N1	59:1A:4247:HOH:O	2.34	0.52
1:1A:922:C:H2'	1:1A:923:U:O4'	2.10	0.52
1:1A:1184:C:O3'	9:1N:25:ARG:NH1	2.41	0.52
1:1A:2052:A:C6	1:1A:2509:C:H1'	2.45	0.52
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.91	0.52
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.90	0.52
32:1a:859:G:OP2	43:1l:12:ARG:NH2	2.42	0.52
32:1a:953:A:H5'	32:1a:953:A:H8	1.73	0.52
32:1a:1056:U:H2'	32:1a:1057:G:C8	2.45	0.52
1:2A:821:G:N3	59:2A:3694:HOH:O	2.33	0.52
1:2A:1342:C:H2'	1:2A:1343:C:H6	1.74	0.52
1:2A:2568:G:H2'	1:2A:2569:C:H6	1.74	0.52
25:23:5:LYS:HE2	25:23:34:GLU:OE2	2.09	0.52
32:2a:136:A:H1'	32:2a:177:U:O2	2.09	0.52
32:2a:1170:A:H2'	32:2a:1171:C:O4'	2.09	0.52
32:2a:1456:C:OP2	59:2a:3330:HOH:O	2.19	0.52
1:1A:1920:G:N3	1:1A:1920:G:H2'	2.24	0.52
33:1b:21:ARG:HB3	33:1b:38:GLY:O	2.09	0.52
1:2A:1873:C:H5'	3:2D:253:GLN:NE2	2.24	0.52
6:2G:73:ALA:HB3	6:2G:85:GLY:H	1.75	0.52
13:2R:21:TYR:OH	13:2R:43:GLU:HG2	2.10	0.52
32:2a:538:C:H2'	32:2a:539:C:C6	2.44	0.52
35:2d:201:GLN:HE22	36:2e:116:THR:HG23	1.75	0.52
37:2f:67:MET:HE1	37:2f:75:LEU:HD12	1.90	0.52
52:2u:9:ARG:O	52:2u:13:ILE:HG13	2.09	0.52
1:1A:1155:G:H21	1:1A:1156:A:H2	1.57	0.52
6:1G:115:ARG:HG3	6:1G:136:ARG:HH22	1.74	0.52
32:1a:658:G:H2'	32:1a:659:A:C8	2.44	0.52
33:1b:32:ILE:HD11	33:1b:190:THR:HG23	1.90	0.52
49:1r:24:ALA:C	49:1r:26:LEU:H	2.18	0.52
1:2A:10:G:N7	59:2A:3696:HOH:O	2.34	0.52
1:2A:732:G:N2	1:2A:834:A:H61	2.07	0.52
1:2A:1924:G:OP1	3:2D:241:PRO:HB2	2.08	0.52
32:2a:1273:G:H2'	32:2a:1274:U:C6	2.45	0.52
33:2b:71:VAL:HA	33:2b:93:VAL:HG23	1.90	0.52
44:2m:37:THR:C	44:2m:55:ARG:HH22	2.17	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:10:LEU:HB3	51:2t:12:ALA:H	1.74	0.52
1:1A:1726:U:OP2	59:1A:4147:HOH:O	2.19	0.52
26:14:15:ILE:HD12	26:14:21:VAL:HG22	1.91	0.52
32:1a:101:G:H2'	32:1a:102:G:O4'	2.10	0.52
32:1a:200:C:H2'	32:1a:201:C:C6	2.45	0.52
32:1a:218:U:H2'	32:1a:219:U:C6	2.44	0.52
32:1a:304:C:H2'	32:1a:305:G:H8	1.75	0.52
32:1a:373:G:OP1	47:1p:3:LYS:HD2	2.08	0.52
33:1b:200:ILE:O	33:1b:202:PRO:HD3	2.10	0.52
3:2D:71:ASP:HB3	3:2D:103:ARG:HH22	1.75	0.52
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.45	0.52
32:2a:615:G:H2'	32:2a:616:A:H8	1.73	0.52
32:2a:1189:G:H2'	32:2a:1190:C:H6	1.74	0.52
33:2b:92:TYR:CD2	33:2b:92:TYR:C	2.88	0.52
38:2g:16:LEU:HD23	40:2i:41:VAL:HG12	1.92	0.52
11:1P:95:VAL:HG22	11:1P:125:VAL:HB	1.92	0.52
32:1a:472:A:H2'	32:1a:473:C:O4'	2.10	0.52
32:1a:1297:U:O2'	32:1a:1342:A:N3	2.32	0.52
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.92	0.52
1:2A:1455:G:H2'	1:2A:1456:C:H6	1.74	0.52
15:2T:1:MET:HE2	15:2T:3:ARG:HG2	1.91	0.52
32:2a:21:U:H2'	32:2a:22:G:O4'	2.09	0.52
32:2a:1095:C:N3	34:2c:178:LEU:HD22	2.24	0.52
32:2a:1379:A:OP2	59:2a:3332:HOH:O	2.19	0.52
33:2b:187:LEU:HD13	33:2b:187:LEU:H	1.75	0.52
43:2l:27:LEU:HD13	43:2l:98:TYR:CE1	2.45	0.52
32:1a:954:G:O6	59:1a:2017:HOH:O	2.19	0.52
32:1a:1184:G:N2	45:1n:43:CYS:HB3	2.25	0.52
32:1a:1205:C:P	50:1s:78:ARG:HH21	2.33	0.52
32:1a:1240:G:H2'	32:1a:1241:C:C6	2.44	0.52
33:1b:87:ARG:NH1	33:1b:233:SER:OG	2.43	0.52
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.92	0.52
51:1t:56:MET:HE2	51:1t:85:MET:HA	1.91	0.52
1:2A:104:C:H2'	1:2A:105:U:H6	1.75	0.52
1:2A:1282:A:OP1	59:2A:3635:HOH:O	2.19	0.52
5:2F:185:ASP:OD1	5:2F:188:ARG:NH1	2.42	0.52
32:2a:209:U:H3'	32:2a:210:U:H6	1.74	0.52
32:2a:228:G:H1'	32:2a:258:A:N1	2.25	0.52
32:2a:623:G:O5'	59:2a:3329:HOH:O	2.19	0.52
32:2a:1088:A:H2'	32:2a:1089:G:H8	1.74	0.52
32:2a:1116:G:H1	32:2a:1124:C:N4	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:11:ARG:HH22	34:2c:180:ALA:HB3	1.75	0.52
41:2j:50:ILE:HD11	41:2j:57:LYS:HD3	1.92	0.52
43:2l:24:VAL:HG23	43:2l:98:TYR:CE1	2.44	0.52
1:1A:2297:A:H4'	1:1A:2298:A:O4'	2.10	0.52
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.26	0.52
26:14:58:ARG:HD2	50:1s:65:ASN:O	2.10	0.52
43:1l:5:PRO:HG2	43:1l:10:LEU:HD21	1.91	0.52
1:2A:1047:G:H2'	1:2A:1048:G:O4'	2.10	0.52
1:2A:2704:A:H2'	1:2A:2705:G:H8	1.74	0.52
32:2a:1267:A:OP2	52:2u:24:ARG:NH1	2.43	0.52
1:1A:286:G:N7	1:1A:447:U:H2'	2.25	0.52
1:1A:1232:U:H4'	17:1V:79:VAL:HG22	1.92	0.52
1:1A:1323:A:OP1	13:1R:36:THR:HG23	2.10	0.52
1:1A:1409:G:N7	23:11:3:LYS:HE2	2.25	0.52
1:1A:2622:U:C4	27:15:3:LYS:HG2	2.45	0.52
1:1A:2723:U:O2'	1:1A:2725:A:H5'	2.10	0.52
32:1a:266:A:H2'	32:1a:267:C:C6	2.45	0.52
32:1a:354:U:H2'	32:1a:355:U:H6	1.75	0.52
1:2A:1625:A:H2'	1:2A:1626:A:C8	2.44	0.52
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.90	0.52
19:2X:35:THR:HG22	19:2X:37:THR:N	2.25	0.52
32:2a:68:C:H2'	32:2a:69:G:C8	2.45	0.52
32:2a:1041:G:H2'	32:2a:1042:C:O4'	2.10	0.52
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.57	0.52
34:2c:121:ALA:HB1	34:2c:189:ALA:HB2	1.90	0.52
49:2r:29:PHE:HD1	49:2r:29:PHE:H	1.57	0.52
1:1A:183:A:OP1	11:1P:46:LYS:NZ	2.43	0.51
1:1A:2043:U:O2'	1:1A:2628:C:H5'	2.10	0.51
14:1S:15:ARG:HE	14:1S:88:ASP:CG	2.18	0.51
23:11:21:ARG:HG2	23:11:21:ARG:NH1	2.16	0.51
29:17:34:ARG:NH1	29:17:41:ARG:O	2.42	0.51
32:1a:94:C:H2'	32:1a:95:A:C8	2.45	0.51
32:1a:924:A:H2'	32:1a:925:G:C8	2.46	0.51
32:1a:1151:A:H2'	32:1a:1152:A:C8	2.45	0.51
44:1m:20:THR:C	44:1m:22:ILE:H	2.18	0.51
50:1s:3:ARG:HH12	50:1s:10:PHE:HB2	1.73	0.51
1:2A:324:G:N2	1:2A:339:C:O2	2.31	0.51
1:2A:1518:A:N6	1:2A:1566:G:O2'	2.43	0.51
32:2a:1191:C:O2'	32:2a:1196:C:N4	2.43	0.51
1:1A:125:C:O3'	59:1A:4149:HOH:O	2.19	0.51
1:1A:2307:U:OP2	14:1S:9:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:179:GLU:HB3	4:1E:181:LEU:HD22	1.92	0.51
8:1I:68:LEU:HD11	8:1I:109:ILE:HD11	1.92	0.51
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.10	0.51
32:1a:68:C:H2'	32:1a:69:G:H8	1.74	0.51
32:1a:124:G:C6	32:1a:189:U:H4'	2.45	0.51
32:1a:143:G:N2	32:1a:169:C:N3	2.53	0.51
32:1a:1286:G:C6	32:1a:1287:G:N1	2.79	0.51
1:2A:173:U:H4'	1:2A:206:A:H4'	1.92	0.51
1:2A:609:C:OP2	11:2P:21:ARG:NH2	2.43	0.51
1:2A:945:A:H2'	1:2A:946:A:H8	1.74	0.51
1:2A:2017:C:H4'	1:2A:2018:G:OP1	2.09	0.51
3:2D:71:ASP:OD2	3:2D:103:ARG:NH2	2.42	0.51
3:2D:137:PRO:O	3:2D:140:THR:HG23	2.11	0.51
5:2F:117:ARG:HH12	11:2P:1:MET:H2	1.56	0.51
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.93	0.51
25:23:39:ASP:OD1	25:23:44:ARG:HD2	2.10	0.51
32:2a:954:G:P	45:2n:32:SER:H	2.33	0.51
1:1A:355:A:OP1	59:1A:4148:HOH:O	2.19	0.51
1:1A:468:A:H1'	1:1A:1245:C:O4'	2.10	0.51
1:1A:1451:U:H2'	1:1A:1452:C:C6	2.46	0.51
1:1A:2207:G:H2'	1:1A:2208:G:H8	1.76	0.51
5:1F:18:ARG:HG2	5:1F:19:GLU:H	1.75	0.51
12:1Q:60:ARG:CZ	12:1Q:60:ARG:N	2.72	0.51
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.92	0.51
32:1a:640:C:O2'	46:1o:28:GLN:NE2	2.37	0.51
32:1a:1271:A:N1	32:1a:1354:G:O2'	2.41	0.51
2:2B:119:G:H2'	2:2B:120:A:O4'	2.10	0.51
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.92	0.51
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.10	0.51
1:1A:859:U:H2'	1:1A:860:C:C6	2.45	0.51
1:1A:942:C:H2'	1:1A:943:C:C6	2.45	0.51
1:1A:1066:A:C8	1:1A:1066:A:H3'	2.45	0.51
1:1A:1873:C:H5'	3:1D:253:GLN:NE2	2.25	0.51
1:1A:2429:A:H2'	1:1A:2430:U:C6	2.45	0.51
1:1A:2640:A:O2'	1:1A:2641:G:OP2	2.25	0.51
3:1D:37:LEU:HD13	3:1D:87:ASN:ND2	2.26	0.51
32:1a:68:C:H2'	32:1a:69:G:C8	2.46	0.51
32:1a:582:U:H2'	32:1a:583:C:C6	2.43	0.51
32:1a:1101:C:H1'	32:1a:1161:A:C5	2.45	0.51
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.45	0.51
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:15:ALA:HA	42:1k:77:MET:HA	1.92	0.51
1:2A:480:C:N3	1:2A:497:A:H2'	2.26	0.51
1:2A:1020:G:C2	1:2A:1035:A:C8	2.98	0.51
1:2A:1092:G:H1'	1:2A:1155:G:N2	2.24	0.51
1:2A:1887:G:O2'	1:2A:1906:A:N6	2.43	0.51
2:2B:44:G:OP1	6:2G:98:ARG:NH2	2.28	0.51
32:2a:669:G:N2	32:2a:670:U:O4	2.43	0.51
32:2a:1362:G:C5	32:2a:1363:U:H5	2.28	0.51
1:1A:216:A:H3'	1:1A:217:A:C5'	2.41	0.51
1:1A:504:A:N3	1:1A:506:G:H5"	2.25	0.51
1:1A:1552:A:O2'	1:1A:1553:A:H8	1.91	0.51
2:1B:7:G:H5'	14:1S:29:PHE:CE2	2.46	0.51
19:1X:57:LEU:CD1	19:1X:78:LYS:HB2	2.41	0.51
27:15:16:ARG:HG2	27:15:16:ARG:HH11	1.76	0.51
32:1a:127:C:H2'	32:1a:128:U:H6	1.76	0.51
32:1a:720:C:H2'	32:1a:721:A:C8	2.45	0.51
35:1d:172:PRO:HB2	35:1d:187:ARG:NH2	2.25	0.51
40:1i:86:VAL:HG13	40:1i:96:LEU:HD12	1.93	0.51
1:2A:356:G:H5"	1:2A:357:C:OP2	2.11	0.51
1:2A:2037:U:H2'	1:2A:2038:U:C6	2.45	0.51
1:2A:2419:U:H2'	1:2A:2420:G:C8	2.46	0.51
3:2D:134:ARG:HD3	3:2D:135:PHE:CE1	2.45	0.51
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.11	0.51
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.90	0.51
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.92	0.51
32:2a:1088:A:H3'	59:2a:3372:HOH:O	2.10	0.51
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.91	0.51
50:2s:3:ARG:NH2	50:2s:8:GLY:O	2.43	0.51
1:1A:2575:A:C2	1:1A:2658:U:H4'	2.46	0.51
59:1A:5442:HOH:O	23:11:33:LYS:HE3	2.10	0.51
2:1B:90:A:N7	2:1B:91:C:H1'	2.25	0.51
3:1D:126:GLN:HE21	3:1D:127:VAL:H	1.58	0.51
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.91	0.51
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.92	0.51
33:1b:74:LYS:HE2	33:1b:166:ASP:HB2	1.91	0.51
41:1j:81:THR:O	41:1j:83:GLU:N	2.44	0.51
47:1p:57:ARG:HH12	47:1p:79:VAL:HA	1.75	0.51
50:1s:63:THR:HG23	50:1s:66:MET:HE3	1.92	0.51
1:2A:172:C:H2'	1:2A:173:U:H6	1.76	0.51
1:2A:2650:A:N7	1:2A:2787:A:H2	2.09	0.51
1:2A:2659:C:H2'	1:2A:2660:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2830:A:H2'	1:2A:2831:G:C8	2.46	0.51
3:2D:77:ALA:HB2	3:2D:97:TYR:CD2	2.46	0.51
6:2G:15:VAL:HG13	6:2G:175:LEU:HD23	1.93	0.51
32:2a:400:U:H2'	32:2a:401:U:H6	1.73	0.51
32:2a:429:C:H2'	32:2a:430:U:C6	2.46	0.51
32:2a:1134:A:O2'	32:2a:1135:A:H8	1.92	0.51
32:2a:1219:C:O3'	32:2a:1282:G:N2	2.43	0.51
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.25	0.51
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.93	0.51
9:1N:8:GLN:HE21	9:1N:8:GLN:HA	1.76	0.51
15:1T:127:ALA:O	15:1T:128:GLU:HB3	2.10	0.51
32:1a:963:C:H2'	32:1a:964:A:C8	2.46	0.51
40:1i:53:VAL:O	40:1i:55:ALA:N	2.44	0.51
44:1m:3:ARG:HG3	44:1m:4:ILE:N	2.25	0.51
1:2A:358:C:H4'	20:2Y:73:ARG:HD2	1.93	0.51
1:2A:913:C:H2'	1:2A:914:U:H6	1.75	0.51
1:2A:968:C:H2'	1:2A:969:C:H6	1.76	0.51
3:2D:145:VAL:HB	3:2D:155:LEU:HB2	1.92	0.51
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.92	0.51
32:2a:925:G:H2'	32:2a:926:C:O4'	2.11	0.51
32:2a:1054:C:OP1	36:2e:27:ARG:NH2	2.43	0.51
44:2m:37:THR:HB	44:2m:55:ARG:NH1	2.15	0.51
1:1A:775:G:C6	3:1D:208:LYS:HB2	2.45	0.51
1:1A:931:C:H3'	1:1A:932:C:H5"	1.92	0.51
1:1A:1086:C:H42	1:1A:1159:G:H1	1.57	0.51
32:1a:198:G:H21	51:1t:102:GLY:C	2.17	0.51
32:1a:893:A:H3'	32:1a:894:G:H5"	1.93	0.51
32:1a:955:A:H2'	32:1a:956:A:H5"	1.91	0.51
32:1a:1198:G:H5"	45:1n:5:ALA:HB2	1.92	0.51
1:2A:117:U:OP1	59:2A:3638:HOH:O	2.19	0.51
1:2A:1104:G:H5"	1:2A:1105:U:H2'	1.92	0.51
1:2A:1210:U:H2'	1:2A:1211:C:C6	2.46	0.51
1:2A:1320:A:N3	1:2A:1321:A:H1'	2.26	0.51
1:2A:2050:G:H2'	1:2A:2052:A:OP1	2.11	0.51
1:2A:2376:G:O6	30:28:39:LYS:HE3	2.11	0.51
7:2H:46:GLU:HB2	7:2H:49:VAL:HG12	1.91	0.51
16:2U:112:ARG:NH2	17:2V:47:VAL:HB	2.25	0.51
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.36	0.51
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.35	0.51
33:2b:13:ALA:HB1	33:2b:17:PHE:HB3	1.91	0.51
12:1Q:21:THR:HG21	12:1Q:101:ARG:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:89:G:H2'	32:1a:90:U:H6	1.76	0.51
32:1a:487:C:H2'	32:1a:488:C:C6	2.45	0.51
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.92	0.51
35:1d:31:CYS:SG	35:1d:33:MET:HB2	2.51	0.51
1:2A:33:C:O2'	1:2A:34:G:OP1	2.28	0.51
1:2A:982:G:OP1	30:28:52:LYS:HD2	2.11	0.51
1:2A:1096:G:H2'	1:2A:1097:C:C6	2.46	0.51
1:2A:1565:U:H2'	1:2A:1566:G:O4'	2.11	0.51
2:2B:54:G:N2	2:2B:55:U:O2	2.44	0.51
7:2H:106:THR:HG22	7:2H:112:PRO:HB3	1.93	0.51
32:2a:1306:A:H4'	32:2a:1344:C:H4'	1.93	0.51
33:2b:170:GLU:O	33:2b:174:VAL:HG23	2.11	0.51
36:2e:68:GLU:HG2	36:2e:70:PRO:HD3	1.92	0.51
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	1.93	0.51
45:2n:11:LYS:NZ	45:2n:11:LYS:HB2	2.26	0.51
32:1a:744:G:O2'	48:1q:98:LEU:HD12	2.11	0.51
37:1f:86:ARG:O	37:1f:87:ARG:HG2	2.11	0.51
45:1n:41:ARG:HG3	45:1n:42:ILE:N	2.25	0.51
1:2A:468:A:H1'	1:2A:1245:C:O4'	2.10	0.51
1:2A:858:C:H2'	1:2A:859:U:H6	1.77	0.51
1:2A:910:G:C6	1:2A:911:C:N4	2.79	0.51
14:2S:23:ARG:NH2	14:2S:84:GLN:HB3	2.25	0.51
32:2a:1067:G:H5'	32:2a:1085:A:OP2	2.11	0.51
34:2c:186:PHE:HB3	34:2c:198:VAL:O	2.11	0.51
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.93	0.51
51:2t:33:ILE:HG13	51:2t:62:LEU:HD22	1.92	0.51
54:2x:47:U:H4'	54:2x:48:C:H5'	1.92	0.51
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.11	0.50
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	1.91	0.50
32:1a:8:G:H5'	32:1a:294:A:O4'	2.11	0.50
32:1a:403:G:O4'	35:1d:119:GLN:NE2	2.44	0.50
32:1a:531:A:OP1	59:1a:2019:HOH:O	2.20	0.50
33:1b:21:ARG:C	33:1b:23:ARG:H	2.14	0.50
43:1l:89:ARG:NH2	43:1l:91:LYS:HG3	2.26	0.50
1:2A:237:C:O2	30:28:12:LYS:NZ	2.31	0.50
1:2A:647:G:H2'	1:2A:648:C:C6	2.46	0.50
1:2A:1090:A:H5"	1:2A:1092:G:O4'	2.11	0.50
1:2A:1096:G:H2'	1:2A:1097:C:H6	1.76	0.50
1:2A:1150:U:H2'	1:2A:1151:G:H8	1.76	0.50
32:2a:395:G:H2'	32:2a:396:C:C6	2.46	0.50
33:2b:119:GLU:HG3	33:2b:142:LEU:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2z:11:ARG:HB3	55:2z:12:PRO:HD2	1.92	0.50
5:1F:28:ILE:HA	5:1F:112:MET:HG2	1.92	0.50
8:1I:14:ASP:O	8:1I:17:GLN:HB3	2.11	0.50
9:1N:68:GLU:HG2	9:1N:88:GLU:OE2	2.12	0.50
32:1a:352:A:N3	32:1a:364:U:O2'	2.36	0.50
32:1a:842:A:H2'	32:1a:843:A:C8	2.46	0.50
32:1a:999:U:H2'	32:1a:1000:G:C8	2.47	0.50
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.93	0.50
42:1k:29:ILE:HG23	42:1k:44:SER:HB3	1.94	0.50
1:2A:720:G:O2'	5:2F:74:ARG:HD3	2.12	0.50
1:2A:1015:C:OP2	59:2A:3634:HOH:O	2.19	0.50
1:2A:1073:A:N6	1:2A:1170:G:H2'	2.27	0.50
1:2A:1682:C:H2'	1:2A:1683:A:C8	2.45	0.50
1:2A:1814:A:OP2	59:2A:3602:HOH:O	2.19	0.50
1:2A:2095:U:H2'	1:2A:2096:U:C6	2.46	0.50
2:2B:50:G:OP1	14:2S:63:THR:N	2.45	0.50
26:24:62:ARG:C	26:24:64:GLY:H	2.19	0.50
32:2a:485:C:H2'	32:2a:486:G:C8	2.46	0.50
32:2a:981:G:H1	32:2a:1021:C:H42	1.59	0.50
34:2c:19:GLU:O	34:2c:40:ARG:NH2	2.44	0.50
34:2c:186:PHE:CE2	34:2c:200:ALA:HB3	2.46	0.50
38:2g:116:ALA:O	38:2g:120:ILE:HG12	2.11	0.50
39:2h:33:GLU:HG2	39:2h:48:TYR:CE1	2.46	0.50
39:2h:51:VAL:CG2	39:2h:60:ARG:HB2	2.39	0.50
1:1A:201:A:H2'	1:1A:202:G:O4'	2.11	0.50
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	1.92	0.50
4:1E:111:ARG:HG3	4:1E:160:TYR:CD2	2.46	0.50
7:1H:56:SER:OG	7:1H:61:HIS:ND1	2.37	0.50
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.46	0.50
32:1a:722:C:H2'	32:1a:723:C:H6	1.77	0.50
32:1a:1328:A:H5"	40:1i:120:ARG:HH12	1.77	0.50
1:2A:1457:A:H2'	1:2A:1458:G:H8	1.76	0.50
7:2H:95:ARG:HG2	7:2H:106:THR:OG1	2.10	0.50
20:2Y:44:ILE:H	20:2Y:44:ILE:HD13	1.75	0.50
44:2m:20:THR:O	44:2m:22:ILE:N	2.42	0.50
50:2s:27:GLU:HB2	50:2s:28:LYS:HD3	1.91	0.50
1:1A:924:A:H2'	1:1A:925:G:H5'	1.94	0.50
1:1A:2254:U:H2'	1:1A:2255:U:C6	2.47	0.50
4:1E:34:VAL:HG13	4:1E:48:GLN:HG2	1.93	0.50
32:1a:39:G:H22	32:1a:393:A:H5'	1.75	0.50
32:1a:648:G:N2	32:1a:725:G:H1	2.06	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.94	0.50
35:1d:117:ALA:O	35:1d:121:VAL:HG23	2.12	0.50
42:1k:20:TYR:HB2	42:1k:31:THR:HG23	1.93	0.50
1:2A:363:A:H2'	1:2A:364:G:O4'	2.12	0.50
1:2A:867:A:H2'	1:2A:990:G:H5"	1.93	0.50
1:2A:2428:C:OP1	11:2P:65:ARG:NH2	2.45	0.50
1:2A:2685:G:H2'	1:2A:2686:A:C8	2.46	0.50
1:2A:2845:U:H2'	1:2A:2846:G:C8	2.46	0.50
15:2T:122:ASP:OD2	32:2a:1426:G:O2'	2.29	0.50
32:2a:501:G:N2	32:2a:517:A:OP2	2.43	0.50
32:2a:1222:U:H3'	32:2a:1223:G:H5'	1.93	0.50
47:2p:28:ARG:HG3	47:2p:29:ASP:N	2.26	0.50
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.10	0.50
48:2q:63:ARG:HG2	48:2q:64:PRO:HD2	1.93	0.50
5:1F:18:ARG:NH2	5:1F:127:GLU:OE2	2.45	0.50
12:1Q:2:LEU:H	12:1Q:2:LEU:HD12	1.76	0.50
20:1Y:13:VAL:HB	20:1Y:72:VAL:HG13	1.93	0.50
26:14:63:TYR:N	26:14:63:TYR:CD1	2.79	0.50
39:1h:119:LEU:HB3	39:1h:123:GLU:HB3	1.93	0.50
1:2A:12:A:N1	1:2A:549:U:H2'	2.27	0.50
6:2G:12:TYR:HA	6:2G:16:ARG:HG3	1.94	0.50
6:2G:48:GLU:HA	6:2G:51:ARG:NE	2.26	0.50
12:2Q:97:VAL:HG21	12:2Q:103:MET:HE3	1.92	0.50
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.94	0.50
32:2a:835:C:H2'	32:2a:836:G:O4'	2.12	0.50
32:2a:927:A:H61	32:2a:1214:U:H3	1.59	0.50
32:2a:1250:A:H2'	32:2a:1251:A:C8	2.47	0.50
33:2b:87:ARG:NH1	33:2b:233:SER:HB3	2.27	0.50
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.92	0.50
43:2l:79:GLU:HG2	43:2l:80:HIS:CD2	2.47	0.50
32:1a:658:G:H2'	32:1a:659:A:H8	1.77	0.50
32:1a:1248:G:N2	32:1a:1252:C:C2	2.79	0.50
41:1j:26:ALA:HB1	41:1j:84:GLN:HE22	1.76	0.50
45:1n:3:ARG:O	45:1n:7:ILE:HG23	2.12	0.50
51:1t:56:MET:HE3	51:1t:88:VAL:HG21	1.93	0.50
1:2A:1067:G:N7	9:2N:66:LYS:HE2	2.27	0.50
1:2A:2539:U:O2'	1:2A:2540:G:H3'	2.12	0.50
32:2a:212:G:H2'	32:2a:213:C:C6	2.47	0.50
32:2a:900:G:N3	32:2a:1381:A:H2	2.09	0.50
32:2a:1049:C:H2'	32:2a:1050:A:C8	2.47	0.50
33:2b:16:HIS:O	33:2b:18:GLY:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:10:LEU:HB2	37:2f:59:TYR:HB3	1.93	0.50
37:2f:22:GLU:O	37:2f:26:ILE:HG13	2.11	0.50
40:2i:17:VAL:HG11	40:2i:80:GLY:C	2.37	0.50
1:1A:206:A:C2	1:1A:223:U:H4'	2.47	0.50
1:1A:353:A:HO2'	1:1A:354:A:H8	1.54	0.50
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.94	0.50
21:1Z:110:GLY:HA3	21:1Z:174:VAL:HG11	1.93	0.50
32:1a:267:C:H2'	32:1a:268:C:C6	2.47	0.50
32:1a:1503:G:OP1	42:1k:120:ARG:NH2	2.45	0.50
34:1c:71:ALA:HB2	34:1c:106:VAL:HB	1.94	0.50
50:1s:27:GLU:HB2	50:1s:28:LYS:HB3	1.93	0.50
1:2A:2272:C:O2'	1:2A:2273:U:H5'	2.12	0.50
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.93	0.50
21:2Z:183:LEU:HD12	21:2Z:186:GLU:OE1	2.11	0.50
32:2a:604:C:C2	35:2d:135:LEU:HG	2.47	0.50
32:2a:1362:G:C4	32:2a:1363:U:H5	2.29	0.50
32:2a:1490:U:H2'	32:2a:1491:A:H8	1.75	0.50
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.80	0.50
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.94	0.50
39:2h:23:SER:HA	39:2h:63:LEU:HD22	1.94	0.50
45:2n:53:LEU:HD13	45:2n:54:PRO:HD2	1.93	0.50
1:1A:1067:G:N2	1:1A:1068:U:O4	2.43	0.50
1:1A:1198:C:OP1	16:1U:92:ARG:NH1	2.44	0.50
1:1A:1475:C:H2'	1:1A:1476:U:C6	2.46	0.50
32:1a:529:C:H5'	35:1d:72:GLU:HG2	1.94	0.50
32:1a:613:G:H2'	32:1a:614:G:O4'	2.11	0.50
34:1c:156:ARG:NH2	34:1c:159:GLY:O	2.44	0.50
38:1g:28:ASN:H	38:1g:28:ASN:HD22	1.59	0.50
1:2A:885:U:H2'	1:2A:886:C:C6	2.46	0.50
1:2A:1211:C:H2'	1:2A:1212:U:C6	2.46	0.50
1:2A:1240:C:H2'	1:2A:1241:G:C8	2.45	0.50
1:2A:2331:A:N3	1:2A:2331:A:H2'	2.27	0.50
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.93	0.50
8:2I:129:THR:HG22	8:2I:139:GLN:NE2	2.24	0.50
16:2U:83:LEU:O	16:2U:87:GLY:N	2.45	0.50
20:2Y:37:VAL:HG21	20:2Y:72:VAL:HG21	1.93	0.50
32:2a:143:G:H2'	32:2a:144:A:C8	2.46	0.50
32:2a:1084:A:N3	32:2a:1085:A:H1'	2.26	0.50
32:2a:1120:C:O2'	32:2a:1121:G:N3	2.45	0.50
34:2c:124:ILE:HD11	34:2c:189:ALA:CB	2.40	0.50
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.77	0.50
1:1A:1223:C:H2'	1:1A:1224:C:H6	1.75	0.50
1:1A:2858:U:H4'	1:1A:2877:A:C2	2.47	0.50
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.47	0.50
10:1O:98:VAL:HG13	10:1O:117:LEU:HB3	1.94	0.50
32:1a:385:A:C6	32:1a:386:C:H1'	2.46	0.50
32:1a:775:G:OP2	59:1a:2018:HOH:O	2.19	0.50
32:1a:954:G:H5'	32:1a:1340:U:O2'	2.12	0.50
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.22	0.50
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.94	0.50
47:1p:74:LEU:HD22	47:1p:79:VAL:HG21	1.94	0.50
55:1z:9:ARG:HB3	55:1z:10:PRO:CD	2.33	0.50
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	1.93	0.50
17:2V:21:ARG:HG2	17:2V:91:TYR:CD2	2.47	0.50
32:2a:543:A:H4'	32:2a:544:U:O5'	2.12	0.50
32:2a:924:A:H2'	32:2a:925:G:C8	2.46	0.50
32:2a:1312:U:H4'	44:2m:23:TYR:CE1	2.47	0.50
1:1A:842:C:H2'	1:1A:843:C:C6	2.47	0.49
32:1a:761:A:OP1	59:1a:2020:HOH:O	2.20	0.49
33:1b:71:VAL:HG11	33:1b:170:GLU:HG2	1.94	0.49
1:2A:396:G:OP2	59:2A:3639:HOH:O	2.20	0.49
29:27:24:THR:O	29:27:28:ARG:HG3	2.11	0.49
32:2a:754:C:OP1	59:2a:3333:HOH:O	2.19	0.49
32:2a:1220:A:C2	32:2a:1285:C:H4'	2.47	0.49
32:2a:1260:U:H5"	32:2a:1261:A:H5'	1.93	0.49
39:2h:12:ARG:HD2	39:2h:26:VAL:HG12	1.93	0.49
1:1A:551:C:C5	1:1A:2791:U:H2'	2.47	0.49
1:1A:637:U:H5"	59:1A:5743:HOH:O	2.11	0.49
1:1A:830:A:H5'	1:1A:831:G:OP1	2.12	0.49
6:1G:170:ARG:HD3	6:1G:174:GLU:HG3	1.93	0.49
32:1a:137:G:H2'	32:1a:138:A:C8	2.45	0.49
32:1a:199:U:H2'	32:1a:200:C:C6	2.47	0.49
32:1a:691:C:OP1	42:1k:85:ARG:NH1	2.45	0.49
32:1a:722:C:H2'	32:1a:723:C:C6	2.47	0.49
42:1k:31:THR:HA	42:1k:42:TRP:HA	1.94	0.49
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.12	0.49
1:2A:324:G:OP2	20:2Y:84:ARG:NH2	2.45	0.49
1:2A:2088:G:O2'	1:2A:2090:G:H5"	2.12	0.49
1:2A:2100:U:O3'	23:21:35:THR:OG1	2.27	0.49
4:2E:119:ARG:HD2	4:2E:120:TRP:NE1	2.27	0.49
17:2V:14:VAL:HA	17:2V:18:LEU:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:612:G:H2'	32:2a:613:G:C8	2.48	0.49
32:2a:952:A:OP2	45:2n:29:ARG:NH1	2.44	0.49
32:2a:1034:C:H2'	32:2a:1035:U:H6	1.77	0.49
32:2a:1325:G:H2'	32:2a:1326:C:C6	2.47	0.49
35:2d:122:ARG:HH12	35:2d:134:ASP:HB2	1.76	0.49
48:2q:66:SER:HB3	48:2q:69:LYS:HB2	1.93	0.49
54:2x:23:C:H2'	54:2x:24:U:H6	1.78	0.49
1:1A:1158:U:H2'	1:1A:1159:G:H8	1.76	0.49
3:1D:68:LYS:HD2	3:1D:70:TRP:CZ2	2.48	0.49
19:1X:57:LEU:HD12	19:1X:78:LYS:HB2	1.94	0.49
32:1a:817:U:H2'	32:1a:818:C:H6	1.76	0.49
32:1a:843:A:H5'	32:1a:1061:U:O4	2.12	0.49
37:1f:21:LEU:O	37:1f:24:GLU:HB3	2.12	0.49
47:1p:18:ARG:HD3	47:1p:35:LYS:HE3	1.94	0.49
1:2A:104:C:H2'	1:2A:105:U:C6	2.46	0.49
1:2A:1231:G:H5'	17:2V:81:TYR:CE1	2.48	0.49
32:2a:507:A:H61	43:2l:53:ARG:HH12	1.59	0.49
39:2h:109:ILE:HD12	39:2h:111:ILE:HG22	1.93	0.49
1:1A:359:C:HO2'	20:1Y:35:TYR:HH	1.61	0.49
1:1A:1153:U:HO2'	1:1A:1154:C:C5'	2.23	0.49
6:1G:118:ARG:O	6:1G:181:ARG:HB3	2.11	0.49
12:1Q:52:VAL:O	12:1Q:56:ARG:HG3	2.12	0.49
32:1a:335:C:H42	32:1a:346:G:H1	1.60	0.49
32:1a:1048:U:O2'	32:1a:1049:C:OP2	2.18	0.49
33:1b:98:LEU:HB2	33:1b:101:MET:HE3	1.94	0.49
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.47	0.49
1:2A:320:C:H2'	1:2A:321:G:O4'	2.12	0.49
1:2A:1556:A:H2'	1:2A:1557:G:C8	2.47	0.49
32:2a:10:G:H2'	32:2a:11:A:C8	2.46	0.49
32:2a:920:G:C2	32:2a:1324:C:C2	3.01	0.49
32:2a:1096:C:H42	32:2a:1169:G:H1	1.60	0.49
32:2a:1169:G:H4'	40:2i:111:ARG:HH11	1.78	0.49
40:2i:46:ALA:HA	40:2i:78:LYS:HB2	1.94	0.49
44:2m:3:ARG:HG3	44:2m:4:ILE:N	2.27	0.49
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.95	0.49
50:2s:63:THR:HG23	50:2s:66:MET:HE3	1.94	0.49
1:1A:277:G:O6	59:1A:4139:HOH:O	2.18	0.49
1:1A:1830:C:OP2	3:1D:183:ARG:NH2	2.46	0.49
4:1E:48:GLN:OE1	4:1E:66:HIS:NE2	2.39	0.49
32:1a:91:G:O2'	32:1a:92:G:H8	1.96	0.49
32:1a:1043:C:C4	34:1c:2:GLY:HA3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:27:ALA:O	41:1j:31:GLY:HA2	2.13	0.49
1:2A:69:A:H5"	1:2A:71:A:C8	2.47	0.49
1:2A:919:G:N2	1:2A:950:U:C2	2.81	0.49
1:2A:1201:A:O4'	16:2U:51:LYS:NZ	2.45	0.49
1:2A:2318:G:N1	6:2G:43:LEU:O	2.39	0.49
32:2a:434:G:O2'	32:2a:479:U:O4	2.29	0.49
32:2a:438:C:H2'	32:2a:439:C:H6	1.76	0.49
32:2a:900:G:C6	32:2a:901:A:C6	3.01	0.49
32:2a:962:C:H2'	32:2a:963:C:C6	2.47	0.49
32:2a:1394:C:H2'	32:2a:1395:C:C6	2.47	0.49
41:2j:81:THR:HA	41:2j:84:GLN:HE21	1.78	0.49
1:1A:714:G:H5'	1:1A:715:G:OP2	2.12	0.49
1:1A:964:G:N2	1:1A:2280:A:OP2	2.45	0.49
1:1A:2651:G:OP1	9:1N:97:ARG:NH2	2.46	0.49
2:1B:45:A:O4'	6:1G:95:ARG:NH1	2.46	0.49
5:1F:129:PHE:CD1	5:1F:163:VAL:HG21	2.47	0.49
28:16:21:TYR:CE2	28:16:38:LYS:HG2	2.48	0.49
32:1a:1057:G:O2'	32:1a:1084:A:N1	2.35	0.49
32:1a:1113:A:OP1	40:1i:16:ARG:NH2	2.39	0.49
32:1a:1328:A:N1	32:1a:1357:A:H5"	2.27	0.49
41:1j:81:THR:C	41:1j:83:GLU:H	2.21	0.49
52:1u:2:GLY:O	52:1u:4:GLY:N	2.45	0.49
1:2A:6:G:H4'	9:2N:13:TRP:CH2	2.47	0.49
1:2A:894:G:H2'	1:2A:895:A:H8	1.78	0.49
1:2A:1820:C:H5"	1:2A:1821:A:OP1	2.12	0.49
1:2A:1920:G:H2'	1:2A:1920:G:N3	2.28	0.49
25:23:7:LYS:NZ	25:23:32:GLN:O	2.46	0.49
32:2a:584:C:H2'	32:2a:585:C:C6	2.47	0.49
32:2a:982:G:H2'	32:2a:983:A:O4'	2.13	0.49
32:2a:1095:C:C4	34:2c:178:LEU:HD22	2.47	0.49
32:2a:1102:C:OP2	40:2i:9:ARG:NH1	2.43	0.49
32:2a:1125:G:H3'	32:2a:1126:G:C8	2.48	0.49
32:2a:1246:C:H2'	32:2a:1247:G:H8	1.78	0.49
33:2b:200:ILE:O	33:2b:202:PRO:HD3	2.12	0.49
37:2f:99:ALA:HB3	49:2r:29:PHE:CE1	2.47	0.49
1:1A:1002:U:OP2	12:1Q:14:ARG:HD3	2.13	0.49
1:1A:1311:G:O4'	18:1W:15:ARG:NH2	2.43	0.49
1:1A:1652:C:H4'	1:1A:1653:A:O5'	2.13	0.49
1:1A:2107:U:H2'	1:1A:2108:G:C8	2.47	0.49
32:1a:143:G:H2'	32:1a:144:A:H8	1.78	0.49
33:1b:144:ARG:O	33:1b:147:LYS:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:80:TYR:O	59:1s:5001:HOH:O	2.20	0.49
1:2A:353:A:H2	1:2A:1254:A:O2'	1.96	0.49
1:2A:1156:A:N3	1:2A:1157:G:H1'	2.28	0.49
1:2A:2691:C:OP2	4:2E:111:ARG:NH2	2.45	0.49
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.48	0.49
31:29:29:ASN:HD22	31:29:32:HIS:CE1	2.31	0.49
32:2a:1308:C:H2'	32:2a:1309:C:C6	2.48	0.49
26:14:16:CYS:SG	26:14:17:GLY:N	2.86	0.49
32:1a:129:A:H1'	32:1a:321:A:C5	2.48	0.49
35:1d:167:GLY:H	35:1d:168:ARG:CZ	2.26	0.49
37:1f:19:LEU:HD11	37:1f:59:TYR:CZ	2.48	0.49
50:1s:80:TYR:O	50:1s:81:ARG:HB2	2.11	0.49
1:2A:895:A:H2	25:23:24:LYS:HB3	1.78	0.49
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.34	0.49
15:2T:23:ARG:HG3	15:2T:120:ARG:NH1	2.27	0.49
21:2Z:100:VAL:HG21	21:2Z:134:PRO:HG2	1.95	0.49
32:2a:407:A:O2'	32:2a:409:G:H5'	2.13	0.49
32:2a:936:A:N3	32:2a:963:C:O2'	2.39	0.49
32:2a:1382:C:C2	32:2a:1480:A:N6	2.80	0.49
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.78	0.49
40:2i:29:ASN:N	40:2i:63:ILE:O	2.32	0.49
43:2l:75:HIS:CD2	43:2l:77:LEU:H	2.28	0.49
12:1Q:34:LEU:HD11	12:1Q:129:THR:HB	1.94	0.49
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.95	0.49
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.35	0.49
32:1a:950:C:O2'	41:1j:55:LYS:O	2.26	0.49
32:1a:1303:C:H5"	32:1a:1304:C:H2'	1.94	0.49
1:2A:183:A:OP1	11:2P:46:LYS:NZ	2.45	0.49
1:2A:670:A:H2'	1:2A:671:G:O4'	2.12	0.49
1:2A:810:A:H5'	3:2D:210:GLY:CA	2.42	0.49
1:2A:1072:A:C2	1:2A:2499:A:H5'	2.48	0.49
1:2A:1336:C:H2'	1:2A:1337:U:C6	2.48	0.49
1:2A:1953:A:H2'	1:2A:1954:G:O4'	2.13	0.49
1:2A:1967:U:H2'	1:2A:1968:C:C6	2.48	0.49
2:2B:55:U:O3'	6:2G:27:ASN:ND2	2.46	0.49
6:2G:41:GLN:HG3	6:2G:60:LEU:HD21	1.95	0.49
14:2S:58:LEU:HD23	14:2S:58:LEU:H	1.77	0.49
14:2S:67:ARG:O	14:2S:71:ARG:HG3	2.13	0.49
20:2Y:49:VAL:HG21	20:2Y:61:ILE:HG23	1.95	0.49
34:2c:18:TRP:CD1	45:2n:55:GLY:H	2.31	0.49
44:2m:92:HIS:CE1	44:2m:98:VAL:HG11	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1826:U:H2'	1:1A:1827:C:H6	1.78	0.49
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.95	0.49
12:1Q:68:ILE:HD13	12:1Q:103:MET:HE2	1.94	0.49
26:14:59:PHE:HD1	50:1s:64:GLU:HB3	1.77	0.49
32:1a:36:G:O2'	43:1l:118:SER:O	2.24	0.49
32:1a:171:C:H2'	32:1a:172:C:C6	2.48	0.49
32:1a:1067:G:C5	32:1a:1068:U:C4	3.00	0.49
44:1m:84:ILE:HD12	50:1s:74:PHE:HZ	1.78	0.49
1:2A:550:A:OP1	59:2A:3637:HOH:O	2.19	0.49
1:2A:1313:A:C2	1:2A:2034:A:C4	3.01	0.49
1:2A:1403:G:O2'	1:2A:1404:A:H5'	2.12	0.49
1:2A:2086:C:H2'	1:2A:2087:C:C6	2.48	0.49
1:2A:2760:A:H3'	1:2A:2761:A:H8	1.78	0.49
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.13	0.49
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.43	0.49
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.95	0.49
18:2W:24:ILE:HA	18:2W:27:LYS:HG3	1.94	0.49
32:2a:139:G:H1	32:2a:173:C:H42	1.59	0.49
32:2a:459:G:H2'	32:2a:460:G:C8	2.47	0.49
32:2a:1125:G:H3'	32:2a:1126:G:H8	1.77	0.49
32:2a:1258:G:H2'	32:2a:1259:C:H6	1.78	0.49
33:2b:54:THR:O	33:2b:58:ILE:HG13	2.13	0.49
1:1A:2207:G:H2'	1:1A:2208:G:C8	2.47	0.48
11:1P:126:VAL:HG12	11:1P:148:LEU:HD13	1.95	0.48
15:1T:127:ALA:C	15:1T:129:ARG:H	2.21	0.48
32:1a:1491:A:H2'	32:1a:1492:C:C6	2.48	0.48
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG3	2.48	0.48
1:2A:359:C:H5"	20:2Y:6:HIS:ND1	2.28	0.48
1:2A:644:G:N3	1:2A:644:G:H5'	2.28	0.48
1:2A:663:U:H2'	1:2A:664:C:H6	1.77	0.48
1:2A:2205:G:H2'	1:2A:2206:C:O4'	2.13	0.48
1:2A:2302:U:O2'	1:2A:2385:C:O2	2.29	0.48
1:2A:2386:G:O2'	1:2A:2388:A:N7	2.40	0.48
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	1.95	0.48
32:2a:887:A:H2'	32:2a:888:C:O4'	2.13	0.48
32:2a:1228:C:H42	32:2a:1273:G:H1	1.61	0.48
32:2a:1306:A:C4'	32:2a:1344:C:H4'	2.43	0.48
36:2e:78:HIS:HD2	36:2e:142:LEU:HD23	1.76	0.48
1:1A:1091:A:H5'	1:1A:1092:G:C8	2.47	0.48
1:1A:1099:A:H2'	1:1A:1100:G:O4'	2.13	0.48
1:1A:1716:C:OP1	59:1A:4154:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:14:ILE:HD11	26:14:24:THR:HG21	1.94	0.48
32:1a:77:G:H1	32:1a:87:C:H42	1.60	0.48
32:1a:595:A:N6	32:1a:613:G:H1	2.10	0.48
32:1a:990:G:H2'	32:1a:991:U:C6	2.48	0.48
33:1b:100:GLY:N	33:1b:176:GLU:OE2	2.37	0.48
34:1c:70:VAL:HG22	34:1c:72:LYS:H	1.78	0.48
47:1p:23:ASP:OD1	47:1p:25:ARG:HG2	2.13	0.48
50:1s:37:ARG:O	50:1s:70:LYS:HD2	2.14	0.48
51:1t:10:LEU:HD22	51:1t:12:ALA:HB2	1.95	0.48
1:2A:614:G:O2'	30:28:4:MET:HG3	2.14	0.48
1:2A:634:C:H2'	1:2A:635:G:O4'	2.13	0.48
1:2A:1513:C:C5	1:2A:1592:C:H2'	2.47	0.48
3:2D:132:PRO:HD3	3:2D:190:TYR:CZ	2.48	0.48
7:2H:71:LEU:HD12	7:2H:71:LEU:HA	1.74	0.48
32:2a:548:C:HO2'	39:2h:91:ARG:HH22	1.54	0.48
32:2a:1074:U:H2'	32:2a:1076:A:OP2	2.12	0.48
32:2a:1236:C:H2'	32:2a:1237:G:O4'	2.13	0.48
32:2a:1281:A:H2'	32:2a:1281:A:N3	2.26	0.48
33:2b:92:TYR:CE2	33:2b:150:SER:N	2.81	0.48
35:2d:122:ARG:HH11	35:2d:122:ARG:HA	1.78	0.48
1:1A:670:A:H2'	1:1A:671:G:O4'	2.13	0.48
1:1A:703:U:H2'	1:1A:704:C:C6	2.48	0.48
29:17:24:THR:O	29:17:28:ARG:HG3	2.13	0.48
32:1a:672:G:H2'	32:1a:673:C:C6	2.48	0.48
32:1a:1315:A:H2'	32:1a:1316:G:O4'	2.13	0.48
54:1x:75:C:H5"	54:1x:76:A:OP2	2.13	0.48
1:2A:822:G:H4'	1:2A:823:A:O5'	2.13	0.48
1:2A:1076:G:H21	31:29:36:GLN:HE22	1.60	0.48
1:2A:1239:G:N2	1:2A:1240:C:C2	2.82	0.48
1:2A:2800:C:P	4:2E:61:ARG:HH21	2.35	0.48
5:2F:101:LEU:O	5:2F:106:ARG:HD3	2.13	0.48
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.95	0.48
32:2a:1334:C:H2'	32:2a:1335:G:C8	2.48	0.48
32:2a:1335:G:H2'	32:2a:1336:C:C6	2.49	0.48
1:1A:120:G:OP2	59:1A:4150:HOH:O	2.19	0.48
1:1A:1073:A:N6	1:1A:1170:G:H2'	2.28	0.48
8:1I:110:ASP:HA	8:1I:111:PRO:HD2	1.67	0.48
32:1a:50:U:O4	32:1a:361:U:H5	1.96	0.48
32:1a:90:U:C2'	32:1a:91:G:H5'	2.44	0.48
32:1a:600:G:C2	32:1a:601:G:C8	3.01	0.48
32:1a:646:G:H2'	32:1a:647:A:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:729:C:OP1	32:1a:829:G:O2'	2.27	0.48
32:1a:1395:C:H2'	32:1a:1396:A:C8	2.48	0.48
32:1a:1431:U:O2'	32:1a:1432:A:H3'	2.13	0.48
1:2A:898:G:H2'	1:2A:899:G:H8	1.77	0.48
1:2A:1685:U:H2'	1:2A:1686:C:H5"	1.94	0.48
1:2A:1826:U:H2'	1:2A:1827:C:H6	1.77	0.48
1:2A:2037:U:H2'	1:2A:2038:U:H6	1.79	0.48
1:2A:2239:G:C5	1:2A:2240:C:C4	3.01	0.48
1:2A:2563:U:H2'	1:2A:2565:U:H5"	1.95	0.48
20:2Y:49:VAL:HG11	20:2Y:55:TYR:CD2	2.48	0.48
32:2a:449:C:OP2	32:2a:450:C:N4	2.46	0.48
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.28	0.48
39:2h:51:VAL:HG11	39:2h:60:ARG:HH11	1.79	0.48
44:2m:33:ALA:HB2	44:2m:64:TRP:HZ3	1.77	0.48
54:2x:59:A:H2'	54:2x:60:U:H5'	1.94	0.48
1:1A:800:C:H2'	1:1A:801:C:C6	2.48	0.48
1:1A:2117:U:H3	1:1A:2214:G:H1	1.62	0.48
1:1A:2338:A:H2'	1:1A:2339:A:C8	2.48	0.48
32:1a:1034:C:H2'	32:1a:1035:U:C6	2.49	0.48
32:1a:1107:G:N2	32:1a:1108:U:O4	2.41	0.48
41:1j:48:THR:OG1	41:1j:62:HIS:ND1	2.45	0.48
1:2A:1064:U:O2'	1:2A:1066:A:H2	1.97	0.48
1:2A:1726:U:O2	1:2A:1793:G:H3'	2.12	0.48
6:2G:111:LEU:HB3	6:2G:117:PHE:CE2	2.49	0.48
21:2Z:7:ALA:HB3	21:2Z:61:LEU:HD12	1.94	0.48
32:2a:1058:C:H3'	59:2a:3349:HOH:O	2.12	0.48
32:2a:1131:U:H2'	32:2a:1132:C:O4'	2.12	0.48
32:2a:1274:U:P	38:2g:41:ARG:HH22	2.35	0.48
43:2l:28:LYS:HE3	43:2l:62:SER:HB2	1.96	0.48
1:1A:2845:U:H2'	1:1A:2846:G:C8	2.48	0.48
32:1a:426:A:OP1	35:1d:9:CYS:HB2	2.13	0.48
32:1a:812:A:H2'	32:1a:813:G:O4'	2.12	0.48
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.47	0.48
1:2A:724:C:H2'	1:2A:725:C:C6	2.49	0.48
18:2W:33:ARG:NH2	18:2W:52:GLU:OE1	2.43	0.48
32:2a:1178:U:H4'	59:2a:3451:HOH:O	2.13	0.48
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.86	0.48
45:2n:41:ARG:HG3	45:2n:42:ILE:HG13	1.96	0.48
1:1A:2095:U:H2'	1:1A:2096:U:C6	2.48	0.48
1:1A:2212:G:H5'	1:1A:2213:G:OP2	2.14	0.48
12:1Q:12:GLN:HG3	12:1Q:73:PRO:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:45:ASP:O	21:1Z:49:ARG:HG3	2.13	0.48
32:1a:747:G:H2'	32:1a:748:C:C6	2.48	0.48
1:2A:105:U:H2'	1:2A:106:G:H8	1.77	0.48
1:2A:623:C:O2	1:2A:627:C:H4'	2.14	0.48
1:2A:964:G:N2	1:2A:2280:A:OP2	2.42	0.48
1:2A:1373:G:H2'	1:2A:1375:C:C5	2.48	0.48
1:2A:1474:G:H2'	1:2A:1475:C:C6	2.48	0.48
1:2A:1980:G:N7	59:2A:3700:HOH:O	2.35	0.48
4:2E:97:LYS:N	4:2E:100:GLU:OE1	2.33	0.48
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.14	0.48
25:23:46:ASN:O	25:23:50:VAL:HG22	2.13	0.48
32:2a:421:G:C2	32:2a:422:G:C8	3.02	0.48
32:2a:544:U:HO2'	32:2a:545:U:P	2.31	0.48
32:2a:1031:G:OP1	45:2n:3:ARG:HB3	2.14	0.48
50:2s:36:ARG:NH2	50:2s:72:GLY:O	2.46	0.48
1:1A:1337:U:H2'	1:1A:1338:C:C6	2.49	0.48
1:1A:1889:A:N6	1:1A:1904:G:O2'	2.46	0.48
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.46	0.48
48:1q:27:PHE:CZ	48:1q:36:ILE:HD11	2.48	0.48
1:2A:555:C:H4'	1:2A:556:A:H5"	1.95	0.48
1:2A:1103:G:H2'	1:2A:1104:G:C8	2.49	0.48
2:2B:1:U:H2'	2:2B:2:C:C5	2.49	0.48
6:2G:41:GLN:NE2	6:2G:153:ARG:HB3	2.24	0.48
15:2T:53:ARG:HB3	15:2T:53:ARG:HH11	1.78	0.48
21:2Z:54:HIS:ND1	21:2Z:101:PRO:HG3	2.28	0.48
32:2a:422:G:OP1	35:2d:38:TYR:OH	2.23	0.48
32:2a:484:G:N2	32:2a:530:G:H1'	2.29	0.48
32:2a:541:G:N1	32:2a:542:G:C2	2.82	0.48
32:2a:937:A:O2'	32:2a:962:C:O2'	2.19	0.48
32:2a:989:G:H2'	32:2a:990:G:C8	2.49	0.48
32:2a:1457:C:H2'	32:2a:1458:G:H8	1.78	0.48
34:2c:113:ALA:HB3	34:2c:114:PRO:HD3	1.96	0.48
37:2f:70:ASP:OD1	37:2f:70:ASP:N	2.45	0.48
41:2j:81:THR:HA	41:2j:84:GLN:NE2	2.28	0.48
1:1A:2123:U:H2'	1:1A:2124:C:C6	2.49	0.48
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.79	0.48
22:10:43:THR:O	22:10:43:THR:HG23	2.14	0.48
32:1a:258:A:C6	32:1a:259:A:C6	3.01	0.48
32:1a:649:A:H1'	32:1a:717:A:O4'	2.14	0.48
35:1d:149:ALA:O	35:1d:153:ARG:N	2.46	0.48
46:1o:17:ARG:HH11	46:1o:17:ARG:HG3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:94:G:H4'	24:22:48:HIS:NE2	2.29	0.48
1:2A:138:A:C8	1:2A:1453:C:O2'	2.66	0.48
1:2A:516:A:H2'	1:2A:517:G:O4'	2.13	0.48
1:2A:830:A:C8	1:2A:838:G:C5	3.02	0.48
1:2A:2207:G:N1	1:2A:2208:G:O6	2.47	0.48
4:2E:14:ILE:HD11	4:2E:173:VAL:HG11	1.94	0.48
15:2T:84:GLN:HG2	15:2T:85:LYS:HD3	1.95	0.48
32:2a:153:G:H2'	32:2a:154:G:H8	1.78	0.48
32:2a:502:C:O2'	32:2a:514:G:N2	2.44	0.48
32:2a:507:A:N6	43:2l:53:ARG:HH12	2.11	0.48
32:2a:1395:C:H2'	32:2a:1396:A:C8	2.49	0.48
32:2a:1406:G:H2'	32:2a:1407:C:C6	2.49	0.48
34:2c:3:ASN:ND2	34:2c:4:LYS:HE2	2.28	0.48
39:2h:51:VAL:HG11	39:2h:60:ARG:NH1	2.29	0.48
45:2n:47:LEU:HB3	45:2n:53:LEU:HD23	1.96	0.48
1:1A:326:U:O4	59:1A:4153:HOH:O	2.20	0.48
1:1A:2356:G:OP2	28:16:38:LYS:NZ	2.46	0.48
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.14	0.48
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.44	0.48
32:1a:942:A:N3	32:1a:947:A:O2'	2.44	0.48
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.43	0.48
50:1s:51:VAL:HB	50:1s:75:ALA:HB2	1.96	0.48
1:2A:209:A:C8	1:2A:254:G:C6	3.02	0.48
1:2A:484:U:H5"	29:27:40:TRP:CD2	2.49	0.48
1:2A:646:G:H2'	1:2A:647:G:H8	1.79	0.48
1:2A:1060:G:O2'	1:2A:1061:G:H5'	2.14	0.48
2:2B:73:A:C4	2:2B:105:A:C2	3.02	0.48
4:2E:127:ASP:OD2	59:2E:401:HOH:O	2.20	0.48
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.44	0.48
6:2G:98:ARG:H	6:2G:98:ARG:HG2	1.39	0.48
12:2Q:75:THR:HG21	12:2Q:87:LYS:NZ	2.29	0.48
14:2S:15:ARG:HB3	14:2S:19:LYS:NZ	2.28	0.48
32:2a:8:G:H21	36:2e:121:LYS:HG2	1.78	0.48
32:2a:270:A:H4'	59:2a:3416:HOH:O	2.14	0.48
32:2a:414:C:H2'	32:2a:415:C:C6	2.48	0.48
32:2a:717:A:OP2	59:2a:3334:HOH:O	2.20	0.48
32:2a:1185:C:H2'	32:2a:1186:A:O4'	2.14	0.48
35:2d:119:GLN:HG2	35:2d:123:HIS:CD2	2.49	0.48
35:2d:205:GLU:OE1	36:2e:100:VAL:HG12	2.13	0.48
1:1A:2659:C:H2'	1:1A:2660:U:C6	2.49	0.47
26:14:67:TYR:HE2	50:1s:43:GLU:OE2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:443:A:OP2	32:1a:470:G:N2	2.41	0.47
32:1a:1105:U:C4	32:1a:1106:A:N7	2.82	0.47
33:1b:37:ASN:C	33:1b:39:ILE:H	2.22	0.47
33:1b:141:GLU:O	33:1b:145:LEU:HB2	2.14	0.47
35:1d:164:ALA:C	35:1d:168:ARG:HH11	2.21	0.47
35:1d:194:LEU:HD12	35:1d:196:LEU:HG	1.94	0.47
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.49	0.47
40:1i:50:LEU:HG	40:1i:55:ALA:O	2.14	0.47
1:2A:94:G:H4'	24:22:48:HIS:CD2	2.49	0.47
1:2A:113:C:H2'	1:2A:114:G:O4'	2.13	0.47
1:2A:903:C:H4'	22:20:23:VAL:HG21	1.96	0.47
1:2A:1620:C:H2'	1:2A:1621:C:C6	2.49	0.47
6:2G:29:TRP:HE3	6:2G:33:ARG:HE	1.61	0.47
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.53	0.47
10:2O:63:VAL:HG12	10:2O:106:LEU:HD11	1.96	0.47
32:2a:448:A:H4'	47:2p:72:ARG:HD2	1.96	0.47
32:2a:499:G:OP2	59:2a:3331:HOH:O	2.19	0.47
33:2b:80:ILE:HD13	33:2b:212:GLN:HA	1.94	0.47
40:2i:4:TYR:O	40:2i:19:LEU:N	2.36	0.47
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.96	0.47
44:2m:80:ARG:HH22	50:2s:69:HIS:CE1	2.29	0.47
1:1A:1520:C:H2'	1:1A:1521:G:H8	1.79	0.47
1:1A:1888:G:N2	1:1A:1904:G:H2'	2.30	0.47
1:1A:2122:G:C2	1:1A:2123:U:H1'	2.48	0.47
9:1N:15:LEU:HD12	9:1N:16:ILE:H	1.79	0.47
23:11:51:VAL:HG21	23:11:74:VAL:HG21	1.96	0.47
48:1q:31:LEU:HD23	48:1q:32:TYR:CZ	2.49	0.47
1:2A:1095:A:H2'	1:2A:1096:G:C8	2.49	0.47
1:2A:2735:C:OP2	4:2E:109:LYS:NZ	2.47	0.47
4:2E:163:GLU:HG2	4:2E:164:ARG:N	2.28	0.47
5:2F:109:GLY:O	5:2F:113:ALA:N	2.43	0.47
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HG12	1.96	0.47
33:2b:127:ILE:C	33:2b:129:GLU:H	2.22	0.47
46:2o:5:LYS:H	46:2o:5:LYS:HZ2	1.62	0.47
2:1B:9:G:P	14:1S:25:ARG:HH22	2.36	0.47
26:14:63:TYR:N	26:14:63:TYR:HD1	2.11	0.47
32:1a:288:G:C5	32:1a:289:G:H1'	2.49	0.47
32:1a:1156:G:H2'	32:1a:1157:G:C8	2.48	0.47
32:1a:1218:A:H2'	32:1a:1219:C:C6	2.49	0.47
35:1d:65:ARG:NH1	35:1d:70:ILE:O	2.48	0.47
42:1k:99:GLN:HG3	42:1k:105:VAL:HG11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:608:A:N1	1:2A:855:G:O2'	2.33	0.47
1:2A:1090:A:N3	1:2A:1092:G:C8	2.82	0.47
1:2A:1104:G:C8	1:2A:1105:U:H2'	2.49	0.47
1:2A:1333:U:O4	13:2R:106:GLY:HA3	2.14	0.47
1:2A:1381:A:H2'	1:2A:1382:G:C8	2.49	0.47
1:2A:1404:A:H2'	1:2A:1405:A:H5'	1.97	0.47
1:2A:1693:G:OP1	59:2A:3601:HOH:O	2.20	0.47
1:2A:2832:A:OP1	4:2E:159:HIS:NE2	2.45	0.47
2:2B:98:G:H2'	2:2B:99:G:O4'	2.13	0.47
7:2H:54:ARG:HB3	7:2H:65:HIS:CG	2.49	0.47
20:2Y:90:LEU:HD13	20:2Y:92:ASN:HD21	1.79	0.47
32:2a:231:C:H5'	48:2q:70:ARG:HG2	1.97	0.47
32:2a:952:A:OP2	45:2n:41:ARG:NH1	2.47	0.47
32:2a:993:A:C2	32:2a:1201:U:H1'	2.50	0.47
1:1A:785:G:OP1	59:1A:4155:HOH:O	2.20	0.47
26:14:55:ARG:HD3	26:14:55:ARG:HA	1.57	0.47
27:15:35:GLU:HG2	59:15:206:HOH:O	2.13	0.47
32:1a:443:A:OP2	32:1a:470:G:N1	2.40	0.47
32:1a:1184:G:H21	45:1n:43:CYS:HB3	1.78	0.47
32:1a:1425:G:O2'	32:1a:1426:G:OP1	2.32	0.47
35:1d:61:LYS:NZ	35:1d:72:GLU:OE2	2.39	0.47
1:2A:2303:C:O2'	1:2A:2304:C:H5'	2.14	0.47
6:2G:126:ASP:CG	6:2G:130:ASN:HD22	2.21	0.47
11:2P:138:LEU:HD23	11:2P:145:PRO:HG3	1.97	0.47
19:2X:88:LYS:HG2	19:2X:93:GLU:HG3	1.96	0.47
32:2a:994:A:C6	32:2a:995:A:C6	3.02	0.47
32:2a:1167:G:H3'	59:2a:3428:HOH:O	2.13	0.47
32:2a:1446:A:H2'	32:2a:1447:G:O4'	2.15	0.47
36:2e:78:HIS:NE2	36:2e:142:LEU:HA	2.30	0.47
44:2m:81:LEU:HD22	44:2m:88:ARG:HB2	1.94	0.47
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.13	0.47
50:2s:3:ARG:NH2	50:2s:10:PHE:HB2	2.29	0.47
1:1A:1176:G:H21	9:1N:73:THR:HG21	1.79	0.47
1:1A:2416:G:H5"	11:1P:75:ILE:HD12	1.96	0.47
2:1B:28:C:H2'	2:1B:29:A:O4'	2.15	0.47
32:1a:299:A:H2'	32:1a:300:U:O4'	2.15	0.47
32:1a:681:U:H2'	32:1a:682:G:H5'	1.96	0.47
33:1b:62:ALA:HB3	33:1b:225:ALA:HB3	1.97	0.47
35:1d:166:LYS:HA	35:1d:178:VAL:HG21	1.97	0.47
1:2A:29:G:H2'	1:2A:30:C:C6	2.49	0.47
1:2A:345:A:OP2	5:2F:169:ASN:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:504:A:N3	1:2A:506:G:H5"	2.29	0.47
1:2A:558:U:H2'	1:2A:559:C:C6	2.50	0.47
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	1.97	0.47
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.50	0.47
26:24:24:THR:OG1	26:24:25:TYR:N	2.47	0.47
32:2a:387:G:P	47:2p:28:ARG:HH22	2.37	0.47
32:2a:765:A:OP1	32:2a:1501:G:H5'	2.15	0.47
32:2a:1286:G:O2'	32:2a:1315:A:N6	2.46	0.47
1:1A:329:U:H2'	1:1A:330:G:O4'	2.14	0.47
1:1A:401:C:H2'	1:1A:402:C:C6	2.49	0.47
1:1A:1778:G:H5"	1:1A:1778:G:H8	1.80	0.47
1:1A:2670:G:O2'	7:1H:175:LYS:NZ	2.48	0.47
5:1F:195:ASP:HB3	5:1F:198:ALA:H	1.79	0.47
18:1W:14:PRO:HG2	18:1W:78:GLU:CG	2.39	0.47
32:1a:982:G:N2	32:1a:1021:C:N3	2.63	0.47
35:1d:100:ARG:HH11	35:1d:137:SER:HB3	1.79	0.47
1:2A:54:A:H2'	1:2A:55:C:O4'	2.15	0.47
1:2A:590:U:H5'	1:2A:989:A:N1	2.30	0.47
1:2A:593:A:N6	1:2A:2510:C:O3'	2.47	0.47
1:2A:610:U:H2'	1:2A:611:C:C6	2.49	0.47
1:2A:1170:G:H5'	31:29:37:GLY:HA2	1.95	0.47
1:2A:2227:G:C3'	1:2A:2228:A:H5"	2.44	0.47
5:2F:29:ASN:H	5:2F:112:MET:CE	2.26	0.47
13:2R:38:VAL:HB	13:2R:39:PRO:HD3	1.97	0.47
32:2a:522:G:H2'	32:2a:523:A:H8	1.80	0.47
32:2a:1236:C:O4'	32:2a:1338:G:H5"	2.14	0.47
37:2f:21:LEU:O	37:2f:25:ILE:HG13	2.14	0.47
1:1A:302:C:N3	1:1A:384:G:N2	2.55	0.47
1:1A:1404:A:N1	1:1A:1417:U:O4	2.48	0.47
1:1A:2650:A:OP2	59:1A:4157:HOH:O	2.21	0.47
1:1A:2730:G:O2'	1:1A:2856:U:OP1	2.32	0.47
2:1B:33:G:C2	2:1B:50:G:C2	3.02	0.47
4:1E:82:ARG:HG2	4:1E:83:ASP:N	2.29	0.47
7:1H:11:VAL:HG13	7:1H:15:VAL:HG22	1.96	0.47
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.14	0.47
20:1Y:38:ILE:HD11	20:1Y:66:PRO:HG3	1.95	0.47
26:14:61:ARG:HH12	50:1s:9:VAL:HG11	1.80	0.47
31:19:17:ILE:HD12	31:19:17:ILE:HA	1.66	0.47
32:1a:932:G:C2	32:1a:933:U:C2	3.02	0.47
32:1a:1118:U:H4'	32:1a:1119:U:H5	1.80	0.47
32:1a:1329:G:O2'	32:1a:1356:G:O6	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1435:G:OP1	51:1t:39:LYS:NZ	2.46	0.47
34:1c:29:TYR:CZ	45:1n:54:PRO:HG2	2.50	0.47
41:1j:30:SER:O	41:1j:81:THR:HB	2.15	0.47
43:1l:28:LYS:HG3	43:1l:62:SER:HB2	1.95	0.47
48:1q:66:SER:OG	48:1q:69:LYS:HB2	2.15	0.47
1:2A:186:C:OP2	59:2A:3636:HOH:O	2.20	0.47
1:2A:264:U:H2'	1:2A:265:C:C6	2.50	0.47
1:2A:592:G:H2'	1:2A:2051:A:C5	2.49	0.47
1:2A:955:A:N1	1:2A:2288:G:H1'	2.30	0.47
1:2A:989:A:OP2	59:2A:3640:HOH:O	2.20	0.47
1:2A:1166:C:H2'	1:2A:1167:G:O4'	2.15	0.47
1:2A:1320:A:N1	1:2A:1340:C:O2'	2.45	0.47
1:2A:2012:U:H2'	1:2A:2013:G:H5"	1.95	0.47
1:2A:2044:G:H5'	1:2A:2628:C:H4'	1.96	0.47
1:2A:2657:C:OP2	1:2A:2744:G:O2'	2.31	0.47
3:2D:3:VAL:HG13	3:2D:17:THR:HB	1.97	0.47
4:2E:50:GLY:HA3	4:2E:75:VAL:HG11	1.96	0.47
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.50	0.47
6:2G:62:LEU:HA	26:24:27:THR:HG21	1.96	0.47
14:2S:95:HIS:CG	14:2S:96:GLY:N	2.82	0.47
24:22:9:GLN:OE1	24:22:56:GLN:HG2	2.15	0.47
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.97	0.47
32:2a:262:G:O2'	48:2q:67:LYS:HB2	2.15	0.47
32:2a:487:C:OP2	43:2l:116:SER:HB3	2.15	0.47
32:2a:523:A:H2'	32:2a:524:G:C8	2.50	0.47
32:2a:601:G:H4'	47:2p:44:THR:O	2.14	0.47
32:2a:646:G:O2'	32:2a:820:G:OP1	2.32	0.47
32:2a:951:G:N3	41:2j:54:PHE:HE1	2.13	0.47
32:2a:1114:G:H2'	32:2a:1115:C:C5	2.50	0.47
32:2a:1172:G:H4'	34:2c:176:HIS:CE1	2.49	0.47
35:2d:117:ALA:O	35:2d:121:VAL:HG23	2.14	0.47
36:2e:11:ILE:HD12	36:2e:31:LEU:HD13	1.96	0.47
40:2i:127:LYS:O	40:2i:128:ARG:HG2	2.15	0.47
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.97	0.47
47:2p:15:PRO:O	47:2p:16:HIS:ND1	2.48	0.47
1:1A:239:A:C5	1:1A:240:G:H1'	2.49	0.47
1:1A:1899:G:H2'	1:1A:1900:C:C6	2.49	0.47
1:1A:2020:C:H4'	1:1A:2735:C:O2	2.14	0.47
1:1A:2699:U:O4	59:1A:4152:HOH:O	2.20	0.47
20:1Y:11:ASP:OD2	20:1Y:97:ARG:NH2	2.47	0.47
32:1a:221:C:H2'	32:1a:222:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1078:U:OP2	59:1a:2021:HOH:O	2.21	0.47
32:1a:1200:C:OP2	45:1n:9:LYS:NZ	2.40	0.47
32:1a:1266:C:H5'	59:1a:2027:HOH:O	2.15	0.47
32:1a:1287:G:N2	32:1a:1313:G:H1'	2.30	0.47
41:1j:47:PHE:CZ	45:1n:37:PHE:HE2	2.31	0.47
1:2A:900:G:H2'	1:2A:901:G:C8	2.41	0.47
1:2A:1176:G:C2	1:2A:1177:A:C4	3.02	0.47
1:2A:1333:U:C2	1:2A:1372:C:O2	2.68	0.47
1:2A:1381:A:H2'	1:2A:1382:G:H8	1.79	0.47
1:2A:1523:A:H2'	1:2A:1524:G:O4'	2.15	0.47
1:2A:1948:A:H2'	1:2A:1949:A:C8	2.49	0.47
1:2A:2830:A:C2	1:2A:2831:G:C4	3.03	0.47
4:2E:119:ARG:HD2	4:2E:120:TRP:CD1	2.49	0.47
8:2I:62:LYS:O	8:2I:66:GLU:HG2	2.15	0.47
12:2Q:48:GLU:OE1	12:2Q:51:ARG:NH2	2.42	0.47
32:2a:124:G:C6	32:2a:189:U:H4'	2.50	0.47
32:2a:1244:C:H2'	32:2a:1245:C:C6	2.49	0.47
32:2a:1280:C:H2'	38:2g:114:ARG:NH1	2.30	0.47
33:2b:163:PHE:HA	33:2b:185:ILE:O	2.15	0.47
45:2n:3:ARG:NH2	45:2n:4:LYS:HE3	2.30	0.47
1:1A:222:C:H2'	1:1A:223:U:H6	1.80	0.47
1:1A:1626:A:OP2	1:1A:1626:A:H8	1.97	0.47
1:1A:1829:G:O2'	3:1D:181:GLU:OE2	2.22	0.47
12:1Q:1:MET:HB3	12:1Q:1:MET:HE2	1.79	0.47
32:1a:721:A:H2'	32:1a:722:C:C6	2.50	0.47
32:1a:1056:U:O2'	33:1b:104:ASN:OD1	2.33	0.47
32:1a:1115:C:C2'	32:1a:1116:G:H5'	2.45	0.47
32:1a:1194:U:H5"	32:1a:1195:A:H5'	1.96	0.47
1:2A:925:G:H2'	1:2A:926:G:O4'	2.15	0.47
1:2A:1036:C:OP2	59:2A:3610:HOH:O	2.21	0.47
1:2A:2256:U:O2'	1:2A:2447:G:OP2	2.27	0.47
3:2D:142:VAL:HG23	3:2D:193:VAL:HA	1.96	0.47
9:2N:34:LEU:HD12	9:2N:34:LEU:HA	1.75	0.47
32:2a:251:G:OP1	48:2q:69:LYS:NZ	2.41	0.47
32:2a:516:A:N6	34:2c:193:TYR:HB2	2.30	0.47
32:2a:1255:G:H3'	32:2a:1256:G:H8	1.79	0.47
32:2a:1328:A:N1	32:2a:1357:A:H5"	2.30	0.47
33:2b:40:HIS:HB3	33:2b:190:THR:HG21	1.97	0.47
33:2b:167:PRO:HG3	33:2b:188:ALA:HB2	1.95	0.47
34:2c:39:ILE:O	34:2c:43:LEU:HB2	2.15	0.47
38:2g:92:SER:O	38:2g:96:GLN:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:17:LYS:H	45:2n:17:LYS:HD3	1.78	0.47
1:1A:271:U:H4'	8:1I:50:ARG:HH12	1.79	0.47
1:1A:963:A:N3	2:1B:80:U:O2'	2.45	0.47
1:1A:1520:C:H2'	1:1A:1521:G:C8	2.50	0.47
8:1I:108:THR:O	8:1I:109:ILE:HD12	2.14	0.47
10:1O:104:ARG:HH22	15:1T:43:GLN:HE22	1.61	0.47
30:18:32:LEU:O	30:18:36:LYS:HE3	2.14	0.47
32:1a:172:C:H2'	32:1a:173:C:C6	2.50	0.47
32:1a:341:C:O2	32:1a:341:C:H2'	2.14	0.47
32:1a:1026:C:H2'	32:1a:1027:A:H5'	1.97	0.47
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.83	0.47
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.15	0.47
41:1j:31:GLY:HA3	41:1j:32:ALA:HA	1.71	0.47
1:2A:947:C:H2'	1:2A:948:C:C6	2.50	0.47
1:2A:981:U:H2'	1:2A:982:G:O4'	2.14	0.47
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.40	0.47
6:2G:148:MET:H	6:2G:148:MET:HG3	1.43	0.47
27:25:16:ARG:O	27:25:20:ARG:HG3	2.15	0.47
32:2a:571:G:N2	32:2a:738:C:OP2	2.47	0.47
32:2a:1208:C:H4'	50:2s:80:TYR:OH	2.15	0.47
47:2p:55:ARG:O	47:2p:58:TYR:HB3	2.15	0.47
49:2r:24:ALA:C	49:2r:26:LEU:H	2.23	0.47
1:1A:1820:C:H5"	1:1A:1821:A:OP1	2.15	0.46
2:1B:66:A:N6	2:1B:108:U:H2'	2.29	0.46
3:1D:102:LYS:C	3:1D:103:ARG:HG2	2.38	0.46
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.71	0.46
18:1W:79:GLY:HA3	18:1W:100:THR:HG22	1.98	0.46
32:1a:221:C:H2'	32:1a:222:G:H8	1.80	0.46
32:1a:677:G:H2'	32:1a:678:A:C8	2.50	0.46
32:1a:703:C:O2'	49:1r:49:LYS:HB3	2.14	0.46
33:1b:15:VAL:HG22	33:1b:210:SER:HB2	1.97	0.46
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.15	0.46
54:1x:61:C:H2'	54:1x:62:C:H6	1.80	0.46
1:2A:323:A:P	20:2Y:86:ARG:HH21	2.37	0.46
1:2A:1013:U:H4'	25:23:14:GLY:O	2.15	0.46
1:2A:1064:U:H3	1:2A:1187:A:N6	2.06	0.46
1:2A:2537:G:H5'	1:2A:2754:C:O2'	2.15	0.46
5:2F:195:ASP:OD1	5:2F:196:LEU:N	2.48	0.46
6:2G:49:ASP:O	6:2G:51:ARG:N	2.48	0.46
8:2I:77:LEU:HB3	8:2I:142:VAL:HG12	1.96	0.46
9:2N:99:LEU:HD22	9:2N:103:VAL:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:300:U:H2'	32:2a:301:G:C8	2.50	0.46
42:2k:92:GLU:CG	42:2k:96:ARG:HH21	2.28	0.46
1:1A:814:G:O2'	1:1A:1424:A:N1	2.48	0.46
1:1A:1391:G:OP2	59:1A:4156:HOH:O	2.20	0.46
2:1B:32:C:C2	2:1B:51:G:N2	2.83	0.46
30:18:61:LEU:O	30:18:63:PRO:HD3	2.15	0.46
31:19:27:CYS:SG	31:19:28:GLU:N	2.88	0.46
32:1a:994:A:H2'	32:1a:995:A:C8	2.50	0.46
40:1i:3:GLN:OE1	40:1i:20:ARG:NH2	2.43	0.46
1:2A:806:G:H2'	1:2A:807:A:O4'	2.15	0.46
1:2A:904:U:O2	1:2A:2279:A:H2'	2.16	0.46
1:2A:1515:A:H2'	1:2A:1516:G:O4'	2.15	0.46
1:2A:2218:U:H1'	1:2A:2219:A:C8	2.50	0.46
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.42	0.46
3:2D:33:LEU:HD11	3:2D:103:ARG:HA	1.97	0.46
3:2D:274:ARG:HG2	3:2D:275:LYS:N	2.29	0.46
12:2Q:97:VAL:HG11	12:2Q:103:MET:HE3	1.98	0.46
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.97	0.46
32:2a:8:G:H5'	32:2a:294:A:O4'	2.16	0.46
32:2a:522:G:H2'	32:2a:523:A:C8	2.50	0.46
32:2a:720:C:H2'	32:2a:721:A:H8	1.79	0.46
32:2a:961:A:H2	32:2a:962:C:C6	2.33	0.46
33:2b:207:ALA:O	33:2b:211:ILE:HG13	2.15	0.46
47:2p:28:ARG:HH11	47:2p:29:ASP:CG	2.23	0.46
1:1A:1248:A:H2	1:1A:1286:A:N6	2.07	0.46
1:1A:2330:G:N2	14:1S:3:ARG:HG2	2.30	0.46
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.97	0.46
26:14:61:ARG:HH21	50:1s:42:PRO:CD	2.27	0.46
32:1a:608:C:H2'	32:1a:609:G:C8	2.50	0.46
32:1a:817:U:H2'	32:1a:818:C:C6	2.50	0.46
32:1a:825:U:OP2	32:1a:825:U:H6	1.98	0.46
32:1a:1325:G:H2'	32:1a:1326:C:C6	2.50	0.46
36:1e:77:PRO:HG2	36:1e:78:HIS:HD2	1.79	0.46
1:2A:364:G:H2'	1:2A:365:G:O4'	2.15	0.46
1:2A:668:A:C2	1:2A:2380:A:H1'	2.51	0.46
1:2A:678:A:H61	1:2A:701:A:H1'	1.80	0.46
1:2A:956:A:H2'	12:2Q:9:TYR:OH	2.15	0.46
1:2A:2314:G:C2	1:2A:2325:C:N3	2.83	0.46
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.47	0.46
25:23:30:ARG:H	25:23:33:GLN:HE21	1.64	0.46
27:25:16:ARG:HG3	27:25:17:ASP:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:136:A:OP1	59:2a:3336:HOH:O	2.20	0.46
32:2a:986:C:N4	32:2a:1001:G:H1	2.13	0.46
34:2c:117:ALA:HB2	34:2c:186:PHE:CD2	2.51	0.46
48:2q:62:SER:HB3	48:2q:72:ARG:HD3	1.97	0.46
1:1A:10:G:H2'	1:1A:11:U:H5"	1.97	0.46
1:1A:501:G:H4'	1:1A:526:A:N1	2.30	0.46
1:1A:663:U:H2'	1:1A:664:C:C6	2.50	0.46
1:1A:671:G:O5'	1:1A:671:G:H8	1.97	0.46
32:1a:620:U:H2'	32:1a:621:G:C8	2.51	0.46
32:1a:1268:A:H2'	32:1a:1269:A:H4'	1.96	0.46
1:2A:183:A:H61	1:2A:186:C:H3'	1.80	0.46
1:2A:1132:G:H2'	1:2A:1134:G:H5'	1.96	0.46
1:2A:1632:A:H2'	1:2A:1633:C:C6	2.51	0.46
1:2A:1684:C:H5"	1:2A:2721:C:O2'	2.15	0.46
1:2A:2554:G:H2'	1:2A:2555:G:C8	2.51	0.46
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.49	0.46
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.63	0.46
4:2E:31:CYS:HA	4:2E:32:PRO:HD2	1.81	0.46
32:2a:798:A:N7	32:2a:800:A:C4	2.83	0.46
32:2a:1149:G:H5'	32:2a:1150:A:OP2	2.14	0.46
32:2a:1358:A:O3'	38:2g:29:LYS:NZ	2.47	0.46
33:2b:16:HIS:C	33:2b:17:PHE:HD1	2.23	0.46
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.97	0.46
36:2e:83:GLU:HA	36:2e:88:LYS:HA	1.96	0.46
38:2g:47:CYS:O	38:2g:50:ILE:HG12	2.14	0.46
1:1A:1002:U:O2	2:1B:90:A:O2'	2.27	0.46
1:1A:1743:G:OP2	1:1A:1744:A:O2'	2.30	0.46
2:1B:50:G:H5"	14:1S:61:ASN:ND2	2.30	0.46
13:1R:57:ARG:HB3	13:1R:59:ASP:OD1	2.16	0.46
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.98	0.46
26:14:33:VAL:HG12	26:14:34:GLU:H	1.81	0.46
32:1a:1223:G:H2'	32:1a:1224:C:H6	1.80	0.46
32:1a:1291:G:N7	44:1m:99:ARG:NH2	2.63	0.46
35:1d:9:CYS:O	35:1d:13:ARG:HG3	2.16	0.46
35:1d:200:GLU:HG2	35:1d:201:GLN:N	2.30	0.46
40:1i:29:ASN:N	40:1i:63:ILE:O	2.26	0.46
44:1m:97:PRO:HA	44:1m:110:ARG:HD3	1.97	0.46
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.50	0.46
1:2A:105:U:H2'	1:2A:106:G:C8	2.51	0.46
1:2A:206:A:C2	1:2A:223:U:H4'	2.50	0.46
1:2A:332:G:N3	1:2A:352:G:O2'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:612:A:OP1	5:2F:95:ARG:NH1	2.49	0.46
1:2A:1266:C:C2	1:2A:1274:G:C2	3.04	0.46
1:2A:1713:G:O2'	1:2A:2012:U:O4	2.24	0.46
1:2A:2284:A:H2'	1:2A:2285:A:H8	1.80	0.46
1:2A:2375:C:H2'	1:2A:2376:G:O4'	2.15	0.46
1:2A:2672:G:H2'	1:2A:2673:A:C8	2.51	0.46
16:2U:66:ASN:O	16:2U:70:ARG:HG3	2.16	0.46
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.98	0.46
18:2W:79:GLY:HA3	18:2W:100:THR:HG22	1.98	0.46
20:2Y:94:LYS:HD3	20:2Y:94:LYS:HA	1.74	0.46
26:24:16:CYS:SG	26:24:17:GLY:N	2.89	0.46
32:2a:417:U:O2'	32:2a:419:G:N7	2.46	0.46
32:2a:546:C:H4'	32:2a:547:A:O5'	2.15	0.46
32:2a:1200:C:OP2	45:2n:9:LYS:NZ	2.23	0.46
33:2b:127:ILE:HG12	33:2b:128:GLU:H	1.80	0.46
34:2c:113:ALA:O	34:2c:116:VAL:N	2.49	0.46
35:2d:3:ARG:HD3	35:2d:118:ARG:CD	2.46	0.46
35:2d:60:GLU:HG2	35:2d:202:LEU:HB2	1.98	0.46
1:1A:806:G:H2'	1:1A:807:A:O4'	2.16	0.46
1:1A:2333:A:H2'	1:1A:2334:G:O4'	2.16	0.46
32:1a:17:A:OP1	59:1a:2022:HOH:O	2.21	0.46
32:1a:77:G:N2	32:1a:88:C:N3	2.64	0.46
32:1a:798:A:H2'	32:1a:800:A:H5"	1.96	0.46
32:1a:964:A:H1'	50:1s:54:GLY:O	2.16	0.46
32:1a:1084:A:OP2	33:1b:96:ARG:HD3	2.16	0.46
34:1c:113:ALA:O	34:1c:116:VAL:N	2.49	0.46
39:1h:124:ALA:O	39:1h:128:GLY:N	2.48	0.46
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.39	0.46
1:2A:338:G:H2'	1:2A:339:C:C6	2.50	0.46
1:2A:554:G:O4'	1:2A:554:G:N3	2.48	0.46
1:2A:1835:U:O2	3:2D:50:THR:HB	2.16	0.46
4:2E:24:THR:HG22	4:2E:186:GLY:O	2.15	0.46
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.74	0.46
32:2a:629:C:H2'	32:2a:630:U:C6	2.51	0.46
32:2a:667:G:H2'	32:2a:668:A:C8	2.50	0.46
32:2a:1110:G:H8	59:2a:3311:HOH:O	1.99	0.46
32:2a:1307:C:C2'	32:2a:1308:C:H5'	2.45	0.46
33:2b:165:VAL:HA	33:2b:187:LEU:CD1	2.45	0.46
34:2c:186:PHE:CB	34:2c:199:LYS:HA	2.45	0.46
41:2j:65:LEU:HD13	45:2n:56:VAL:HG22	1.97	0.46
43:2l:110:VAL:HG23	43:2l:120:TYR:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.80	0.46
1:1A:680:C:H2'	1:1A:681:G:O4'	2.16	0.46
1:1A:1603:C:OP2	1:1A:1604:A:O2'	2.19	0.46
1:1A:1953:A:H2'	1:1A:1954:G:O4'	2.15	0.46
2:1B:2:C:H2'	2:1B:3:C:C6	2.51	0.46
24:12:22:GLU:HG2	24:12:64:LEU:HD11	1.97	0.46
32:1a:476:G:H2'	32:1a:477:G:O4'	2.15	0.46
40:1i:15:ALA:HB2	40:1i:65:VAL:HG23	1.98	0.46
49:1r:53:ARG:HD2	49:1r:59:SER:O	2.15	0.46
54:1x:46:G:H3'	54:1x:47:U:C2	2.51	0.46
1:2A:1703:C:H2'	1:2A:1704:C:C6	2.51	0.46
1:2A:1874:C:OP1	3:2D:257:LEU:HD23	2.14	0.46
1:2A:2566:U:H5"	1:2A:2567:C:OP2	2.15	0.46
1:2A:2829:A:OP1	13:2R:2:ARG:NH2	2.48	0.46
21:2Z:5:LEU:HD13	21:2Z:47:VAL:HG21	1.98	0.46
32:2a:209:U:H3'	32:2a:210:U:C6	2.51	0.46
32:2a:460:G:H2'	32:2a:461:G:C8	2.47	0.46
33:2b:188:ALA:HB1	33:2b:192:SER:HB2	1.98	0.46
34:2c:32:LEU:CB	34:2c:59:ARG:HH12	2.29	0.46
37:2f:61:LEU:HB3	37:2f:63:TYR:HE1	1.81	0.46
41:2j:6:ILE:O	41:2j:71:LEU:HD12	2.16	0.46
1:1A:899:G:H1	1:1A:969:C:H42	1.64	0.46
2:1B:24:G:N7	2:1B:56:G:H2'	2.30	0.46
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.16	0.46
26:14:44:THR:O	26:14:44:THR:OG1	2.32	0.46
32:1a:1290:U:H5"	44:1m:98:VAL:HG23	1.98	0.46
33:1b:71:VAL:O	33:1b:165:VAL:HG23	2.16	0.46
33:1b:81:VAL:HG23	33:1b:82:ARG:H	1.81	0.46
35:1d:184:LYS:HE3	35:1d:184:LYS:HB3	1.70	0.46
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.98	0.46
42:1k:34:ASP:HB3	42:1k:40:ILE:HD11	1.98	0.46
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.72	0.46
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.16	0.46
1:2A:488:G:O6	59:2A:3641:HOH:O	2.21	0.46
1:2A:948:C:H2'	1:2A:949:C:C6	2.50	0.46
1:2A:2889:C:O3'	13:2R:90:ARG:NH1	2.49	0.46
3:2D:67:PHE:CD1	3:2D:153:ALA:HB3	2.51	0.46
6:2G:47:LYS:HB3	6:2G:48:GLU:H	1.39	0.46
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.96	0.46
26:24:44:THR:O	26:24:46:GLN:N	2.49	0.46
26:24:59:PHE:HA	26:24:60:GLN:C	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:45:G:H2'	32:2a:46:U:O4'	2.16	0.46
32:2a:810:C:H2'	32:2a:811:U:H6	1.81	0.46
32:2a:1137:G:H2'	32:2a:1138:G:H8	1.81	0.46
32:2a:1221:A:H62	32:2a:1281:A:N6	2.14	0.46
32:2a:1270:A:H2'	32:2a:1271:A:C8	2.51	0.46
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.98	0.46
39:2h:39:LEU:HB3	39:2h:45:ILE:HG12	1.98	0.46
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.16	0.46
1:1A:440:C:H2'	1:1A:441:A:C8	2.51	0.46
1:1A:1500:U:O2'	1:1A:1501:G:N7	2.45	0.46
1:1A:2584:C:N3	55:1z:1:VAL:HA	2.30	0.46
32:1a:521:G:H5"	43:1l:113:ARG:NH1	2.30	0.46
32:1a:1140:A:H4'	32:1a:1141:C:O5'	2.16	0.46
35:1d:8:VAL:HG23	35:1d:11:LEU:HD22	1.97	0.46
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.98	0.46
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.97	0.46
1:2A:998:G:H5"	12:2Q:13:GLN:HB3	1.98	0.46
1:2A:1409:G:OP2	23:21:3:LYS:HG3	2.16	0.46
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	1.97	0.46
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.98	0.46
9:2N:37:LYS:HG3	9:2N:42:TRP:NE1	2.31	0.46
21:2Z:19:ARG:NH1	21:2Z:84:GLU:HB2	2.31	0.46
26:24:26:SER:OG	26:24:27:THR:N	2.49	0.46
32:2a:722:C:OP1	37:2f:2:ARG:NH1	2.48	0.46
33:2b:81:VAL:HG23	33:2b:82:ARG:H	1.81	0.46
38:2g:16:LEU:H	38:2g:16:LEU:HD22	1.80	0.46
41:2j:33:GLN:H	41:2j:76:ASN:H	1.63	0.46
1:1A:1176:G:H21	9:1N:73:THR:CG2	2.29	0.46
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	1.98	0.46
7:1H:101:ARG:HA	7:1H:101:ARG:HD2	1.72	0.46
10:1O:103:ALA:HB1	10:1O:105:GLU:HG2	1.98	0.46
32:1a:1056:U:H2'	32:1a:1057:G:H8	1.78	0.46
32:1a:1254:G:H2'	32:1a:1255:G:O4'	2.15	0.46
32:1a:1385:C:H2'	32:1a:1386:C:O4'	2.14	0.46
35:1d:173:TRP:CE2	35:1d:189:PRO:HB3	2.51	0.46
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.16	0.46
44:1m:15:VAL:O	44:1m:19:LEU:HD22	2.15	0.46
50:1s:27:GLU:HG3	50:1s:28:LYS:NZ	2.31	0.46
51:1t:39:LYS:HB2	51:1t:39:LYS:HE3	1.84	0.46
1:2A:552:A:C2	1:2A:2064:C:H4'	2.51	0.46
1:2A:791:G:H2'	1:2A:792:A:H5'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1856:G:H4'	3:2D:242:ARG:CZ	2.46	0.46
1:2A:2347:A:H61	22:20:43:THR:CG2	2.29	0.46
11:2P:2:LYS:NZ	11:2P:4:SER:OG	2.37	0.46
12:2Q:12:GLN:HG3	12:2Q:72:LYS:HZ2	1.81	0.46
12:2Q:59:ARG:O	12:2Q:60:ARG:HB2	2.16	0.46
32:2a:1087:G:H4'	33:2b:111:ARG:NH1	2.30	0.46
32:2a:1116:G:H2'	32:2a:1117:G:H8	1.80	0.46
32:2a:1202:G:H5'	50:2s:34:TRP:O	2.15	0.46
32:2a:1302:C:C2	50:2s:72:GLY:HA3	2.51	0.46
34:2c:63:ASN:HA	34:2c:98:ASN:HB2	1.98	0.46
1:1A:624:G:O2'	1:1A:701:A:N6	2.48	0.45
1:1A:1475:C:H2'	1:1A:1476:U:H6	1.81	0.45
1:1A:2578:G:H2'	1:1A:2579:C:C6	2.50	0.45
6:1G:97:ASP:O	6:1G:101:ILE:HG13	2.16	0.45
26:14:58:ARG:NH1	50:1s:68:GLY:H	2.14	0.45
32:1a:197:U:H3'	32:1a:197:U:H6	1.81	0.45
32:1a:392:G:O2'	32:1a:394:C:OP1	2.26	0.45
32:1a:972:A:N1	32:1a:1030:G:H4'	2.31	0.45
32:1a:1219:C:O2'	32:1a:1282:G:N1	2.45	0.45
1:2A:309:C:H2'	1:2A:310:C:C6	2.50	0.45
1:2A:623:C:OP1	5:2F:108:LYS:NZ	2.35	0.45
1:2A:665:C:O2'	1:2A:2361:C:OP1	2.16	0.45
1:2A:945:A:H2'	1:2A:946:A:C8	2.51	0.45
5:2F:112:MET:HE3	5:2F:112:MET:HB3	1.63	0.45
7:2H:127:GLU:C	7:2H:129:THR:H	2.24	0.45
12:2Q:12:GLN:HG2	12:2Q:73:PRO:HD2	1.98	0.45
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.52	0.45
21:2Z:89:PHE:HE2	21:2Z:96:VAL:HG21	1.81	0.45
32:2a:655:G:O6	59:2a:3335:HOH:O	2.20	0.45
32:2a:1117:G:C6	32:2a:1118:U:H1'	2.52	0.45
32:2a:1256:G:N2	32:2a:1257:A:N7	2.64	0.45
32:2a:1302:C:H2'	32:2a:1303:C:O4'	2.16	0.45
33:2b:47:THR:OG1	33:2b:202:PRO:O	2.34	0.45
40:2i:77:ILE:O	40:2i:81:ILE:HG23	2.16	0.45
1:1A:591:U:C4	1:1A:592:G:C6	3.04	0.45
1:1A:867:A:H2'	1:1A:990:G:H5"	1.98	0.45
1:1A:1404:A:H5'	1:1A:1404:A:N3	2.32	0.45
1:1A:2290:G:N7	22:10:14:ARG:NH1	2.64	0.45
3:1D:71:ASP:CB	3:1D:103:ARG:HH22	2.19	0.45
32:1a:725:G:H2'	32:1a:726:G:O4'	2.16	0.45
32:1a:843:A:C2	32:1a:896:A:H4'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1086:C:H2'	32:1a:1087:G:O4'	2.16	0.45
1:2A:358:C:H2'	1:2A:359:C:H6	1.80	0.45
1:2A:704:C:H2'	1:2A:705:C:C6	2.50	0.45
1:2A:885:U:H1'	1:2A:1235:G:H1'	1.98	0.45
1:2A:1548:U:H2'	1:2A:1549:C:C6	2.51	0.45
2:2B:11:C:H3'	2:2B:12:C:C6	2.51	0.45
18:2W:38:TYR:O	27:25:28:PRO:HB3	2.15	0.45
21:2Z:72:ARG:HA	21:2Z:72:ARG:HD3	1.80	0.45
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.16	0.45
39:2h:81:HIS:N	39:2h:138:TRP:O	2.49	0.45
43:2l:24:VAL:HG23	43:2l:98:TYR:HE1	1.82	0.45
44:2m:80:ARG:NH2	50:2s:69:HIS:HE1	2.11	0.45
49:2r:29:PHE:N	49:2r:29:PHE:CD1	2.79	0.45
1:1A:253:A:C8	1:1A:254:G:H1'	2.51	0.45
1:1A:1500:U:OP1	13:1R:77:ARG:NH1	2.44	0.45
1:1A:1531:A:H2'	1:1A:1532:G:C8	2.51	0.45
1:1A:1633:C:H2'	1:1A:1634:C:C6	2.50	0.45
1:1A:2282:G:OP1	22:10:18:ALA:HB1	2.16	0.45
3:1D:108:PRO:HG3	3:1D:143:HIS:CE1	2.51	0.45
20:1Y:1:MET:HE3	20:1Y:2:ARG:HG2	1.97	0.45
21:1Z:155:LEU:HD12	21:1Z:155:LEU:HA	1.75	0.45
26:14:20:ASN:OD1	26:14:21:VAL:N	2.50	0.45
32:1a:296:A:H1'	32:1a:549:U:O2	2.17	0.45
32:1a:820:G:OP2	49:1r:61:LYS:HE3	2.15	0.45
37:1f:22:GLU:O	37:1f:26:ILE:HG13	2.17	0.45
1:2A:1100:G:N2	1:2A:1149:C:O2	2.45	0.45
1:2A:1150:U:H2'	1:2A:1151:G:C8	2.52	0.45
1:2A:1627:G:H2'	1:2A:1628:C:O4'	2.16	0.45
1:2A:2573:U:H1'	10:2O:23:ARG:HH11	1.81	0.45
1:2A:2698:U:H2'	1:2A:2699:U:O4'	2.17	0.45
17:2V:20:LEU:HD12	17:2V:20:LEU:HA	1.77	0.45
32:2a:1315:A:H2'	32:2a:1316:G:O4'	2.16	0.45
32:2a:1342:A:H3'	32:2a:1343:G:C8	2.51	0.45
34:2c:130:VAL:O	34:2c:134:ILE:HG12	2.16	0.45
35:2d:153:ARG:NH1	35:2d:181:MET:HE3	2.31	0.45
36:2e:68:GLU:HG2	36:2e:69:VAL:N	2.31	0.45
1:1A:2302:U:H2'	1:1A:2303:C:C6	2.52	0.45
1:1A:2563:U:C2	1:1A:2565:U:H5'	2.52	0.45
2:1B:13:A:N1	2:1B:69:G:O2'	2.48	0.45
8:1I:6:LEU:HG	8:1I:36:ALA:HA	1.99	0.45
13:1R:11:ASN:OD1	59:1R:301:HOH:O	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.17	0.45
21:1Z:180:VAL:O	21:1Z:183:LEU:HB2	2.16	0.45
32:1a:897:A:O2'	32:1a:898:U:H5'	2.17	0.45
32:1a:1179:G:OP2	59:1a:2016:HOH:O	2.21	0.45
33:1b:18:GLY:HA2	33:1b:42:ILE:HG13	1.98	0.45
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.71	0.45
33:1b:230:VAL:HG12	33:1b:231:GLU:N	2.30	0.45
35:1d:194:LEU:HD22	35:1d:194:LEU:HA	1.65	0.45
39:1h:25:ASP:OD1	39:1h:60:ARG:HG3	2.16	0.45
50:1s:36:ARG:HB3	50:1s:72:GLY:HA3	1.99	0.45
1:2A:530:G:O3'	1:2A:531:A:H8	1.99	0.45
1:2A:1098:C:H2'	1:2A:1099:A:H5'	1.98	0.45
1:2A:1424:A:H4'	1:2A:1425:G:OP2	2.17	0.45
1:2A:1702:C:O2'	1:2A:1703:C:H5'	2.16	0.45
1:2A:1830:C:OP2	3:2D:183:ARG:NH2	2.48	0.45
1:2A:2254:U:H2'	1:2A:2255:U:C6	2.51	0.45
1:2A:2756:G:N2	7:2H:143:GLN:OE1	2.49	0.45
2:2B:29:A:O2'	2:2B:58:A:N1	2.37	0.45
3:2D:5:LYS:HE3	3:2D:5:LYS:HB3	1.67	0.45
6:2G:115:ARG:HH11	6:2G:115:ARG:CG	2.29	0.45
9:2N:20:GLY:HA2	9:2N:61:ARG:NE	2.30	0.45
12:2Q:16:ARG:O	12:2Q:17:LEU:HD23	2.17	0.45
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.98	0.45
21:2Z:1:MET:HA	21:2Z:55:HIS:HB3	1.97	0.45
32:2a:295:G:H2'	32:2a:296:A:C8	2.51	0.45
32:2a:430:U:H2'	32:2a:431:C:C6	2.52	0.45
32:2a:837:A:H2'	32:2a:838:A:O4'	2.17	0.45
32:2a:1045:U:H2'	32:2a:1046:C:C6	2.51	0.45
32:2a:1188:G:O2'	34:2c:193:TYR:HA	2.16	0.45
1:1A:1359:C:OP1	59:1A:4132:HOH:O	2.21	0.45
1:1A:2644:G:H5'	1:1A:2820:G:O2'	2.16	0.45
2:1B:50:G:H5"	14:1S:61:ASN:HD21	1.82	0.45
4:1E:55:ASN:HB3	4:1E:58:ARG:HG3	1.97	0.45
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.16	0.45
32:1a:544:U:HO2'	32:1a:545:U:P	2.38	0.45
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.51	0.45
50:1s:27:GLU:HB2	50:1s:28:LYS:HZ2	1.81	0.45
1:2A:1044:U:O2'	1:2A:1045:A:H5'	2.17	0.45
1:2A:1050:C:C2	1:2A:1188:A:C5	3.04	0.45
1:2A:1404:A:H2'	1:2A:1405:A:C5'	2.47	0.45
1:2A:2330:G:C2	14:2S:3:ARG:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:97:ASP:O	6:2G:101:ILE:HG13	2.16	0.45
9:2N:36:GLY:HA2	9:2N:38:HIS:CE1	2.51	0.45
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.57	0.45
32:2a:126:C:H2'	32:2a:127:C:C6	2.51	0.45
32:2a:584:C:H2'	32:2a:585:C:H6	1.81	0.45
32:2a:1354:G:C2	32:2a:1355:U:C2	3.04	0.45
41:2j:13:HIS:CD2	41:2j:68:HIS:CE1	3.04	0.45
1:1A:222:C:H2'	1:1A:223:U:C6	2.52	0.45
1:1A:671:G:H2'	1:1A:672:G:O4'	2.16	0.45
1:1A:2035:A:H2'	1:1A:2036:A:C8	2.52	0.45
1:1A:2300:G:OP1	59:1A:4158:HOH:O	2.21	0.45
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.99	0.45
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.73	0.45
20:1Y:92:ASN:N	20:1Y:92:ASN:HD22	2.14	0.45
21:1Z:152:ALA:O	21:1Z:155:LEU:HB2	2.17	0.45
32:1a:141:G:C2	32:1a:172:C:N3	2.85	0.45
32:1a:184:G:C2	32:1a:196:G:C2	3.05	0.45
32:1a:480:A:H4'	32:1a:481:A:OP1	2.16	0.45
32:1a:1107:G:O2'	32:1a:1128:C:C4	2.66	0.45
32:1a:1188:G:C6	32:1a:1189:G:C5	3.05	0.45
32:1a:1240:G:H2'	32:1a:1241:C:H6	1.81	0.45
33:1b:147:LYS:HE3	33:1b:147:LYS:HB3	1.78	0.45
33:1b:178:ARG:NH2	39:1h:68:ARG:HH22	2.14	0.45
35:1d:119:GLN:HG2	35:1d:123:HIS:CD2	2.52	0.45
37:1f:9:VAL:HB	37:1f:87:ARG:HB2	1.98	0.45
39:1h:41:ARG:HH22	39:1h:123:GLU:CD	2.25	0.45
40:1i:43:ALA:C	40:1i:45:ALA:H	2.24	0.45
40:1i:47:LEU:O	40:1i:50:LEU:HB2	2.16	0.45
44:1m:15:VAL:HG23	44:1m:43:THR:O	2.16	0.45
1:2A:141:G:H2'	1:2A:142:C:C6	2.52	0.45
4:2E:33:VAL:HG13	4:2E:89:ASP:C	2.41	0.45
7:2H:3:ARG:NE	7:2H:54:ARG:HH12	2.14	0.45
8:2I:72:LEU:HA	8:2I:75:LEU:HD22	1.97	0.45
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	1.99	0.45
24:22:3:LEU:HD23	24:22:3:LEU:HA	1.82	0.45
32:2a:103:A:C6	32:2a:322:G:C6	3.05	0.45
32:2a:448:A:C5	32:2a:449:C:C4	3.05	0.45
32:2a:609:G:H4'	47:2p:16:HIS:CD2	2.52	0.45
32:2a:825:U:H6	32:2a:825:U:OP1	1.98	0.45
32:2a:965:G:N2	32:2a:1201:U:C2	2.85	0.45
40:2i:49:PRO:HG2	40:2i:81:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:6:ILE:HG12	41:2j:98:ILE:HD11	1.99	0.45
51:2t:33:ILE:O	51:2t:37:SER:OG	2.26	0.45
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.82	0.45
1:1A:609:C:OP2	11:1P:21:ARG:NH2	2.50	0.45
59:1A:4195:HOH:O	15:1T:119:LYS:NZ	2.50	0.45
7:1H:71:LEU:HD12	7:1H:71:LEU:HA	1.77	0.45
11:1P:76:LYS:HE2	11:1P:76:LYS:HB3	1.84	0.45
25:13:38:GLU:HB3	25:13:40:THR:HG23	1.98	0.45
32:1a:170:C:H2'	32:1a:171:C:H6	1.82	0.45
32:1a:295:G:H2'	32:1a:296:A:C8	2.52	0.45
32:1a:429:C:H2'	32:1a:430:U:H6	1.81	0.45
32:1a:641:G:C2	32:1a:642:G:C8	3.05	0.45
32:1a:747:G:H2'	32:1a:748:C:H6	1.81	0.45
48:1q:45:HIS:NE2	48:1q:47:PRO:HG3	2.32	0.45
50:1s:63:THR:OG1	50:1s:64:GLU:N	2.50	0.45
1:2A:182:G:H2'	1:2A:183:A:O4'	2.17	0.45
1:2A:232:A:C2	1:2A:243:A:C4	3.05	0.45
1:2A:325:C:OP2	20:2Y:73:ARG:NH1	2.50	0.45
1:2A:1305:G:C6	1:2A:1306:C:C4	3.04	0.45
1:2A:2326:G:H2'	1:2A:2327:C:C6	2.51	0.45
4:2E:182:LEU:HA	4:2E:182:LEU:HD12	1.65	0.45
10:2O:6:THR:HG22	10:2O:8:LEU:HD22	1.99	0.45
10:2O:64:ARG:NH1	10:2O:81:ASP:OD1	2.48	0.45
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.51	0.45
18:2W:45:TYR:CZ	18:2W:49:LYS:HE3	2.52	0.45
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	1.99	0.45
32:2a:958:C:H1'	45:2n:19:ARG:HA	1.99	0.45
32:2a:1101:C:H42	32:2a:1139:G:N2	2.14	0.45
32:2a:1239:U:H5'	32:2a:1240:G:O5'	2.17	0.45
35:2d:191:ARG:O	35:2d:191:ARG:NH1	2.49	0.45
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.99	0.45
37:2f:44:GLY:HA2	37:2f:59:TYR:CZ	2.52	0.45
41:2j:48:THR:HB	41:2j:62:HIS:ND1	2.32	0.45
44:2m:80:ARG:O	44:2m:84:ILE:HG23	2.17	0.45
49:2r:43:PHE:C	49:2r:51:LEU:HD12	2.42	0.45
1:1A:433:G:OP2	59:1A:4160:HOH:O	2.21	0.45
1:1A:509:C:H2'	1:1A:510:C:C6	2.52	0.45
1:1A:645:A:OP2	11:1P:108:LYS:NZ	2.48	0.45
1:1A:1067:G:H22	1:1A:1187:A:H2	1.60	0.45
1:1A:2358:C:H2'	1:1A:2359:U:C6	2.52	0.45
1:1A:2878:G:H2'	1:1A:2879:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:41:C:H2'	32:1a:42:G:H8	1.82	0.45
32:1a:669:G:O2'	32:1a:670:U:H5'	2.17	0.45
32:1a:850:A:C8	32:1a:852:G:C8	3.04	0.45
32:1a:1297:U:H2'	32:1a:1298:G:O4'	2.16	0.45
33:1b:84:GLU:O	33:1b:219:VAL:HG11	2.17	0.45
33:1b:145:LEU:HD13	33:1b:145:LEU:HA	1.74	0.45
35:1d:49:ARG:H	35:1d:49:ARG:NE	2.15	0.45
39:1h:49:GLU:HG2	39:1h:62:TYR:HE1	1.81	0.45
42:1k:44:SER:OG	42:1k:47:VAL:HG23	2.17	0.45
44:1m:44:ARG:HD3	44:1m:44:ARG:HA	1.72	0.45
1:2A:1104:G:H5'	1:2A:1105:U:H5"	1.99	0.45
1:2A:1311:G:O2'	1:2A:2033:G:O6	2.33	0.45
1:2A:1735:A:N6	1:2A:1744:A:H2	2.04	0.45
1:2A:1906:A:H2'	1:2A:1907:C:O4'	2.16	0.45
1:2A:2709:U:H2'	1:2A:2710:C:C6	2.51	0.45
1:2A:2818:A:H62	1:2A:2899:G:H2'	1.81	0.45
2:2B:66:A:H61	2:2B:108:U:H2'	1.81	0.45
4:2E:116:VAL:HG21	4:2E:138:PRO:HB3	1.98	0.45
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.17	0.45
8:2I:44:LEU:HD12	8:2I:44:LEU:HA	1.82	0.45
22:20:43:THR:HG23	22:20:43:THR:O	2.17	0.45
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.52	0.45
32:2a:1302:C:N4	50:2s:36:ARG:HB2	2.32	0.45
34:2c:185:GLY:O	34:2c:186:PHE:HB2	2.16	0.45
35:2d:57:ARG:HB3	35:2d:206:PHE:HB2	1.98	0.45
50:2s:52:TYR:HD1	50:2s:57:HIS:CD2	2.34	0.45
1:1A:942:C:H2'	1:1A:943:C:H6	1.82	0.45
1:1A:2696:G:H5'	10:1O:68:GLU:OE1	2.16	0.45
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.98	0.45
32:1a:610:U:H2'	32:1a:611:G:C8	2.52	0.45
32:1a:675:G:H2'	32:1a:676:U:C6	2.52	0.45
32:1a:900:G:C6	32:1a:901:A:C6	3.05	0.45
32:1a:1111:C:H4'	32:1a:1131:U:O2	2.17	0.45
33:1b:51:LEU:O	33:1b:55:PHE:HD2	2.00	0.45
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.98	0.45
50:1s:43:GLU:OE1	50:1s:43:GLU:N	2.50	0.45
1:2A:242:G:N7	30:28:5:LYS:HE2	2.32	0.45
1:2A:1051:C:C2	1:2A:1182:G:N2	2.84	0.45
32:2a:378:A:H2'	32:2a:379:A:C8	2.52	0.45
32:2a:859:G:OP2	43:2l:12:ARG:NH2	2.49	0.45
32:2a:1369:G:C2	32:2a:1370:G:C8	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.16	0.45
1:1A:235:G:H4'	1:1A:412:G:C5	2.52	0.45
1:1A:301:A:H2'	1:1A:302:C:C6	2.52	0.45
1:1A:1614:G:H5'	3:1D:60:ARG:HA	1.99	0.45
1:1A:1835:U:O2	3:1D:50:THR:HB	2.16	0.45
1:1A:2342:G:O2'	1:1A:2347:A:N1	2.42	0.45
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.98	0.45
26:14:62:ARG:HD3	26:14:62:ARG:HA	1.68	0.45
30:18:61:LEU:C	30:18:63:PRO:HD3	2.42	0.45
32:1a:46:U:H2'	32:1a:47:G:C8	2.52	0.45
32:1a:397:C:H1'	32:1a:606:A:H1'	1.98	0.45
32:1a:1257:A:H2'	32:1a:1258:G:O4'	2.17	0.45
36:1e:76:ILE:HD12	36:1e:142:LEU:HD21	1.98	0.45
1:2A:563:G:H2'	1:2A:564:C:C6	2.52	0.45
1:2A:598:U:H2'	1:2A:599:G:C8	2.52	0.45
1:2A:929:G:O6	1:2A:938:C:N4	2.49	0.45
1:2A:942:C:H2'	1:2A:943:C:H6	1.82	0.45
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.17	0.45
1:2A:1404:A:C6	1:2A:1417:U:O4	2.70	0.45
1:2A:2124:C:H1'	1:2A:2208:G:N1	2.32	0.45
1:2A:2494:C:H2'	1:2A:2495:G:O4'	2.17	0.45
2:2B:6:C:N4	2:2B:115:G:H1	2.12	0.45
5:2F:106:ARG:H	5:2F:106:ARG:HG2	1.50	0.45
6:2G:41:GLN:O	6:2G:43:LEU:HB2	2.17	0.45
10:2O:23:ARG:HG3	10:2O:24:VAL:N	2.32	0.45
21:2Z:179:ASP:O	21:2Z:182:LYS:HB2	2.17	0.45
25:23:23:LEU:HD13	25:23:50:VAL:HG11	1.99	0.45
31:29:17:ILE:HG22	31:29:24:TYR:HB2	1.99	0.45
32:2a:144:A:H2'	32:2a:145:C:H6	1.82	0.45
32:2a:365:C:H2'	32:2a:366:C:H6	1.81	0.45
32:2a:438:C:H2'	32:2a:439:C:C6	2.52	0.45
32:2a:571:G:O3'	59:2a:3337:HOH:O	2.21	0.45
32:2a:712:A:H2'	32:2a:713:A:H8	1.80	0.45
34:2c:43:LEU:O	34:2c:47:LEU:HB3	2.17	0.45
1:1A:720:G:O2'	5:1F:74:ARG:HD3	2.16	0.44
1:1A:1187:A:C4	1:1A:1189:G:C8	3.05	0.44
1:1A:1792:A:H2'	59:1A:5466:HOH:O	2.16	0.44
1:1A:2205:G:H5'	1:1A:2206:C:OP2	2.17	0.44
1:1A:2554:G:H2'	1:1A:2555:G:C8	2.51	0.44
1:1A:2744:G:H3'	1:1A:2745:A:O4'	2.17	0.44
6:1G:181:ARG:HG3	6:1G:182:LYS:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:46:LYS:HE3	11:1P:46:LYS:HB3	1.75	0.44
32:1a:354:U:H2'	32:1a:355:U:C6	2.52	0.44
32:1a:720:C:H2'	32:1a:721:A:H8	1.82	0.44
32:1a:983:A:H2'	32:1a:984:A:H5'	1.98	0.44
32:1a:1132:C:H2'	32:1a:1133:U:O4'	2.17	0.44
35:1d:39:PRO:HA	35:1d:40:PRO:HD3	1.86	0.44
51:1t:36:LEU:HD13	51:1t:58:LYS:HG3	1.99	0.44
1:2A:1042:G:N3	1:2A:1042:G:H2'	2.32	0.44
1:2A:1061:G:H2'	1:2A:1062:G:H8	1.83	0.44
1:2A:1567:G:H2'	1:2A:1568:U:O4'	2.18	0.44
1:2A:1854:G:OP1	3:2D:52:ARG:NH1	2.50	0.44
2:2B:12:C:H2'	22:20:73:GLY:HA3	1.99	0.44
5:2F:9:ILE:HG21	5:2F:125:LEU:HD13	1.99	0.44
11:2P:126:VAL:HG12	11:2P:148:LEU:CD2	2.46	0.44
21:2Z:57:ILE:HD12	21:2Z:71:VAL:HG23	1.99	0.44
32:2a:11:A:OP2	36:2e:126:ARG:HD2	2.17	0.44
32:2a:423:U:H3'	32:2a:424:G:H2'	2.00	0.44
32:2a:538:C:H2'	32:2a:539:C:H6	1.81	0.44
32:2a:1189:G:H2'	32:2a:1190:C:C6	2.52	0.44
35:2d:31:CYS:SG	35:2d:33:MET:N	2.90	0.44
35:2d:146:ILE:N	35:2d:146:ILE:HD12	2.31	0.44
38:2g:113:GLU:O	38:2g:119:ARG:HD3	2.17	0.44
45:2n:4:LYS:O	45:2n:7:ILE:HG12	2.18	0.44
55:2z:11:ARG:HB3	55:2z:12:PRO:CD	2.46	0.44
1:1A:387:A:H2'	1:1A:388:G:C8	2.52	0.44
6:1G:41:GLN:NE2	6:1G:154:GLY:O	2.43	0.44
32:1a:610:U:C2	32:1a:611:G:C8	3.05	0.44
32:1a:1101:C:H1'	32:1a:1161:A:C4	2.52	0.44
33:1b:97:TRP:HZ2	33:1b:102:LEU:HD13	1.82	0.44
35:1d:174:LEU:N	35:1d:186:LEU:HD12	2.32	0.44
35:1d:175:SER:O	35:1d:183:GLY:HA2	2.17	0.44
40:1i:23:ASN:HD22	40:1i:23:ASN:C	2.25	0.44
1:2A:47:A:H4'	1:2A:48:U:H5"	1.99	0.44
1:2A:791:G:C2'	1:2A:792:A:H5'	2.47	0.44
1:2A:1426:G:H1'	1:2A:1617:A:N1	2.32	0.44
1:2A:2494:C:N3	12:2Q:124:LYS:NZ	2.61	0.44
6:2G:43:LEU:HB3	6:2G:44:GLY:H	1.59	0.44
8:2I:90:GLY:O	8:2I:121:LYS:HE3	2.17	0.44
11:2P:125:VAL:HG13	11:2P:138:LEU:HD21	1.98	0.44
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.98	0.44
28:26:35:GLU:HG3	28:26:50:ARG:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:91:G:O2'	32:2a:92:G:H8	2.01	0.44
32:2a:551:G:H2'	32:2a:552:G:O4'	2.18	0.44
32:2a:1443:C:H2'	32:2a:1444:C:O4'	2.17	0.44
33:2b:28:PHE:CD1	33:2b:190:THR:HA	2.52	0.44
33:2b:92:TYR:OH	33:2b:153:ARG:HG2	2.17	0.44
48:2q:43:LEU:O	48:2q:69:LYS:HG2	2.17	0.44
1:1A:170:A:H2'	1:1A:171:C:O4'	2.17	0.44
1:1A:482:A:H5"	59:1A:4893:HOH:O	2.18	0.44
1:1A:517:G:H2'	1:1A:518:G:O4'	2.17	0.44
1:1A:1868:C:N4	1:1A:1919:U:H2'	2.32	0.44
1:1A:1924:G:OP1	3:1D:241:PRO:HB2	2.17	0.44
1:1A:2428:C:OP1	11:1P:65:ARG:NH2	2.50	0.44
6:1G:139:LEU:H	6:1G:139:LEU:HD12	1.83	0.44
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.54	0.44
14:1S:36:TYR:N	14:1S:36:TYR:CD1	2.85	0.44
25:13:23:LEU:HD13	25:13:50:VAL:HG11	1.99	0.44
32:1a:200:C:H2'	32:1a:201:C:H6	1.82	0.44
32:1a:1150:A:H2'	32:1a:1151:A:C8	2.52	0.44
33:1b:73:THR:HG23	33:1b:95:GLN:O	2.18	0.44
34:1c:87:LEU:O	34:1c:91:LEU:HB2	2.18	0.44
1:2A:448:A:H2'	1:2A:449:A:C8	2.53	0.44
1:2A:898:G:N2	1:2A:971:A:H1'	2.32	0.44
1:2A:1423:A:O2'	1:2A:1425:G:N7	2.47	0.44
1:2A:2020:C:H4'	1:2A:2735:C:O2	2.18	0.44
1:2A:2760:A:H5'	7:2H:4:ILE:HD12	1.98	0.44
1:2A:2763:G:C6	7:2H:2:SER:HB2	2.53	0.44
20:2Y:5:MET:HE2	20:2Y:5:MET:HB2	1.57	0.44
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.90	0.44
26:24:61:ARG:HA	26:24:61:ARG:HD2	1.67	0.44
32:2a:547:A:N7	32:2a:551:G:H1'	2.33	0.44
32:2a:1078:U:H2'	32:2a:1079:C:O4'	2.17	0.44
32:2a:1335:G:H2'	32:2a:1336:C:H6	1.82	0.44
33:2b:15:VAL:O	33:2b:16:HIS:ND1	2.50	0.44
34:2c:107:GLN:O	34:2c:108:ASN:C	2.60	0.44
34:2c:113:ALA:O	34:2c:115:LEU:N	2.51	0.44
38:2g:49:ILE:HA	38:2g:52:GLU:OE1	2.17	0.44
39:2h:58:TYR:O	39:2h:59:LEU:HD23	2.17	0.44
1:1A:2210:U:H2'	1:1A:2211:G:C8	2.47	0.44
1:1A:2899:G:OP2	59:1A:4159:HOH:O	2.21	0.44
7:1H:113:VAL:HG11	7:1H:151:ILE:HD13	1.99	0.44
14:1S:67:ARG:O	14:1S:71:ARG:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:118:ARG:HG2	32:1a:1426:G:C8	2.52	0.44
26:14:35:VAL:HG22	26:14:36:CYS:H	1.82	0.44
31:19:15:LYS:HE2	31:19:17:ILE:HD13	2.00	0.44
32:1a:453:C:H3'	32:1a:454:G:H8	1.82	0.44
32:1a:751:A:H2'	32:1a:752:A:O4'	2.18	0.44
1:2A:592:G:OP2	59:2A:3642:HOH:O	2.21	0.44
1:2A:1101:G:H21	1:2A:1148:A:H62	1.65	0.44
1:2A:1268:G:C2	1:2A:1272:G:C5	3.05	0.44
1:2A:2824:C:C5'	27:25:29:THR:HG21	2.47	0.44
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.62	0.44
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	2.00	0.44
18:2W:41:LYS:HE3	27:25:25:LEU:HD11	1.99	0.44
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.71	0.44
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.52	0.44
32:2a:1400:G:C6	32:2a:1460:G:C6	3.06	0.44
33:2b:16:HIS:HB3	33:2b:210:SER:HB3	1.99	0.44
36:2e:51:VAL:O	36:2e:55:VAL:HG23	2.16	0.44
43:2l:55:VAL:HG23	43:2l:69:TYR:HA	1.98	0.44
54:2x:50:U:H2'	54:2x:51:C:C6	2.51	0.44
1:1A:25:G:C6	1:1A:26:G:N1	2.86	0.44
1:1A:775:G:C5	3:1D:208:LYS:HB2	2.53	0.44
1:1A:810:A:H2	3:1D:219:PRO:HG3	1.82	0.44
1:1A:1573:A:OP2	59:1A:4162:HOH:O	2.21	0.44
1:1A:1734:U:O2	1:1A:1746:A:H5'	2.17	0.44
1:1A:1845:A:H8	1:1A:1845:A:OP1	2.00	0.44
1:1A:2316:A:H5"	6:1G:134:GLY:HA3	1.98	0.44
1:1A:2648:U:H5"	4:1E:82:ARG:NH2	2.32	0.44
1:1A:2855:G:H2'	1:1A:2856:U:O4'	2.18	0.44
1:1A:2896:U:H2'	1:1A:2897:C:C6	2.53	0.44
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.81	0.44
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	2.00	0.44
32:1a:256:G:H2'	32:1a:257:U:C6	2.52	0.44
32:1a:432:C:H2'	32:1a:433:U:H6	1.82	0.44
32:1a:485:C:H1'	32:1a:533:C:H1'	1.99	0.44
32:1a:756:U:H2'	32:1a:757:G:O4'	2.18	0.44
32:1a:1171:C:P	41:1j:51:ARG:HH22	2.38	0.44
32:1a:1395:C:H2'	32:1a:1396:A:H8	1.83	0.44
34:1c:111:LEU:HD21	34:1c:144:SER:O	2.17	0.44
34:1c:115:LEU:HD22	34:1c:115:LEU:N	2.30	0.44
35:1d:8:VAL:O	35:1d:10:ARG:N	2.47	0.44
41:1j:64:GLU:OE2	41:1j:66:ARG:HD2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:1n:43:CYS:HA	45:1n:46:GLU:HB2	1.99	0.44
1:2A:53:G:O2'	1:2A:124:A:N1	2.47	0.44
1:2A:239:A:C5	1:2A:240:G:H1'	2.53	0.44
1:2A:335:G:H5"	1:2A:336:C:OP2	2.18	0.44
1:2A:483:G:C8	29:27:37:LYS:HG2	2.53	0.44
1:2A:706:G:H5'	5:2F:99:TYR:CD2	2.52	0.44
1:2A:945:A:C4	1:2A:946:A:C8	3.06	0.44
1:2A:1561:U:H2'	1:2A:1562:G:H8	1.83	0.44
7:2H:139:GLN:O	7:2H:143:GLN:N	2.47	0.44
11:2P:65:ARG:HG3	30:28:25:MET:CG	2.45	0.44
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.50	0.44
16:2U:104:GLN:OE1	16:2U:105:VAL:HG23	2.18	0.44
23:21:18:ILE:HG12	23:21:37:ILE:HG23	1.99	0.44
26:24:59:PHE:HA	26:24:61:ARG:H	1.81	0.44
32:2a:108:U:H2'	32:2a:109:G:C8	2.52	0.44
32:2a:159:U:H2'	32:2a:160:C:C6	2.51	0.44
32:2a:564:U:H2'	32:2a:565:G:O4'	2.17	0.44
32:2a:959:U:H2'	32:2a:960:U:C5	2.53	0.44
32:2a:1151:A:H2'	32:2a:1152:A:C8	2.52	0.44
32:2a:1273:G:H2'	32:2a:1274:U:H6	1.82	0.44
32:2a:1299:C:H2'	32:2a:1300:A:O4'	2.18	0.44
41:2j:24:VAL:O	41:2j:34:VAL:HG11	2.17	0.44
44:2m:33:ALA:HB2	44:2m:64:TRP:CZ3	2.53	0.44
46:2o:20:GLY:O	46:2o:22:THR:HG22	2.17	0.44
46:2o:26:GLU:H	46:2o:26:GLU:HG2	1.37	0.44
47:2p:18:ARG:NH1	47:2p:32:TYR:OH	2.51	0.44
54:2x:61:C:H2'	54:2x:62:C:H6	1.83	0.44
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.15	0.44
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.90	0.44
32:1a:288:G:N7	32:1a:289:G:H1'	2.33	0.44
32:1a:341:C:H4'	32:1a:342:G:C2	2.53	0.44
32:1a:828:U:H2'	32:1a:829:G:H5"	1.98	0.44
32:1a:1142:U:O4'	32:1a:1164:G:N2	2.51	0.44
36:1e:90:VAL:O	36:1e:120:THR:HA	2.17	0.44
37:1f:61:LEU:HD13	37:1f:61:LEU:HA	1.86	0.44
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	2.00	0.44
1:2A:503:A:C6	1:2A:505:A:C6	3.05	0.44
1:2A:610:U:H1'	5:2F:90:PHE:CG	2.53	0.44
1:2A:636:U:H4'	1:2A:639:A:N6	2.33	0.44
1:2A:875:A:N7	1:2A:2259:C:H5'	2.32	0.44
1:2A:2043:U:O2'	1:2A:2628:C:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:95:C:H2'	2:2B:96:U:C6	2.52	0.44
6:2G:13:GLU:O	6:2G:17:PRO:HD2	2.17	0.44
10:2O:35:VAL:HG13	10:2O:65:THR:HG23	1.99	0.44
32:2a:101:G:H2'	32:2a:102:G:O4'	2.17	0.44
32:2a:1030:G:OP1	45:2n:4:LYS:NZ	2.42	0.44
33:2b:165:VAL:HG23	33:2b:166:ASP:H	1.83	0.44
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.53	0.44
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.31	0.44
43:2l:34:ARG:O	43:2l:61:THR:HG23	2.18	0.44
1:1A:1939:A:O2'	1:1A:1941:C:N4	2.50	0.44
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.50	0.44
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.53	0.44
21:1Z:138:GLU:HB2	21:1Z:156:LYS:HE2	2.00	0.44
32:1a:45:G:C2	32:1a:46:U:H1'	2.53	0.44
32:1a:73:C:N3	32:1a:91:G:O6	2.51	0.44
32:1a:104:C:O2'	47:1p:25:ARG:O	2.34	0.44
32:1a:524:G:H2'	32:1a:525:G:O4'	2.18	0.44
32:1a:1259:C:H1'	32:1a:1264:C:C2	2.52	0.44
35:1d:132:ARG:HG2	35:1d:133:VAL:N	2.33	0.44
44:1m:4:ILE:HG13	44:1m:57:ARG:HA	1.98	0.44
1:2A:972:G:H2'	1:2A:973:G:O4'	2.18	0.44
1:2A:1000:G:H2'	1:2A:1001:A:H2'	1.99	0.44
1:2A:1549:C:H2'	1:2A:1550:C:H6	1.83	0.44
1:2A:1714:A:OP1	10:2O:5:GLN:HG3	2.17	0.44
1:2A:1886:G:C2'	1:2A:1887:G:H5'	2.48	0.44
1:2A:2113:U:H4'	1:2A:2114:G:O5'	2.18	0.44
1:2A:2363:A:H2'	1:2A:2364:G:H5'	2.00	0.44
1:2A:2484:U:O2	1:2A:2484:U:H2'	2.16	0.44
1:2A:2700:U:P	1:2A:2731:G:H22	2.40	0.44
1:2A:2715:C:H2'	1:2A:2716:A:O4'	2.18	0.44
4:2E:175:VAL:O	4:2E:177:PRO:HD3	2.17	0.44
12:2Q:12:GLN:HE21	12:2Q:72:LYS:NZ	2.14	0.44
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	2.00	0.44
23:21:76:ARG:HB2	23:21:97:LEU:HD13	1.98	0.44
32:2a:677:G:H2'	32:2a:678:A:C8	2.53	0.44
33:2b:84:GLU:O	33:2b:219:VAL:HG21	2.17	0.44
35:2d:19:LEU:HD22	35:2d:67:ILE:HG13	2.00	0.44
35:2d:50:ARG:HA	35:2d:51:PRO:HD3	1.85	0.44
35:2d:135:LEU:HA	35:2d:136:PRO:HD2	1.85	0.44
49:2r:25:THR:O	49:2r:25:THR:OG1	2.30	0.44
1:1A:933:A:H1'	1:1A:935:C:OP2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1840:A:H2'	1:1A:1841:G:O4'	2.18	0.44
1:1A:2244:U:H2'	1:1A:2245:G:C8	2.53	0.44
5:1F:53:THR:HB	5:1F:56:GLU:OE2	2.18	0.44
5:1F:132:VAL:HG22	5:1F:163:VAL:HG22	2.00	0.44
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	2.00	0.44
20:1Y:6:HIS:H	20:1Y:6:HIS:HD2	1.64	0.44
26:14:9:LEU:HD23	26:14:9:LEU:HA	1.81	0.44
32:1a:77:G:H1'	32:1a:78:G:H8	1.83	0.44
32:1a:1109:U:O4	41:1j:71:LEU:HD22	2.18	0.44
32:1a:1208:C:N4	44:1m:104:ARG:HG3	2.33	0.44
32:1a:1329:G:C5	40:1i:107:ARG:NH1	2.86	0.44
32:1a:1332:A:C5	32:1a:1333:U:C4	3.06	0.44
32:1a:1489:G:H2'	32:1a:1490:U:O4'	2.18	0.44
1:2A:241:C:O2'	59:2A:3643:HOH:O	2.21	0.44
1:2A:786:U:H2'	1:2A:787:G:C8	2.53	0.44
1:2A:1047:G:H22	1:2A:1199:G:H1'	1.83	0.44
1:2A:1887:G:C6	1:2A:1888:G:N1	2.86	0.44
1:2A:2076:C:H5'	1:2A:2077:G:O5'	2.18	0.44
1:2A:2115:G:N2	1:2A:2217:C:H1'	2.33	0.44
3:2D:206:LEU:HD23	3:2D:206:LEU:HA	1.70	0.44
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.18	0.44
25:23:48:GLU:HA	25:23:51:ALA:HB2	2.00	0.44
30:28:34:TRP:CE2	30:28:35:GLN:HB2	2.53	0.44
32:2a:24:C:H5	32:2a:545:U:O4	2.01	0.44
32:2a:969:U:H4'	32:2a:970:U:OP2	2.17	0.44
32:2a:1221:A:H4'	32:2a:1222:U:H5'	2.00	0.44
32:2a:1299:C:C5'	45:2n:17:LYS:HZ2	2.30	0.44
34:2c:156:ARG:HD3	34:2c:193:TYR:O	2.18	0.44
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.98	0.44
42:2k:16:SER:O	42:2k:35:PRO:HG3	2.18	0.44
1:1A:644:G:N3	1:1A:644:G:H5'	2.32	0.44
1:1A:1423:A:OP1	29:17:10:ARG:NH2	2.50	0.44
1:1A:2596:U:H4'	1:1A:2597:C:OP1	2.17	0.44
14:1S:32:LEU:HD23	14:1S:32:LEU:HA	1.75	0.44
32:1a:377:C:H2'	32:1a:378:A:O4'	2.18	0.44
32:1a:611:G:H2'	32:1a:612:G:C8	2.49	0.44
32:1a:991:U:H2'	32:1a:992:G:O4'	2.18	0.44
32:1a:1320:G:H2'	32:1a:1321:A:C8	2.52	0.44
33:1b:55:PHE:CE1	33:1b:218:ALA:HA	2.51	0.44
36:1e:68:GLU:HG3	36:1e:69:VAL:N	2.32	0.44
38:1g:16:LEU:HD12	38:1g:16:LEU:HA	1.88	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:11:ARG:C	44:1m:13:LYS:H	2.25	0.44
1:2A:151:G:H2'	1:2A:152:C:C6	2.53	0.44
1:2A:250:A:H2'	1:2A:251:C:O4'	2.18	0.44
1:2A:263:G:C2	1:2A:264:U:C2	3.06	0.44
1:2A:416:A:H4'	1:2A:417:G:H5'	2.00	0.44
1:2A:1059:U:H2'	1:2A:1060:G:H8	1.83	0.44
1:2A:1309:G:H2'	1:2A:2035:A:N6	2.32	0.44
1:2A:1553:A:H4'	1:2A:1555:A:C5	2.53	0.44
1:2A:2091:G:C2	1:2A:2453:C:C2	3.06	0.44
1:2A:2307:U:OP2	14:2S:9:ARG:NH2	2.46	0.44
1:2A:2314:G:C2'	1:2A:2315:G:H5'	2.48	0.44
1:2A:2370:C:H2'	1:2A:2371:A:O4'	2.17	0.44
1:2A:2623:C:OP2	27:25:2:ALA:N	2.51	0.44
1:2A:2788:A:H4'	1:2A:2789:G:H5"	1.99	0.44
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.46	0.44
6:2G:11:TYR:OH	6:2G:16:ARG:NE	2.51	0.44
6:2G:102:PHE:CE1	6:2G:141:PHE:CE1	3.05	0.44
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.17	0.44
15:2T:56:GLY:O	15:2T:59:THR:HG23	2.18	0.44
25:23:26:LEU:HD21	25:23:46:ASN:HB2	1.99	0.44
32:2a:36:G:H2'	32:2a:37:C:C6	2.53	0.44
32:2a:199:U:H2'	32:2a:200:C:C6	2.53	0.44
32:2a:262:G:H5"	32:2a:264:C:H41	1.82	0.44
32:2a:1047:G:H1'	32:2a:1048:U:OP2	2.18	0.44
32:2a:1245:C:H2'	32:2a:1246:C:C6	2.53	0.44
32:2a:1284:U:OP2	44:2m:21:TYR:OH	2.16	0.44
42:2k:22:HIS:O	42:2k:28:THR:HA	2.17	0.44
43:2l:24:VAL:CG2	43:2l:27:LEU:HD22	2.48	0.44
47:2p:3:LYS:O	47:2p:21:VAL:HA	2.17	0.44
1:1A:682:G:O5'	1:1A:682:G:H8	2.01	0.43
1:1A:863:C:O2'	1:1A:885:U:H5"	2.18	0.43
1:1A:1288:G:O2'	11:1P:7:ARG:NH2	2.51	0.43
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	1.99	0.43
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.53	0.43
32:1a:548:C:C6	48:1q:31:LEU:HD11	2.53	0.43
32:1a:551:G:H2'	32:1a:552:G:O4'	2.18	0.43
32:1a:568:G:O6	59:1a:2023:HOH:O	2.21	0.43
32:1a:597:C:H42	32:1a:611:G:H1	1.66	0.43
32:1a:699:A:H2'	32:1a:700:A:C8	2.53	0.43
32:1a:1203:G:OP1	32:1a:1302:C:N4	2.50	0.43
33:1b:222:ILE:O	33:1b:226:ARG:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:20:TYR:HA	35:1d:26:CYS:SG	2.57	0.43
35:1d:194:LEU:HD13	35:1d:195:ALA:N	2.32	0.43
36:1e:152:ARG:HB3	39:1h:43:GLY:HA3	2.00	0.43
39:1h:78:GLN:HE21	39:1h:78:GLN:HB2	1.48	0.43
40:1i:40:LEU:O	40:1i:43:ALA:N	2.44	0.43
48:1q:86:GLU:O	48:1q:90:ILE:HG13	2.18	0.43
49:1r:33:ASP:OD2	49:1r:36:ASN:HB2	2.18	0.43
1:2A:330:G:H21	1:2A:353:A:N6	2.12	0.43
1:2A:605:G:OP2	16:2U:10:ARG:HD2	2.18	0.43
1:2A:1480:G:H2'	1:2A:1481:G:O4'	2.18	0.43
1:2A:1884:A:N1	1:2A:2108:G:O2'	2.43	0.43
1:2A:1940:A:O3'	32:2a:1495:G:H1'	2.18	0.43
11:2P:47:ASP:HA	11:2P:48:PRO:HD3	1.80	0.43
18:2W:14:PRO:HG2	18:2W:78:GLU:CG	2.43	0.43
24:22:4:SER:HA	24:22:7:ARG:NH1	2.33	0.43
24:22:32:LEU:HA	24:22:35:LEU:HB2	1.99	0.43
32:2a:475:G:H2'	32:2a:476:G:H8	1.82	0.43
32:2a:675:G:H2'	32:2a:676:U:C6	2.53	0.43
32:2a:676:U:O4	42:2k:26:ASN:ND2	2.51	0.43
32:2a:1078:U:H5"	32:2a:1092:C:O2	2.18	0.43
32:2a:1308:C:H5"	52:2u:18:TYR:O	2.17	0.43
32:2a:1354:G:C6	32:2a:1355:U:C4	3.06	0.43
48:2q:62:SER:CB	48:2q:72:ARG:HD3	2.48	0.43
48:2q:89:LEU:HD23	48:2q:89:LEU:HA	1.78	0.43
1:1A:1073:A:H61	1:1A:1170:G:H2'	1.83	0.43
1:1A:1218:A:O2'	1:1A:1219:U:H6	2.01	0.43
1:1A:2398:U:OP1	22:10:55:ARG:NH2	2.51	0.43
1:1A:2759:G:O6	1:1A:2767:C:H5"	2.18	0.43
2:1B:90:A:C5	2:1B:91:C:H1'	2.53	0.43
14:1S:26:LEU:HD22	14:1S:87:PHE:CE1	2.53	0.43
30:18:28:GLY:O	30:18:36:LYS:NZ	2.41	0.43
32:1a:156:A:H2	32:1a:343:G:N2	2.15	0.43
32:1a:441:G:H5"	59:1a:2075:HOH:O	2.18	0.43
32:1a:1073:U:H2'	32:1a:1074:U:C6	2.53	0.43
33:1b:19:HIS:HA	33:1b:39:ILE:CG2	2.48	0.43
33:1b:90:MET:HA	33:1b:91:PRO:HD3	1.90	0.43
33:1b:97:TRP:CH2	33:1b:173:ALA:HA	2.53	0.43
35:1d:112:VAL:HG23	35:1d:116:GLN:OE1	2.18	0.43
1:2A:235:G:H4'	1:2A:412:G:C6	2.53	0.43
1:2A:596:C:N3	4:2E:145:LYS:NZ	2.60	0.43
1:2A:982:G:OP2	30:28:52:LYS:NZ	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1133:A:N3	1:2A:1133:A:H2'	2.33	0.43
1:2A:1185:U:H2'	9:2N:63:THR:HG21	1.99	0.43
1:2A:2125:G:N2	1:2A:2207:G:H1'	2.30	0.43
1:2A:2798:U:O2'	4:2E:65:GLY:HA3	2.18	0.43
2:2B:78:A:H2'	2:2B:79:C:O4'	2.19	0.43
4:2E:101:ARG:O	4:2E:201:THR:HG22	2.19	0.43
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	2.00	0.43
7:2H:7:LEU:O	7:2H:69:ARG:HD3	2.19	0.43
32:2a:661:U:H3	32:2a:697:G:H22	1.65	0.43
32:2a:775:G:H2'	32:2a:776:A:H5'	2.00	0.43
32:2a:846:C:H2'	32:2a:847:G:O4'	2.18	0.43
32:2a:1109:U:H4'	32:2a:1263:U:H1'	2.00	0.43
34:2c:111:LEU:HD13	34:2c:204:LEU:HD22	2.01	0.43
46:2o:5:LYS:H	46:2o:5:LYS:HD3	1.82	0.43
53:2v:14:A:C8	53:2v:15:A:C8	3.07	0.43
53:2v:14:A:H2'	53:2v:15:A:O4'	2.18	0.43
1:1A:885:U:H2'	1:1A:886:C:C6	2.53	0.43
1:1A:2083:A:C2	1:1A:2514:A:N6	2.86	0.43
5:1F:140:LEU:HD13	5:1F:140:LEU:HA	1.82	0.43
5:1F:164:ARG:O	5:1F:168:ARG:HG3	2.18	0.43
6:1G:41:GLN:HE22	6:1G:153:ARG:HB3	1.83	0.43
13:1R:111:LEU:O	59:1R:302:HOH:O	2.21	0.43
32:1a:911:G:O6	38:1g:3:ARG:NH2	2.51	0.43
32:1a:925:G:O3'	44:1m:109:THR:OG1	2.35	0.43
32:1a:1145:C:C2	32:1a:1157:G:C2	3.06	0.43
32:1a:1407:C:H2'	32:1a:1408:U:O4'	2.19	0.43
33:1b:180:LEU:O	33:1b:181:PHE:HB2	2.18	0.43
46:1o:26:GLU:H	46:1o:26:GLU:HG2	1.37	0.43
48:1q:67:LYS:C	48:1q:69:LYS:H	2.27	0.43
49:1r:53:ARG:HG2	49:1r:58:LEU:O	2.18	0.43
55:1z:11:ARG:CB	55:1z:12:PRO:HD2	2.47	0.43
1:2A:25:G:C6	1:2A:26:G:N1	2.87	0.43
1:2A:139:A:HO2'	1:2A:1452:C:HO2'	1.62	0.43
1:2A:224:C:H2'	1:2A:225:C:C6	2.54	0.43
1:2A:508:A:O4'	20:2Y:48:ALA:HB1	2.18	0.43
1:2A:552:A:N1	1:2A:2063:A:H2'	2.34	0.43
1:2A:560:A:H2'	1:2A:561:C:C6	2.52	0.43
1:2A:922:C:H2'	1:2A:923:U:O4'	2.19	0.43
1:2A:931:C:H2'	1:2A:932:C:H4'	1.99	0.43
1:2A:2858:U:H4'	1:2A:2877:A:C2	2.53	0.43
6:2G:114:ILE:HA	6:2G:136:ARG:HH22	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:49:ARG:NH1	32:2a:1406:G:OP1	2.49	0.43
21:2Z:48:PHE:HE1	21:2Z:71:VAL:HG11	1.83	0.43
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.33	0.43
32:2a:431:C:H2'	32:2a:432:C:H6	1.82	0.43
32:2a:1115:C:C2	32:2a:1116:G:C8	3.07	0.43
32:2a:1145:C:H2'	32:2a:1146:C:H6	1.84	0.43
32:2a:1286:G:C6	32:2a:1287:G:N1	2.86	0.43
34:2c:117:ALA:HA	34:2c:186:PHE:CE1	2.54	0.43
1:1A:838:G:O6	59:1A:4146:HOH:O	2.19	0.43
1:1A:2224:U:O4'	3:1D:151:LYS:HE2	2.18	0.43
7:1H:7:LEU:HA	7:1H:8:PRO:HD3	1.89	0.43
7:1H:125:VAL:HG12	7:1H:127:GLU:O	2.18	0.43
8:1I:31:LEU:HD21	8:1I:38:LEU:HG	2.00	0.43
8:1I:72:LEU:HD21	8:1I:107:VAL:HG11	1.99	0.43
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.68	0.43
30:18:23:VAL:HG11	30:18:47:LYS:HD3	2.00	0.43
32:1a:17:A:O2'	36:1e:16:THR:HB	2.18	0.43
32:1a:107:G:H2'	32:1a:108:U:C6	2.53	0.43
32:1a:162:G:N2	32:1a:163:G:N7	2.66	0.43
32:1a:598:A:C2	32:1a:599:C:C2	3.06	0.43
32:1a:651:G:H4'	46:1o:51:HIS:ND1	2.33	0.43
32:1a:1027:A:H2'	32:1a:1028:C:O4'	2.19	0.43
32:1a:1120:C:H3'	32:1a:1120:C:H6	1.82	0.43
32:1a:1132:C:O2'	32:1a:1262:A:N1	2.48	0.43
32:1a:1267:A:H4'	32:1a:1268:A:O5'	2.18	0.43
38:1g:73:MET:HE2	38:1g:73:MET:HB2	1.90	0.43
42:1k:63:LEU:H	42:1k:63:LEU:HD12	1.84	0.43
43:1l:77:LEU:HD21	43:1l:107:ALA:HA	2.00	0.43
1:2A:26:G:O2'	1:2A:27:A:OP2	2.34	0.43
1:2A:1142:U:H2'	1:2A:1143:A:O4'	2.19	0.43
1:2A:1561:U:H2'	1:2A:1562:G:C8	2.54	0.43
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	2.00	0.43
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	2.00	0.43
7:2H:8:PRO:O	7:2H:10:PRO:HD3	2.18	0.43
7:2H:69:ARG:HG3	7:2H:70:THR:N	2.33	0.43
8:2I:4:ILE:HD11	8:2I:44:LEU:CD1	2.47	0.43
9:2N:42:TRP:HA	9:2N:48:MET:HE1	1.99	0.43
11:2P:84:ASN:OD1	11:2P:117:GLU:HB2	2.18	0.43
15:2T:1:MET:HE2	15:2T:3:ARG:CG	2.49	0.43
32:2a:459:G:H2'	32:2a:460:G:H8	1.83	0.43
32:2a:818:C:H2'	32:2a:819:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1218:A:H4'	32:2a:1286:G:H4'	2.00	0.43
32:2a:1243:A:C6	32:2a:1244:C:C2	3.07	0.43
33:2b:92:TYR:CZ	33:2b:150:SER:CA	3.01	0.43
44:2m:87:TYR:O	44:2m:91:ARG:HG2	2.17	0.43
45:2n:17:LYS:HE2	45:2n:17:LYS:N	2.29	0.43
1:1A:387:A:H2'	1:1A:388:G:H8	1.83	0.43
1:1A:2331:A:H2'	1:1A:2331:A:N3	2.33	0.43
1:1A:2734:G:H2'	1:1A:2735:C:C6	2.54	0.43
2:1B:80:U:H2'	2:1B:81:G:C8	2.54	0.43
3:1D:242:ARG:N	3:1D:242:ARG:HD3	2.33	0.43
4:1E:31:CYS:HA	4:1E:32:PRO:HD2	1.79	0.43
22:10:82:ARG:HA	22:10:83:PRO:HD3	1.73	0.43
32:1a:68:C:O2'	32:1a:166:A:N3	2.33	0.43
33:1b:15:VAL:O	33:1b:16:HIS:HB3	2.18	0.43
33:1b:170:GLU:O	33:1b:174:VAL:HG23	2.19	0.43
33:1b:193:ASP:HA	33:1b:194:PRO:HD3	1.87	0.43
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.99	0.43
1:2A:310:C:H2'	1:2A:311:C:C6	2.51	0.43
1:2A:703:U:H2'	1:2A:704:C:H6	1.81	0.43
1:2A:1003:A:C6	1:2A:1004:A:C6	3.07	0.43
1:2A:1024:G:H3'	1:2A:1025:A:H5"	2.00	0.43
1:2A:2387:A:H5"	1:2A:2388:A:OP2	2.18	0.43
3:2D:71:ASP:HB3	3:2D:72:LYS:HG3	1.99	0.43
3:2D:232:PRO:O	59:2D:401:HOH:O	2.21	0.43
8:2I:62:LYS:HE2	8:2I:133:HIS:HE1	1.82	0.43
13:2R:13:HIS:CE1	13:2R:16:HIS:HB2	2.53	0.43
32:2a:543:A:OP1	36:2e:126:ARG:NH2	2.49	0.43
32:2a:1148:C:H2'	32:2a:1149:G:O4'	2.18	0.43
33:2b:92:TYR:CE2	33:2b:149:LEU:C	2.96	0.43
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.51	0.43
41:2j:49:VAL:HG13	45:2n:41:ARG:HD2	2.00	0.43
44:2m:17:VAL:HG12	44:2m:27:LYS:NZ	2.34	0.43
1:1A:1247:G:H5'	11:1P:3:LEU:HD23	2.00	0.43
16:1U:34:LYS:HE2	16:1U:34:LYS:HA	2.01	0.43
32:1a:503:C:OP2	43:1l:50:SER:OG	2.36	0.43
32:1a:726:G:OP2	46:1o:35:ARG:NH2	2.48	0.43
32:1a:961:A:H5"	32:1a:962:C:OP2	2.18	0.43
32:1a:1194:U:H4'	32:1a:1195:A:C8	2.53	0.43
33:1b:22:LYS:C	33:1b:24:TRP:H	2.25	0.43
36:1e:15:ARG:HD2	36:1e:26:PHE:CD2	2.54	0.43
36:1e:147:ASP:O	36:1e:151:LEU:HG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.19	0.43
1:2A:1000:G:OP2	12:2Q:14:ARG:NH2	2.52	0.43
1:2A:1887:G:O6	1:2A:1888:G:N1	2.52	0.43
1:2A:2249:G:N7	59:2A:3701:HOH:O	2.35	0.43
1:2A:2298:A:C4	1:2A:2300:G:C8	3.07	0.43
1:2A:2327:C:O2'	1:2A:2328:C:H5'	2.19	0.43
1:2A:2548:U:N3	1:2A:2549:C:C4	2.87	0.43
2:2B:11:C:H3'	2:2B:12:C:C5	2.54	0.43
6:2G:80:PHE:C	6:2G:82:LEU:N	2.76	0.43
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.99	0.43
14:2S:111:GLU:H	14:2S:111:GLU:HG2	1.70	0.43
17:2V:43:GLU:N	17:2V:43:GLU:OE2	2.51	0.43
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.84	0.43
32:2a:147:A:N6	32:2a:165:U:C2	2.87	0.43
32:2a:372:G:H5"	47:2p:5:ARG:HD3	2.01	0.43
32:2a:455:A:O2'	32:2a:457:G:N7	2.43	0.43
32:2a:498:C:H3'	59:2a:3331:HOH:O	2.19	0.43
32:2a:738:C:H6	46:2o:69:TYR:CE2	2.36	0.43
32:2a:1390:C:O2'	59:2a:3338:HOH:O	2.21	0.43
33:2b:179:LYS:HA	39:2h:72:PRO:HG3	1.99	0.43
42:2k:99:GLN:C	42:2k:101:SER:H	2.27	0.43
54:2x:55:PSU:H5'	54:2x:56:C:OP2	2.19	0.43
1:1A:1216:G:H2'	1:1A:1217:G:H5'	2.00	0.43
1:1A:1524:G:O2'	1:1A:1604:A:C2	2.72	0.43
1:1A:1633:C:H2'	1:1A:1634:C:H6	1.83	0.43
1:1A:2485:C:H5"	1:1A:2486:C:OP2	2.18	0.43
1:1A:2704:A:H2'	1:1A:2705:G:H8	1.84	0.43
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.84	0.43
7:1H:5:GLY:HA2	7:1H:69:ARG:HB3	2.00	0.43
7:1H:103:LEU:HD23	7:1H:148:ILE:HD12	2.00	0.43
11:1P:42:SER:O	59:1P:301:HOH:O	2.22	0.43
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.51	0.43
30:18:31:HIS:CE1	30:18:32:LEU:HD22	2.53	0.43
32:1a:142:G:H1	32:1a:170:C:H42	1.65	0.43
32:1a:355:U:H2'	32:1a:356:A:C8	2.53	0.43
32:1a:493:A:C6	32:1a:494:A:N1	2.87	0.43
32:1a:729:C:H2'	32:1a:730:A:C8	2.54	0.43
32:1a:1055:G:C5	32:1a:1056:U:C4	3.07	0.43
32:1a:1298:G:N2	32:1a:1300:A:H3'	2.34	0.43
32:1a:1352:C:H2'	32:1a:1353:G:C8	2.54	0.43
1:2A:537:A:C2	1:2A:538:A:C4	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:588:U:H2'	1:2A:589:A:O4'	2.19	0.43
1:2A:955:A:C6	1:2A:956:A:C6	3.07	0.43
1:2A:1041:A:C6	1:2A:1205:G:N1	2.87	0.43
1:2A:1404:A:N1	1:2A:1417:U:O4	2.52	0.43
1:2A:1944:U:O2'	54:2x:12:G:H1'	2.19	0.43
1:2A:2784:C:H2'	1:2A:2785:C:C6	2.53	0.43
2:2B:59:A:H3'	2:2B:60:C:C6	2.53	0.43
2:2B:90:A:N7	2:2B:91:C:H1'	2.33	0.43
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.99	0.43
3:2D:33:LEU:HA	3:2D:33:LEU:HD23	1.75	0.43
5:2F:33:LEU:HB3	11:2P:6:LEU:HD21	2.01	0.43
6:2G:16:ARG:NH2	6:2G:31:VAL:HG13	2.33	0.43
9:2N:96:GLU:HB2	9:2N:122:VAL:HG12	2.01	0.43
11:2P:82:GLY:HA3	11:2P:115:LEU:HD11	2.00	0.43
26:24:61:ARG:NH2	50:2s:9:VAL:HG11	2.34	0.43
32:2a:647:A:O3'	49:2r:64:ARG:NH2	2.41	0.43
32:2a:698:G:H2'	32:2a:699:A:C8	2.53	0.43
32:2a:818:C:H2'	32:2a:819:U:H6	1.83	0.43
32:2a:1140:A:C6	32:2a:1162:A:C5	3.06	0.43
32:2a:1287:G:H5"	52:2u:4:GLY:HA3	2.00	0.43
32:2a:1302:C:OP1	50:2s:70:LYS:HE2	2.17	0.43
32:2a:1457:C:H2'	32:2a:1458:G:C8	2.54	0.43
32:2a:1487:C:H2'	32:2a:1488:U:O4'	2.19	0.43
33:2b:16:HIS:CD2	33:2b:204:ASN:H	2.37	0.43
35:2d:88:VAL:O	35:2d:92:VAL:HG23	2.19	0.43
35:2d:100:ARG:NH2	35:2d:102:ASP:OD2	2.52	0.43
36:2e:71:LEU:H	36:2e:71:LEU:CD2	2.31	0.43
43:2l:119:LYS:O	43:2l:120:TYR:HB2	2.19	0.43
1:1A:124:A:H5"	1:1A:125:C:C6	2.54	0.43
1:1A:628:U:H4'	1:1A:704:C:H4'	2.00	0.43
1:1A:878:G:H5'	11:1P:45:LEU:HD21	2.01	0.43
1:1A:2514:A:P	59:1A:4236:HOH:O	2.76	0.43
2:1B:48:A:H4'	14:1S:95:HIS:CD2	2.51	0.43
6:1G:138:GLN:HE21	6:1G:153:ARG:HH21	1.67	0.43
7:1H:4:ILE:O	7:1H:69:ARG:HG2	2.19	0.43
10:1O:21:CYS:HB2	10:1O:39:ILE:HD12	2.01	0.43
21:1Z:31:ARG:H	21:1Z:31:ARG:HG3	1.63	0.43
26:14:14:ILE:HG23	26:14:31:ILE:HB	2.00	0.43
32:1a:510:C:H5"	32:1a:511:G:OP2	2.19	0.43
32:1a:610:U:H2'	32:1a:611:G:H8	1.83	0.43
32:1a:824:C:H5'	32:1a:825:U:H5	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:107:ARG:HH12	35:1d:194:LEU:HG	1.83	0.43
38:1g:69:VAL:HG12	38:1g:100:ALA:HA	2.00	0.43
39:1h:51:VAL:HG11	39:1h:60:ARG:NH1	2.33	0.43
51:1t:43:LEU:HD23	51:1t:43:LEU:HA	1.88	0.43
2:2B:80:U:O2'	2:2B:81:G:H8	2.02	0.43
4:2E:77:ILE:HD13	4:2E:195:LEU:HD22	2.00	0.43
5:2F:196:LEU:HD13	5:2F:196:LEU:HA	1.83	0.43
12:2Q:2:LEU:H	12:2Q:2:LEU:HD12	1.83	0.43
32:2a:298:G:N3	32:2a:540:C:H4'	2.32	0.43
32:2a:911:G:C6	32:2a:1368:G:C6	3.07	0.43
32:2a:938:U:O2	32:2a:938:U:H2'	2.19	0.43
32:2a:1134:A:C5'	41:2j:41:PRO:HA	2.49	0.43
32:2a:1233:A:H2'	32:2a:1234:A:C8	2.54	0.43
32:2a:1469:G:H5'	59:2a:3414:HOH:O	2.18	0.43
33:2b:12:GLU:O	33:2b:15:VAL:HG22	2.19	0.43
33:2b:97:TRP:CH2	33:2b:101:MET:HB2	2.54	0.43
34:2c:29:TYR:OH	45:2n:54:PRO:HG2	2.18	0.43
38:2g:151:TYR:O	38:2g:154:TYR:HB2	2.18	0.43
44:2m:82:MET:HE3	44:2m:93:ARG:HG2	1.99	0.43
1:1A:475:G:OP2	59:1A:4161:HOH:O	2.21	0.43
1:1A:1614:G:H4'	3:1D:59:LYS:HG2	2.01	0.43
1:1A:2225:C:O2	1:1A:2231:G:C2	2.71	0.43
4:1E:78:LEU:O	4:1E:79:ARG:HD3	2.19	0.43
32:1a:127:C:H2'	32:1a:128:U:C6	2.53	0.43
32:1a:409:G:N7	35:1d:35:ARG:NH1	2.67	0.43
32:1a:447:A:H4'	47:1p:72:ARG:NH2	2.34	0.43
32:1a:1133:U:C2'	32:1a:1134:A:H5'	2.49	0.43
32:1a:1148:C:H2'	32:1a:1149:G:O4'	2.19	0.43
33:1b:97:TRP:CZ2	33:1b:102:LEU:HD13	2.54	0.43
41:1j:46:ARG:HA	41:1j:46:ARG:HD3	1.72	0.43
1:2A:38:C:H2'	1:2A:39:C:C6	2.54	0.43
1:2A:514:G:N7	18:2W:49:LYS:NZ	2.67	0.43
1:2A:795:C:O2	1:2A:1663:A:H2'	2.19	0.43
1:2A:1132:G:C6	1:2A:1134:G:C4	3.07	0.43
1:2A:1883:A:N3	1:2A:2244:U:O2'	2.51	0.43
1:2A:1915:C:H2'	1:2A:1916:C:H6	1.84	0.43
2:2B:32:C:H42	2:2B:50:G:H1	1.67	0.43
8:2I:140:LEU:HD23	8:2I:140:LEU:HA	1.83	0.43
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.18	0.43
32:2a:20:C:H5"	36:2e:86:ALA:CB	2.48	0.43
32:2a:124:G:C2	32:2a:190:U:H5"	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1184:G:H21	45:2n:43:CYS:HB3	1.84	0.43
32:2a:1273:G:O2'	40:2i:38:GLN:HG2	2.18	0.43
34:2c:32:LEU:O	34:2c:35:GLU:HB3	2.18	0.43
34:2c:52:LEU:HD22	34:2c:53:ALA:N	2.34	0.43
49:2r:29:PHE:HD2	49:2r:39:VAL:HG11	1.82	0.43
1:1A:894:G:N9	1:1A:977:A:H8	2.17	0.43
1:1A:2203:G:N2	1:1A:2204:C:N3	2.66	0.43
1:1A:2283:U:H5"	1:1A:2284:A:OP1	2.19	0.43
1:1A:2694:C:O2	10:1O:70:LYS:NZ	2.34	0.43
3:1D:164:GLN:NE2	3:1D:166:GLN:OE1	2.52	0.43
16:1U:112:ARG:NH2	17:1V:47:VAL:HB	2.34	0.43
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.54	0.43
32:1a:585:C:H2'	32:1a:586:A:C8	2.54	0.43
32:1a:1051:G:N7	32:1a:1077:G:H2'	2.33	0.43
32:1a:1243:A:H3'	32:1a:1244:C:C6	2.54	0.43
33:1b:10:LEU:HB3	33:1b:48:MET:HE1	2.01	0.43
40:1i:104:ARG:HH11	40:1i:104:ARG:CG	2.26	0.43
44:1m:108:ARG:HA	44:1m:108:ARG:HD3	1.92	0.43
45:1n:11:LYS:HE2	45:1n:11:LYS:HB3	1.84	0.43
1:2A:323:A:H5"	1:2A:324:G:OP2	2.18	0.43
1:2A:1039:C:O2'	1:2A:1041:A:OP1	2.29	0.43
1:2A:1072:A:N6	1:2A:1171:A:C4	2.86	0.43
1:2A:1332:A:H5"	1:2A:1333:U:OP2	2.19	0.43
1:2A:2898:C:H2'	1:2A:2899:G:O4'	2.19	0.43
19:2X:52:VAL:HG12	19:2X:82:GLN:O	2.19	0.43
20:2Y:20:TYR:CZ	20:2Y:43:ASN:HA	2.54	0.43
26:24:58:ARG:NH1	50:2s:68:GLY:H	2.16	0.43
30:28:26:LYS:HG2	30:28:48:PHE:CD1	2.54	0.43
32:2a:585:C:C2	32:2a:622:G:N2	2.87	0.43
32:2a:959:U:H5'	45:2n:21:TYR:CE2	2.54	0.43
32:2a:1370:G:H2'	32:2a:1371:C:C6	2.54	0.43
38:2g:120:ILE:HG12	38:2g:120:ILE:H	1.34	0.43
43:2l:83:VAL:HG11	43:2l:100:ILE:HG12	2.01	0.43
47:2p:76:GLN:C	47:2p:78:GLY:H	2.26	0.43
1:1A:11:U:O2	1:1A:11:U:H2'	2.18	0.42
1:1A:503:A:N1	1:1A:524:G:H4'	2.33	0.42
1:1A:921:G:O2'	21:1Z:151:HIS:HE1	2.02	0.42
1:1A:1209:G:H2'	1:1A:1210:U:C6	2.54	0.42
1:1A:1929:C:O2	54:1x:12:G:H4'	2.19	0.42
1:1A:1992:A:OP2	3:1D:242:ARG:NH2	2.52	0.42
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:86:GLU:OE1	7:1H:132:ARG:NH2	2.52	0.42
10:1O:23:ARG:HG3	10:1O:24:VAL:N	2.33	0.42
23:11:21:ARG:HD3	23:11:35:THR:HG21	2.01	0.42
32:1a:252:U:H2'	32:1a:253:G:C8	2.54	0.42
32:1a:719:C:H2'	32:1a:720:C:H6	1.84	0.42
32:1a:934:U:H2'	32:1a:935:U:O4'	2.19	0.42
32:1a:1281:A:H5"	32:1a:1281:A:N3	2.33	0.42
33:1b:162:ILE:HD11	33:1b:184:VAL:HG22	2.01	0.42
35:1d:196:LEU:O	35:1d:198:VAL:N	2.46	0.42
42:1k:98:LEU:O	42:1k:101:SER:OG	2.35	0.42
44:1m:79:LYS:HA	44:1m:82:MET:HE3	2.00	0.42
1:2A:338:G:H2'	1:2A:339:C:O4'	2.18	0.42
1:2A:903:C:OP2	22:20:77:ARG:NH2	2.52	0.42
1:2A:1262:C:H42	1:2A:1276:G:H1	1.65	0.42
1:2A:1897:A:H2'	1:2A:1898:A:C8	2.54	0.42
1:2A:2537:G:H2'	1:2A:2538:C:C6	2.54	0.42
2:2B:51:G:H2'	2:2B:52:A:C8	2.54	0.42
6:2G:36:LYS:HG2	6:2G:160:VAL:HB	2.01	0.42
6:2G:109:VAL:C	6:2G:112:PRO:HD2	2.44	0.42
6:2G:173:LEU:C	6:2G:178:PHE:HB2	2.44	0.42
8:2I:48:GLU:HG3	8:2I:52:ARG:NH1	2.34	0.42
28:26:10:LEU:HG	28:26:54:ILE:HG13	2.01	0.42
32:2a:1149:G:H8	32:2a:1149:G:H5"	1.84	0.42
32:2a:1163:G:O2'	32:2a:1164:G:N7	2.52	0.42
1:1A:159:G:C2'	1:1A:160:C:H5'	2.49	0.42
6:1G:102:PHE:CE1	6:1G:141:PHE:HE2	2.37	0.42
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.54	0.42
32:1a:904:G:C6	32:1a:1483:G:C6	3.07	0.42
32:1a:954:G:C8	32:1a:1344:C:N4	2.87	0.42
32:1a:1218:A:H4'	32:1a:1286:G:H4'	2.01	0.42
37:1f:89:MET:HG2	37:1f:91:VAL:HG23	2.00	0.42
1:2A:732:G:H21	1:2A:834:A:H61	1.66	0.42
1:2A:754:C:H42	1:2A:769:G:H1	1.67	0.42
1:2A:794:G:C8	18:2W:89:ALA:HB1	2.54	0.42
1:2A:820:A:N3	1:2A:820:A:H2'	2.33	0.42
1:2A:846:A:H8	1:2A:846:A:OP1	2.01	0.42
1:2A:921:G:O2'	21:2Z:151:HIS:HE1	2.02	0.42
1:2A:1109:C:O2	1:2A:1109:C:H2'	2.19	0.42
1:2A:1116:G:H1'	1:2A:1134:G:C8	2.55	0.42
1:2A:1258:A:H61	1:2A:1280:G:H1'	1.84	0.42
1:2A:1869:G:C8	1:2A:1948:A:H1'	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:42:C:H2'	2:2B:43:C:H6	1.84	0.42
2:2B:50:G:OP2	14:2S:62:LYS:HE3	2.19	0.42
2:2B:78:A:C2	2:2B:100:A:C4	3.08	0.42
5:2F:157:VAL:HG21	5:2F:181:LEU:HD13	2.00	0.42
6:2G:123:ASN:C	6:2G:125:PHE:H	2.27	0.42
8:2I:75:LEU:HD11	8:2I:105:HIS:CG	2.54	0.42
13:2R:52:ILE:O	13:2R:55:ALA:N	2.52	0.42
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.19	0.42
21:2Z:127:LYS:O	21:2Z:128:VAL:HG12	2.19	0.42
26:24:41:PRO:HG3	26:24:49:PHE:CZ	2.54	0.42
32:2a:104:C:H2'	32:2a:105:G:O4'	2.19	0.42
32:2a:606:A:C8	32:2a:607:C:C6	3.06	0.42
32:2a:967:C:H42	32:2a:1198:G:H1	1.67	0.42
33:2b:17:PHE:HB2	33:2b:44:LEU:HD11	2.00	0.42
34:2c:6:HIS:HD2	34:2c:7:PRO:CD	2.32	0.42
44:2m:91:ARG:HB2	44:2m:98:VAL:HG12	2.01	0.42
45:2n:21:TYR:HE1	45:2n:23:ARG:HE	1.67	0.42
51:2t:20:LEU:HD23	51:2t:20:LEU:HA	1.77	0.42
54:2x:17:C:OP2	54:2x:18:G:H5'	2.18	0.42
1:1A:209:A:N1	1:1A:253:A:O2'	2.46	0.42
1:1A:271:U:H4'	8:1I:50:ARG:NH1	2.34	0.42
1:1A:601:G:H2'	1:1A:602:C:C6	2.54	0.42
1:1A:1090:A:H4'	1:1A:1091:A:H5"	2.02	0.42
1:1A:2022:A:H2'	1:1A:2023:G:C8	2.55	0.42
24:12:28:LYS:HG3	24:12:53:LEU:HD21	2.00	0.42
26:14:14:ILE:H	26:14:14:ILE:HG12	1.57	0.42
32:1a:96:G:H2'	32:1a:97:C:H6	1.84	0.42
32:1a:870:A:H2'	32:1a:871:C:C6	2.54	0.42
32:1a:1050:A:N1	32:1a:1091:G:O2'	2.45	0.42
32:1a:1346:A:H4'	32:1a:1347:U:H2'	2.01	0.42
34:1c:58:GLU:O	34:1c:59:ARG:HG3	2.19	0.42
38:1g:91:VAL:HG12	38:1g:95:ARG:HB3	2.00	0.42
39:1h:14:ARG:O	39:1h:18:ARG:HD3	2.19	0.42
43:1l:27:LEU:HD13	43:1l:98:TYR:CE2	2.54	0.42
1:2A:31:C:O2'	1:2A:32:U:H5'	2.19	0.42
1:2A:646:G:H2'	1:2A:647:G:C8	2.54	0.42
1:2A:772:G:OP2	1:2A:772:G:H8	2.02	0.42
1:2A:1386:U:H3'	1:2A:1442:U:O2	2.20	0.42
1:2A:2207:G:H8	1:2A:2207:G:OP2	2.03	0.42
1:2A:2278:A:H5"	1:2A:2279:A:C5'	2.48	0.42
1:2A:2303:C:C2'	1:2A:2304:C:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2657:C:H2'	1:2A:2658:U:O4'	2.20	0.42
1:2A:2890:C:H2'	1:2A:2891:A:O4'	2.20	0.42
5:2F:160:ASN:HB3	5:2F:163:VAL:HB	2.01	0.42
12:2Q:32:TYR:OH	12:2Q:111:GLU:HB2	2.19	0.42
13:2R:54:LEU:HD12	13:2R:54:LEU:HA	1.84	0.42
25:23:4:LEU:O	25:23:36:VAL:HA	2.19	0.42
32:2a:74:G:C6	32:2a:91:G:C6	3.07	0.42
32:2a:615:G:H2'	32:2a:616:A:C8	2.52	0.42
32:2a:844:C:C4	32:2a:845:G:H1'	2.55	0.42
32:2a:910:C:H2'	32:2a:911:G:C8	2.54	0.42
32:2a:1328:A:H5"	40:2i:120:ARG:NH1	2.32	0.42
33:2b:218:ALA:O	33:2b:222:ILE:HG23	2.20	0.42
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.52	0.42
43:2l:110:VAL:CG2	43:2l:120:TYR:HB3	2.50	0.42
1:1A:122:G:N2	59:1A:4291:HOH:O	2.47	0.42
1:1A:141:G:O2'	19:1X:35:THR:HG21	2.19	0.42
1:1A:216:A:H8	1:1A:217:A:H5'	1.84	0.42
1:1A:241:C:OP2	30:18:5:LYS:NZ	2.41	0.42
1:1A:989:A:C4	1:1A:2459:A:C2	3.07	0.42
1:1A:1066:A:H3'	1:1A:1066:A:H8	1.84	0.42
1:1A:1072:A:C2	1:1A:2499:A:H5'	2.54	0.42
1:1A:1151:G:N3	1:1A:1151:G:H2'	2.34	0.42
1:1A:2657:C:H2'	1:1A:2658:U:O4'	2.19	0.42
5:1F:74:ARG:H	5:1F:74:ARG:HG3	1.54	0.42
6:1G:47:LYS:H	6:1G:47:LYS:HG2	1.67	0.42
7:1H:157:TYR:CE1	7:1H:172:LYS:HG3	2.55	0.42
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	2.01	0.42
19:1X:57:LEU:HD11	19:1X:78:LYS:HE2	2.00	0.42
21:1Z:5:LEU:O	21:1Z:59:LEU:HA	2.19	0.42
21:1Z:92:SER:O	21:1Z:94:GLU:N	2.53	0.42
32:1a:697:G:H2'	32:1a:698:G:C8	2.54	0.42
32:1a:1272:G:C4	32:1a:1273:G:C8	3.07	0.42
38:1g:46:ALA:HB1	38:1g:121:ALA:HB2	2.01	0.42
48:1q:29:HIS:HA	48:1q:30:PRO:HD3	1.92	0.42
1:2A:238:G:C6	1:2A:239:A:C6	3.08	0.42
1:2A:827:A:H2	1:2A:1806:G:N3	2.17	0.42
1:2A:996:G:C6	1:2A:997:A:N7	2.88	0.42
1:2A:1024:G:H3'	1:2A:1025:A:C5'	2.49	0.42
1:2A:1058:C:O2'	1:2A:1059:U:H5'	2.19	0.42
1:2A:1098:C:N4	1:2A:1151:G:H1	1.95	0.42
1:2A:2059:G:H2'	1:2A:2060:C:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2325:C:H2'	1:2A:2326:G:H8	1.81	0.42
1:2A:2358:C:H2'	1:2A:2359:U:C6	2.53	0.42
2:2B:54:G:C2	2:2B:55:U:O2	2.72	0.42
2:2B:83:G:H4'	25:23:52:HIS:CG	2.54	0.42
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	2.02	0.42
10:2O:80:ASP:OD1	15:2T:64:ARG:NH2	2.52	0.42
14:2S:68:GLN:HE21	14:2S:71:ARG:HH11	1.66	0.42
20:2Y:76:CYS:SG	20:2Y:78:ALA:HB3	2.60	0.42
21:2Z:155:LEU:HD12	21:2Z:155:LEU:HA	1.92	0.42
32:2a:870:A:H2'	32:2a:871:C:C6	2.54	0.42
32:2a:1261:A:O2'	32:2a:1264:C:N4	2.52	0.42
32:2a:1374:U:H2'	32:2a:1375:G:C8	2.55	0.42
33:2b:68:ILE:HG12	33:2b:161:ALA:HB3	2.02	0.42
35:2d:9:CYS:O	35:2d:13:ARG:HG3	2.19	0.42
38:2g:66:VAL:HG12	38:2g:70:LYS:NZ	2.34	0.42
40:2i:38:GLN:C	40:2i:38:GLN:CD	2.87	0.42
41:2j:30:SER:OG	41:2j:84:GLN:NE2	2.52	0.42
1:1A:346:G:C8	5:1F:171:PRO:HG3	2.55	0.42
1:1A:930:C:H2'	1:1A:931:C:C1'	2.50	0.42
1:1A:2346:A:C8	1:1A:2348:G:C5	3.07	0.42
3:1D:8:PRO:HB3	3:1D:14:ARG:HB2	2.01	0.42
6:1G:126:ASP:CG	6:1G:130:ASN:HD22	2.27	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	2.00	0.42
10:1O:104:ARG:HH22	15:1T:43:GLN:NE2	2.18	0.42
32:1a:39:G:N2	32:1a:393:A:H5'	2.34	0.42
36:1e:28:PHE:CD2	36:1e:51:VAL:HG22	2.55	0.42
45:1n:11:LYS:H	45:1n:11:LYS:HG2	1.66	0.42
51:1t:9:ASN:HD22	51:1t:10:LEU:N	2.13	0.42
1:2A:184:A:H62	11:2P:38:GLN:HE22	1.66	0.42
1:2A:243:A:C6	1:2A:244:A:C5	3.08	0.42
1:2A:323:A:H1'	1:2A:342:C:H1'	2.02	0.42
1:2A:1280:G:C2	1:2A:1281:G:N2	2.87	0.42
1:2A:1557:G:H2'	1:2A:1558:C:O4'	2.19	0.42
1:2A:1643:C:H2'	1:2A:1644:C:C6	2.55	0.42
1:2A:2219:A:OP1	8:2I:33:ARG:NH2	2.53	0.42
1:2A:2302:U:H2'	1:2A:2303:C:H6	1.81	0.42
1:2A:2706:C:H2'	1:2A:2707:U:H6	1.85	0.42
1:2A:2848:G:H5'	13:2R:46:GLY:HA2	2.02	0.42
2:2B:16:G:H1	2:2B:68:C:H42	1.66	0.42
4:2E:37:ARG:HA	4:2E:42:ASP:OD2	2.19	0.42
6:2G:128:ARG:HE	6:2G:128:ARG:HB2	1.69	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:136:ARG:HD2	6:2G:136:ARG:C	2.44	0.42
13:2R:67:LEU:HD23	13:2R:76:VAL:HG21	2.01	0.42
30:28:31:HIS:CE1	30:28:32:LEU:HD13	2.55	0.42
32:2a:440:G:C6	32:2a:475:G:C6	3.08	0.42
32:2a:751:A:H2'	32:2a:752:A:O4'	2.19	0.42
32:2a:935:U:H2'	32:2a:937:A:OP2	2.18	0.42
32:2a:1312:U:H4'	44:2m:23:TYR:CZ	2.54	0.42
33:2b:58:ILE:HG13	33:2b:58:ILE:H	1.66	0.42
36:2e:100:VAL:HG23	36:2e:118:ILE:HG22	2.01	0.42
37:2f:43:LEU:HD22	37:2f:46:ARG:HD2	2.01	0.42
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	2.01	0.42
51:2t:64:ASP:OD2	51:2t:81:LYS:NZ	2.37	0.42
1:1A:115:A:C8	1:1A:116:A:C8	3.07	0.42
1:1A:214:G:N2	1:1A:216:A:H62	2.13	0.42
1:1A:1153:U:C6	1:1A:1154:C:C6	3.07	0.42
1:1A:1402:U:H2'	1:1A:1403:G:O4'	2.19	0.42
6:1G:5:VAL:HG22	6:1G:8:LYS:H	1.84	0.42
11:1P:77:ARG:HB2	11:1P:78:PRO:HD2	2.01	0.42
32:1a:1104:U:H2'	32:1a:1105:U:O4'	2.20	0.42
32:1a:1382:C:C2	32:1a:1384:G:C5	3.08	0.42
38:1g:37:ASN:O	38:1g:41:ARG:HG3	2.19	0.42
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.53	0.42
43:1l:88:GLY:O	43:1l:99:HIS:HD2	2.02	0.42
44:1m:74:VAL:O	44:1m:78:ILE:HG13	2.20	0.42
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.55	0.42
54:1x:17:C:OP2	54:1x:18:G:H5"	2.19	0.42
1:2A:330:G:H2'	1:2A:332:G:OP2	2.19	0.42
1:2A:651:A:C6	1:2A:661:A:C8	3.08	0.42
1:2A:1104:G:H5'	1:2A:1105:U:P	2.59	0.42
1:2A:2107:U:H2'	1:2A:2108:G:C8	2.54	0.42
1:2A:2286:C:H6	1:2A:2286:C:H5'	1.85	0.42
1:2A:2828:G:H2'	1:2A:2830:A:N7	2.35	0.42
2:2B:55:U:H1'	6:2G:29:TRP:HE1	1.84	0.42
10:2O:98:VAL:HG13	10:2O:117:LEU:HB3	2.02	0.42
32:2a:407:A:H2'	32:2a:408:A:H4'	2.02	0.42
32:2a:908:C:H2'	32:2a:909:C:O4'	2.20	0.42
32:2a:1060:G:N1	32:2a:1064:G:C6	2.87	0.42
35:2d:98:GLU:C	35:2d:100:ARG:H	2.26	0.42
35:2d:162:LEU:HD23	35:2d:178:VAL:HG13	2.00	0.42
41:2j:74:ILE:HD13	41:2j:74:ILE:HA	1.80	0.42
45:2n:3:ARG:HH21	45:2n:4:LYS:HE3	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2o:4:THR:OG1	46:2o:7:GLU:HG3	2.20	0.42
46:2o:48:LYS:HA	46:2o:48:LYS:HD3	1.78	0.42
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.54	0.42
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	2.01	0.42
1:1A:1404:A:C6	1:1A:1417:U:O4	2.73	0.42
1:1A:1553:A:H4'	1:1A:1555:A:C4	2.55	0.42
1:1A:2544:A:H2'	1:1A:2545:A:O4'	2.20	0.42
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.28	0.42
11:1P:91:PHE:CE1	11:1P:99:LEU:HD11	2.55	0.42
23:11:97:LEU:HD23	23:11:97:LEU:HA	1.92	0.42
32:1a:209:U:H3'	32:1a:210:U:C5	2.55	0.42
32:1a:951:G:H3'	32:1a:952:A:H5"	2.02	0.42
32:1a:982:G:C2	32:1a:983:A:H1'	2.53	0.42
32:1a:1331:A:C2	32:1a:1357:A:C4	3.08	0.42
34:1c:45:LYS:HG3	34:1c:46:GLU:HG2	2.00	0.42
39:1h:44:PHE:HE2	39:1h:109:ILE:HG12	1.84	0.42
41:1j:47:PHE:N	41:1j:63:PHE:O	2.34	0.42
42:1k:38:ASN:HA	42:1k:39:PRO:HD3	1.85	0.42
1:2A:80:G:N1	1:2A:100:A:OP2	2.46	0.42
1:2A:604:G:H2'	1:2A:605:G:C8	2.54	0.42
1:2A:769:G:H2'	1:2A:770:U:O4'	2.20	0.42
1:2A:966:G:C6	1:2A:967:U:C4	3.08	0.42
1:2A:967:U:H2'	1:2A:968:C:C6	2.55	0.42
1:2A:1898:A:H3'	1:2A:1899:G:O4'	2.20	0.42
1:2A:2305:C:P	14:2S:89:ARG:HH22	2.42	0.42
1:2A:2367:C:OP1	22:20:24:LYS:NZ	2.44	0.42
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.20	0.42
7:2H:27:LYS:HZ1	7:2H:32:GLU:HG3	1.84	0.42
10:2O:70:LYS:HB3	10:2O:70:LYS:HE2	1.93	0.42
16:2U:17:ILE:HD13	16:2U:17:ILE:HA	1.89	0.42
21:2Z:75:ASN:HB2	21:2Z:85:HIS:HB3	2.01	0.42
26:24:58:ARG:HB3	26:24:59:PHE:CD1	2.55	0.42
29:27:30:VAL:O	29:27:34:ARG:HG3	2.19	0.42
32:2a:399:C:O2'	32:2a:400:U:H5'	2.20	0.42
32:2a:703:C:H42	49:2r:71:LYS:HE2	1.83	0.42
32:2a:910:C:H2'	32:2a:911:G:H8	1.85	0.42
32:2a:1102:C:H2'	32:2a:1103:G:C8	2.55	0.42
32:2a:1222:U:H3'	32:2a:1223:G:C5'	2.50	0.42
34:2c:61:ALA:C	34:2c:63:ASN:H	2.28	0.42
35:2d:173:TRP:CD2	35:2d:189:PRO:HB3	2.54	0.42
1:1A:1399:A:H2'	1:1A:1400:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1409:G:OP2	23:11:3:LYS:HD2	2.20	0.42
1:1A:1925:G:O2'	1:1A:1949:A:N1	2.50	0.42
1:1A:2107:U:H2'	1:1A:2108:G:H8	1.84	0.42
1:1A:2429:A:H2'	1:1A:2430:U:H6	1.85	0.42
5:1F:11:VAL:HB	5:1F:18:ARG:HB3	2.00	0.42
7:1H:76:VAL:O	7:1H:80:SER:OG	2.38	0.42
15:1T:118:ARG:HH11	15:1T:118:ARG:CG	2.32	0.42
20:1Y:5:MET:HE2	20:1Y:5:MET:HB2	1.66	0.42
32:1a:604:C:H2'	32:1a:605:A:O4'	2.19	0.42
32:1a:1053:U:H2'	32:1a:1054:C:C6	2.55	0.42
33:1b:77:ALA:O	33:1b:81:VAL:HG22	2.19	0.42
34:1c:32:LEU:HD22	34:1c:59:ARG:HH12	1.84	0.42
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	2.02	0.42
44:1m:96:LEU:O	44:1m:110:ARG:NH1	2.45	0.42
1:2A:647:G:C2	1:2A:648:C:C2	3.08	0.42
1:2A:680:C:H2'	1:2A:681:G:O4'	2.19	0.42
1:2A:850:A:H5"	1:2A:851:G:OP1	2.20	0.42
1:2A:866:A:H2'	1:2A:867:A:O4'	2.20	0.42
1:2A:991:G:N2	1:2A:1015:C:C2	2.88	0.42
1:2A:1765:G:H8	1:2A:1769:A:H62	1.66	0.42
1:2A:2567:C:H2'	1:2A:2568:G:O4'	2.19	0.42
1:2A:2690:A:H4'	4:2E:165:VAL:HG11	2.02	0.42
1:2A:2854:G:H2'	1:2A:2855:G:C8	2.55	0.42
10:2O:68:GLU:CB	10:2O:78:ARG:HB2	2.49	0.42
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.51	0.42
15:2T:116:ALA:HB1	15:2T:121:ILE:HD11	2.02	0.42
19:2X:84:ALA:HB3	19:2X:87:GLN:CD	2.44	0.42
32:2a:825:U:H6	32:2a:825:U:P	2.43	0.42
32:2a:1287:G:C5'	52:2u:4:GLY:HA3	2.49	0.42
32:2a:1320:G:H21	54:2x:41:C:H1'	1.85	0.42
32:2a:1348:G:H2'	32:2a:1349:C:O4'	2.20	0.42
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.20	0.42
34:2c:120:VAL:HA	34:2c:123:GLN:HE21	1.84	0.42
40:2i:105:ASP:C	40:2i:107:ARG:H	2.28	0.42
42:2k:85:ARG:HA	42:2k:112:THR:OG1	2.19	0.42
44:2m:27:LYS:HD2	44:2m:27:LYS:HA	1.80	0.42
54:2x:75:C:OP1	59:2x:3101:HOH:O	2.22	0.42
1:1A:1732:C:H2'	1:1A:1733:G:O4'	2.20	0.42
1:1A:2638:G:O2'	1:1A:2793:A:N1	2.47	0.42
8:1I:109:ILE:HG23	8:1I:110:ASP:N	2.35	0.42
26:14:47:GLN:NE2	44:1m:62:ASN:OD1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:18:U:H2'	32:1a:19:C:C6	2.55	0.42
32:1a:461:G:O2'	32:1a:462:G:H5'	2.20	0.42
32:1a:590:G:H1'	32:1a:616:A:H61	1.84	0.42
33:1b:208:ILE:H	33:1b:208:ILE:HG13	1.52	0.42
34:1c:56:ASP:O	34:1c:57:ILE:HG13	2.20	0.42
34:1c:120:VAL:HA	34:1c:123:GLN:HE21	1.84	0.42
38:1g:47:CYS:HB3	38:1g:58:PRO:HB3	2.01	0.42
39:1h:23:SER:HA	39:1h:63:LEU:HD22	2.02	0.42
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.45	0.42
40:1i:38:GLN:HE21	40:1i:39:GLY:N	2.17	0.42
1:2A:1067:G:C5	1:2A:1184:C:C4	3.08	0.42
1:2A:1546:C:O4'	3:2D:100:GLY:HA2	2.20	0.42
1:2A:2224:U:H2'	1:2A:2225:C:C6	2.54	0.42
3:2D:71:ASP:CG	3:2D:103:ARG:HH22	2.27	0.42
6:2G:44:GLY:HA2	6:2G:88:ILE:HG22	2.02	0.42
6:2G:142:PRO:HG2	6:2G:143:GLU:OE2	2.19	0.42
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.54	0.42
11:2P:95:VAL:HG13	11:2P:125:VAL:HB	2.02	0.42
32:2a:126:C:H2'	32:2a:127:C:H6	1.84	0.42
32:2a:138:A:O3'	32:2a:139:G:H8	2.02	0.42
32:2a:426:A:P	35:2d:22:LYS:HZ1	2.42	0.42
32:2a:528:G:OP1	35:2d:62:GLN:NE2	2.32	0.42
32:2a:1107:G:C2	32:2a:1110:G:C2	3.07	0.42
32:2a:1198:G:H5"	45:2n:5:ALA:CB	2.50	0.42
32:2a:1356:G:O6	40:2i:107:ARG:NH1	2.53	0.42
35:2d:31:CYS:O	35:2d:35:ARG:HG3	2.19	0.42
38:2g:129:GLU:H	38:2g:129:GLU:HG2	1.59	0.42
43:2l:24:VAL:HG21	43:2l:27:LEU:HD22	2.02	0.42
45:2n:32:SER:O	45:2n:40:CYS:HA	2.19	0.42
1:1A:485:A:H2'	1:1A:486:C:O4'	2.19	0.42
1:1A:908:G:H2'	1:1A:909:A:O4'	2.20	0.42
1:1A:1313:A:C2	1:1A:2034:A:C4	3.08	0.42
1:1A:1531:A:H2'	1:1A:1532:G:H8	1.84	0.42
1:1A:2224:U:O2'	1:1A:2225:C:H5'	2.20	0.42
1:1A:2330:G:H22	14:1S:3:ARG:NE	2.18	0.42
6:1G:43:LEU:HD12	6:1G:43:LEU:HA	1.85	0.42
20:1Y:55:TYR:CD1	20:1Y:55:TYR:N	2.87	0.42
23:11:82:LEU:HA	23:11:85:LEU:HD12	2.02	0.42
26:14:68:ARG:HB3	26:14:68:ARG:NH2	2.35	0.42
32:1a:523:A:H2'	32:1a:524:G:H8	1.84	0.42
32:1a:609:G:H2'	32:1a:610:U:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1040:G:C4	32:1a:1186:A:C2	3.08	0.42
32:1a:1045:U:H2'	32:1a:1046:C:C6	2.55	0.42
32:1a:1494:G:H2'	32:1a:1496:A:OP2	2.20	0.42
33:1b:78:GLN:NE2	33:1b:94:ASN:O	2.46	0.42
36:1e:69:VAL:HA	36:1e:70:PRO:HD2	1.98	0.42
36:1e:78:HIS:CD2	36:1e:142:LEU:HD23	2.55	0.42
39:1h:81:HIS:N	39:1h:138:TRP:O	2.53	0.42
49:1r:58:LEU:HA	49:1r:58:LEU:HD13	1.81	0.42
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.20	0.42
1:2A:115:A:H3'	1:2A:116:A:H5"	2.02	0.42
1:2A:946:A:C5	1:2A:947:C:C4	3.08	0.42
1:2A:1047:G:N2	1:2A:1199:G:H1'	2.35	0.42
1:2A:1198:C:H2'	1:2A:1199:G:O4'	2.20	0.42
1:2A:1334:C:H2'	1:2A:1335:C:C6	2.55	0.42
1:2A:1878:A:C4	1:2A:1879:G:C8	3.07	0.42
1:2A:2588:A:O4'	27:25:3:LYS:HB2	2.20	0.42
2:2B:2:C:H3'	2:2B:2:C:P	2.60	0.42
9:2N:73:THR:HB	9:2N:82:LEU:HD11	2.00	0.42
9:2N:131:GLN:H	9:2N:131:GLN:HG2	1.58	0.42
12:2Q:77:LYS:HE3	12:2Q:84:GLY:O	2.20	0.42
21:2Z:128:VAL:HG23	21:2Z:160:GLY:O	2.20	0.42
25:23:29:ARG:H	25:23:33:GLN:NE2	2.18	0.42
32:2a:6:U:H5"	32:2a:7:G:C5	2.55	0.42
32:2a:402:G:H5'	35:2d:5:ILE:HD11	2.01	0.42
32:2a:1101:C:H1'	32:2a:1161:A:C5	2.54	0.42
33:2b:204:ASN:OD1	33:2b:205:ASP:N	2.52	0.42
33:2b:229:VAL:O	33:2b:231:GLU:N	2.44	0.42
38:2g:70:LYS:HB3	38:2g:96:GLN:HB3	2.01	0.42
43:2l:51:ALA:HB3	43:2l:53:ARG:HE	1.85	0.42
47:2p:43:LYS:HB3	47:2p:48:TRP:CD1	2.55	0.42
50:2s:63:THR:OG1	50:2s:64:GLU:N	2.53	0.42
1:1A:761:G:H2'	1:1A:762:A:O4'	2.20	0.41
1:1A:1149:C:H2'	1:1A:1150:U:C5	2.53	0.41
1:1A:2284:A:H2'	1:1A:2285:A:C8	2.54	0.41
2:1B:57:A:H1'	6:1G:29:TRP:HB2	2.01	0.41
4:1E:101:ARG:HB2	4:1E:201:THR:HG21	2.01	0.41
5:1F:37:VAL:HG21	11:1P:6:LEU:HD11	2.00	0.41
15:1T:127:ALA:C	15:1T:129:ARG:N	2.76	0.41
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	2.02	0.41
23:11:4:VAL:HG22	23:11:11:ARG:HB3	2.01	0.41
32:1a:487:C:O2'	32:1a:488:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:609:G:C4	32:1a:610:U:C5	3.08	0.41
32:1a:1334:C:P	52:1u:3:LYS:HZ1	2.40	0.41
43:1l:60:LEU:HD21	43:1l:66:VAL:HG22	2.02	0.41
47:1p:59:TRP:HB3	47:1p:64:ALA:HB2	2.02	0.41
1:2A:772:G:OP2	1:2A:772:G:C8	2.73	0.41
1:2A:2438:C:H5"	1:2A:2439:G:OP1	2.19	0.41
1:2A:2700:U:H5'	1:2A:2700:U:O2	2.19	0.41
1:2A:2881:G:C2	1:2A:2882:A:N6	2.87	0.41
2:2B:1:U:O2'	2:2B:2:C:O5'	2.35	0.41
8:2I:104:GLN:HG3	8:2I:105:HIS:CD2	2.55	0.41
19:2X:65:ARG:HD3	19:2X:70:LEU:HG	2.01	0.41
32:2a:200:C:H2'	32:2a:201:C:C6	2.54	0.41
32:2a:914:C:H2'	32:2a:915:A:O4'	2.20	0.41
32:2a:952:A:P	45:2n:41:ARG:HH12	2.43	0.41
32:2a:960:U:N3	32:2a:1205:C:N3	2.60	0.41
32:2a:965:G:N2	32:2a:1201:U:O2	2.53	0.41
38:2g:54:THR:O	38:2g:56:GLN:N	2.53	0.41
54:2x:17:C:H2'	54:2x:17(A):U:H2'	2.02	0.41
1:1A:955:A:N3	1:1A:2275:C:O2'	2.49	0.41
3:1D:134:ARG:NH1	3:1D:188:GLU:OE2	2.53	0.41
5:1F:106:ARG:H	5:1F:106:ARG:HG2	1.49	0.41
20:1Y:1:MET:H1	20:1Y:1:MET:HG3	1.72	0.41
37:1f:18:GLN:O	37:1f:21:LEU:HB2	2.19	0.41
43:1l:102:ARG:HE	43:1l:102:ARG:HB3	1.75	0.41
49:1r:44:LEU:HD21	49:1r:70:ILE:HG21	2.01	0.41
50:1s:2:PRO:HB2	50:1s:3:ARG:H	1.57	0.41
1:2A:16:G:H2'	1:2A:17:C:C6	2.55	0.41
1:2A:75:C:OP1	24:22:59:ARG:HD3	2.19	0.41
1:2A:345:A:H5'	1:2A:363:A:H1'	2.01	0.41
1:2A:539:A:H1'	1:2A:603:C:H1'	2.03	0.41
1:2A:622:G:N2	1:2A:627:C:O3'	2.53	0.41
1:2A:909:A:H2'	1:2A:910:G:H8	1.85	0.41
1:2A:1439:U:C4	1:2A:1440:A:C5	3.08	0.41
1:2A:1739:U:O2'	3:2D:14:ARG:NH2	2.53	0.41
1:2A:1840:A:H8	1:2A:1840:A:O5'	2.03	0.41
1:2A:1890:G:H8	1:2A:1890:G:OP2	2.03	0.41
1:2A:2249:G:N3	1:2A:2249:G:H2'	2.35	0.41
1:2A:2796:C:H2'	1:2A:2797:C:H6	1.84	0.41
2:2B:45:A:O2'	2:2B:46:A:OP1	2.37	0.41
2:2B:111:G:H2'	2:2B:112:U:O4'	2.19	0.41
12:2Q:72:LYS:HB3	12:2Q:94:VAL:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:442:G:H8	32:2a:442:G:O5'	2.02	0.41
32:2a:741:U:H2'	32:2a:742:G:O4'	2.21	0.41
32:2a:1110:G:H2'	32:2a:1111:C:C6	2.55	0.41
32:2a:1375:G:N2	32:2a:1480:A:H8	2.18	0.41
33:2b:180:LEU:O	33:2b:181:PHE:HB2	2.18	0.41
36:2e:90:VAL:O	36:2e:120:THR:HA	2.20	0.41
47:2p:45:THR:HG22	47:2p:47:ASP:H	1.84	0.41
1:1A:182:G:OP2	59:1A:4163:HOH:O	2.21	0.41
1:1A:1614:G:H5"	3:1D:61:LEU:HD22	2.01	0.41
1:1A:2115:G:P	8:1I:22:LYS:HD2	2.60	0.41
1:1A:2783:C:H2'	1:1A:2784:C:C6	2.55	0.41
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.20	0.41
21:1Z:67:LEU:HA	21:1Z:68:PRO:HD3	1.94	0.41
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.50	0.41
32:1a:89:G:H2'	32:1a:90:U:C6	2.55	0.41
32:1a:125:A:N7	48:1q:63:ARG:HB2	2.35	0.41
32:1a:291:C:H2'	32:1a:292:U:O4'	2.20	0.41
32:1a:371:U:C2	32:1a:372:G:C8	3.08	0.41
40:1i:24:GLY:HA2	40:1i:57:GLY:HA2	2.01	0.41
50:1s:63:THR:HG23	50:1s:65:ASN:HD21	1.85	0.41
1:2A:534:C:H2'	1:2A:535:U:O4'	2.21	0.41
1:2A:554:G:C5	1:2A:2043:U:H5"	2.55	0.41
1:2A:719:C:H5"	5:2F:81:PRO:HD2	2.02	0.41
1:2A:1095:A:H2'	1:2A:1096:G:H8	1.85	0.41
1:2A:1096:G:C4	1:2A:1097:C:C5	3.08	0.41
1:2A:2596:U:H4'	1:2A:2597:C:OP1	2.19	0.41
1:2A:2602:C:H2'	1:2A:2603:G:C8	2.56	0.41
3:2D:43:ARG:HA	3:2D:48:ARG:O	2.21	0.41
4:2E:101:ARG:NH2	4:2E:171:GLU:HB2	2.36	0.41
6:2G:44:GLY:N	6:2G:88:ILE:O	2.54	0.41
7:2H:95:ARG:HA	7:2H:128:PRO:O	2.21	0.41
15:2T:6:LEU:HA	15:2T:6:LEU:HD13	1.78	0.41
16:2U:44:ASN:HD22	16:2U:44:ASN:N	2.18	0.41
32:2a:26:C:H5'	32:2a:508:G:H1'	2.02	0.41
32:2a:255:G:H2'	32:2a:256:G:O4'	2.20	0.41
32:2a:506:C:OP2	43:2l:69:TYR:OH	2.29	0.41
32:2a:1087:G:O5'	33:2b:111:ARG:HD2	2.20	0.41
32:2a:1155:G:H2'	32:2a:1156:G:C8	2.55	0.41
49:2r:58:LEU:HD12	49:2r:62:GLU:HB3	2.02	0.41
1:1A:553:A:C2	59:1A:4190:HOH:O	2.73	0.41
1:1A:1055:A:N3	1:1A:1198:C:H1'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1248:A:N6	1:1A:1285:U:H2'	2.35	0.41
1:1A:1477:C:H2'	1:1A:1478:U:O4'	2.20	0.41
1:1A:1763:G:C6	1:1A:1764:U:C4	3.08	0.41
3:1D:68:LYS:O	3:1D:69:ARG:HB2	2.21	0.41
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.50	0.41
7:1H:7:LEU:HG	7:1H:69:ARG:NH1	2.34	0.41
10:1O:87:ILE:HD12	10:1O:91:LEU:HA	2.02	0.41
14:1S:41:ASP:OD2	14:1S:44:LYS:HG3	2.20	0.41
16:1U:8:VAL:HG22	16:1U:11:ARG:HH21	1.85	0.41
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	2.01	0.41
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.41	0.41
19:1X:31:HIS:HD2	19:1X:33:LYS:N	2.07	0.41
32:1a:414:C:H1'	32:1a:524:G:O2'	2.19	0.41
32:1a:448:A:H4'	47:1p:72:ARG:HB2	2.03	0.41
32:1a:749:G:C6	32:1a:796:C:C2	3.08	0.41
32:1a:1176:U:H4'	36:1e:22:GLY:O	2.21	0.41
32:1a:1328:A:H5"	40:1i:120:ARG:NH1	2.35	0.41
33:1b:28:PHE:HD2	33:1b:194:PRO:HG3	1.85	0.41
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.21	0.41
40:1i:53:VAL:HB	40:1i:92:TYR:CZ	2.55	0.41
44:1m:33:ALA:O	44:1m:37:THR:OG1	2.33	0.41
1:2A:348:G:H2'	1:2A:349:G:O4'	2.21	0.41
1:2A:909:A:OP1	12:2Q:22:LYS:HG3	2.21	0.41
1:2A:1056:G:C6	1:2A:1058:C:C4	3.09	0.41
1:2A:1080:U:H2'	1:2A:1081:G:C8	2.56	0.41
1:2A:1307:A:H2	27:25:10:LYS:HD2	1.85	0.41
1:2A:1308:U:C4	1:2A:1309:G:C6	3.08	0.41
1:2A:1330:G:N2	1:2A:1373:G:H5"	2.35	0.41
1:2A:2080:A:O2'	5:2F:69:HIS:HD2	2.03	0.41
1:2A:2495:G:C2	1:2A:2496:G:C8	3.08	0.41
2:2B:102:A:O5'	2:2B:102:A:H8	2.04	0.41
4:2E:115:GLY:O	4:2E:119:ARG:HB2	2.21	0.41
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.83	0.41
6:2G:27:ASN:HB3	6:2G:30:GLU:HG3	2.02	0.41
6:2G:33:ARG:HH12	6:2G:162:THR:CB	2.33	0.41
32:2a:759:G:N2	32:2a:788:U:O4	2.54	0.41
32:2a:877:C:O5'	32:2a:877:C:H6	2.03	0.41
32:2a:925:G:O2'	32:2a:1288:A:H4'	2.21	0.41
32:2a:969:U:C4	32:2a:1194:U:H1'	2.55	0.41
32:2a:1140:A:C5	32:2a:1162:A:C6	3.08	0.41
32:2a:1188:G:H4'	34:2c:192:THR:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1260:U:H3'	32:2a:1260:U:H6	1.85	0.41
32:2a:1375:G:H21	32:2a:1480:A:H8	1.68	0.41
33:2b:90:MET:HA	33:2b:90:MET:HE3	2.03	0.41
33:2b:158:LEU:HA	33:2b:159:PRO:HD2	1.90	0.41
34:2c:20:SER:O	45:2n:54:PRO:HB3	2.21	0.41
36:2e:107:ARG:O	36:2e:111:GLU:HB2	2.20	0.41
37:2f:35:ALA:HB1	37:2f:65:VAL:HG11	2.02	0.41
49:2r:66:LEU:O	49:2r:70:ILE:HG13	2.20	0.41
1:1A:345:A:H3'	5:1F:169:ASN:HD21	1.85	0.41
1:1A:488:G:OP2	59:1A:4164:HOH:O	2.22	0.41
1:1A:830:A:O4'	3:1D:227:ASN:ND2	2.53	0.41
1:1A:1424:A:H4'	1:1A:1425:G:OP2	2.19	0.41
1:1A:1451:U:H2'	1:1A:1452:C:H6	1.84	0.41
1:1A:1474:G:H2'	1:1A:1475:C:H6	1.83	0.41
1:1A:2388:A:H2'	1:1A:2389:A:C8	2.55	0.41
1:1A:2400:G:H5"	1:1A:2401:U:O4'	2.21	0.41
2:1B:78:A:C2	2:1B:100:A:C4	3.08	0.41
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	2.02	0.41
7:1H:3:ARG:HG3	7:1H:4:ILE:N	2.35	0.41
17:1V:49:THR:HG22	17:1V:49:THR:O	2.20	0.41
21:1Z:24:LEU:HB2	21:1Z:41:LEU:HD23	2.00	0.41
28:16:2:ALA:N	59:16:201:HOH:O	2.54	0.41
32:1a:140:G:C2	32:1a:173:C:N3	2.89	0.41
32:1a:149:C:C5	32:1a:150:C:H5	2.39	0.41
32:1a:165:U:H1'	59:1a:2150:HOH:O	2.20	0.41
32:1a:638:G:C5	32:1a:639:A:C8	3.08	0.41
32:1a:952:A:H8	32:1a:952:A:OP1	2.04	0.41
32:1a:1342:A:H2'	32:1a:1343:G:O4'	2.20	0.41
33:1b:71:VAL:HA	33:1b:93:VAL:HG23	2.02	0.41
37:1f:97:PHE:HB2	49:1r:32:ARG:HD3	2.01	0.41
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.20	0.41
40:1i:96:LEU:H	40:1i:98:PRO:HD2	1.86	0.41
1:2A:1059:U:H2'	1:2A:1060:G:C8	2.55	0.41
1:2A:1109:C:H42	1:2A:1119:G:H1	1.69	0.41
1:2A:1155:G:H8	1:2A:1155:G:O5'	2.03	0.41
1:2A:1683:A:H4'	1:2A:2722:A:O2'	2.20	0.41
1:2A:1697:G:H2'	1:2A:1698:A:O4'	2.21	0.41
1:2A:2371:A:H2'	1:2A:2372:A:O4'	2.20	0.41
1:2A:2405:C:P	30:28:30:ARG:NH1	2.93	0.41
1:2A:2421:G:C2	1:2A:2422:A:H1'	2.55	0.41
2:2B:4:C:C2	2:2B:118:G:N2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:53:A:H2'	2:2B:54:G:O4'	2.21	0.41
2:2B:75:G:O2'	21:2Z:85:HIS:NE2	2.44	0.41
6:2G:76:SER:CB	6:2G:84:LYS:H	2.34	0.41
8:2I:29:TYR:CD2	8:2I:30:LEU:HD23	2.55	0.41
11:2P:59:LEU:HD23	11:2P:59:LEU:HA	1.87	0.41
14:2S:62:LYS:HB3	14:2S:97:ARG:NE	2.36	0.41
16:2U:110:VAL:O	16:2U:113:ALA:HB3	2.21	0.41
32:2a:1032:U:C6	32:2a:1183:A:H5'	2.56	0.41
32:2a:1288:A:N6	32:2a:1313:G:O4'	2.53	0.41
33:2b:90:MET:HG3	33:2b:91:PRO:HD2	2.02	0.41
33:2b:175:ARG:HB3	33:2b:175:ARG:NH1	2.36	0.41
34:2c:52:LEU:CD1	34:2c:118:GLN:HE22	2.34	0.41
37:2f:52:ILE:HD13	37:2f:87:ARG:NH1	2.35	0.41
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	2.01	0.41
54:2x:19:G:C4	54:2x:57:A:C2	3.08	0.41
54:2x:29:G:C6	54:2x:30:G:C5	3.09	0.41
1:1A:612:A:OP1	5:1F:95:ARG:NH1	2.54	0.41
1:1A:830:A:C5	3:1D:229:VAL:HG21	2.56	0.41
1:1A:885:U:H1'	1:1A:1235:G:H1'	2.03	0.41
1:1A:1185:U:OP1	9:1N:25:ARG:NH1	2.52	0.41
1:1A:2659:C:H2'	1:1A:2660:U:H6	1.85	0.41
1:1A:2797:C:H2'	1:1A:2798:U:O4'	2.21	0.41
4:1E:85:ASN:HA	4:1E:86:PRO:HD2	1.94	0.41
20:1Y:38:ILE:HD13	20:1Y:66:PRO:HA	2.03	0.41
21:1Z:40:ASP:OD2	21:1Z:42:VAL:HG13	2.20	0.41
24:12:51:ARG:HD3	24:12:55:ARG:NH1	2.35	0.41
24:12:61:LEU:HD23	24:12:61:LEU:HA	1.93	0.41
32:1a:614:G:H2'	32:1a:615:G:C8	2.56	0.41
35:1d:141:ARG:H	35:1d:141:ARG:HG2	1.62	0.41
38:1g:68:ASN:ND2	38:1g:128:ALA:O	2.54	0.41
41:1j:12:ASP:HB3	41:1j:15:THR:OG1	2.20	0.41
47:1p:57:ARG:HG3	47:1p:57:ARG:HH11	1.85	0.41
1:2A:183:A:H5"	1:2A:184:A:O5'	2.21	0.41
1:2A:745:A:H2'	1:2A:746:G:O4'	2.20	0.41
1:2A:1038:G:OP1	16:2U:50:ARG:NH2	2.50	0.41
1:2A:2333:A:H2'	1:2A:2334:G:O4'	2.20	0.41
1:2A:2704:A:H2'	1:2A:2705:G:C8	2.54	0.41
1:2A:2706:C:H2'	1:2A:2707:U:C6	2.56	0.41
3:2D:147:LEU:HD12	3:2D:147:LEU:HA	1.88	0.41
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.21	0.41
11:2P:135:LEU:HD23	11:2P:135:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2U:16:LYS:HE2	16:2U:16:LYS:HB3	1.88	0.41
32:2a:952:A:H8	32:2a:952:A:OP1	2.04	0.41
32:2a:1091:G:H5'	34:2c:176:HIS:CD2	2.56	0.41
32:2a:1108:U:H6	32:2a:1109:U:O2'	2.02	0.41
35:2d:107:ARG:HA	35:2d:107:ARG:HD2	1.89	0.41
44:2m:14:ARG:O	44:2m:17:VAL:HG22	2.20	0.41
45:2n:51:GLY:C	45:2n:53:LEU:H	2.29	0.41
45:2n:52:GLN:O	45:2n:53:LEU:HD22	2.21	0.41
55:2z:4:PRO:HA	55:2z:5:PRO:HD3	1.85	0.41
1:1A:210:A:H5"	1:1A:447:U:OP1	2.20	0.41
1:1A:1311:G:O5'	18:1W:15:ARG:NH2	2.53	0.41
1:1A:1777:G:H2'	1:1A:1778:G:H5"	2.02	0.41
3:1D:38:LYS:HA	3:1D:38:LYS:HD2	1.83	0.41
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.34	0.41
8:1I:129:THR:HG22	8:1I:139:GLN:NE2	2.19	0.41
19:1X:57:LEU:HD11	19:1X:78:LYS:CE	2.51	0.41
26:14:46:GLN:O	26:14:48:ARG:HG2	2.21	0.41
32:1a:569:G:N3	32:1a:857:C:H4'	2.35	0.41
32:1a:630:U:H2'	32:1a:631:C:H6	1.85	0.41
32:1a:1255:G:C6	32:1a:1256:G:C4	3.09	0.41
33:1b:70:PHE:O	33:1b:93:VAL:N	2.46	0.41
34:1c:22:TRP:HB2	34:1c:23:TYR:H	1.77	0.41
34:1c:148:GLY:HA3	34:1c:172:ARG:H	1.85	0.41
35:1d:110:PHE:HE1	35:1d:176:LEU:HD13	1.86	0.41
43:1l:117:ARG:HB3	43:1l:122:THR:HB	2.03	0.41
45:1n:13:THR:HA	45:1n:14:PRO:HD3	1.72	0.41
49:1r:20:ALA:O	49:1r:55:ARG:NH2	2.53	0.41
1:2A:253:A:C8	1:2A:254:G:H1'	2.56	0.41
1:2A:1313:A:H2'	1:2A:1314:A:O4'	2.21	0.41
1:2A:1585:G:H2'	1:2A:1586:U:C6	2.55	0.41
1:2A:1643:C:H2'	1:2A:1644:C:H6	1.85	0.41
1:2A:1684:C:H4'	1:2A:2721:C:O2	2.21	0.41
1:2A:1840:A:H2'	1:2A:1841:G:O4'	2.20	0.41
1:2A:2753:A:H2'	1:2A:2754:C:O4'	2.19	0.41
2:2B:10:C:C4	2:2B:11:C:C5	3.08	0.41
3:2D:10:THR:OG1	3:2D:13:ARG:HG2	2.20	0.41
4:2E:89:ASP:OD2	4:2E:89:ASP:N	2.53	0.41
6:2G:173:LEU:HB3	6:2G:178:PHE:CG	2.55	0.41
7:2H:44:VAL:HG21	7:2H:51:ARG:HB2	2.01	0.41
15:2T:64:ARG:NH1	15:2T:103:ARG:HA	2.35	0.41
21:2Z:132:ASN:O	21:2Z:134:PRO:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:524:G:C4	32:2a:525:G:C8	3.08	0.41
32:2a:1105:U:C2	32:2a:1106:A:C8	3.08	0.41
34:2c:6:HIS:HA	34:2c:7:PRO:HD3	1.97	0.41
36:2e:42:GLY:HA2	36:2e:65:ASN:O	2.20	0.41
43:2l:33:ARG:O	43:2l:85:ILE:HG12	2.21	0.41
46:2o:36:ILE:O	46:2o:39:LEU:N	2.54	0.41
49:2r:76:LEU:HD12	49:2r:76:LEU:HA	1.68	0.41
6:1G:138:GLN:HE21	6:1G:153:ARG:NH2	2.19	0.41
27:15:11:THR:HG23	27:15:15:ARG:HB3	2.03	0.41
32:1a:343:G:N1	32:1a:344:G:H1'	2.36	0.41
32:1a:620:U:H2'	32:1a:621:G:H8	1.86	0.41
32:1a:843:A:H2	32:1a:896:A:H4'	1.84	0.41
33:1b:211:ILE:H	33:1b:211:ILE:HG13	1.72	0.41
35:1d:188:LEU:H	35:1d:188:LEU:CD2	2.30	0.41
1:2A:6:G:H4'	9:2N:13:TRP:HH2	1.85	0.41
1:2A:20:A:O2'	1:2A:21:C:H5'	2.21	0.41
1:2A:184:A:C4	1:2A:851:G:C6	3.09	0.41
1:2A:376:G:H2'	1:2A:377:G:C8	2.55	0.41
1:2A:666:G:H21	1:2A:670:A:H2	1.69	0.41
1:2A:793:U:O2	1:2A:2035:A:H1'	2.21	0.41
1:2A:989:A:C4	1:2A:2459:A:C2	3.09	0.41
1:2A:1248:A:C8	1:2A:1250:G:C6	3.08	0.41
1:2A:1593:C:H2'	1:2A:1594:C:C6	2.55	0.41
1:2A:2114:G:C6	1:2A:2236:A:C8	3.08	0.41
1:2A:2305:C:H5'	14:2S:10:ARG:HD2	2.02	0.41
1:2A:2662:C:H2'	1:2A:2663:C:H6	1.86	0.41
1:2A:2691:C:H5'	4:2E:189:PRO:HA	2.01	0.41
2:2B:25:A:H2'	2:2B:26:A:O4'	2.20	0.41
3:2D:68:LYS:O	3:2D:69:ARG:HB2	2.20	0.41
6:2G:28:VAL:O	6:2G:31:VAL:HG12	2.21	0.41
13:2R:97:VAL:CG2	13:2R:114:VAL:HG13	2.51	0.41
14:2S:62:LYS:O	14:2S:65:VAL:HB	2.21	0.41
17:2V:48:GLY:HA3	17:2V:52:VAL:HG12	2.02	0.41
21:2Z:30:ASN:ND2	21:2Z:90:VAL:HB	2.36	0.41
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.36	0.41
32:2a:103:A:H2'	32:2a:322:G:N2	2.35	0.41
32:2a:176:G:N2	32:2a:177:U:O4	2.43	0.41
32:2a:324:C:H4'	32:2a:325:A:H5'	2.03	0.41
32:2a:429:C:H2'	32:2a:430:U:H6	1.83	0.41
32:2a:570:C:O2'	32:2a:856:G:H4'	2.20	0.41
38:2g:73:MET:HE2	38:2g:73:MET:HB2	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:27:GLU:HB3	50:2s:28:LYS:HA	2.03	0.41
1:1A:238:G:P	30:18:13:ARG:HH22	2.43	0.41
1:1A:554:G:C5	1:1A:2043:U:H5"	2.56	0.41
1:1A:610:U:O4	1:1A:716:A:H1'	2.21	0.41
1:1A:1066:A:H8	1:1A:1067:G:H5"	1.85	0.41
1:1A:1091:A:OP1	1:1A:1091:A:H8	2.03	0.41
1:1A:1220:G:H1'	1:1A:1221:A:O5'	2.21	0.41
1:1A:1540:A:C6	1:1A:1541:A:C6	3.08	0.41
1:1A:2416:G:H8	1:1A:2416:G:OP2	2.04	0.41
2:1B:88:C:H2'	2:1B:89:G:O4'	2.21	0.41
6:1G:128:ARG:HE	6:1G:128:ARG:HB2	1.64	0.41
7:1H:23:ARG:HD2	7:1H:34:GLU:OE1	2.20	0.41
11:1P:81:GLN:NE2	11:1P:105:LEU:O	2.54	0.41
20:1Y:28:LYS:HD2	20:1Y:40:GLU:HG3	2.03	0.41
24:12:3:LEU:O	24:12:7:ARG:HG3	2.21	0.41
26:14:48:ARG:O	26:14:50:VAL:N	2.53	0.41
32:1a:204:A:N1	32:1a:216:G:O2'	2.45	0.41
32:1a:369:A:C2	32:1a:467:A:C6	3.09	0.41
32:1a:429:C:H2'	32:1a:430:U:C6	2.55	0.41
32:1a:434:G:O2'	32:1a:479:U:O4	2.39	0.41
32:1a:719:C:H2'	32:1a:720:C:C6	2.56	0.41
32:1a:1043:C:N4	34:1c:2:GLY:HA3	2.36	0.41
32:1a:1243:A:H3'	32:1a:1244:C:H6	1.85	0.41
34:1c:22:TRP:CH2	45:1n:54:PRO:HG3	2.56	0.41
34:1c:59:ARG:O	41:1j:92:THR:HG22	2.20	0.41
35:1d:146:ILE:HD12	35:1d:146:ILE:N	2.36	0.41
35:1d:167:GLY:H	35:1d:168:ARG:NH2	2.18	0.41
38:1g:29:LYS:HD3	38:1g:29:LYS:HA	1.97	0.41
38:1g:125:MET:HE2	38:1g:125:MET:HB3	1.98	0.41
40:1i:8:GLY:O	40:1i:76:ALA:HB1	2.20	0.41
47:1p:3:LYS:O	47:1p:21:VAL:HA	2.21	0.41
48:1q:45:HIS:O	48:1q:73:VAL:HG23	2.21	0.41
49:1r:54:ARG:CZ	49:1r:54:ARG:HB3	2.51	0.41
50:1s:30:LEU:HD12	50:1s:30:LEU:HA	1.86	0.41
50:1s:51:VAL:O	50:1s:58:VAL:N	2.35	0.41
51:1t:82:SER:O	51:1t:86:ARG:HG3	2.21	0.41
52:1u:2:GLY:C	52:1u:4:GLY:H	2.28	0.41
1:2A:138:A:H8	1:2A:1453:C:O2'	2.02	0.41
1:2A:153:G:O6	1:2A:160:C:N4	2.42	0.41
1:2A:223:U:O2	1:2A:456:G:C2	2.74	0.41
1:2A:671:G:H8	1:2A:671:G:O5'	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1146:U:C2	1:2A:1147:C:C5	3.09	0.41
1:2A:2086:C:H2'	1:2A:2087:C:H6	1.86	0.41
1:2A:2207:G:C2	1:2A:2208:G:C6	3.08	0.41
1:2A:2311:G:C2	1:2A:2328:C:N3	2.88	0.41
1:2A:2390:G:H2'	1:2A:2391:C:C6	2.55	0.41
1:2A:2622:U:H6	1:2A:2622:U:H5'	1.85	0.41
2:2B:33:G:C6	2:2B:34:U:C4	3.08	0.41
2:2B:33:G:C2	2:2B:50:G:C2	3.09	0.41
2:2B:61:G:C6	2:2B:62:C:C4	3.09	0.41
4:2E:52:LEU:HB2	4:2E:76:ARG:HB3	2.03	0.41
14:2S:39:ILE:HB	14:2S:49:VAL:HG22	2.02	0.41
15:2T:122:ASP:O	15:2T:126:ALA:N	2.53	0.41
17:2V:89:GLN:HA	17:2V:90:PRO:HD3	1.94	0.41
21:2Z:92:SER:O	21:2Z:94:GLU:N	2.54	0.41
31:29:14:CYS:HA	31:29:27:CYS:HB2	2.02	0.41
32:2a:99:G:C6	32:2a:100:C:C4	3.08	0.41
32:2a:954:G:C8	32:2a:1340:U:C2	3.08	0.41
32:2a:1037:C:OP2	32:2a:1037:C:H4'	2.21	0.41
32:2a:1508:G:H2'	32:2a:1509:A:O4'	2.21	0.41
33:2b:55:PHE:HD1	33:2b:58:ILE:HD12	1.86	0.41
33:2b:56:ARG:NH1	33:2b:59:GLU:OE1	2.53	0.41
33:2b:67:THR:HA	33:2b:90:MET:HE2	2.01	0.41
33:2b:153:ARG:HG3	33:2b:154:LEU:N	2.36	0.41
33:2b:188:ALA:HB1	33:2b:192:SER:CB	2.51	0.41
34:2c:20:SER:HB3	34:2c:22:TRP:NE1	2.35	0.41
35:2d:52:SER:O	35:2d:56:VAL:HG23	2.21	0.41
35:2d:158:ILE:O	35:2d:162:LEU:HD12	2.20	0.41
35:2d:204:ILE:H	35:2d:204:ILE:HG12	1.73	0.41
36:2e:5:ASP:OD1	36:2e:5:ASP:N	2.54	0.41
37:2f:82:ARG:HB2	37:2f:85:VAL:HG23	2.03	0.41
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.20	0.41
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.20	0.41
43:2l:8:ASN:OD1	48:2q:34:LYS:HE2	2.21	0.41
46:2o:5:LYS:H	46:2o:5:LYS:CD	2.34	0.41
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.20	0.41
51:2t:39:LYS:HE3	51:2t:39:LYS:HB2	1.67	0.41
54:2x:69:C:H2'	54:2x:70:G:O4'	2.20	0.41
1:1A:173:U:H4'	1:1A:206:A:H4'	2.03	0.41
1:1A:904:U:O2	1:1A:2279:A:H2'	2.21	0.41
1:1A:1215:G:N2	1:1A:1224:C:C2	2.89	0.41
1:1A:1616:A:H2'	1:1A:1617:A:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2225:C:C2	1:1A:2231:G:C2	3.09	0.41
1:1A:2719:G:H1'	13:1R:71:GLN:HE22	1.86	0.41
9:1N:39:ARG:HA	9:1N:40:PRO:HD3	1.98	0.41
11:1P:63:PRO:HG2	30:18:25:MET:HB2	2.03	0.41
12:1Q:97:VAL:HG21	12:1Q:103:MET:HE3	2.02	0.41
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.50	0.41
15:1T:26:ASP:OD1	15:1T:120:ARG:NH2	2.40	0.41
32:1a:71:G:H2'	32:1a:72:C:C6	2.56	0.41
32:1a:188:C:O2	32:1a:192:G:C6	2.73	0.41
32:1a:741:U:O2'	32:1a:857:C:O2	2.33	0.41
32:1a:952:A:P	45:1n:41:ARG:HH12	2.44	0.41
32:1a:970:U:H4'	32:1a:971:G:C5'	2.51	0.41
32:1a:1248:G:H5"	32:1a:1249:C:OP2	2.21	0.41
40:1i:46:ALA:HA	40:1i:78:LYS:HB2	2.02	0.41
43:1l:71:PRO:O	43:1l:102:ARG:HD3	2.21	0.41
54:1x:8:4SU:O2	54:1x:21:A:H2	2.04	0.41
1:2A:6:G:H2'	1:2A:7:A:C8	2.55	0.41
1:2A:107:G:C2	1:2A:108:A:C8	3.09	0.41
1:2A:716:A:H4'	1:2A:717:C:O5'	2.21	0.41
1:2A:784:G:C6	1:2A:785:G:C2	3.09	0.41
1:2A:894:G:C4	1:2A:977:A:H8	2.38	0.41
1:2A:1067:G:C6	1:2A:1184:C:C4	3.09	0.41
1:2A:1342:C:OP1	1:2A:2721:C:H4'	2.21	0.41
1:2A:1633:C:H2'	1:2A:1634:C:H6	1.86	0.41
1:2A:2040:A:OP2	27:25:9:LYS:NZ	2.52	0.41
1:2A:2124:C:H1'	1:2A:2208:G:H1	1.86	0.41
1:2A:2419:U:H2'	1:2A:2420:G:H8	1.84	0.41
1:2A:2622:U:O4	27:25:3:LYS:HG2	2.21	0.41
1:2A:2845:U:C4	1:2A:2892:A:N6	2.89	0.41
9:2N:37:LYS:HA	9:2N:42:TRP:CD1	2.55	0.41
13:2R:60:LEU:HD23	13:2R:60:LEU:HA	1.86	0.41
14:2S:62:LYS:HE3	14:2S:62:LYS:HB2	1.96	0.41
21:2Z:67:LEU:HA	21:2Z:68:PRO:HD3	1.95	0.41
30:28:8:LYS:HB3	30:28:12:LYS:HE3	2.03	0.41
32:2a:108:U:C2'	32:2a:109:G:H5'	2.51	0.41
32:2a:182:C:O2'	51:2t:89:ARG:NH2	2.54	0.41
32:2a:674:G:O5'	32:2a:674:G:H8	2.04	0.41
32:2a:983:A:C8	32:2a:984:A:H4'	2.56	0.41
32:2a:1037:C:O2'	32:2a:1038:A:H5'	2.20	0.41
32:2a:1102:C:H2'	32:2a:1103:G:H8	1.85	0.41
32:2a:1283:U:O2'	32:2a:1284:U:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1296:C:H2'	32:2a:1297:U:C6	2.56	0.41
33:2b:16:HIS:CD2	33:2b:17:PHE:N	2.89	0.41
1:1A:286:G:O2'	1:1A:447:U:OP2	2.32	0.40
1:1A:307:U:H2'	1:1A:308:C:C6	2.56	0.40
1:1A:1387:A:O2'	1:1A:1389:G:OP2	2.30	0.40
1:1A:1714:A:H4'	1:1A:1715:A:O5'	2.20	0.40
1:1A:2086:C:H2'	1:1A:2087:C:C6	2.56	0.40
1:1A:2415:C:O3'	11:1P:77:ARG:NH2	2.54	0.40
1:1A:2811:A:N3	1:1A:2903:U:H1'	2.35	0.40
5:1F:101:LEU:O	5:1F:106:ARG:HD3	2.21	0.40
19:1X:31:HIS:HA	19:1X:32:PRO:HD3	1.93	0.40
25:13:7:LYS:NZ	25:13:32:GLN:O	2.54	0.40
26:14:61:ARG:O	26:14:62:ARG:C	2.64	0.40
32:1a:184:G:C6	32:1a:196:G:C6	3.09	0.40
32:1a:369:A:OP1	59:1a:2024:HOH:O	2.22	0.40
32:1a:393:A:H3'	32:1a:393:A:N3	2.36	0.40
32:1a:836:G:O2'	32:1a:837:A:H5'	2.21	0.40
32:1a:1034:C:H2'	32:1a:1035:U:H6	1.86	0.40
32:1a:1165:A:H3'	32:1a:1166:G:C5'	2.51	0.40
32:1a:1296:C:H2'	32:1a:1297:U:C6	2.56	0.40
32:1a:1503:G:P	42:1k:120:ARG:HH22	2.44	0.40
35:1d:171:GLY:C	35:1d:173:TRP:H	2.29	0.40
38:1g:104:LEU:HD13	38:1g:104:LEU:HA	1.84	0.40
39:1h:138:TRP:CD1	39:1h:138:TRP:C	2.99	0.40
45:1n:44:LEU:O	45:1n:44:LEU:HD12	2.21	0.40
46:1o:3:ILE:H	46:1o:3:ILE:HG12	1.60	0.40
46:1o:74:ASP:CG	46:1o:77:ARG:HG3	2.46	0.40
1:2A:195:A:H2'	1:2A:196:C:O4'	2.21	0.40
1:2A:630:A:C6	1:2A:631:A:C6	3.08	0.40
1:2A:673:G:C5	1:2A:674:C:C4	3.09	0.40
1:2A:830:A:H3'	59:2A:3891:HOH:O	2.20	0.40
1:2A:1682:C:H2'	1:2A:1683:A:H8	1.87	0.40
1:2A:1813:A:C2	1:2A:2598:A:C5	3.09	0.40
1:2A:2282:G:H2'	1:2A:2283:U:C6	2.55	0.40
3:2D:13:ARG:HA	3:2D:13:ARG:HD2	1.73	0.40
10:2O:9:GLU:O	10:2O:83:ALA:HA	2.22	0.40
13:2R:92:GLY:HA2	13:2R:94:TYR:CZ	2.56	0.40
16:2U:83:LEU:HD12	16:2U:88:ILE:HD12	2.04	0.40
21:2Z:19:ARG:HH11	21:2Z:19:ARG:HD3	1.75	0.40
25:23:18:ASP:OD1	25:23:18:ASP:N	2.53	0.40
30:28:22:VAL:CG2	30:28:59:LYS:HG3	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:28:33:ASN:HA	30:28:36:LYS:HD2	2.02	0.40
32:2a:228:G:O2'	32:2a:259:A:N1	2.52	0.40
32:2a:507:A:N6	43:2l:92:ASP:HB2	2.28	0.40
32:2a:982:G:H2'	32:2a:982:G:N3	2.36	0.40
32:2a:1043:C:C2	32:2a:1180:G:C2	3.09	0.40
32:2a:1051:G:N7	32:2a:1077:G:C8	2.90	0.40
32:2a:1146:C:C2	32:2a:1156:G:N2	2.89	0.40
32:2a:1295:U:OP1	50:2s:5:LEU:HB2	2.21	0.40
32:2a:1308:C:O5'	52:2u:12:LYS:NZ	2.54	0.40
34:2c:111:LEU:HD23	34:2c:111:LEU:HA	1.76	0.40
44:2m:96:LEU:HD23	44:2m:96:LEU:HA	1.92	0.40
51:2t:54:LYS:HA	51:2t:57:ARG:CZ	2.50	0.40
51:2t:67:ALA:HA	51:2t:72:LEU:O	2.21	0.40
1:1A:454:A:OP2	1:1A:454:A:H8	2.05	0.40
1:1A:878:G:H5'	11:1P:45:LEU:CD2	2.51	0.40
1:1A:1474:G:O2'	1:1A:1475:C:H5'	2.21	0.40
1:1A:1536:G:O2'	3:1D:101:GLU:HB2	2.21	0.40
1:1A:2802:A:H2'	1:1A:2802:A:N3	2.36	0.40
3:1D:123:ALA:HA	3:1D:124:PRO:HD3	1.92	0.40
7:1H:56:SER:OG	7:1H:58:GLU:HG2	2.22	0.40
12:1Q:7:MET:HB2	12:1Q:7:MET:HE3	1.49	0.40
12:1Q:42:ILE:HG12	12:1Q:103:MET:HE1	2.02	0.40
32:1a:125:A:O2'	32:1a:126:C:O5'	2.33	0.40
32:1a:180:A:H2'	32:1a:181:C:C6	2.57	0.40
32:1a:202:A:C2	32:1a:219:U:H1'	2.56	0.40
32:1a:566:U:OP1	46:1o:64:ARG:NH1	2.54	0.40
32:1a:911:G:C6	32:1a:1368:G:C6	3.09	0.40
32:1a:1100:G:H5"	40:1i:104:ARG:HH21	1.86	0.40
32:1a:1195:A:C5	32:1a:1197:G:C5	3.09	0.40
33:1b:92:TYR:CE1	33:1b:94:ASN:HB2	2.56	0.40
33:1b:145:LEU:HD12	33:1b:149:LEU:HD12	2.03	0.40
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	2.02	0.40
39:1h:36:LEU:HD23	39:1h:36:LEU:HA	1.88	0.40
50:1s:33:THR:OG1	50:1s:34:TRP:N	2.54	0.40
50:1s:52:TYR:HA	50:1s:56:GLN:O	2.20	0.40
1:2A:332:G:C5	1:2A:353:A:C6	3.10	0.40
1:2A:466:U:H2'	1:2A:467:G:C8	2.57	0.40
1:2A:591:U:C4	1:2A:592:G:C6	3.09	0.40
1:2A:1104:G:H5'	1:2A:1105:U:OP2	2.22	0.40
1:2A:1675:G:H2'	1:2A:1676:C:C6	2.56	0.40
4:2E:188:VAL:HA	4:2E:189:PRO:HD3	1.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:109:PHE:HB2	7:2H:111:HIS:O	2.22	0.40
11:2P:120:ALA:HB1	11:2P:138:LEU:HA	2.04	0.40
12:2Q:38:GLU:OE2	12:2Q:128:LYS:N	2.35	0.40
12:2Q:84:GLY:O	12:2Q:85:LYS:HB2	2.22	0.40
18:2W:51:LEU:HD23	18:2W:105:VAL:HG11	2.03	0.40
18:2W:83:LYS:O	18:2W:84:ARG:HD3	2.21	0.40
22:20:82:ARG:HA	22:20:83:PRO:HD3	1.64	0.40
24:22:51:ARG:HH11	24:22:51:ARG:HG3	1.86	0.40
32:2a:288:G:N7	32:2a:289:G:H1'	2.36	0.40
32:2a:504:A:OP2	59:2a:3339:HOH:O	2.22	0.40
32:2a:729:C:H2'	32:2a:730:A:H8	1.85	0.40
32:2a:1305:G:H4'	32:2a:1345:C:C2	2.56	0.40
32:2a:1385:C:O2	32:2a:1478:A:N1	2.54	0.40
35:2d:67:ILE:O	35:2d:114:ARG:HD2	2.22	0.40
36:2e:36:ASP:C	36:2e:38:GLN:N	2.72	0.40
37:2f:35:ALA:HA	37:2f:67:MET:HB3	2.04	0.40
38:2g:26:PHE:HD2	38:2g:101:LEU:HD22	1.87	0.40
38:2g:66:VAL:O	38:2g:70:LYS:HG3	2.21	0.40
49:2r:58:LEU:HD13	49:2r:58:LEU:HA	1.92	0.40
1:1A:75:C:OP1	24:12:59:ARG:HD3	2.21	0.40
1:1A:955:A:N1	1:1A:2288:G:H1'	2.36	0.40
1:1A:1897:A:H2'	1:1A:1898:A:C8	2.56	0.40
1:1A:2206:C:O2'	1:1A:2207:G:H5'	2.22	0.40
4:1E:175:VAL:HB	4:1E:182:LEU:HD12	2.03	0.40
11:1P:83:VAL:HG23	11:1P:87:ASP:HB2	2.03	0.40
20:1Y:90:LEU:HD12	20:1Y:90:LEU:HA	1.88	0.40
29:17:3:ARG:HD3	29:17:3:ARG:HA	1.91	0.40
32:1a:353:G:O2'	32:1a:354:U:H5'	2.21	0.40
32:1a:443:A:P	32:1a:470:G:H22	2.44	0.40
32:1a:799:A:N7	32:1a:1487:C:O2'	2.46	0.40
32:1a:931:G:C5'	32:1a:943:A:H61	2.35	0.40
32:1a:982:G:N2	32:1a:1021:C:C4	2.90	0.40
32:1a:1122:G:N2	32:1a:1126:G:C6	2.89	0.40
39:1h:87:SER:HA	39:1h:93:VAL:HG23	2.02	0.40
1:2A:29:G:C6	1:2A:30:C:C4	3.08	0.40
1:2A:384:G:O2'	1:2A:385:U:H5'	2.21	0.40
1:2A:792:A:H2'	1:2A:2623:C:H5"	2.02	0.40
1:2A:996:G:C6	1:2A:1010:G:C6	3.10	0.40
1:2A:1100:G:H3'	1:2A:1101:G:H8	1.86	0.40
1:2A:1596:C:H2'	1:2A:1597:C:C6	2.56	0.40
1:2A:1715:A:H5"	1:2A:2561:G:OP1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2700:U:OP2	1:2A:2731:G:N2	2.53	0.40
1:2A:2854:G:H2'	1:2A:2855:G:H8	1.86	0.40
3:2D:245:PRO:HA	3:2D:246:PRO:HD3	1.92	0.40
5:2F:102:PRO:O	5:2F:106:ARG:HG2	2.22	0.40
5:2F:129:PHE:O	5:2F:132:VAL:HG13	2.19	0.40
7:2H:123:PHE:CE1	7:2H:133:VAL:HG22	2.56	0.40
10:2O:29:ASN:N	10:2O:29:ASN:OD1	2.51	0.40
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	2.02	0.40
18:2W:4:LYS:CB	18:2W:106:ILE:HG12	2.47	0.40
18:2W:54:ALA:HB1	18:2W:107:LEU:HD22	2.02	0.40
24:22:16:LEU:HB3	24:22:20:GLU:HB2	2.03	0.40
32:2a:298:G:O2'	32:2a:540:C:H5"	2.21	0.40
32:2a:567:A:H2'	32:2a:568:G:O4'	2.22	0.40
32:2a:674:G:C6	32:2a:675:G:C6	3.09	0.40
32:2a:1254:G:C5	32:2a:1255:G:C8	3.10	0.40
32:2a:1309:C:H2'	32:2a:1310:C:H6	1.85	0.40
33:2b:25:ASN:HA	33:2b:26:PRO:HD3	1.89	0.40
36:2e:99:GLY:O	36:2e:117:ASP:HA	2.22	0.40
46:2o:39:LEU:HD23	46:2o:39:LEU:HA	1.90	0.40
46:2o:82:ILE:O	46:2o:86:GLY:N	2.55	0.40
1:1A:2341:G:H2'	1:1A:2342:G:O4'	2.22	0.40
1:1A:2898:C:H2'	1:1A:2899:G:O4'	2.20	0.40
3:1D:25:THR:HG21	3:1D:113:VAL:HG11	2.04	0.40
3:1D:38:LYS:HE3	3:1D:39:LYS:O	2.21	0.40
3:1D:72:LYS:HE3	3:1D:75:ILE:HD12	2.04	0.40
4:1E:82:ARG:HG2	4:1E:83:ASP:H	1.85	0.40
5:1F:150:GLY:HA2	5:1F:172:TRP:CE3	2.56	0.40
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.21	0.40
6:1G:111:LEU:HB2	6:1G:112:PRO:HD3	2.03	0.40
10:1O:80:ASP:OD1	15:1T:64:ARG:NH2	2.54	0.40
11:1P:59:LEU:HD21	30:18:10:ALA:HA	2.04	0.40
26:14:35:VAL:HG22	26:14:36:CYS:N	2.36	0.40
32:1a:220:C:H2'	32:1a:221:C:C6	2.56	0.40
32:1a:753:G:H4'	32:1a:1491:A:H4'	2.02	0.40
32:1a:1048:U:OP1	32:1a:1048:U:H4'	2.21	0.40
32:1a:1197:G:C2	32:1a:1198:G:C8	3.09	0.40
32:1a:1325:G:O2'	40:1i:121:ARG:HD2	2.21	0.40
32:1a:1412:C:H2'	32:1a:1413:C:H6	1.86	0.40
33:1b:19:HIS:HA	33:1b:39:ILE:HG21	2.01	0.40
34:1c:114:PRO:C	34:1c:118:GLN:HE21	2.22	0.40
38:1g:151:TYR:OH	42:1k:54:ARG:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:57:ARG:HH12	47:1p:79:VAL:CA	2.34	0.40
51:1t:48:LYS:HA	51:1t:48:LYS:HD3	1.82	0.40
1:2A:798:A:P	29:27:3:ARG:HH22	2.44	0.40
1:2A:1041:A:N6	1:2A:1205:G:C6	2.89	0.40
1:2A:1054:A:H8	1:2A:1054:A:O5'	2.05	0.40
1:2A:1228:G:OP1	25:23:30:ARG:NH1	2.49	0.40
1:2A:1399:A:H2'	1:2A:1400:G:O4'	2.21	0.40
1:2A:2288:G:H2'	1:2A:2289:A:H5"	2.04	0.40
1:2A:2343:U:H5'	1:2A:2347:A:N6	2.36	0.40
2:2B:13:A:N1	2:2B:69:G:O2'	2.45	0.40
5:2F:23:ASP:O	5:2F:24:LEU:HD13	2.21	0.40
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.21	0.40
13:2R:28:LEU:HD23	13:2R:28:LEU:HA	1.90	0.40
14:2S:3:ARG:HH11	14:2S:3:ARG:HG2	1.86	0.40
16:2U:76:TYR:CE2	16:2U:80:ILE:HD11	2.56	0.40
32:2a:156:A:H2'	32:2a:157:A:C8	2.57	0.40
32:2a:428:A:C8	32:2a:429:C:C5	3.10	0.40
32:2a:919:G:C2	32:2a:1325:G:C2	3.09	0.40
32:2a:969:U:H2'	32:2a:1194:U:C4	2.56	0.40
1:1A:173:U:H2'	1:1A:174:G:H8	1.86	0.40
1:1A:1223:C:O2'	1:1A:1224:C:H5'	2.20	0.40
1:1A:1591:A:H2'	1:1A:1592:C:O4'	2.22	0.40
6:1G:15:VAL:HG13	6:1G:175:LEU:HB3	2.04	0.40
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.46	0.40
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	2.03	0.40
21:1Z:102:LEU:HD13	21:1Z:123:ASP:HA	2.04	0.40
32:1a:916:A:C6	32:1a:917:G:C5	3.09	0.40
32:1a:1040:G:H2'	32:1a:1041:G:O4'	2.21	0.40
32:1a:1234:A:H2'	32:1a:1235:G:O4'	2.22	0.40
33:1b:80:ILE:O	33:1b:84:GLU:HG2	2.21	0.40
34:1c:16:ARG:HE	34:1c:16:ARG:HB3	1.73	0.40
35:1d:3:ARG:O	35:1d:5:ILE:HG22	2.22	0.40
37:1f:61:LEU:HB3	37:1f:63:TYR:HE1	1.85	0.40
44:1m:19:LEU:HD12	44:1m:19:LEU:HA	1.91	0.40
45:1n:53:LEU:HA	45:1n:54:PRO:HD2	1.97	0.40
50:1s:23:ASN:HA	50:1s:27:GLU:OE1	2.21	0.40
1:2A:437:G:C5	11:2P:72:PRO:HB3	2.56	0.40
1:2A:673:G:C6	1:2A:674:C:C4	3.09	0.40
1:2A:828:A:N1	3:2D:226:MET:HE2	2.37	0.40
1:2A:901:G:H2'	1:2A:902:C:C6	2.56	0.40
1:2A:1048:G:N2	1:2A:1198:C:C2	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1699:G:C6	13:2R:9:LYS:HB2	2.56	0.40
1:2A:1834:C:O5'	1:2A:1834:C:H6	2.05	0.40
4:2E:55:ASN:HA	4:2E:56:PRO:HD3	1.95	0.40
6:2G:108:ASN:O	26:24:37:SER:N	2.51	0.40
10:2O:108:GLU:H	10:2O:108:GLU:HG3	1.60	0.40
11:2P:85:LEU:HG	11:2P:115:LEU:O	2.22	0.40
14:2S:88:ASP:C	14:2S:90:GLY:H	2.30	0.40
19:2X:47:PHE:O	19:2X:49:VAL:HG13	2.21	0.40
21:2Z:97:GLU:HA	21:2Z:126:VAL:O	2.22	0.40
32:2a:156:A:H2'	32:2a:157:A:H8	1.86	0.40
32:2a:566:U:OP1	46:2o:68:ARG:NH1	2.42	0.40
32:2a:811:U:H5"	32:2a:812:A:OP2	2.22	0.40
32:2a:1084:A:H4'	32:2a:1085:A:O5'	2.21	0.40
32:2a:1380:C:O2	32:2a:1380:C:H2'	2.22	0.40
32:2a:1393:G:H2'	32:2a:1394:C:H6	1.85	0.40
32:2a:1477:A:H1'	32:2a:1498:G:OP1	2.22	0.40
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.21	0.40
40:2i:96:LEU:HD23	40:2i:96:LEU:HA	1.99	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	258 (94%)	15 (6%)	0	100	100
3	2D	273/276 (99%)	250 (92%)	21 (8%)	2 (1%)	18	47
4	1E	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	24	55
4	2E	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	24	55
5	1F	201/210 (96%)	190 (94%)	10 (5%)	1 (0%)	24	55
5	2F	201/210 (96%)	192 (96%)	8 (4%)	1 (0%)	24	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
6	1G	179/182 (98%)	161 (90%)	14 (8%)	4 (2%)	5 19
6	2G	179/182 (98%)	152 (85%)	22 (12%)	5 (3%)	4 14
7	1H	172/180 (96%)	158 (92%)	13 (8%)	1 (1%)	21 51
7	2H	172/180 (96%)	157 (91%)	13 (8%)	2 (1%)	10 34
8	1I	144/148 (97%)	119 (83%)	24 (17%)	1 (1%)	18 47
8	2I	144/148 (97%)	117 (81%)	26 (18%)	1 (1%)	18 47
9	1N	138/140 (99%)	135 (98%)	3 (2%)	0	100 100
9	2N	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	18 47
10	1O	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	16 44
10	2O	120/122 (98%)	116 (97%)	3 (2%)	1 (1%)	16 44
11	1P	147/150 (98%)	139 (95%)	7 (5%)	1 (1%)	18 47
11	2P	147/150 (98%)	135 (92%)	10 (7%)	2 (1%)	9 30
12	1Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
12	2Q	139/141 (99%)	127 (91%)	10 (7%)	2 (1%)	9 30
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100 100
13	2R	116/118 (98%)	111 (96%)	5 (4%)	0	100 100
14	1S	108/112 (96%)	101 (94%)	7 (6%)	0	100 100
14	2S	108/112 (96%)	99 (92%)	8 (7%)	1 (1%)	14 41
15	1T	129/146 (88%)	123 (95%)	5 (4%)	1 (1%)	16 44
15	2T	129/146 (88%)	125 (97%)	4 (3%)	0	100 100
16	1U	114/118 (97%)	111 (97%)	3 (3%)	0	100 100
16	2U	114/118 (97%)	111 (97%)	3 (3%)	0	100 100
17	1V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12 38
17	2V	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12 38
18	1W	110/113 (97%)	108 (98%)	2 (2%)	0	100 100
18	2W	110/113 (97%)	109 (99%)	1 (1%)	0	100 100
19	1X	93/96 (97%)	90 (97%)	3 (3%)	0	100 100
19	2X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11 36
20	1Y	105/110 (96%)	91 (87%)	12 (11%)	2 (2%)	6 22
20	2Y	105/110 (96%)	94 (90%)	10 (10%)	1 (1%)	12 38
21	1Z	184/206 (89%)	170 (92%)	13 (7%)	1 (0%)	24 55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
21	2Z	184/206 (89%)	166 (90%)	14 (8%)	4 (2%)	5 19
22	10	73/85 (86%)	69 (94%)	3 (4%)	1 (1%)	9 30
22	20	73/85 (86%)	70 (96%)	3 (4%)	0	100 100
23	11	95/98 (97%)	94 (99%)	1 (1%)	0	100 100
23	21	95/98 (97%)	93 (98%)	2 (2%)	0	100 100
24	12	68/72 (94%)	66 (97%)	2 (3%)	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%)	54 (95%)	3 (5%)	0	100 100
26	14	67/71 (94%)	49 (73%)	9 (13%)	9 (13%)	0 0
26	24	67/71 (94%)	49 (73%)	12 (18%)	6 (9%)	0 1
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
28	16	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
28	26	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
29	17	46/49 (94%)	46 (100%)	0	0	100 100
29	27	46/49 (94%)	45 (98%)	0	1 (2%)	5 19
30	18	62/65 (95%)	60 (97%)	2 (3%)	0	100 100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100 100
31	19	35/37 (95%)	35 (100%)	0	0	100 100
31	29	35/37 (95%)	35 (100%)	0	0	100 100
33	1b	229/256 (90%)	178 (78%)	42 (18%)	9 (4%)	2 8
33	2b	229/256 (90%)	183 (80%)	41 (18%)	5 (2%)	5 19
34	1c	204/239 (85%)	169 (83%)	33 (16%)	2 (1%)	12 38
34	2c	204/239 (85%)	167 (82%)	34 (17%)	3 (2%)	8 28
35	1d	206/209 (99%)	179 (87%)	25 (12%)	2 (1%)	12 38
35	2d	206/209 (99%)	182 (88%)	18 (9%)	6 (3%)	3 13
36	1e	146/162 (90%)	130 (89%)	13 (9%)	3 (2%)	5 20
36	2e	146/162 (90%)	130 (89%)	14 (10%)	2 (1%)	9 30
37	1f	98/101 (97%)	91 (93%)	6 (6%)	1 (1%)	12 38
37	2f	98/101 (97%)	92 (94%)	5 (5%)	1 (1%)	12 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	1g	153/156 (98%)	136 (89%)	17 (11%)	0	100	100
38	2g	153/156 (98%)	134 (88%)	19 (12%)	0	100	100
39	1h	135/138 (98%)	129 (96%)	6 (4%)	0	100	100
39	2h	135/138 (98%)	127 (94%)	8 (6%)	0	100	100
40	1i	125/128 (98%)	105 (84%)	15 (12%)	5 (4%)	2	8
40	2i	125/128 (98%)	104 (83%)	14 (11%)	7 (6%)	1	4
41	1j	95/105 (90%)	77 (81%)	12 (13%)	6 (6%)	1	3
41	2j	94/105 (90%)	81 (86%)	11 (12%)	2 (2%)	5	20
42	1k	112/129 (87%)	97 (87%)	13 (12%)	2 (2%)	6	23
42	2k	112/129 (87%)	100 (89%)	11 (10%)	1 (1%)	14	41
43	1l	120/132 (91%)	112 (93%)	8 (7%)	0	100	100
43	2l	120/132 (91%)	111 (92%)	9 (8%)	0	100	100
44	1m	116/126 (92%)	100 (86%)	13 (11%)	3 (3%)	4	15
44	2m	114/126 (90%)	96 (84%)	15 (13%)	3 (3%)	4	15
45	1n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	7	25
45	2n	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
46	1o	86/89 (97%)	75 (87%)	10 (12%)	1 (1%)	10	34
46	2o	86/89 (97%)	77 (90%)	7 (8%)	2 (2%)	5	18
47	1p	80/88 (91%)	67 (84%)	11 (14%)	2 (2%)	4	16
47	2p	80/88 (91%)	68 (85%)	12 (15%)	0	100	100
48	1q	97/105 (92%)	90 (93%)	6 (6%)	1 (1%)	12	38
48	2q	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
49	1r	66/88 (75%)	58 (88%)	6 (9%)	2 (3%)	3	12
49	2r	66/88 (75%)	60 (91%)	5 (8%)	1 (2%)	8	28
50	1s	82/93 (88%)	70 (85%)	12 (15%)	0	100	100
50	2s	81/93 (87%)	67 (83%)	14 (17%)	0	100	100
51	1t	94/106 (89%)	81 (86%)	11 (12%)	2 (2%)	5	20
51	2t	94/106 (89%)	81 (86%)	10 (11%)	3 (3%)	3	11
52	1u	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2	6
52	2u	21/27 (78%)	17 (81%)	3 (14%)	1 (5%)	2	6
55	1z	10/14 (71%)	6 (60%)	1 (10%)	3 (30%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
55	2z	10/14 (71%)	8 (80%)	1 (10%)	1 (10%)	0 1
All	All	11430/12156 (94%)	10379 (91%)	909 (8%)	142 (1%)	10 34

All (142) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	1G	47	LYS
6	1G	50	ALA
6	1G	51	ARG
6	1G	126	ASP
7	1H	126	PRO
17	1V	79	VAL
26	14	45	GLY
26	14	46	GLN
26	14	47	GLN
26	14	48	ARG
26	14	50	VAL
26	14	53	GLU
26	14	62	ARG
26	14	68	ARG
33	1b	16	HIS
33	1b	17	PHE
33	1b	121	LEU
33	1b	125	PRO
40	1i	54	ASP
41	1j	55	LYS
41	1j	56	HIS
41	1j	82	ILE
44	1m	4	ILE
45	1n	3	ARG
46	1o	19	PRO
47	1p	76	GLN
48	1q	68	ARG
55	1z	10	PRO
55	1z	11	ARG
3	2D	239	ARG
6	2G	14	GLU
6	2G	47	LYS
6	2G	50	ALA
6	2G	81	LYS
6	2G	126	ASP
7	2H	55	PRO

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Mol	Chain	Res	Type
7	2H	126	PRO
8	2I	10	GLU
21	2Z	128	VAL
21	2Z	135	GLU
26	24	47	GLN
26	24	50	VAL
26	24	68	ARG
29	27	46	VAL
33	2b	17	PHE
33	2b	230	VAL
35	2d	47	ARG
41	2j	78	ASN
42	2k	49	GLY
55	2z	11	ARG
5	1F	130	ALA
10	1O	5	GLN
21	1Z	93	ASP
33	1b	22	LYS
33	1b	23	ARG
33	1b	231	GLU
34	1c	205	GLY
36	1e	98	THR
40	1i	44	VAL
40	1i	56	LEU
41	1j	31	GLY
42	1k	49	GLY
49	1r	32	ARG
51	1t	47	GLY
3	2D	3	VAL
5	2F	130	ALA
10	2O	5	GLN
12	2Q	60	ARG
14	2S	57	LYS
17	2V	79	VAL
20	2Y	54	LYS
21	2Z	93	ASP
26	24	45	GLY
26	24	54	GLY
33	2b	93	VAL
33	2b	97	TRP
33	2b	125	PRO
35	2d	20	TYR

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Mol	Chain	Res	Type
36	2e	37	ARG
44	2m	21	TYR
44	2m	106	ASN
49	2r	25	THR
51	2t	47	GLY
51	2t	99	LEU
52	2u	3	LYS
4	1E	52	LEU
20	1Y	53	PRO
20	1Y	54	LYS
26	14	49	PHE
33	1b	52	GLU
36	1e	85	GLY
41	1j	78	ASN
44	1m	21	TYR
47	1p	77	ALA
49	1r	25	THR
52	1u	3	LYS
4	2E	52	LEU
26	24	62	ARG
34	2c	66	VAL
35	2d	46	LYS
35	2d	129	ASN
40	2i	56	LEU
46	2o	19	PRO
11	1P	122	PRO
37	1f	40	VAL
55	1z	9	ARG
9	2N	2	LYS
11	2P	45	LEU
12	2Q	59	ARG
40	2i	54	ASP
41	2j	82	ILE
51	2t	10	LEU
8	1I	107	VAL
34	1c	66	VAL
51	1t	100	ILE
11	2P	122	PRO
36	2e	69	VAL
40	2i	96	LEU
46	2o	88	ARG
33	1b	128	GLU

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Mol	Chain	Res	Type
36	1e	69	VAL
40	1i	11	LYS
40	1i	96	LEU
44	1m	67	GLU
21	2Z	127	LYS
34	2c	91	LEU
35	2d	45	GLN
37	2f	40	VAL
40	2i	11	LYS
19	2X	94	GLY
35	2d	136	PRO
40	2i	44	VAL
44	2m	4	ILE
15	1T	37	GLY
35	1d	8	VAL
35	1d	136	PRO
42	1k	105	VAL
40	2i	39	GLY
40	2i	41	VAL
22	10	13	GLY
41	1j	77	PRO
34	2c	108	ASN

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%)	188 (87%)	27 (13%)	4 15
3	2D	216/218 (99%)	186 (86%)	30 (14%)	3 12
4	1E	164/166 (99%)	139 (85%)	25 (15%)	3 10
4	2E	164/166 (99%)	138 (84%)	26 (16%)	2 9
5	1F	160/166 (96%)	135 (84%)	25 (16%)	2 9
5	2F	159/166 (96%)	136 (86%)	23 (14%)	3 11
6	1G	143/156 (92%)	124 (87%)	19 (13%)	4 14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	2G	142/156 (91%)	115 (81%)	27 (19%)	1 5
7	1H	144/148 (97%)	129 (90%)	15 (10%)	7 22
7	2H	144/148 (97%)	125 (87%)	19 (13%)	4 14
8	1I	110/124 (89%)	86 (78%)	24 (22%)	1 3
8	2I	104/124 (84%)	88 (85%)	16 (15%)	2 10
9	1N	118/119 (99%)	101 (86%)	17 (14%)	3 11
9	2N	118/119 (99%)	100 (85%)	18 (15%)	3 10
10	1O	100/100 (100%)	91 (91%)	9 (9%)	9 28
10	2O	100/100 (100%)	90 (90%)	10 (10%)	7 24
11	1P	116/116 (100%)	100 (86%)	16 (14%)	3 12
11	2P	115/116 (99%)	98 (85%)	17 (15%)	3 10
12	1Q	111/111 (100%)	99 (89%)	12 (11%)	6 21
12	2Q	111/111 (100%)	101 (91%)	10 (9%)	9 28
13	1R	101/101 (100%)	81 (80%)	20 (20%)	1 5
13	2R	101/101 (100%)	81 (80%)	20 (20%)	1 5
14	1S	87/88 (99%)	77 (88%)	10 (12%)	5 18
14	2S	85/88 (97%)	65 (76%)	20 (24%)	1 3
15	1T	115/127 (91%)	99 (86%)	16 (14%)	3 12
15	2T	113/127 (89%)	97 (86%)	16 (14%)	3 12
16	1U	93/94 (99%)	83 (89%)	10 (11%)	6 21
16	2U	93/94 (99%)	84 (90%)	9 (10%)	8 25
17	1V	80/82 (98%)	65 (81%)	15 (19%)	1 5
17	2V	80/82 (98%)	69 (86%)	11 (14%)	3 12
18	1W	90/92 (98%)	80 (89%)	10 (11%)	6 20
18	2W	90/92 (98%)	80 (89%)	10 (11%)	6 20
19	1X	77/78 (99%)	70 (91%)	7 (9%)	9 28
19	2X	77/78 (99%)	72 (94%)	5 (6%)	15 43
20	1Y	85/91 (93%)	76 (89%)	9 (11%)	6 22
20	2Y	85/91 (93%)	78 (92%)	7 (8%)	10 33
21	1Z	159/179 (89%)	140 (88%)	19 (12%)	5 17
21	2Z	156/179 (87%)	139 (89%)	17 (11%)	6 21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
22	10	60/67 (90%)	57 (95%)	3 (5%)	22 54
22	20	60/67 (90%)	57 (95%)	3 (5%)	22 54
23	11	80/83 (96%)	70 (88%)	10 (12%)	4 15
23	21	80/83 (96%)	68 (85%)	12 (15%)	3 10
24	12	65/67 (97%)	57 (88%)	8 (12%)	4 16
24	22	65/67 (97%)	57 (88%)	8 (12%)	4 16
25	13	51/52 (98%)	42 (82%)	9 (18%)	2 7
25	23	50/52 (96%)	45 (90%)	5 (10%)	7 24
26	14	60/63 (95%)	51 (85%)	9 (15%)	3 10
26	24	53/63 (84%)	46 (87%)	7 (13%)	4 14
27	15	50/52 (96%)	45 (90%)	5 (10%)	7 24
27	25	50/52 (96%)	44 (88%)	6 (12%)	5 17
28	16	51/52 (98%)	48 (94%)	3 (6%)	18 48
28	26	50/52 (96%)	43 (86%)	7 (14%)	3 12
29	17	41/42 (98%)	37 (90%)	4 (10%)	7 25
29	27	41/42 (98%)	38 (93%)	3 (7%)	13 38
30	18	54/55 (98%)	50 (93%)	4 (7%)	13 37
30	28	54/55 (98%)	52 (96%)	2 (4%)	30 65
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 73
31	29	34/34 (100%)	32 (94%)	2 (6%)	18 48
33	1b	177/220 (80%)	141 (80%)	36 (20%)	1 4
33	2b	158/220 (72%)	127 (80%)	31 (20%)	1 5
34	1c	127/188 (68%)	115 (91%)	12 (9%)	8 27
34	2c	108/188 (57%)	90 (83%)	18 (17%)	2 8
35	1d	161/181 (89%)	139 (86%)	22 (14%)	3 13
35	2d	164/181 (91%)	138 (84%)	26 (16%)	2 9
36	1e	113/123 (92%)	96 (85%)	17 (15%)	3 10
36	2e	106/123 (86%)	88 (83%)	18 (17%)	2 7
37	1f	83/90 (92%)	75 (90%)	8 (10%)	8 26
37	2f	86/90 (96%)	77 (90%)	9 (10%)	6 22
38	1g	111/127 (87%)	93 (84%)	18 (16%)	2 8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	2g	107/127 (84%)	91 (85%)	16 (15%)	3 10
39	1h	114/119 (96%)	96 (84%)	18 (16%)	2 9
39	2h	111/119 (93%)	95 (86%)	16 (14%)	3 11
40	1i	89/99 (90%)	72 (81%)	17 (19%)	1 5
40	2i	80/99 (81%)	71 (89%)	9 (11%)	5 19
41	1j	60/92 (65%)	48 (80%)	12 (20%)	1 4
41	2j	62/92 (67%)	46 (74%)	16 (26%)	0 2
42	1k	82/99 (83%)	74 (90%)	8 (10%)	7 25
42	2k	82/99 (83%)	71 (87%)	11 (13%)	4 13
43	1l	95/109 (87%)	84 (88%)	11 (12%)	5 18
43	2l	94/109 (86%)	86 (92%)	8 (8%)	10 31
44	1m	90/101 (89%)	81 (90%)	9 (10%)	7 24
44	2m	87/101 (86%)	81 (93%)	6 (7%)	14 41
45	1n	47/50 (94%)	38 (81%)	9 (19%)	1 5
45	2n	43/50 (86%)	35 (81%)	8 (19%)	1 5
46	1o	75/80 (94%)	67 (89%)	8 (11%)	6 21
46	2o	78/80 (98%)	67 (86%)	11 (14%)	3 12
47	1p	67/74 (90%)	55 (82%)	12 (18%)	2 6
47	2p	68/74 (92%)	59 (87%)	9 (13%)	4 14
48	1q	91/97 (94%)	83 (91%)	8 (9%)	9 29
48	2q	94/97 (97%)	86 (92%)	8 (8%)	10 31
49	1r	59/77 (77%)	48 (81%)	11 (19%)	1 5
49	2r	59/77 (77%)	48 (81%)	11 (19%)	1 5
50	1s	65/80 (81%)	59 (91%)	6 (9%)	8 27
50	2s	67/80 (84%)	56 (84%)	11 (16%)	2 8
51	1t	66/82 (80%)	56 (85%)	10 (15%)	3 10
51	2t	71/82 (87%)	67 (94%)	4 (6%)	19 50
52	1u	16/22 (73%)	16 (100%)	0	100 100
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19 50
55	1z	12/14 (86%)	11 (92%)	1 (8%)	10 32
55	2z	12/14 (86%)	11 (92%)	1 (8%)	10 32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9159/10094 (91%)	7931 (87%)	1228 (13%)	4 13

All (1228) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	34	VAL
3	1D	37	LEU
3	1D	39	LYS
3	1D	61	LEU
3	1D	94	LEU
3	1D	99	ASP
3	1D	103	ARG
3	1D	111	LEU
3	1D	113	VAL
3	1D	138	VAL
3	1D	142	VAL
3	1D	150	LYS
3	1D	155	LEU
3	1D	162	SER
3	1D	164	GLN
3	1D	165	ILE
3	1D	173	VAL
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	257	LEU
3	1D	259	THR
3	1D	260	ARG
3	1D	275	LYS
4	1E	7	VAL
4	1E	9	VAL
4	1E	12	THR
4	1E	21	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	40	GLU
4	1E	49	LEU
4	1E	54	GLN
4	1E	73	GLU

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Mol	Chain	Res	Type
4	1E	75	VAL
4	1E	77	ILE
4	1E	78	LEU
4	1E	79	ARG
4	1E	82	ARG
4	1E	111	ARG
4	1E	116	VAL
4	1E	119	ARG
4	1E	144	ARG
4	1E	154	LYS
4	1E	167	VAL
4	1E	170	LEU
4	1E	175	VAL
4	1E	181	LEU
4	1E	184	VAL
5	1F	12	LEU
5	1F	17	ARG
5	1F	20	LEU
5	1F	24	LEU
5	1F	28	ILE
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	108	LYS
5	1F	110	LEU
5	1F	112	MET
5	1F	125	LEU
5	1F	132	VAL
5	1F	140	LEU
5	1F	162	LEU
5	1F	165	ARG
5	1F	169	ASN
5	1F	170	LEU
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU
5	1F	201	VAL
6	1G	3	LEU
6	1G	5	VAL

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Mol	Chain	Res	Type
6	1G	7	LEU
6	1G	31	VAL
6	1G	35	GLU
6	1G	43	LEU
6	1G	45	GLU
6	1G	60	LEU
6	1G	82	LEU
6	1G	88	ILE
6	1G	139	LEU
6	1G	140	ILE
6	1G	143	GLU
6	1G	148	MET
6	1G	153	ARG
6	1G	159	VAL
6	1G	165	THR
6	1G	170	ARG
6	1G	175	LEU
7	1H	13	LYS
7	1H	15	VAL
7	1H	24	VAL
7	1H	25	LYS
7	1H	43	VAL
7	1H	45	VAL
7	1H	49	VAL
7	1H	69	ARG
7	1H	71	LEU
7	1H	80	SER
7	1H	84	SER
7	1H	98	LEU
7	1H	124	GLU
7	1H	129	THR
7	1H	139	GLN
8	1I	9	LEU
8	1I	10	GLU
8	1I	20	ASP
8	1I	38	LEU
8	1I	43	ASN
8	1I	44	LEU
8	1I	47	LEU
8	1I	57	ARG
8	1I	61	ARG
8	1I	64	GLU

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Mol	Chain	Res	Type
8	1I	66	GLU
8	1I	68	LEU
8	1I	74	ASN
8	1I	75	LEU
8	1I	76	THR
8	1I	77	LEU
8	1I	78	THR
8	1I	87	LYS
8	1I	92	VAL
8	1I	101	LEU
8	1I	108	THR
8	1I	109	ILE
8	1I	116	LEU
8	1I	127	VAL
9	1N	5	VAL
9	1N	8	GLN
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	61	ARG
9	1N	62	VAL
9	1N	65	LYS
9	1N	67	LEU
9	1N	73	THR
9	1N	87	LEU
9	1N	97	ARG
9	1N	99	LEU
9	1N	120	LEU
9	1N	137	LYS
10	1O	8	LEU
10	1O	10	VAL
10	1O	20	MET
10	1O	23	ARG
10	1O	24	VAL
10	1O	45	GLU
10	1O	69	ILE
10	1O	98	VAL
10	1O	105	GLU
11	1P	3	LEU
11	1P	21	ARG

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Mol	Chain	Res	Type
11	1P	55	ARG
11	1P	59	LEU
11	1P	70	GLN
11	1P	75	ILE
11	1P	83	VAL
11	1P	95	VAL
11	1P	98	GLU
11	1P	99	LEU
11	1P	106	LEU
11	1P	112	LEU
11	1P	121	LYS
11	1P	125	VAL
11	1P	148	LEU
11	1P	149	GLU
12	1Q	5	ARG
12	1Q	7	MET
12	1Q	8	LYS
12	1Q	16	ARG
12	1Q	35	VAL
12	1Q	45	GLN
12	1Q	55	VAL
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	81	VAL
12	1Q	109	VAL
12	1Q	110	THR
13	1R	1	MET
13	1R	6	SER
13	1R	18	LEU
13	1R	28	LEU
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	60	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	73	VAL
13	1R	75	LEU
13	1R	79	LEU
13	1R	91	GLN

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Mol	Chain	Res	Type
13	1R	100	LEU
13	1R	102	GLU
13	1R	111	LEU
13	1R	114	VAL
14	1S	3	ARG
14	1S	4	LEU
14	1S	14	VAL
14	1S	20	ARG
14	1S	36	TYR
14	1S	46	VAL
14	1S	50	SER
14	1S	59	LYS
14	1S	69	VAL
14	1S	110	LEU
15	1T	17	THR
15	1T	23	ARG
15	1T	28	VAL
15	1T	34	VAL
15	1T	39	ARG
15	1T	49	VAL
15	1T	59	THR
15	1T	64	ARG
15	1T	67	SER
15	1T	78	LEU
15	1T	85	LYS
15	1T	89	VAL
15	1T	96	ARG
15	1T	107	ASP
15	1T	108	ARG
15	1T	118	ARG
16	1U	5	LYS
16	1U	8	VAL
16	1U	36	ARG
16	1U	60	LEU
16	1U	74	LEU
16	1U	83	LEU
16	1U	95	LEU
16	1U	104	GLN
16	1U	108	GLU
16	1U	117	GLN
17	1V	18	LEU
17	1V	21	ARG

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Mol	Chain	Res	Type
17	1V	28	GLU
17	1V	43	GLU
17	1V	46	VAL
17	1V	51	VAL
17	1V	52	VAL
17	1V	57	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	73	SER
17	1V	79	VAL
17	1V	95	LEU
17	1V	100	ARG
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	51	LEU
18	1W	78	GLU
18	1W	96	ILE
18	1W	100	THR
18	1W	103	ILE
18	1W	107	LEU
19	1X	35	THR
19	1X	52	VAL
19	1X	70	LEU
19	1X	72	LYS
19	1X	76	ARG
19	1X	88	LYS
19	1X	92	LEU
20	1Y	1	MET
20	1Y	7	VAL
20	1Y	23	ARG
20	1Y	43	ASN
20	1Y	67	LEU
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	90	LEU
20	1Y	92	ASN
21	1Z	11	GLU
21	1Z	18	LEU
21	1Z	31	ARG

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Mol	Chain	Res	Type
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	46	LYS
21	1Z	58	VAL
21	1Z	74	VAL
21	1Z	76	LEU
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	107	THR
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	163	LEU
21	1Z	165	VAL
21	1Z	170	THR
22	10	10	THR
22	10	20	ARG
22	10	82	ARG
23	11	11	ARG
23	11	21	ARG
23	11	23	LYS
23	11	30	VAL
23	11	40	ARG
23	11	50	ARG
23	11	53	VAL
23	11	59	THR
23	11	78	LYS
23	11	95	LEU
24	12	19	VAL
24	12	30	ARG
24	12	32	LEU
24	12	38	GLN
24	12	49	LYS
24	12	53	LEU
24	12	64	LEU
24	12	70	GLN
25	13	3	ARG
25	13	6	VAL
25	13	8	LEU
25	13	17	LYS
25	13	23	LEU

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Mol	Chain	Res	Type
25	13	31	LEU
25	13	38	GLU
25	13	54	VAL
25	13	56	VAL
26	14	14	ILE
26	14	33	VAL
26	14	34	GLU
26	14	49	PHE
26	14	56	VAL
26	14	60	GLN
26	14	63	TYR
26	14	68	ARG
26	14	69	LYS
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
27	15	40	LYS
27	15	57	VAL
28	16	9	LEU
28	16	38	LYS
28	16	48	VAL
29	17	1	MET
29	17	9	ARG
29	17	24	THR
29	17	43	THR
30	18	14	VAL
30	18	23	VAL
30	18	32	LEU
30	18	46	ARG
31	19	17	ILE
33	1b	8	LYS
33	1b	10	LEU
33	1b	11	LEU
33	1b	17	PHE
33	1b	21	ARG
33	1b	32	ILE
33	1b	47	THR
33	1b	48	MET
33	1b	67	THR
33	1b	68	ILE
33	1b	71	VAL
33	1b	74	LYS

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Mol	Chain	Res	Type
33	1b	76	GLN
33	1b	80	ILE
33	1b	82	ARG
33	1b	86	GLU
33	1b	93	VAL
33	1b	112	VAL
33	1b	116	GLU
33	1b	127	ILE
33	1b	128	GLU
33	1b	143	GLU
33	1b	144	ARG
33	1b	145	LEU
33	1b	164	VAL
33	1b	170	GLU
33	1b	179	LYS
33	1b	185	ILE
33	1b	187	LEU
33	1b	190	THR
33	1b	198	ASP
33	1b	208	ILE
33	1b	217	ARG
33	1b	221	LEU
33	1b	223	ILE
33	1b	226	ARG
34	1c	3	ASN
34	1c	15	THR
34	1c	17	ASP
34	1c	32	LEU
34	1c	47	LEU
34	1c	70	VAL
34	1c	82	GLU
34	1c	115	LEU
34	1c	131	ARG
34	1c	150	LYS
34	1c	151	VAL
34	1c	188	LEU
35	1d	3	ARG
35	1d	5	ILE
35	1d	15	GLU
35	1d	17	VAL
35	1d	31	CYS
35	1d	45	GLN

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Mol	Chain	Res	Type
35	1d	49	ARG
35	1d	58	LEU
35	1d	70	ILE
35	1d	101	LEU
35	1d	104	VAL
35	1d	107	ARG
35	1d	108	LEU
35	1d	112	VAL
35	1d	122	ARG
35	1d	155	LEU
35	1d	162	LEU
35	1d	168	ARG
35	1d	188	LEU
35	1d	194	LEU
35	1d	196	LEU
35	1d	200	GLU
36	1e	12	LEU
36	1e	18	ARG
36	1e	24	ARG
36	1e	31	LEU
36	1e	41	VAL
36	1e	47	LYS
36	1e	67	VAL
36	1e	73	ASN
36	1e	75	THR
36	1e	79	GLU
36	1e	80	ILE
36	1e	81	GLU
36	1e	83	GLU
36	1e	91	LEU
36	1e	100	VAL
36	1e	147	ASP
36	1e	148	VAL
37	1f	40	VAL
37	1f	43	LEU
37	1f	46	ARG
37	1f	61	LEU
37	1f	65	VAL
37	1f	72	VAL
37	1f	74	ASP
37	1f	75	LEU
38	1g	8	GLU

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Mol	Chain	Res	Type
38	1g	12	LEU
38	1g	13	GLN
38	1g	15	ASP
38	1g	16	LEU
38	1g	21	VAL
38	1g	38	LEU
38	1g	50	ILE
38	1g	51	GLN
38	1g	56	GLN
38	1g	91	VAL
38	1g	104	LEU
38	1g	106	GLN
38	1g	110	GLN
38	1g	113	GLU
38	1g	114	ARG
38	1g	131	LYS
38	1g	135	VAL
39	1h	2	LEU
39	1h	19	VAL
39	1h	26	VAL
39	1h	50	ARG
39	1h	51	VAL
39	1h	52	ASP
39	1h	53	VAL
39	1h	54	ASP
39	1h	63	LEU
39	1h	75	ARG
39	1h	78	GLN
39	1h	91	ARG
39	1h	99	GLU
39	1h	109	ILE
39	1h	112	LEU
39	1h	120	THR
39	1h	127	LEU
39	1h	137	VAL
40	1i	23	ASN
40	1i	27	THR
40	1i	29	ASN
40	1i	42	ARG
40	1i	50	LEU
40	1i	54	ASP
40	1i	64	THR

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Mol	Chain	Res	Type
40	1i	81	ILE
40	1i	83	ARG
40	1i	86	VAL
40	1i	92	TYR
40	1i	102	LEU
40	1i	104	ARG
40	1i	107	ARG
40	1i	108	VAL
40	1i	113	LYS
40	1i	128	ARG
41	1j	30	SER
41	1j	34	VAL
41	1j	44	VAL
41	1j	46	ARG
41	1j	48	THR
41	1j	49	VAL
41	1j	84	GLN
41	1j	92	THR
41	1j	94	VAL
41	1j	95	GLU
41	1j	96	ILE
41	1j	98	ILE
42	1k	18	ARG
42	1k	25	TYR
42	1k	31	THR
42	1k	48	ILE
42	1k	84	VAL
42	1k	106	LYS
42	1k	109	VAL
42	1k	114	VAL
43	1l	10	LEU
43	1l	27	LEU
43	1l	33	ARG
43	1l	52	LEU
43	1l	60	LEU
43	1l	67	THR
43	1l	70	ILE
43	1l	83	VAL
43	1l	84	LEU
43	1l	97	ARG
43	1l	104	VAL
44	1m	4	ILE

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Mol	Chain	Res	Type
44	1m	11	ARG
44	1m	19	LEU
44	1m	35	GLU
44	1m	56	LEU
44	1m	65	LYS
44	1m	70	LEU
44	1m	102	ARG
44	1m	110	ARG
45	1n	6	LEU
45	1n	8	GLU
45	1n	13	THR
45	1n	18	VAL
45	1n	22	THR
45	1n	33	VAL
45	1n	35	ARG
45	1n	44	LEU
45	1n	46	GLU
46	1o	3	ILE
46	1o	26	GLU
46	1o	38	ARG
46	1o	39	LEU
46	1o	41	GLU
46	1o	83	GLU
46	1o	84	LYS
46	1o	87	ILE
47	1p	1	MET
47	1p	2	VAL
47	1p	5	ARG
47	1p	11	SER
47	1p	19	ILE
47	1p	20	VAL
47	1p	21	VAL
47	1p	47	ASP
47	1p	60	LEU
47	1p	62	VAL
47	1p	67	THR
47	1p	69	THR
48	1q	9	VAL
48	1q	37	LYS
48	1q	53	LEU
48	1q	60	ILE
48	1q	74	LEU

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Mol	Chain	Res	Type
48	1q	82	MET
48	1q	89	LEU
48	1q	98	LEU
49	1r	26	LEU
49	1r	31	LEU
49	1r	37	VAL
49	1r	38	GLU
49	1r	54	ARG
49	1r	55	ARG
49	1r	58	LEU
49	1r	68	LYS
49	1r	76	LEU
49	1r	82	THR
49	1r	86	VAL
50	1s	3	ARG
50	1s	22	LEU
50	1s	28	LYS
50	1s	37	ARG
50	1s	63	THR
50	1s	65	ASN
51	1t	9	ASN
51	1t	10	LEU
51	1t	24	LEU
51	1t	30	LYS
51	1t	45	GLN
51	1t	60	GLU
51	1t	62	LEU
51	1t	71	THR
51	1t	84	LEU
51	1t	93	GLU
55	1z	1	VAL
3	2D	3	VAL
3	2D	13	ARG
3	2D	61	LEU
3	2D	64	ILE
3	2D	71	ASP
3	2D	82	ILE
3	2D	87	ASN
3	2D	94	LEU
3	2D	103	ARG
3	2D	106	ILE
3	2D	113	VAL

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Mol	Chain	Res	Type
3	2D	126	GLN
3	2D	134	ARG
3	2D	138	VAL
3	2D	142	VAL
3	2D	155	LEU
3	2D	173	VAL
3	2D	183	ARG
3	2D	193	VAL
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	239	ARG
3	2D	242	ARG
3	2D	257	LEU
3	2D	259	THR
3	2D	260	ARG
3	2D	262	ARG
3	2D	274	ARG
4	2E	9	VAL
4	2E	12	THR
4	2E	21	VAL
4	2E	24	THR
4	2E	33	VAL
4	2E	34	VAL
4	2E	40	GLU
4	2E	49	LEU
4	2E	52	LEU
4	2E	75	VAL
4	2E	76	ARG
4	2E	77	ILE
4	2E	79	ARG
4	2E	82	ARG
4	2E	111	ARG
4	2E	116	VAL
4	2E	119	ARG
4	2E	144	ARG
4	2E	154	LYS
4	2E	163	GLU
4	2E	167	VAL
4	2E	170	LEU
4	2E	175	VAL

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Mol	Chain	Res	Type
4	2E	181	LEU
4	2E	184	VAL
4	2E	202	LYS
5	2F	12	LEU
5	2F	20	LEU
5	2F	24	LEU
5	2F	33	LEU
5	2F	53	THR
5	2F	57	VAL
5	2F	74	ARG
5	2F	88	VAL
5	2F	106	ARG
5	2F	107	LYS
5	2F	112	MET
5	2F	122	LYS
5	2F	132	VAL
5	2F	135	LYS
5	2F	140	LEU
5	2F	165	ARG
5	2F	169	ASN
5	2F	183	VAL
5	2F	188	ARG
5	2F	192	LEU
5	2F	196	LEU
5	2F	197	ASP
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	13	GLU
6	2G	14	GLU
6	2G	16	ARG
6	2G	28	VAL
6	2G	33	ARG
6	2G	35	GLU
6	2G	43	LEU
6	2G	60	LEU
6	2G	88	ILE
6	2G	98	ARG
6	2G	111	LEU
6	2G	113	ARG
6	2G	115	ARG
6	2G	130	ASN

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Mol	Chain	Res	Type
6	2G	133	LEU
6	2G	136	ARG
6	2G	139	LEU
6	2G	140	ILE
6	2G	143	GLU
6	2G	145	THR
6	2G	148	MET
6	2G	149	VAL
6	2G	159	VAL
6	2G	162	THR
6	2G	165	THR
7	2H	3	ARG
7	2H	15	VAL
7	2H	23	ARG
7	2H	24	VAL
7	2H	33	LEU
7	2H	41	MET
7	2H	42	ARG
7	2H	43	VAL
7	2H	45	VAL
7	2H	49	VAL
7	2H	59	ARG
7	2H	63	SER
7	2H	69	ARG
7	2H	71	LEU
7	2H	98	LEU
7	2H	115	VAL
7	2H	124	GLU
7	2H	131	VAL
7	2H	139	GLN
8	2I	15	VAL
8	2I	43	ASN
8	2I	44	LEU
8	2I	47	LEU
8	2I	54	GLN
8	2I	61	ARG
8	2I	75	LEU
8	2I	77	LEU
8	2I	92	VAL
8	2I	101	LEU
8	2I	108	THR
8	2I	116	LEU

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Mol	Chain	Res	Type
8	2I	121	LYS
8	2I	127	VAL
8	2I	140	LEU
8	2I	142	VAL
9	2N	5	VAL
9	2N	10	GLU
9	2N	14	VAL
9	2N	33	LEU
9	2N	34	LEU
9	2N	43	THR
9	2N	46	VAL
9	2N	48	MET
9	2N	61	ARG
9	2N	62	VAL
9	2N	63	THR
9	2N	87	LEU
9	2N	97	ARG
9	2N	99	LEU
9	2N	120	LEU
9	2N	131	GLN
9	2N	133	GLN
9	2N	137	LYS
10	2O	8	LEU
10	2O	10	VAL
10	2O	20	MET
10	2O	23	ARG
10	2O	24	VAL
10	2O	45	GLU
10	2O	53	LYS
10	2O	69	ILE
10	2O	98	VAL
10	2O	113	LYS
11	2P	3	LEU
11	2P	15	ARG
11	2P	21	ARG
11	2P	55	ARG
11	2P	59	LEU
11	2P	65	ARG
11	2P	70	GLN
11	2P	83	VAL
11	2P	95	VAL
11	2P	96	THR

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Mol	Chain	Res	Type
11	2P	99	LEU
11	2P	106	LEU
11	2P	112	LEU
11	2P	121	LYS
11	2P	123	LEU
11	2P	125	VAL
11	2P	148	LEU
12	2Q	1	MET
12	2Q	7	MET
12	2Q	35	VAL
12	2Q	45	GLN
12	2Q	48	GLU
12	2Q	64	ILE
12	2Q	81	VAL
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	115	MET
13	2R	1	MET
13	2R	6	SER
13	2R	18	LEU
13	2R	24	GLN
13	2R	28	LEU
13	2R	29	LEU
13	2R	44	LEU
13	2R	54	LEU
13	2R	60	LEU
13	2R	65	LEU
13	2R	73	VAL
13	2R	75	LEU
13	2R	79	LEU
13	2R	82	GLU
13	2R	86	ARG
13	2R	91	GLN
13	2R	100	LEU
13	2R	102	GLU
13	2R	111	LEU
13	2R	114	VAL
14	2S	4	LEU
14	2S	13	ARG
14	2S	14	VAL
14	2S	19	LYS
14	2S	20	ARG

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Mol	Chain	Res	Type
14	2S	21	THR
14	2S	35	ILE
14	2S	36	TYR
14	2S	44	LYS
14	2S	46	VAL
14	2S	48	LEU
14	2S	49	VAL
14	2S	50	SER
14	2S	58	LEU
14	2S	67	ARG
14	2S	69	VAL
14	2S	75	GLU
14	2S	83	LYS
14	2S	110	LEU
14	2S	111	GLU
15	2T	8	LYS
15	2T	23	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	49	VAL
15	2T	53	ARG
15	2T	59	THR
15	2T	64	ARG
15	2T	67	SER
15	2T	78	LEU
15	2T	85	LYS
15	2T	89	VAL
15	2T	96	ARG
15	2T	107	ASP
15	2T	113	LYS
15	2T	118	ARG
16	2U	17	ILE
16	2U	59	ARG
16	2U	60	LEU
16	2U	74	LEU
16	2U	83	LEU
16	2U	92	ARG
16	2U	104	GLN
16	2U	108	GLU
16	2U	117	GLN
17	2V	15	GLU
17	2V	18	LEU

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Mol	Chain	Res	Type
17	2V	21	ARG
17	2V	35	LEU
17	2V	46	VAL
17	2V	52	VAL
17	2V	57	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	95	LEU
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	51	LEU
18	2W	52	GLU
18	2W	92	ARG
18	2W	96	ILE
18	2W	100	THR
18	2W	107	LEU
19	2X	57	LEU
19	2X	72	LYS
19	2X	76	ARG
19	2X	78	LYS
19	2X	92	LEU
20	2Y	5	MET
20	2Y	7	VAL
20	2Y	8	LYS
20	2Y	21	LYS
20	2Y	44	ILE
20	2Y	67	LEU
20	2Y	72	VAL
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	86	VAL
21	2Z	91	LEU
21	2Z	94	GLU
21	2Z	107	THR
21	2Z	126	VAL
21	2Z	131	ARG
21	2Z	135	GLU
21	2Z	136	PHE
21	2Z	150	LEU

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Mol	Chain	Res	Type
21	2Z	155	LEU
21	2Z	161	VAL
21	2Z	163	LEU
21	2Z	165	VAL
21	2Z	170	THR
21	2Z	185	GLU
22	20	10	THR
22	20	20	ARG
22	20	49	LYS
23	21	4	VAL
23	21	21	ARG
23	21	30	VAL
23	21	35	THR
23	21	37	ILE
23	21	40	ARG
23	21	50	ARG
23	21	53	VAL
23	21	56	GLN
23	21	59	THR
23	21	69	LYS
23	21	95	LEU
24	22	2	LYS
24	22	30	ARG
24	22	32	LEU
24	22	35	LEU
24	22	53	LEU
24	22	64	LEU
24	22	68	ARG
24	22	70	GLN
25	23	3	ARG
25	23	5	LYS
25	23	8	LEU
25	23	31	LEU
25	23	54	VAL
26	24	14	ILE
26	24	33	VAL
26	24	56	VAL
26	24	58	ARG
26	24	61	ARG
26	24	63	TYR
26	24	68	ARG
27	25	6	VAL

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Mol	Chain	Res	Type
27	25	16	ARG
27	25	40	LYS
27	25	55	ARG
27	25	57	VAL
27	25	60	VAL
28	26	9	LEU
28	26	14	THR
28	26	28	ARG
28	26	33	LYS
28	26	34	LEU
28	26	38	LYS
28	26	48	VAL
29	27	9	ARG
29	27	32	LYS
29	27	43	THR
30	28	14	VAL
30	28	26	LYS
31	29	17	ILE
31	29	26	ILE
33	2b	8	LYS
33	2b	17	PHE
33	2b	19	HIS
33	2b	32	ILE
33	2b	47	THR
33	2b	48	MET
33	2b	51	LEU
33	2b	63	MET
33	2b	67	THR
33	2b	68	ILE
33	2b	71	VAL
33	2b	80	ILE
33	2b	81	VAL
33	2b	83	MET
33	2b	90	MET
33	2b	93	VAL
33	2b	108	ILE
33	2b	117	GLU
33	2b	127	ILE
33	2b	128	GLU
33	2b	154	LEU
33	2b	160	ASP
33	2b	165	VAL

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Mol	Chain	Res	Type
33	2b	175	ARG
33	2b	179	LYS
33	2b	185	ILE
33	2b	187	LEU
33	2b	198	ASP
33	2b	222	ILE
33	2b	223	ILE
33	2b	224	GLN
34	2c	3	ASN
34	2c	5	ILE
34	2c	8	ILE
34	2c	14	ILE
34	2c	16	ARG
34	2c	47	LEU
34	2c	49	SER
34	2c	52	LEU
34	2c	70	VAL
34	2c	125	GLU
34	2c	131	ARG
34	2c	143	GLU
34	2c	152	ILE
34	2c	162	GLN
34	2c	178	LEU
34	2c	182	ILE
34	2c	198	VAL
34	2c	202	ILE
35	2d	3	ARG
35	2d	5	ILE
35	2d	8	VAL
35	2d	17	VAL
35	2d	25	ARG
35	2d	26	CYS
35	2d	31	CYS
35	2d	34	GLU
35	2d	38	TYR
35	2d	49	ARG
35	2d	58	LEU
35	2d	70	ILE
35	2d	73	ARG
35	2d	86	LYS
35	2d	96	LEU
35	2d	101	LEU

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Mol	Chain	Res	Type
35	2d	104	VAL
35	2d	122	ARG
35	2d	132	ARG
35	2d	135	LEU
35	2d	157	LEU
35	2d	170	VAL
35	2d	181	MET
35	2d	187	ARG
35	2d	194	LEU
35	2d	200	GLU
36	2e	12	LEU
36	2e	27	ARG
36	2e	31	LEU
36	2e	34	VAL
36	2e	40	ARG
36	2e	41	VAL
36	2e	47	LYS
36	2e	50	GLU
36	2e	51	VAL
36	2e	68	GLU
36	2e	69	VAL
36	2e	71	LEU
36	2e	91	LEU
36	2e	115	VAL
36	2e	116	THR
36	2e	143	ARG
36	2e	148	VAL
36	2e	152	ARG
37	2f	23	LYS
37	2f	28	ARG
37	2f	37	VAL
37	2f	40	VAL
37	2f	43	LEU
37	2f	46	ARG
37	2f	65	VAL
37	2f	72	VAL
37	2f	75	LEU
38	2g	12	LEU
38	2g	15	ASP
38	2g	16	LEU
38	2g	21	VAL
38	2g	38	LEU

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Mol	Chain	Res	Type
38	2g	42	ILE
38	2g	45	ASP
38	2g	56	GLN
38	2g	104	LEU
38	2g	106	GLN
38	2g	110	GLN
38	2g	114	ARG
38	2g	120	ILE
38	2g	129	GLU
38	2g	131	LYS
38	2g	135	VAL
39	2h	50	ARG
39	2h	51	VAL
39	2h	52	ASP
39	2h	53	VAL
39	2h	63	LEU
39	2h	78	GLN
39	2h	84	ARG
39	2h	91	ARG
39	2h	99	GLU
39	2h	107	LEU
39	2h	111	ILE
39	2h	112	LEU
39	2h	120	THR
39	2h	122	ARG
39	2h	127	LEU
39	2h	137	VAL
40	2i	3	GLN
40	2i	38	GLN
40	2i	50	LEU
40	2i	64	THR
40	2i	81	ILE
40	2i	89	ASN
40	2i	102	LEU
40	2i	124	GLN
40	2i	128	ARG
41	2j	6	ILE
41	2j	8	LEU
41	2j	13	HIS
41	2j	16	LEU
41	2j	19	SER
41	2j	21	GLN

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Mol	Chain	Res	Type
41	2j	23	ILE
41	2j	25	GLU
41	2j	44	VAL
41	2j	48	THR
41	2j	49	VAL
41	2j	68	HIS
41	2j	94	VAL
41	2j	95	GLU
41	2j	96	ILE
41	2j	98	ILE
42	2k	18	ARG
42	2k	30	VAL
42	2k	48	ILE
42	2k	70	LYS
42	2k	75	TYR
42	2k	77	MET
42	2k	78	GLN
42	2k	84	VAL
42	2k	109	VAL
42	2k	114	VAL
42	2k	126	ARG
43	2l	23	LYS
43	2l	27	LEU
43	2l	55	VAL
43	2l	70	ILE
43	2l	83	VAL
43	2l	84	LEU
43	2l	97	ARG
43	2l	104	VAL
44	2m	3	ARG
44	2m	35	GLU
44	2m	82	MET
44	2m	106	ASN
44	2m	110	ARG
44	2m	116	THR
45	2n	11	LYS
45	2n	17	LYS
45	2n	18	VAL
45	2n	22	THR
45	2n	33	VAL
45	2n	44	LEU
45	2n	50	LYS

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Mol	Chain	Res	Type
45	2n	53	LEU
46	2o	3	ILE
46	2o	5	LYS
46	2o	10	LYS
46	2o	22	THR
46	2o	26	GLU
46	2o	39	LEU
46	2o	41	GLU
46	2o	71	GLN
46	2o	83	GLU
46	2o	84	LYS
46	2o	87	ILE
47	2p	1	MET
47	2p	2	VAL
47	2p	5	ARG
47	2p	11	SER
47	2p	21	VAL
47	2p	27	LYS
47	2p	60	LEU
47	2p	62	VAL
47	2p	69	THR
48	2q	6	LEU
48	2q	9	VAL
48	2q	24	GLU
48	2q	37	LYS
48	2q	53	LEU
48	2q	60	ILE
48	2q	74	LEU
48	2q	77	VAL
49	2r	26	LEU
49	2r	29	PHE
49	2r	31	LEU
49	2r	35	ARG
49	2r	37	VAL
49	2r	38	GLU
49	2r	41	LYS
49	2r	54	ARG
49	2r	58	LEU
49	2r	76	LEU
49	2r	86	VAL
50	2s	3	ARG
50	2s	18	LYS

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Mol	Chain	Res	Type
50	2s	22	LEU
50	2s	28	LYS
50	2s	37	ARG
50	2s	41	VAL
50	2s	48	THR
50	2s	63	THR
50	2s	71	LEU
50	2s	77	THR
50	2s	78	ARG
51	2t	10	LEU
51	2t	24	LEU
51	2t	62	LEU
51	2t	71	THR
52	2u	10	ARG
55	2z	7	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (160) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	126	GLN
3	1D	143	HIS
3	1D	164	GLN
3	1D	253	GLN
4	1E	54	GLN
5	1F	69	HIS
5	1F	169	ASN
5	1F	203	GLN
5	1F	204	ASN
6	1G	130	ASN
7	1H	158	HIS
8	1I	43	ASN
8	1I	104	GLN
8	1I	105	HIS
8	1I	139	GLN
9	1N	8	GLN
11	1P	38	GLN
11	1P	70	GLN
13	1R	71	GLN
13	1R	91	GLN
14	1S	95	HIS
15	1T	43	GLN

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Mol	Chain	Res	Type
15	1T	84	GLN
15	1T	123	GLN
16	1U	94	ASN
18	1W	60	ASN
19	1X	31	HIS
20	1Y	6	HIS
20	1Y	43	ASN
20	1Y	92	ASN
21	1Z	73	GLN
21	1Z	151	HIS
24	12	38	GLN
24	12	70	GLN
30	18	35	GLN
30	18	43	GLN
31	19	36	GLN
33	1b	78	GLN
33	1b	146	GLN
34	1c	6	HIS
34	1c	69	HIS
34	1c	102	ASN
34	1c	123	GLN
34	1c	170	GLN
35	1d	45	GLN
35	1d	77	ASN
35	1d	123	HIS
35	1d	125	HIS
35	1d	160	GLN
36	1e	20	GLN
36	1e	73	ASN
36	1e	141	GLN
37	1f	32	ASN
37	1f	100	ASN
38	1g	64	GLN
38	1g	86	GLN
38	1g	110	GLN
38	1g	148	ASN
40	1i	23	ASN
40	1i	38	GLN
40	1i	58	HIS
40	1i	89	ASN
40	1i	117	HIS
40	1i	124	GLN

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Mol	Chain	Res	Type
41	1j	56	HIS
42	1k	93	GLN
42	1k	116	HIS
43	1l	78	GLN
43	1l	99	HIS
44	1m	92	HIS
48	1q	26	GLN
50	1s	47	HIS
50	1s	56	GLN
50	1s	57	HIS
50	1s	69	HIS
51	1t	9	ASN
51	1t	16	HIS
51	1t	26	ASN
51	1t	45	GLN
3	2D	126	GLN
3	2D	164	GLN
3	2D	253	GLN
4	2E	85	ASN
5	2F	69	HIS
5	2F	203	GLN
6	2G	40	ASN
6	2G	41	GLN
6	2G	130	ASN
8	2I	43	ASN
8	2I	54	GLN
8	2I	133	HIS
8	2I	139	GLN
10	2O	90	GLN
11	2P	38	GLN
12	2Q	12	GLN
12	2Q	45	GLN
12	2Q	123	HIS
13	2R	24	GLN
13	2R	50	HIS
14	2S	68	GLN
15	2T	84	GLN
15	2T	123	GLN
16	2U	44	ASN
16	2U	94	ASN
17	2V	64	HIS
19	2X	31	HIS

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Mol	Chain	Res	Type
20	2Y	43	ASN
20	2Y	92	ASN
21	2Z	55	HIS
21	2Z	73	GLN
21	2Z	121	HIS
23	21	56	GLN
25	23	33	GLN
28	26	32	ASN
30	28	35	GLN
31	29	36	GLN
33	2b	19	HIS
33	2b	40	HIS
33	2b	45	GLN
33	2b	78	GLN
33	2b	110	GLN
34	2c	3	ASN
34	2c	6	HIS
34	2c	123	GLN
34	2c	136	GLN
34	2c	176	HIS
35	2d	123	HIS
35	2d	125	HIS
35	2d	160	GLN
36	2e	141	GLN
37	2f	73	ASN
38	2g	86	GLN
38	2g	97	GLN
38	2g	110	GLN
38	2g	122	HIS
38	2g	148	ASN
40	2i	3	GLN
40	2i	34	ASN
40	2i	58	HIS
40	2i	89	ASN
40	2i	117	HIS
41	2j	21	GLN
41	2j	56	HIS
41	2j	84	GLN
42	2k	22	HIS
42	2k	26	ASN
42	2k	93	GLN
42	2k	104	GLN

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Mol	Chain	Res	Type
42	2k	116	HIS
43	2l	75	HIS
43	2l	78	GLN
44	2m	77	ASN
46	2o	28	GLN
46	2o	71	GLN
48	2q	26	GLN
50	2s	69	HIS
51	2t	18	GLN
51	2t	42	GLN
51	2t	75	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2737/2915 (93%)	396 (14%)	28 (1%)
1	2A	2781/2915 (95%)	475 (17%)	26 (0%)
2	1B	119/121 (98%)	9 (7%)	0
2	2B	119/121 (98%)	34 (28%)	2 (1%)
32	1a	1472/1521 (96%)	271 (18%)	0
32	2a	1479/1521 (97%)	282 (19%)	0
53	1v	4/24 (16%)	1 (25%)	0
53	2v	4/24 (16%)	1 (25%)	0
54	1x	75/77 (97%)	12 (16%)	0
54	2x	75/77 (97%)	15 (20%)	0
All	All	8865/9316 (95%)	1496 (16%)	56 (0%)

All (1496) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	11	U
1	1A	32	U
1	1A	33	C
1	1A	35	G
1	1A	44	C
1	1A	69	A
1	1A	72	A
1	1A	73	G
1	1A	82	A
1	1A	91	C
1	1A	115	A

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Mol	Chain	Res	Type
1	1A	116	A
1	1A	117	U
1	1A	137	G
1	1A	148	A
1	1A	154	C
1	1A	160	C
1	1A	184	A
1	1A	187	A
1	1A	188	U
1	1A	189	C
1	1A	193	G
1	1A	202	G
1	1A	203	G
1	1A	204	A
1	1A	209	A
1	1A	210	A
1	1A	212	G
1	1A	216	A
1	1A	217	A
1	1A	221	A
1	1A	236	G
1	1A	238	G
1	1A	249	G
1	1A	268	G
1	1A	270	U
1	1A	271	U
1	1A	272	G
1	1A	273	U
1	1A	288	G
1	1A	295	U
1	1A	298	G
1	1A	302	C
1	1A	334	A
1	1A	347	A
1	1A	352	G
1	1A	353	A
1	1A	368	A
1	1A	375	G
1	1A	377	G
1	1A	380	A
1	1A	386	G
1	1A	406	U

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Mol	Chain	Res	Type
1	1A	412	G
1	1A	422	G
1	1A	431	U
1	1A	432	G
1	1A	433	G
1	1A	437	G
1	1A	447	U
1	1A	454	A
1	1A	467	G
1	1A	469	C
1	1A	473	U
1	1A	476	C
1	1A	481	C
1	1A	482	A
1	1A	495	A
1	1A	506	G
1	1A	528	U
1	1A	529	A
1	1A	533	C
1	1A	554	G
1	1A	555	C
1	1A	556	A
1	1A	557	G
1	1A	572	G
1	1A	585	G
1	1A	595	G
1	1A	597	A
1	1A	608	A
1	1A	614	G
1	1A	615	G
1	1A	625	A
1	1A	626	G
1	1A	629	U
1	1A	638	G
1	1A	640	G
1	1A	661	A
1	1A	670	A
1	1A	671	G
1	1A	682	G
1	1A	696	C
1	1A	715	G
1	1A	732	G

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Mol	Chain	Res	Type
1	1A	763	G
1	1A	776	C
1	1A	792	A
1	1A	793	U
1	1A	810	A
1	1A	820	A
1	1A	821	G
1	1A	822	G
1	1A	828	A
1	1A	830	A
1	1A	831	G
1	1A	836	C
1	1A	838	G
1	1A	848	A
1	1A	851	G
1	1A	858	C
1	1A	873	U
1	1A	874	U
1	1A	876	G
1	1A	878	G
1	1A	883	C
1	1A	905	G
1	1A	912	A
1	1A	915	G
1	1A	925	G
1	1A	931	C
1	1A	932	C
1	1A	933	A
1	1A	934	C
1	1A	935	C
1	1A	936	A
1	1A	938	C
1	1A	941	A
1	1A	942	C
1	1A	955	A
1	1A	976	G
1	1A	985	A
1	1A	989	A
1	1A	990	G
1	1A	1002	U
1	1A	1003	A
1	1A	1005	C

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Mol	Chain	Res	Type
1	1A	1018	G
1	1A	1019	C
1	1A	1028	A
1	1A	1041	A
1	1A	1050	C
1	1A	1057	U
1	1A	1058	C
1	1A	1067	G
1	1A	1071	U
1	1A	1078	U
1	1A	1083	C
1	1A	1086	C
1	1A	1091	A
1	1A	1092	G
1	1A	1096	G
1	1A	1150	U
1	1A	1151	G
1	1A	1152	G
1	1A	1154	C
1	1A	1157	G
1	1A	1173	A
1	1A	1174	A
1	1A	1175	U
1	1A	1179	C
1	1A	1180	G
1	1A	1183	G
1	1A	1186	U
1	1A	1200	A
1	1A	1215	G
1	1A	1217	G
1	1A	1218	A
1	1A	1219	U
1	1A	1220	G
1	1A	1221	A
1	1A	1262	C
1	1A	1264	A
1	1A	1285	U
1	1A	1286	A
1	1A	1289	G
1	1A	1298	A
1	1A	1301	G
1	1A	1316	G

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Mol	Chain	Res	Type
1	1A	1317	A
1	1A	1318	U
1	1A	1345	U
1	1A	1346	A
1	1A	1348	G
1	1A	1366	A
1	1A	1397	U
1	1A	1404	A
1	1A	1405	A
1	1A	1410	A
1	1A	1415	C
1	1A	1418	A
1	1A	1429	A
1	1A	1430	G
1	1A	1440	A
1	1A	1461	G
1	1A	1462	C
1	1A	1466	G
1	1A	1467	G
1	1A	1473	C
1	1A	1482	C
1	1A	1490	A
1	1A	1496	G
1	1A	1507	G
1	1A	1513	C
1	1A	1517	A
1	1A	1524	G
1	1A	1528	G
1	1A	1538	C
1	1A	1539	A
1	1A	1541	A
1	1A	1553	A
1	1A	1554	C
1	1A	1555	A
1	1A	1570	G
1	1A	1578	C
1	1A	1588	A
1	1A	1589	C
1	1A	1604	A
1	1A	1612	A
1	1A	1615	A
1	1A	1624	U

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Mol	Chain	Res	Type
1	1A	1627	G
1	1A	1630	C
1	1A	1631	A
1	1A	1632	A
1	1A	1653	A
1	1A	1654	A
1	1A	1655	A
1	1A	1693	G
1	1A	1694	C
1	1A	1720	G
1	1A	1746	A
1	1A	1747	A
1	1A	1766	A
1	1A	1767	U
1	1A	1768	G
1	1A	1778	G
1	1A	1786	G
1	1A	1793	G
1	1A	1794	G
1	1A	1803	A
1	1A	1810	A
1	1A	1812	C
1	1A	1821	A
1	1A	1830	C
1	1A	1831	G
1	1A	1832	A
1	1A	1846	G
1	1A	1858	G
1	1A	1859	A
1	1A	1869	G
1	1A	1877	A
1	1A	1899	G
1	1A	1910	A
1	1A	1921	A
1	1A	1927	G
1	1A	1934	A
1	1A	1936	U
1	1A	1940	A
1	1A	1948	A
1	1A	1950	G
1	1A	1951	G
1	1A	1952	U

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Mol	Chain	Res	Type
1	1A	1953	A
1	1A	1958	A
1	1A	1959	A
1	1A	1973	A
1	1A	1976	U
1	1A	1984	U
1	1A	1986	C
1	1A	1988	C
1	1A	1991	A
1	1A	1992	A
1	1A	1993	A
1	1A	2013	G
1	1A	2014	U
1	1A	2018	G
1	1A	2044	G
1	1A	2052	A
1	1A	2053	G
1	1A	2054	A
1	1A	2060	C
1	1A	2064	C
1	1A	2076	C
1	1A	2077	G
1	1A	2081	A
1	1A	2082	G
1	1A	2083	A
1	1A	2090	G
1	1A	2091	G
1	1A	2101	G
1	1A	2204	C
1	1A	2205	G
1	1A	2206	C
1	1A	2207	G
1	1A	2209	C
1	1A	2212	G
1	1A	2213	G
1	1A	2216	C
1	1A	2219	A
1	1A	2226	G
1	1A	2227	G
1	1A	2228	A
1	1A	2229	U
1	1A	2236	A

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Mol	Chain	Res	Type
1	1A	2249	G
1	1A	2250	G
1	1A	2251	C
1	1A	2279	A
1	1A	2280	A
1	1A	2284	A
1	1A	2286	C
1	1A	2294	C
1	1A	2298	A
1	1A	2316	A
1	1A	2331	A
1	1A	2332	G
1	1A	2336	G
1	1A	2338	A
1	1A	2347	A
1	1A	2354	C
1	1A	2358	C
1	1A	2361	C
1	1A	2390	G
1	1A	2394	G
1	1A	2396	C
1	1A	2416	G
1	1A	2417	U
1	1A	2418	G
1	1A	2421	G
1	1A	2433	A
1	1A	2434	U
1	1A	2436	A
1	1A	2440	G
1	1A	2441	A
1	1A	2442	U
1	1A	2443	A
1	1A	2446	A
1	1A	2450	A
1	1A	2451	C
1	1A	2456	G
1	1A	2459	A
1	1A	2479	G
1	1A	2485	C
1	1A	2487	A
1	1A	2489	A
1	1A	2513	G

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Mol	Chain	Res	Type
1	1A	2516	G
1	1A	2517	U
1	1A	2529	A
1	1A	2536	G
1	1A	2540	G
1	1A	2560	G
1	1A	2565	U
1	1A	2566	U
1	1A	2577	A
1	1A	2578	G
1	1A	2584	C
1	1A	2593	G
1	1A	2613	A
1	1A	2620	U
1	1A	2621	C
1	1A	2622	U
1	1A	2623	C
1	1A	2640	A
1	1A	2641	G
1	1A	2665	A
1	1A	2700	U
1	1A	2701	C
1	1A	2702	C
1	1A	2713	U
1	1A	2714	C
1	1A	2724	A
1	1A	2725	A
1	1A	2726	G
1	1A	2738	U
1	1A	2745	A
1	1A	2770	A
1	1A	2773	G
1	1A	2776	A
1	1A	2777	A
1	1A	2778	G
1	1A	2790	A
1	1A	2792	G
1	1A	2802	A
1	1A	2803	C
1	1A	2806	C
1	1A	2812	G
1	1A	2829	A

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Mol	Chain	Res	Type
1	1A	2830	A
1	1A	2842	G
1	1A	2844	A
1	1A	2881	G
1	1A	2889	C
1	1A	2902	G
1	1A	2903	U
2	1B	13	A
2	1B	15	A
2	1B	25	A
2	1B	56	G
2	1B	65	C
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	10	G
32	1a	23	G
32	1a	33	A
32	1a	40	G
32	1a	45	G
32	1a	49	C
32	1a	52	A
32	1a	62	G
32	1a	65	G
32	1a	66	U
32	1a	74	G
32	1a	75	C
32	1a	76	G
32	1a	77	G
32	1a	78	G
32	1a	88	C
32	1a	91	G
32	1a	95	A
32	1a	109	G
32	1a	110	A
32	1a	115	C
32	1a	126	C
32	1a	133	G
32	1a	136	A
32	1a	139	G
32	1a	155	A

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Mol	Chain	Res	Type
32	1a	159	U
32	1a	161	G
32	1a	162	G
32	1a	163	G
32	1a	168	U
32	1a	169	C
32	1a	178	G
32	1a	190	U
32	1a	202	A
32	1a	203	A
32	1a	204	A
32	1a	206	G
32	1a	208	C
32	1a	209	U
32	1a	210	U
32	1a	211	U
32	1a	212	G
32	1a	218	U
32	1a	243	G
32	1a	247	G
32	1a	254	G
32	1a	258	A
32	1a	262	G
32	1a	263	C
32	1a	276	C
32	1a	277	G
32	1a	285	G
32	1a	317	A
32	1a	324	C
32	1a	325	A
32	1a	326	C
32	1a	339	U
32	1a	342	G
32	1a	343	G
32	1a	344	G
32	1a	348	C
32	1a	349	A
32	1a	350	G
32	1a	352	A
32	1a	363	U
32	1a	368	C
32	1a	369	A

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Mol	Chain	Res	Type
32	1a	380	G
32	1a	393	A
32	1a	394	C
32	1a	402	G
32	1a	408	A
32	1a	409	G
32	1a	419	G
32	1a	420	G
32	1a	425	U
32	1a	435	A
32	1a	441	G
32	1a	443	A
32	1a	447	A
32	1a	449	C
32	1a	455	A
32	1a	456	C
32	1a	457	G
32	1a	467	A
32	1a	469	G
32	1a	470	G
32	1a	477	G
32	1a	481	A
32	1a	482	U
32	1a	489	G
32	1a	493	A
32	1a	494	A
32	1a	495	C
32	1a	496	U
32	1a	497	C
32	1a	502	C
32	1a	503	C
32	1a	505	G
32	1a	510	C
32	1a	511	G
32	1a	515	U
32	1a	516	A
32	1a	517	A
32	1a	531	A
32	1a	543	A
32	1a	545	U
32	1a	547	A
32	1a	556	A

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Mol	Chain	Res	Type
32	1a	557	A
32	1a	560	G
32	1a	561	G
32	1a	576	G
32	1a	580	C
32	1a	602	C
32	1a	614	G
32	1a	637	A
32	1a	649	A
32	1a	671	A
32	1a	672	G
32	1a	677	G
32	1a	678	A
32	1a	707	U
32	1a	708	G
32	1a	715	G
32	1a	731	C
32	1a	733	C
32	1a	736	G
32	1a	739	G
32	1a	743	A
32	1a	761	A
32	1a	776	A
32	1a	777	U
32	1a	778	A
32	1a	799	A
32	1a	800	A
32	1a	801	C
32	1a	805	G
32	1a	812	A
32	1a	813	G
32	1a	820	G
32	1a	824	C
32	1a	825	U
32	1a	826	C
32	1a	829	G
32	1a	838	A
32	1a	850	A
32	1a	880	G
32	1a	892	A
32	1a	893	A
32	1a	894	G

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Mol	Chain	Res	Type
32	1a	904	G
32	1a	905	G
32	1a	912	C
32	1a	938	U
32	1a	939	U
32	1a	946	A
32	1a	947	A
32	1a	949	G
32	1a	950	C
32	1a	952	A
32	1a	953	A
32	1a	954	G
32	1a	955	A
32	1a	959	U
32	1a	961	A
32	1a	970	U
32	1a	971	G
32	1a	972	A
32	1a	977	C
32	1a	980	G
32	1a	982	G
32	1a	983	A
32	1a	984	A
32	1a	988	G
32	1a	990	G
32	1a	992	G
32	1a	995	A
32	1a	999	U
32	1a	1025	G
32	1a	1027	A
32	1a	1029	A
32	1a	1036	G
32	1a	1037	C
32	1a	1039	U
32	1a	1048	U
32	1a	1049	C
32	1a	1077	G
32	1a	1078	U
32	1a	1084	A
32	1a	1091	G
32	1a	1103	G
32	1a	1107	G

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Mol	Chain	Res	Type
32	1a	1115	C
32	1a	1116	G
32	1a	1117	G
32	1a	1119	U
32	1a	1120	C
32	1a	1121	G
32	1a	1122	G
32	1a	1128	C
32	1a	1134	A
32	1a	1135	A
32	1a	1139	G
32	1a	1142	U
32	1a	1143	G
32	1a	1149	G
32	1a	1158	A
32	1a	1165	A
32	1a	1166	G
32	1a	1171	C
32	1a	1175	G
32	1a	1178	U
32	1a	1179	G
32	1a	1183	A
32	1a	1184	G
32	1a	1195	A
32	1a	1196	C
32	1a	1200	C
32	1a	1209	A
32	1a	1220	A
32	1a	1222	U
32	1a	1235	G
32	1a	1238	A
32	1a	1239	U
32	1a	1240	G
32	1a	1242	C
32	1a	1245	C
32	1a	1248	G
32	1a	1252	C
32	1a	1260	U
32	1a	1261	A
32	1a	1262	A
32	1a	1268	A
32	1a	1269	A

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Mol	Chain	Res	Type
32	1a	1281	A
32	1a	1282	G
32	1a	1284	U
32	1a	1294	G
32	1a	1301	A
32	1a	1304	C
32	1a	1320	G
32	1a	1322	A
32	1a	1328	A
32	1a	1329	G
32	1a	1335	G
32	1a	1342	A
32	1a	1345	C
32	1a	1348	G
32	1a	1353	G
32	1a	1360	A
32	1a	1379	A
32	1a	1380	C
32	1a	1381	A
32	1a	1402	G
32	1a	1425	G
32	1a	1426	G
32	1a	1432	A
32	1a	1433	C
32	1a	1434	G
32	1a	1465	G
32	1a	1475	G
32	1a	1480	A
32	1a	1481	A
32	1a	1482	G
32	1a	1484	U
32	1a	1495	G
32	1a	1497	A
32	1a	1507	G
32	1a	1508	G
53	1v	15	A
54	1x	9	G
54	1x	13	C
54	1x	17(A)	U
54	1x	18	G
54	1x	19	G
54	1x	20	U

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Mol	Chain	Res	Type
54	1x	21	A
54	1x	34	C
54	1x	44	A
54	1x	47	U
54	1x	51	C
54	1x	76	A
1	2A	7	A
1	2A	9	G
1	2A	11	U
1	2A	13	A
1	2A	14	G
1	2A	33	C
1	2A	34	G
1	2A	44	C
1	2A	48	U
1	2A	49	G
1	2A	56	G
1	2A	59	G
1	2A	69	A
1	2A	72	A
1	2A	73	G
1	2A	82	A
1	2A	88	U
1	2A	91	C
1	2A	93	G
1	2A	98	G
1	2A	99	G
1	2A	115	A
1	2A	116	A
1	2A	117	U
1	2A	122	G
1	2A	125	C
1	2A	137	G
1	2A	138	A
1	2A	154	C
1	2A	155	U
1	2A	161	G
1	2A	169	A
1	2A	170	A
1	2A	184	A
1	2A	185	A
1	2A	187	A

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Mol	Chain	Res	Type
1	2A	193	G
1	2A	203	G
1	2A	204	A
1	2A	209	A
1	2A	210	A
1	2A	212	G
1	2A	216	A
1	2A	217	A
1	2A	218	U
1	2A	221	A
1	2A	236	G
1	2A	238	G
1	2A	268	G
1	2A	270	U
1	2A	271	U
1	2A	272	G
1	2A	273	U
1	2A	274	C
1	2A	287	U
1	2A	288	G
1	2A	300	C
1	2A	301	A
1	2A	327	G
1	2A	333	A
1	2A	334	A
1	2A	335	G
1	2A	347	A
1	2A	350	G
1	2A	352	G
1	2A	353	A
1	2A	356	G
1	2A	361	G
1	2A	365	G
1	2A	375	G
1	2A	385	U
1	2A	386	G
1	2A	412	G
1	2A	431	U
1	2A	437	G
1	2A	438	A
1	2A	441	A
1	2A	453	U

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Mol	Chain	Res	Type
1	2A	454	A
1	2A	461	C
1	2A	468	A
1	2A	469	C
1	2A	479	A
1	2A	480	C
1	2A	482	A
1	2A	495	A
1	2A	506	G
1	2A	528	U
1	2A	529	A
1	2A	533	C
1	2A	552	A
1	2A	554	G
1	2A	555	C
1	2A	556	A
1	2A	557	G
1	2A	568	G
1	2A	573	G
1	2A	585	G
1	2A	590	U
1	2A	595	G
1	2A	596	C
1	2A	597	A
1	2A	608	A
1	2A	625	A
1	2A	626	G
1	2A	629	U
1	2A	640	G
1	2A	651	A
1	2A	658	C
1	2A	661	A
1	2A	669	C
1	2A	670	A
1	2A	678	A
1	2A	681	G
1	2A	697	G
1	2A	732	G
1	2A	763	G
1	2A	772	G
1	2A	776	C
1	2A	784	G

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Mol	Chain	Res	Type
1	2A	810	A
1	2A	811	G
1	2A	820	A
1	2A	821	G
1	2A	822	G
1	2A	828	A
1	2A	829	A
1	2A	830	A
1	2A	831	G
1	2A	836	C
1	2A	838	G
1	2A	851	G
1	2A	858	C
1	2A	865	A
1	2A	873	U
1	2A	874	U
1	2A	894	G
1	2A	903	C
1	2A	905	G
1	2A	912	A
1	2A	913	C
1	2A	925	G
1	2A	928	G
1	2A	930	C
1	2A	931	C
1	2A	932	C
1	2A	933	A
1	2A	934	C
1	2A	935	C
1	2A	936	A
1	2A	938	C
1	2A	941	A
1	2A	942	C
1	2A	944	A
1	2A	945	A
1	2A	946	A
1	2A	947	C
1	2A	951	G
1	2A	955	A
1	2A	956	A
1	2A	962	A
1	2A	964	G

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Mol	Chain	Res	Type
1	2A	976	G
1	2A	982	G
1	2A	985	A
1	2A	989	A
1	2A	990	G
1	2A	997	A
1	2A	1003	A
1	2A	1005	C
1	2A	1018	G
1	2A	1019	C
1	2A	1028	A
1	2A	1041	A
1	2A	1042	G
1	2A	1043	C
1	2A	1050	C
1	2A	1057	U
1	2A	1058	C
1	2A	1065	A
1	2A	1067	G
1	2A	1070	G
1	2A	1071	U
1	2A	1078	U
1	2A	1081	G
1	2A	1083	C
1	2A	1088	C
1	2A	1090	A
1	2A	1091	A
1	2A	1092	G
1	2A	1093	A
1	2A	1098	C
1	2A	1103	G
1	2A	1104	G
1	2A	1105	U
1	2A	1106	U
1	2A	1107	G
1	2A	1108	G
1	2A	1109	C
1	2A	1110	U
1	2A	1115	A
1	2A	1118	A
1	2A	1120	C
1	2A	1121	C

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Mol	Chain	Res	Type
1	2A	1128	U
1	2A	1133	A
1	2A	1136	G
1	2A	1142	U
1	2A	1143	A
1	2A	1146	U
1	2A	1154	C
1	2A	1156	A
1	2A	1157	G
1	2A	1158	U
1	2A	1159	G
1	2A	1161	C
1	2A	1163	C
1	2A	1175	U
1	2A	1178	U
1	2A	1179	C
1	2A	1180	G
1	2A	1183	G
1	2A	1200	A
1	2A	1216	G
1	2A	1256	G
1	2A	1263	G
1	2A	1264	A
1	2A	1274	G
1	2A	1281	G
1	2A	1285	U
1	2A	1289	G
1	2A	1295	G
1	2A	1298	A
1	2A	1301	G
1	2A	1316	G
1	2A	1317	A
1	2A	1318	U
1	2A	1329	A
1	2A	1332	A
1	2A	1345	U
1	2A	1346	A
1	2A	1348	G
1	2A	1359	C
1	2A	1366	A
1	2A	1374	U
1	2A	1387	A

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Mol	Chain	Res	Type
1	2A	1390	C
1	2A	1399	A
1	2A	1404	A
1	2A	1405	A
1	2A	1410	A
1	2A	1413	G
1	2A	1415	C
1	2A	1429	A
1	2A	1430	G
1	2A	1431	C
1	2A	1461	G
1	2A	1462	C
1	2A	1465	U
1	2A	1466	G
1	2A	1473	C
1	2A	1490	A
1	2A	1495	A
1	2A	1496	G
1	2A	1501	G
1	2A	1505	G
1	2A	1508	C
1	2A	1513	C
1	2A	1517	A
1	2A	1528	G
1	2A	1534	U
1	2A	1535	A
1	2A	1538	C
1	2A	1542	U
1	2A	1554	C
1	2A	1555	A
1	2A	1570	G
1	2A	1577	C
1	2A	1579	G
1	2A	1589	C
1	2A	1593	C
1	2A	1604	A
1	2A	1605	G
1	2A	1612	A
1	2A	1615	A
1	2A	1624	U
1	2A	1630	C
1	2A	1631	A

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Mol	Chain	Res	Type
1	2A	1640	G
1	2A	1653	A
1	2A	1654	A
1	2A	1655	A
1	2A	1658	G
1	2A	1686	C
1	2A	1694	C
1	2A	1720	G
1	2A	1746	A
1	2A	1766	A
1	2A	1771	C
1	2A	1786	G
1	2A	1788	G
1	2A	1792	A
1	2A	1793	G
1	2A	1794	G
1	2A	1799	G
1	2A	1803	A
1	2A	1810	A
1	2A	1812	C
1	2A	1821	A
1	2A	1830	C
1	2A	1831	G
1	2A	1846	G
1	2A	1858	G
1	2A	1859	A
1	2A	1869	G
1	2A	1877	A
1	2A	1880	G
1	2A	1887	G
1	2A	1889	A
1	2A	1891	G
1	2A	1898	A
1	2A	1899	G
1	2A	1905	A
1	2A	1910	A
1	2A	1921	A
1	2A	1927	G
1	2A	1934	A
1	2A	1935	C
1	2A	1950	G
1	2A	1951	G

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Mol	Chain	Res	Type
1	2A	1952	U
1	2A	1955	C
1	2A	1959	A
1	2A	1976	U
1	2A	1984	U
1	2A	1988	C
1	2A	1991	A
1	2A	1992	A
1	2A	1993	A
1	2A	2005	G
1	2A	2014	U
1	2A	2018	G
1	2A	2026	A
1	2A	2041	A
1	2A	2044	G
1	2A	2052	A
1	2A	2054	A
1	2A	2060	C
1	2A	2064	C
1	2A	2067	G
1	2A	2073	G
1	2A	2076	C
1	2A	2077	G
1	2A	2081	A
1	2A	2082	G
1	2A	2083	A
1	2A	2090	G
1	2A	2103	A
1	2A	2120	U
1	2A	2123	U
1	2A	2207	G
1	2A	2209	C
1	2A	2210	U
1	2A	2213	G
1	2A	2219	A
1	2A	2226	G
1	2A	2227	G
1	2A	2228	A
1	2A	2229	U
1	2A	2236	A
1	2A	2246	G
1	2A	2249	G

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Mol	Chain	Res	Type
1	2A	2250	G
1	2A	2251	C
1	2A	2268	U
1	2A	2279	A
1	2A	2280	A
1	2A	2286	C
1	2A	2289	A
1	2A	2294	C
1	2A	2298	A
1	2A	2304	C
1	2A	2308	C
1	2A	2316	A
1	2A	2318	G
1	2A	2319	G
1	2A	2323	U
1	2A	2328	C
1	2A	2329	G
1	2A	2330	G
1	2A	2331	A
1	2A	2336	G
1	2A	2345	G
1	2A	2346	A
1	2A	2347	A
1	2A	2354	C
1	2A	2358	C
1	2A	2361	C
1	2A	2387	A
1	2A	2394	G
1	2A	2396	C
1	2A	2407	G
1	2A	2411	G
1	2A	2413	C
1	2A	2417	U
1	2A	2418	G
1	2A	2421	G
1	2A	2433	A
1	2A	2434	U
1	2A	2436	A
1	2A	2439	G
1	2A	2440	G
1	2A	2441	A
1	2A	2442	U

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Mol	Chain	Res	Type
1	2A	2445	A
1	2A	2446	A
1	2A	2450	A
1	2A	2451	C
1	2A	2456	G
1	2A	2459	A
1	2A	2476	C
1	2A	2487	A
1	2A	2497	G
1	2A	2501	G
1	2A	2508	A
1	2A	2513	G
1	2A	2516	G
1	2A	2517	U
1	2A	2529	A
1	2A	2531	C
1	2A	2540	G
1	2A	2565	U
1	2A	2566	U
1	2A	2577	A
1	2A	2578	G
1	2A	2584	C
1	2A	2585	G
1	2A	2613	A
1	2A	2620	U
1	2A	2622	U
1	2A	2623	C
1	2A	2626	U
1	2A	2641	G
1	2A	2665	A
1	2A	2674	G
1	2A	2700	U
1	2A	2701	C
1	2A	2702	C
1	2A	2713	U
1	2A	2724	A
1	2A	2725	A
1	2A	2726	G
1	2A	2738	U
1	2A	2745	A
1	2A	2776	A
1	2A	2777	A

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Mol	Chain	Res	Type
1	2A	2778	G
1	2A	2790	A
1	2A	2805	G
1	2A	2812	G
1	2A	2817	U
1	2A	2819	A
1	2A	2827	G
1	2A	2829	A
1	2A	2830	A
1	2A	2842	G
1	2A	2844	A
1	2A	2881	G
1	2A	2884	C
1	2A	2888	C
1	2A	2889	C
1	2A	2900	A
1	2A	2902	G
1	2A	2903	U
1	2A	2904	C
2	2B	2	C
2	2B	4	C
2	2B	7	G
2	2B	8	U
2	2B	9	G
2	2B	13	A
2	2B	22	U
2	2B	23	G
2	2B	28	C
2	2B	30	C
2	2B	31	C
2	2B	34	U
2	2B	35	U
2	2B	37	C
2	2B	42	C
2	2B	43	C
2	2B	45	A
2	2B	46	A
2	2B	50	G
2	2B	52	A
2	2B	53	A
2	2B	56	G
2	2B	58	A

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Mol	Chain	Res	Type
2	2B	59	A
2	2B	65	C
2	2B	67	G
2	2B	73	A
2	2B	85	G
2	2B	90	A
2	2B	110	G
2	2B	111	G
2	2B	116	G
2	2B	117	G
2	2B	120	A
32	2a	6	U
32	2a	10	G
32	2a	15	U
32	2a	23	G
32	2a	33	A
32	2a	40	G
32	2a	48	C
32	2a	49	C
32	2a	51	A
32	2a	52	A
32	2a	53	G
32	2a	60	A
32	2a	66	U
32	2a	67	G
32	2a	75	C
32	2a	79	G
32	2a	84	A
32	2a	85	C
32	2a	95	A
32	2a	99	G
32	2a	109	G
32	2a	110	A
32	2a	114	A
32	2a	115	C
32	2a	126	C
32	2a	138	A
32	2a	146	A
32	2a	158	C
32	2a	168	U
32	2a	169	C
32	2a	177	U

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Mol	Chain	Res	Type
32	2a	189	U
32	2a	190	U
32	2a	202	A
32	2a	204	A
32	2a	210	U
32	2a	211	U
32	2a	212	G
32	2a	213	C
32	2a	239	A
32	2a	243	G
32	2a	247	G
32	2a	262	G
32	2a	263	C
32	2a	275	A
32	2a	277	G
32	2a	285	G
32	2a	294	A
32	2a	297	G
32	2a	302	G
32	2a	317	A
32	2a	324	C
32	2a	328	G
32	2a	340	A
32	2a	346	G
32	2a	347	G
32	2a	348	C
32	2a	349	A
32	2a	350	G
32	2a	361	U
32	2a	363	U
32	2a	365	C
32	2a	368	C
32	2a	380	G
32	2a	394	C
32	2a	400	U
32	2a	402	G
32	2a	408	A
32	2a	410	A
32	2a	419	G
32	2a	425	U
32	2a	426	A
32	2a	435	A

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Mol	Chain	Res	Type
32	2a	437	C
32	2a	446	A
32	2a	447	A
32	2a	455	A
32	2a	456	C
32	2a	469	G
32	2a	470	G
32	2a	481	A
32	2a	482	U
32	2a	489	G
32	2a	493	A
32	2a	494	A
32	2a	495	C
32	2a	502	C
32	2a	505	G
32	2a	511	G
32	2a	515	U
32	2a	516	A
32	2a	517	A
32	2a	531	A
32	2a	543	A
32	2a	544	U
32	2a	545	U
32	2a	546	C
32	2a	548	C
32	2a	550	G
32	2a	552	G
32	2a	556	A
32	2a	557	A
32	2a	560	G
32	2a	576	G
32	2a	580	C
32	2a	614	G
32	2a	615	G
32	2a	636	U
32	2a	637	A
32	2a	645	G
32	2a	649	A
32	2a	658	G
32	2a	671	A
32	2a	672	G
32	2a	677	G

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Mol	Chain	Res	Type
32	2a	679	A
32	2a	704	C
32	2a	705	G
32	2a	707	U
32	2a	708	G
32	2a	715	G
32	2a	726	G
32	2a	733	C
32	2a	739	G
32	2a	758	G
32	2a	761	A
32	2a	772	U
32	2a	776	A
32	2a	777	U
32	2a	778	A
32	2a	800	A
32	2a	801	C
32	2a	803	A
32	2a	805	G
32	2a	811	U
32	2a	812	A
32	2a	813	G
32	2a	820	G
32	2a	824	C
32	2a	825	U
32	2a	826	C
32	2a	829	G
32	2a	837	A
32	2a	852	G
32	2a	862	U
32	2a	863	G
32	2a	880	G
32	2a	891	A
32	2a	892	A
32	2a	893	A
32	2a	904	G
32	2a	905	G
32	2a	909	C
32	2a	911	G
32	2a	912	C
32	2a	913	A
32	2a	920	G

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Mol	Chain	Res	Type
32	2a	938	U
32	2a	939	U
32	2a	946	A
32	2a	947	A
32	2a	949	G
32	2a	952	A
32	2a	953	A
32	2a	954	G
32	2a	955	A
32	2a	956	A
32	2a	967	C
32	2a	970	U
32	2a	971	G
32	2a	977	C
32	2a	979	A
32	2a	981	G
32	2a	982	G
32	2a	984	A
32	2a	995	A
32	2a	1000	G
32	2a	1001	G
32	2a	1028	C
32	2a	1033	G
32	2a	1036	G
32	2a	1037	C
32	2a	1038	A
32	2a	1039	U
32	2a	1048	U
32	2a	1049	C
32	2a	1064	G
32	2a	1077	G
32	2a	1078	U
32	2a	1084	A
32	2a	1096	C
32	2a	1100	G
32	2a	1101	C
32	2a	1105	U
32	2a	1108	U
32	2a	1109	U
32	2a	1112	C
32	2a	1113	A
32	2a	1117	G

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Mol	Chain	Res	Type
32	2a	1118	U
32	2a	1119	U
32	2a	1120	C
32	2a	1121	G
32	2a	1122	G
32	2a	1129	A
32	2a	1140	A
32	2a	1142	U
32	2a	1149	G
32	2a	1165	A
32	2a	1168	G
32	2a	1171	C
32	2a	1172	G
32	2a	1173	A
32	2a	1178	U
32	2a	1179	G
32	2a	1184	G
32	2a	1191	C
32	2a	1193	U
32	2a	1194	U
32	2a	1195	A
32	2a	1196	C
32	2a	1220	A
32	2a	1222	U
32	2a	1223	G
32	2a	1228	C
32	2a	1238	A
32	2a	1239	U
32	2a	1240	G
32	2a	1242	C
32	2a	1244	C
32	2a	1255	G
32	2a	1260	U
32	2a	1262	A
32	2a	1263	U
32	2a	1264	C
32	2a	1268	A
32	2a	1269	A
32	2a	1279	C
32	2a	1281	A
32	2a	1284	U
32	2a	1285	C

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Mol	Chain	Res	Type
32	2a	1287	G
32	2a	1293	G
32	2a	1302	C
32	2a	1304	C
32	2a	1305	G
32	2a	1307	C
32	2a	1308	C
32	2a	1320	G
32	2a	1328	A
32	2a	1329	G
32	2a	1339	A
32	2a	1341	C
32	2a	1342	A
32	2a	1345	C
32	2a	1347	U
32	2a	1351	G
32	2a	1353	G
32	2a	1361	C
32	2a	1380	C
32	2a	1381	A
32	2a	1388	G
32	2a	1402	G
32	2a	1407	C
32	2a	1425	G
32	2a	1426	G
32	2a	1431	U
32	2a	1433	C
32	2a	1434	G
32	2a	1477	A
32	2a	1480	A
32	2a	1481	A
32	2a	1482	G
32	2a	1483	G
32	2a	1484	U
32	2a	1495	G
32	2a	1497	A
32	2a	1498	G
32	2a	1507	G
32	2a	1508	G
32	2a	1509	A
32	2a	1510	U
53	2v	15	A

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Mol	Chain	Res	Type
54	2x	9	G
54	2x	13	C
54	2x	16	C
54	2x	17	C
54	2x	17(A)	U
54	2x	20	U
54	2x	21	A
54	2x	31	G
54	2x	42	G
54	2x	47	U
54	2x	51	C
54	2x	55	PSU
54	2x	56	C
54	2x	65	C
54	2x	76	A

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	183	A
1	1A	184	A
1	1A	187	A
1	1A	237	C
1	1A	301	A
1	1A	516	A
1	1A	715	G
1	1A	792	A
1	1A	810	A
1	1A	820	A
1	1A	822	G
1	1A	873	U
1	1A	1002	U
1	1A	1018	G
1	1A	1153	U
1	1A	1218	A
1	1A	1220	G
1	1A	1285	U
1	1A	1425	G
1	1A	1465	U
1	1A	1653	A
1	1A	2013	G
1	1A	2208	G

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Mol	Chain	Res	Type
1	1A	2417	U
1	1A	2433	A
1	1A	2441	A
1	1A	2450	A
1	1A	2700	U
1	2A	184	A
1	2A	237	C
1	2A	270	U
1	2A	272	G
1	2A	300	C
1	2A	333	A
1	2A	516	A
1	2A	669	C
1	2A	820	A
1	2A	902	C
1	2A	945	A
1	2A	1047	G
1	2A	1090	A
1	2A	1102	A
1	2A	1114	A
1	2A	1238	A
1	2A	1425	G
1	2A	1465	U
1	2A	1604	A
1	2A	1653	A
1	2A	1934	A
1	2A	2013	G
1	2A	2328	C
1	2A	2417	U
1	2A	2450	A
1	2A	2700	U
2	2B	42	C
2	2B	45	A

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

8 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	$\#\|Z\| > 2$
54	5MC	1x	32	54	19,22,23	1.51	3 (15%)	26,32,35	1.29	2 (7%)
54	PSU	1x	55	54	18,21,22	1.28	2 (11%)	21,30,33	1.97	4 (19%)
54	4SU	2x	8	54	18,21,22	1.88	5 (27%)	25,30,33	1.07	3 (12%)
54	5MU	2x	54	54	19,22,23	1.41	4 (21%)	27,32,35	1.90	6 (22%)
54	PSU	2x	55	54	18,21,22	1.44	1 (5%)	21,30,33	2.00	3 (14%)
54	4SU	1x	8	54	18,21,22	2.17	5 (27%)	25,30,33	1.61	5 (20%)
54	5MC	2x	32	54	19,22,23	1.62	2 (10%)	26,32,35	1.45	3 (11%)
54	5MU	1x	54	54	19,22,23	1.46	4 (21%)	27,32,35	1.95	6 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	5MC	1x	32	54	-	0/7/25/26	0/2/2/2
54	PSU	1x	55	54	-	0/7/25/26	0/2/2/2
54	4SU	2x	8	54	-	0/7/25/26	0/2/2/2
54	5MU	2x	54	54	-	0/7/25/26	0/2/2/2
54	PSU	2x	55	54	-	2/7/25/26	0/2/2/2
54	4SU	1x	8	54	-	0/7/25/26	0/2/2/2
54	5MC	2x	32	54	-	1/7/25/26	0/2/2/2
54	5MU	1x	54	54	-	0/7/25/26	0/2/2/2

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2x	32	5MC	C5-C4	5.45	1.48	1.44
54	1x	8	4SU	C4-N3	-5.42	1.32	1.37
54	1x	32	5MC	C5-C4	5.12	1.48	1.44
54	2x	55	PSU	C6-C5	4.48	1.40	1.35
54	1x	8	4SU	C4-S4	-4.44	1.60	1.68
54	2x	8	4SU	C4-N3	-4.39	1.33	1.37
54	1x	8	4SU	C2-N3	-3.98	1.31	1.38
54	2x	8	4SU	C4-S4	-3.98	1.61	1.68
54	1x	55	PSU	C6-C5	3.54	1.39	1.35
54	2x	8	4SU	C2-N3	-3.14	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2x	32	5MC	C6-C5	3.14	1.39	1.34
54	1x	54	5MU	C4-N3	-3.13	1.33	1.38
54	1x	8	4SU	C5-C4	-3.07	1.38	1.42
54	2x	54	5MU	C6-C5	2.97	1.39	1.34
54	1x	54	5MU	C6-C5	2.97	1.39	1.34
54	1x	32	5MC	C6-C5	2.87	1.39	1.34
54	2x	8	4SU	C5-C4	-2.62	1.39	1.42
54	2x	54	5MU	C2-N1	2.43	1.42	1.38
54	1x	32	5MC	C6-N1	-2.43	1.33	1.38
54	2x	54	5MU	C4-N3	-2.39	1.34	1.38
54	1x	55	PSU	C4-N3	-2.36	1.34	1.38
54	2x	54	5MU	C4-C5	2.29	1.48	1.44
54	2x	8	4SU	C6-C5	2.21	1.40	1.35
54	1x	54	5MU	C2-N3	-2.17	1.34	1.38
54	1x	54	5MU	C2-N1	2.16	1.41	1.38
54	1x	8	4SU	C6-C5	2.11	1.40	1.35

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2x	55	PSU	N1-C2-N3	6.14	121.64	115.17
54	1x	55	PSU	N1-C2-N3	5.60	121.08	115.17
54	2x	54	5MU	N3-C2-N1	4.75	121.07	114.89
54	1x	8	4SU	C6-C5-C4	-4.74	115.84	119.95
54	1x	54	5MU	C5-C4-N3	4.69	119.40	115.32
54	1x	54	5MU	C4-N3-C2	-4.43	121.53	127.34
54	1x	55	PSU	C4-N3-C2	-4.41	120.30	126.37
54	1x	54	5MU	C5-C6-N1	-4.34	118.60	123.31
54	2x	54	5MU	C4-N3-C2	-4.33	121.66	127.34
54	2x	32	5MC	O2-C2-N3	-4.25	115.63	122.33
54	1x	32	5MC	C5-C6-N1	-4.24	118.71	123.31
54	1x	54	5MU	N3-C2-N1	4.05	120.16	114.89
54	1x	54	5MU	O4-C4-C5	-3.88	120.48	124.92
54	2x	54	5MU	O4-C4-C5	-3.87	120.48	124.92
54	2x	55	PSU	O2-C2-N1	-3.86	118.81	122.79
54	2x	55	PSU	C4-N3-C2	-3.82	121.11	126.37
54	2x	54	5MU	C5-C4-N3	3.48	118.35	115.32
54	2x	32	5MC	C5-C6-N1	-3.26	119.77	123.31
54	1x	8	4SU	C4-N3-C2	3.15	130.34	127.31
54	1x	8	4SU	S4-C4-N3	-3.15	116.91	120.20
54	2x	32	5MC	C5-C4-N3	-3.04	118.64	121.75
54	1x	32	5MC	C5-C4-N3	-3.04	118.64	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1x	8	4SU	O2-C2-N1	2.67	126.27	122.80
54	2x	54	5MU	C5-C6-N1	-2.65	120.44	123.31
54	1x	55	PSU	O2-C2-N1	-2.62	120.08	122.79
54	2x	8	4SU	C6-C5-C4	-2.48	117.80	119.95
54	2x	54	5MU	O2-C2-N1	-2.45	119.60	122.80
54	1x	8	4SU	C5-C4-N3	2.33	116.92	114.75
54	1x	55	PSU	C5-C6-N1	-2.24	119.03	122.14
54	2x	8	4SU	C5-C4-N3	2.20	116.80	114.75
54	2x	8	4SU	C1'-N1-C2	2.09	121.34	117.59
54	1x	54	5MU	O2-C2-N1	-2.09	120.08	122.80

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	2x	55	PSU	O4'-C4'-C5'-O5'
54	2x	55	PSU	C3'-C4'-C5'-O5'
54	2x	32	5MC	C2'-C1'-N1-C6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	2x	55	PSU	1	0
54	1x	8	4SU	2	0
54	2x	32	5MC	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2444 ligands modelled in this entry, 2442 are monoatomic - leaving 2 for Mogul analysis.

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
58	SF4	1d	301	35	0,12,12	-	-	-		
58	SF4	2d	501	35	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SF4	1d	301	35	-	-	0/6/5/5
58	SF4	2d	501	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	2746/2915 (94%)	-0.53	31 (1%) 78 70	23, 42, 86, 108	0
1	2A	2790/2915 (95%)	-0.42	16 (0%) 85 80	27, 47, 93, 110	0
2	1B	120/121 (99%)	-0.03	0 100 100	36, 64, 82, 95	0
2	2B	120/121 (99%)	0.65	4 (3%) 49 39	43, 70, 85, 96	0
3	1D	275/276 (99%)	-0.32	2 (0%) 84 77	21, 41, 57, 80	0
3	2D	275/276 (99%)	-0.31	3 (1%) 78 70	24, 43, 60, 80	0
4	1E	204/206 (99%)	-0.27	1 (0%) 87 82	20, 44, 67, 83	0
4	2E	204/206 (99%)	-0.19	0 100 100	24, 48, 69, 84	0
5	1F	203/210 (96%)	0.02	1 (0%) 87 82	23, 51, 77, 93	0
5	2F	203/210 (96%)	0.08	1 (0%) 87 82	27, 55, 79, 94	0
6	1G	181/182 (99%)	0.51	10 (5%) 30 23	52, 70, 83, 96	0
6	2G	181/182 (99%)	1.13	22 (12%) 8 6	58, 74, 85, 96	0
7	1H	174/180 (96%)	0.61	5 (2%) 53 43	49, 65, 77, 89	0
7	2H	174/180 (96%)	0.97	8 (4%) 37 29	55, 70, 81, 91	0
8	1I	146/148 (98%)	0.38	5 (3%) 48 39	48, 75, 85, 89	0
8	2I	146/148 (98%)	0.44	4 (2%) 56 46	51, 76, 86, 91	0
9	1N	140/140 (100%)	0.02	1 (0%) 84 77	33, 47, 69, 82	0
9	2N	140/140 (100%)	0.01	0 100 100	36, 52, 71, 84	0
10	1O	122/122 (100%)	-0.23	0 100 100	32, 44, 63, 71	0
10	2O	122/122 (100%)	-0.18	0 100 100	35, 47, 64, 72	0
11	1P	149/150 (99%)	0.07	0 100 100	24, 54, 76, 85	0
11	2P	149/150 (99%)	0.17	0 100 100	27, 58, 78, 88	0
12	1Q	141/141 (100%)	0.14	3 (2%) 63 54	33, 50, 66, 88	0
12	2Q	141/141 (100%)	0.22	3 (2%) 63 54	37, 54, 69, 85	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.11	0 100 100	31, 40, 55, 66	0
13	2R	118/118 (100%)	-0.19	0 100 100	34, 44, 56, 69	0
14	1S	110/112 (98%)	0.32	2 (1%) 67 58	46, 63, 73, 77	0
14	2S	110/112 (98%)	1.13	13 (11%) 9 7	52, 67, 77, 80	0
15	1T	131/146 (89%)	0.07	4 (3%) 51 41	37, 50, 75, 86	0
15	2T	131/146 (89%)	0.03	2 (1%) 72 63	39, 53, 76, 85	0
16	1U	116/118 (98%)	-0.09	1 (0%) 81 74	28, 40, 56, 75	0
16	2U	116/118 (98%)	-0.00	0 100 100	32, 45, 62, 76	0
17	1V	101/101 (100%)	0.03	0 100 100	29, 49, 68, 80	0
17	2V	101/101 (100%)	0.15	0 100 100	32, 56, 73, 80	0
18	1W	112/113 (99%)	-0.30	0 100 100	27, 37, 57, 91	0
18	2W	112/113 (99%)	-0.26	1 (0%) 81 74	31, 40, 61, 91	0
19	1X	95/96 (98%)	0.10	2 (2%) 63 54	28, 47, 69, 80	0
19	2X	95/96 (98%)	0.32	3 (3%) 50 40	33, 51, 70, 81	0
20	1Y	107/110 (97%)	0.46	1 (0%) 81 74	45, 59, 78, 87	0
20	2Y	107/110 (97%)	0.74	6 (5%) 30 23	51, 63, 81, 90	0
21	1Z	186/206 (90%)	0.33	2 (1%) 78 70	52, 68, 83, 93	0
21	2Z	186/206 (90%)	0.79	8 (4%) 40 31	55, 72, 85, 94	0
22	10	75/85 (88%)	-0.44	0 100 100	16, 36, 52, 67	0
22	20	75/85 (88%)	0.58	3 (4%) 42 33	40, 64, 77, 80	0
23	11	97/98 (98%)	-0.07	1 (1%) 79 72	30, 48, 75, 79	0
23	21	97/98 (98%)	0.13	2 (2%) 63 54	34, 51, 76, 81	0
24	12	70/72 (97%)	0.42	4 (5%) 29 22	42, 59, 73, 82	0
24	22	70/72 (97%)	0.58	2 (2%) 53 43	47, 63, 76, 80	0
25	13	59/60 (98%)	0.17	0 100 100	32, 46, 67, 78	0
25	23	59/60 (98%)	0.19	1 (1%) 69 60	37, 51, 71, 82	0
26	14	69/71 (97%)	0.84	12 (17%) 4 3	63, 82, 95, 99	0
26	24	69/71 (97%)	1.39	17 (24%) 2 1	69, 85, 96, 100	0
27	15	59/60 (98%)	-0.45	0 100 100	22, 38, 57, 73	0
27	25	59/60 (98%)	-0.32	0 100 100	27, 42, 61, 74	0
28	16	53/54 (98%)	-0.22	0 100 100	37, 48, 66, 70	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.06	0 100 100	40, 52, 63, 69	0
29	17	48/49 (97%)	-0.21	2 (4%) 40 32	26, 31, 65, 78	0
29	27	48/49 (97%)	-0.19	2 (4%) 40 32	29, 34, 65, 80	0
30	18	64/65 (98%)	-0.02	0 100 100	34, 41, 53, 61	0
30	28	64/65 (98%)	0.12	0 100 100	37, 45, 57, 64	0
31	19	37/37 (100%)	0.39	2 (5%) 31 24	40, 49, 69, 74	0
31	29	37/37 (100%)	0.74	2 (5%) 31 24	44, 54, 70, 76	0
32	1a	1477/1521 (97%)	0.05	28 (1%) 66 57	35, 71, 97, 112	0
32	2a	1483/1521 (97%)	0.24	26 (1%) 67 58	45, 79, 100, 110	0
33	1b	231/256 (90%)	0.93	24 (10%) 11 8	66, 83, 94, 100	0
33	2b	231/256 (90%)	1.18	35 (15%) 5 4	72, 89, 96, 104	0
34	1c	206/239 (86%)	0.93	18 (8%) 16 11	68, 83, 91, 96	0
34	2c	206/239 (86%)	1.22	26 (12%) 8 6	70, 85, 92, 95	0
35	1d	208/209 (99%)	0.85	13 (6%) 26 19	54, 76, 88, 96	0
35	2d	208/209 (99%)	0.67	6 (2%) 53 43	62, 75, 86, 92	0
36	1e	148/162 (91%)	0.24	3 (2%) 65 56	46, 66, 78, 89	0
36	2e	148/162 (91%)	0.57	4 (2%) 56 46	60, 75, 84, 92	0
37	1f	100/101 (99%)	0.43	3 (3%) 52 42	58, 74, 83, 90	0
37	2f	100/101 (99%)	0.27	1 (1%) 79 72	60, 74, 84, 88	0
38	1g	155/156 (99%)	0.66	12 (7%) 19 14	61, 79, 93, 97	0
38	2g	155/156 (99%)	0.87	21 (13%) 7 5	69, 80, 92, 97	0
39	1h	137/138 (99%)	0.32	0 100 100	54, 69, 79, 86	0
39	2h	137/138 (99%)	0.65	7 (5%) 33 25	65, 77, 86, 91	0
40	1i	127/128 (99%)	1.12	21 (16%) 4 3	64, 86, 93, 96	0
40	2i	127/128 (99%)	1.94	50 (39%) 1 0	64, 88, 95, 96	0
41	1j	97/105 (92%)	1.44	21 (21%) 2 2	63, 86, 95, 98	0
41	2j	96/105 (91%)	1.88	41 (42%) 0 0	76, 91, 99, 101	0
42	1k	114/129 (88%)	0.24	3 (2%) 57 47	40, 69, 83, 92	0
42	2k	114/129 (88%)	0.38	4 (3%) 47 38	53, 76, 86, 93	0
43	1l	122/132 (92%)	0.34	6 (4%) 35 27	46, 62, 73, 79	0
43	2l	122/132 (92%)	0.46	3 (2%) 58 48	56, 69, 78, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	118/126 (93%)	0.67	6 (5%) 33 25	65, 80, 87, 92	0
44	2m	116/126 (92%)	1.32	15 (12%) 7 6	70, 83, 89, 93	0
45	1n	60/61 (98%)	1.10	8 (13%) 7 5	63, 75, 88, 89	0
45	2n	60/61 (98%)	2.23	32 (53%) 0 0	76, 87, 92, 96	0
46	1o	88/89 (98%)	0.29	1 (1%) 78 70	51, 67, 82, 90	0
46	2o	88/89 (98%)	0.32	0 100 100	59, 73, 83, 89	0
47	1p	82/88 (93%)	1.07	8 (9%) 13 9	60, 78, 87, 93	0
47	2p	82/88 (93%)	0.71	2 (2%) 59 49	62, 70, 82, 91	0
48	1q	99/105 (94%)	0.41	0 100 100	51, 69, 80, 84	0
48	2q	99/105 (94%)	0.48	4 (4%) 42 33	59, 73, 83, 90	0
49	1r	68/88 (77%)	0.31	1 (1%) 72 63	58, 70, 84, 87	0
49	2r	68/88 (77%)	0.33	0 100 100	63, 73, 85, 90	0
50	1s	84/93 (90%)	0.91	6 (7%) 22 16	68, 81, 90, 95	0
50	2s	83/93 (89%)	1.78	30 (36%) 1 0	82, 91, 99, 104	0
51	1t	96/106 (90%)	0.81	8 (8%) 17 12	61, 75, 84, 93	0
51	2t	96/106 (90%)	0.59	7 (7%) 21 15	55, 73, 84, 88	0
52	1u	23/27 (85%)	1.44	5 (21%) 2 2	71, 78, 80, 84	0
52	2u	23/27 (85%)	2.26	14 (60%) 0 0	73, 80, 85, 86	0
53	1v	5/24 (20%)	1.06	1 (20%) 3 2	61, 64, 90, 97	0
53	2v	5/24 (20%)	0.71	1 (20%) 3 2	65, 68, 91, 97	0
54	1x	72/77 (93%)	-0.43	0 100 100	28, 58, 83, 92	0
54	2x	72/77 (93%)	0.06	1 (1%) 73 64	41, 79, 91, 102	0
55	1z	12/14 (85%)	1.12	4 (33%) 1 1	23, 39, 59, 84	0
55	2z	12/14 (85%)	0.79	2 (16%) 4 3	26, 42, 64, 85	0
All	All	20520/21472 (95%)	0.14	747 (3%) 46 37	16, 62, 92, 112	0

All (747) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
55	2z	12	PRO	7.2
32	1a	980	G	6.1
7	1H	2	SER	5.8
55	1z	12	PRO	5.8
32	1a	981	G	5.6

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Mol	Chain	Res	Type	RSRZ
20	1Y	1	MET	5.4
1	1A	2815	G	5.2
45	1n	2	ALA	5.1
40	2i	29	ASN	5.0
32	2a	980	G	4.9
38	1g	80	VAL	4.9
29	17	48	LYS	4.8
45	2n	21	TYR	4.8
41	2j	40	LEU	4.7
26	24	49	PHE	4.7
45	2n	17	LYS	4.6
38	2g	16	LEU	4.6
41	2j	63	PHE	4.6
50	2s	13	ASP	4.6
34	2c	186	PHE	4.6
41	2j	100	THR	4.6
32	2a	981	G	4.6
45	2n	18	VAL	4.5
38	1g	83	ALA	4.4
23	11	2	SER	4.3
45	2n	2	ALA	4.3
50	2s	35	SER	4.3
12	1Q	59	ARG	4.3
45	2n	34	TYR	4.3
51	2t	9	ASN	4.3
50	2s	2	PRO	4.2
32	2a	1268	A	4.2
40	2i	102	LEU	4.2
33	2b	133	LYS	4.2
52	2u	14	TRP	4.1
52	2u	17	THR	4.1
44	2m	102	ARG	4.1
41	2j	44	VAL	4.0
32	1a	979	A	4.0
26	24	56	VAL	4.0
1	1A	2813	C	4.0
40	1i	2	GLU	4.0
38	1g	78	ARG	3.9
1	1A	1149	C	3.9
40	2i	126	SER	3.9
40	2i	7	THR	3.9
31	29	37	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
32	2a	1184	G	3.9
45	2n	33	VAL	3.9
35	1d	23	GLY	3.9
50	2s	84	GLY	3.9
45	2n	25	VAL	3.9
40	2i	9	ARG	3.9
40	2i	66	ARG	3.9
15	2T	131	ALA	3.9
1	1A	33	C	3.9
36	1e	22	GLY	3.8
38	2g	78	ARG	3.8
51	1t	10	LEU	3.8
33	2b	134	GLU	3.8
34	1c	184	TYR	3.8
33	2b	187	LEU	3.8
41	2j	65	LEU	3.8
33	1b	214	ILE	3.7
1	1A	8	U	3.7
34	2c	2	GLY	3.7
38	1g	84	ASN	3.7
53	1v	14	A	3.7
31	19	12	ASP	3.7
51	1t	18	GLN	3.7
47	1p	68	ASP	3.7
50	2s	49	ILE	3.7
1	2A	1582	C	3.6
50	1s	13	ASP	3.6
29	27	48	LYS	3.6
40	2i	10	ARG	3.6
40	2i	42	ARG	3.6
41	2j	47	PHE	3.6
26	14	57	GLU	3.6
40	2i	36	TYR	3.6
50	1s	9	VAL	3.6
23	21	2	SER	3.6
34	1c	28	GLN	3.6
45	2n	16	PHE	3.6
32	1a	1268	A	3.6
26	24	50	VAL	3.6
1	2A	2815	G	3.5
51	1t	103	GLY	3.5
38	2g	5	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
40	2i	68	GLY	3.5
6	2G	28	VAL	3.5
33	2b	196	LEU	3.5
22	20	10	THR	3.5
15	1T	131	ALA	3.5
40	2i	119	ALA	3.5
24	12	70	GLN	3.5
34	1c	2	GLY	3.5
34	1c	201	TYR	3.5
1	1A	2814	C	3.4
40	2i	16	ARG	3.4
40	1i	106	ALA	3.4
40	2i	15	ALA	3.4
51	1t	9	ASN	3.4
40	1i	15	ALA	3.4
33	2b	236	TYR	3.4
26	14	59	PHE	3.4
41	1j	63	PHE	3.4
52	2u	16	GLY	3.4
1	1A	2812	G	3.4
32	1a	982	G	3.4
33	1b	237	ALA	3.4
40	2i	5	TYR	3.4
26	14	49	PHE	3.4
38	2g	156	TRP	3.4
32	2a	979	A	3.4
50	2s	71	LEU	3.3
52	2u	11	GLY	3.3
15	1T	130	ALA	3.3
20	2Y	1	MET	3.3
40	1i	13	ALA	3.3
41	1j	46	ARG	3.3
45	2n	3	ARG	3.3
15	1T	37	GLY	3.3
26	24	65	ASP	3.3
40	2i	105	ASP	3.3
50	2s	12	ASP	3.3
12	1Q	60	ARG	3.3
50	2s	40	ILE	3.3
33	2b	97	TRP	3.3
45	2n	37	PHE	3.2
52	1u	24	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
40	2i	11	LYS	3.2
40	2i	2	GLU	3.2
50	2s	14	HIS	3.2
6	1G	51	ARG	3.2
33	2b	190	THR	3.2
32	1a	1509	A	3.2
35	2d	154	ASN	3.2
38	1g	79	ARG	3.2
41	2j	76	ASN	3.2
44	2m	60	VAL	3.2
41	2j	58	ASP	3.1
1	1A	934	C	3.1
40	2i	67	GLY	3.1
6	1G	35	GLU	3.1
35	1d	155	LEU	3.1
38	1g	156	TRP	3.1
45	2n	30	ALA	3.1
33	2b	101	MET	3.1
41	2j	75	ILE	3.1
41	1j	31	GLY	3.1
45	2n	15	LYS	3.1
51	2t	10	LEU	3.1
33	2b	152	PHE	3.0
38	2g	80	VAL	3.0
50	2s	9	VAL	3.0
50	2s	4	SER	3.0
25	23	2	PRO	3.0
1	1A	9	G	3.0
1	1A	1220	G	3.0
34	2c	6	HIS	3.0
45	2n	49	HIS	3.0
1	1A	2806	C	3.0
14	2S	7	TYR	3.0
33	2b	150	SER	3.0
36	1e	20	GLN	3.0
41	2j	78	ASN	3.0
24	12	69	ARG	3.0
45	2n	13	THR	3.0
14	2S	34	HIS	3.0
43	2l	18	VAL	3.0
41	1j	10	GLY	3.0
43	1l	91	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
38	2g	38	LEU	3.0
40	1i	64	THR	3.0
34	2c	180	ALA	3.0
40	2i	17	VAL	3.0
16	1U	117	GLN	3.0
1	2A	2812	G	3.0
33	2b	237	ALA	3.0
26	14	56	VAL	3.0
40	2i	14	VAL	3.0
40	2i	109	VAL	3.0
41	2j	5	ARG	2.9
52	2u	15	ARG	2.9
52	2u	13	ILE	2.9
6	2G	53	LEU	2.9
38	2g	12	LEU	2.9
8	1I	10	GLU	2.9
55	1z	10	PRO	2.9
2	2B	23	G	2.9
1	1A	1554	C	2.9
45	2n	20	ALA	2.9
52	2u	6	ARG	2.9
45	2n	42	ILE	2.9
47	1p	19	ILE	2.9
20	2Y	90	LEU	2.9
40	2i	62	TYR	2.9
41	1j	64	GLU	2.9
40	1i	126	SER	2.9
50	2s	38	SER	2.9
45	2n	5	ALA	2.9
1	2A	2801	C	2.9
32	1a	158	C	2.9
14	2S	58	LEU	2.9
35	1d	154	ASN	2.9
33	1b	165	VAL	2.9
14	2S	20	ARG	2.9
45	2n	35	ARG	2.9
51	2t	8	ARG	2.9
40	2i	19	LEU	2.9
32	1a	1121	G	2.9
32	2a	1265	G	2.9
40	2i	21	PRO	2.9
26	14	53	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
33	2b	136	VAL	2.9
44	2m	118	ALA	2.9
34	1c	158	GLY	2.8
38	1g	81	GLY	2.8
36	2e	20	GLN	2.8
51	1t	14	LYS	2.8
40	2i	65	VAL	2.8
38	2g	37	ASN	2.8
45	1n	59	ALA	2.8
40	2i	37	PHE	2.8
52	2u	9	ARG	2.8
45	2n	39	LEU	2.8
1	1A	571	A	2.8
26	24	45	GLY	2.8
32	1a	211	U	2.8
33	2b	92	TYR	2.8
50	2s	29	ARG	2.8
42	1k	36	ASP	2.8
48	2q	98	LEU	2.8
26	14	50	VAL	2.8
33	2b	21	ARG	2.8
45	1n	5	ALA	2.8
2	2B	88	C	2.8
43	1l	126	LYS	2.8
32	2a	1206	G	2.8
26	24	57	GLU	2.8
52	1u	15	ARG	2.8
29	27	46	VAL	2.8
22	20	69	PHE	2.8
33	1b	188	ALA	2.8
35	2d	155	LEU	2.8
50	2s	31	ILE	2.8
8	2I	11	ASN	2.8
6	2G	74	LYS	2.8
41	2j	55	LYS	2.8
38	2g	82	GLY	2.8
51	2t	103	GLY	2.8
33	2b	135	GLN	2.7
12	2Q	59	ARG	2.7
40	2i	125	TYR	2.7
41	1j	76	ASN	2.7
7	2H	82	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
52	1u	2	GLY	2.7
44	1m	94	ARG	2.7
1	1A	1098	C	2.7
38	1g	2	ALA	2.7
14	2S	35	ILE	2.7
39	2h	94	TYR	2.7
43	2l	126	LYS	2.7
40	1i	105	ASP	2.7
47	2p	82	GLN	2.7
34	1c	207	VAL	2.7
32	2a	1231	C	2.7
40	1i	102	LEU	2.7
51	2t	74	LYS	2.7
40	1i	67	GLY	2.7
41	2j	87	THR	2.7
32	2a	1025	G	2.7
34	2c	124	ILE	2.7
41	2j	38	ILE	2.7
50	1s	85	LYS	2.7
20	2Y	5	MET	2.7
12	2Q	60	ARG	2.7
40	2i	107	ARG	2.7
45	2n	22	THR	2.7
32	2a	1207	A	2.7
33	1b	12	GLU	2.7
45	2n	7	ILE	2.6
3	2D	2	ALA	2.6
41	2j	32	ALA	2.6
1	2A	1216	G	2.6
1	2A	1579	G	2.6
1	2A	2902	G	2.6
32	2a	1172	G	2.6
44	2m	64	TRP	2.6
19	1X	65	ARG	2.6
39	2h	122	ARG	2.6
1	1A	2209	C	2.6
41	2j	99	LYS	2.6
44	1m	2	ALA	2.6
45	1n	16	PHE	2.6
41	1j	62	HIS	2.6
2	2B	118	G	2.6
43	2l	64	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
41	1j	100	THR	2.6
34	2c	129	ALA	2.6
1	1A	553	A	2.6
51	2t	25	ARG	2.6
55	2z	11	ARG	2.6
38	1g	82	GLY	2.6
41	2j	37	PRO	2.6
7	1H	133	VAL	2.6
33	1b	7	VAL	2.6
34	2c	44	GLU	2.6
41	1j	78	ASN	2.6
45	2n	8	GLU	2.6
44	2m	33	ALA	2.6
44	2m	75	ALA	2.6
32	1a	978	U	2.6
26	14	55	ARG	2.6
18	2W	112	GLY	2.6
35	2d	87	GLY	2.6
45	2n	38	GLY	2.6
33	2b	197	VAL	2.6
41	1j	98	ILE	2.6
3	2D	28	GLU	2.6
14	2S	29	PHE	2.6
38	2g	84	ASN	2.6
40	2i	13	ALA	2.6
44	2m	76	ALA	2.6
50	2s	74	PHE	2.6
32	1a	1239	U	2.5
34	1c	190	ARG	2.5
44	1m	102	ARG	2.5
52	2u	3	LYS	2.5
1	1A	2811	A	2.5
33	1b	97	TRP	2.5
14	2S	32	LEU	2.5
14	2S	45	GLY	2.5
34	2c	155	GLY	2.5
34	1c	193	TYR	2.5
35	1d	188	LEU	2.5
39	2h	2	LEU	2.5
44	2m	90	LEU	2.5
8	2I	81	VAL	2.5
21	2Z	1	MET	2.5

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Mol	Chain	Res	Type	RSRZ
37	1f	88	VAL	2.5
40	1i	65	VAL	2.5
40	2i	108	VAL	2.5
55	1z	1	VAL	2.5
33	1b	28	PHE	2.5
47	1p	82	GLN	2.5
41	2j	66	ARG	2.5
55	1z	11	ARG	2.5
6	2G	32	PRO	2.5
19	1X	95	LEU	2.5
40	2i	63	ILE	2.5
51	1t	55	ILE	2.5
26	24	63	TYR	2.5
33	2b	144	ARG	2.5
32	2a	1239	U	2.5
40	2i	99	LEU	2.5
41	1j	93	GLY	2.5
7	2H	79	VAL	2.5
32	2a	1021	C	2.5
38	2g	154	TYR	2.5
41	1j	47	PHE	2.5
48	2q	24	GLU	2.5
33	2b	188	ALA	2.5
33	2b	137	ARG	2.5
38	2g	4	ARG	2.5
40	1i	10	ARG	2.5
42	2k	126	ARG	2.5
35	2d	2	GLY	2.5
41	2j	93	GLY	2.5
51	2t	11	SER	2.5
33	1b	93	VAL	2.5
40	2i	41	VAL	2.5
7	1H	58	GLU	2.5
33	2b	70	PHE	2.5
15	2T	130	ALA	2.5
34	2c	179	ARG	2.5
35	1d	164	ALA	2.5
41	1j	32	ALA	2.5
42	2k	13	GLN	2.5
1	1A	2206	C	2.5
32	1a	1120	C	2.5
44	2m	31	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2901	G	2.5
32	2a	993	A	2.5
32	2a	1165	A	2.5
37	2f	89	MET	2.4
6	2G	20	ILE	2.4
14	2S	28	VAL	2.4
34	1c	185	GLY	2.4
34	2c	185	GLY	2.4
43	1l	89	ARG	2.4
50	2s	34	TRP	2.4
6	1G	80	PHE	2.4
34	2c	170	GLN	2.4
36	1e	21	ALA	2.4
44	1m	27	LYS	2.4
33	1b	10	LEU	2.4
34	2c	178	LEU	2.4
50	1s	71	LEU	2.4
40	2i	81	ILE	2.4
40	1i	28	VAL	2.4
41	2j	49	VAL	2.4
40	1i	12	GLU	2.4
41	2j	27	ALA	2.4
33	1b	236	TYR	2.4
47	2p	69	THR	2.4
6	2G	175	LEU	2.4
19	2X	92	LEU	2.4
1	1A	2904	C	2.4
1	2A	1120	C	2.4
41	2j	77	PRO	2.4
6	2G	31	VAL	2.4
14	1S	93	LYS	2.4
35	2d	49	ARG	2.4
41	1j	5	ARG	2.4
50	2s	3	ARG	2.4
24	12	37	PHE	2.4
32	1a	1025	G	2.4
32	2a	1337	G	2.4
33	1b	70	PHE	2.4
45	2n	36	PHE	2.4
38	2g	83	ALA	2.4
2	2B	1	U	2.4
32	1a	209	U	2.4

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Mol	Chain	Res	Type	RSRZ
32	2a	1510	U	2.4
21	2Z	9	TYR	2.4
26	24	67	TYR	2.4
42	1k	25	TYR	2.4
47	1p	39	TYR	2.4
34	2c	5	ILE	2.4
33	1b	229	VAL	2.4
12	2Q	22	LYS	2.4
40	1i	69	GLY	2.4
44	2m	6	GLY	2.4
29	17	47	ARG	2.4
45	2n	9	LYS	2.4
1	1A	2205	G	2.4
1	1A	2905	U	2.4
26	14	52	THR	2.4
26	24	44	THR	2.4
52	2u	8	THR	2.4
6	2G	19	LEU	2.4
34	1c	39	ILE	2.4
33	1b	130	ARG	2.3
38	2g	79	ARG	2.3
42	2k	117	ASN	2.3
44	2m	100	GLY	2.3
6	1G	48	GLU	2.3
6	2G	61	ALA	2.3
15	1T	126	ALA	2.3
35	2d	156	GLU	2.3
41	2j	20	ALA	2.3
41	2j	26	ALA	2.3
41	2j	64	GLU	2.3
1	1A	1934	A	2.3
33	1b	187	LEU	2.3
33	2b	31	TYR	2.3
41	1j	8	LEU	2.3
41	2j	48	THR	2.3
44	2m	87	TYR	2.3
45	1n	13	THR	2.3
24	22	8	LYS	2.3
1	2A	1089	G	2.3
38	2g	76	ARG	2.3
40	2i	28	VAL	2.3
41	2j	43	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
45	2n	19	ARG	2.3
52	1u	10	ARG	2.3
33	2b	99	GLY	2.3
39	2h	131	GLY	2.3
50	2s	8	GLY	2.3
6	2G	102	PHE	2.3
33	1b	134	GLU	2.3
8	1I	35	LEU	2.3
38	1g	77	SER	2.3
7	2H	111	HIS	2.3
26	24	40	HIS	2.3
1	2A	1091	A	2.3
8	1I	29	TYR	2.3
26	24	52	THR	2.3
45	1n	7	ILE	2.3
50	2s	33	THR	2.3
32	1a	1024	A	2.3
47	1p	3	LYS	2.3
7	2H	112	PRO	2.3
14	2S	3	ARG	2.3
45	2n	29	ARG	2.3
34	2c	64	VAL	2.3
39	2h	53	VAL	2.3
34	2c	10	PHE	2.3
1	1A	2804	G	2.3
6	2G	35	GLU	2.3
32	1a	1002	G	2.3
40	2i	45	ALA	2.3
21	2Z	5	LEU	2.3
45	2n	44	LEU	2.3
14	1S	59	LYS	2.3
45	2n	4	LYS	2.3
51	1t	21	LYS	2.3
41	2j	81	THR	2.3
52	1u	9	ARG	2.3
47	1p	41	PRO	2.3
1	1A	669	C	2.3
8	1I	90	GLY	2.3
23	21	29	GLY	2.3
40	2i	39	GLY	2.3
3	1D	28	GLU	2.3
34	1c	206	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
41	2j	83	GLU	2.3
6	2G	172	LEU	2.3
24	22	70	GLN	2.3
40	2i	96	LEU	2.3
44	2m	78	ILE	2.3
35	1d	159	ARG	2.3
41	2j	30	SER	2.3
52	2u	10	ARG	2.3
21	2Z	175	VAL	2.3
40	2i	53	VAL	2.3
1	2A	2900	A	2.2
34	2c	128	PHE	2.2
6	2G	50	ALA	2.2
8	2I	10	GLU	2.2
31	19	28	GLU	2.2
40	2i	73	GLN	2.2
26	24	51	ASP	2.2
46	1o	3	ILE	2.2
33	1b	40	HIS	2.2
47	1p	22	THR	2.2
50	2s	67	VAL	2.2
1	2A	2816	G	2.2
32	1a	614	G	2.2
32	2a	951	G	2.2
32	2a	982	G	2.2
26	14	54	GLY	2.2
1	2A	1071	U	2.2
8	2I	146	ALA	2.2
21	2Z	184	ALA	2.2
32	1a	160	C	2.2
32	2a	957	C	2.2
41	1j	33	GLN	2.2
20	2Y	107	ASP	2.2
34	1c	6	HIS	2.2
35	1d	102	ASP	2.2
5	2F	6	VAL	2.2
7	2H	169	VAL	2.2
34	2c	130	VAL	2.2
41	2j	42	THR	2.2
44	2m	63	THR	2.2
7	2H	2	SER	2.2
26	24	54	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
34	2c	158	GLY	2.2
6	2G	139	LEU	2.2
32	1a	96	G	2.2
32	1a	376	G	2.2
34	1c	52	LEU	2.2
34	1c	90	GLU	2.2
20	2Y	57	GLN	2.2
26	24	58	ARG	2.2
33	2b	189	ASP	2.2
6	2G	15	VAL	2.2
6	2G	160	VAL	2.2
7	2H	115	VAL	2.2
33	2b	131	PRO	2.2
40	1i	14	VAL	2.2
41	1j	24	VAL	2.2
6	1G	25	TYR	2.2
33	2b	148	TYR	2.2
35	1d	137	SER	2.2
44	1m	59	TYR	2.2
3	2D	38	LYS	2.2
6	1G	182	LYS	2.2
20	2Y	34	LYS	2.2
45	1n	4	LYS	2.2
35	1d	162	LEU	2.2
41	1j	40	LEU	2.2
50	2s	16	LEU	2.2
31	29	5	ALA	2.2
34	1c	160	ALA	2.2
36	2e	81	GLU	2.2
39	2h	99	GLU	2.2
40	2i	61	ALA	2.2
40	2i	106	ALA	2.2
34	2c	182	ILE	2.2
38	1g	5	ARG	2.2
50	1s	56	GLN	2.2
1	1A	10	G	2.2
33	2b	16	HIS	2.2
1	2A	678	A	2.2
32	1a	516	A	2.2
32	1a	1432	A	2.2
38	2g	21	VAL	2.2
41	1j	34	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
3	1D	276	LYS	2.2
40	1i	68	GLY	2.2
40	2i	30	GLY	2.2
34	1c	23	TYR	2.2
40	2i	59	PHE	2.2
52	2u	21	TYR	2.2
4	1E	195	LEU	2.2
40	1i	19	LEU	2.2
36	2e	94	ALA	2.2
40	2i	46	ALA	2.2
50	2s	36	ARG	2.1
1	1A	270	U	2.1
1	1A	1150	U	2.1
32	2a	1201	U	2.1
33	2b	140	HIS	2.1
6	1G	2	PRO	2.1
43	1l	18	VAL	2.1
51	1t	74	LYS	2.1
1	1A	2802	A	2.1
32	2a	1339	A	2.1
34	1c	78	GLY	2.1
1	1A	1097	C	2.1
45	2n	6	LEU	2.1
6	1G	54	GLU	2.1
33	1b	201	ILE	2.1
33	2b	172	ILE	2.1
6	2G	2	PRO	2.1
6	2G	17	PRO	2.1
32	1a	66	U	2.1
33	1b	234	PRO	2.1
36	2e	10	MET	2.1
44	2m	97	PRO	2.1
14	2S	59	LYS	2.1
12	1Q	33	GLY	2.1
41	2j	52	GLY	2.1
50	2s	68	GLY	2.1
33	2b	138	LEU	2.1
6	2G	46	ALA	2.1
7	1H	3	ARG	2.1
32	2a	1432	A	2.1
34	2c	184	TYR	2.1
40	1i	125	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
53	2v	14	A	2.1
6	1G	30	GLU	2.1
1	1A	935	C	2.1
14	2S	31	SER	2.1
32	1a	988	G	2.1
32	2a	1469	G	2.1
35	1d	80	GLU	2.1
41	1j	4	ILE	2.1
41	2j	59	SER	2.1
7	2H	8	PRO	2.1
24	12	15	LYS	2.1
34	2c	26	LYS	2.1
35	1d	8	VAL	2.1
41	2j	24	VAL	2.1
48	2q	9	VAL	2.1
39	2h	101	PRO	2.1
40	2i	85	LEU	2.1
41	2j	8	LEU	2.1
41	2j	10	GLY	2.1
43	1l	63	GLY	2.1
22	20	43	THR	2.1
38	1g	32	ARG	2.1
6	2G	48	GLU	2.1
33	1b	127	ILE	2.1
37	1f	99	ALA	2.1
40	1i	63	ILE	2.1
43	1l	64	TYR	2.1
50	2s	80	TYR	2.1
26	24	66	SER	2.1
9	1N	140	VAL	2.1
14	2S	93	LYS	2.1
26	24	69	LYS	2.1
32	1a	162	G	2.1
33	1b	132	LYS	2.1
50	2s	69	HIS	2.1
40	1i	109	VAL	2.1
49	1r	86	VAL	2.1
8	1I	8	PRO	2.1
34	1c	7	PRO	2.1
50	2s	59	PRO	2.1
33	1b	149	LEU	2.1
41	1j	90	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
32	1a	1023	U	2.1
34	2c	25	GLY	2.1
21	1Z	69	THR	2.1
40	2i	128	ARG	2.1
42	2k	36	ASP	2.1
45	1n	12	ARG	2.1
47	1p	42	ARG	2.1
33	2b	80	ILE	2.1
34	2c	167	TRP	2.1
41	2j	6	ILE	2.1
6	2G	137	GLU	2.1
21	2Z	11	GLU	2.1
26	14	63	TYR	2.1
48	2q	100	LYS	2.0
1	2A	1129	A	2.0
7	1H	131	VAL	2.0
21	1Z	180	VAL	2.0
33	2b	81	VAL	2.0
42	1k	14	VAL	2.0
5	1F	14	PRO	2.0
52	2u	23	PRO	2.0
32	1a	64	C	2.0
1	1A	2901	G	2.0
19	2X	68	ARG	2.0
32	2a	1202	G	2.0
35	1d	2	GLY	2.0
35	1d	153	ARG	2.0
38	2g	34	GLY	2.0
41	2j	60	ARG	2.0
50	2s	10	PHE	2.0
50	2s	37	ARG	2.0
32	1a	168	U	2.0
21	2Z	87	ASP	2.0
33	2b	108	ILE	2.0
33	2b	171	ALA	2.0
34	2c	187	ALA	2.0
38	2g	7	ALA	2.0
44	1m	118	ALA	2.0
45	2n	10	ALA	2.0
6	2G	146	TYR	2.0
26	14	67	TYR	2.0
40	2i	117	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
41	2j	34	VAL	2.0
41	2j	72	VAL	2.0
21	2Z	95	PRO	2.0
19	2X	95	LEU	2.0
33	2b	44	LEU	2.0
34	2c	52	LEU	2.0
50	2s	5	LEU	2.0
38	2g	32	ARG	2.0
38	2g	109	ASN	2.0
50	1s	65	ASN	2.0
26	14	64	GLY	2.0
26	24	42	PHE	2.0
38	2g	43	PHE	2.0
40	1i	8	GLY	2.0
40	2i	18	PHE	2.0
52	2u	19	GLY	2.0
32	2a	1132	C	2.0
33	1b	222	ILE	2.0
33	2b	201	ILE	2.0
6	1G	50	ALA	2.0
41	2j	67	THR	2.0
54	2x	47	U	2.0
34	2c	45	LYS	2.0
40	2i	127	LYS	2.0
45	2n	61	TRP	2.0
33	1b	136	VAL	2.0
37	1f	90	VAL	2.0
50	2s	60	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
54	PSU	2x	55	20/21	0.77	0.13	67,79,90,98	0
54	5MU	2x	54	21/22	0.87	0.11	66,79,92,102	0
54	5MC	2x	32	21/22	0.89	0.14	72,77,87,99	0
54	4SU	2x	8	20/21	0.91	0.09	68,80,91,95	0
54	5MU	1x	54	21/22	0.92	0.09	48,57,75,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
54	PSU	1x	55	20/21	0.93	0.08	49,60,75,77	0
54	5MC	1x	32	21/22	0.94	0.10	50,57,66,75	0
54	4SU	1x	8	20/21	0.96	0.07	51,58,69,71	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
56	MG	1a	1791	1/1	0.21	0.29	89,89,89,89	0
56	MG	2a	3137	1/1	0.24	0.22	97,97,97,97	0
56	MG	1A	3409	1/1	0.35	0.37	81,81,81,81	0
56	MG	1a	1780	1/1	0.49	0.23	93,93,93,93	0
56	MG	1B	214	1/1	0.52	0.24	80,80,80,80	0
56	MG	2A	3469	1/1	0.60	0.29	67,67,67,67	0
56	MG	1A	3893	1/1	0.60	0.19	69,69,69,69	0
56	MG	2a	3244	1/1	0.60	0.20	76,76,76,76	0
56	MG	1a	1787	1/1	0.61	0.30	70,70,70,70	0
56	MG	2a	3152	1/1	0.61	0.26	89,89,89,89	0
56	MG	2a	3077	1/1	0.61	0.24	95,95,95,95	0
56	MG	1a	1788	1/1	0.62	0.31	81,81,81,81	0
56	MG	2a	3027	1/1	0.63	0.13	88,88,88,88	0
56	MG	2A	3495	1/1	0.64	0.36	75,75,75,75	0
56	MG	1a	1812	1/1	0.64	0.30	78,78,78,78	0
56	MG	1a	1789	1/1	0.64	0.26	78,78,78,78	0
56	MG	1A	3451	1/1	0.65	0.17	81,81,81,81	0
56	MG	2a	3168	1/1	0.65	0.17	83,83,83,83	0
56	MG	2a	3220	1/1	0.65	0.44	87,87,87,87	0
56	MG	1A	3339	1/1	0.65	0.25	78,78,78,78	0
56	MG	2a	3213	1/1	0.66	0.18	87,87,87,87	0
56	MG	1A	3954	1/1	0.66	0.23	83,83,83,83	0
56	MG	1a	1804	1/1	0.66	0.23	88,88,88,88	0
56	MG	1A	3940	1/1	0.67	0.20	78,78,78,78	0
56	MG	1a	1786	1/1	0.67	0.25	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1881	1/1	0.67	0.27	84,84,84,84	0
56	MG	2a	3040	1/1	0.67	0.27	83,83,83,83	0
56	MG	2A	3459	1/1	0.67	0.26	70,70,70,70	0
56	MG	2a	3108	1/1	0.67	0.23	79,79,79,79	0
56	MG	1A	4020	1/1	0.68	0.21	67,67,67,67	0
56	MG	1A	3481	1/1	0.68	0.18	76,76,76,76	0
56	MG	1a	1760	1/1	0.69	0.33	78,78,78,78	0
56	MG	1a	1813	1/1	0.69	0.15	99,99,99,99	0
56	MG	2a	3149	1/1	0.69	0.30	100,100,100,100	0
56	MG	2A	3502	1/1	0.69	0.27	75,75,75,75	0
56	MG	1a	1762	1/1	0.70	0.16	80,80,80,80	0
56	MG	2a	3178	1/1	0.70	0.31	75,75,75,75	0
56	MG	2a	3023	1/1	0.70	0.35	74,74,74,74	0
56	MG	1A	3340	1/1	0.70	0.16	56,56,56,56	0
56	MG	2a	3155	1/1	0.70	0.22	91,91,91,91	0
56	MG	2A	3578	1/1	0.71	0.14	58,58,58,58	0
56	MG	1A	3262	1/1	0.71	0.16	58,58,58,58	0
56	MG	2a	3186	1/1	0.71	0.22	80,80,80,80	0
56	MG	2a	3191	1/1	0.71	0.28	66,66,66,66	0
56	MG	1a	1667	1/1	0.71	0.45	68,68,68,68	0
56	MG	1a	1753	1/1	0.71	0.15	83,83,83,83	0
56	MG	2A	3437	1/1	0.71	0.26	83,83,83,83	0
56	MG	1a	1613	1/1	0.72	0.27	76,76,76,76	0
56	MG	1A	3476	1/1	0.72	0.16	66,66,66,66	0
56	MG	1a	1688	1/1	0.72	0.25	76,76,76,76	0
56	MG	1A	3990	1/1	0.72	0.28	64,64,64,64	0
56	MG	2A	3525	1/1	0.72	0.16	53,53,53,53	0
56	MG	1a	1826	1/1	0.72	0.26	80,80,80,80	0
56	MG	2B	3008	1/1	0.72	0.23	73,73,73,73	0
56	MG	1a	1756	1/1	0.72	0.26	93,93,93,93	0
56	MG	1r	3002	1/1	0.72	0.20	85,85,85,85	0
56	MG	2A	3256	1/1	0.72	0.16	79,79,79,79	0
56	MG	2a	3041	1/1	0.72	0.24	79,79,79,79	0
56	MG	2a	3243	1/1	0.72	0.16	58,58,58,58	0
56	MG	1B	225	1/1	0.72	0.14	77,77,77,77	0
56	MG	2a	3056	1/1	0.73	0.48	79,79,79,79	0
56	MG	1a	1889	1/1	0.73	0.22	64,64,64,64	0
56	MG	1A	3994	1/1	0.73	0.15	51,51,51,51	0
56	MG	2A	3180	1/1	0.73	0.23	52,52,52,52	0
56	MG	1A	3068	1/1	0.73	0.25	67,67,67,67	0
56	MG	1a	1768	1/1	0.74	0.20	90,90,90,90	0
56	MG	11	101	1/1	0.74	0.15	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3197	1/1	0.74	0.22	74,74,74,74	0
56	MG	1A	3984	1/1	0.74	0.21	77,77,77,77	0
56	MG	1A	3069	1/1	0.74	0.10	65,65,65,65	0
56	MG	2G	3001	1/1	0.74	0.15	60,60,60,60	0
56	MG	1E	307	1/1	0.74	0.19	74,74,74,74	0
56	MG	1A	3508	1/1	0.75	0.15	64,64,64,64	0
56	MG	2a	3084	1/1	0.75	0.22	75,75,75,75	0
56	MG	1A	3964	1/1	0.75	0.25	76,76,76,76	0
56	MG	1A	3322	1/1	0.75	0.20	63,63,63,63	0
56	MG	1A	3901	1/1	0.75	0.21	68,68,68,68	0
56	MG	1G	3002	1/1	0.75	0.24	69,69,69,69	0
56	MG	1x	110	1/1	0.75	0.26	78,78,78,78	0
56	MG	2B	3002	1/1	0.75	0.21	70,70,70,70	0
56	MG	2a	3176	1/1	0.75	0.34	87,87,87,87	0
56	MG	2A	3023	1/1	0.75	0.07	55,55,55,55	0
56	MG	1N	204	1/1	0.75	0.15	59,59,59,59	0
56	MG	1A	3364	1/1	0.75	0.26	57,57,57,57	0
56	MG	2A	3288	1/1	0.75	0.20	70,70,70,70	0
56	MG	2A	3394	1/1	0.75	0.27	61,61,61,61	0
56	MG	2A	3395	1/1	0.75	0.19	78,78,78,78	0
56	MG	2a	3047	1/1	0.75	0.11	89,89,89,89	0
56	MG	14	502	1/1	0.75	0.23	79,79,79,79	0
56	MG	1B	221	1/1	0.76	0.17	63,63,63,63	0
56	MG	2a	3048	1/1	0.76	0.15	91,91,91,91	0
56	MG	1A	3514	1/1	0.76	0.19	72,72,72,72	0
56	MG	1a	1891	1/1	0.76	0.32	82,82,82,82	0
56	MG	1A	3817	1/1	0.76	0.26	61,61,61,61	0
56	MG	18	101	1/1	0.76	0.21	66,66,66,66	0
56	MG	1a	1759	1/1	0.76	0.23	82,82,82,82	0
56	MG	2a	3215	1/1	0.76	0.32	80,80,80,80	0
56	MG	1a	1820	1/1	0.76	0.31	82,82,82,82	0
56	MG	1A	3439	1/1	0.76	0.17	50,50,50,50	0
56	MG	2A	3503	1/1	0.76	0.13	61,61,61,61	0
56	MG	2a	3014	1/1	0.77	0.28	74,74,74,74	0
56	MG	1A	3665	1/1	0.77	0.23	64,64,64,64	0
56	MG	2a	3153	1/1	0.77	0.16	99,99,99,99	0
56	MG	1A	3745	1/1	0.77	0.26	54,54,54,54	0
56	MG	2a	3158	1/1	0.77	0.32	72,72,72,72	0
56	MG	2A	3498	1/1	0.77	0.13	69,69,69,69	0
56	MG	1a	1766	1/1	0.77	0.21	79,79,79,79	0
56	MG	1a	1752	1/1	0.77	0.21	72,72,72,72	0
56	MG	2a	3124	1/1	0.78	0.33	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3133	1/1	0.78	0.17	93,93,93,93	0
56	MG	2A	3278	1/1	0.78	0.17	65,65,65,65	0
56	MG	1A	3921	1/1	0.78	0.18	80,80,80,80	0
56	MG	1N	201	1/1	0.78	0.23	70,70,70,70	0
56	MG	2a	3010	1/1	0.78	0.26	83,83,83,83	0
56	MG	1A	3501	1/1	0.78	0.14	83,83,83,83	0
56	MG	2A	3404	1/1	0.78	0.24	69,69,69,69	0
56	MG	1P	201	1/1	0.78	0.21	55,55,55,55	0
56	MG	2a	3034	1/1	0.78	0.42	72,72,72,72	0
56	MG	1A	3941	1/1	0.78	0.22	73,73,73,73	0
56	MG	1A	3472	1/1	0.78	0.17	66,66,66,66	0
56	MG	1a	1795	1/1	0.78	0.16	64,64,64,64	0
56	MG	1A	3303	1/1	0.78	0.24	48,48,48,48	0
56	MG	2A	3137	1/1	0.78	0.15	55,55,55,55	0
56	MG	1A	3980	1/1	0.78	0.39	63,63,63,63	0
56	MG	2a	3081	1/1	0.78	0.25	69,69,69,69	0
56	MG	2a	3233	1/1	0.78	0.25	66,66,66,66	0
56	MG	2A	3206	1/1	0.78	0.19	64,64,64,64	0
56	MG	1A	3098	1/1	0.78	0.30	71,71,71,71	0
56	MG	2d	503	1/1	0.78	0.21	72,72,72,72	0
56	MG	2A	3202	1/1	0.79	0.10	50,50,50,50	0
56	MG	2a	3088	1/1	0.79	0.26	73,73,73,73	0
56	MG	1A	3368	1/1	0.79	0.22	50,50,50,50	0
56	MG	2A	3529	1/1	0.79	0.16	62,62,62,62	0
56	MG	1A	3815	1/1	0.79	0.14	52,52,52,52	0
56	MG	2A	3267	1/1	0.79	0.24	63,63,63,63	0
56	MG	1A	3415	1/1	0.79	0.19	73,73,73,73	0
56	MG	2B	3010	1/1	0.79	0.26	66,66,66,66	0
56	MG	1A	3842	1/1	0.79	0.29	55,55,55,55	0
56	MG	2a	3004	1/1	0.79	0.12	87,87,87,87	0
56	MG	2A	3320	1/1	0.79	0.19	67,67,67,67	0
56	MG	2a	3159	1/1	0.79	0.24	76,76,76,76	0
56	MG	1T	203	1/1	0.79	0.17	69,69,69,69	0
56	MG	2a	3020	1/1	0.79	0.15	72,72,72,72	0
56	MG	1a	1906	1/1	0.79	0.12	83,83,83,83	0
56	MG	1A	3852	1/1	0.79	0.21	72,72,72,72	0
56	MG	1B	223	1/1	0.79	0.17	74,74,74,74	0
56	MG	2A	3438	1/1	0.79	0.33	70,70,70,70	0
56	MG	2a	3201	1/1	0.79	0.15	83,83,83,83	0
56	MG	2a	3210	1/1	0.79	0.25	69,69,69,69	0
56	MG	2A	3457	1/1	0.79	0.20	55,55,55,55	0
56	MG	1A	3438	1/1	0.79	0.15	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3083	1/1	0.79	0.23	66,66,66,66	0
56	MG	2A	3093	1/1	0.79	0.27	64,64,64,64	0
56	MG	2a	3058	1/1	0.79	0.13	66,66,66,66	0
56	MG	1A	3376	1/1	0.79	0.17	60,60,60,60	0
56	MG	1a	1617	1/1	0.79	0.39	74,74,74,74	0
56	MG	2A	3360	1/1	0.80	0.20	73,73,73,73	0
56	MG	1A	3011	1/1	0.80	0.39	65,65,65,65	0
56	MG	2a	3144	1/1	0.80	0.25	75,75,75,75	0
56	MG	2a	3002	1/1	0.80	0.25	68,68,68,68	0
56	MG	1A	3949	1/1	0.80	0.17	59,59,59,59	0
56	MG	1A	3330	1/1	0.80	0.23	62,62,62,62	0
56	MG	2a	3154	1/1	0.80	0.25	84,84,84,84	0
56	MG	2A	3431	1/1	0.80	0.19	68,68,68,68	0
56	MG	1a	1663	1/1	0.80	0.18	67,67,67,67	0
56	MG	1A	3850	1/1	0.80	0.23	80,80,80,80	0
56	MG	1A	3073	1/1	0.80	0.12	74,74,74,74	0
56	MG	2a	3169	1/1	0.80	0.13	75,75,75,75	0
56	MG	1a	1712	1/1	0.80	0.27	65,65,65,65	0
56	MG	2A	3462	1/1	0.80	0.27	74,74,74,74	0
56	MG	1A	3867	1/1	0.80	0.33	40,40,40,40	0
56	MG	1a	1800	1/1	0.80	0.21	84,84,84,84	0
56	MG	1A	3989	1/1	0.80	0.27	70,70,70,70	0
56	MG	1a	1810	1/1	0.80	0.18	86,86,86,86	0
56	MG	1A	3402	1/1	0.80	0.17	73,73,73,73	0
56	MG	1A	3462	1/1	0.80	0.20	45,45,45,45	0
56	MG	1T	205	1/1	0.80	0.23	66,66,66,66	0
56	MG	1A	3091	1/1	0.80	0.21	61,61,61,61	0
56	MG	2a	3226	1/1	0.80	0.36	75,75,75,75	0
56	MG	2A	3580	1/1	0.80	0.17	51,51,51,51	0
56	MG	2a	3099	1/1	0.80	0.27	63,63,63,63	0
56	MG	1a	1866	1/1	0.80	0.39	72,72,72,72	0
56	MG	1A	3412	1/1	0.80	0.29	77,77,77,77	0
56	MG	2n	502	1/1	0.80	0.43	73,73,73,73	0
56	MG	2A	3364	1/1	0.81	0.15	55,55,55,55	0
56	MG	2A	3390	1/1	0.81	0.21	63,63,63,63	0
56	MG	1A	3816	1/1	0.81	0.11	67,67,67,67	0
56	MG	1x	107	1/1	0.81	0.16	64,64,64,64	0
56	MG	2a	3007	1/1	0.81	0.20	91,91,91,91	0
56	MG	1A	3307	1/1	0.81	0.20	75,75,75,75	0
56	MG	1A	3702	1/1	0.81	0.20	73,73,73,73	0
56	MG	2a	3017	1/1	0.81	0.31	68,68,68,68	0
56	MG	2A	3025	1/1	0.81	0.20	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3074	1/1	0.81	0.12	47,47,47,47	0
56	MG	2a	3164	1/1	0.81	0.30	65,65,65,65	0
56	MG	2A	3451	1/1	0.81	0.18	63,63,63,63	0
56	MG	1A	3963	1/1	0.81	0.20	54,54,54,54	0
56	MG	1B	208	1/1	0.81	0.20	61,61,61,61	0
56	MG	2A	3135	1/1	0.81	0.10	48,48,48,48	0
56	MG	2a	3045	1/1	0.81	0.10	81,81,81,81	0
56	MG	1a	1680	1/1	0.81	0.20	57,57,57,57	0
56	MG	1a	1770	1/1	0.81	0.16	87,87,87,87	0
56	MG	1A	3296	1/1	0.81	0.20	47,47,47,47	0
56	MG	2a	3205	1/1	0.81	0.32	78,78,78,78	0
56	MG	1a	1827	1/1	0.81	0.22	63,63,63,63	0
56	MG	1a	1843	1/1	0.81	0.21	71,71,71,71	0
56	MG	1a	1695	1/1	0.81	0.20	77,77,77,77	0
56	MG	1A	3922	1/1	0.81	0.19	75,75,75,75	0
56	MG	1A	3640	1/1	0.81	0.16	70,70,70,70	0
56	MG	1A	3986	1/1	0.81	0.16	44,44,44,44	0
56	MG	2a	3102	1/1	0.81	0.32	72,72,72,72	0
56	MG	2A	3333	1/1	0.81	0.25	61,61,61,61	0
56	MG	1a	1754	1/1	0.81	0.13	53,53,53,53	0
56	MG	2a	3125	1/1	0.81	0.31	66,66,66,66	0
56	MG	1A	3297	1/1	0.82	0.29	59,59,59,59	0
56	MG	2A	3359	1/1	0.82	0.20	75,75,75,75	0
56	MG	2a	3140	1/1	0.82	0.23	83,83,83,83	0
56	MG	1b	3001	1/1	0.82	0.25	83,83,83,83	0
56	MG	1q	202	1/1	0.82	0.26	62,62,62,62	0
56	MG	1A	3022	1/1	0.82	0.14	66,66,66,66	0
56	MG	1A	3444	1/1	0.82	0.17	65,65,65,65	0
56	MG	1A	3450	1/1	0.82	0.19	64,64,64,64	0
56	MG	1a	1748	1/1	0.82	0.25	61,61,61,61	0
56	MG	1A	3575	1/1	0.82	0.10	39,39,39,39	0
56	MG	2A	3068	1/1	0.82	0.29	68,68,68,68	0
56	MG	1A	3585	1/1	0.82	0.09	68,68,68,68	0
56	MG	2A	3441	1/1	0.82	0.15	51,51,51,51	0
56	MG	1A	3866	1/1	0.82	0.17	65,65,65,65	0
56	MG	2a	3175	1/1	0.82	0.17	53,53,53,53	0
56	MG	2a	3038	1/1	0.82	0.18	85,85,85,85	0
56	MG	2A	3453	1/1	0.82	0.29	83,83,83,83	0
56	MG	1A	3277	1/1	0.82	0.23	68,68,68,68	0
56	MG	2a	3188	1/1	0.82	0.27	74,74,74,74	0
56	MG	2A	3132	1/1	0.82	0.12	62,62,62,62	0
56	MG	1A	3341	1/1	0.82	0.14	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3686	1/1	0.82	0.16	58,58,58,58	0
56	MG	1A	3345	1/1	0.82	0.22	64,64,64,64	0
56	MG	1A	3001	1/1	0.82	0.15	45,45,45,45	0
56	MG	1a	1836	1/1	0.82	0.25	59,59,59,59	0
56	MG	2A	3246	1/1	0.82	0.18	67,67,67,67	0
56	MG	2A	3509	1/1	0.82	0.17	80,80,80,80	0
56	MG	1A	3808	1/1	0.82	0.32	57,57,57,57	0
56	MG	1a	1624	1/1	0.82	0.16	65,65,65,65	0
56	MG	2A	3565	1/1	0.82	0.17	62,62,62,62	0
56	MG	1a	1774	1/1	0.82	0.26	63,63,63,63	0
56	MG	1A	3811	1/1	0.82	0.12	50,50,50,50	0
56	MG	1A	3943	1/1	0.82	0.22	35,35,35,35	0
56	MG	1a	1775	1/1	0.83	0.28	65,65,65,65	0
56	MG	1A	3480	1/1	0.83	0.20	75,75,75,75	0
56	MG	2a	3089	1/1	0.83	0.21	75,75,75,75	0
56	MG	2A	3032	1/1	0.83	0.24	50,50,50,50	0
56	MG	1a	1782	1/1	0.83	0.12	67,67,67,67	0
56	MG	1A	4006	1/1	0.83	0.11	77,77,77,77	0
56	MG	1a	1601	1/1	0.83	0.15	66,66,66,66	0
56	MG	2A	3500	1/1	0.83	0.13	57,57,57,57	0
56	MG	1A	3716	1/1	0.83	0.14	53,53,53,53	0
56	MG	1A	3244	1/1	0.83	0.24	55,55,55,55	0
56	MG	2a	3138	1/1	0.83	0.20	73,73,73,73	0
56	MG	1A	3491	1/1	0.83	0.13	83,83,83,83	0
56	MG	1a	1654	1/1	0.83	0.15	67,67,67,67	0
56	MG	1B	215	1/1	0.83	0.13	68,68,68,68	0
56	MG	1A	3020	1/1	0.83	0.16	56,56,56,56	0
56	MG	2A	3205	1/1	0.83	0.17	62,62,62,62	0
56	MG	1A	3442	1/1	0.83	0.40	57,57,57,57	0
56	MG	2A	3240	1/1	0.83	0.29	57,57,57,57	0
56	MG	1A	3401	1/1	0.83	0.15	67,67,67,67	0
56	MG	1A	3516	1/1	0.83	0.13	75,75,75,75	0
56	MG	1A	3839	1/1	0.83	0.12	54,54,54,54	0
56	MG	2a	3001	1/1	0.83	0.23	54,54,54,54	0
56	MG	1a	1735	1/1	0.83	0.19	72,72,72,72	0
56	MG	1H	204	1/1	0.83	0.12	62,62,62,62	0
56	MG	2A	3297	1/1	0.83	0.13	49,49,49,49	0
56	MG	1A	3556	1/1	0.83	0.17	70,70,70,70	0
56	MG	2a	3182	1/1	0.83	0.10	64,64,64,64	0
56	MG	1N	202	1/1	0.83	0.30	49,49,49,49	0
56	MG	2A	3335	1/1	0.83	0.18	52,52,52,52	0
56	MG	1A	3304	1/1	0.83	0.18	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3194	1/1	0.83	0.39	75,75,75,75	0
56	MG	1a	1867	1/1	0.83	0.14	51,51,51,51	0
56	MG	1O	201	1/1	0.83	0.13	54,54,54,54	0
56	MG	1A	3161	1/1	0.83	0.18	61,61,61,61	0
56	MG	2A	3393	1/1	0.83	0.19	71,71,71,71	0
56	MG	1A	3308	1/1	0.83	0.30	64,64,64,64	0
56	MG	1A	3167	1/1	0.83	0.19	59,59,59,59	0
56	MG	1Y	502	1/1	0.83	0.23	59,59,59,59	0
56	MG	1Z	303	1/1	0.83	0.11	64,64,64,64	0
56	MG	2a	3227	1/1	0.83	0.24	81,81,81,81	0
56	MG	10	105	1/1	0.83	0.24	57,57,57,57	0
56	MG	1x	101	1/1	0.83	0.24	69,69,69,69	0
56	MG	1a	1771	1/1	0.83	0.15	75,75,75,75	0
56	MG	1A	3422	1/1	0.83	0.10	72,72,72,72	0
56	MG	1x	111	1/1	0.83	0.26	80,80,80,80	0
56	MG	2q	201	1/1	0.83	0.25	71,71,71,71	0
56	MG	2x	3004	1/1	0.83	0.15	74,74,74,74	0
56	MG	1a	1604	1/1	0.84	0.32	70,70,70,70	0
56	MG	1A	3315	1/1	0.84	0.08	51,51,51,51	0
56	MG	1A	3798	1/1	0.84	0.16	59,59,59,59	0
56	MG	1A	3054	1/1	0.84	0.30	56,56,56,56	0
56	MG	1a	1625	1/1	0.84	0.22	78,78,78,78	0
56	MG	1a	1650	1/1	0.84	0.30	72,72,72,72	0
56	MG	1a	1652	1/1	0.84	0.33	65,65,65,65	0
56	MG	1A	3219	1/1	0.84	0.23	63,63,63,63	0
56	MG	2A	3076	1/1	0.84	0.27	61,61,61,61	0
56	MG	2A	3482	1/1	0.84	0.23	63,63,63,63	0
56	MG	2a	3134	1/1	0.84	0.33	79,79,79,79	0
56	MG	2A	3082	1/1	0.84	0.19	56,56,56,56	0
56	MG	1E	303	1/1	0.84	0.30	51,51,51,51	0
56	MG	1A	3331	1/1	0.84	0.12	53,53,53,53	0
56	MG	2a	3142	1/1	0.84	0.18	83,83,83,83	0
56	MG	2A	3098	1/1	0.84	0.16	53,53,53,53	0
56	MG	2A	3129	1/1	0.84	0.13	55,55,55,55	0
56	MG	2a	3150	1/1	0.84	0.18	63,63,63,63	0
56	MG	1a	1677	1/1	0.84	0.25	61,61,61,61	0
56	MG	2A	3521	1/1	0.84	0.12	59,59,59,59	0
56	MG	1A	3067	1/1	0.84	0.11	64,64,64,64	0
56	MG	1A	3517	1/1	0.84	0.25	56,56,56,56	0
56	MG	2a	3157	1/1	0.84	0.33	66,66,66,66	0
56	MG	2A	3174	1/1	0.84	0.17	48,48,48,48	0
56	MG	1a	1807	1/1	0.84	0.13	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1690	1/1	0.84	0.25	82,82,82,82	0
56	MG	1A	3837	1/1	0.84	0.23	74,74,74,74	0
56	MG	1A	3039	1/1	0.84	0.13	54,54,54,54	0
56	MG	1A	3459	1/1	0.84	0.20	57,57,57,57	0
56	MG	1A	3053	1/1	0.84	0.18	38,38,38,38	0
56	MG	1A	3413	1/1	0.84	0.14	60,60,60,60	0
56	MG	1A	3859	1/1	0.84	0.16	59,59,59,59	0
56	MG	1A	3991	1/1	0.84	0.20	53,53,53,53	0
56	MG	1a	1864	1/1	0.84	0.20	68,68,68,68	0
56	MG	2a	3008	1/1	0.84	0.27	60,60,60,60	0
56	MG	2A	3292	1/1	0.84	0.13	60,60,60,60	0
56	MG	1a	1865	1/1	0.84	0.13	65,65,65,65	0
56	MG	1a	1755	1/1	0.84	0.17	60,60,60,60	0
56	MG	1A	3414	1/1	0.84	0.17	79,79,79,79	0
56	MG	1a	1758	1/1	0.84	0.10	64,64,64,64	0
56	MG	1A	3678	1/1	0.84	0.12	67,67,67,67	0
56	MG	1A	4010	1/1	0.84	0.31	58,58,58,58	0
56	MG	2a	3036	1/1	0.84	0.16	73,73,73,73	0
56	MG	1a	1892	1/1	0.84	0.32	67,67,67,67	0
56	MG	2A	3369	1/1	0.84	0.17	65,65,65,65	0
56	MG	1A	3285	1/1	0.84	0.50	79,79,79,79	0
56	MG	2a	3234	1/1	0.84	0.32	79,79,79,79	0
56	MG	1A	4035	1/1	0.84	0.20	81,81,81,81	0
56	MG	1f	3001	1/1	0.84	0.19	66,66,66,66	0
56	MG	1A	3350	1/1	0.84	0.14	65,65,65,65	0
56	MG	2A	3396	1/1	0.84	0.15	44,44,44,44	0
56	MG	1a	1769	1/1	0.84	0.19	74,74,74,74	0
56	MG	1A	3487	1/1	0.84	0.21	64,64,64,64	0
56	MG	1A	3975	1/1	0.85	0.11	63,63,63,63	0
56	MG	1H	203	1/1	0.85	0.17	60,60,60,60	0
56	MG	1A	3642	1/1	0.85	0.09	67,67,67,67	0
56	MG	1A	3239	1/1	0.85	0.19	41,41,41,41	0
56	MG	2a	3093	1/1	0.85	0.20	62,62,62,62	0
56	MG	1A	3269	1/1	0.85	0.16	56,56,56,56	0
56	MG	2A	3097	1/1	0.85	0.18	54,54,54,54	0
56	MG	1A	3513	1/1	0.85	0.12	72,72,72,72	0
56	MG	2a	3109	1/1	0.85	0.37	73,73,73,73	0
56	MG	1a	1732	1/1	0.85	0.24	53,53,53,53	0
56	MG	1A	3090	1/1	0.85	0.19	53,53,53,53	0
56	MG	1A	3479	1/1	0.85	0.17	78,78,78,78	0
56	MG	2A	3497	1/1	0.85	0.14	49,49,49,49	0
56	MG	1a	1750	1/1	0.85	0.18	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3138	1/1	0.85	0.14	62,62,62,62	0
56	MG	1a	1829	1/1	0.85	0.21	73,73,73,73	0
56	MG	1A	3720	1/1	0.85	0.26	64,64,64,64	0
56	MG	2A	3189	1/1	0.85	0.26	61,61,61,61	0
56	MG	2a	3148	1/1	0.85	0.15	77,77,77,77	0
56	MG	2A	3511	1/1	0.85	0.10	50,50,50,50	0
56	MG	1A	3253	1/1	0.85	0.21	81,81,81,81	0
56	MG	1A	3899	1/1	0.85	0.20	53,53,53,53	0
56	MG	1A	4012	1/1	0.85	0.30	81,81,81,81	0
56	MG	2A	3535	1/1	0.85	0.12	69,69,69,69	0
56	MG	2A	3213	1/1	0.85	0.14	67,67,67,67	0
56	MG	1A	4018	1/1	0.85	0.18	62,62,62,62	0
56	MG	2A	3244	1/1	0.85	0.15	73,73,73,73	0
56	MG	1A	3765	1/1	0.85	0.16	56,56,56,56	0
56	MG	1A	3550	1/1	0.85	0.18	58,58,58,58	0
56	MG	1a	1885	1/1	0.85	0.18	66,66,66,66	0
56	MG	2E	305	1/1	0.85	0.14	68,68,68,68	0
56	MG	1B	207	1/1	0.85	0.34	70,70,70,70	0
56	MG	1A	3385	1/1	0.85	0.17	51,51,51,51	0
56	MG	2A	3290	1/1	0.85	0.17	57,57,57,57	0
56	MG	1B	213	1/1	0.85	0.33	65,65,65,65	0
56	MG	1A	3386	1/1	0.85	0.11	51,51,51,51	0
56	MG	1A	3580	1/1	0.85	0.12	68,68,68,68	0
56	MG	1a	1618	1/1	0.85	0.09	65,65,65,65	0
56	MG	1h	3001	1/1	0.85	0.19	74,74,74,74	0
56	MG	1o	3001	1/1	0.85	0.14	77,77,77,77	0
56	MG	1A	3305	1/1	0.85	0.13	83,83,83,83	0
56	MG	1A	3599	1/1	0.85	0.17	51,51,51,51	0
56	MG	1a	1641	1/1	0.85	0.17	70,70,70,70	0
56	MG	2a	3030	1/1	0.85	0.15	59,59,59,59	0
56	MG	1a	1645	1/1	0.85	0.19	71,71,71,71	0
56	MG	1A	3823	1/1	0.85	0.14	39,39,39,39	0
56	MG	1D	305	1/1	0.85	0.17	58,58,58,58	0
56	MG	2a	3039	1/1	0.85	0.23	75,75,75,75	0
56	MG	2A	3006	1/1	0.85	0.08	71,71,71,71	0
56	MG	1A	3828	1/1	0.85	0.17	55,55,55,55	0
56	MG	2a	3241	1/1	0.85	0.31	67,67,67,67	0
56	MG	2A	3397	1/1	0.85	0.20	64,64,64,64	0
56	MG	1a	1658	1/1	0.85	0.13	68,68,68,68	0
56	MG	2A	3417	1/1	0.85	0.17	62,62,62,62	0
56	MG	2A	3425	1/1	0.85	0.40	72,72,72,72	0
56	MG	2p	101	1/1	0.85	0.29	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3492	1/1	0.85	0.08	81,81,81,81	0
56	MG	1F	306	1/1	0.85	0.14	64,64,64,64	0
56	MG	2x	3006	1/1	0.85	0.16	78,78,78,78	0
56	MG	1a	1642	1/1	0.86	0.30	68,68,68,68	0
56	MG	2A	3007	1/1	0.86	0.15	50,50,50,50	0
56	MG	2A	3013	1/1	0.86	0.25	67,67,67,67	0
56	MG	2A	3022	1/1	0.86	0.08	63,63,63,63	0
56	MG	1A	3230	1/1	0.86	0.16	61,61,61,61	0
56	MG	1A	3433	1/1	0.86	0.17	50,50,50,50	0
56	MG	1A	3436	1/1	0.86	0.12	68,68,68,68	0
56	MG	2A	3038	1/1	0.86	0.21	50,50,50,50	0
56	MG	2A	3063	1/1	0.86	0.17	56,56,56,56	0
56	MG	1A	3961	1/1	0.86	0.19	47,47,47,47	0
56	MG	1E	304	1/1	0.86	0.10	64,64,64,64	0
56	MG	1A	3306	1/1	0.86	0.19	62,62,62,62	0
56	MG	1F	302	1/1	0.86	0.30	56,56,56,56	0
56	MG	1A	3594	1/1	0.86	0.23	62,62,62,62	0
56	MG	1A	3295	1/1	0.86	0.20	63,63,63,63	0
56	MG	2A	3467	1/1	0.86	0.20	58,58,58,58	0
56	MG	1A	3490	1/1	0.86	0.15	66,66,66,66	0
56	MG	1A	3982	1/1	0.86	0.24	74,74,74,74	0
56	MG	2A	3483	1/1	0.86	0.13	47,47,47,47	0
56	MG	1a	1816	1/1	0.86	0.14	88,88,88,88	0
56	MG	2a	3143	1/1	0.86	0.11	90,90,90,90	0
56	MG	1A	3146	1/1	0.86	0.09	43,43,43,43	0
56	MG	1a	1821	1/1	0.86	0.11	77,77,77,77	0
56	MG	1a	1824	1/1	0.86	0.19	52,52,52,52	0
56	MG	1a	1700	1/1	0.86	0.28	80,80,80,80	0
56	MG	2A	3154	1/1	0.86	0.28	55,55,55,55	0
56	MG	1A	3342	1/1	0.86	0.11	40,40,40,40	0
56	MG	2A	3178	1/1	0.86	0.16	59,59,59,59	0
56	MG	1a	1718	1/1	0.86	0.25	64,64,64,64	0
56	MG	1A	3988	1/1	0.86	0.32	38,38,38,38	0
56	MG	2A	3198	1/1	0.86	0.28	53,53,53,53	0
56	MG	1A	3848	1/1	0.86	0.22	57,57,57,57	0
56	MG	2A	3537	1/1	0.86	0.21	59,59,59,59	0
56	MG	1A	3264	1/1	0.86	0.23	66,66,66,66	0
56	MG	1A	3505	1/1	0.86	0.10	66,66,66,66	0
56	MG	1A	3317	1/1	0.86	0.15	67,67,67,67	0
56	MG	2A	3225	1/1	0.86	0.21	42,42,42,42	0
56	MG	1A	3709	1/1	0.86	0.20	54,54,54,54	0
56	MG	1a	1878	1/1	0.86	0.17	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2E	304	1/1	0.86	0.57	74,74,74,74	0
56	MG	1A	3454	1/1	0.86	0.21	50,50,50,50	0
56	MG	1A	3021	1/1	0.86	0.17	48,48,48,48	0
56	MG	1a	1888	1/1	0.86	0.24	75,75,75,75	0
56	MG	2A	3268	1/1	0.86	0.15	63,63,63,63	0
56	MG	10	106	1/1	0.86	0.15	62,62,62,62	0
56	MG	1A	3247	1/1	0.86	0.35	72,72,72,72	0
56	MG	1A	3374	1/1	0.86	0.08	59,59,59,59	0
56	MG	2A	3291	1/1	0.86	0.20	56,56,56,56	0
56	MG	1A	4031	1/1	0.86	0.37	54,54,54,54	0
56	MG	2a	3217	1/1	0.86	0.22	59,59,59,59	0
56	MG	18	102	1/1	0.86	0.15	66,66,66,66	0
56	MG	2a	3225	1/1	0.86	0.31	67,67,67,67	0
56	MG	1A	3916	1/1	0.86	0.17	60,60,60,60	0
56	MG	2A	3324	1/1	0.86	0.11	64,64,64,64	0
56	MG	1B	203	1/1	0.86	0.27	66,66,66,66	0
56	MG	1a	1609	1/1	0.86	0.26	60,60,60,60	0
56	MG	2A	3357	1/1	0.86	0.15	75,75,75,75	0
56	MG	1A	3770	1/1	0.86	0.16	68,68,68,68	0
56	MG	1A	3793	1/1	0.86	0.16	72,72,72,72	0
56	MG	2d	502	1/1	0.86	0.37	61,61,61,61	0
56	MG	1t	3001	1/1	0.86	0.21	64,64,64,64	0
56	MG	1A	3927	1/1	0.86	0.30	59,59,59,59	0
56	MG	2A	3386	1/1	0.86	0.15	57,57,57,57	0
56	MG	1A	3938	1/1	0.86	0.17	47,47,47,47	0
56	MG	1A	3528	1/1	0.86	0.21	54,54,54,54	0
56	MG	1A	3474	1/1	0.86	0.12	59,59,59,59	0
56	MG	1a	1697	1/1	0.87	0.26	70,70,70,70	0
56	MG	2A	3027	1/1	0.87	0.18	64,64,64,64	0
56	MG	2A	3030	1/1	0.87	0.17	57,57,57,57	0
56	MG	2A	3391	1/1	0.87	0.16	61,61,61,61	0
56	MG	1A	3485	1/1	0.87	0.18	67,67,67,67	0
56	MG	1A	3378	1/1	0.87	0.15	53,53,53,53	0
56	MG	2a	3054	1/1	0.87	0.10	83,83,83,83	0
56	MG	2A	3048	1/1	0.87	0.25	57,57,57,57	0
56	MG	1A	3597	1/1	0.87	0.13	49,49,49,49	0
56	MG	1a	1722	1/1	0.87	0.22	60,60,60,60	0
56	MG	1a	1815	1/1	0.87	0.18	70,70,70,70	0
56	MG	1A	3337	1/1	0.87	0.18	48,48,48,48	0
56	MG	1A	3088	1/1	0.87	0.21	52,52,52,52	0
56	MG	1a	1737	1/1	0.87	0.34	66,66,66,66	0
56	MG	1a	1743	1/1	0.87	0.39	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3393	1/1	0.87	0.21	46,46,46,46	0
56	MG	1a	1749	1/1	0.87	0.15	66,66,66,66	0
56	MG	2A	3099	1/1	0.87	0.23	45,45,45,45	0
56	MG	2A	3115	1/1	0.87	0.27	54,54,54,54	0
56	MG	2a	3118	1/1	0.87	0.24	68,68,68,68	0
56	MG	1A	3834	1/1	0.87	0.23	58,58,58,58	0
56	MG	1A	3240	1/1	0.87	0.14	48,48,48,48	0
56	MG	1A	3309	1/1	0.87	0.19	65,65,65,65	0
56	MG	1a	1848	1/1	0.87	0.12	85,85,85,85	0
56	MG	1a	1855	1/1	0.87	0.32	75,75,75,75	0
56	MG	2A	3475	1/1	0.87	0.23	67,67,67,67	0
56	MG	2A	3140	1/1	0.87	0.21	62,62,62,62	0
56	MG	1A	3680	1/1	0.87	0.21	71,71,71,71	0
56	MG	2A	3486	1/1	0.87	0.12	51,51,51,51	0
56	MG	2A	3167	1/1	0.87	0.22	58,58,58,58	0
56	MG	1A	3507	1/1	0.87	0.15	93,93,93,93	0
56	MG	1a	1619	1/1	0.87	0.17	71,71,71,71	0
56	MG	1a	1621	1/1	0.87	0.17	83,83,83,83	0
56	MG	1A	3983	1/1	0.87	0.18	62,62,62,62	0
56	MG	2A	3192	1/1	0.87	0.08	45,45,45,45	0
56	MG	2A	3196	1/1	0.87	0.09	37,37,37,37	0
56	MG	1A	3698	1/1	0.87	0.20	46,46,46,46	0
56	MG	2A	3520	1/1	0.87	0.29	75,75,75,75	0
56	MG	1a	1627	1/1	0.87	0.20	68,68,68,68	0
56	MG	2A	3523	1/1	0.87	0.15	57,57,57,57	0
56	MG	1a	1639	1/1	0.87	0.07	70,70,70,70	0
56	MG	1A	3199	1/1	0.87	0.26	48,48,48,48	0
56	MG	2A	3212	1/1	0.87	0.25	58,58,58,58	0
56	MG	1A	3858	1/1	0.87	0.14	52,52,52,52	0
56	MG	2A	3220	1/1	0.87	0.30	50,50,50,50	0
56	MG	2A	3572	1/1	0.87	0.25	61,61,61,61	0
56	MG	1a	1644	1/1	0.87	0.17	68,68,68,68	0
56	MG	1a	1895	1/1	0.87	0.14	56,56,56,56	0
56	MG	1A	3316	1/1	0.87	0.10	81,81,81,81	0
56	MG	2B	3003	1/1	0.87	0.22	64,64,64,64	0
56	MG	2a	3193	1/1	0.87	0.20	76,76,76,76	0
56	MG	1A	3151	1/1	0.87	0.10	49,49,49,49	0
56	MG	2a	3195	1/1	0.87	0.15	53,53,53,53	0
56	MG	2B	3009	1/1	0.87	0.34	57,57,57,57	0
56	MG	1A	3009	1/1	0.87	0.19	50,50,50,50	0
56	MG	1a	1779	1/1	0.87	0.13	73,73,73,73	0
56	MG	1A	3738	1/1	0.87	0.10	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3276	1/1	0.87	0.16	58,58,58,58	0
56	MG	26	101	1/1	0.87	0.08	46,46,46,46	0
56	MG	1A	3288	1/1	0.87	0.12	70,70,70,70	0
56	MG	1a	1783	1/1	0.87	0.19	75,75,75,75	0
56	MG	1a	1785	1/1	0.87	0.14	66,66,66,66	0
56	MG	1A	3421	1/1	0.87	0.10	65,65,65,65	0
56	MG	1A	3292	1/1	0.87	0.10	44,44,44,44	0
56	MG	1A	3779	1/1	0.87	0.11	45,45,45,45	0
56	MG	1A	3426	1/1	0.87	0.32	67,67,67,67	0
56	MG	2A	3005	1/1	0.87	0.22	70,70,70,70	0
56	MG	2a	3018	1/1	0.87	0.18	66,66,66,66	0
56	MG	1A	3336	1/1	0.87	0.16	61,61,61,61	0
56	MG	1A	3936	1/1	0.87	0.12	39,39,39,39	0
56	MG	2A	3345	1/1	0.87	0.19	68,68,68,68	0
56	MG	2k	3001	1/1	0.87	0.20	70,70,70,70	0
56	MG	2A	3008	1/1	0.87	0.21	59,59,59,59	0
56	MG	1A	3435	1/1	0.87	0.10	62,62,62,62	0
56	MG	2a	3035	1/1	0.87	0.20	76,76,76,76	0
56	MG	1a	1802	1/1	0.87	0.10	77,77,77,77	0
56	MG	1a	1803	1/1	0.87	0.14	80,80,80,80	0
56	MG	1A	3283	1/1	0.88	0.13	60,60,60,60	0
56	MG	1A	3903	1/1	0.88	0.15	66,66,66,66	0
56	MG	2A	3423	1/1	0.88	0.32	71,71,71,71	0
56	MG	1a	1860	1/1	0.88	0.24	61,61,61,61	0
56	MG	2A	3426	1/1	0.88	0.30	67,67,67,67	0
56	MG	2A	3429	1/1	0.88	0.27	64,64,64,64	0
56	MG	1A	3723	1/1	0.88	0.13	49,49,49,49	0
56	MG	2a	3057	1/1	0.88	0.20	75,75,75,75	0
56	MG	2A	3433	1/1	0.88	0.16	62,62,62,62	0
56	MG	2a	3076	1/1	0.88	0.29	68,68,68,68	0
56	MG	1A	3917	1/1	0.88	0.20	60,60,60,60	0
56	MG	1A	3249	1/1	0.88	0.20	53,53,53,53	0
56	MG	1B	209	1/1	0.88	0.19	61,61,61,61	0
56	MG	1A	3744	1/1	0.88	0.15	63,63,63,63	0
56	MG	1A	3012	1/1	0.88	0.10	45,45,45,45	0
56	MG	2A	3455	1/1	0.88	0.18	67,67,67,67	0
56	MG	2A	3162	1/1	0.88	0.15	47,47,47,47	0
56	MG	1A	3259	1/1	0.88	0.15	66,66,66,66	0
56	MG	1A	3075	1/1	0.88	0.20	60,60,60,60	0
56	MG	2A	3463	1/1	0.88	0.11	58,58,58,58	0
56	MG	2a	3117	1/1	0.88	0.26	68,68,68,68	0
56	MG	2A	3466	1/1	0.88	0.07	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3120	1/1	0.88	0.19	66,66,66,66	0
56	MG	1a	1626	1/1	0.88	0.25	69,69,69,69	0
56	MG	1A	3515	1/1	0.88	0.24	75,75,75,75	0
56	MG	1a	1636	1/1	0.88	0.26	68,68,68,68	0
56	MG	1B	224	1/1	0.88	0.20	69,69,69,69	0
56	MG	2a	3135	1/1	0.88	0.16	61,61,61,61	0
56	MG	1a	1772	1/1	0.88	0.14	66,66,66,66	0
56	MG	1A	3786	1/1	0.88	0.17	67,67,67,67	0
56	MG	2A	3492	1/1	0.88	0.15	45,45,45,45	0
56	MG	2A	3200	1/1	0.88	0.13	41,41,41,41	0
56	MG	1D	302	1/1	0.88	0.16	33,33,33,33	0
56	MG	2A	3203	1/1	0.88	0.17	58,58,58,58	0
56	MG	1a	1776	1/1	0.88	0.19	76,76,76,76	0
56	MG	1h	3003	1/1	0.88	0.27	79,79,79,79	0
56	MG	1A	3400	1/1	0.88	0.11	48,48,48,48	0
56	MG	1A	3311	1/1	0.88	0.09	57,57,57,57	0
56	MG	2A	3215	1/1	0.88	0.15	63,63,63,63	0
56	MG	1r	3001	1/1	0.88	0.17	68,68,68,68	0
56	MG	1A	3182	1/1	0.88	0.12	59,59,59,59	0
56	MG	1a	1651	1/1	0.88	0.17	61,61,61,61	0
56	MG	1A	3406	1/1	0.88	0.12	56,56,56,56	0
56	MG	1x	106	1/1	0.88	0.34	54,54,54,54	0
56	MG	1A	3408	1/1	0.88	0.19	66,66,66,66	0
56	MG	1A	3468	1/1	0.88	0.09	59,59,59,59	0
56	MG	2A	3541	1/1	0.88	0.11	67,67,67,67	0
56	MG	2a	3172	1/1	0.88	0.20	78,78,78,78	0
56	MG	1A	3344	1/1	0.88	0.14	54,54,54,54	0
56	MG	2A	3270	1/1	0.88	0.18	61,61,61,61	0
56	MG	1A	3979	1/1	0.88	0.19	59,59,59,59	0
56	MG	2a	3181	1/1	0.88	0.26	71,71,71,71	0
56	MG	1A	3268	1/1	0.88	0.16	50,50,50,50	0
56	MG	2B	3001	1/1	0.88	0.23	65,65,65,65	0
56	MG	2a	3187	1/1	0.88	0.12	56,56,56,56	0
56	MG	2A	3279	1/1	0.88	0.18	71,71,71,71	0
56	MG	2A	3286	1/1	0.88	0.11	47,47,47,47	0
56	MG	1a	1794	1/1	0.88	0.22	63,63,63,63	0
56	MG	1A	3981	1/1	0.88	0.24	63,63,63,63	0
56	MG	1A	3349	1/1	0.88	0.20	51,51,51,51	0
56	MG	1A	3300	1/1	0.88	0.22	51,51,51,51	0
56	MG	2a	3198	1/1	0.88	0.21	76,76,76,76	0
56	MG	2A	3294	1/1	0.88	0.20	58,58,58,58	0
56	MG	1A	3360	1/1	0.88	0.16	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3362	1/1	0.88	0.18	42,42,42,42	0
56	MG	1A	3029	1/1	0.88	0.19	57,57,57,57	0
56	MG	1A	3424	1/1	0.88	0.15	62,62,62,62	0
56	MG	1a	1715	1/1	0.88	0.14	76,76,76,76	0
56	MG	2A	3339	1/1	0.88	0.12	55,55,55,55	0
56	MG	1A	3489	1/1	0.88	0.19	55,55,55,55	0
56	MG	1Z	301	1/1	0.88	0.12	74,74,74,74	0
56	MG	2A	3052	1/1	0.88	0.33	66,66,66,66	0
56	MG	2a	3231	1/1	0.88	0.26	79,79,79,79	0
56	MG	1a	1728	1/1	0.88	0.27	55,55,55,55	0
56	MG	1A	3365	1/1	0.88	0.35	44,44,44,44	0
56	MG	1a	1734	1/1	0.88	0.32	66,66,66,66	0
56	MG	2a	3022	1/1	0.88	0.31	70,70,70,70	0
56	MG	2A	3075	1/1	0.88	0.32	75,75,75,75	0
56	MG	1A	3429	1/1	0.88	0.17	53,53,53,53	0
56	MG	1A	3325	1/1	0.88	0.10	75,75,75,75	0
56	MG	1A	3495	1/1	0.88	0.23	51,51,51,51	0
56	MG	2A	3084	1/1	0.88	0.11	51,51,51,51	0
56	MG	1A	3704	1/1	0.88	0.14	34,34,34,34	0
56	MG	2a	3037	1/1	0.88	0.20	72,72,72,72	0
56	MG	1A	3070	1/1	0.88	0.08	65,65,65,65	0
56	MG	1A	3503	1/1	0.88	0.16	82,82,82,82	0
56	MG	1A	4027	1/1	0.89	0.17	72,72,72,72	0
56	MG	1A	3327	1/1	0.89	0.12	64,64,64,64	0
56	MG	2A	3184	1/1	0.89	0.21	59,59,59,59	0
56	MG	2a	3060	1/1	0.89	0.31	63,63,63,63	0
56	MG	2a	3070	1/1	0.89	0.14	57,57,57,57	0
56	MG	1A	3208	1/1	0.89	0.17	57,57,57,57	0
56	MG	1Z	302	1/1	0.89	0.36	73,73,73,73	0
56	MG	1A	4036	1/1	0.89	0.30	44,44,44,44	0
56	MG	2a	3083	1/1	0.89	0.10	43,43,43,43	0
56	MG	1A	3946	1/1	0.89	0.10	51,51,51,51	0
56	MG	2A	3460	1/1	0.89	0.10	53,53,53,53	0
56	MG	1A	3662	1/1	0.89	0.12	55,55,55,55	0
56	MG	1A	3425	1/1	0.89	0.09	57,57,57,57	0
56	MG	1A	3147	1/1	0.89	0.15	49,49,49,49	0
56	MG	1x	102	1/1	0.89	0.18	69,69,69,69	0
56	MG	2a	3107	1/1	0.89	0.18	63,63,63,63	0
56	MG	1x	105	1/1	0.89	0.23	57,57,57,57	0
56	MG	1A	3679	1/1	0.89	0.15	51,51,51,51	0
56	MG	2a	3112	1/1	0.89	0.18	67,67,67,67	0
56	MG	1A	3371	1/1	0.89	0.15	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1x	109	1/1	0.89	0.20	73,73,73,73	0
56	MG	1a	1717	1/1	0.89	0.14	69,69,69,69	0
56	MG	2a	3121	1/1	0.89	0.21	57,57,57,57	0
56	MG	2a	3122	1/1	0.89	0.27	69,69,69,69	0
56	MG	1A	3800	1/1	0.89	0.08	55,55,55,55	0
56	MG	2A	3239	1/1	0.89	0.13	49,49,49,49	0
56	MG	2a	3129	1/1	0.89	0.24	73,73,73,73	0
56	MG	2A	3002	1/1	0.89	0.16	59,59,59,59	0
56	MG	2A	3243	1/1	0.89	0.14	62,62,62,62	0
56	MG	1A	3977	1/1	0.89	0.20	50,50,50,50	0
56	MG	1a	1723	1/1	0.89	0.16	60,60,60,60	0
56	MG	1a	1606	1/1	0.89	0.20	73,73,73,73	0
56	MG	2A	3505	1/1	0.89	0.08	48,48,48,48	0
56	MG	1A	3868	1/1	0.89	0.17	65,65,65,65	0
56	MG	1A	3874	1/1	0.89	0.09	45,45,45,45	0
56	MG	1A	3883	1/1	0.89	0.11	66,66,66,66	0
56	MG	2a	3147	1/1	0.89	0.13	74,74,74,74	0
56	MG	1a	1736	1/1	0.89	0.14	63,63,63,63	0
56	MG	1D	301	1/1	0.89	0.24	58,58,58,58	0
56	MG	1A	3805	1/1	0.89	0.13	47,47,47,47	0
56	MG	2A	3029	1/1	0.89	0.23	59,59,59,59	0
56	MG	1a	1620	1/1	0.89	0.10	79,79,79,79	0
56	MG	1A	3332	1/1	0.89	0.18	61,61,61,61	0
56	MG	1A	3183	1/1	0.89	0.10	59,59,59,59	0
56	MG	2A	3544	1/1	0.89	0.18	61,61,61,61	0
56	MG	2A	3039	1/1	0.89	0.21	65,65,65,65	0
56	MG	2A	3566	1/1	0.89	0.20	58,58,58,58	0
56	MG	2A	3293	1/1	0.89	0.11	57,57,57,57	0
56	MG	2A	3044	1/1	0.89	0.10	46,46,46,46	0
56	MG	1a	1751	1/1	0.89	0.29	63,63,63,63	0
56	MG	1A	3902	1/1	0.89	0.10	41,41,41,41	0
56	MG	2A	3323	1/1	0.89	0.08	54,54,54,54	0
56	MG	1E	306	1/1	0.89	0.39	74,74,74,74	0
56	MG	1A	3195	1/1	0.89	0.16	45,45,45,45	0
56	MG	1a	1837	1/1	0.89	0.25	50,50,50,50	0
56	MG	1a	1635	1/1	0.89	0.12	64,64,64,64	0
56	MG	1a	1845	1/1	0.89	0.18	52,52,52,52	0
56	MG	2A	3346	1/1	0.89	0.33	65,65,65,65	0
56	MG	2A	3352	1/1	0.89	0.21	66,66,66,66	0
56	MG	1A	3576	1/1	0.89	0.17	48,48,48,48	0
56	MG	2A	3358	1/1	0.89	0.21	53,53,53,53	0
56	MG	1a	1638	1/1	0.89	0.28	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3357	1/1	0.89	0.14	50,50,50,50	0
56	MG	1A	3819	1/1	0.89	0.12	89,89,89,89	0
56	MG	1a	1761	1/1	0.89	0.17	66,66,66,66	0
56	MG	2A	3384	1/1	0.89	0.20	47,47,47,47	0
56	MG	1A	3477	1/1	0.89	0.22	67,67,67,67	0
56	MG	2a	3206	1/1	0.89	0.25	62,62,62,62	0
56	MG	2a	3015	1/1	0.89	0.08	79,79,79,79	0
56	MG	2A	3388	1/1	0.89	0.14	46,46,46,46	0
56	MG	1a	1763	1/1	0.89	0.09	76,76,76,76	0
56	MG	1A	3999	1/1	0.89	0.16	71,71,71,71	0
56	MG	2A	3392	1/1	0.89	0.23	43,43,43,43	0
56	MG	2A	3126	1/1	0.89	0.18	54,54,54,54	0
56	MG	1A	3926	1/1	0.89	0.26	66,66,66,66	0
56	MG	1a	1646	1/1	0.89	0.17	68,68,68,68	0
56	MG	1A	3051	1/1	0.89	0.18	57,57,57,57	0
56	MG	1A	3391	1/1	0.89	0.16	56,56,56,56	0
56	MG	1A	4015	1/1	0.89	0.25	61,61,61,61	0
56	MG	2a	3239	1/1	0.89	0.32	60,60,60,60	0
56	MG	1a	1653	1/1	0.89	0.10	70,70,70,70	0
56	MG	1A	3206	1/1	0.89	0.13	51,51,51,51	0
56	MG	1a	1900	1/1	0.89	0.22	62,62,62,62	0
56	MG	2A	3163	1/1	0.89	0.26	64,64,64,64	0
56	MG	2A	3166	1/1	0.89	0.15	51,51,51,51	0
56	MG	2a	3043	1/1	0.89	0.10	85,85,85,85	0
56	MG	1A	3631	1/1	0.89	0.10	55,55,55,55	0
56	MG	2a	3046	1/1	0.89	0.12	77,77,77,77	0
56	MG	2A	3432	1/1	0.89	0.23	64,64,64,64	0
56	MG	2A	3171	1/1	0.89	0.12	52,52,52,52	0
56	MG	2x	3005	1/1	0.89	0.14	70,70,70,70	0
56	MG	1a	1778	1/1	0.89	0.24	78,78,78,78	0
56	MG	1A	4034	1/1	0.90	0.14	44,44,44,44	0
56	MG	2F	301	1/1	0.90	0.16	63,63,63,63	0
56	MG	2A	3249	1/1	0.90	0.17	57,57,57,57	0
56	MG	2Q	201	1/1	0.90	0.27	55,55,55,55	0
56	MG	2A	3251	1/1	0.90	0.22	55,55,55,55	0
56	MG	1a	1608	1/1	0.90	0.17	68,68,68,68	0
56	MG	2A	3257	1/1	0.90	0.18	62,62,62,62	0
56	MG	2a	3003	1/1	0.90	0.25	60,60,60,60	0
56	MG	1h	3002	1/1	0.90	0.12	64,64,64,64	0
56	MG	1A	3419	1/1	0.90	0.22	52,52,52,52	0
56	MG	1A	3266	1/1	0.90	0.15	78,78,78,78	0
56	MG	1A	4039	1/1	0.90	0.18	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3141	1/1	0.90	0.15	56,56,56,56	0
56	MG	1A	3423	1/1	0.90	0.21	62,62,62,62	0
56	MG	2A	3280	1/1	0.90	0.13	46,46,46,46	0
56	MG	1A	3184	1/1	0.90	0.06	61,61,61,61	0
56	MG	1A	3270	1/1	0.90	0.25	63,63,63,63	0
56	MG	1A	3271	1/1	0.90	0.25	66,66,66,66	0
56	MG	1A	3612	1/1	0.90	0.10	24,24,24,24	0
56	MG	1a	1765	1/1	0.90	0.14	65,65,65,65	0
56	MG	1A	3428	1/1	0.90	0.09	55,55,55,55	0
56	MG	2a	3033	1/1	0.90	0.21	76,76,76,76	0
56	MG	1A	3488	1/1	0.90	0.20	53,53,53,53	0
56	MG	1a	1629	1/1	0.90	0.22	54,54,54,54	0
56	MG	2A	3301	1/1	0.90	0.09	48,48,48,48	0
56	MG	2A	3318	1/1	0.90	0.23	64,64,64,64	0
56	MG	1a	1633	1/1	0.90	0.19	52,52,52,52	0
56	MG	2A	3001	1/1	0.90	0.14	55,55,55,55	0
56	MG	1A	3381	1/1	0.90	0.10	61,61,61,61	0
56	MG	2A	3331	1/1	0.90	0.12	36,36,36,36	0
56	MG	2A	3004	1/1	0.90	0.12	55,55,55,55	0
56	MG	1A	3430	1/1	0.90	0.27	41,41,41,41	0
56	MG	1A	3827	1/1	0.90	0.09	27,27,27,27	0
56	MG	1A	3028	1/1	0.90	0.15	58,58,58,58	0
56	MG	1A	3956	1/1	0.90	0.14	69,69,69,69	0
56	MG	2a	3051	1/1	0.90	0.22	76,76,76,76	0
56	MG	2a	3053	1/1	0.90	0.07	83,83,83,83	0
56	MG	1A	3830	1/1	0.90	0.15	54,54,54,54	0
56	MG	2a	3055	1/1	0.90	0.11	70,70,70,70	0
56	MG	1D	316	1/1	0.90	0.15	76,76,76,76	0
56	MG	1A	3278	1/1	0.90	0.16	72,72,72,72	0
56	MG	1A	3246	1/1	0.90	0.32	65,65,65,65	0
56	MG	1a	1647	1/1	0.90	0.20	58,58,58,58	0
56	MG	2A	3028	1/1	0.90	0.10	48,48,48,48	0
56	MG	2A	3366	1/1	0.90	0.20	58,58,58,58	0
56	MG	2A	3367	1/1	0.90	0.10	52,52,52,52	0
56	MG	1E	305	1/1	0.90	0.08	58,58,58,58	0
56	MG	2A	3381	1/1	0.90	0.19	45,45,45,45	0
56	MG	2A	3382	1/1	0.90	0.11	71,71,71,71	0
56	MG	1A	3313	1/1	0.90	0.15	71,71,71,71	0
56	MG	1A	3840	1/1	0.90	0.22	67,67,67,67	0
56	MG	2a	3092	1/1	0.90	0.36	65,65,65,65	0
56	MG	2A	3034	1/1	0.90	0.14	61,61,61,61	0
56	MG	1A	3978	1/1	0.90	0.11	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3050	1/1	0.90	0.24	63,63,63,63	0
56	MG	1A	3845	1/1	0.90	0.17	57,57,57,57	0
56	MG	1a	1662	1/1	0.90	0.15	73,73,73,73	0
56	MG	1A	3693	1/1	0.90	0.14	58,58,58,58	0
56	MG	1a	1664	1/1	0.90	0.15	57,57,57,57	0
56	MG	1a	1801	1/1	0.90	0.12	70,70,70,70	0
56	MG	1A	3348	1/1	0.90	0.16	63,63,63,63	0
56	MG	2a	3119	1/1	0.90	0.35	62,62,62,62	0
56	MG	2A	3398	1/1	0.90	0.08	57,57,57,57	0
56	MG	1a	1671	1/1	0.90	0.23	61,61,61,61	0
56	MG	1a	1672	1/1	0.90	0.12	61,61,61,61	0
56	MG	2A	3077	1/1	0.90	0.39	63,63,63,63	0
56	MG	1a	1676	1/1	0.90	0.29	51,51,51,51	0
56	MG	2a	3126	1/1	0.90	0.09	66,66,66,66	0
56	MG	2a	3128	1/1	0.90	0.37	63,63,63,63	0
56	MG	1A	3014	1/1	0.90	0.11	58,58,58,58	0
56	MG	2a	3130	1/1	0.90	0.21	58,58,58,58	0
56	MG	2a	3131	1/1	0.90	0.15	63,63,63,63	0
56	MG	1a	1678	1/1	0.90	0.16	60,60,60,60	0
56	MG	2A	3430	1/1	0.90	0.17	57,57,57,57	0
56	MG	1a	1679	1/1	0.90	0.15	52,52,52,52	0
56	MG	2A	3095	1/1	0.90	0.14	48,48,48,48	0
56	MG	1A	3854	1/1	0.90	0.26	76,76,76,76	0
56	MG	2a	3139	1/1	0.90	0.14	94,94,94,94	0
56	MG	1A	3448	1/1	0.90	0.13	58,58,58,58	0
56	MG	1a	1818	1/1	0.90	0.08	78,78,78,78	0
56	MG	2A	3105	1/1	0.90	0.10	55,55,55,55	0
56	MG	2A	3448	1/1	0.90	0.12	65,65,65,65	0
56	MG	1A	3512	1/1	0.90	0.08	53,53,53,53	0
56	MG	2A	3116	1/1	0.90	0.15	55,55,55,55	0
56	MG	2A	3117	1/1	0.90	0.26	51,51,51,51	0
56	MG	1a	1693	1/1	0.90	0.17	65,65,65,65	0
56	MG	2A	3128	1/1	0.90	0.28	61,61,61,61	0
56	MG	1A	3861	1/1	0.90	0.14	68,68,68,68	0
56	MG	1a	1825	1/1	0.90	0.25	61,61,61,61	0
56	MG	1A	3052	1/1	0.90	0.10	48,48,48,48	0
56	MG	2A	3465	1/1	0.90	0.14	46,46,46,46	0
56	MG	1a	1698	1/1	0.90	0.18	75,75,75,75	0
56	MG	1a	1828	1/1	0.90	0.14	67,67,67,67	0
56	MG	1T	204	1/1	0.90	0.14	72,72,72,72	0
56	MG	2A	3151	1/1	0.90	0.17	45,45,45,45	0
56	MG	1a	1834	1/1	0.90	0.18	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1702	1/1	0.90	0.17	67,67,67,67	0
56	MG	1A	3351	1/1	0.90	0.14	59,59,59,59	0
56	MG	1U	204	1/1	0.90	0.34	44,44,44,44	0
56	MG	1A	3993	1/1	0.90	0.15	73,73,73,73	0
56	MG	1A	3257	1/1	0.90	0.31	68,68,68,68	0
56	MG	1A	3728	1/1	0.90	0.10	23,23,23,23	0
56	MG	1A	4001	1/1	0.90	0.22	52,52,52,52	0
56	MG	1a	1725	1/1	0.90	0.30	59,59,59,59	0
56	MG	2A	3183	1/1	0.90	0.20	58,58,58,58	0
56	MG	2a	3189	1/1	0.90	0.16	57,57,57,57	0
56	MG	1A	3217	1/1	0.90	0.11	48,48,48,48	0
56	MG	2A	3508	1/1	0.90	0.13	61,61,61,61	0
56	MG	1A	3127	1/1	0.90	0.19	50,50,50,50	0
56	MG	1A	3463	1/1	0.90	0.22	53,53,53,53	0
56	MG	2A	3513	1/1	0.90	0.16	38,38,38,38	0
56	MG	2A	3514	1/1	0.90	0.10	58,58,58,58	0
56	MG	2a	3200	1/1	0.90	0.18	56,56,56,56	0
56	MG	2A	3518	1/1	0.90	0.18	67,67,67,67	0
56	MG	1a	1869	1/1	0.90	0.13	63,63,63,63	0
56	MG	1a	1876	1/1	0.90	0.14	61,61,61,61	0
56	MG	13	101	1/1	0.90	0.22	52,52,52,52	0
56	MG	2a	3212	1/1	0.90	0.20	56,56,56,56	0
56	MG	1A	3329	1/1	0.90	0.14	50,50,50,50	0
56	MG	15	105	1/1	0.90	0.10	57,57,57,57	0
56	MG	2A	3534	1/1	0.90	0.09	52,52,52,52	0
56	MG	1a	1887	1/1	0.90	0.27	66,66,66,66	0
56	MG	1a	1742	1/1	0.90	0.18	61,61,61,61	0
56	MG	1A	3128	1/1	0.90	0.24	49,49,49,49	0
56	MG	2A	3542	1/1	0.90	0.18	50,50,50,50	0
56	MG	2A	3543	1/1	0.90	0.07	66,66,66,66	0
56	MG	1a	1745	1/1	0.90	0.20	62,62,62,62	0
56	MG	2A	3552	1/1	0.90	0.20	50,50,50,50	0
56	MG	1a	1747	1/1	0.90	0.27	59,59,59,59	0
56	MG	2A	3216	1/1	0.90	0.24	44,44,44,44	0
56	MG	2A	3567	1/1	0.90	0.13	54,54,54,54	0
56	MG	1A	3574	1/1	0.90	0.13	57,57,57,57	0
56	MG	18	104	1/1	0.90	0.16	59,59,59,59	0
56	MG	2A	3227	1/1	0.90	0.25	49,49,49,49	0
56	MG	2e	3001	1/1	0.90	0.13	68,68,68,68	0
56	MG	2A	3231	1/1	0.90	0.18	53,53,53,53	0
56	MG	2k	3002	1/1	0.90	0.09	66,66,66,66	0
56	MG	2l	202	1/1	0.90	0.11	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3233	1/1	0.90	0.29	62,62,62,62	0
56	MG	2A	3234	1/1	0.90	0.32	52,52,52,52	0
56	MG	1A	3906	1/1	0.90	0.10	42,42,42,42	0
56	MG	2x	3001	1/1	0.90	0.15	79,79,79,79	0
56	MG	2x	3002	1/1	0.90	0.18	58,58,58,58	0
56	MG	1A	3915	1/1	0.90	0.11	38,38,38,38	0
56	MG	1b	3002	1/1	0.90	0.07	87,87,87,87	0
56	MG	1e	202	1/1	0.90	0.15	66,66,66,66	0
56	MG	1A	3159	1/1	0.91	0.16	42,42,42,42	0
56	MG	2a	3019	1/1	0.91	0.17	67,67,67,67	0
56	MG	2A	3337	1/1	0.91	0.10	41,41,41,41	0
56	MG	1a	1808	1/1	0.91	0.14	85,85,85,85	0
56	MG	1A	3673	1/1	0.91	0.18	52,52,52,52	0
56	MG	2a	3026	1/1	0.91	0.52	72,72,72,72	0
56	MG	2A	3053	1/1	0.91	0.20	49,49,49,49	0
56	MG	2A	3055	1/1	0.91	0.25	46,46,46,46	0
56	MG	2A	3056	1/1	0.91	0.23	57,57,57,57	0
56	MG	1a	1811	1/1	0.91	0.13	71,71,71,71	0
56	MG	2A	3066	1/1	0.91	0.17	54,54,54,54	0
56	MG	1A	3496	1/1	0.91	0.14	68,68,68,68	0
56	MG	2A	3362	1/1	0.91	0.20	54,54,54,54	0
56	MG	2A	3363	1/1	0.91	0.18	53,53,53,53	0
56	MG	2A	3073	1/1	0.91	0.11	37,37,37,37	0
56	MG	1A	3499	1/1	0.91	0.12	81,81,81,81	0
56	MG	1N	205	1/1	0.91	0.12	53,53,53,53	0
56	MG	2a	3042	1/1	0.91	0.18	78,78,78,78	0
56	MG	1A	3359	1/1	0.91	0.21	51,51,51,51	0
56	MG	1A	3841	1/1	0.91	0.18	41,41,41,41	0
56	MG	1Q	3003	1/1	0.91	0.10	54,54,54,54	0
56	MG	1Q	3004	1/1	0.91	0.17	46,46,46,46	0
56	MG	1R	205	1/1	0.91	0.19	52,52,52,52	0
56	MG	2A	3088	1/1	0.91	0.09	46,46,46,46	0
56	MG	2A	3092	1/1	0.91	0.20	55,55,55,55	0
56	MG	1A	3445	1/1	0.91	0.10	58,58,58,58	0
56	MG	1A	3263	1/1	0.91	0.17	56,56,56,56	0
56	MG	1A	3846	1/1	0.91	0.09	43,43,43,43	0
56	MG	1A	3449	1/1	0.91	0.32	77,77,77,77	0
56	MG	1W	3004	1/1	0.91	0.17	43,43,43,43	0
56	MG	1a	1714	1/1	0.91	0.10	58,58,58,58	0
56	MG	2a	3065	1/1	0.91	0.08	84,84,84,84	0
56	MG	2A	3109	1/1	0.91	0.27	66,66,66,66	0
56	MG	1A	3110	1/1	0.91	0.11	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3166	1/1	0.91	0.18	47,47,47,47	0
56	MG	1A	3992	1/1	0.91	0.10	50,50,50,50	0
56	MG	2a	3082	1/1	0.91	0.32	61,61,61,61	0
56	MG	2A	3124	1/1	0.91	0.10	62,62,62,62	0
56	MG	1A	3114	1/1	0.91	0.21	48,48,48,48	0
56	MG	10	101	1/1	0.91	0.19	68,68,68,68	0
56	MG	2A	3428	1/1	0.91	0.15	64,64,64,64	0
56	MG	1a	1849	1/1	0.91	0.13	54,54,54,54	0
56	MG	1a	1853	1/1	0.91	0.06	56,56,56,56	0
56	MG	2a	3094	1/1	0.91	0.20	51,51,51,51	0
56	MG	1A	3171	1/1	0.91	0.20	47,47,47,47	0
56	MG	2a	3100	1/1	0.91	0.25	57,57,57,57	0
56	MG	1a	1858	1/1	0.91	0.18	69,69,69,69	0
56	MG	1A	3461	1/1	0.91	0.24	46,46,46,46	0
56	MG	1a	1861	1/1	0.91	0.20	68,68,68,68	0
56	MG	2A	3149	1/1	0.91	0.25	59,59,59,59	0
56	MG	2A	3439	1/1	0.91	0.12	54,54,54,54	0
56	MG	2A	3440	1/1	0.91	0.13	62,62,62,62	0
56	MG	1A	3417	1/1	0.91	0.11	60,60,60,60	0
56	MG	1a	1733	1/1	0.91	0.27	53,53,53,53	0
56	MG	2A	3157	1/1	0.91	0.18	47,47,47,47	0
56	MG	1A	3025	1/1	0.91	0.14	60,60,60,60	0
56	MG	13	102	1/1	0.91	0.16	63,63,63,63	0
56	MG	1A	3521	1/1	0.91	0.17	46,46,46,46	0
56	MG	1A	3522	1/1	0.91	0.20	62,62,62,62	0
56	MG	17	104	1/1	0.91	0.22	57,57,57,57	0
56	MG	2A	3461	1/1	0.91	0.08	78,78,78,78	0
56	MG	2A	3172	1/1	0.91	0.14	47,47,47,47	0
56	MG	1a	1879	1/1	0.91	0.14	51,51,51,51	0
56	MG	1A	3873	1/1	0.91	0.11	25,25,25,25	0
56	MG	1a	1884	1/1	0.91	0.21	56,56,56,56	0
56	MG	1A	3245	1/1	0.91	0.24	64,64,64,64	0
56	MG	1A	3758	1/1	0.91	0.13	66,66,66,66	0
56	MG	2A	3187	1/1	0.91	0.09	53,53,53,53	0
56	MG	2A	3480	1/1	0.91	0.14	74,74,74,74	0
56	MG	19	502	1/1	0.91	0.16	46,46,46,46	0
56	MG	2A	3190	1/1	0.91	0.24	61,61,61,61	0
56	MG	2a	3141	1/1	0.91	0.08	57,57,57,57	0
56	MG	1A	4023	1/1	0.91	0.22	40,40,40,40	0
56	MG	2A	3487	1/1	0.91	0.17	60,60,60,60	0
56	MG	2A	3195	1/1	0.91	0.23	58,58,58,58	0
56	MG	1A	4025	1/1	0.91	0.14	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3272	1/1	0.91	0.15	70,70,70,70	0
56	MG	1A	3055	1/1	0.91	0.20	55,55,55,55	0
56	MG	1a	1898	1/1	0.91	0.26	65,65,65,65	0
56	MG	1A	3778	1/1	0.91	0.09	20,20,20,20	0
56	MG	1a	1905	1/1	0.91	0.12	83,83,83,83	0
56	MG	1A	3567	1/1	0.91	0.17	51,51,51,51	0
56	MG	2A	3507	1/1	0.91	0.10	48,48,48,48	0
56	MG	2a	3156	1/1	0.91	0.19	70,70,70,70	0
56	MG	1a	1615	1/1	0.91	0.07	83,83,83,83	0
56	MG	1A	3062	1/1	0.91	0.24	57,57,57,57	0
56	MG	1A	4037	1/1	0.91	0.11	62,62,62,62	0
56	MG	2a	3160	1/1	0.91	0.21	59,59,59,59	0
56	MG	2a	3162	1/1	0.91	0.10	47,47,47,47	0
56	MG	1A	3787	1/1	0.91	0.08	45,45,45,45	0
56	MG	1A	4049	1/1	0.91	0.15	57,57,57,57	0
56	MG	1A	4050	1/1	0.91	0.09	53,53,53,53	0
56	MG	2A	3519	1/1	0.91	0.14	53,53,53,53	0
56	MG	1B	201	1/1	0.91	0.07	44,44,44,44	0
56	MG	1A	3788	1/1	0.91	0.06	25,25,25,25	0
56	MG	1A	3384	1/1	0.91	0.11	66,66,66,66	0
56	MG	1A	3794	1/1	0.91	0.19	62,62,62,62	0
56	MG	2A	3526	1/1	0.91	0.11	54,54,54,54	0
56	MG	2a	3184	1/1	0.91	0.17	56,56,56,56	0
56	MG	2A	3237	1/1	0.91	0.19	48,48,48,48	0
56	MG	1A	3071	1/1	0.91	0.10	52,52,52,52	0
56	MG	1r	3003	1/1	0.91	0.08	58,58,58,58	0
56	MG	2A	3536	1/1	0.91	0.15	67,67,67,67	0
56	MG	1A	3799	1/1	0.91	0.28	54,54,54,54	0
56	MG	1a	1634	1/1	0.91	0.18	66,66,66,66	0
56	MG	1A	3044	1/1	0.91	0.15	50,50,50,50	0
56	MG	2A	3247	1/1	0.91	0.18	63,63,63,63	0
56	MG	1A	3389	1/1	0.91	0.12	50,50,50,50	0
56	MG	2A	3550	1/1	0.91	0.25	37,37,37,37	0
56	MG	1A	3806	1/1	0.91	0.23	56,56,56,56	0
56	MG	2A	3563	1/1	0.91	0.17	58,58,58,58	0
56	MG	2a	3204	1/1	0.91	0.21	62,62,62,62	0
56	MG	1A	3482	1/1	0.91	0.19	61,61,61,61	0
56	MG	1A	3346	1/1	0.91	0.21	33,33,33,33	0
56	MG	2a	3208	1/1	0.91	0.15	68,68,68,68	0
56	MG	2a	3209	1/1	0.91	0.21	76,76,76,76	0
56	MG	2A	3259	1/1	0.91	0.14	40,40,40,40	0
56	MG	1A	3813	1/1	0.91	0.17	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3256	1/1	0.91	0.14	51,51,51,51	0
56	MG	1A	3148	1/1	0.91	0.23	42,42,42,42	0
56	MG	2a	3216	1/1	0.91	0.15	57,57,57,57	0
56	MG	1A	3629	1/1	0.91	0.22	58,58,58,58	0
56	MG	2A	3277	1/1	0.91	0.11	36,36,36,36	0
56	MG	1A	3952	1/1	0.91	0.14	57,57,57,57	0
56	MG	1a	1784	1/1	0.91	0.12	73,73,73,73	0
56	MG	1A	3294	1/1	0.91	0.16	60,60,60,60	0
56	MG	2a	3228	1/1	0.91	0.09	67,67,67,67	0
56	MG	1A	3820	1/1	0.91	0.10	50,50,50,50	0
56	MG	2a	3232	1/1	0.91	0.20	62,62,62,62	0
56	MG	1A	3437	1/1	0.91	0.25	56,56,56,56	0
56	MG	2A	3010	1/1	0.91	0.16	51,51,51,51	0
56	MG	2a	3238	1/1	0.91	0.23	61,61,61,61	0
56	MG	2E	306	1/1	0.91	0.28	43,43,43,43	0
56	MG	1A	3826	1/1	0.91	0.11	35,35,35,35	0
56	MG	1A	3100	1/1	0.91	0.12	31,31,31,31	0
56	MG	2O	203	1/1	0.91	0.17	57,57,57,57	0
56	MG	1E	308	1/1	0.91	0.18	70,70,70,70	0
56	MG	25	502	1/1	0.91	0.30	56,56,56,56	0
56	MG	1a	1660	1/1	0.91	0.18	54,54,54,54	0
56	MG	1A	3967	1/1	0.91	0.13	53,53,53,53	0
56	MG	1A	3970	1/1	0.91	0.27	53,53,53,53	0
56	MG	2A	3311	1/1	0.91	0.15	44,44,44,44	0
56	MG	2A	3316	1/1	0.91	0.19	43,43,43,43	0
56	MG	1A	3405	1/1	0.91	0.09	59,59,59,59	0
56	MG	1H	201	1/1	0.91	0.30	54,54,54,54	0
56	MG	2a	3009	1/1	0.91	0.23	81,81,81,81	0
56	MG	1a	1669	1/1	0.91	0.33	62,62,62,62	0
56	MG	1A	3829	1/1	0.91	0.11	56,56,56,56	0
56	MG	1a	1805	1/1	0.91	0.16	70,70,70,70	0
56	MG	1a	1806	1/1	0.91	0.20	67,67,67,67	0
57	ZN	24	501	1/1	0.91	0.08	126,126,126,126	0
56	MG	1A	3911	1/1	0.92	0.10	66,66,66,66	0
56	MG	1A	3706	1/1	0.92	0.08	38,38,38,38	0
56	MG	2A	3229	1/1	0.92	0.10	46,46,46,46	0
56	MG	1A	3131	1/1	0.92	0.07	32,32,32,32	0
56	MG	2B	3004	1/1	0.92	0.25	59,59,59,59	0
56	MG	1A	3710	1/1	0.92	0.08	48,48,48,48	0
56	MG	1A	3498	1/1	0.92	0.29	50,50,50,50	0
56	MG	1A	3434	1/1	0.92	0.31	41,41,41,41	0
56	MG	2D	302	1/1	0.92	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2D	303	1/1	0.92	0.14	60,60,60,60	0
56	MG	2E	302	1/1	0.92	0.34	63,63,63,63	0
56	MG	1a	1729	1/1	0.92	0.28	57,57,57,57	0
56	MG	1a	1730	1/1	0.92	0.24	49,49,49,49	0
56	MG	1A	3379	1/1	0.92	0.08	47,47,47,47	0
56	MG	1A	3334	1/1	0.92	0.09	55,55,55,55	0
56	MG	2A	3245	1/1	0.92	0.15	78,78,78,78	0
56	MG	2O	201	1/1	0.92	0.12	54,54,54,54	0
56	MG	1e	204	1/1	0.92	0.10	64,64,64,64	0
56	MG	1A	3730	1/1	0.92	0.08	33,33,33,33	0
56	MG	2Q	203	1/1	0.92	0.11	52,52,52,52	0
56	MG	20	8001	1/1	0.92	0.13	72,72,72,72	0
56	MG	1A	3250	1/1	0.92	0.15	42,42,42,42	0
56	MG	2A	3250	1/1	0.92	0.16	61,61,61,61	0
56	MG	1Q	3006	1/1	0.92	0.16	48,48,48,48	0
56	MG	1A	3139	1/1	0.92	0.12	28,28,28,28	0
56	MG	1k	3001	1/1	0.92	0.22	65,65,65,65	0
56	MG	1A	3190	1/1	0.92	0.11	59,59,59,59	0
56	MG	2a	3005	1/1	0.92	0.28	51,51,51,51	0
56	MG	2a	3006	1/1	0.92	0.14	66,66,66,66	0
56	MG	2A	3265	1/1	0.92	0.15	59,59,59,59	0
56	MG	1A	3751	1/1	0.92	0.10	40,40,40,40	0
56	MG	1A	3511	1/1	0.92	0.20	51,51,51,51	0
56	MG	1A	3140	1/1	0.92	0.14	50,50,50,50	0
56	MG	2a	3013	1/1	0.92	0.08	73,73,73,73	0
56	MG	2A	3271	1/1	0.92	0.19	36,36,36,36	0
56	MG	1A	3768	1/1	0.92	0.12	82,82,82,82	0
56	MG	1W	3006	1/1	0.92	0.17	42,42,42,42	0
56	MG	1A	3197	1/1	0.92	0.13	30,30,30,30	0
56	MG	1A	3771	1/1	0.92	0.07	54,54,54,54	0
56	MG	1A	3959	1/1	0.92	0.15	57,57,57,57	0
56	MG	1A	3038	1/1	0.92	0.10	52,52,52,52	0
56	MG	1A	3446	1/1	0.92	0.09	52,52,52,52	0
56	MG	2a	3024	1/1	0.92	0.20	58,58,58,58	0
56	MG	1A	3782	1/1	0.92	0.07	43,43,43,43	0
56	MG	1A	3966	1/1	0.92	0.08	52,52,52,52	0
56	MG	2a	3029	1/1	0.92	0.26	59,59,59,59	0
56	MG	1A	3783	1/1	0.92	0.08	22,22,22,22	0
56	MG	2a	3032	1/1	0.92	0.25	65,65,65,65	0
56	MG	1A	3447	1/1	0.92	0.14	75,75,75,75	0
56	MG	1A	3399	1/1	0.92	0.16	68,68,68,68	0
56	MG	1A	3006	1/1	0.92	0.26	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	15	103	1/1	0.92	0.17	45,45,45,45	0
56	MG	1A	3789	1/1	0.92	0.13	31,31,31,31	0
56	MG	1A	3016	1/1	0.92	0.23	49,49,49,49	0
56	MG	2A	3317	1/1	0.92	0.14	40,40,40,40	0
56	MG	1A	3265	1/1	0.92	0.11	55,55,55,55	0
56	MG	2A	3319	1/1	0.92	0.21	57,57,57,57	0
56	MG	1A	3796	1/1	0.92	0.47	42,42,42,42	0
56	MG	1A	3532	1/1	0.92	0.14	43,43,43,43	0
56	MG	2a	3044	1/1	0.92	0.10	95,95,95,95	0
56	MG	2A	3018	1/1	0.92	0.21	57,57,57,57	0
56	MG	2A	3327	1/1	0.92	0.14	68,68,68,68	0
56	MG	2A	3020	1/1	0.92	0.22	60,60,60,60	0
56	MG	1A	3536	1/1	0.92	0.21	62,62,62,62	0
56	MG	2a	3050	1/1	0.92	0.18	71,71,71,71	0
56	MG	1A	3347	1/1	0.92	0.20	41,41,41,41	0
56	MG	2a	3052	1/1	0.92	0.06	73,73,73,73	0
56	MG	1A	3985	1/1	0.92	0.23	73,73,73,73	0
56	MG	2A	3026	1/1	0.92	0.16	56,56,56,56	0
56	MG	2A	3340	1/1	0.92	0.18	51,51,51,51	0
56	MG	1a	1605	1/1	0.92	0.10	84,84,84,84	0
56	MG	1A	3552	1/1	0.92	0.15	58,58,58,58	0
56	MG	1a	1607	1/1	0.92	0.13	66,66,66,66	0
56	MG	2A	3354	1/1	0.92	0.25	75,75,75,75	0
56	MG	1a	1777	1/1	0.92	0.17	73,73,73,73	0
56	MG	1A	3456	1/1	0.92	0.11	58,58,58,58	0
56	MG	2a	3072	1/1	0.92	0.14	64,64,64,64	0
56	MG	2A	3033	1/1	0.92	0.23	55,55,55,55	0
56	MG	1A	3214	1/1	0.92	0.18	34,34,34,34	0
56	MG	1A	3460	1/1	0.92	0.10	51,51,51,51	0
56	MG	1a	1614	1/1	0.92	0.26	57,57,57,57	0
56	MG	1A	3407	1/1	0.92	0.10	71,71,71,71	0
56	MG	2A	3046	1/1	0.92	0.25	62,62,62,62	0
56	MG	2a	3086	1/1	0.92	0.35	65,65,65,65	0
56	MG	1A	3103	1/1	0.92	0.26	41,41,41,41	0
56	MG	1A	3057	1/1	0.92	0.11	56,56,56,56	0
56	MG	2a	3090	1/1	0.92	0.12	60,60,60,60	0
56	MG	2a	3091	1/1	0.92	0.29	63,63,63,63	0
56	MG	2A	3375	1/1	0.92	0.15	50,50,50,50	0
56	MG	2A	3378	1/1	0.92	0.14	53,53,53,53	0
56	MG	2A	3380	1/1	0.92	0.12	45,45,45,45	0
56	MG	1A	3227	1/1	0.92	0.21	65,65,65,65	0
56	MG	1A	3818	1/1	0.92	0.16	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4000	1/1	0.92	0.17	54,54,54,54	0
56	MG	2A	3057	1/1	0.92	0.26	50,50,50,50	0
56	MG	2A	3062	1/1	0.92	0.21	33,33,33,33	0
56	MG	1a	1622	1/1	0.92	0.28	74,74,74,74	0
56	MG	2a	3110	1/1	0.92	0.18	53,53,53,53	0
56	MG	2A	3064	1/1	0.92	0.24	56,56,56,56	0
56	MG	2a	3115	1/1	0.92	0.19	52,52,52,52	0
56	MG	2a	3116	1/1	0.92	0.31	51,51,51,51	0
56	MG	2A	3065	1/1	0.92	0.29	58,58,58,58	0
56	MG	1A	3588	1/1	0.92	0.20	69,69,69,69	0
56	MG	1A	3591	1/1	0.92	0.13	45,45,45,45	0
56	MG	1A	4007	1/1	0.92	0.14	58,58,58,58	0
56	MG	1a	1799	1/1	0.92	0.14	76,76,76,76	0
56	MG	1A	3822	1/1	0.92	0.07	34,34,34,34	0
56	MG	1A	3155	1/1	0.92	0.15	51,51,51,51	0
56	MG	2A	3402	1/1	0.92	0.18	55,55,55,55	0
56	MG	1A	3595	1/1	0.92	0.17	47,47,47,47	0
56	MG	2A	3411	1/1	0.92	0.17	39,39,39,39	0
56	MG	2A	3415	1/1	0.92	0.14	43,43,43,43	0
56	MG	2A	3416	1/1	0.92	0.10	56,56,56,56	0
56	MG	2A	3080	1/1	0.92	0.06	37,37,37,37	0
56	MG	1A	3473	1/1	0.92	0.12	63,63,63,63	0
56	MG	2A	3424	1/1	0.92	0.12	50,50,50,50	0
56	MG	1A	3005	1/1	0.92	0.31	60,60,60,60	0
56	MG	2a	3136	1/1	0.92	0.21	72,72,72,72	0
56	MG	1A	3276	1/1	0.92	0.25	74,74,74,74	0
56	MG	1A	3623	1/1	0.92	0.15	40,40,40,40	0
56	MG	2A	3089	1/1	0.92	0.06	45,45,45,45	0
56	MG	1A	3627	1/1	0.92	0.10	20,20,20,20	0
56	MG	1a	1640	1/1	0.92	0.19	77,77,77,77	0
56	MG	1A	3835	1/1	0.92	0.15	49,49,49,49	0
56	MG	1A	3416	1/1	0.92	0.21	70,70,70,70	0
56	MG	2A	3435	1/1	0.92	0.09	53,53,53,53	0
56	MG	2a	3145	1/1	0.92	0.09	91,91,91,91	0
56	MG	1A	3122	1/1	0.92	0.37	60,60,60,60	0
56	MG	1A	3635	1/1	0.92	0.09	56,56,56,56	0
56	MG	2A	3102	1/1	0.92	0.09	41,41,41,41	0
56	MG	1a	1814	1/1	0.92	0.20	63,63,63,63	0
56	MG	2A	3107	1/1	0.92	0.17	50,50,50,50	0
56	MG	2A	3447	1/1	0.92	0.19	77,77,77,77	0
56	MG	2A	3108	1/1	0.92	0.15	47,47,47,47	0
56	MG	1A	3126	1/1	0.92	0.18	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3452	1/1	0.92	0.12	59,59,59,59	0
56	MG	2A	3113	1/1	0.92	0.10	54,54,54,54	0
56	MG	1A	3420	1/1	0.92	0.06	50,50,50,50	0
56	MG	1a	1817	1/1	0.92	0.14	49,49,49,49	0
56	MG	1A	4046	1/1	0.92	0.08	56,56,56,56	0
56	MG	1a	1819	1/1	0.92	0.12	58,58,58,58	0
56	MG	1A	3650	1/1	0.92	0.17	46,46,46,46	0
56	MG	2a	3166	1/1	0.92	0.26	63,63,63,63	0
56	MG	2A	3127	1/1	0.92	0.11	54,54,54,54	0
56	MG	1A	3658	1/1	0.92	0.08	21,21,21,21	0
56	MG	1a	1823	1/1	0.92	0.16	69,69,69,69	0
56	MG	2a	3174	1/1	0.92	0.14	56,56,56,56	0
56	MG	2A	3130	1/1	0.92	0.11	50,50,50,50	0
56	MG	1A	3659	1/1	0.92	0.16	73,73,73,73	0
56	MG	1A	3013	1/1	0.92	0.20	64,64,64,64	0
56	MG	2A	3473	1/1	0.92	0.08	40,40,40,40	0
56	MG	2A	3474	1/1	0.92	0.08	58,58,58,58	0
56	MG	1A	3366	1/1	0.92	0.24	46,46,46,46	0
56	MG	1A	3853	1/1	0.92	0.20	49,49,49,49	0
56	MG	2A	3139	1/1	0.92	0.21	47,47,47,47	0
56	MG	1A	3668	1/1	0.92	0.26	84,84,84,84	0
56	MG	1A	3670	1/1	0.92	0.10	56,56,56,56	0
56	MG	2A	3150	1/1	0.92	0.15	56,56,56,56	0
56	MG	2A	3489	1/1	0.92	0.18	43,43,43,43	0
56	MG	1A	3486	1/1	0.92	0.12	65,65,65,65	0
56	MG	2A	3494	1/1	0.92	0.15	69,69,69,69	0
56	MG	1a	1666	1/1	0.92	0.07	55,55,55,55	0
56	MG	1A	3860	1/1	0.92	0.15	72,72,72,72	0
56	MG	1a	1838	1/1	0.92	0.14	62,62,62,62	0
56	MG	1A	3284	1/1	0.92	0.16	52,52,52,52	0
56	MG	1A	3370	1/1	0.92	0.26	53,53,53,53	0
56	MG	1A	3037	1/1	0.92	0.15	65,65,65,65	0
56	MG	2A	3169	1/1	0.92	0.31	54,54,54,54	0
56	MG	2A	3170	1/1	0.92	0.11	35,35,35,35	0
56	MG	1A	3681	1/1	0.92	0.07	39,39,39,39	0
56	MG	1a	1852	1/1	0.92	0.12	77,77,77,77	0
56	MG	2a	3211	1/1	0.92	0.20	60,60,60,60	0
56	MG	2A	3173	1/1	0.92	0.17	49,49,49,49	0
56	MG	1A	3869	1/1	0.92	0.18	85,85,85,85	0
56	MG	1A	3372	1/1	0.92	0.08	56,56,56,56	0
56	MG	2A	3516	1/1	0.92	0.08	38,38,38,38	0
56	MG	2A	3517	1/1	0.92	0.10	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3218	1/1	0.92	0.27	55,55,55,55	0
56	MG	1A	3690	1/1	0.92	0.20	41,41,41,41	0
56	MG	1A	3876	1/1	0.92	0.20	68,68,68,68	0
56	MG	1A	3691	1/1	0.92	0.14	59,59,59,59	0
56	MG	2A	3185	1/1	0.92	0.33	43,43,43,43	0
56	MG	2A	3522	1/1	0.92	0.14	39,39,39,39	0
56	MG	2a	3229	1/1	0.92	0.21	66,66,66,66	0
56	MG	2A	3186	1/1	0.92	0.19	43,43,43,43	0
56	MG	1a	1863	1/1	0.92	0.15	47,47,47,47	0
56	MG	1A	3885	1/1	0.92	0.09	56,56,56,56	0
56	MG	1A	3887	1/1	0.92	0.07	29,29,29,29	0
56	MG	2A	3533	1/1	0.92	0.11	47,47,47,47	0
56	MG	1A	3692	1/1	0.92	0.16	57,57,57,57	0
56	MG	2A	3193	1/1	0.92	0.28	63,63,63,63	0
56	MG	1A	3894	1/1	0.92	0.20	58,58,58,58	0
56	MG	1A	3286	1/1	0.92	0.06	45,45,45,45	0
56	MG	1a	1873	1/1	0.92	0.10	56,56,56,56	0
56	MG	1a	1699	1/1	0.92	0.22	71,71,71,71	0
56	MG	1A	3130	1/1	0.92	0.29	48,48,48,48	0
56	MG	1a	1701	1/1	0.92	0.22	50,50,50,50	0
56	MG	2A	3547	1/1	0.92	0.18	37,37,37,37	0
56	MG	1A	3700	1/1	0.92	0.23	37,37,37,37	0
56	MG	2l	203	1/1	0.92	0.20	67,67,67,67	0
56	MG	2A	3551	1/1	0.92	0.33	55,55,55,55	0
56	MG	1a	1883	1/1	0.92	0.19	58,58,58,58	0
56	MG	2A	3559	1/1	0.92	0.16	61,61,61,61	0
56	MG	2A	3209	1/1	0.92	0.37	49,49,49,49	0
56	MG	1a	1711	1/1	0.92	0.13	54,54,54,54	0
56	MG	1F	307	1/1	0.92	0.21	49,49,49,49	0
56	MG	1a	1713	1/1	0.92	0.35	65,65,65,65	0
56	MG	1A	3493	1/1	0.92	0.06	63,63,63,63	0
56	MG	1A	3377	1/1	0.92	0.29	67,67,67,67	0
56	MG	2a	3012	1/1	0.93	0.31	69,69,69,69	0
56	MG	1a	1842	1/1	0.93	0.11	61,61,61,61	0
56	MG	1A	3441	1/1	0.93	0.12	50,50,50,50	0
56	MG	1T	201	1/1	0.93	0.10	59,59,59,59	0
56	MG	1A	3671	1/1	0.93	0.13	47,47,47,47	0
56	MG	1A	3387	1/1	0.93	0.10	64,64,64,64	0
56	MG	2A	3100	1/1	0.93	0.29	62,62,62,62	0
56	MG	1A	3338	1/1	0.93	0.08	55,55,55,55	0
56	MG	2A	3104	1/1	0.93	0.09	42,42,42,42	0
56	MG	2A	3372	1/1	0.93	0.20	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3373	1/1	0.93	0.06	47,47,47,47	0
56	MG	1A	3251	1/1	0.93	0.12	60,60,60,60	0
56	MG	2A	3377	1/1	0.93	0.07	21,21,21,21	0
56	MG	1A	3392	1/1	0.93	0.09	55,55,55,55	0
56	MG	1a	1716	1/1	0.93	0.12	68,68,68,68	0
56	MG	1A	3832	1/1	0.93	0.20	68,68,68,68	0
56	MG	2A	3111	1/1	0.93	0.40	62,62,62,62	0
56	MG	2A	3383	1/1	0.93	0.19	64,64,64,64	0
56	MG	1A	3252	1/1	0.93	0.16	53,53,53,53	0
56	MG	2A	3385	1/1	0.93	0.12	43,43,43,43	0
56	MG	1A	3152	1/1	0.93	0.22	50,50,50,50	0
56	MG	1A	3255	1/1	0.93	0.12	44,44,44,44	0
56	MG	1a	1724	1/1	0.93	0.23	70,70,70,70	0
56	MG	2A	3119	1/1	0.93	0.21	46,46,46,46	0
56	MG	1A	3298	1/1	0.93	0.20	52,52,52,52	0
56	MG	1a	1726	1/1	0.93	0.19	66,66,66,66	0
56	MG	1A	3023	1/1	0.93	0.25	57,57,57,57	0
56	MG	1A	3518	1/1	0.93	0.18	52,52,52,52	0
56	MG	1a	1874	1/1	0.93	0.17	64,64,64,64	0
56	MG	1a	1875	1/1	0.93	0.27	65,65,65,65	0
56	MG	2A	3131	1/1	0.93	0.13	48,48,48,48	0
56	MG	2A	3399	1/1	0.93	0.10	49,49,49,49	0
56	MG	1A	3453	1/1	0.93	0.11	49,49,49,49	0
56	MG	1a	1877	1/1	0.93	0.22	56,56,56,56	0
56	MG	2A	3405	1/1	0.93	0.20	45,45,45,45	0
56	MG	2A	3409	1/1	0.93	0.15	59,59,59,59	0
56	MG	1A	3844	1/1	0.93	0.17	63,63,63,63	0
56	MG	2A	3412	1/1	0.93	0.10	45,45,45,45	0
56	MG	1A	3404	1/1	0.93	0.07	82,82,82,82	0
56	MG	1A	3523	1/1	0.93	0.18	59,59,59,59	0
56	MG	1a	1882	1/1	0.93	0.17	55,55,55,55	0
56	MG	2A	3418	1/1	0.93	0.22	62,62,62,62	0
56	MG	2A	3143	1/1	0.93	0.20	51,51,51,51	0
56	MG	1A	3302	1/1	0.93	0.10	33,33,33,33	0
56	MG	1A	3204	1/1	0.93	0.07	38,38,38,38	0
56	MG	1A	3205	1/1	0.93	0.15	55,55,55,55	0
56	MG	2A	3152	1/1	0.93	0.13	48,48,48,48	0
56	MG	2a	3080	1/1	0.93	0.26	61,61,61,61	0
56	MG	1a	1739	1/1	0.93	0.22	72,72,72,72	0
56	MG	16	103	1/1	0.93	0.08	57,57,57,57	0
56	MG	2A	3158	1/1	0.93	0.23	52,52,52,52	0
56	MG	1A	3540	1/1	0.93	0.18	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	3085	1/1	0.93	0.24	61,61,61,61	0
56	MG	1a	1890	1/1	0.93	0.25	58,58,58,58	0
56	MG	1A	4003	1/1	0.93	0.17	24,24,24,24	0
56	MG	1A	4005	1/1	0.93	0.20	31,31,31,31	0
56	MG	1A	3712	1/1	0.93	0.10	58,58,58,58	0
56	MG	1A	3856	1/1	0.93	0.16	52,52,52,52	0
56	MG	19	503	1/1	0.93	0.14	61,61,61,61	0
56	MG	1a	1903	1/1	0.93	0.18	56,56,56,56	0
56	MG	2A	3442	1/1	0.93	0.27	66,66,66,66	0
56	MG	2A	3446	1/1	0.93	0.11	47,47,47,47	0
56	MG	1A	3548	1/1	0.93	0.12	65,65,65,65	0
56	MG	2a	3101	1/1	0.93	0.36	64,64,64,64	0
56	MG	1a	1603	1/1	0.93	0.08	59,59,59,59	0
56	MG	2A	3175	1/1	0.93	0.06	40,40,40,40	0
56	MG	1A	3040	1/1	0.93	0.21	58,58,58,58	0
56	MG	1A	3722	1/1	0.93	0.20	56,56,56,56	0
56	MG	2A	3181	1/1	0.93	0.21	43,43,43,43	0
56	MG	2a	3111	1/1	0.93	0.18	46,46,46,46	0
56	MG	1d	302	1/1	0.93	0.17	70,70,70,70	0
56	MG	1A	3017	1/1	0.93	0.11	47,47,47,47	0
56	MG	1e	203	1/1	0.93	0.13	76,76,76,76	0
56	MG	1A	3725	1/1	0.93	0.11	39,39,39,39	0
56	MG	1A	3209	1/1	0.93	0.19	41,41,41,41	0
56	MG	2A	3188	1/1	0.93	0.18	49,49,49,49	0
56	MG	1A	3353	1/1	0.93	0.17	57,57,57,57	0
56	MG	1a	1611	1/1	0.93	0.09	85,85,85,85	0
56	MG	1A	3573	1/1	0.93	0.09	74,74,74,74	0
56	MG	2a	3123	1/1	0.93	0.24	57,57,57,57	0
56	MG	1A	3165	1/1	0.93	0.15	48,48,48,48	0
56	MG	2A	3194	1/1	0.93	0.26	45,45,45,45	0
56	MG	1A	3358	1/1	0.93	0.13	54,54,54,54	0
56	MG	1o	3002	1/1	0.93	0.14	55,55,55,55	0
56	MG	1a	1764	1/1	0.93	0.11	67,67,67,67	0
56	MG	1a	1616	1/1	0.93	0.13	76,76,76,76	0
56	MG	1A	3875	1/1	0.93	0.12	50,50,50,50	0
56	MG	1A	3045	1/1	0.93	0.07	53,53,53,53	0
56	MG	2A	3204	1/1	0.93	0.09	53,53,53,53	0
56	MG	1A	3877	1/1	0.93	0.17	61,61,61,61	0
56	MG	1A	4038	1/1	0.93	0.14	66,66,66,66	0
56	MG	2A	3493	1/1	0.93	0.09	41,41,41,41	0
56	MG	1A	3880	1/1	0.93	0.09	42,42,42,42	0
56	MG	1x	103	1/1	0.93	0.14	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4041	1/1	0.93	0.11	39,39,39,39	0
56	MG	1A	3757	1/1	0.93	0.09	41,41,41,41	0
56	MG	1A	3099	1/1	0.93	0.17	42,42,42,42	0
56	MG	2A	3218	1/1	0.93	0.15	64,64,64,64	0
56	MG	2A	3219	1/1	0.93	0.23	38,38,38,38	0
56	MG	1A	3418	1/1	0.93	0.22	43,43,43,43	0
56	MG	2a	3146	1/1	0.93	0.10	66,66,66,66	0
56	MG	1A	3766	1/1	0.93	0.11	49,49,49,49	0
56	MG	1a	1628	1/1	0.93	0.09	57,57,57,57	0
56	MG	1A	3170	1/1	0.93	0.18	32,32,32,32	0
56	MG	2A	3510	1/1	0.93	0.16	62,62,62,62	0
56	MG	1a	1631	1/1	0.93	0.17	44,44,44,44	0
56	MG	1A	3897	1/1	0.93	0.23	33,33,33,33	0
56	MG	1A	3589	1/1	0.93	0.25	65,65,65,65	0
56	MG	2A	3515	1/1	0.93	0.10	63,63,63,63	0
56	MG	1A	3900	1/1	0.93	0.32	42,42,42,42	0
56	MG	1A	3314	1/1	0.93	0.14	57,57,57,57	0
56	MG	1A	3228	1/1	0.93	0.20	51,51,51,51	0
56	MG	1A	3048	1/1	0.93	0.11	41,41,41,41	0
56	MG	1A	3596	1/1	0.93	0.14	53,53,53,53	0
56	MG	1A	3907	1/1	0.93	0.07	13,13,13,13	0
56	MG	1a	1790	1/1	0.93	0.11	33,33,33,33	0
56	MG	2A	3021	1/1	0.93	0.20	60,60,60,60	0
56	MG	2A	3524	1/1	0.93	0.08	33,33,33,33	0
56	MG	1A	3484	1/1	0.93	0.06	70,70,70,70	0
56	MG	2a	3171	1/1	0.93	0.08	77,77,77,77	0
56	MG	1a	1792	1/1	0.93	0.11	59,59,59,59	0
56	MG	2A	3527	1/1	0.93	0.15	68,68,68,68	0
56	MG	1a	1793	1/1	0.93	0.17	68,68,68,68	0
56	MG	2A	3254	1/1	0.93	0.20	60,60,60,60	0
56	MG	1A	3237	1/1	0.93	0.16	52,52,52,52	0
56	MG	2a	3180	1/1	0.93	0.08	79,79,79,79	0
56	MG	1B	226	1/1	0.93	0.11	47,47,47,47	0
56	MG	1a	1798	1/1	0.93	0.08	64,64,64,64	0
56	MG	2A	3264	1/1	0.93	0.21	65,65,65,65	0
56	MG	2a	3185	1/1	0.93	0.13	79,79,79,79	0
56	MG	2A	3538	1/1	0.93	0.18	52,52,52,52	0
56	MG	2A	3539	1/1	0.93	0.21	48,48,48,48	0
56	MG	1A	3602	1/1	0.93	0.13	41,41,41,41	0
56	MG	1A	3605	1/1	0.93	0.12	35,35,35,35	0
56	MG	1A	3607	1/1	0.93	0.12	50,50,50,50	0
56	MG	1A	3321	1/1	0.93	0.33	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3177	1/1	0.93	0.18	56,56,56,56	0
56	MG	2A	3275	1/1	0.93	0.09	34,34,34,34	0
56	MG	1A	3179	1/1	0.93	0.09	47,47,47,47	0
56	MG	1A	3243	1/1	0.93	0.15	43,43,43,43	0
56	MG	2A	3043	1/1	0.93	0.21	58,58,58,58	0
56	MG	1A	3937	1/1	0.93	0.29	51,51,51,51	0
56	MG	1A	3328	1/1	0.93	0.19	56,56,56,56	0
56	MG	2A	3282	1/1	0.93	0.08	31,31,31,31	0
56	MG	1A	3280	1/1	0.93	0.17	70,70,70,70	0
56	MG	2A	3570	1/1	0.93	0.07	50,50,50,50	0
56	MG	1E	310	1/1	0.93	0.17	45,45,45,45	0
56	MG	2A	3574	1/1	0.93	0.10	53,53,53,53	0
56	MG	2A	3575	1/1	0.93	0.31	47,47,47,47	0
56	MG	2A	3576	1/1	0.93	0.19	50,50,50,50	0
56	MG	1A	3801	1/1	0.93	0.12	52,52,52,52	0
56	MG	1F	305	1/1	0.93	0.23	28,28,28,28	0
56	MG	1A	3804	1/1	0.93	0.14	50,50,50,50	0
56	MG	1A	3004	1/1	0.93	0.29	44,44,44,44	0
56	MG	2A	3059	1/1	0.93	0.13	50,50,50,50	0
56	MG	2A	3061	1/1	0.93	0.14	44,44,44,44	0
56	MG	2A	3300	1/1	0.93	0.09	42,42,42,42	0
56	MG	1A	3058	1/1	0.93	0.06	49,49,49,49	0
56	MG	2A	3302	1/1	0.93	0.12	64,64,64,64	0
56	MG	1A	3950	1/1	0.93	0.13	55,55,55,55	0
56	MG	1A	3647	1/1	0.93	0.12	55,55,55,55	0
56	MG	2a	3230	1/1	0.93	0.09	70,70,70,70	0
56	MG	1A	3061	1/1	0.93	0.29	51,51,51,51	0
56	MG	1A	3655	1/1	0.93	0.19	56,56,56,56	0
56	MG	1A	3958	1/1	0.93	0.14	46,46,46,46	0
56	MG	2A	3069	1/1	0.93	0.19	55,55,55,55	0
56	MG	2E	307	1/1	0.93	0.10	70,70,70,70	0
56	MG	2A	3070	1/1	0.93	0.32	58,58,58,58	0
56	MG	1A	3383	1/1	0.93	0.12	51,51,51,51	0
56	MG	2a	3242	1/1	0.93	0.13	57,57,57,57	0
56	MG	2A	3326	1/1	0.93	0.13	34,34,34,34	0
56	MG	1a	1682	1/1	0.93	0.15	70,70,70,70	0
56	MG	2A	3328	1/1	0.93	0.09	45,45,45,45	0
56	MG	1a	1684	1/1	0.93	0.19	58,58,58,58	0
56	MG	2V	201	1/1	0.93	0.33	51,51,51,51	0
56	MG	1A	3076	1/1	0.93	0.14	42,42,42,42	0
56	MG	1N	208	1/1	0.93	0.07	60,60,60,60	0
56	MG	2A	3336	1/1	0.93	0.16	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3078	1/1	0.93	0.08	53,53,53,53	0
56	MG	1a	1691	1/1	0.93	0.11	50,50,50,50	0
56	MG	1A	3080	1/1	0.93	0.14	52,52,52,52	0
56	MG	1A	3664	1/1	0.93	0.09	57,57,57,57	0
56	MG	2t	201	1/1	0.93	0.20	62,62,62,62	0
56	MG	1P	202	1/1	0.93	0.13	46,46,46,46	0
56	MG	2A	3348	1/1	0.93	0.21	72,72,72,72	0
56	MG	2A	3086	1/1	0.93	0.06	30,30,30,30	0
56	MG	1A	3196	1/1	0.93	0.17	45,45,45,45	0
56	MG	1A	3667	1/1	0.93	0.14	42,42,42,42	0
56	MG	1A	3440	1/1	0.93	0.09	51,51,51,51	0
56	MG	2A	3094	1/1	0.94	0.12	48,48,48,48	0
56	MG	1a	1686	1/1	0.94	0.19	53,53,53,53	0
56	MG	2A	3096	1/1	0.94	0.13	40,40,40,40	0
56	MG	1a	1846	1/1	0.94	0.08	71,71,71,71	0
56	MG	1a	1847	1/1	0.94	0.18	54,54,54,54	0
56	MG	1A	3395	1/1	0.94	0.14	59,59,59,59	0
56	MG	1A	3396	1/1	0.94	0.11	58,58,58,58	0
56	MG	2A	3101	1/1	0.94	0.12	60,60,60,60	0
56	MG	1a	1851	1/1	0.94	0.16	49,49,49,49	0
56	MG	1A	3944	1/1	0.94	0.21	19,19,19,19	0
56	MG	2A	3368	1/1	0.94	0.22	63,63,63,63	0
56	MG	1A	3398	1/1	0.94	0.10	47,47,47,47	0
56	MG	2A	3106	1/1	0.94	0.14	33,33,33,33	0
56	MG	1A	3669	1/1	0.94	0.08	55,55,55,55	0
56	MG	2A	3374	1/1	0.94	0.13	57,57,57,57	0
56	MG	2a	3021	1/1	0.94	0.07	78,78,78,78	0
56	MG	1A	3242	1/1	0.94	0.23	48,48,48,48	0
56	MG	1a	1859	1/1	0.94	0.14	72,72,72,72	0
56	MG	1N	203	1/1	0.94	0.22	46,46,46,46	0
56	MG	1A	3951	1/1	0.94	0.07	31,31,31,31	0
56	MG	2A	3114	1/1	0.94	0.13	34,34,34,34	0
56	MG	1A	3008	1/1	0.94	0.19	51,51,51,51	0
56	MG	1A	3115	1/1	0.94	0.19	40,40,40,40	0
56	MG	1A	3675	1/1	0.94	0.14	39,39,39,39	0
56	MG	2A	3118	1/1	0.94	0.22	56,56,56,56	0
56	MG	1a	1709	1/1	0.94	0.13	54,54,54,54	0
56	MG	2A	3121	1/1	0.94	0.15	42,42,42,42	0
56	MG	1a	1710	1/1	0.94	0.18	54,54,54,54	0
56	MG	1a	1868	1/1	0.94	0.14	49,49,49,49	0
56	MG	1A	3677	1/1	0.94	0.12	50,50,50,50	0
56	MG	1a	1870	1/1	0.94	0.07	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1872	1/1	0.94	0.10	67,67,67,67	0
56	MG	1A	3143	1/1	0.94	0.22	55,55,55,55	0
56	MG	1Q	3001	1/1	0.94	0.26	47,47,47,47	0
56	MG	1A	3274	1/1	0.94	0.06	69,69,69,69	0
56	MG	1A	3310	1/1	0.94	0.09	65,65,65,65	0
56	MG	1Q	3005	1/1	0.94	0.17	53,53,53,53	0
56	MG	1A	3458	1/1	0.94	0.12	72,72,72,72	0
56	MG	1R	203	1/1	0.94	0.12	56,56,56,56	0
56	MG	1a	1720	1/1	0.94	0.23	43,43,43,43	0
56	MG	1R	204	1/1	0.94	0.12	48,48,48,48	0
56	MG	2A	3144	1/1	0.94	0.21	53,53,53,53	0
56	MG	1A	3684	1/1	0.94	0.11	41,41,41,41	0
56	MG	1A	3275	1/1	0.94	0.08	53,53,53,53	0
56	MG	1A	3968	1/1	0.94	0.15	65,65,65,65	0
56	MG	1A	3352	1/1	0.94	0.28	49,49,49,49	0
56	MG	2A	3153	1/1	0.94	0.19	42,42,42,42	0
56	MG	2A	3419	1/1	0.94	0.23	51,51,51,51	0
56	MG	1A	3312	1/1	0.94	0.09	60,60,60,60	0
56	MG	1A	3976	1/1	0.94	0.20	49,49,49,49	0
56	MG	2a	3061	1/1	0.94	0.07	72,72,72,72	0
56	MG	2a	3063	1/1	0.94	0.11	66,66,66,66	0
56	MG	1W	3001	1/1	0.94	0.29	52,52,52,52	0
56	MG	2A	3161	1/1	0.94	0.16	46,46,46,46	0
56	MG	2a	3071	1/1	0.94	0.23	58,58,58,58	0
56	MG	2A	3427	1/1	0.94	0.14	68,68,68,68	0
56	MG	1A	3354	1/1	0.94	0.16	54,54,54,54	0
56	MG	1W	3005	1/1	0.94	0.07	41,41,41,41	0
56	MG	1a	1893	1/1	0.94	0.19	59,59,59,59	0
56	MG	1a	1894	1/1	0.94	0.21	56,56,56,56	0
56	MG	1A	3410	1/1	0.94	0.08	51,51,51,51	0
56	MG	1A	3838	1/1	0.94	0.10	45,45,45,45	0
56	MG	1A	3696	1/1	0.94	0.08	62,62,62,62	0
56	MG	1A	3464	1/1	0.94	0.13	43,43,43,43	0
56	MG	1a	1738	1/1	0.94	0.08	59,59,59,59	0
56	MG	1A	3466	1/1	0.94	0.11	48,48,48,48	0
56	MG	1A	3701	1/1	0.94	0.06	22,22,22,22	0
56	MG	1A	3356	1/1	0.94	0.09	49,49,49,49	0
56	MG	1c	3001	1/1	0.94	0.23	68,68,68,68	0
56	MG	2A	3443	1/1	0.94	0.10	52,52,52,52	0
56	MG	1A	3559	1/1	0.94	0.07	36,36,36,36	0
56	MG	1d	303	1/1	0.94	0.15	62,62,62,62	0
56	MG	10	107	1/1	0.94	0.10	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3450	1/1	0.94	0.19	52,52,52,52	0
56	MG	1A	3470	1/1	0.94	0.08	57,57,57,57	0
56	MG	1A	3987	1/1	0.94	0.11	35,35,35,35	0
56	MG	1A	3847	1/1	0.94	0.06	81,81,81,81	0
56	MG	2A	3454	1/1	0.94	0.22	58,58,58,58	0
56	MG	1A	3116	1/1	0.94	0.12	47,47,47,47	0
56	MG	1A	3065	1/1	0.94	0.09	60,60,60,60	0
56	MG	15	104	1/1	0.94	0.25	49,49,49,49	0
56	MG	2A	3191	1/1	0.94	0.15	45,45,45,45	0
56	MG	1A	3002	1/1	0.94	0.17	43,43,43,43	0
56	MG	1A	3279	1/1	0.94	0.09	46,46,46,46	0
56	MG	1A	3212	1/1	0.94	0.15	49,49,49,49	0
56	MG	1q	201	1/1	0.94	0.19	68,68,68,68	0
56	MG	1A	3581	1/1	0.94	0.15	51,51,51,51	0
56	MG	1A	3857	1/1	0.94	0.11	51,51,51,51	0
56	MG	2A	3199	1/1	0.94	0.19	47,47,47,47	0
56	MG	2A	3472	1/1	0.94	0.11	54,54,54,54	0
56	MG	18	103	1/1	0.94	0.10	49,49,49,49	0
56	MG	1A	3583	1/1	0.94	0.11	33,33,33,33	0
56	MG	1A	3724	1/1	0.94	0.19	55,55,55,55	0
56	MG	1A	3319	1/1	0.94	0.07	55,55,55,55	0
56	MG	1A	4004	1/1	0.94	0.29	31,31,31,31	0
56	MG	1A	3282	1/1	0.94	0.23	47,47,47,47	0
56	MG	2A	3208	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3862	1/1	0.94	0.09	25,25,25,25	0
56	MG	2a	3132	1/1	0.94	0.14	71,71,71,71	0
56	MG	1A	3863	1/1	0.94	0.16	49,49,49,49	0
56	MG	2A	3491	1/1	0.94	0.07	39,39,39,39	0
56	MG	1A	3865	1/1	0.94	0.15	32,32,32,32	0
56	MG	2A	3214	1/1	0.94	0.22	49,49,49,49	0
56	MG	1A	3018	1/1	0.94	0.32	58,58,58,58	0
56	MG	1A	3323	1/1	0.94	0.06	46,46,46,46	0
56	MG	2A	3217	1/1	0.94	0.26	45,45,45,45	0
56	MG	1A	4016	1/1	0.94	0.13	58,58,58,58	0
56	MG	1A	4017	1/1	0.94	0.17	41,41,41,41	0
56	MG	2A	3501	1/1	0.94	0.10	43,43,43,43	0
56	MG	1a	1612	1/1	0.94	0.07	63,63,63,63	0
56	MG	2A	3221	1/1	0.94	0.15	35,35,35,35	0
56	MG	2A	3003	1/1	0.94	0.07	58,58,58,58	0
56	MG	1A	3741	1/1	0.94	0.12	32,32,32,32	0
56	MG	1A	4019	1/1	0.94	0.15	93,93,93,93	0
56	MG	1A	3592	1/1	0.94	0.12	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4022	1/1	0.94	0.17	66,66,66,66	0
56	MG	1A	3871	1/1	0.94	0.19	67,67,67,67	0
56	MG	2a	3151	1/1	0.94	0.06	64,64,64,64	0
56	MG	2A	3009	1/1	0.94	0.18	56,56,56,56	0
56	MG	1A	3483	1/1	0.94	0.14	65,65,65,65	0
56	MG	1A	3077	1/1	0.94	0.11	53,53,53,53	0
56	MG	2A	3016	1/1	0.94	0.08	59,59,59,59	0
56	MG	2A	3017	1/1	0.94	0.08	52,52,52,52	0
56	MG	1A	3326	1/1	0.94	0.08	63,63,63,63	0
56	MG	1A	4032	1/1	0.94	0.25	47,47,47,47	0
56	MG	1A	3031	1/1	0.94	0.10	51,51,51,51	0
56	MG	1A	3223	1/1	0.94	0.18	55,55,55,55	0
56	MG	1A	3601	1/1	0.94	0.11	28,28,28,28	0
56	MG	1A	3881	1/1	0.94	0.12	63,63,63,63	0
56	MG	2a	3165	1/1	0.94	0.25	50,50,50,50	0
56	MG	2A	3252	1/1	0.94	0.27	56,56,56,56	0
56	MG	2A	3253	1/1	0.94	0.15	68,68,68,68	0
56	MG	1A	3882	1/1	0.94	0.07	36,36,36,36	0
56	MG	1A	3375	1/1	0.94	0.11	59,59,59,59	0
56	MG	2A	3528	1/1	0.94	0.07	56,56,56,56	0
56	MG	1A	3287	1/1	0.94	0.12	57,57,57,57	0
56	MG	1A	4042	1/1	0.94	0.11	51,51,51,51	0
56	MG	2A	3262	1/1	0.94	0.14	55,55,55,55	0
56	MG	2a	3177	1/1	0.94	0.16	52,52,52,52	0
56	MG	1A	3224	1/1	0.94	0.14	36,36,36,36	0
56	MG	1A	3888	1/1	0.94	0.22	37,37,37,37	0
56	MG	1a	1796	1/1	0.94	0.12	50,50,50,50	0
56	MG	1A	3889	1/1	0.94	0.09	53,53,53,53	0
56	MG	2A	3035	1/1	0.94	0.17	59,59,59,59	0
56	MG	2A	3540	1/1	0.94	0.16	39,39,39,39	0
56	MG	2A	3036	1/1	0.94	0.15	35,35,35,35	0
56	MG	1A	3891	1/1	0.94	0.12	51,51,51,51	0
56	MG	1a	1637	1/1	0.94	0.23	64,64,64,64	0
56	MG	2A	3040	1/1	0.94	0.12	43,43,43,43	0
56	MG	1B	202	1/1	0.94	0.20	59,59,59,59	0
56	MG	2a	3192	1/1	0.94	0.17	56,56,56,56	0
56	MG	1A	3772	1/1	0.94	0.09	61,61,61,61	0
56	MG	1B	206	1/1	0.94	0.10	38,38,38,38	0
56	MG	1A	3777	1/1	0.94	0.14	43,43,43,43	0
56	MG	2A	3555	1/1	0.94	0.06	43,43,43,43	0
56	MG	2A	3283	1/1	0.94	0.06	51,51,51,51	0
56	MG	1A	3609	1/1	0.94	0.14	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3287	1/1	0.94	0.07	46,46,46,46	0
56	MG	2a	3202	1/1	0.94	0.19	70,70,70,70	0
56	MG	2a	3203	1/1	0.94	0.12	53,53,53,53	0
56	MG	1A	3898	1/1	0.94	0.20	36,36,36,36	0
56	MG	1A	3291	1/1	0.94	0.07	55,55,55,55	0
56	MG	2A	3569	1/1	0.94	0.10	41,41,41,41	0
56	MG	1A	3226	1/1	0.94	0.17	53,53,53,53	0
56	MG	1A	3258	1/1	0.94	0.07	45,45,45,45	0
56	MG	1A	3628	1/1	0.94	0.15	63,63,63,63	0
56	MG	2A	3060	1/1	0.94	0.14	42,42,42,42	0
56	MG	1A	3188	1/1	0.94	0.15	54,54,54,54	0
56	MG	2A	3577	1/1	0.94	0.11	54,54,54,54	0
56	MG	1A	3105	1/1	0.94	0.09	39,39,39,39	0
56	MG	2A	3579	1/1	0.94	0.07	42,42,42,42	0
56	MG	1A	3160	1/1	0.94	0.08	42,42,42,42	0
56	MG	2A	3582	1/1	0.94	0.14	50,50,50,50	0
56	MG	1A	3232	1/1	0.94	0.11	57,57,57,57	0
56	MG	1A	3136	1/1	0.94	0.18	47,47,47,47	0
56	MG	1A	3019	1/1	0.94	0.13	61,61,61,61	0
56	MG	1a	1661	1/1	0.94	0.13	57,57,57,57	0
56	MG	2B	3005	1/1	0.94	0.23	51,51,51,51	0
56	MG	1A	3797	1/1	0.94	0.13	73,73,73,73	0
56	MG	1D	310	1/1	0.94	0.17	33,33,33,33	0
56	MG	2A	3071	1/1	0.94	0.21	56,56,56,56	0
56	MG	2D	301	1/1	0.94	0.10	54,54,54,54	0
56	MG	2A	3321	1/1	0.94	0.11	53,53,53,53	0
56	MG	1D	315	1/1	0.94	0.08	56,56,56,56	0
56	MG	2a	3237	1/1	0.94	0.10	69,69,69,69	0
56	MG	1A	3920	1/1	0.94	0.11	23,23,23,23	0
56	MG	1A	3649	1/1	0.94	0.10	28,28,28,28	0
56	MG	1a	1668	1/1	0.94	0.08	71,71,71,71	0
56	MG	1A	3390	1/1	0.94	0.10	54,54,54,54	0
56	MG	1A	3925	1/1	0.94	0.10	54,54,54,54	0
56	MG	1A	3506	1/1	0.94	0.16	57,57,57,57	0
56	MG	1A	3267	1/1	0.94	0.19	57,57,57,57	0
56	MG	2N	8001	1/1	0.94	0.07	59,59,59,59	0
56	MG	1a	1832	1/1	0.94	0.10	54,54,54,54	0
56	MG	2f	3001	1/1	0.94	0.07	58,58,58,58	0
56	MG	1A	3932	1/1	0.94	0.13	46,46,46,46	0
56	MG	2A	3338	1/1	0.94	0.11	54,54,54,54	0
56	MG	2Q	202	1/1	0.94	0.13	51,51,51,51	0
56	MG	1A	3934	1/1	0.94	0.14	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2R	8001	1/1	0.94	0.14	50,50,50,50	0
56	MG	2U	201	1/1	0.94	0.08	40,40,40,40	0
56	MG	1A	3343	1/1	0.94	0.16	31,31,31,31	0
56	MG	2A	3343	1/1	0.94	0.17	60,60,60,60	0
56	MG	1A	3509	1/1	0.94	0.15	60,60,60,60	0
56	MG	2A	3091	1/1	0.94	0.21	37,37,37,37	0
56	MG	28	8001	1/1	0.94	0.24	56,56,56,56	0
56	MG	2A	3347	1/1	0.94	0.08	55,55,55,55	0
56	MG	1A	3663	1/1	0.94	0.18	55,55,55,55	0
56	MG	1A	3198	1/1	0.94	0.13	41,41,41,41	0
56	MG	1A	3809	1/1	0.95	0.17	40,40,40,40	0
56	MG	1A	4021	1/1	0.95	0.09	33,33,33,33	0
56	MG	1a	1850	1/1	0.95	0.18	46,46,46,46	0
56	MG	1A	3810	1/1	0.95	0.11	63,63,63,63	0
56	MG	1A	3361	1/1	0.95	0.12	59,59,59,59	0
56	MG	2A	3242	1/1	0.95	0.11	55,55,55,55	0
56	MG	1A	3225	1/1	0.95	0.21	40,40,40,40	0
56	MG	15	101	1/1	0.95	0.16	43,43,43,43	0
56	MG	1A	3904	1/1	0.95	0.13	44,44,44,44	0
56	MG	1A	4029	1/1	0.95	0.32	40,40,40,40	0
56	MG	1A	3905	1/1	0.95	0.13	39,39,39,39	0
56	MG	1a	1727	1/1	0.95	0.21	39,39,39,39	0
56	MG	1a	1862	1/1	0.95	0.13	53,53,53,53	0
56	MG	2A	3468	1/1	0.95	0.09	64,64,64,64	0
56	MG	2A	3072	1/1	0.95	0.20	55,55,55,55	0
56	MG	2A	3470	1/1	0.95	0.06	42,42,42,42	0
56	MG	1A	3814	1/1	0.95	0.10	58,58,58,58	0
56	MG	1A	4033	1/1	0.95	0.10	50,50,50,50	0
56	MG	1A	3154	1/1	0.95	0.32	44,44,44,44	0
56	MG	1A	3261	1/1	0.95	0.32	68,68,68,68	0
56	MG	2a	3067	1/1	0.95	0.17	56,56,56,56	0
56	MG	2a	3069	1/1	0.95	0.24	65,65,65,65	0
56	MG	2A	3478	1/1	0.95	0.07	47,47,47,47	0
56	MG	1A	3587	1/1	0.95	0.15	42,42,42,42	0
56	MG	2A	3258	1/1	0.95	0.08	32,32,32,32	0
56	MG	2a	3074	1/1	0.95	0.14	63,63,63,63	0
56	MG	1A	3135	1/1	0.95	0.19	44,44,44,44	0
56	MG	1A	3497	1/1	0.95	0.22	56,56,56,56	0
56	MG	1A	3157	1/1	0.95	0.29	30,30,30,30	0
56	MG	2A	3488	1/1	0.95	0.10	31,31,31,31	0
56	MG	1a	1871	1/1	0.95	0.18	58,58,58,58	0
56	MG	19	504	1/1	0.95	0.09	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3085	1/1	0.95	0.07	34,34,34,34	0
56	MG	1A	3699	1/1	0.95	0.07	17,17,17,17	0
56	MG	2A	3087	1/1	0.95	0.07	36,36,36,36	0
56	MG	2a	3087	1/1	0.95	0.29	60,60,60,60	0
56	MG	2A	3272	1/1	0.95	0.21	61,61,61,61	0
56	MG	1A	3229	1/1	0.95	0.12	55,55,55,55	0
56	MG	1a	1741	1/1	0.95	0.44	68,68,68,68	0
56	MG	1A	3924	1/1	0.95	0.14	67,67,67,67	0
56	MG	1A	3452	1/1	0.95	0.20	42,42,42,42	0
56	MG	1A	3158	1/1	0.95	0.09	37,37,37,37	0
56	MG	1a	1746	1/1	0.95	0.25	60,60,60,60	0
56	MG	2a	3096	1/1	0.95	0.12	72,72,72,72	0
56	MG	2A	3504	1/1	0.95	0.07	45,45,45,45	0
56	MG	1A	4051	1/1	0.95	0.11	44,44,44,44	0
56	MG	1A	3074	1/1	0.95	0.20	61,61,61,61	0
56	MG	2A	3285	1/1	0.95	0.12	58,58,58,58	0
56	MG	2a	3103	1/1	0.95	0.25	59,59,59,59	0
56	MG	1A	3931	1/1	0.95	0.12	49,49,49,49	0
56	MG	1A	3455	1/1	0.95	0.14	52,52,52,52	0
56	MG	1B	204	1/1	0.95	0.14	53,53,53,53	0
56	MG	2A	3289	1/1	0.95	0.19	44,44,44,44	0
56	MG	1A	3301	1/1	0.95	0.20	33,33,33,33	0
56	MG	1A	3831	1/1	0.95	0.10	54,54,54,54	0
56	MG	2a	3114	1/1	0.95	0.18	70,70,70,70	0
56	MG	1A	3236	1/1	0.95	0.10	49,49,49,49	0
56	MG	1A	3833	1/1	0.95	0.16	56,56,56,56	0
56	MG	1B	212	1/1	0.95	0.19	47,47,47,47	0
56	MG	2A	3296	1/1	0.95	0.09	39,39,39,39	0
56	MG	1A	3095	1/1	0.95	0.08	41,41,41,41	0
56	MG	1A	3046	1/1	0.95	0.08	60,60,60,60	0
56	MG	1A	3836	1/1	0.95	0.06	36,36,36,36	0
56	MG	1A	3718	1/1	0.95	0.10	18,18,18,18	0
56	MG	2A	3304	1/1	0.95	0.08	40,40,40,40	0
56	MG	2A	3305	1/1	0.95	0.13	38,38,38,38	0
56	MG	2A	3308	1/1	0.95	0.19	41,41,41,41	0
56	MG	1a	1896	1/1	0.95	0.09	45,45,45,45	0
56	MG	1A	3945	1/1	0.95	0.20	30,30,30,30	0
56	MG	1A	3118	1/1	0.95	0.17	20,20,20,20	0
56	MG	2A	3531	1/1	0.95	0.17	58,58,58,58	0
56	MG	2A	3532	1/1	0.95	0.09	56,56,56,56	0
56	MG	1a	1902	1/1	0.95	0.18	59,59,59,59	0
56	MG	1A	3241	1/1	0.95	0.20	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3380	1/1	0.95	0.15	39,39,39,39	0
56	MG	1A	3618	1/1	0.95	0.12	40,40,40,40	0
56	MG	1A	3203	1/1	0.95	0.50	47,47,47,47	0
56	MG	1A	3624	1/1	0.95	0.11	35,35,35,35	0
56	MG	2A	3123	1/1	0.95	0.13	51,51,51,51	0
56	MG	1A	3142	1/1	0.95	0.15	43,43,43,43	0
56	MG	1A	3957	1/1	0.95	0.09	44,44,44,44	0
56	MG	1A	3007	1/1	0.95	0.11	53,53,53,53	0
56	MG	2A	3332	1/1	0.95	0.11	50,50,50,50	0
56	MG	1e	201	1/1	0.95	0.10	59,59,59,59	0
56	MG	2A	3334	1/1	0.95	0.10	44,44,44,44	0
56	MG	2A	3549	1/1	0.95	0.13	43,43,43,43	0
56	MG	1A	3739	1/1	0.95	0.10	22,22,22,22	0
56	MG	1A	3010	1/1	0.95	0.28	53,53,53,53	0
56	MG	1A	3630	1/1	0.95	0.11	50,50,50,50	0
56	MG	1A	3851	1/1	0.95	0.10	42,42,42,42	0
56	MG	2A	3556	1/1	0.95	0.07	41,41,41,41	0
56	MG	2A	3558	1/1	0.95	0.08	37,37,37,37	0
56	MG	2A	3134	1/1	0.95	0.07	35,35,35,35	0
56	MG	2A	3561	1/1	0.95	0.07	41,41,41,41	0
56	MG	1A	3519	1/1	0.95	0.12	33,33,33,33	0
56	MG	2A	3136	1/1	0.95	0.21	45,45,45,45	0
56	MG	2A	3344	1/1	0.95	0.15	32,32,32,32	0
56	MG	1A	3632	1/1	0.95	0.16	45,45,45,45	0
56	MG	1E	309	1/1	0.95	0.13	32,32,32,32	0
56	MG	1A	3035	1/1	0.95	0.14	58,58,58,58	0
56	MG	1A	3638	1/1	0.95	0.14	22,22,22,22	0
56	MG	2A	3573	1/1	0.95	0.10	42,42,42,42	0
56	MG	2a	3163	1/1	0.95	0.14	55,55,55,55	0
56	MG	2A	3351	1/1	0.95	0.17	62,62,62,62	0
56	MG	1A	3972	1/1	0.95	0.06	22,22,22,22	0
56	MG	1A	3973	1/1	0.95	0.10	49,49,49,49	0
56	MG	2A	3145	1/1	0.95	0.13	50,50,50,50	0
56	MG	2A	3146	1/1	0.95	0.19	41,41,41,41	0
56	MG	2a	3170	1/1	0.95	0.17	53,53,53,53	0
56	MG	1A	3759	1/1	0.95	0.05	54,54,54,54	0
56	MG	1q	204	1/1	0.95	0.18	58,58,58,58	0
56	MG	1a	1648	1/1	0.95	0.40	64,64,64,64	0
56	MG	1A	3762	1/1	0.95	0.10	51,51,51,51	0
56	MG	1G	3003	1/1	0.95	0.06	59,59,59,59	0
56	MG	1A	3173	1/1	0.95	0.14	24,24,24,24	0
56	MG	2A	3156	1/1	0.95	0.11	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3427	1/1	0.95	0.18	41,41,41,41	0
56	MG	2B	3007	1/1	0.95	0.11	55,55,55,55	0
56	MG	1A	3525	1/1	0.95	0.06	60,60,60,60	0
56	MG	2a	3183	1/1	0.95	0.23	54,54,54,54	0
56	MG	1a	1657	1/1	0.95	0.08	72,72,72,72	0
56	MG	1A	3769	1/1	0.95	0.11	37,37,37,37	0
56	MG	1a	1659	1/1	0.95	0.18	60,60,60,60	0
56	MG	1A	3648	1/1	0.95	0.15	51,51,51,51	0
56	MG	1a	1797	1/1	0.95	0.12	42,42,42,42	0
56	MG	2E	301	1/1	0.95	0.08	24,24,24,24	0
56	MG	1A	3248	1/1	0.95	0.21	60,60,60,60	0
56	MG	2E	303	1/1	0.95	0.25	53,53,53,53	0
56	MG	1A	3530	1/1	0.95	0.11	29,29,29,29	0
56	MG	1A	3654	1/1	0.95	0.16	60,60,60,60	0
56	MG	1A	3175	1/1	0.95	0.20	36,36,36,36	0
56	MG	2a	3196	1/1	0.95	0.10	54,54,54,54	0
56	MG	1A	3534	1/1	0.95	0.27	65,65,65,65	0
56	MG	1A	3281	1/1	0.95	0.22	59,59,59,59	0
56	MG	2a	3199	1/1	0.95	0.24	59,59,59,59	0
56	MG	1A	3660	1/1	0.95	0.13	38,38,38,38	0
56	MG	2A	3176	1/1	0.95	0.15	44,44,44,44	0
56	MG	1P	203	1/1	0.95	0.10	67,67,67,67	0
56	MG	1A	3538	1/1	0.95	0.10	14,14,14,14	0
56	MG	1Q	3002	1/1	0.95	0.21	38,38,38,38	0
56	MG	1a	1673	1/1	0.95	0.08	46,46,46,46	0
56	MG	1a	1809	1/1	0.95	0.09	67,67,67,67	0
56	MG	2a	3207	1/1	0.95	0.10	58,58,58,58	0
56	MG	2Q	204	1/1	0.95	0.15	46,46,46,46	0
56	MG	2Q	205	1/1	0.95	0.06	57,57,57,57	0
56	MG	1A	3056	1/1	0.95	0.13	49,49,49,49	0
56	MG	2A	3015	1/1	0.95	0.14	72,72,72,72	0
56	MG	1A	3541	1/1	0.95	0.14	56,56,56,56	0
56	MG	1A	3149	1/1	0.95	0.12	34,34,34,34	0
56	MG	2a	3214	1/1	0.95	0.15	75,75,75,75	0
56	MG	1A	3878	1/1	0.95	0.21	60,60,60,60	0
56	MG	1A	3791	1/1	0.95	0.10	60,60,60,60	0
56	MG	1A	3394	1/1	0.95	0.07	58,58,58,58	0
56	MG	1A	3218	1/1	0.95	0.20	52,52,52,52	0
56	MG	1A	3355	1/1	0.95	0.11	51,51,51,51	0
56	MG	2a	3222	1/1	0.95	0.13	67,67,67,67	0
56	MG	2A	3408	1/1	0.95	0.07	47,47,47,47	0
56	MG	1A	4002	1/1	0.95	0.09	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3884	1/1	0.95	0.12	63,63,63,63	0
56	MG	1A	3558	1/1	0.95	0.10	27,27,27,27	0
56	MG	2A	3197	1/1	0.95	0.10	47,47,47,47	0
56	MG	1U	201	1/1	0.95	0.09	38,38,38,38	0
56	MG	1a	1694	1/1	0.95	0.08	41,41,41,41	0
56	MG	1U	203	1/1	0.95	0.40	40,40,40,40	0
56	MG	2a	3011	1/1	0.95	0.36	68,68,68,68	0
56	MG	2A	3201	1/1	0.95	0.13	52,52,52,52	0
56	MG	2a	3235	1/1	0.95	0.17	64,64,64,64	0
56	MG	2a	3236	1/1	0.95	0.14	67,67,67,67	0
56	MG	2A	3422	1/1	0.95	0.16	52,52,52,52	0
56	MG	1a	1696	1/1	0.95	0.08	67,67,67,67	0
56	MG	1A	3181	1/1	0.95	0.23	46,46,46,46	0
56	MG	2a	3240	1/1	0.95	0.19	65,65,65,65	0
56	MG	1U	205	1/1	0.95	0.25	43,43,43,43	0
56	MG	1A	3220	1/1	0.95	0.09	43,43,43,43	0
56	MG	1A	3570	1/1	0.95	0.12	18,18,18,18	0
56	MG	2A	3037	1/1	0.95	0.28	62,62,62,62	0
56	MG	1A	3572	1/1	0.95	0.11	51,51,51,51	0
56	MG	2A	3210	1/1	0.95	0.08	49,49,49,49	0
56	MG	1A	4011	1/1	0.95	0.15	48,48,48,48	0
56	MG	1a	1707	1/1	0.95	0.21	46,46,46,46	0
56	MG	2A	3041	1/1	0.95	0.15	49,49,49,49	0
56	MG	1A	3802	1/1	0.95	0.12	64,64,64,64	0
56	MG	2l	201	1/1	0.95	0.13	64,64,64,64	0
56	MG	1A	4013	1/1	0.95	0.12	47,47,47,47	0
56	MG	1a	1839	1/1	0.95	0.09	62,62,62,62	0
56	MG	2A	3047	1/1	0.95	0.11	46,46,46,46	0
56	MG	1a	1840	1/1	0.95	0.13	67,67,67,67	0
56	MG	1A	3109	1/1	0.95	0.12	69,69,69,69	0
56	MG	1A	3895	1/1	0.95	0.21	38,38,38,38	0
56	MG	2A	3223	1/1	0.95	0.18	39,39,39,39	0
56	MG	1A	3066	1/1	0.95	0.27	63,63,63,63	0
56	MG	2A	3226	1/1	0.95	0.38	52,52,52,52	0
56	MG	1A	3289	1/1	0.95	0.19	49,49,49,49	0
56	MG	1A	3403	1/1	0.95	0.17	49,49,49,49	0
56	MG	2A	3058	1/1	0.95	0.14	56,56,56,56	0
56	MG	1A	3965	1/1	0.96	0.09	35,35,35,35	0
56	MG	2A	3434	1/1	0.96	0.09	55,55,55,55	0
56	MG	1A	3210	1/1	0.96	0.16	46,46,46,46	0
56	MG	2A	3436	1/1	0.96	0.16	68,68,68,68	0
56	MG	2A	3031	1/1	0.96	0.23	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3211	1/1	0.96	0.12	52,52,52,52	0
56	MG	1A	3726	1/1	0.96	0.07	29,29,29,29	0
56	MG	1G	3001	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3606	1/1	0.96	0.12	43,43,43,43	0
56	MG	1A	3211	1/1	0.96	0.21	46,46,46,46	0
56	MG	1A	3849	1/1	0.96	0.09	55,55,55,55	0
56	MG	1A	3363	1/1	0.96	0.12	42,42,42,42	0
56	MG	1a	1665	1/1	0.96	0.10	47,47,47,47	0
56	MG	2a	3049	1/1	0.96	0.05	91,91,91,91	0
56	MG	1A	3974	1/1	0.96	0.18	48,48,48,48	0
56	MG	2A	3449	1/1	0.96	0.12	62,62,62,62	0
56	MG	1A	3457	1/1	0.96	0.11	48,48,48,48	0
56	MG	1A	3613	1/1	0.96	0.10	30,30,30,30	0
56	MG	1A	3742	1/1	0.96	0.15	60,60,60,60	0
56	MG	1a	1670	1/1	0.96	0.15	60,60,60,60	0
56	MG	1A	3743	1/1	0.96	0.06	60,60,60,60	0
56	MG	1a	1822	1/1	0.96	0.07	74,74,74,74	0
56	MG	2A	3456	1/1	0.96	0.07	41,41,41,41	0
56	MG	2a	3059	1/1	0.96	0.18	58,58,58,58	0
56	MG	2A	3228	1/1	0.96	0.19	44,44,44,44	0
56	MG	1A	3324	1/1	0.96	0.07	66,66,66,66	0
56	MG	2a	3062	1/1	0.96	0.06	66,66,66,66	0
56	MG	2A	3050	1/1	0.96	0.05	44,44,44,44	0
56	MG	2A	3051	1/1	0.96	0.16	49,49,49,49	0
56	MG	1A	3620	1/1	0.96	0.10	19,19,19,19	0
56	MG	2a	3068	1/1	0.96	0.07	43,43,43,43	0
56	MG	2A	3235	1/1	0.96	0.42	55,55,55,55	0
56	MG	2A	3464	1/1	0.96	0.10	53,53,53,53	0
56	MG	1A	3747	1/1	0.96	0.11	28,28,28,28	0
56	MG	2A	3054	1/1	0.96	0.06	41,41,41,41	0
56	MG	1O	202	1/1	0.96	0.07	51,51,51,51	0
56	MG	2A	3241	1/1	0.96	0.17	56,56,56,56	0
56	MG	1A	3072	1/1	0.96	0.09	53,53,53,53	0
56	MG	2a	3078	1/1	0.96	0.08	49,49,49,49	0
56	MG	2a	3079	1/1	0.96	0.32	55,55,55,55	0
56	MG	1A	3753	1/1	0.96	0.08	67,67,67,67	0
56	MG	1A	3027	1/1	0.96	0.09	60,60,60,60	0
56	MG	1a	1830	1/1	0.96	0.08	55,55,55,55	0
56	MG	1a	1681	1/1	0.96	0.09	44,44,44,44	0
56	MG	1a	1833	1/1	0.96	0.14	47,47,47,47	0
56	MG	1A	3367	1/1	0.96	0.13	51,51,51,51	0
56	MG	1a	1683	1/1	0.96	0.23	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3520	1/1	0.96	0.09	41,41,41,41	0
56	MG	1A	3761	1/1	0.96	0.07	52,52,52,52	0
56	MG	2A	3484	1/1	0.96	0.09	37,37,37,37	0
56	MG	1A	3036	1/1	0.96	0.25	52,52,52,52	0
56	MG	2A	3067	1/1	0.96	0.24	57,57,57,57	0
56	MG	1a	1689	1/1	0.96	0.04	60,60,60,60	0
56	MG	1A	3764	1/1	0.96	0.06	54,54,54,54	0
56	MG	1A	3369	1/1	0.96	0.14	49,49,49,49	0
56	MG	1a	1692	1/1	0.96	0.16	50,50,50,50	0
56	MG	2a	3097	1/1	0.96	0.20	47,47,47,47	0
56	MG	2A	3261	1/1	0.96	0.08	34,34,34,34	0
56	MG	1A	3093	1/1	0.96	0.17	46,46,46,46	0
56	MG	2A	3263	1/1	0.96	0.12	24,24,24,24	0
56	MG	1A	3465	1/1	0.96	0.34	36,36,36,36	0
56	MG	1A	3872	1/1	0.96	0.10	46,46,46,46	0
56	MG	1A	3526	1/1	0.96	0.14	50,50,50,50	0
56	MG	1T	202	1/1	0.96	0.07	43,43,43,43	0
56	MG	1A	3527	1/1	0.96	0.10	32,32,32,32	0
56	MG	1A	3290	1/1	0.96	0.12	47,47,47,47	0
56	MG	2A	3079	1/1	0.96	0.20	51,51,51,51	0
56	MG	2A	3273	1/1	0.96	0.07	36,36,36,36	0
56	MG	2a	3113	1/1	0.96	0.30	51,51,51,51	0
56	MG	1A	3176	1/1	0.96	0.07	50,50,50,50	0
56	MG	1A	3775	1/1	0.96	0.10	22,22,22,22	0
56	MG	1A	3776	1/1	0.96	0.09	44,44,44,44	0
56	MG	1a	1703	1/1	0.96	0.10	48,48,48,48	0
56	MG	1a	1706	1/1	0.96	0.14	52,52,52,52	0
56	MG	2A	3512	1/1	0.96	0.06	40,40,40,40	0
56	MG	1A	3531	1/1	0.96	0.15	56,56,56,56	0
56	MG	1A	3373	1/1	0.96	0.06	49,49,49,49	0
56	MG	1V	201	1/1	0.96	0.24	45,45,45,45	0
56	MG	2A	3284	1/1	0.96	0.22	65,65,65,65	0
56	MG	1A	3533	1/1	0.96	0.09	37,37,37,37	0
56	MG	1W	3003	1/1	0.96	0.19	37,37,37,37	0
56	MG	1A	3781	1/1	0.96	0.06	28,28,28,28	0
56	MG	2a	3127	1/1	0.96	0.23	51,51,51,51	0
56	MG	1A	4008	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	3145	1/1	0.96	0.08	37,37,37,37	0
56	MG	1X	3001	1/1	0.96	0.11	44,44,44,44	0
56	MG	1X	3002	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3221	1/1	0.96	0.19	56,56,56,56	0
56	MG	1a	1719	1/1	0.96	0.17	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3886	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3333	1/1	0.96	0.13	51,51,51,51	0
56	MG	1A	3178	1/1	0.96	0.21	50,50,50,50	0
56	MG	1A	3117	1/1	0.96	0.06	41,41,41,41	0
56	MG	10	102	1/1	0.96	0.07	56,56,56,56	0
56	MG	10	104	1/1	0.96	0.08	46,46,46,46	0
56	MG	2A	3303	1/1	0.96	0.06	42,42,42,42	0
56	MG	1A	3546	1/1	0.96	0.08	41,41,41,41	0
56	MG	1A	3547	1/1	0.96	0.10	38,38,38,38	0
56	MG	1A	3478	1/1	0.96	0.30	51,51,51,51	0
56	MG	2A	3309	1/1	0.96	0.17	44,44,44,44	0
56	MG	2A	3310	1/1	0.96	0.06	46,46,46,46	0
56	MG	1A	3024	1/1	0.96	0.06	52,52,52,52	0
56	MG	2A	3312	1/1	0.96	0.17	39,39,39,39	0
56	MG	2A	3313	1/1	0.96	0.08	49,49,49,49	0
56	MG	2A	3315	1/1	0.96	0.12	40,40,40,40	0
56	MG	2A	3110	1/1	0.96	0.17	49,49,49,49	0
56	MG	1A	3896	1/1	0.96	0.23	32,32,32,32	0
56	MG	1A	3119	1/1	0.96	0.13	35,35,35,35	0
56	MG	1A	3299	1/1	0.96	0.26	30,30,30,30	0
56	MG	1A	3097	1/1	0.96	0.09	40,40,40,40	0
56	MG	1A	4026	1/1	0.96	0.18	41,41,41,41	0
56	MG	1A	3150	1/1	0.96	0.14	40,40,40,40	0
56	MG	2A	3554	1/1	0.96	0.16	44,44,44,44	0
56	MG	1A	4028	1/1	0.96	0.10	68,68,68,68	0
56	MG	1A	3564	1/1	0.96	0.06	42,42,42,42	0
56	MG	2A	3557	1/1	0.96	0.13	45,45,45,45	0
56	MG	1a	1740	1/1	0.96	0.10	57,57,57,57	0
56	MG	17	101	1/1	0.96	0.27	34,34,34,34	0
56	MG	2A	3560	1/1	0.96	0.10	41,41,41,41	0
56	MG	2A	3330	1/1	0.96	0.12	58,58,58,58	0
56	MG	2A	3562	1/1	0.96	0.14	37,37,37,37	0
56	MG	17	102	1/1	0.96	0.09	33,33,33,33	0
56	MG	2A	3125	1/1	0.96	0.09	43,43,43,43	0
56	MG	1A	3566	1/1	0.96	0.10	42,42,42,42	0
56	MG	1a	1897	1/1	0.96	0.10	50,50,50,50	0
56	MG	2A	3568	1/1	0.96	0.10	43,43,43,43	0
56	MG	1A	3186	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3803	1/1	0.96	0.12	33,33,33,33	0
56	MG	1A	3568	1/1	0.96	0.12	51,51,51,51	0
56	MG	1A	3569	1/1	0.96	0.12	25,25,25,25	0
56	MG	1A	3432	1/1	0.96	0.23	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3571	1/1	0.96	0.14	66,66,66,66	0
56	MG	2A	3341	1/1	0.96	0.06	39,39,39,39	0
56	MG	1A	3124	1/1	0.96	0.29	54,54,54,54	0
56	MG	1A	3231	1/1	0.96	0.21	42,42,42,42	0
56	MG	1a	1602	1/1	0.96	0.20	51,51,51,51	0
56	MG	1A	3388	1/1	0.96	0.17	42,42,42,42	0
56	MG	2A	3581	1/1	0.96	0.05	51,51,51,51	0
56	MG	1A	3919	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	4045	1/1	0.96	0.28	50,50,50,50	0
56	MG	1a	1757	1/1	0.96	0.08	64,64,64,64	0
56	MG	2a	3190	1/1	0.96	0.08	67,67,67,67	0
56	MG	1A	3812	1/1	0.96	0.06	54,54,54,54	0
56	MG	1A	3685	1/1	0.96	0.13	47,47,47,47	0
56	MG	1A	3125	1/1	0.96	0.10	49,49,49,49	0
56	MG	2B	3006	1/1	0.96	0.17	50,50,50,50	0
56	MG	1A	3234	1/1	0.96	0.17	54,54,54,54	0
56	MG	1A	3194	1/1	0.96	0.13	41,41,41,41	0
56	MG	1A	3153	1/1	0.96	0.07	43,43,43,43	0
56	MG	1A	3582	1/1	0.96	0.09	44,44,44,44	0
56	MG	1A	3928	1/1	0.96	0.17	51,51,51,51	0
56	MG	1B	205	1/1	0.96	0.11	49,49,49,49	0
56	MG	1a	1767	1/1	0.96	0.07	84,84,84,84	0
56	MG	1A	3694	1/1	0.96	0.07	43,43,43,43	0
56	MG	1A	3695	1/1	0.96	0.12	63,63,63,63	0
56	MG	2A	3159	1/1	0.96	0.14	31,31,31,31	0
56	MG	2A	3160	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3273	1/1	0.96	0.26	45,45,45,45	0
56	MG	1A	3584	1/1	0.96	0.10	52,52,52,52	0
56	MG	1B	211	1/1	0.96	0.20	54,54,54,54	0
56	MG	2A	3164	1/1	0.96	0.09	42,42,42,42	0
56	MG	2A	3165	1/1	0.96	0.10	54,54,54,54	0
56	MG	1a	1773	1/1	0.96	0.13	57,57,57,57	0
56	MG	1A	3824	1/1	0.96	0.05	31,31,31,31	0
56	MG	2O	202	1/1	0.96	0.18	53,53,53,53	0
56	MG	2A	3168	1/1	0.96	0.19	51,51,51,51	0
56	MG	1A	3033	1/1	0.96	0.20	47,47,47,47	0
56	MG	1a	1623	1/1	0.96	0.09	79,79,79,79	0
56	MG	1x	104	1/1	0.96	0.15	47,47,47,47	0
56	MG	1A	3939	1/1	0.96	0.16	57,57,57,57	0
56	MG	2A	3387	1/1	0.96	0.10	51,51,51,51	0
56	MG	1A	3586	1/1	0.96	0.10	32,32,32,32	0
56	MG	2a	3224	1/1	0.96	0.11	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3034	1/1	0.96	0.14	42,42,42,42	0
56	MG	1x	108	1/1	0.96	0.08	57,57,57,57	0
56	MG	2Y	502	1/1	0.96	0.15	57,57,57,57	0
56	MG	1A	3942	1/1	0.96	0.32	34,34,34,34	0
56	MG	1A	3443	1/1	0.96	0.08	47,47,47,47	0
56	MG	2A	3179	1/1	0.96	0.15	43,43,43,43	0
56	MG	1A	3079	1/1	0.96	0.08	31,31,31,31	0
56	MG	1A	3705	1/1	0.96	0.20	35,35,35,35	0
56	MG	2A	3182	1/1	0.96	0.15	37,37,37,37	0
56	MG	1A	3397	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	3708	1/1	0.96	0.14	45,45,45,45	0
56	MG	1D	303	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3049	1/1	0.96	0.09	49,49,49,49	0
56	MG	1A	3104	1/1	0.96	0.04	38,38,38,38	0
56	MG	2A	3406	1/1	0.96	0.15	49,49,49,49	0
56	MG	1A	3134	1/1	0.96	0.14	31,31,31,31	0
56	MG	1A	3953	1/1	0.96	0.18	61,61,61,61	0
56	MG	2A	3410	1/1	0.96	0.08	40,40,40,40	0
56	MG	1D	317	1/1	0.96	0.07	69,69,69,69	0
56	MG	1E	301	1/1	0.96	0.07	58,58,58,58	0
56	MG	2A	3413	1/1	0.96	0.15	44,44,44,44	0
56	MG	1A	3715	1/1	0.96	0.10	49,49,49,49	0
56	MG	1a	1643	1/1	0.96	0.16	52,52,52,52	0
56	MG	1A	3083	1/1	0.96	0.06	29,29,29,29	0
56	MG	1A	3107	1/1	0.96	0.28	50,50,50,50	0
56	MG	1A	3318	1/1	0.96	0.06	46,46,46,46	0
56	MG	2A	3420	1/1	0.96	0.15	59,59,59,59	0
56	MG	2A	3019	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3600	1/1	0.96	0.11	31,31,31,31	0
56	MG	1A	3960	1/1	0.96	0.08	41,41,41,41	0
56	MG	2a	3025	1/1	0.96	0.08	58,58,58,58	0
56	MG	1a	1649	1/1	0.96	0.15	56,56,56,56	0
56	MG	1A	3137	1/1	0.96	0.20	49,49,49,49	0
56	MG	2A	3024	1/1	0.96	0.18	67,67,67,67	0
56	MG	1A	3843	1/1	0.96	0.06	37,37,37,37	0
56	MG	2x	3003	1/1	0.96	0.14	51,51,51,51	0
56	MG	1F	301	1/1	0.96	0.20	39,39,39,39	0
56	MG	1A	3085	1/1	0.96	0.10	41,41,41,41	0
56	MG	1F	304	1/1	0.96	0.18	40,40,40,40	0
56	MG	2A	3207	1/1	0.96	0.16	23,23,23,23	0
56	MG	1A	3590	1/1	0.97	0.09	56,56,56,56	0
56	MG	2A	3314	1/1	0.97	0.07	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3682	1/1	0.97	0.10	59,59,59,59	0
56	MG	1A	3469	1/1	0.97	0.07	47,47,47,47	0
56	MG	1A	3032	1/1	0.97	0.07	65,65,65,65	0
56	MG	1A	3593	1/1	0.97	0.10	30,30,30,30	0
56	MG	2a	3073	1/1	0.97	0.11	68,68,68,68	0
56	MG	1P	204	1/1	0.97	0.31	31,31,31,31	0
56	MG	1P	205	1/1	0.97	0.22	49,49,49,49	0
56	MG	1A	3892	1/1	0.97	0.11	46,46,46,46	0
56	MG	2A	3322	1/1	0.97	0.05	29,29,29,29	0
56	MG	2A	3155	1/1	0.97	0.11	33,33,33,33	0
56	MG	1A	3471	1/1	0.97	0.06	66,66,66,66	0
56	MG	1A	3041	1/1	0.97	0.17	56,56,56,56	0
56	MG	1A	3189	1/1	0.97	0.25	28,28,28,28	0
56	MG	1A	3060	1/1	0.97	0.12	51,51,51,51	0
56	MG	1A	4009	1/1	0.97	0.20	48,48,48,48	0
56	MG	1R	201	1/1	0.97	0.08	38,38,38,38	0
56	MG	1R	202	1/1	0.97	0.25	68,68,68,68	0
56	MG	1A	3475	1/1	0.97	0.07	61,61,61,61	0
56	MG	1A	3191	1/1	0.97	0.07	40,40,40,40	0
56	MG	2A	3011	1/1	0.97	0.20	42,42,42,42	0
56	MG	2A	3012	1/1	0.97	0.06	52,52,52,52	0
56	MG	1a	1675	1/1	0.97	0.10	62,62,62,62	0
56	MG	2A	3014	1/1	0.97	0.17	44,44,44,44	0
56	MG	1A	3431	1/1	0.97	0.05	14,14,14,14	0
56	MG	1R	206	1/1	0.97	0.09	34,34,34,34	0
56	MG	2A	3530	1/1	0.97	0.12	48,48,48,48	0
56	MG	1A	3192	1/1	0.97	0.06	50,50,50,50	0
56	MG	2a	3098	1/1	0.97	0.14	49,49,49,49	0
56	MG	1A	3604	1/1	0.97	0.07	26,26,26,26	0
56	MG	1A	3807	1/1	0.97	0.07	58,58,58,58	0
56	MG	1A	3047	1/1	0.97	0.28	46,46,46,46	0
56	MG	1A	3233	1/1	0.97	0.32	54,54,54,54	0
56	MG	1A	3081	1/1	0.97	0.17	62,62,62,62	0
56	MG	2a	3104	1/1	0.97	0.06	40,40,40,40	0
56	MG	2a	3105	1/1	0.97	0.28	58,58,58,58	0
56	MG	2a	3106	1/1	0.97	0.24	59,59,59,59	0
56	MG	2A	3177	1/1	0.97	0.20	40,40,40,40	0
56	MG	1U	202	1/1	0.97	0.08	43,43,43,43	0
56	MG	1A	3703	1/1	0.97	0.07	58,58,58,58	0
56	MG	1A	3162	1/1	0.97	0.18	38,38,38,38	0
56	MG	1A	3910	1/1	0.97	0.10	34,34,34,34	0
56	MG	1A	3163	1/1	0.97	0.16	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3537	1/1	0.97	0.07	37,37,37,37	0
56	MG	1W	3002	1/1	0.97	0.18	47,47,47,47	0
56	MG	2A	3545	1/1	0.97	0.09	50,50,50,50	0
56	MG	2A	3361	1/1	0.97	0.08	72,72,72,72	0
56	MG	2A	3548	1/1	0.97	0.11	42,42,42,42	0
56	MG	1A	3616	1/1	0.97	0.07	28,28,28,28	0
56	MG	1A	3238	1/1	0.97	0.20	53,53,53,53	0
56	MG	1A	3619	1/1	0.97	0.05	16,16,16,16	0
56	MG	1A	3164	1/1	0.97	0.22	51,51,51,51	0
56	MG	2A	3553	1/1	0.97	0.12	35,35,35,35	0
56	MG	1A	3714	1/1	0.97	0.10	32,32,32,32	0
56	MG	1A	3042	1/1	0.97	0.24	47,47,47,47	0
56	MG	1A	3923	1/1	0.97	0.05	37,37,37,37	0
56	MG	2A	3371	1/1	0.97	0.06	49,49,49,49	0
56	MG	1A	3821	1/1	0.97	0.06	26,26,26,26	0
56	MG	1A	3543	1/1	0.97	0.10	41,41,41,41	0
56	MG	1A	3717	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	3625	1/1	0.97	0.13	30,30,30,30	0
56	MG	1a	1704	1/1	0.97	0.16	40,40,40,40	0
56	MG	2A	3042	1/1	0.97	0.17	50,50,50,50	0
56	MG	2A	3379	1/1	0.97	0.11	42,42,42,42	0
56	MG	1a	1705	1/1	0.97	0.09	64,64,64,64	0
56	MG	1A	3200	1/1	0.97	0.09	54,54,54,54	0
56	MG	2A	3045	1/1	0.97	0.10	45,45,45,45	0
56	MG	10	103	1/1	0.97	0.07	69,69,69,69	0
56	MG	1A	3929	1/1	0.97	0.11	27,27,27,27	0
56	MG	2A	3571	1/1	0.97	0.18	43,43,43,43	0
56	MG	1A	4040	1/1	0.97	0.23	35,35,35,35	0
56	MG	2A	3049	1/1	0.97	0.10	33,33,33,33	0
56	MG	1A	3930	1/1	0.97	0.04	23,23,23,23	0
56	MG	1A	3201	1/1	0.97	0.21	39,39,39,39	0
56	MG	1A	4043	1/1	0.97	0.06	45,45,45,45	0
56	MG	1A	4044	1/1	0.97	0.39	39,39,39,39	0
56	MG	1A	3320	1/1	0.97	0.14	49,49,49,49	0
56	MG	1A	3933	1/1	0.97	0.14	54,54,54,54	0
56	MG	1A	4047	1/1	0.97	0.09	36,36,36,36	0
56	MG	1A	3549	1/1	0.97	0.11	68,68,68,68	0
56	MG	1a	1854	1/1	0.97	0.15	51,51,51,51	0
56	MG	2A	3583	1/1	0.97	0.11	42,42,42,42	0
56	MG	1A	3120	1/1	0.97	0.09	37,37,37,37	0
56	MG	1A	3121	1/1	0.97	0.24	42,42,42,42	0
56	MG	1a	1721	1/1	0.97	0.13	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3400	1/1	0.97	0.08	31,31,31,31	0
56	MG	2A	3401	1/1	0.97	0.08	39,39,39,39	0
56	MG	16	101	1/1	0.97	0.14	51,51,51,51	0
56	MG	2A	3403	1/1	0.97	0.05	34,34,34,34	0
56	MG	1A	3727	1/1	0.97	0.07	25,25,25,25	0
56	MG	1A	3633	1/1	0.97	0.06	29,29,29,29	0
56	MG	1A	3634	1/1	0.97	0.10	19,19,19,19	0
56	MG	2A	3407	1/1	0.97	0.08	31,31,31,31	0
56	MG	1A	3731	1/1	0.97	0.09	29,29,29,29	0
56	MG	1A	3733	1/1	0.97	0.07	37,37,37,37	0
56	MG	1A	3737	1/1	0.97	0.14	29,29,29,29	0
56	MG	1A	3168	1/1	0.97	0.09	41,41,41,41	0
56	MG	1A	3637	1/1	0.97	0.12	29,29,29,29	0
56	MG	1a	1731	1/1	0.97	0.07	55,55,55,55	0
56	MG	2A	3414	1/1	0.97	0.12	39,39,39,39	0
56	MG	18	105	1/1	0.97	0.12	43,43,43,43	0
56	MG	2a	3173	1/1	0.97	0.22	57,57,57,57	0
56	MG	1A	3169	1/1	0.97	0.21	41,41,41,41	0
56	MG	1B	210	1/1	0.97	0.04	45,45,45,45	0
56	MG	1A	3102	1/1	0.97	0.17	37,37,37,37	0
56	MG	1A	3641	1/1	0.97	0.06	22,22,22,22	0
56	MG	1A	3562	1/1	0.97	0.15	50,50,50,50	0
56	MG	2a	3179	1/1	0.97	0.04	47,47,47,47	0
56	MG	2A	3238	1/1	0.97	0.17	48,48,48,48	0
56	MG	1A	3563	1/1	0.97	0.11	50,50,50,50	0
56	MG	2P	201	1/1	0.97	0.15	33,33,33,33	0
56	MG	1A	3123	1/1	0.97	0.15	25,25,25,25	0
56	MG	1B	218	1/1	0.97	0.12	60,60,60,60	0
56	MG	2A	3081	1/1	0.97	0.06	37,37,37,37	0
56	MG	1A	3749	1/1	0.97	0.05	27,27,27,27	0
56	MG	1B	222	1/1	0.97	0.07	58,58,58,58	0
56	MG	1A	3955	1/1	0.97	0.16	47,47,47,47	0
56	MG	1A	3565	1/1	0.97	0.05	17,17,17,17	0
56	MG	2U	202	1/1	0.97	0.10	45,45,45,45	0
56	MG	1a	1610	1/1	0.97	0.05	52,52,52,52	0
56	MG	1A	3752	1/1	0.97	0.08	55,55,55,55	0
56	MG	1a	1886	1/1	0.97	0.16	53,53,53,53	0
56	MG	1A	3172	1/1	0.97	0.13	32,32,32,32	0
56	MG	2A	3090	1/1	0.97	0.04	51,51,51,51	0
56	MG	1A	3754	1/1	0.97	0.06	20,20,20,20	0
56	MG	1A	3755	1/1	0.97	0.05	65,65,65,65	0
56	MG	1A	3651	1/1	0.97	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
56	MG	1D	304	1/1	0.97	0.17	50,50,50,50	0
56	MG	1A	3652	1/1	0.97	0.03	24,24,24,24	0
56	MG	1D	306	1/1	0.97	0.14	43,43,43,43	0
56	MG	2A	3260	1/1	0.97	0.18	54,54,54,54	0
56	MG	1A	3063	1/1	0.97	0.17	52,52,52,52	0
56	MG	2A	3444	1/1	0.97	0.13	39,39,39,39	0
56	MG	1D	312	1/1	0.97	0.05	47,47,47,47	0
56	MG	1D	313	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	3086	1/1	0.97	0.09	31,31,31,31	0
56	MG	1A	3657	1/1	0.97	0.06	19,19,19,19	0
56	MG	2A	3266	1/1	0.97	0.11	54,54,54,54	0
56	MG	1A	3411	1/1	0.97	0.09	51,51,51,51	0
56	MG	2A	3103	1/1	0.97	0.08	50,50,50,50	0
56	MG	2a	3016	1/1	0.97	0.07	58,58,58,58	0
56	MG	1a	1901	1/1	0.97	0.10	46,46,46,46	0
56	MG	1A	3502	1/1	0.97	0.10	77,77,77,77	0
56	MG	1A	3064	1/1	0.97	0.08	41,41,41,41	0
56	MG	1a	1904	1/1	0.97	0.06	53,53,53,53	0
56	MG	2A	3274	1/1	0.97	0.09	47,47,47,47	0
56	MG	2A	3458	1/1	0.97	0.10	31,31,31,31	0
56	MG	2a	3219	1/1	0.97	0.09	58,58,58,58	0
56	MG	1A	3971	1/1	0.97	0.10	61,61,61,61	0
56	MG	2a	3221	1/1	0.97	0.14	57,57,57,57	0
56	MG	1A	3767	1/1	0.97	0.10	21,21,21,21	0
56	MG	2a	3223	1/1	0.97	0.13	57,57,57,57	0
56	MG	1A	3504	1/1	0.97	0.15	52,52,52,52	0
56	MG	1A	3216	1/1	0.97	0.11	66,66,66,66	0
56	MG	2A	3112	1/1	0.97	0.15	36,36,36,36	0
56	MG	2a	3028	1/1	0.97	0.27	61,61,61,61	0
56	MG	1a	1632	1/1	0.97	0.10	53,53,53,53	0
56	MG	2A	3281	1/1	0.97	0.20	50,50,50,50	0
56	MG	2a	3031	1/1	0.97	0.23	48,48,48,48	0
56	MG	1A	3254	1/1	0.97	0.13	32,32,32,32	0
56	MG	1A	3089	1/1	0.97	0.22	44,44,44,44	0
56	MG	1A	3108	1/1	0.97	0.33	49,49,49,49	0
56	MG	1A	3335	1/1	0.97	0.11	43,43,43,43	0
56	MG	1A	3510	1/1	0.97	0.17	39,39,39,39	0
56	MG	2A	3471	1/1	0.97	0.14	54,54,54,54	0
56	MG	1F	303	1/1	0.97	0.05	40,40,40,40	0
56	MG	1A	3043	1/1	0.97	0.06	49,49,49,49	0
56	MG	1A	3003	1/1	0.97	0.08	58,58,58,58	0
56	MG	1A	3672	1/1	0.97	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3476	1/1	0.97	0.05	45,45,45,45	0
56	MG	1A	3780	1/1	0.97	0.05	48,48,48,48	0
56	MG	2A	3479	1/1	0.97	0.06	31,31,31,31	0
56	MG	1A	3132	1/1	0.97	0.16	17,17,17,17	0
56	MG	2A	3481	1/1	0.97	0.07	41,41,41,41	0
56	MG	1l	201	1/1	0.97	0.12	62,62,62,62	0
56	MG	1A	3674	1/1	0.97	0.04	30,30,30,30	0
56	MG	2A	3295	1/1	0.97	0.05	50,50,50,50	0
56	MG	1A	3260	1/1	0.97	0.14	49,49,49,49	0
56	MG	1a	1781	1/1	0.97	0.09	87,87,87,87	0
56	MG	2A	3299	1/1	0.97	0.09	44,44,44,44	0
56	MG	1A	3784	1/1	0.97	0.12	31,31,31,31	0
56	MG	1q	203	1/1	0.97	0.20	64,64,64,64	0
56	MG	1A	3879	1/1	0.97	0.06	24,24,24,24	0
56	MG	1A	3785	1/1	0.97	0.05	57,57,57,57	0
56	MG	1A	3222	1/1	0.97	0.14	38,38,38,38	0
56	MG	1A	3112	1/1	0.97	0.17	35,35,35,35	0
56	MG	2A	3496	1/1	0.97	0.06	59,59,59,59	0
56	MG	1A	3156	1/1	0.97	0.23	49,49,49,49	0
56	MG	1A	3185	1/1	0.97	0.07	44,44,44,44	0
56	MG	1A	3790	1/1	0.97	0.09	21,21,21,21	0
56	MG	1A	3998	1/1	0.97	0.11	51,51,51,51	0
56	MG	2a	3064	1/1	0.97	0.30	51,51,51,51	0
57	ZN	14	501	1/1	0.97	0.05	102,102,102,102	0
56	MG	1a	1655	1/1	0.97	0.05	60,60,60,60	0
57	ZN	2n	501	1/1	0.97	0.06	105,105,105,105	0
56	MG	1A	3092	1/1	0.98	0.08	40,40,40,40	0
56	MG	1A	4048	1/1	0.98	0.04	32,32,32,32	0
56	MG	1A	3707	1/1	0.98	0.07	40,40,40,40	0
56	MG	1A	3193	1/1	0.98	0.15	20,20,20,20	0
56	MG	1A	3653	1/1	0.98	0.04	10,10,10,10	0
56	MG	1a	1630	1/1	0.98	0.08	38,38,38,38	0
56	MG	1A	3101	1/1	0.98	0.10	35,35,35,35	0
56	MG	1A	3711	1/1	0.98	0.04	45,45,45,45	0
56	MG	1A	3467	1/1	0.98	0.13	44,44,44,44	0
56	MG	1A	3656	1/1	0.98	0.07	56,56,56,56	0
56	MG	1A	3180	1/1	0.98	0.05	50,50,50,50	0
56	MG	1A	3535	1/1	0.98	0.08	24,24,24,24	0
56	MG	1A	3213	1/1	0.98	0.04	23,23,23,23	0
56	MG	1A	3912	1/1	0.98	0.06	49,49,49,49	0
56	MG	1n	502	1/1	0.98	0.03	47,47,47,47	0
56	MG	1A	3913	1/1	0.98	0.04	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3421	1/1	0.98	0.04	50,50,50,50	0
56	MG	2A	3298	1/1	0.98	0.04	45,45,45,45	0
56	MG	2a	3161	1/1	0.98	0.09	62,62,62,62	0
56	MG	1A	3914	1/1	0.98	0.10	22,22,22,22	0
56	MG	1A	3608	1/1	0.98	0.08	39,39,39,39	0
56	MG	1A	3719	1/1	0.98	0.05	7,7,7,7	0
56	MG	2A	3546	1/1	0.98	0.05	42,42,42,42	0
56	MG	1A	3661	1/1	0.98	0.10	51,51,51,51	0
56	MG	1A	3918	1/1	0.98	0.11	25,25,25,25	0
56	MG	1A	3111	1/1	0.98	0.16	39,39,39,39	0
56	MG	1A	3610	1/1	0.98	0.07	33,33,33,33	0
56	MG	1B	220	1/1	0.98	0.05	27,27,27,27	0
56	MG	1a	1831	1/1	0.98	0.09	63,63,63,63	0
56	MG	1A	3087	1/1	0.98	0.10	32,32,32,32	0
56	MG	1A	3094	1/1	0.98	0.10	24,24,24,24	0
56	MG	1A	3614	1/1	0.98	0.06	26,26,26,26	0
56	MG	1a	1835	1/1	0.98	0.11	34,34,34,34	0
56	MG	1A	3995	1/1	0.98	0.13	10,10,10,10	0
56	MG	1A	3996	1/1	0.98	0.06	29,29,29,29	0
56	MG	1a	1744	1/1	0.98	0.05	80,80,80,80	0
56	MG	1A	3997	1/1	0.98	0.04	18,18,18,18	0
56	MG	1A	3026	1/1	0.98	0.25	36,36,36,36	0
56	MG	1A	3617	1/1	0.98	0.11	28,28,28,28	0
56	MG	1a	1656	1/1	0.98	0.06	25,25,25,25	0
56	MG	2A	3564	1/1	0.98	0.31	34,34,34,34	0
56	MG	1a	1844	1/1	0.98	0.05	38,38,38,38	0
56	MG	1A	3729	1/1	0.98	0.06	22,22,22,22	0
56	MG	2A	3445	1/1	0.98	0.06	74,74,74,74	0
56	MG	1A	3542	1/1	0.98	0.07	29,29,29,29	0
56	MG	1A	3577	1/1	0.98	0.04	38,38,38,38	0
56	MG	1A	3732	1/1	0.98	0.05	32,32,32,32	0
56	MG	2a	3066	1/1	0.98	0.10	50,50,50,50	0
56	MG	1D	307	1/1	0.98	0.08	39,39,39,39	0
56	MG	1D	308	1/1	0.98	0.04	13,13,13,13	0
56	MG	2A	3329	1/1	0.98	0.06	39,39,39,39	0
56	MG	1D	309	1/1	0.98	0.04	37,37,37,37	0
56	MG	1A	3578	1/1	0.98	0.07	39,39,39,39	0
56	MG	1D	311	1/1	0.98	0.05	49,49,49,49	0
56	MG	1A	3734	1/1	0.98	0.07	27,27,27,27	0
56	MG	1A	3735	1/1	0.98	0.08	27,27,27,27	0
56	MG	2a	3075	1/1	0.98	0.12	60,60,60,60	0
56	MG	1a	1857	1/1	0.98	0.14	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1D	314	1/1	0.98	0.04	48,48,48,48	0
56	MG	1A	3736	1/1	0.98	0.07	30,30,30,30	0
56	MG	1A	3579	1/1	0.98	0.13	49,49,49,49	0
56	MG	2A	3222	1/1	0.98	0.11	45,45,45,45	0
56	MG	1A	3935	1/1	0.98	0.06	20,20,20,20	0
56	MG	1A	3494	1/1	0.98	0.11	58,58,58,58	0
56	MG	2A	3342	1/1	0.98	0.23	46,46,46,46	0
56	MG	1A	3544	1/1	0.98	0.07	30,30,30,30	0
56	MG	1a	1674	1/1	0.98	0.14	57,57,57,57	0
56	MG	2A	3120	1/1	0.98	0.03	23,23,23,23	0
56	MG	1A	3740	1/1	0.98	0.07	13,13,13,13	0
56	MG	2A	3230	1/1	0.98	0.30	51,51,51,51	0
56	MG	2A	3122	1/1	0.98	0.20	43,43,43,43	0
56	MG	1A	3870	1/1	0.98	0.07	41,41,41,41	0
56	MG	1A	4014	1/1	0.98	0.07	51,51,51,51	0
56	MG	1A	3626	1/1	0.98	0.04	24,24,24,24	0
56	MG	1A	3545	1/1	0.98	0.11	31,31,31,31	0
56	MG	2D	304	1/1	0.98	0.17	34,34,34,34	0
56	MG	1A	3138	1/1	0.98	0.11	55,55,55,55	0
56	MG	1A	3078	1/1	0.98	0.09	21,21,21,21	0
56	MG	1A	3202	1/1	0.98	0.11	50,50,50,50	0
56	MG	1A	3187	1/1	0.98	0.05	54,54,54,54	0
56	MG	1A	3382	1/1	0.98	0.08	29,29,29,29	0
56	MG	1a	1685	1/1	0.98	0.06	23,23,23,23	0
56	MG	1A	3948	1/1	0.98	0.05	18,18,18,18	0
56	MG	1a	1687	1/1	0.98	0.12	54,54,54,54	0
56	MG	1A	3750	1/1	0.98	0.04	18,18,18,18	0
56	MG	1A	4024	1/1	0.98	0.06	29,29,29,29	0
56	MG	2A	3248	1/1	0.98	0.11	56,56,56,56	0
56	MG	1a	1880	1/1	0.98	0.08	50,50,50,50	0
56	MG	1A	3551	1/1	0.98	0.09	32,32,32,32	0
56	MG	2A	3490	1/1	0.98	0.05	30,30,30,30	0
56	MG	1A	3500	1/1	0.98	0.05	51,51,51,51	0
56	MG	2A	3142	1/1	0.98	0.15	39,39,39,39	0
56	MG	1A	3553	1/1	0.98	0.04	38,38,38,38	0
56	MG	2A	3376	1/1	0.98	0.11	29,29,29,29	0
56	MG	1A	3636	1/1	0.98	0.06	19,19,19,19	0
56	MG	2A	3255	1/1	0.98	0.06	42,42,42,42	0
56	MG	1A	3555	1/1	0.98	0.05	39,39,39,39	0
56	MG	1H	202	1/1	0.98	0.12	59,59,59,59	0
56	MG	2A	3499	1/1	0.98	0.06	31,31,31,31	0
56	MG	2A	3147	1/1	0.98	0.11	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3148	1/1	0.98	0.11	41,41,41,41	0
56	MG	1A	4030	1/1	0.98	0.10	41,41,41,41	0
56	MG	1A	3174	1/1	0.98	0.10	40,40,40,40	0
56	MG	1A	3557	1/1	0.98	0.09	44,44,44,44	0
56	MG	1A	3293	1/1	0.98	0.07	36,36,36,36	0
56	MG	1A	3760	1/1	0.98	0.08	42,42,42,42	0
56	MG	1A	3825	1/1	0.98	0.05	33,33,33,33	0
56	MG	2A	3389	1/1	0.98	0.08	36,36,36,36	0
56	MG	1A	3106	1/1	0.98	0.15	26,26,26,26	0
56	MG	1N	206	1/1	0.98	0.06	34,34,34,34	0
56	MG	1N	207	1/1	0.98	0.22	45,45,45,45	0
56	MG	2n	503	1/1	0.98	0.04	64,64,64,64	0
56	MG	1A	3890	1/1	0.98	0.10	62,62,62,62	0
56	MG	1A	3643	1/1	0.98	0.07	22,22,22,22	0
56	MG	1A	3644	1/1	0.98	0.08	38,38,38,38	0
56	MG	1a	1899	1/1	0.98	0.05	50,50,50,50	0
56	MG	1a	1708	1/1	0.98	0.09	61,61,61,61	0
56	MG	1A	3645	1/1	0.98	0.05	32,32,32,32	0
56	MG	1A	3646	1/1	0.98	0.08	21,21,21,21	0
56	MG	1A	3015	1/1	0.98	0.17	40,40,40,40	0
56	MG	1A	3030	1/1	0.98	0.17	52,52,52,52	0
56	MG	1A	3969	1/1	0.98	0.05	39,39,39,39	0
57	ZN	1n	501	1/1	0.98	0.05	86,86,86,86	0
56	MG	1A	3598	1/1	0.98	0.04	21,21,21,21	0
57	ZN	29	501	1/1	0.98	0.03	65,65,65,65	0
56	MG	1A	3529	1/1	0.98	0.07	62,62,62,62	0
58	SF4	2d	501	8/8	0.98	0.04	58,77,81,90	0
56	MG	1A	3560	1/1	0.99	0.09	24,24,24,24	0
56	MG	2A	3232	1/1	0.99	0.14	38,38,38,38	0
56	MG	1A	3855	1/1	0.99	0.06	15,15,15,15	0
56	MG	1A	3697	1/1	0.99	0.04	44,44,44,44	0
56	MG	2A	3141	1/1	0.99	0.14	35,35,35,35	0
56	MG	2A	3236	1/1	0.99	0.16	41,41,41,41	0
56	MG	1A	3561	1/1	0.99	0.14	34,34,34,34	0
56	MG	1A	3215	1/1	0.99	0.07	26,26,26,26	0
56	MG	1A	3113	1/1	0.99	0.04	42,42,42,42	0
56	MG	1A	3792	1/1	0.99	0.06	47,47,47,47	0
56	MG	1A	3524	1/1	0.99	0.11	24,24,24,24	0
56	MG	1A	3611	1/1	0.99	0.09	28,28,28,28	0
56	MG	1A	3207	1/1	0.99	0.09	40,40,40,40	0
56	MG	1A	3864	1/1	0.99	0.03	15,15,15,15	0
56	MG	1A	3763	1/1	0.99	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3349	1/1	0.99	0.09	49,49,49,49	0
56	MG	2A	3350	1/1	0.99	0.07	46,46,46,46	0
56	MG	1A	3129	1/1	0.99	0.14	35,35,35,35	0
56	MG	1A	3144	1/1	0.99	0.14	22,22,22,22	0
56	MG	2A	3353	1/1	0.99	0.08	54,54,54,54	0
56	MG	1A	3615	1/1	0.99	0.09	57,57,57,57	0
56	MG	2A	3355	1/1	0.99	0.03	42,42,42,42	0
56	MG	2A	3356	1/1	0.99	0.04	37,37,37,37	0
56	MG	2A	3477	1/1	0.99	0.09	61,61,61,61	0
56	MG	2a	3167	1/1	0.99	0.12	40,40,40,40	0
56	MG	1A	3084	1/1	0.99	0.03	25,25,25,25	0
56	MG	1A	3554	1/1	0.99	0.08	38,38,38,38	0
56	MG	1E	302	1/1	0.99	0.07	19,19,19,19	0
56	MG	2F	302	1/1	0.99	0.07	44,44,44,44	0
56	MG	1A	3082	1/1	0.99	0.10	28,28,28,28	0
56	MG	1A	3683	1/1	0.99	0.07	40,40,40,40	0
56	MG	1A	3908	1/1	0.99	0.05	20,20,20,20	0
56	MG	1A	3909	1/1	0.99	0.03	25,25,25,25	0
56	MG	2A	3306	1/1	0.99	0.06	26,26,26,26	0
56	MG	2A	3365	1/1	0.99	0.06	44,44,44,44	0
56	MG	2A	3307	1/1	0.99	0.07	32,32,32,32	0
56	MG	1A	3639	1/1	0.99	0.05	11,11,11,11	0
56	MG	1A	3059	1/1	0.99	0.03	46,46,46,46	0
56	MG	1A	3773	1/1	0.99	0.05	22,22,22,22	0
56	MG	2A	3370	1/1	0.99	0.03	62,62,62,62	0
56	MG	1a	1841	1/1	0.99	0.04	40,40,40,40	0
56	MG	1A	3774	1/1	0.99	0.08	21,21,21,21	0
56	MG	1A	3713	1/1	0.99	0.03	38,38,38,38	0
56	MG	17	103	1/1	0.99	0.05	53,53,53,53	0
56	MG	1A	3133	1/1	0.99	0.03	32,32,32,32	0
56	MG	1A	3687	1/1	0.99	0.08	21,21,21,21	0
56	MG	1B	216	1/1	0.99	0.04	47,47,47,47	0
56	MG	1B	217	1/1	0.99	0.06	36,36,36,36	0
56	MG	1A	3688	1/1	0.99	0.06	23,23,23,23	0
56	MG	1B	219	1/1	0.99	0.06	53,53,53,53	0
56	MG	2A	3269	1/1	0.99	0.11	43,43,43,43	0
56	MG	1A	3621	1/1	0.99	0.03	24,24,24,24	0
56	MG	1A	3622	1/1	0.99	0.06	21,21,21,21	0
56	MG	2A	3506	1/1	0.99	0.04	34,34,34,34	0
56	MG	1A	3748	1/1	0.99	0.05	36,36,36,36	0
56	MG	2A	3325	1/1	0.99	0.06	32,32,32,32	0
56	MG	1A	3603	1/1	0.99	0.07	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3224	1/1	0.99	0.04	33,33,33,33	0
57	ZN	1Y	501	1/1	0.99	0.02	63,63,63,63	0
56	MG	1A	3666	1/1	0.99	0.02	9,9,9,9	0
56	MG	2A	3133	1/1	0.99	0.06	40,40,40,40	0
57	ZN	2Y	501	1/1	0.99	0.04	88,88,88,88	0
56	MG	1a	1856	1/1	0.99	0.08	70,70,70,70	0
57	ZN	25	501	1/1	0.99	0.03	49,49,49,49	0
57	ZN	26	102	1/1	0.99	0.05	68,68,68,68	0
56	MG	1A	3721	1/1	0.99	0.05	45,45,45,45	0
56	MG	1A	3096	1/1	0.99	0.05	40,40,40,40	0
58	SF4	1d	301	8/8	0.99	0.05	64,69,73,86	0
56	MG	1A	3235	1/1	0.99	0.04	42,42,42,42	0
56	MG	1A	3962	1/1	1.00	0.03	34,34,34,34	0
57	ZN	15	102	1/1	1.00	0.02	43,43,43,43	0
57	ZN	16	102	1/1	1.00	0.04	45,45,45,45	0
57	ZN	19	501	1/1	1.00	0.04	44,44,44,44	0
56	MG	1A	3756	1/1	1.00	0.04	46,46,46,46	0
56	MG	1A	3539	1/1	1.00	0.04	26,26,26,26	0
56	MG	1A	3676	1/1	1.00	0.02	23,23,23,23	0
56	MG	1A	3746	1/1	1.00	0.07	15,15,15,15	0
56	MG	1A	3795	1/1	1.00	0.06	24,24,24,24	0
56	MG	1A	3689	1/1	1.00	0.05	14,14,14,14	0
56	MG	2A	3485	1/1	1.00	0.02	35,35,35,35	0
56	MG	1A	3947	1/1	1.00	0.02	37,37,37,37	0
56	MG	2a	3095	1/1	1.00	0.02	58,58,58,58	0

6.5 Other polymers (i)

There are no such residues in this entry.