



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 10:17 AM UTC

PDB ID : 8W2N / pdb_00008w2n
EMDB ID : EMD-43752
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) in the P/P conformation on a slippery CCC-C codon and Elongation Factor P bound (uL1 in the open conformation)
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2024-02-20
Resolution : 3.20 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

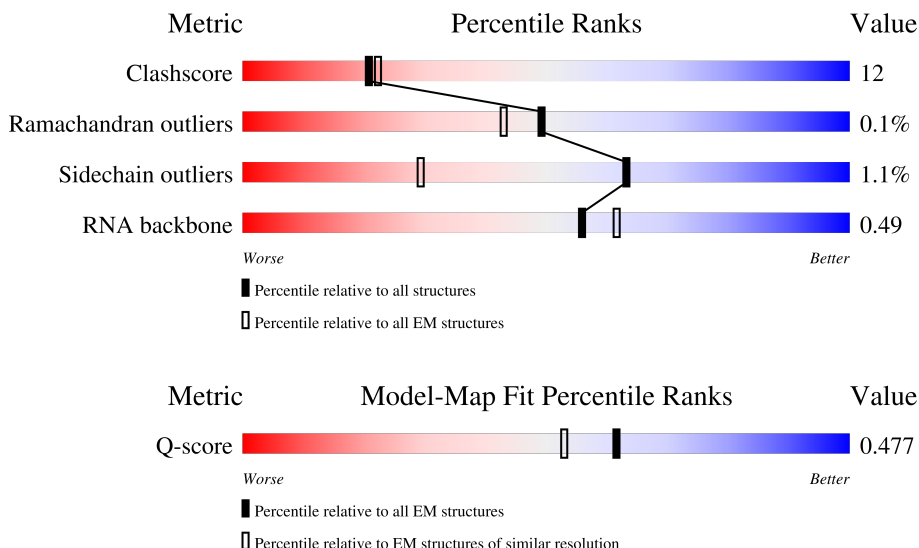
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



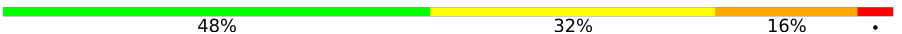
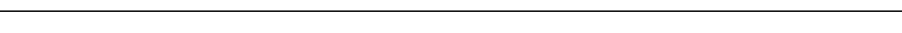
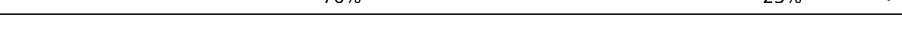
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	2904	
2	2	1540	
3	3	120	

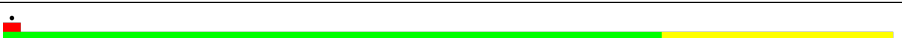
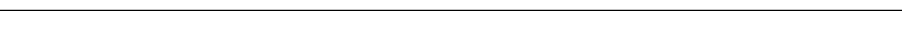
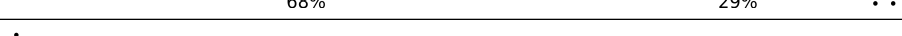
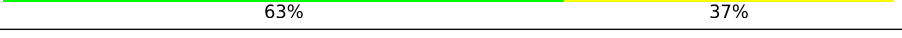
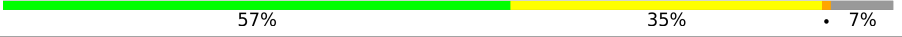
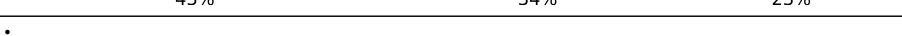
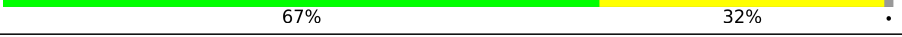
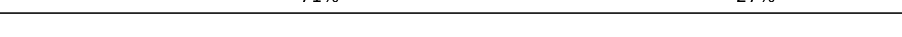
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Mol	Chain	Length	Quality of chain
4	4	18	
5	5	77	
6	6	188	
7	B	273	
8	C	209	
9	D	201	
10	E	179	
11	F	177	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	127	
18	O	117	
19	P	115	
20	Q	118	
21	R	103	
22	S	110	
23	T	100	
24	U	104	
25	V	94	
26	W	84	
27	X	78	
28	Y	63	

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Mol	Chain	Length	Quality of chain
29	Z	59	
30	a	70	
31	b	57	
32	c	55	
33	d	46	
34	e	65	
35	f	38	
36	g	241	
37	h	233	
38	i	206	
39	j	167	
40	k	135	
41	l	179	
42	m	130	
43	n	130	
44	o	103	
45	p	129	
46	q	124	
47	r	118	
48	s	101	
49	t	89	
50	u	82	
51	v	84	
52	w	75	
53	x	92	

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Mol	Chain	Length	Quality of chain
54	y	87	76% 23%
55	z	71	23% 68% 31%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145329 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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					AltConf	Trace
1	1	2815	Total	C	N	O	P	0	0
			60445	26964	11140	19526	2815		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1914786293
1	887	A	U	conflict	GB 1914786293
1	1847	G	A	conflict	GB 1914786293
1	2069	A	G	conflict	GB 1914786293

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1532	Total	C	N	O	P	0	0
			32887	14674	6033	10648	1532		

- Molecule 3 is a RNA chain called 5S mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	6	Total	C	N	O	P	0	0
			125	56	21	42	6		

- Molecule 5 is a RNA chain called tRNA^{ProL} (GGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Elongation factor P.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	188	Total	C	N	O	S	0	0
			1461	928	242	286	5		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 13 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 16 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 19 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 21 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 22 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O	S	0	0
			788	498	148	142			

- Molecule 25 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 33 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 34 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 35 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 48 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 51 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 53 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

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

Mol	Chain	Residues	Atoms		AltConf
56	1	290	Total	Mg	0
			290	290	
56	2	138	Total	Mg	0
			138	138	
56	3	10	Total	Mg	0
			10	10	
56	B	3	Total	Mg	0
			3	3	
56	C	2	Total	Mg	0
			2	2	
56	D	4	Total	Mg	0
			4	4	
56	E	1	Total	Mg	0
			1	1	
56	J	1	Total	Mg	0
			1	1	
56	L	2	Total	Mg	0
			2	2	
56	M	1	Total	Mg	0
			1	1	
56	P	2	Total	Mg	0
			2	2	
56	Q	2	Total	Mg	0
			2	2	
56	R	2	Total	Mg	0
			2	2	
56	S	1	Total	Mg	0
			1	1	
56	T	1	Total	Mg	0
			1	1	
56	Z	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
56	b	2	Total 2	Mg 2	0
56	d	1	Total 1	Mg 1	0
56	e	3	Total 3	Mg 3	0
56	f	2	Total 2	Mg 2	0
56	i	3	Total 3	Mg 3	0
56	j	2	Total 2	Mg 2	0
56	l	2	Total 2	Mg 2	0
56	m	2	Total 2	Mg 2	0
56	q	1	Total 1	Mg 1	0
56	y	1	Total 1	Mg 1	0

- Molecule 57 is water.

Mol	Chain	Residues	Atoms		AltConf
57	1	508	Total 508	O 508	0
57	2	395	Total 395	O 395	0
57	3	17	Total 17	O 17	0
57	5	5	Total 5	O 5	0
57	C	1	Total 1	O 1	0
57	D	2	Total 2	O 2	0
57	E	7	Total 7	O 7	0
57	F	3	Total 3	O 3	0
57	G	4	Total 4	O 4	0

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Mol	Chain	Residues	Atoms		AltConf
57	J	2	Total 2	O 2	0
57	L	1	Total 1	O 1	0
57	N	1	Total 1	O 1	0
57	O	1	Total 1	O 1	0
57	P	2	Total 2	O 2	0
57	T	1	Total 1	O 1	0
57	V	2	Total 2	O 2	0
57	W	1	Total 1	O 1	0
57	X	1	Total 1	O 1	0
57	Y	8	Total 8	O 8	0
57	Z	1	Total 1	O 1	0
57	a	2	Total 2	O 2	0
57	c	2	Total 2	O 2	0
57	g	10	Total 10	O 10	0
57	h	11	Total 11	O 11	0
57	i	1	Total 1	O 1	0
57	k	5	Total 5	O 5	0
57	l	9	Total 9	O 9	0
57	m	5	Total 5	O 5	0
57	n	4	Total 4	O 4	0
57	p	2	Total 2	O 2	0

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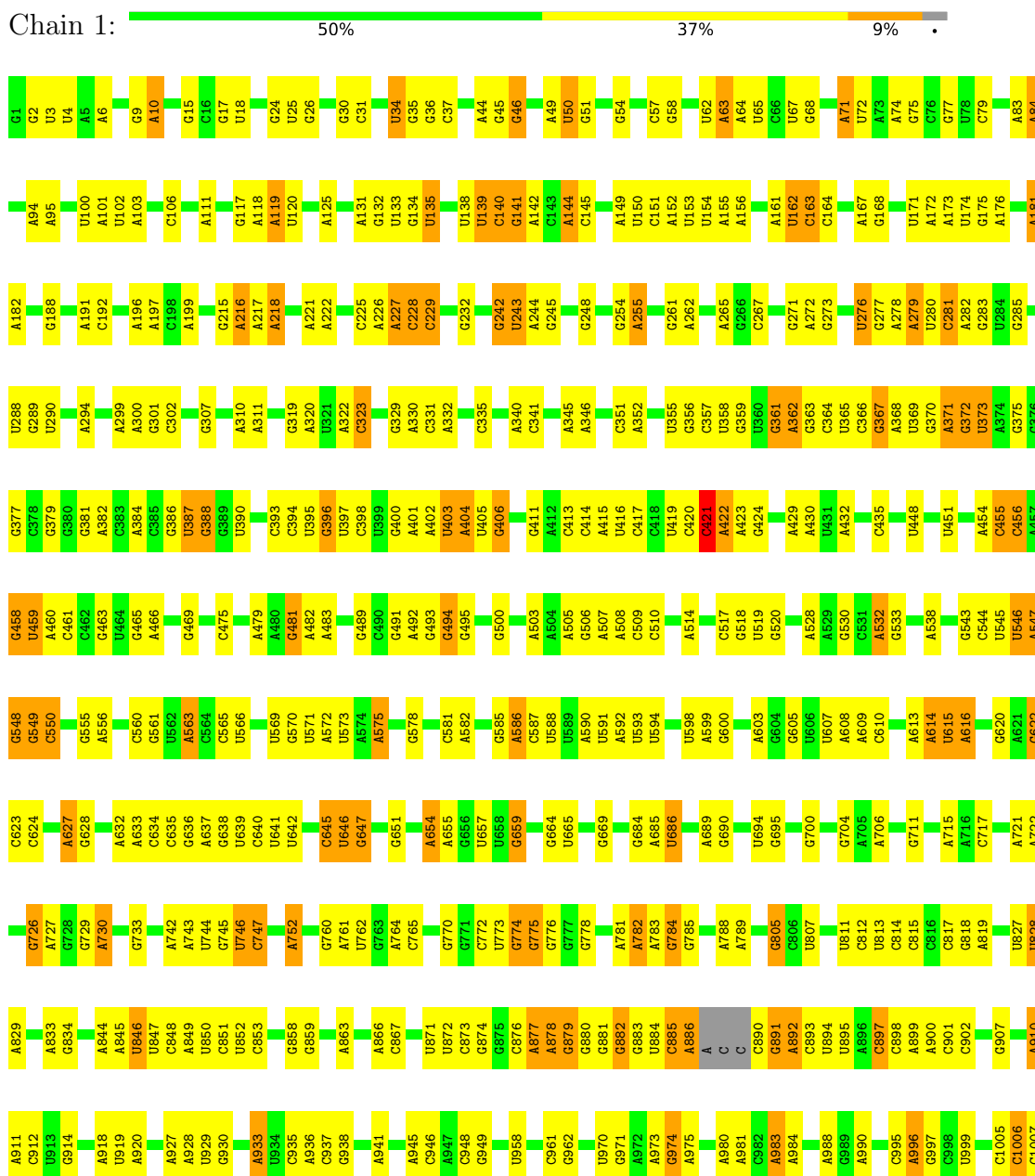
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Mol	Chain	Residues	Atoms		AltConf
57	q	3	Total 3	O 3	0
57	r	6	Total 6	O 6	0
57	s	1	Total 1	O 1	0
57	t	5	Total 5	O 5	0
57	u	1	Total 1	O 1	0
57	v	3	Total 3	O 3	0
57	w	6	Total 6	O 6	0
57	x	5	Total 5	O 5	0
57	y	3	Total 3	O 3	0
57	z	7	Total 7	O 7	0

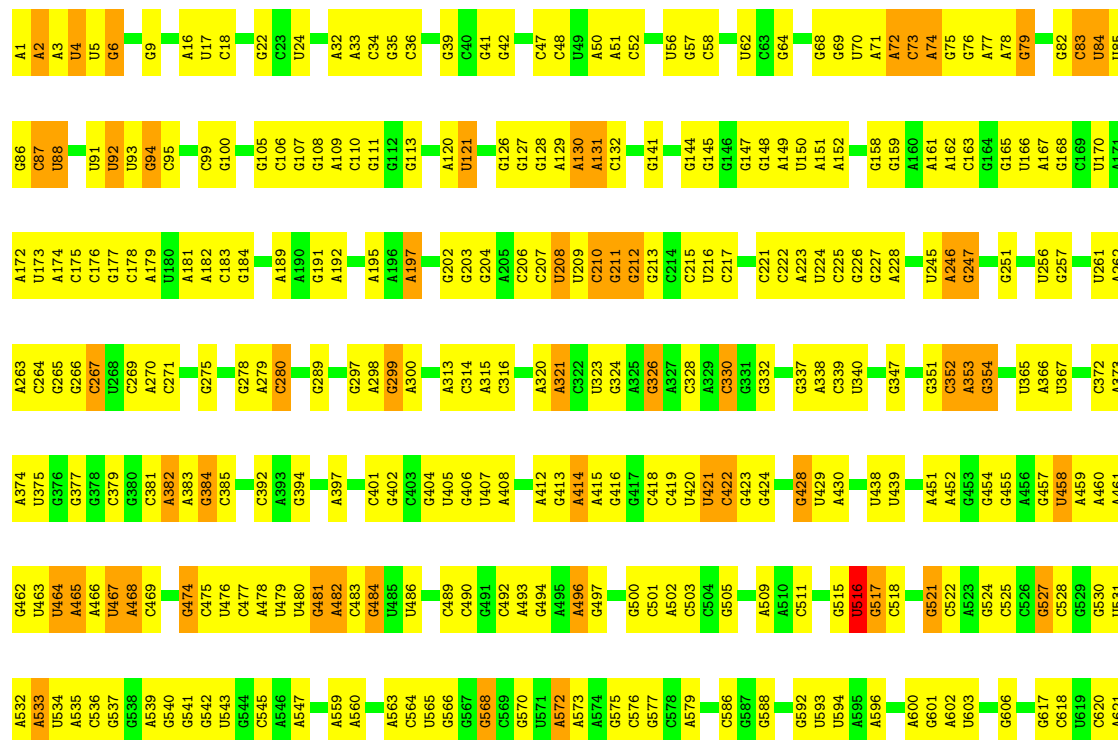
3 Residue-property plots

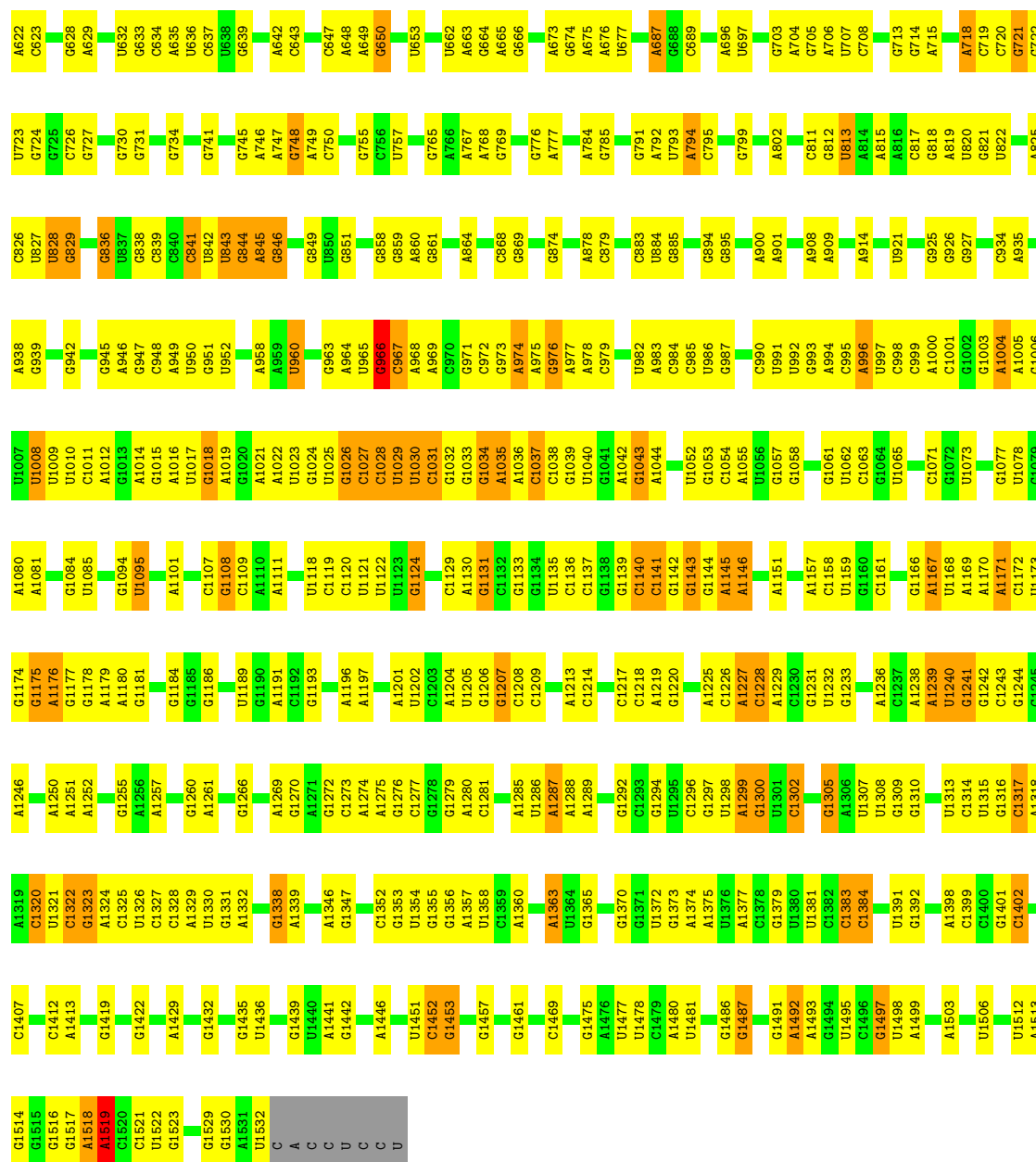
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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

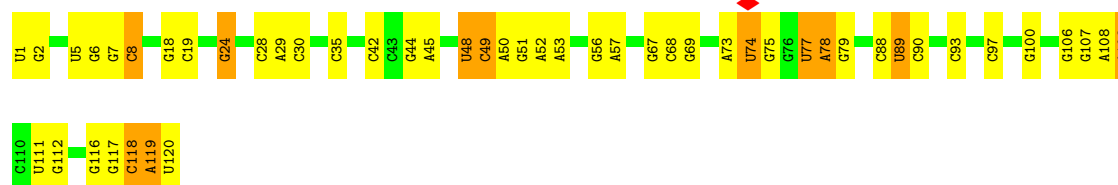


U2244	A2020	G1907	G1799	G1722	U1599	U1523	A1433	G1343	G1250	G1160	U1081	A1008
U2245	C2021	A1913	C1800	A1722	C1600	G1524	A1434	U1344	A1253	G1169	U1082	A1009
A2246	U2022	G1914	A1801	G1723	C1607	A1528	C1437	C1345	A1254	C1170	A1083	A1010
A2247	C2023	A1915	A1802	G1724	A1608	G1529	G1437	U1352	U1255	G1171	A1084	G1011
U2248	G2024	U1916	A1803	U1725	A1614	A1532	G1441	C1357	G1256	U1173	A1086	U1012
G2250	U2026	U1917	A1808	C1727	A1614	A1532	U1442	U1357	U1263	U1174	G1087	C1013
G2251	G2027	A1918	A1809	C1728	A1618	C1533	U1443	A1359	U1264	U1175	A1088	A1014
C2252	A2030	C1920	C1816	U1729	G1618	U1534	U1444	A1365	A1265	U1176	A1089	U1019
C2263	A2031	C1920	G1817	C1730	G1619	C1535	U1445	A1366	A1266	U1177	A1090	A1020
C2264	G2032	U1923	U1818	G1731	U1621	C1536	C1446	A1367	A1268	C1178	G1092	G1022
C2265	A2033	U1923	A1819	G1732	G1622	G1537	U1447	G1368	A1269	U1179	G1093	U1023
C2266	C2034	A1928	G1826	G1734	G1622	U1539	G1448	U1369	C1270	U1180	U1094	G1024
G2271	A2037	G1929	G1826	A1735	G1627	C1540	A1453	G1371	A1271	U1183	A1095	G1025
U2272	G2038	G1930	A1829	U1736	G1628	C1541	U1458	U1379	A1272	U1184	A1096	G1026
A2273	U2039	U1931	A1830	C1737	U1642	U1542	G1459	G1380	A1275	U1185	U1097	A1027
A2274	G2040	A1932	C1830	G1738	A1632	G1543	U1460	U1381	G1283	G1186	A1098	A1028
A2275	U2041	G1933	G1831	U1742	U1636	A1551	A1461	U1382	A1285	U1188	U1100	A1032
A2276	C2043	A1936	C1832	G1743	A1637	A1552	A1469	G1383	G1295	G1193	C1102	U1033
G2277	A2051	A1937	G1840	A1746	G1645	C1558	A1470	A1384	C1296	G1196	A1103	A1039
G2278	G2052	U1938	U1841	U1747	C1646	U1559	G1471	A1385	G1296	C1197	C1104	A1040
G2282	A2053	U1940	G1842	U1751	U1647	G1560	G1475	C1386	G1296	U1198	U1105	G1041
A2284	A2054	C1941	C1843	U1752	U1648	G1561	U1476	A1387	G1300	U1199	G1106	G1042
C2285	G2055	U1942	G1847	G1753	G1651	U1562	A1477	U1400	A1301	U1199	C1043	C1043
G2286	U2056	U1943	A1848	G1754	A1652	C1564	G1478	A1392	A1302	C1200	U1108	C1044
A2287	A2060	U1955	U1856	G1756	G1653	C1565	G1482	A1395	C1306	G1210	G1110	A1046
G2288	G2061	U1956	G1857	A1757	A1655	A1566	G1483	U1396	A1307	U1203	A1111	G1047
G2289	A2062	C1957	U1858	U1758	G1656	A1569	U1484	U1397	A1204	U1204	U1112	A1048
G2290	C2063	C1958	C1859	A1759	G1667	A1570	U1485	C1398	G1309	A1205	U1113	G1054
U2291	A2064	G1964	G1862	C1760	G1674	A1571	U1486	C1399	G1315	G1211	C1114	G1055
G2292	G2065	G1964	U1863	G1765	C1675	A1572	U1487	U1400	G1316	G1212	G1115	G1056
G2293	A2069	C1967	U1864	U1766	A1676	C1574	C1489	G1401	G1317	U1212	G1116	A1057
G2294	A2070	G1968	U1865	G1766	A1676	C1574	A1490	G1407	U1318	G1125	U1058	U1058
G2295	A2071	A1969	C1870	A1773	A1679	C1577	G1491	U1408	C1319	A1126	G1059	G1060
U2296	C2072	U1970	A1871	G1776	G1680	U1578	G1492	U1409	A1320	U1130	U1061	U1061
A2297	C2073	G1972	A1872	G1776	G1681	A1579	A1494	G1410	A1321	G1131	G1062	G1062
U2299	C2074	U1971	G1873	G1779	U1683	C1581	A1495	U1411	A1322	U1132	G1063	G1063
U2300	A2078	A1987	G1874	U1779	U1683	C1582	U1497	G1412	G1323	G1223	C1064	C1064
G2302	G2079	U1987	G1875	A1780	U1693	C1583	C1498	G1416	U1324	U1224	A1133	U1065
G2303	U2086	U1991	C1881	A1783	C1694	U1584	A1504	C1417	G1325	G1225	A1134	U1066
G2304	G2087	U1992	U1882	A1784	G1695	C1585	A1505	A1418	A1327	U1226	G1136	U1066
U2305	C2088	U1993	U1883	G1787	G1696	A1586	A1506	A1419	A1328	G1227	G1139	A1067
G2306	U2092	C1996	A1884	A1788	A1698	G1587	U1507	A1420	U1329	A1230	C1140	G1068
G2307	G2093	C1997	A1885	G1788	G1699	G1588	C1507	G1421	C1330	U1231	U1141	A1069
G2308	C2096	C2006	G1888	A1789	U1709	G1589	U1508	G1422	G1333	G1236	A1142	A1070
A2309	A2097	G2006	G1889	C1790	U1710	A1590	A1509	G1425	G1334	A1237	A1143	C1072
G2310	U2098	G2010	A1896	A1791	U1711	C1592	G1510	G1428	U1240	U1241	G1149	A1073
U2311	G2100	A2014	A1900	A1794	A1712	C1593	U1513	G1429	A1241	C1150	G1150	C1074
U2312	A2101	C2102	A1901	C1795	A1713	U1594	G1514	G1430	A1247	C1153	U1159	C1075
C2313	G2103	U2015	G1715	U1796	G1714	U1597	A1515	A1431	G1248	U1159	U1159	G1076
G2314	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	U1078
G2315	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	G1079
G2316	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080
G2317	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080
G2318	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080
G2319	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080
G2320	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080
G2321	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080
G2322	C2104	C2104	G1716	U1798	U1716	A1598	G1516	G1432	U1249	U1159	U1159	A1080



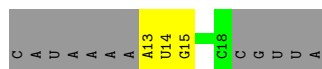


• Molecule 3: 5S mRNA



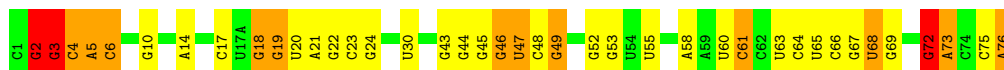
• Molecule 4: mRNA





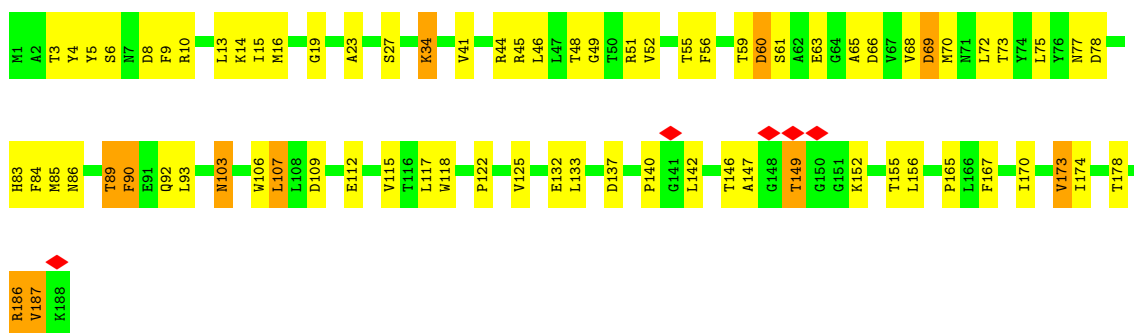
• Molecule 5: tRNA^{ProL} (GGG)

Chain 5: 48% 32% 16%



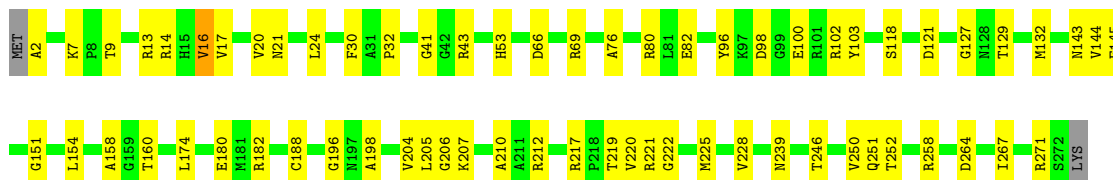
• Molecule 6: Elongation factor P

Chain 6: 60% 35% 6%



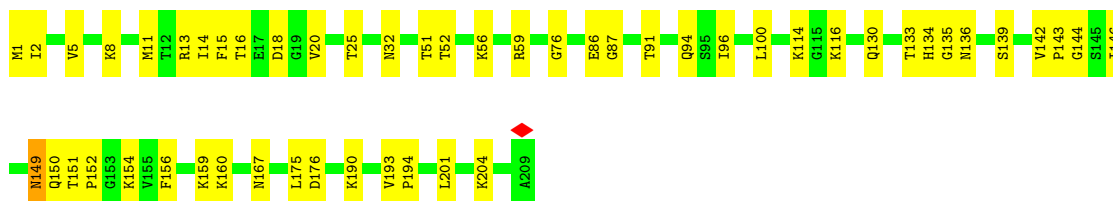
• Molecule 7: 50S ribosomal protein L2

Chain B: 75% 23%



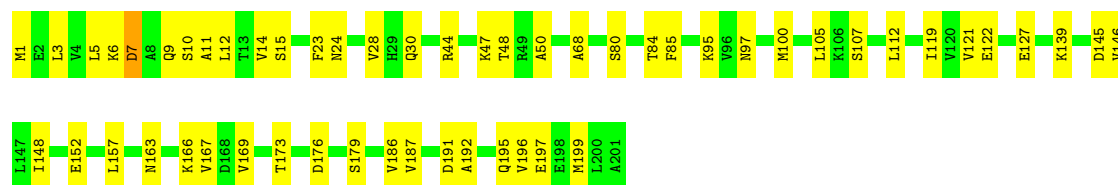
• Molecule 8: 50S ribosomal protein L3

Chain C: 75% 24%



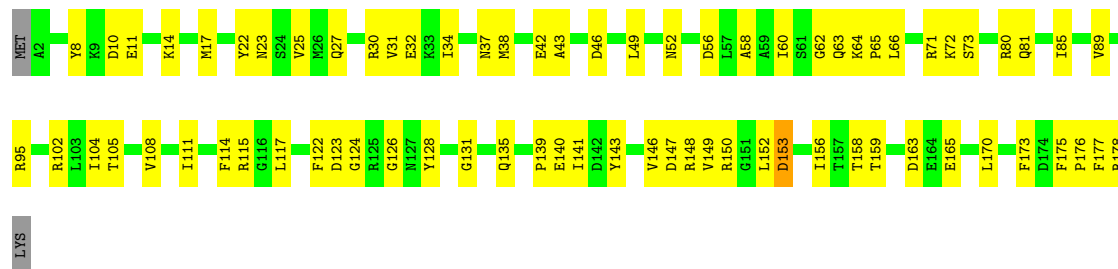
• Molecule 9: 50S ribosomal protein L4

Chain D: 73% 26%



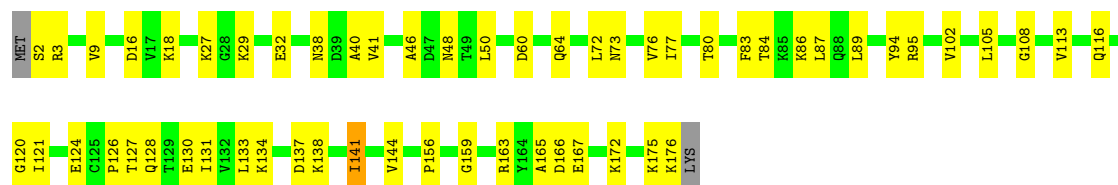
• Molecule 10: 50S ribosomal protein L5

Chain E: 58% 40% ..



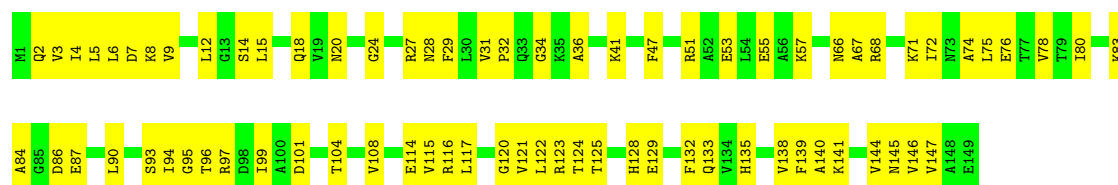
• Molecule 11: 50S ribosomal protein L6

Chain F: 67% 31% ..



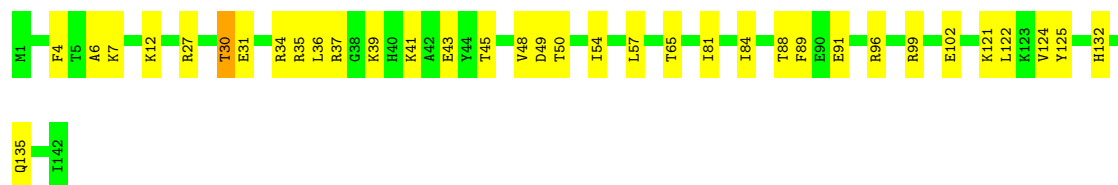
• Molecule 12: 50S ribosomal protein L9

Chain G: 50% 50%



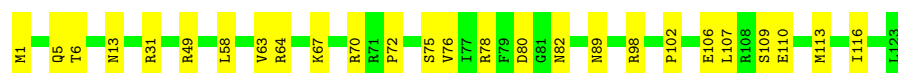
• Molecule 13: 50S ribosomal protein L13

Chain J: 75% 24%



• Molecule 14: 50S ribosomal protein L14

Chain K:  79% 21%



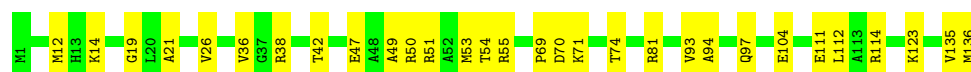
- Molecule 15: 50S ribosomal protein L15

Chain L:  74% 26%



- Molecule 16: 50S ribosomal protein L16

Chain M:  78% 22%



- Molecule 17: 50S ribosomal protein L17

Chain N:  68% 26% 6%



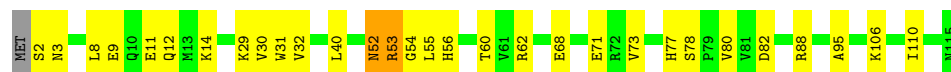
- Molecule 18: 50S ribosomal protein L18

Chain O:  76% 23%



- Molecule 19: 50S ribosomal protein L19

Chain P:  73% 24% ..



- Molecule 20: 50S ribosomal protein L20

Chain Q:  74% 25% ..



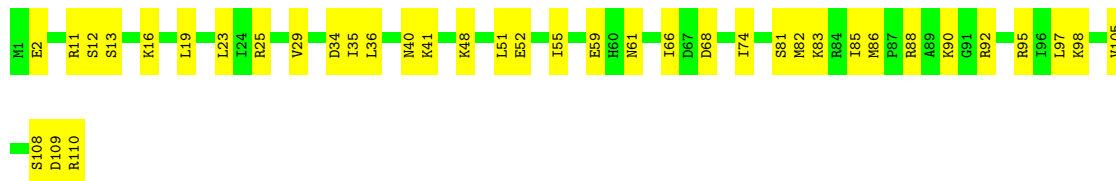
- Molecule 21: 50S ribosomal protein L21

Chain R:  67% 33%



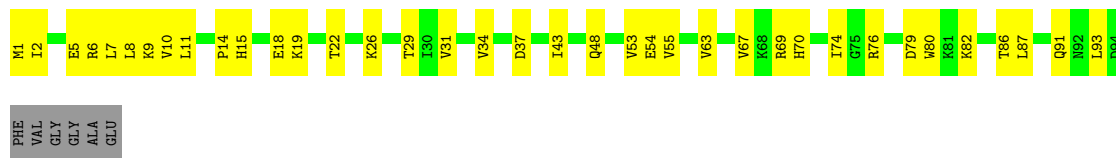
- Molecule 22: 50S ribosomal protein L22

Chain S:  65% 35%



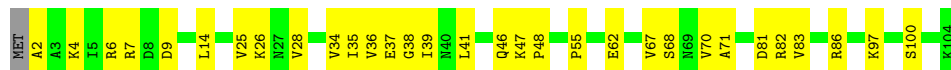
- Molecule 23: 50S ribosomal protein L23

Chain T:  57% 37% 6%



- Molecule 24: 50S ribosomal protein L24

Chain U:  69% 30%



- Molecule 25: 50S ribosomal protein L25

Chain V:  63% 37%



- Molecule 26: 50S ribosomal protein L27

Chain W:  64% 26% 10%



- Molecule 27: 50S ribosomal protein L28

Chain X: 



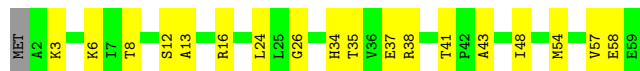
- Molecule 28: 50S ribosomal protein L29

Chain Y: 



- Molecule 29: 50S ribosomal protein L30

Chain Z: 



- Molecule 30: 50S ribosomal protein L31

Chain a: 



- Molecule 31: 50S ribosomal protein L32

Chain b: 



- Molecule 32: 50S ribosomal protein L33

Chain c: 



- Molecule 33: 50S ribosomal protein L34

Chain d: 



- Molecule 34: 50S ribosomal protein L35

Chain e: 68% 29%



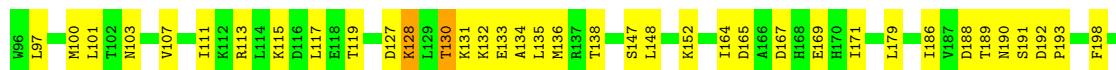
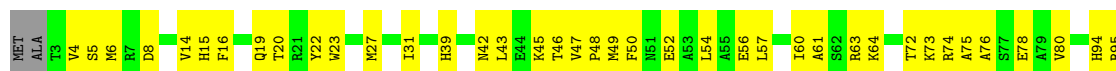
- Molecule 35: 50S ribosomal protein L36

Chain f: 63% 37%



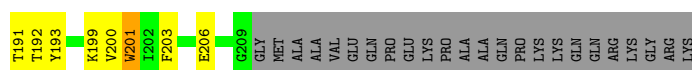
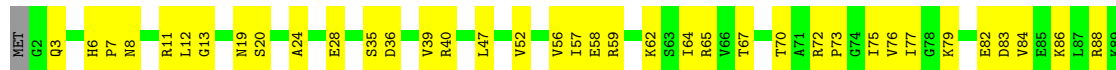
- Molecule 36: 30S ribosomal protein S2

Chain g: 57% 35% 7%



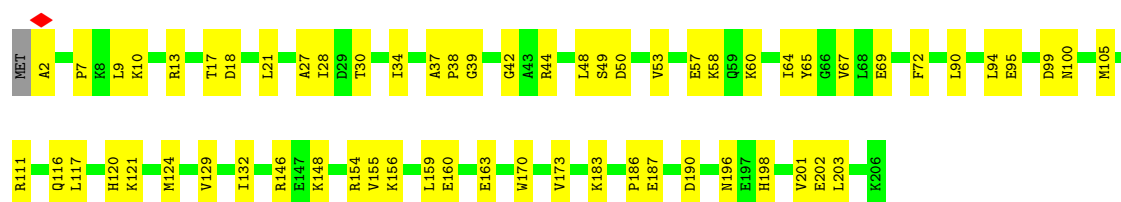
- Molecule 37: 30S ribosomal protein S3

Chain h: 54% 35% 11%

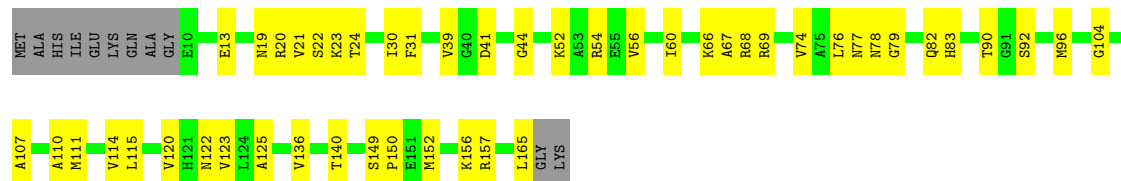


- Molecule 38: 30S ribosomal protein S4

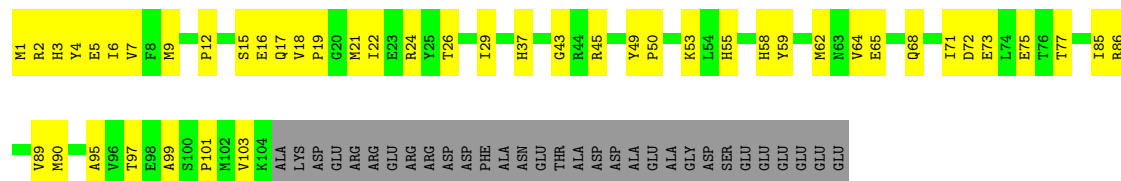
Chain i: 69% 30%



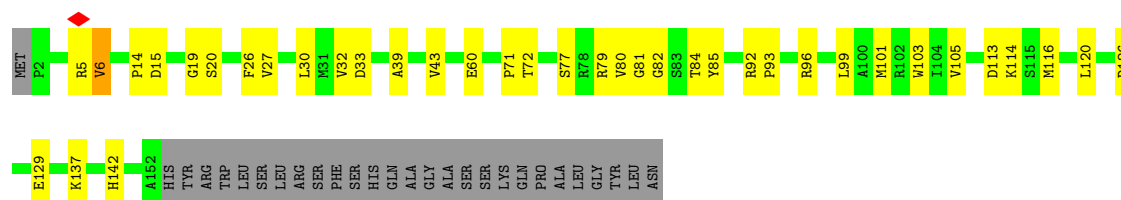
- Molecule 39: 30S ribosomal protein S5



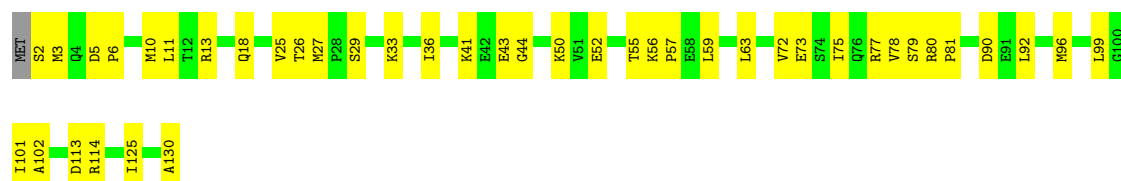
- Molecule 40: 30S ribosomal protein S6



- Molecule 41: 30S ribosomal protein S7

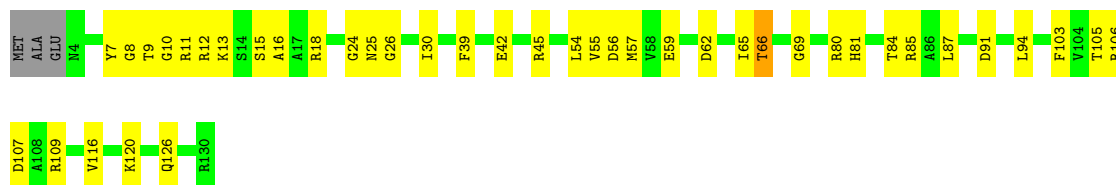


- Molecule 42: 30S ribosomal protein S8



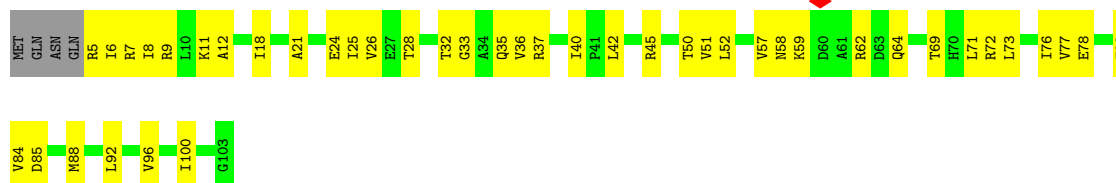
- Molecule 43: 30S ribosomal protein S9

Chain n:  66% 31% ..



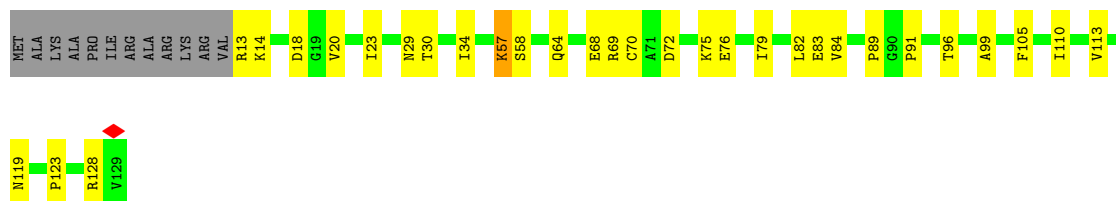
- Molecule 44: 30S ribosomal protein S10

Chain o:  54% 42% .



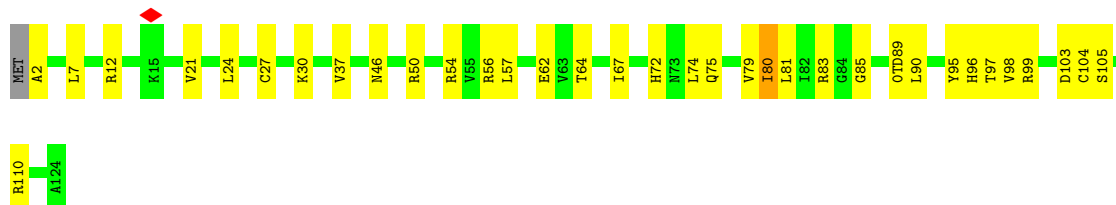
- Molecule 45: 30S ribosomal protein S11

Chain p:  67% 23% 9% .



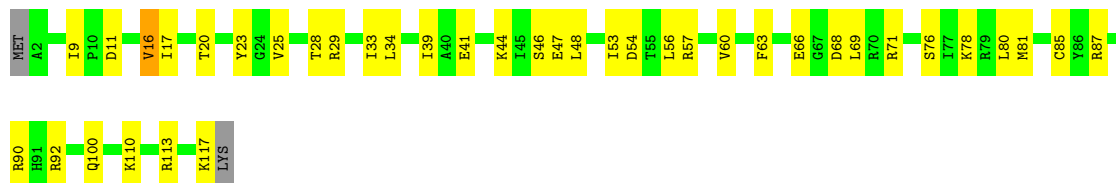
- Molecule 46: 30S ribosomal protein S12

Chain q:  71% 27% ..



- Molecule 47: 30S ribosomal protein S13

Chain r:  65% 32% ..



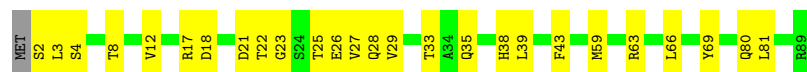
- Molecule 48: 30S ribosomal protein S14

Chain s:  69% 29% ..



- Molecule 49: 30S ribosomal protein S15

Chain t:  70% 29% .



- Molecule 50: 30S ribosomal protein S16

Chain u:  60% 40%



- Molecule 51: 30S ribosomal protein S17

Chain v:  56% 39% 5%



- Molecule 52: 30S ribosomal protein S18

Chain w:  5% 40% 48% 12%



- Molecule 53: 30S ribosomal protein S19

Chain x:  58% 33% 10%



- Molecule 54: 30S ribosomal protein S20

Chain y:  76% 23% .



● Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.07	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00251	Depositor
Map size ($\text{\AA}$)	547.328, 547.328, 547.328	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.069, 1.069, 1.069	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, 4OC, MA6, PSU, UR3, MG, G7M, 0TD, 2MG, KEO

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	1	0.74	1/67700 (0.0%)	0.47	7/105611 (0.0%)
2	2	0.62	0/36543	0.42	1/57001 (0.0%)
3	3	0.60	0/2872	0.46	0/4478
4	4	0.53	0/138	0.65	0/212
5	5	0.49	0/1841	0.64	3/2870 (0.1%)
6	6	0.90	1/1470 (0.1%)	1.06	6/1992 (0.3%)
7	B	0.82	2/2121 (0.1%)	0.68	0/2852
8	C	0.75	0/1586	0.70	1/2134 (0.0%)
9	D	0.66	0/1571	0.57	0/2113
10	E	0.54	0/1434	0.60	0/1926
11	F	0.54	0/1333	0.58	0/1805
12	G	0.38	0/1122	0.58	0/1515
13	J	0.67	0/1152	0.62	0/1551
14	K	0.76	0/955	0.62	0/1279
15	L	0.77	0/1062	0.80	2/1413 (0.1%)
16	M	0.66	0/1093	0.58	0/1460
17	N	0.81	0/964	0.70	1/1289 (0.1%)
18	O	0.55	0/902	0.62	1/1209 (0.1%)
19	P	0.80	1/929 (0.1%)	0.70	1/1242 (0.1%)
20	Q	0.93	2/960 (0.2%)	0.66	1/1278 (0.1%)
21	R	0.75	1/829 (0.1%)	0.61	0/1107
22	S	0.69	0/864	0.61	0/1156
23	T	0.62	0/752	0.59	0/1005
24	U	0.55	0/796	0.55	0/1062
25	V	0.64	0/766	0.59	0/1025
26	W	0.71	0/589	0.62	0/779
27	X	0.74	0/635	0.61	0/848
28	Y	0.53	0/502	0.55	0/667
29	Z	0.68	0/452	0.57	0/605
30	a	0.28	0/531	0.49	0/709
31	b	0.68	0/450	0.64	0/599
32	c	0.71	0/433	0.60	0/576

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.78	0/380	0.59	0/498
34	e	0.86	0/513	0.72	0/676
35	f	0.79	0/303	0.72	0/397
36	g	0.37	0/1791	0.52	0/2413
37	h	0.59	1/1663 (0.1%)	0.66	0/2241
38	i	0.50	0/1665	0.56	0/2227
39	j	0.63	0/1165	0.59	0/1568
40	k	0.49	0/867	0.53	0/1171
41	l	0.57	0/1195	0.63	0/1602
42	m	0.66	0/989	0.56	0/1326
43	n	0.55	0/1034	0.61	0/1375
44	o	0.50	0/800	0.56	0/1082
45	p	0.59	1/893 (0.1%)	0.58	0/1205
46	q	0.60	0/960	0.61	0/1286
47	r	0.52	0/909	0.59	0/1215
48	s	0.62	0/817	0.57	0/1088
49	t	0.61	0/722	0.55	0/964
50	u	0.63	0/659	0.73	2/884 (0.2%)
51	v	0.54	0/657	0.55	0/881
52	w	0.53	0/553	0.55	0/743
53	x	0.46	0/680	0.57	0/915
54	y	0.51	0/675	0.49	0/895
55	z	0.27	0/597	0.47	0/792
All	All	0.68	10/155834 (0.0%)	0.51	26/232812 (0.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	143	ASN	CA-C	-7.59	1.46	1.53
1	1	2102	G	C1'-N9	-7.38	1.36	1.48
20	Q	25	TYR	CA-C	-6.36	1.44	1.52
6	6	77	ASN	CA-C	-6.12	1.45	1.52
20	Q	48	ARG	CA-C	-5.88	1.44	1.52
21	R	79	ARG	CA-C	-5.80	1.45	1.52
37	h	192	THR	CA-C	-5.51	1.45	1.52
19	P	52	ASN	CA-C	-5.41	1.46	1.52
7	B	158	ALA	CA-C	-5.30	1.45	1.52
45	p	57	LYS	CA-C	-5.24	1.45	1.52

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	149	ASN	N-CA-C	10.53	125.08	109.59
6	6	149	THR	N-CA-C	9.82	121.58	111.07
15	L	36	LYS	N-CA-C	9.01	131.70	113.31
5	5	2	G	C4'-C3'-O3'	8.30	121.85	109.40
6	6	60	ASP	N-CA-C	8.23	121.98	109.23
6	6	103	ASN	N-CA-C	-7.55	102.29	113.61
5	5	72	G	C4'-C3'-O3'	7.22	120.23	109.40
17	N	105	GLY	N-CA-C	6.92	121.03	112.73
50	u	45	GLU	N-CA-C	-6.76	101.61	110.53
15	L	35	HIS	N-CA-C	6.64	120.09	107.75
19	P	55	LEU	N-CA-C	-6.37	104.61	112.38
20	Q	50	ARG	N-CA-C	-6.35	104.45	111.82
6	6	78	ASP	N-CA-C	-6.21	98.77	108.90
5	5	3	G	C4'-C3'-O3'	6.21	118.71	109.40
2	2	1491	G	C2'-C3'-O3'	-5.66	105.21	113.70
1	1	547	A	C4'-C3'-O3'	-5.58	104.63	113.00
1	1	546	U	C1'-C2'-O2'	-5.56	100.06	108.40
1	1	1236	G	C2'-C3'-O3'	5.53	117.79	109.50
1	1	884	U	C4'-C3'-O3'	5.48	121.22	113.00
1	1	1490	A	C4'-C3'-O3'	-5.45	104.82	113.00
1	1	2190	G	C2'-C3'-O3'	5.45	121.87	113.70
1	1	421	C	C2'-C3'-O3'	5.40	117.60	109.50
6	6	55	THR	N-CA-C	-5.23	100.65	109.07
6	6	52	VAL	N-CA-C	-5.23	100.34	108.81
18	O	54	VAL	N-CA-C	-5.07	106.98	113.22
50	u	48	GLU	N-CA-C	-5.07	102.55	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	60445	0	30406	1004	0
2	2	32887	0	16565	590	0
3	3	2569	0	1301	40	0
4	4	125	0	66	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	5	1648	0	834	24	0
6	6	1461	0	1421	52	0
7	B	2082	0	2154	47	0
8	C	1565	0	1616	47	0
9	D	1552	0	1619	41	0
10	E	1410	0	1444	63	0
11	F	1313	0	1358	38	0
12	G	1111	0	1148	58	0
13	J	1129	0	1162	37	0
14	K	946	0	1023	24	0
15	L	1053	0	1128	31	0
16	M	1074	0	1157	21	0
17	N	951	0	994	21	0
18	O	892	0	923	19	0
19	P	917	0	962	24	0
20	Q	947	0	1019	22	0
21	R	816	0	839	27	0
22	S	857	0	922	27	0
23	T	746	0	811	27	0
24	U	788	0	844	23	0
25	V	753	0	780	25	0
26	W	582	0	599	17	0
27	X	625	0	652	16	0
28	Y	501	0	531	15	0
29	Z	448	0	488	15	0
30	a	522	0	524	28	0
31	b	444	0	458	16	0
32	c	426	0	464	15	0
33	d	377	0	418	10	0
34	e	504	0	572	19	0
35	f	302	0	343	12	0
36	g	1760	0	1787	61	0
37	h	1636	0	1710	64	0
38	i	1643	0	1706	43	0
39	j	1152	0	1196	42	0
40	k	848	0	846	35	0
41	l	1181	0	1238	29	0
42	m	979	0	1031	33	0
43	n	1022	0	1070	36	0
44	o	790	0	831	37	0
45	p	877	0	887	25	0
46	q	957	0	1017	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	r	900	0	965	31	0
48	s	805	0	844	26	0
49	t	714	0	734	25	0
50	u	649	0	666	33	0
51	v	648	0	691	28	0
52	w	544	0	560	31	0
53	x	663	0	688	25	0
54	y	669	0	719	17	0
55	z	589	0	629	19	0
56	1	290	0	0	0	0
56	2	138	0	0	0	0
56	3	10	0	0	0	0
56	B	3	0	0	0	0
56	C	2	0	0	0	0
56	D	4	0	0	0	0
56	E	1	0	0	0	0
56	J	1	0	0	0	0
56	L	2	0	0	0	0
56	M	1	0	0	0	0
56	P	2	0	0	0	0
56	Q	2	0	0	0	0
56	R	2	0	0	0	0
56	S	1	0	0	0	0
56	T	1	0	0	0	0
56	Z	2	0	0	0	0
56	b	2	0	0	0	0
56	d	1	0	0	0	0
56	e	3	0	0	0	0
56	f	2	0	0	0	0
56	i	3	0	0	0	0
56	j	2	0	0	0	0
56	l	2	0	0	0	0
56	m	2	0	0	0	0
56	q	1	0	0	0	0
56	y	1	0	0	0	0
57	1	508	0	0	44	0
57	2	395	0	0	36	0
57	3	17	0	0	1	0
57	5	5	0	0	2	0
57	C	1	0	0	0	0
57	D	2	0	0	3	0
57	E	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	F	3	0	0	0	0
57	G	4	0	0	0	0
57	J	2	0	0	0	0
57	L	1	0	0	0	0
57	N	1	0	0	0	0
57	O	1	0	0	0	0
57	P	2	0	0	0	0
57	T	1	0	0	0	0
57	V	2	0	0	1	0
57	W	1	0	0	0	0
57	X	1	0	0	0	0
57	Y	8	0	0	1	0
57	Z	1	0	0	3	0
57	a	2	0	0	1	0
57	c	2	0	0	0	0
57	g	10	0	0	0	0
57	h	11	0	0	3	0
57	i	1	0	0	0	0
57	k	5	0	0	0	0
57	l	9	0	0	0	0
57	m	5	0	0	0	0
57	n	4	0	0	0	0
57	p	2	0	0	2	0
57	q	3	0	0	0	0
57	r	6	0	0	1	0
57	s	1	0	0	0	0
57	t	5	0	0	1	0
57	u	1	0	0	4	0
57	v	3	0	0	3	0
57	w	6	0	0	0	0
57	x	5	0	0	0	0
57	y	3	0	0	0	0
57	z	7	0	0	2	0
All	All	145329	0	97360	2856	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 12.

All (2856) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2799:A:H5''	57:1:3407:HOH:O	1.32	1.22
29:Z:3:LYS:HE2	57:Z:201:HOH:O	1.46	1.14
51:v:75:LEU:HD11	57:v:101:HOH:O	1.62	0.98
50:u:14:ARG:HG2	57:u:101:HOH:O	1.63	0.98
46:q:72:HIS:HB3	46:q:99:ARG:HH22	1.29	0.96
1:1:853:C:H5''	57:1:3532:HOH:O	1.64	0.96
1:1:2802:G:H5''	57:1:3608:HOH:O	1.66	0.94
1:1:1176:U:H6	57:1:3356:HOH:O	1.51	0.94
11:F:16:ASP:HB2	11:F:27:LYS:HB2	1.49	0.91
24:U:28:VAL:HG12	24:U:34:VAL:HG12	1.53	0.90
1:1:2840:C:H5''	17:N:53:THR:HG21	1.55	0.89
2:2:1061:G:H1'	57:2:2170:HOH:O	1.73	0.88
42:m:18:GLN:HE21	42:m:72:VAL:HG22	1.39	0.88
1:1:1597:A:H5''	1:1:1598:A:H5'	1.59	0.85
11:F:95:ARG:HG3	11:F:128:GLN:HB2	1.58	0.85
2:2:91:U:C6	57:2:1902:HOH:O	2.29	0.84
1:1:495:G:H21	22:S:61:ASN:HD21	1.25	0.84
2:2:844:G:H8	57:2:1817:HOH:O	1.60	0.83
9:D:121:VAL:HG11	57:D:402:HOH:O	1.78	0.83
1:1:2797:U:C4	57:1:3332:HOH:O	2.29	0.83
2:2:91:U:H5''	57:2:1902:HOH:O	1.79	0.82
2:2:843:U:H2'	57:2:1911:HOH:O	1.79	0.82
1:1:2483:C:N3	16:M:123:LYS:NZ	2.28	0.82
1:1:272:A:H5'	57:1:3499:HOH:O	1.79	0.81
2:2:1001:C:C6	57:2:1881:HOH:O	2.33	0.81
6:6:75:LEU:HD11	6:6:85:MET:HG2	1.60	0.81
19:P:29:LYS:HB3	19:P:40:LEU:HD12	1.64	0.80
27:X:16:ASN:HD22	27:X:24:ALA:HB1	1.47	0.80
1:1:586:A:H5'	9:D:84:THR:HG21	1.60	0.80
2:2:76:G:H1	2:2:93:U:H3	1.29	0.79
1:1:2327:A:H2'	1:1:2328:A:C8	2.17	0.79
1:1:1936:A:H2	1:1:1943:U:H3	1.31	0.78
1:1:846:U:C5'	57:1:3521:HOH:O	2.31	0.78
2:2:121:U:H1'	57:2:1893:HOH:O	1.83	0.78
2:2:206:C:H2'	2:2:207:C:H6	1.48	0.78
1:1:1092:C:H2'	1:1:1099:G:H22	1.49	0.78
2:2:1135:U:H4'	57:2:2013:HOH:O	1.82	0.78
2:2:942:G:H21	43:n:126:GLN:HE22	1.32	0.78
1:1:2391:G:H2'	1:1:2424:C:H41	1.49	0.77
2:2:673:A:H2'	2:2:674:G:C8	2.20	0.77
2:2:1052:U:H5	57:2:1883:HOH:O	1.67	0.77
2:2:1008:U:N3	2:2:1021:A:N1	2.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:636:G:N7	15:L:109:LYS:NZ	2.33	0.76
2:2:337:G:H2'	2:2:338:A:H8	1.50	0.76
2:2:1356:G:H2'	2:2:1357:A:C8	2.19	0.76
50:u:14:ARG:CG	57:u:101:HOH:O	2.28	0.76
15:L:19:LEU:HD23	15:L:27:LEU:HD23	1.67	0.76
38:i:95:GLU:HA	38:i:100:ASN:HD22	1.51	0.76
1:1:1169:A:H5'	57:1:3515:HOH:O	1.85	0.75
49:t:33:THR:HG22	49:t:63:ARG:HH11	1.50	0.75
2:2:405:U:O4	38:i:2:ALA:N	2.20	0.75
6:6:34:KEO:O02	6:6:34:KEO:N02	2.17	0.75
22:S:109:ASP:O	22:S:110:ARG:NH2	2.20	0.75
7:B:16:VAL:HG12	7:B:206:GLY:HA3	1.67	0.75
40:k:99:ALA:HB1	40:k:103:VAL:HG11	1.69	0.75
2:2:1023:U:H3'	2:2:1024:G:H8	1.50	0.75
44:o:51:VAL:HG23	48:s:81:ARG:HB2	1.69	0.75
9:D:6:LYS:O	9:D:9:GLN:NE2	2.20	0.75
27:X:33:LEU:HD12	27:X:50:ARG:HG2	1.69	0.75
52:w:33:ILE:HD11	52:w:37:GLY:HA2	1.68	0.75
1:1:368:A:H5''	57:1:3731:HOH:O	1.87	0.74
23:T:15:HIS:HB3	23:T:31:VAL:HG23	1.69	0.74
13:J:45:THR:HB	13:J:48:VAL:HG22	1.68	0.74
24:U:26:LYS:HD3	24:U:37:GLU:HB3	1.69	0.74
33:d:9:VAL:HG12	33:d:12:ARG:HH12	1.51	0.74
1:1:1847:G:O2'	1:1:1848:A:H8	1.69	0.74
24:U:35:ILE:HD11	24:U:62:GLU:HB3	1.70	0.74
43:n:54:LEU:HD23	43:n:55:VAL:HG13	1.70	0.74
38:i:95:GLU:HA	38:i:100:ASN:ND2	2.01	0.74
22:S:82:MET:HG3	22:S:98:LYS:HB2	1.69	0.74
27:X:59:ILE:HD12	27:X:64:ILE:HG22	1.68	0.74
7:B:144:VAL:HB	7:B:154:LEU:HB2	1.69	0.74
9:D:1:MET:HB3	9:D:14:VAL:HG23	1.69	0.74
44:o:25:ILE:HD11	44:o:92:LEU:HD21	1.69	0.73
12:G:27:ARG:NH1	27:X:60:ASP:OD2	2.21	0.73
1:1:846:U:H5'	57:1:3521:HOH:O	1.88	0.73
1:1:2439:A:OP1	6:6:34:KEO:N02	2.20	0.73
2:2:337:G:H2'	2:2:338:A:C8	2.23	0.73
4:4:14:U:H3	6:6:147:ALA:H	1.33	0.73
9:D:47:LYS:NZ	57:D:401:HOH:O	2.20	0.73
1:1:2328:A:H2'	1:1:2329:U:C6	2.24	0.73
10:E:140:GLU:HA	30:a:28:VAL:HG22	1.71	0.73
11:F:175:LYS:HZ2	11:F:176:LYS:H	1.35	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:h:72:ARG:HD2	37:h:75:ILE:HD13	1.71	0.73
52:w:14:THR:HG21	52:w:48:ARG:HE	1.51	0.73
50:u:14:ARG:CD	57:u:101:HOH:O	2.37	0.73
1:1:1565:C:O2'	1:1:1566:A:H2'	1.89	0.72
29:Z:6:LYS:HB2	29:Z:58:GLU:HB3	1.71	0.72
2:2:91:U:H6	57:2:1902:HOH:O	1.70	0.72
2:2:1279:G:OP1	44:o:9:ARG:NH2	2.22	0.72
6:6:9:PHE:HB3	6:6:13:LEU:HD23	1.71	0.72
1:1:1143:A:N7	13:J:27:ARG:NH1	2.38	0.72
1:1:563:A:OP1	20:Q:41:LYS:NZ	2.22	0.72
1:1:1570:A:H2'	1:1:1571:A:C8	2.24	0.72
53:x:52:HIS:NE2	53:x:54:GLY:O	2.22	0.72
14:K:63:VAL:HG23	14:K:64:ARG:HG3	1.71	0.71
2:2:459:A:H2'	2:2:460:A:C8	2.26	0.71
2:2:1042:A:H5'	57:2:2071:HOH:O	1.89	0.71
1:1:1045:C:O2	1:1:1047:G:N2	2.24	0.71
46:q:72:HIS:HB3	46:q:99:ARG:NH2	2.05	0.71
38:i:198:HIS:O	38:i:202:GLU:HG3	1.91	0.71
47:r:23:TYR:HB3	47:r:66:GLU:HG3	1.71	0.71
1:1:111:A:O2'	28:Y:58:ASN:ND2	2.23	0.70
1:1:155:A:H5'	57:1:3373:HOH:O	1.90	0.70
6:6:142:LEU:HD22	41:l:77:SER:HB3	1.72	0.70
1:1:1086:A:O2'	1:1:1087:G:N7	2.24	0.70
39:j:157:ARG:NH1	42:m:99:LEU:O	2.22	0.70
9:D:7:ASP:OD1	9:D:7:ASP:N	2.20	0.70
1:1:320:A:N3	9:D:163:ASN:ND2	2.40	0.70
1:1:587:C:OP2	15:L:21:ARG:NH2	2.24	0.70
1:1:1058:U:H3	1:1:1081:U:H3	1.38	0.70
1:1:1264:A:OP1	31:b:16:ARG:NH1	2.22	0.70
24:U:34:VAL:HG13	24:U:67:VAL:HG22	1.72	0.70
27:X:32:ASN:OD1	27:X:34:HIS:NE2	2.25	0.70
51:v:60:GLU:OE2	51:v:77:ARG:NH2	2.24	0.70
51:v:76:VAL:HG23	51:v:77:ARG:HG2	1.72	0.70
1:1:1695:G:N7	7:B:14:ARG:NH2	2.40	0.70
7:B:2:ALA:N	7:B:20:VAL:O	2.24	0.70
39:j:157:ARG:NH2	42:m:43:GLU:OE2	2.23	0.70
41:l:79:ARG:HA	41:l:84:THR:HA	1.73	0.70
2:2:1124:G:O2'	2:2:1145:A:N6	2.25	0.70
20:Q:100:VAL:O	20:Q:103:LYS:NZ	2.24	0.70
10:E:108:VAL:HG11	10:E:176:PRO:HG2	1.74	0.69
37:h:200:VAL:C	37:h:201:TRP:HD1	2.00	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:V:20:LEU:HD22	25:V:25:LYS:HB2	1.74	0.69
45:p:64:GLN:HB2	45:p:99:ALA:HB2	1.73	0.69
41:l:79:ARG:NH1	41:l:82:GLY:O	2.25	0.69
1:1:191:A:H2'	1:1:192:C:H6	1.57	0.69
1:1:2405:G:O2'	1:1:2406:A:OP2	2.11	0.69
7:B:17:VAL:HG22	7:B:204:VAL:HG22	1.74	0.69
10:E:153:ASP:OD1	10:E:153:ASP:N	2.25	0.69
2:2:108:G:H5'	2:2:109:A:H5''	1.73	0.69
36:g:111:ILE:HD12	36:g:152:LYS:HA	1.75	0.69
1:1:1250:G:N7	15:L:18:ARG:NH2	2.37	0.69
2:2:517:G:N2	2:2:530:G:OP1	2.23	0.69
37:h:73:PRO:HA	37:h:76:VAL:HG12	1.73	0.69
1:1:1056:G:O2'	1:1:1103:A:N6	2.26	0.69
1:1:2451:A:H1'	5:5:76:A:H2'	1.75	0.69
2:2:78:A:H2'	2:2:79:G:H8	1.58	0.69
9:D:145:ASP:HB3	9:D:166:LYS:HD2	1.74	0.69
22:S:59:GLU:HG3	22:S:66:ILE:HD11	1.75	0.69
25:V:21:ARG:NH2	25:V:87:GLN:O	2.25	0.69
1:1:1012:U:O4	13:J:30:THR:HG21	1.93	0.69
6:6:4:TYR:O	6:6:61:SER:HB2	1.92	0.69
1:1:2191:A:H2'	1:1:2192:U:C6	2.28	0.68
1:1:2308:G:N2	57:1:3316:HOH:O	2.27	0.68
10:E:117:LEU:H	10:E:177:PHE:HA	1.57	0.68
1:1:396:G:OP2	27:X:10:LYS:NZ	2.27	0.68
2:2:1176:A:H2'	2:2:1177:G:C8	2.28	0.68
41:l:71:PRO:HG3	41:l:99:LEU:HD11	1.76	0.68
5:5:4:C:H3'	6:6:10:ARG:NH2	2.09	0.68
2:2:1377:A:OP1	41:l:92:ARG:NH1	2.26	0.68
37:h:35:SER:OG	37:h:59:ARG:NH2	2.26	0.68
2:2:1021:A:H5''	57:2:1885:HOH:O	1.93	0.68
9:D:15:SER:N	9:D:197:GLU:OE2	2.24	0.68
20:Q:47:TYR:OH	20:Q:51:ARG:NH2	2.27	0.68
39:j:115:LEU:HD13	39:j:123:VAL:HG11	1.74	0.68
48:s:39:GLU:O	48:s:43:ASN:ND2	2.26	0.68
2:2:1023:U:H3'	2:2:1024:G:C8	2.29	0.68
2:2:996:A:H2'	2:2:997:U:H6	1.59	0.67
45:p:113:VAL:HA	52:w:73:ARG:HD3	1.76	0.67
2:2:1038:C:H2'	2:2:1039:G:H8	1.57	0.67
8:C:114:LYS:O	8:C:167:ASN:N	2.26	0.67
1:1:805:G:N2	1:1:829:A:OP1	2.27	0.67
50:u:14:ARG:HD2	57:u:101:HOH:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1565:C:HO2'	1:1:1566:A:H2'	1.59	0.67
3:3:44:G:OP2	30:a:1:MET:N	2.26	0.67
35:f:14:CYS:SG	35:f:33:HIS:ND1	2.68	0.67
1:1:2514:U:H2'	1:1:2515:C:H6	1.60	0.67
2:2:202:G:H21	2:2:466:A:H61	1.41	0.67
2:2:958:A:OP1	53:x:55:ARG:NH2	2.27	0.67
42:m:10:MET:HG3	42:m:27:MET:HE1	1.76	0.67
43:n:81:HIS:CE1	43:n:85:ARG:HH21	2.13	0.67
1:1:2304:G:H22	1:1:2312:U:H3	1.43	0.67
6:6:117:LEU:HA	6:6:122:PRO:HA	1.77	0.67
1:1:1779:U:OP2	1:1:1784:A:N6	2.28	0.67
49:t:12:VAL:HG21	49:t:22:THR:HG22	1.77	0.67
1:1:1666:G:H4'	14:K:6:THR:HG23	1.76	0.67
1:1:1931:U:OP2	1:1:1968:G:N1	2.26	0.67
1:1:2098:U:H1'	57:1:3319:HOH:O	1.93	0.67
37:h:110:GLU:HB2	37:h:144:LEU:HD12	1.77	0.67
43:n:55:VAL:HG11	43:n:94:LEU:HD12	1.76	0.67
1:1:1789:A:OP2	7:B:221:ARG:NH1	2.28	0.67
2:2:181:A:H1'	2:2:182:A:C8	2.30	0.66
5:5:68:U:H6	57:5:103:HOH:O	1.78	0.66
1:1:2469:A:H4'	16:M:55:ARG:HD3	1.78	0.66
2:2:1298:U:H5	41:l:114:LYS:HD3	1.59	0.66
10:E:147:ASP:OD1	10:E:148:ARG:N	2.25	0.66
23:T:5:GLU:OE1	23:T:5:GLU:N	2.19	0.66
43:n:26:GLY:N	43:n:62:ASP:OD1	2.28	0.66
1:1:1090:A:H2'	1:1:1091:G:C8	2.29	0.66
2:2:460:A:H2'	2:2:461:A:C8	2.30	0.66
1:1:1614:A:N6	22:S:92:ARG:O	2.27	0.66
39:j:44:GLY:O	39:j:74:VAL:N	2.29	0.66
1:1:886:A:N3	1:1:891:G:N1	2.44	0.66
2:2:1025:U:H4'	2:2:1026:G:C8	2.30	0.66
2:2:1266:G:N2	2:2:1269:A:OP2	2.23	0.66
34:e:6:THR:HG23	34:e:63:PRO:HD2	1.78	0.66
1:1:627:A:OP1	15:L:78:ARG:NH1	2.26	0.66
10:E:102:ARG:NH1	30:a:9:TYR:OH	2.29	0.66
44:o:11:LYS:HB3	44:o:71:LEU:HD23	1.77	0.66
1:1:1469:A:H2'	1:1:1470:A:H8	1.61	0.66
1:1:2291:U:H2'	1:1:2292:U:C6	2.30	0.66
36:g:45:LYS:O	36:g:49:MET:HE2	1.96	0.66
1:1:45:G:H5''	1:1:46:G:H5'	1.78	0.66
1:1:2319:G:O2'	1:1:2320:U:O5'	2.13	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:674:G:H2'	2:2:675:A:H8	1.61	0.66
43:n:91:ASP:HB3	43:n:94:LEU:HD22	1.78	0.66
1:1:1590:A:H2'	1:1:1591:A:H8	1.61	0.66
2:2:71:A:H61	2:2:99:C:H1'	1.61	0.65
1:1:1093:G:O2'	1:1:1098:A:N6	2.29	0.65
1:1:2006:C:O2'	1:1:2823:A:N3	2.29	0.65
21:R:52:PRO:HG2	21:R:53:PHE:CD1	2.31	0.65
52:w:21:ILE:HG21	52:w:54:GLN:HB3	1.78	0.65
1:1:1048:A:OP2	1:1:1110:G:N2	2.29	0.65
13:J:49:ASP:OD1	13:J:121:LYS:NZ	2.29	0.65
43:n:12:ARG:HG3	43:n:13:LYS:HG3	1.77	0.65
47:r:81:MET:HG2	47:r:92:ARG:HG3	1.77	0.65
1:1:355:U:H2'	1:1:356:G:H8	1.61	0.65
2:2:1040:U:H5''	57:2:2005:HOH:O	1.96	0.65
37:h:191:THR:HG23	37:h:193:TYR:H	1.60	0.65
51:v:68:SER:OG	51:v:69:LYS:N	2.28	0.65
1:1:2193:G:HO2'	1:1:2194:U:H6	1.44	0.65
24:U:47:LYS:HE3	24:U:48:PRO:HD2	1.78	0.65
1:1:2867:G:O2'	1:1:2868:A:H8	1.79	0.65
2:2:946:A:H2'	2:2:947:G:H8	1.62	0.65
2:2:996:A:H2'	2:2:997:U:C6	2.31	0.65
6:6:72:LEU:HD21	6:6:93:LEU:HD13	1.78	0.65
23:T:6:ARG:O	23:T:10:VAL:HG23	1.97	0.65
30:a:46:GLY:O	30:a:50:ASP:HB3	1.96	0.65
37:h:58:GLU:OE2	37:h:65:ARG:NH2	2.30	0.65
9:D:121:VAL:CG1	57:D:402:HOH:O	2.38	0.65
11:F:126:PRO:HD2	11:F:130:GLU:HB2	1.79	0.65
21:R:44:GLY:O	21:R:45:GLU:HG3	1.97	0.65
23:T:69:ARG:HG2	23:T:74:ILE:HG12	1.79	0.65
1:1:1799:G:N2	1:1:1818:U:O2'	2.27	0.65
2:2:459:A:H2'	2:2:460:A:H8	1.61	0.65
2:2:945:G:C2	2:2:946:A:C8	2.85	0.65
7:B:100:GLU:OE2	7:B:102:ARG:NE	2.30	0.65
18:O:114:GLY:O	18:O:116:GLN:NE2	2.30	0.65
47:r:16:VAL:HG23	47:r:17:ILE:HD12	1.78	0.65
2:2:908:A:H2'	2:2:909:A:H8	1.61	0.65
2:2:1071:C:OP1	39:j:54:ARG:NH2	2.30	0.65
6:6:16:MET:HB2	6:6:65:ALA:HB2	1.78	0.65
7:B:196:GLY:O	7:B:198:ALA:N	2.30	0.64
39:j:136:VAL:O	39:j:140:THR:HG23	1.97	0.64
1:1:1607:C:N4	1:1:1622:G:OP2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:844:G:H3'	2:2:844:G:N3	2.11	0.64
1:1:2291:U:H2'	1:1:2292:U:H6	1.62	0.64
2:2:1037:C:H2'	2:2:1038:C:H6	1.62	0.64
14:K:78:ARG:NH1	19:P:71:GLU:OE2	2.30	0.64
1:1:2780:G:N1	13:J:102:GLU:OE2	2.29	0.64
7:B:132:MET:HE1	7:B:174:LEU:HD21	1.79	0.64
38:i:57:GLU:OE2	38:i:196:ASN:N	2.29	0.64
1:1:1072:C:O2	1:1:1092:C:N4	2.29	0.64
1:1:1236:G:O2'	1:1:1237:A:H8	1.81	0.64
2:2:1451:U:H5''	2:2:1452:C:H5	1.61	0.64
11:F:127:THR:HG22	11:F:128:GLN:H	1.62	0.64
1:1:863:A:O3'	3:3:100:G:N2	2.30	0.64
2:2:776:G:N1	2:2:802:A:OP1	2.25	0.64
39:j:111:MET:HG3	39:j:140:THR:HG21	1.80	0.64
1:1:877:A:H3'	57:1:3420:HOH:O	1.96	0.64
1:1:877:A:O2'	1:1:900:A:N6	2.31	0.64
1:1:2813:A:H2'	1:1:2814:A:H8	1.63	0.64
6:6:27:SER:HB2	6:6:41:VAL:HG12	1.80	0.64
38:i:100:ASN:OD1	38:i:111:ARG:NH1	2.29	0.64
55:z:17:ARG:HE	55:z:21:ARG:HH12	1.45	0.64
1:1:280:U:O4	1:1:361:G:N2	2.31	0.64
1:1:746:U:O2'	1:1:747:C:OP2	2.13	0.64
1:1:1315:C:O2'	1:1:1392:A:N3	2.30	0.64
1:1:2595:G:N2	1:1:2598:A:OP2	2.26	0.64
1:1:2655:G:N2	1:1:2665:A:OP2	2.29	0.64
2:2:1229:A:OP2	47:r:113:ARG:NH1	2.31	0.64
11:F:2:SER:OG	11:F:3:ARG:N	2.20	0.64
39:j:77:ASN:OD1	39:j:78:ASN:N	2.29	0.64
2:2:841:C:H2'	2:2:843:U:H5'	1.79	0.64
37:h:121:THR:HG23	37:h:189:ALA:HA	1.80	0.64
2:2:859:G:H2'	2:2:860:A:H8	1.63	0.64
2:2:946:A:H2'	2:2:947:G:C8	2.33	0.64
6:6:106:TRP:HB3	6:6:178:THR:HG22	1.80	0.63
1:1:191:A:H2'	1:1:192:C:C6	2.33	0.63
2:2:439:U:H5''	38:i:121:LYS:HD2	1.80	0.63
2:2:460:A:H2'	2:2:461:A:H8	1.63	0.63
2:2:750:C:H4'	49:t:21:ASP:HA	1.80	0.63
2:2:1352:C:H2'	2:2:1353:G:C8	2.34	0.63
43:n:84:THR:HG21	43:n:103:PHE:HB3	1.80	0.63
1:1:242:G:N2	1:1:255:A:OP2	2.24	0.63
50:u:40:ASN:ND2	50:u:42:ILE:O	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:704:G:H2'	1:1:726:G:H22	1.63	0.63
1:1:1469:A:H2'	1:1:1470:A:C8	2.33	0.63
1:1:2660:A:N6	57:1:3326:HOH:O	2.32	0.63
42:m:77:ARG:NE	42:m:79:SER:O	2.31	0.63
1:1:1176:U:H2'	1:1:1177:G:C8	2.33	0.63
2:2:859:G:H2'	2:2:860:A:C8	2.33	0.63
6:6:44:ARG:NH1	6:6:49:GLY:O	2.31	0.63
10:E:64:LYS:HD2	30:a:5:ILE:HG12	1.81	0.63
1:1:1712:U:OP2	1:1:1713:A:O2'	2.14	0.63
1:1:307:G:N1	1:1:310:A:OP2	2.25	0.63
1:1:414:C:H2'	1:1:415:A:H8	1.64	0.63
1:1:2800:A:C2	1:1:2895:G:H1'	2.34	0.63
2:2:845:A:N6	57:2:1817:HOH:O	2.32	0.63
41:l:5:ARG:HH12	41:l:6:VAL:HG22	1.63	0.63
51:v:25:ILE:HB	51:v:42:THR:HG23	1.80	0.63
1:1:1796:U:H2'	1:1:1797:G:H8	1.63	0.63
12:G:121:VAL:HB	12:G:123:ARG:HE	1.64	0.63
1:1:172:A:H2'	1:1:173:A:H8	1.63	0.63
42:m:13:ARG:NH1	42:m:26:THR:O	2.31	0.63
1:1:2287:A:OP1	32:c:30:LYS:NZ	2.31	0.62
2:2:191:G:H2'	2:2:192:A:H8	1.64	0.62
27:X:40:VAL:HA	27:X:64:ILE:HD11	1.80	0.62
1:1:1105:U:H2'	1:1:1106:G:H8	1.64	0.62
2:2:1021:A:C5'	57:2:1885:HOH:O	2.45	0.62
40:k:37:HIS:HB3	40:k:97:THR:HG22	1.80	0.62
40:k:43:GLY:HA2	40:k:58:HIS:CE1	2.33	0.62
1:1:414:C:H2'	1:1:415:A:C8	2.33	0.62
2:2:1228:C:OP2	47:r:110:LYS:NZ	2.28	0.62
2:2:522:C:H41	46:q:50:ARG:NH1	1.97	0.62
10:E:46:ASP:HB3	10:E:49:LEU:HD13	1.82	0.62
36:g:134:ALA:O	36:g:138:THR:HG23	1.99	0.62
1:1:1447:C:H2'	1:1:1448:G:H8	1.65	0.62
1:1:2405:G:HO2'	1:1:2406:A:P	2.22	0.62
2:2:500:G:H2'	2:2:501:C:C6	2.35	0.62
2:2:1008:U:O4	2:2:1021:A:N6	2.32	0.62
1:1:371:A:O2'	27:X:61:LYS:NZ	2.26	0.62
2:2:1004:A:H2'	2:2:1005:A:C8	2.34	0.62
46:q:85:GLY:O	46:q:96:HIS:ND1	2.26	0.62
2:2:768:A:N3	2:2:1512:U:O2'	2.32	0.62
2:2:1218:C:H2'	2:2:1219:A:H8	1.63	0.62
1:1:458:G:O2'	1:1:459:U:OP2	2.17	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2547:A:H2'	1:1:2548:U:C6	2.34	0.62
2:2:521:G:N7	46:q:50:ARG:NH2	2.48	0.62
39:j:76:LEU:HD11	39:j:120:VAL:HG12	1.81	0.62
41:l:113:ASP:OD1	41:l:114:LYS:N	2.25	0.62
45:p:69:ARG:HD3	57:p:202:HOH:O	2.00	0.62
1:1:1712:U:H3'	1:1:1713:A:H2'	1.81	0.62
1:1:2521:C:C2	1:1:2545:G:N2	2.68	0.62
2:2:765:G:N2	2:2:813:U:OP2	2.30	0.62
2:2:1038:C:H2'	2:2:1039:G:C8	2.34	0.62
6:6:142:LEU:HD23	41:l:79:ARG:HB2	1.81	0.62
8:C:1:MET:HG2	8:C:2:ILE:HG22	1.82	0.62
22:S:25:ARG:NH1	22:S:74:ILE:O	2.28	0.62
25:V:77:VAL:HG12	25:V:89:ILE:HG23	1.80	0.62
40:k:49:TYR:HB3	52:w:74:HIS:CE1	2.35	0.62
1:1:1996:C:OP1	14:K:31:ARG:NE	2.33	0.62
1:1:2193:G:O2'	1:1:2194:U:H5''	2.00	0.62
12:G:84:ALA:HB2	12:G:90:LEU:HD23	1.80	0.62
32:c:33:LYS:HD2	32:c:51:GLU:HG2	1.82	0.62
36:g:60:ILE:HD13	36:g:63:ARG:HH21	1.64	0.62
1:1:1263:U:OP1	31:b:13:ARG:NH1	2.32	0.61
1:1:2802:G:C5'	57:1:3608:HOH:O	2.34	0.61
2:2:1314:C:H2'	2:2:1315:U:H6	1.65	0.61
2:2:1522:U:OP1	45:p:128:ARG:NH2	2.33	0.61
6:6:133:LEU:HD12	6:6:156:LEU:HD23	1.83	0.61
19:P:9:GLU:O	19:P:12:GLN:N	2.33	0.61
47:r:39:ILE:HG13	47:r:56:LEU:HD21	1.81	0.61
49:t:29:VAL:HG11	49:t:81:LEU:HD21	1.81	0.61
1:1:1270:C:H5''	1:1:1271:G:H5'	1.82	0.61
1:1:1799:G:H22	1:1:1818:U:HO2'	1.47	0.61
22:S:109:ASP:OD1	22:S:110:ARG:N	2.34	0.61
32:c:53:LYS:HB2	32:c:55:LYS:HE3	1.82	0.61
1:1:1914:C:H1'	57:1:3301:HOH:O	2.00	0.61
1:1:2308:G:H5''	1:1:2309:A:OP2	2.01	0.61
2:2:1121:U:H2'	2:2:1122:U:C6	2.34	0.61
2:2:1338:G:H2'	2:2:1339:A:C8	2.36	0.61
7:B:69:ARG:NH2	7:B:127:GLY:O	2.29	0.61
37:h:6:HIS:CE1	57:h:304:HOH:O	2.53	0.61
2:2:1328:C:H5''	47:r:28:THR:HG21	1.83	0.61
6:6:13:LEU:HD12	6:6:14:LYS:H	1.66	0.61
43:n:55:VAL:O	43:n:57:MET:N	2.33	0.61
2:2:1323:G:H2'	2:2:1324:A:C8	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Z:3:LYS:CE	57:Z:201:HOH:O	2.20	0.61
2:2:1297:G:O2'	41:l:114:LYS:NZ	2.33	0.61
11:F:105:LEU:HB2	11:F:113:VAL:HB	1.83	0.61
42:m:78:VAL:HG21	42:m:125:ILE:HG22	1.82	0.61
1:1:700:G:O2'	1:1:1632:A:N3	2.27	0.61
1:1:1171:G:N2	1:1:1177:G:H1	1.99	0.61
1:1:2831:G:OP2	8:C:59:ARG:NH2	2.34	0.61
2:2:1111:A:N1	37:h:177:THR:HG22	2.16	0.61
1:1:1055:G:H1	1:1:1104:C:H42	1.49	0.61
1:1:2514:U:H2'	1:1:2515:C:C6	2.34	0.61
1:1:639:U:H2'	1:1:640:C:C6	2.36	0.60
2:2:150:U:H2'	2:2:151:A:H8	1.66	0.60
2:2:216:U:H4'	2:2:464:U:H4'	1.83	0.60
2:2:842:U:H3'	2:2:843:U:C5'	2.31	0.60
5:5:66:C:H2'	5:5:67:G:C8	2.36	0.60
30:a:30:HIS:ND1	30:a:31:ASP:O	2.32	0.60
1:1:747:C:OP2	22:S:90:LYS:NZ	2.30	0.60
1:1:2098:U:C1'	57:1:3319:HOH:O	2.49	0.60
8:C:152:PRO:HB2	8:C:154:LYS:HG2	1.83	0.60
14:K:76:VAL:HG22	19:P:73:VAL:HG22	1.82	0.60
1:1:1800:C:OP2	7:B:182:ARG:NH1	2.33	0.60
6:6:132:GLU:HG3	6:6:187:VAL:HG21	1.82	0.60
9:D:97:ASN:HB2	9:D:100:MET:HG3	1.84	0.60
43:n:106:ARG:NH1	43:n:107:ASP:O	2.33	0.60
1:1:1802:A:H2'	1:1:1803:A:C8	2.37	0.60
1:1:2861:U:H2'	1:1:2862:G:H8	1.65	0.60
2:2:842:U:H2'	2:2:844:G:H5'	1.83	0.60
37:h:56:VAL:HG22	37:h:67:THR:HB	1.82	0.60
43:n:25:ASN:N	43:n:62:ASP:OD1	2.35	0.60
50:u:40:ASN:HD22	50:u:43:ALA:HB2	1.66	0.60
51:v:52:GLU:O	51:v:81:LYS:NZ	2.33	0.60
1:1:883:G:H22	1:1:893:C:H42	1.48	0.60
1:1:1753:G:N2	1:1:1756:G:OP2	2.35	0.60
7:B:118:SER:HB2	7:B:129:THR:HG22	1.82	0.60
50:u:61:VAL:HG21	50:u:67:ILE:HD11	1.84	0.60
55:z:69:ARG:NH2	57:z:101:HOH:O	2.35	0.60
14:K:113:MET:SD	14:K:116:ILE:HD11	2.40	0.60
22:S:34:ASP:OD1	22:S:35:ILE:N	2.34	0.60
22:S:81:SER:HB3	22:S:97:LEU:HD12	1.83	0.60
54:y:9:LYS:HE2	54:y:13:GLN:HE21	1.67	0.60
1:1:155:A:H2'	1:1:156:A:C8	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2285:C:P	32:c:6:ARG:HH21	2.23	0.60
2:2:1261:A:N6	2:2:1274:A:O2'	2.33	0.60
1:1:1523:U:H5''	1:1:1524:G:C8	2.36	0.60
1:1:1857:G:O2'	1:1:1858:A:O5'	2.20	0.60
13:J:96:ARG:NE	13:J:99:ARG:HG3	2.16	0.60
38:i:170:TRP:CD2	38:i:186:PRO:HB3	2.37	0.60
48:s:49:GLN:HE22	53:x:13:LEU:H	1.47	0.60
2:2:181:A:N6	2:2:195:A:N7	2.50	0.60
10:E:62:GLY:HA3	10:E:95:ARG:HH21	1.67	0.60
52:w:42:SER:HA	52:w:45:THR:HG22	1.84	0.60
1:1:1103:A:H5''	1:1:1104:C:C5	2.37	0.60
2:2:1171:A:H2'	2:2:1172:C:H6	1.65	0.60
6:6:72:LEU:HD22	6:6:115:VAL:HG21	1.84	0.60
22:S:2:GLU:HA	22:S:108:SER:HB3	1.83	0.60
38:i:28:ILE:HD12	38:i:34:ILE:HG12	1.83	0.60
40:k:22:ILE:O	40:k:26:THR:HG23	2.02	0.60
1:1:299:A:N3	1:1:319:G:O2'	2.32	0.59
1:1:1590:A:H2'	1:1:1591:A:C8	2.36	0.59
29:Z:24:LEU:HD11	29:Z:54:MET:SD	2.42	0.59
6:6:86:ASN:HB2	6:6:89:THR:H	1.67	0.59
1:1:1710:G:H2'	1:1:1711:A:H8	1.66	0.59
1:1:1746:A:H2'	1:1:1747:U:C6	2.37	0.59
1:1:1940:U:H4'	1:1:1941:C:O5'	2.02	0.59
2:2:41:G:H2'	2:2:42:G:H8	1.67	0.59
2:2:524:G:H2'	2:2:525:C:C6	2.37	0.59
2:2:1037:C:H2'	2:2:1038:C:C6	2.37	0.59
44:o:85:ASP:HA	44:o:88:MET:HE3	1.83	0.59
2:2:202:G:HO2'	2:2:468:A:H8	1.48	0.59
2:2:1298:U:OP2	41:l:114:LYS:NZ	2.34	0.59
13:J:31:GLU:OE2	13:J:34:ARG:NH2	2.36	0.59
38:i:187:GLU:N	38:i:190:ASP:OD2	2.35	0.59
48:s:33:ASP:OD1	48:s:35:ASN:N	2.32	0.59
1:1:1858:A:N6	1:1:1884:G:O2'	2.36	0.59
23:T:67:VAL:HG22	23:T:76:ARG:HB2	1.84	0.59
28:Y:34:SER:OG	28:Y:36:GLN:NE2	2.29	0.59
1:1:2101:A:H5''	57:1:3354:HOH:O	2.03	0.59
44:o:57:VAL:O	44:o:58:ASN:ND2	2.35	0.59
2:2:256:U:H2'	2:2:257:G:H8	1.68	0.59
2:2:1218:C:H2'	2:2:1219:A:C8	2.37	0.59
9:D:146:VAL:HG12	9:D:167:VAL:HG22	1.85	0.59
10:E:10:ASP:OD1	10:E:11:GLU:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:7:ASP:OD1	12:G:8:LYS:N	2.35	0.59
45:p:29:ASN:OD1	45:p:30:THR:N	2.34	0.59
45:p:119:ASN:ND2	55:z:35:ARG:HH22	2.01	0.59
1:1:367:G:C5'	57:1:3425:HOH:O	2.50	0.59
2:2:35:G:H2'	2:2:36:C:C6	2.38	0.59
2:2:995:C:H2'	2:2:996:A:H5''	1.84	0.59
3:3:5:U:H2'	3:3:6:G:H8	1.68	0.59
3:3:29:A:H2'	3:3:30:C:C6	2.37	0.59
15:L:123:ARG:NH2	15:L:143:GLU:OE2	2.35	0.59
31:b:38:HIS:HB3	31:b:44:THR:HG22	1.85	0.59
44:o:12:ALA:HB2	44:o:96:VAL:HA	1.83	0.59
1:1:1010:A:OP1	20:Q:66:ASN:ND2	2.30	0.59
1:1:1020:A:H5'	1:1:1021:A:C8	2.38	0.59
2:2:113:G:H1'	2:2:354:G:H5'	1.84	0.59
2:2:1081:A:N7	39:j:52:LYS:NZ	2.50	0.59
7:B:66:ASP:OD2	7:B:102:ARG:NH1	2.34	0.59
2:2:56:U:H2'	2:2:57:G:H8	1.67	0.59
11:F:38:ASN:O	11:F:41:VAL:HG12	2.03	0.59
19:P:88:ARG:NH2	19:P:110:ILE:O	2.27	0.59
45:p:75:LYS:HG3	45:p:76:GLU:N	2.17	0.59
1:1:774:G:O2'	1:1:775:G:O5'	2.21	0.58
1:1:1710:G:H2'	1:1:1711:A:C8	2.38	0.58
1:1:1932:A:H2'	1:1:1933:G:O4'	2.02	0.58
2:2:464:U:N3	2:2:467:U:OP2	2.24	0.58
10:E:126:GLY:HA2	10:E:163:ASP:HA	1.84	0.58
36:g:5:SER:HB3	36:g:8:ASP:HB2	1.85	0.58
51:v:78:VAL:HG11	51:v:81:LYS:HE2	1.83	0.58
53:x:52:HIS:HD2	53:x:54:GLY:H	1.51	0.58
1:1:2329:U:H2'	1:1:2330:G:C8	2.38	0.58
2:2:1167:A:O2'	2:2:1169:A:N7	2.32	0.58
10:E:52:ASN:HB2	10:E:150:ARG:NH2	2.17	0.58
48:s:88:ALA:HB1	48:s:96:LEU:HD22	1.85	0.58
1:1:139:U:H2'	1:1:140:C:H5	1.68	0.58
1:1:2298:A:OP1	10:E:71:ARG:NH2	2.36	0.58
2:2:465:A:H2'	2:2:466:A:C8	2.38	0.58
2:2:769:G:H4'	2:2:1513:A:H4'	1.85	0.58
2:2:1143:G:H2'	2:2:1144:G:H8	1.67	0.58
2:2:1176:A:H2'	2:2:1177:G:H8	1.68	0.58
1:1:1171:G:H22	1:1:1177:G:H1	1.50	0.58
1:1:2478:A:OP2	35:f:2:LYS:NZ	2.32	0.58
8:C:14:ILE:HA	19:P:12:GLN:HE22	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:26:SER:OG	30:a:27:THR:N	2.36	0.58
42:m:2:SER:OG	42:m:3:MET:N	2.27	0.58
1:1:2813:A:H2'	1:1:2814:A:C8	2.38	0.58
2:2:784:A:H2'	2:2:785:G:C8	2.38	0.58
6:6:15:ILE:HG22	6:6:16:MET:H	1.67	0.58
20:Q:58:ARG:O	20:Q:62:ILE:HG12	2.03	0.58
23:T:54:GLU:OE2	23:T:91:GLN:NE2	2.35	0.58
27:X:40:VAL:HG22	27:X:64:ILE:HD12	1.85	0.58
31:b:30:VAL:HG12	31:b:37:LYS:HG2	1.84	0.58
36:g:15:HIS:HB3	36:g:43:LEU:HD11	1.84	0.58
36:g:73:LYS:NZ	36:g:165:ASP:OD2	2.36	0.58
2:2:256:U:H2'	2:2:257:G:C8	2.39	0.58
2:2:908:A:H2'	2:2:909:A:C8	2.38	0.58
12:G:93:SER:HB3	12:G:121:VAL:HG12	1.84	0.58
52:w:14:THR:HG21	52:w:48:ARG:NE	2.18	0.58
1:1:706:A:OP1	7:B:7:LYS:NZ	2.23	0.58
1:1:2543:G:H2'	1:1:2544:G:C8	2.39	0.58
10:E:111:ILE:HG23	10:E:114:PHE:HB2	1.86	0.58
25:V:34:LYS:NZ	57:V:101:HOH:O	2.36	0.58
31:b:31:ASP:OD2	31:b:34:SER:N	2.36	0.58
36:g:100:MET:HA	36:g:107:VAL:HG21	1.84	0.58
51:v:58:VAL:HG13	51:v:79:VAL:HB	1.86	0.58
2:2:1532:U:O4	55:z:46:LYS:NZ	2.35	0.58
15:L:85:VAL:HG11	15:L:90:VAL:HG12	1.86	0.58
46:q:50:ARG:HG3	46:q:90:LEU:HD21	1.86	0.58
47:r:54:ASP:OD1	47:r:57:ARG:NH1	2.36	0.58
1:1:356:G:H2'	1:1:357:C:C6	2.39	0.58
2:2:1175:G:HO2'	2:2:1176:A:H8	1.52	0.58
2:2:1229:A:O2'	5:5:30:U:OP1	2.20	0.58
6:6:72:LEU:HB3	6:6:84:PHE:CD1	2.39	0.58
10:E:22:TYR:OH	10:E:165:GLU:OE1	2.21	0.58
23:T:6:ARG:NH1	23:T:37:ASP:OD1	2.35	0.58
39:j:13:GLU:HB3	39:j:39:VAL:HG12	1.86	0.58
1:1:833:A:H2'	1:1:834:G:C8	2.39	0.58
1:1:1103:A:H5''	1:1:1104:C:H5	1.68	0.58
1:1:1429:G:H2'	1:1:1430:G:H8	1.69	0.58
1:1:2246:G:H2'	1:1:2247:A:H8	1.68	0.58
2:2:375:U:O2'	50:u:6:LEU:O	2.22	0.58
2:2:1279:G:N2	57:2:1826:HOH:O	2.36	0.58
7:B:205:LEU:HD12	7:B:210:ALA:HB1	1.86	0.58
8:C:86:GLU:OE2	8:C:87:GLY:N	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:34:GLU:HG2	21:R:60:LYS:HG2	1.86	0.58
1:1:622:G:H2'	1:1:623:C:H6	1.69	0.57
1:1:2793:C:H5'	57:1:3395:HOH:O	2.03	0.57
2:2:33:A:H2'	2:2:34:C:C6	2.40	0.57
2:2:384:G:H2'	2:2:385:C:C6	2.39	0.57
2:2:864:A:H4'	39:j:90:THR:HG23	1.85	0.57
2:2:1171:A:H2'	2:2:1172:C:C6	2.38	0.57
9:D:10:SER:OG	9:D:11:ALA:N	2.35	0.57
49:t:29:VAL:HG23	49:t:63:ARG:HG3	1.86	0.57
1:1:1203:U:O2'	15:L:4:ASN:ND2	2.36	0.57
1:1:2229:U:O2	27:X:34:HIS:HE1	1.88	0.57
2:2:689:C:HO2'	2:2:705:G:HO2'	1.49	0.57
10:E:140:GLU:N	10:E:140:GLU:OE1	2.38	0.57
37:h:47:LEU:HD22	37:h:76:VAL:HG23	1.86	0.57
38:i:27:ALA:HB3	38:i:30:THR:HG23	1.86	0.57
1:1:1055:G:H1'	1:1:1085:A:H2	1.69	0.57
1:1:1112:G:H2'	1:1:1113:U:H6	1.68	0.57
1:1:2016:U:O2	31:b:4:GLN:NE2	2.32	0.57
5:5:5:A:O2'	5:5:6:C:O5'	2.21	0.57
8:C:51:THR:OG1	8:C:76:GLY:HA3	2.05	0.57
46:q:83:ARG:HD3	46:q:98:VAL:HG12	1.86	0.57
51:v:9:GLN:HG2	51:v:60:GLU:HB3	1.86	0.57
55:z:10:GLU:OE2	55:z:14:VAL:HG13	2.04	0.57
1:1:614:A:OP1	1:1:616:A:N6	2.37	0.57
1:1:654:A:H2	57:1:3612:HOH:O	1.86	0.57
1:1:1735:A:H2'	1:1:1736:U:C6	2.39	0.57
2:2:1014:A:C2	2:2:1219:A:H1'	2.39	0.57
3:3:74:U:O4	25:V:37:PRO:HG2	2.04	0.57
10:E:135:GLN:HE22	10:E:149:VAL:HA	1.70	0.57
36:g:113:ARG:NH1	36:g:117:LEU:HB2	2.19	0.57
37:h:184:TYR:HE2	57:h:304:HOH:O	1.86	0.57
49:t:21:ASP:OD1	49:t:21:ASP:N	2.35	0.57
2:2:421:U:H5''	2:2:422:C:H5	1.69	0.57
2:2:1010:U:H2'	2:2:1011:C:C6	2.39	0.57
8:C:5:VAL:H	8:C:32:ASN:HD21	1.52	0.57
44:o:84:VAL:HG22	44:o:88:MET:HE2	1.86	0.57
53:x:52:HIS:CD2	53:x:54:GLY:H	2.22	0.57
2:2:1352:C:H2'	2:2:1353:G:H8	1.68	0.57
11:F:86:LYS:HB2	11:F:165:ALA:HB2	1.87	0.57
44:o:40:ILE:N	44:o:73:LEU:O	2.38	0.57
52:w:34:THR:HG23	52:w:36:SER:H	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1475:G:HO2'	1:1:1476:U:H6	1.51	0.57
10:E:73:SER:OG	10:E:80:ARG:HA	2.05	0.57
10:E:143:TYR:HA	10:E:146:VAL:HG13	1.87	0.57
40:k:2:ARG:HD2	40:k:68:GLN:HE21	1.67	0.57
1:1:155:A:H1'	57:1:3305:HOH:O	2.03	0.57
1:1:227:A:O2'	1:1:228:C:O5'	2.22	0.57
1:1:402:A:H2'	1:1:403:U:O4'	2.03	0.57
1:1:528:A:H8	1:1:528:A:H3'	1.69	0.57
44:o:52:LEU:HD12	44:o:62:ARG:HD3	1.87	0.57
51:v:30:LYS:HB2	51:v:37:PHE:CE2	2.39	0.57
1:1:1020:A:H4'	1:1:1021:A:O5'	2.05	0.57
1:1:1593:A:H2'	1:1:1594:U:C6	2.40	0.57
2:2:635:A:H2'	2:2:636:U:C6	2.40	0.57
2:2:1451:U:OP2	2:2:1452:C:N4	2.33	0.57
7:B:246:THR:HG22	7:B:250:VAL:O	2.05	0.57
11:F:102:VAL:HG12	11:F:116:GLN:HG2	1.86	0.57
2:2:844:G:H2'	2:2:845:A:C8	2.39	0.57
15:L:51:GLU:OE2	15:L:56:PRO:HA	2.05	0.57
26:W:21:LEU:HD21	26:W:41:ARG:HH21	1.69	0.57
38:i:18:ASP:HB2	38:i:28:ILE:HD13	1.86	0.57
42:m:43:GLU:HG2	42:m:101:ILE:HG21	1.87	0.57
50:u:21:VAL:HG21	50:u:60:TRP:CD1	2.40	0.57
53:x:27:ASP:N	53:x:27:ASP:OD1	2.36	0.57
1:1:458:G:HO2'	1:1:469:G:H1	1.52	0.56
1:1:1022:G:H22	1:1:1142:A:H2	1.53	0.56
1:1:2802:G:H4'	57:1:3608:HOH:O	2.05	0.56
7:B:145:GLU:HB2	7:B:188:CYS:HB3	1.87	0.56
12:G:135:HIS:HB3	12:G:138:VAL:HG22	1.86	0.56
30:a:9:TYR:HD1	30:a:27:THR:HG23	1.69	0.56
1:1:2243:U:H2'	1:1:2244:U:C6	2.40	0.56
1:1:2867:G:O2'	1:1:2868:A:O5'	2.22	0.56
2:2:73:C:H2'	2:2:74:A:H5'	1.86	0.56
1:1:94:A:H2'	1:1:95:A:C8	2.40	0.56
1:1:355:U:H2'	1:1:356:G:C8	2.40	0.56
1:1:752:A:H62	1:1:2609:U:H3	1.51	0.56
1:1:2246:G:H2'	1:1:2247:A:C8	2.40	0.56
1:1:2384:U:OP2	26:W:55:ARG:NH2	2.33	0.56
1:1:2899:A:H2'	1:1:2900:A:C8	2.40	0.56
6:6:16:MET:HE3	6:6:19:GLY:HA2	1.86	0.56
10:E:177:PHE:O	10:E:178:ARG:HG3	2.05	0.56
34:e:31:HIS:ND1	34:e:32:ILE:HG13	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:q:74:LEU:HD21	46:q:80:ILE:HD11	1.86	0.56
1:1:962:G:H21	1:1:2250:G:H22	1.53	0.56
2:2:821:G:H2'	2:2:822:U:C6	2.40	0.56
2:2:999:C:H2'	2:2:1000:A:H8	1.70	0.56
42:m:25:VAL:HG13	42:m:63:LEU:HD11	1.87	0.56
52:w:21:ILE:HG12	52:w:55:LEU:HD23	1.88	0.56
2:2:452:A:H62	2:2:480:U:H3	1.52	0.56
2:2:972:C:OP2	44:o:59:LYS:NZ	2.39	0.56
38:i:37:ALA:HB3	38:i:42:GLY:HA2	1.87	0.56
1:1:548:G:H2'	1:1:549:G:O4'	2.05	0.56
1:1:833:A:H2'	1:1:834:G:H8	1.70	0.56
1:1:1447:C:H2'	1:1:1448:G:C8	2.41	0.56
1:1:2097:A:C6	1:1:2193:G:C6	2.94	0.56
1:1:2391:G:H2'	1:1:2424:C:N4	2.18	0.56
2:2:202:G:O2'	2:2:468:A:H8	1.87	0.56
2:2:208:U:H2'	2:2:210:C:C2	2.41	0.56
2:2:269:C:H2'	2:2:270:A:C8	2.40	0.56
2:2:784:A:H2'	2:2:785:G:H8	1.69	0.56
12:G:117:LEU:HD12	12:G:120:GLY:H	1.71	0.56
1:1:882:G:C2	1:1:883:G:H1'	2.41	0.56
1:1:1105:U:H2'	1:1:1106:G:C8	2.40	0.56
1:1:2661:G:H2'	1:1:2662:A:C8	2.41	0.56
2:2:1157:A:C2	2:2:1181:G:C4	2.94	0.56
3:3:51:G:H2'	3:3:52:A:C8	2.39	0.56
10:E:38:MET:HG2	10:E:152:LEU:HB3	1.88	0.56
12:G:125:THR:OG1	12:G:146:VAL:O	2.21	0.56
16:M:47:GLU:OE2	16:M:51:ARG:NE	2.24	0.56
25:V:75:GLN:HB2	25:V:92:VAL:HG13	1.86	0.56
40:k:6:ILE:HB	40:k:62:MET:HG3	1.87	0.56
40:k:73:GLU:O	40:k:77:THR:HG23	2.04	0.56
52:w:30:LYS:HA	52:w:33:ILE:HG22	1.88	0.56
1:1:2071:A:H2'	1:1:2072:C:C6	2.41	0.56
1:1:2881:U:O2'	17:N:95:THR:O	2.24	0.56
2:2:1457:G:OP1	54:y:34:LYS:NZ	2.32	0.56
3:3:119:A:H2'	3:3:120:U:O4'	2.05	0.56
10:E:104:ILE:HG23	10:E:105:THR:HG23	1.87	0.56
13:J:4:PHE:O	20:Q:64:ARG:NH2	2.35	0.56
13:J:96:ARG:HE	13:J:99:ARG:HG3	1.69	0.56
44:o:5:ARG:HH11	44:o:7:ARG:HG3	1.71	0.56
44:o:28:THR:O	44:o:32:THR:HG22	2.06	0.56
1:1:2312:U:H5'	10:E:85:ILE:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:216:U:H2'	2:2:217:C:C6	2.41	0.56
2:2:533:A:O2'	2:2:535:A:OP2	2.21	0.56
12:G:14:SER:OG	12:G:15:LEU:N	2.32	0.56
12:G:132:PHE:HB2	12:G:140:ALA:HB3	1.87	0.56
37:h:150:LYS:HB2	37:h:169:ARG:HG3	1.88	0.56
45:p:13:ARG:NH2	57:p:201:HOH:O	2.39	0.56
1:1:1058:U:H2'	1:1:1059:G:C8	2.41	0.56
2:2:1173:U:N3	2:2:1174:G:N7	2.53	0.56
5:5:2:G:O2'	5:5:3:G:H8	1.88	0.56
5:5:18:G:H1	5:5:55:U:H6	1.54	0.56
10:E:56:ASP:O	10:E:60:ILE:HG12	2.06	0.56
1:1:49:A:H4'	1:1:50:U:H5''	1.88	0.55
1:1:639:U:H2'	1:1:640:C:H6	1.69	0.55
1:1:2286:G:H4'	1:1:2287:A:O5'	2.05	0.55
2:2:560:A:H5'	2:2:566:G:N2	2.21	0.55
2:2:1250:A:OP1	43:n:69:GLY:N	2.34	0.55
22:S:68:ASP:OD1	22:S:110:ARG:NH1	2.40	0.55
33:d:34:ARG:NE	33:d:42:LEU:O	2.36	0.55
40:k:29:ILE:HD13	40:k:64:VAL:HG11	1.89	0.55
47:r:80:LEU:HD12	47:r:87:ARG:HB2	1.88	0.55
52:w:16:GLU:HG3	52:w:18:VAL:HG23	1.88	0.55
1:1:549:G:H2'	1:1:550:C:H6	1.70	0.55
1:1:1506:U:H2'	1:1:1507:C:C6	2.41	0.55
1:1:1506:U:H2'	1:1:1507:C:H6	1.71	0.55
8:C:11:MET:HG2	8:C:25:THR:HG22	1.88	0.55
10:E:43:ALA:HA	10:E:46:ASP:O	2.05	0.55
10:E:115:ARG:HH21	47:r:71:ARG:NH2	2.04	0.55
33:d:24:THR:HG1	33:d:27:GLY:H	1.54	0.55
19:P:2:SER:OG	19:P:3:ASN:N	2.40	0.55
1:1:1149:G:H2'	1:1:1150:C:C6	2.41	0.55
1:1:2321:U:H5''	1:1:2322:A:OP2	2.06	0.55
1:1:2899:A:H2'	1:1:2900:A:H8	1.71	0.55
2:2:84:U:H2'	2:2:86:G:H21	1.71	0.55
2:2:844:G:N2	2:2:846:G:N3	2.55	0.55
6:6:70:MET:HE1	6:6:117:LEU:HD21	1.87	0.55
8:C:16:THR:HG23	8:C:18:ASP:H	1.71	0.55
44:o:85:ASP:HA	44:o:88:MET:HG2	1.87	0.55
1:1:356:G:H2'	1:1:357:C:H6	1.72	0.55
1:1:1495:A:H2'	1:1:1496:A:C8	2.41	0.55
1:1:2192:U:H1'	1:1:2193:G:H5'	1.88	0.55
2:2:366:A:O2'	2:2:394:G:N2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:j:82:GLN:OE1	39:j:150:PRO:HD3	2.05	0.55
1:1:645:C:H2'	1:1:647:G:C8	2.42	0.55
1:1:1125:G:OP2	1:1:1126:A:O2'	2.18	0.55
1:1:1171:G:H2'	1:1:1172:C:C6	2.42	0.55
9:D:148:ILE:HG21	9:D:157:LEU:HD21	1.88	0.55
35:f:25:VAL:HB	35:f:35:GLN:HG2	1.89	0.55
37:h:8:ASN:ND2	48:s:89:MET:O	2.40	0.55
1:1:2629:U:O2'	1:1:2630:G:H5''	2.06	0.55
2:2:1073:U:O2	36:g:103:ASN:ND2	2.40	0.55
3:3:8:C:OP1	18:O:15:ARG:NH2	2.28	0.55
11:F:137:ASP:O	11:F:141:ILE:HG23	2.06	0.55
17:N:103:ARG:HD3	17:N:110:MET:HE2	1.89	0.55
27:X:59:ILE:HG23	27:X:64:ILE:HG22	1.89	0.55
32:c:8:LYS:HB3	32:c:24:THR:HG22	1.89	0.55
43:n:56:ASP:OD1	43:n:56:ASP:N	2.38	0.55
52:w:12:ARG:NH2	52:w:16:GLU:OE1	2.40	0.55
1:1:935:C:H2'	1:1:936:A:H8	1.72	0.55
1:1:2294:G:P	18:O:94:ARG:HH12	2.30	0.55
1:1:2676:C:P	14:K:31:ARG:HH22	2.29	0.55
29:Z:12:SER:OG	29:Z:13:ALA:N	2.40	0.55
37:h:79:LYS:HB3	37:h:82:GLU:CD	2.32	0.55
1:1:659:G:N2	9:D:30:GLN:OE1	2.38	0.55
1:1:2639:A:O3'	13:J:96:ARG:NH2	2.39	0.55
2:2:500:G:H2'	2:2:501:C:H6	1.71	0.55
2:2:1004:A:H2'	2:2:1005:A:H8	1.72	0.55
2:2:1023:U:H2'	2:2:1024:G:O4'	2.06	0.55
12:G:94:ILE:HG23	12:G:122:LEU:HB3	1.89	0.55
18:O:35:ILE:HD12	18:O:106:LEU:HD12	1.89	0.55
35:f:5:ALA:O	35:f:37:GLN:NE2	2.38	0.55
1:1:155:A:H2'	1:1:156:A:H8	1.71	0.55
1:1:828:U:H2'	1:1:829:A:C8	2.41	0.55
1:1:1865:U:H2'	57:1:3547:HOH:O	2.06	0.55
2:2:925:G:C2	2:2:927:G:C8	2.95	0.55
2:2:1077:G:N2	2:2:1080:A:OP2	2.39	0.55
2:2:1497:G:H1'	2:2:1518:MA6:H2	1.88	0.55
12:G:9:VAL:HG21	12:G:12:LEU:HD12	1.87	0.55
29:Z:41:THR:HG22	29:Z:43:ALA:H	1.72	0.55
40:k:1:MET:HG2	40:k:2:ARG:H	1.72	0.55
1:1:2297:A:N1	1:1:2321:U:H5	2.05	0.54
12:G:128:HIS:HB2	12:G:144:VAL:HG13	1.88	0.54
30:a:37:CYS:SG	30:a:39:LYS:HG2	2.46	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:19:GLN:HB2	36:g:22:TYR:HD2	1.71	0.54
48:s:79:LEU:HB2	48:s:84:VAL:HG23	1.88	0.54
1:1:1751:U:H1'	57:1:3421:HOH:O	2.08	0.54
2:2:505:G:H5'	2:2:534:U:H2'	1.90	0.54
12:G:129:GLU:OE2	12:G:141:LYS:HB3	2.07	0.54
39:j:165:LEU:HD22	42:m:114:ARG:HD3	1.89	0.54
1:1:1667:G:H5''	14:K:5:GLN:O	2.08	0.54
6:6:6:SER:HA	6:6:9:PHE:CZ	2.42	0.54
7:B:21:ASN:HB2	7:B:24:LEU:HG	1.89	0.54
23:T:14:PRO:HD3	28:Y:30:MET:SD	2.47	0.54
23:T:48:GLN:HG3	23:T:55:VAL:HG12	1.89	0.54
1:1:3:U:H2'	1:1:4:U:C6	2.43	0.54
1:1:1176:U:H5''	57:1:3356:HOH:O	2.07	0.54
1:1:1340:U:OP1	23:T:19:LYS:NZ	2.36	0.54
1:1:1730:C:H1'	1:1:1731:G:C6	2.43	0.54
3:3:106:G:H2'	3:3:107:G:O4'	2.08	0.54
7:B:69:ARG:HG2	7:B:129:THR:HG21	1.89	0.54
34:e:11:ALA:HA	34:e:62:LEU:HD21	1.88	0.54
36:g:20:THR:HG22	36:g:39:HIS:CE1	2.43	0.54
41:l:72:THR:HG22	41:l:142:HIS:NE2	2.22	0.54
1:1:2848:G:C8	19:P:95:ALA:HB2	2.42	0.54
2:2:275:G:H5'	51:v:16:LYS:HD2	1.90	0.54
2:2:1298:U:C5	41:l:114:LYS:HD3	2.42	0.54
7:B:121:ASP:OD2	12:G:83:LYS:NZ	2.36	0.54
10:E:131:GLY:HA2	10:E:153:ASP:HA	1.90	0.54
23:T:18:GLU:O	23:T:22:THR:HG23	2.08	0.54
47:r:78:LYS:HG2	57:r:206:HOH:O	2.07	0.54
1:1:634:C:H2'	1:1:635:C:C6	2.43	0.54
1:1:1009:A:OP1	13:J:39:LYS:NZ	2.35	0.54
1:1:1111:A:O2'	1:1:1112:G:OP1	2.24	0.54
1:1:1179:G:H3'	1:1:1180:U:H4'	1.90	0.54
1:1:2691:C:HO2'	1:1:2871:U:HO2'	1.55	0.54
2:2:147:G:H2'	2:2:148:G:C8	2.43	0.54
2:2:841:C:H1'	57:2:1997:HOH:O	2.07	0.54
2:2:1173:U:C2	2:2:1174:G:C8	2.95	0.54
12:G:68:ARG:O	12:G:72:ILE:HG12	2.08	0.54
20:Q:47:TYR:CZ	20:Q:51:ARG:NH2	2.76	0.54
24:U:48:PRO:HB3	24:U:55:PRO:O	2.08	0.54
36:g:164:ILE:O	36:g:186:ILE:HB	2.08	0.54
44:o:35:GLN:HE21	44:o:78:GLU:HG2	1.72	0.54
47:r:17:ILE:O	47:r:20:THR:OG1	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1019:U:H3	1:1:1142:A:H62	1.55	0.54
1:1:2402:U:O2'	1:1:2403:C:O5'	2.23	0.54
1:1:2554:U:H2'	1:1:2555:U:C6	2.42	0.54
2:2:1360:A:OP2	48:s:75:ARG:NH2	2.40	0.54
11:F:166:ASP:OD2	11:F:167:GLU:N	2.39	0.54
36:g:64:LYS:HA	36:g:225:ARG:NH1	2.22	0.54
43:n:12:ARG:NH2	43:n:107:ASP:OD2	2.40	0.54
54:y:43:ASP:OD1	54:y:43:ASP:N	2.39	0.54
1:1:549:G:H2'	1:1:550:C:C6	2.43	0.54
10:E:58:ALA:HB2	10:E:65:PRO:HD3	1.88	0.54
44:o:51:VAL:CG2	48:s:81:ARG:HB2	2.37	0.54
53:x:40:ILE:HG23	53:x:44:MET:HE2	1.88	0.54
1:1:784:G:N1	7:B:228:VAL:HG21	2.22	0.54
1:1:1197:G:H2'	1:1:1198:U:H6	1.73	0.54
1:1:1883:U:H2'	1:1:1884:G:O4'	2.08	0.54
2:2:821:G:H2'	2:2:822:U:H6	1.72	0.54
2:2:951:G:C6	2:2:1231:G:C6	2.96	0.54
12:G:86:ASP:HB3	40:k:24:ARG:NH1	2.22	0.54
1:1:79:C:O2'	1:1:346:A:N3	2.39	0.54
1:1:2591:C:H2'	1:1:2592:G:C8	2.43	0.54
2:2:176:C:H2'	2:2:177:G:N3	2.23	0.54
2:2:979:C:H1'	2:2:1317:C:H41	1.73	0.54
2:2:1145:A:O2'	2:2:1146:A:O5'	2.23	0.54
3:3:49:C:OP1	18:O:102:ARG:HB2	2.09	0.54
3:3:93:C:OP2	25:V:18:ARG:NH1	2.41	0.54
8:C:13:ARG:HH11	19:P:56:HIS:HA	1.73	0.54
10:E:141:ILE:HD11	10:E:146:VAL:HG12	1.90	0.54
40:k:7:VAL:HG11	52:w:65:LEU:HD11	1.90	0.54
1:1:2243:U:H2'	1:1:2244:U:H6	1.73	0.53
1:1:2469:A:H2'	1:1:2470:G:O4'	2.08	0.53
2:2:56:U:H2'	2:2:57:G:C8	2.43	0.53
2:2:87:C:H2'	2:2:88:U:C6	2.43	0.53
2:2:206:C:H2'	2:2:207:C:C6	2.38	0.53
2:2:1175:G:N3	2:2:1176:A:C8	2.76	0.53
2:2:1219:A:H2'	2:2:1220:G:C8	2.43	0.53
14:K:109:SER:OG	14:K:110:GLU:N	2.37	0.53
22:S:86:MET:HE2	22:S:88:ARG:HD3	1.90	0.53
24:U:86:ARG:NH1	24:U:100:SER:O	2.27	0.53
30:a:54:GLY:HA2	30:a:59:ARG:HH21	1.73	0.53
1:1:288:U:H2'	1:1:289:G:C8	2.43	0.53
1:1:382:A:C2	1:1:393:C:C2	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1091:G:H2'	1:1:1092:C:C6	2.44	0.53
1:1:1236:G:O2'	1:1:1237:A:P	2.66	0.53
1:1:1523:U:H5''	1:1:1524:G:H8	1.72	0.53
2:2:1239:A:H4'	2:2:1240:U:H5''	1.91	0.53
1:1:1071:G:N2	1:1:1089:A:O2'	2.41	0.53
1:1:1589:U:H2'	1:1:1590:A:H8	1.73	0.53
9:D:3:LEU:N	9:D:12:LEU:O	2.36	0.53
37:h:155:GLY:HA2	37:h:163:ALA:HB1	1.89	0.53
39:j:30:ILE:HG13	39:j:30:ILE:O	2.08	0.53
1:1:1062:G:OP1	1:1:1070:A:H5'	2.09	0.53
1:1:2508:G:H1	1:1:2580:U:H5	1.56	0.53
1:1:2698:U:H2'	1:1:2699:C:C6	2.44	0.53
15:L:109:LYS:HD2	15:L:126:ARG:HB2	1.91	0.53
36:g:27:MET:HE2	36:g:193:PRO:HD3	1.90	0.53
37:h:111:LEU:HD11	37:h:146:ALA:HB2	1.90	0.53
37:h:112:ASP:OD2	37:h:115:LEU:HB2	2.08	0.53
1:1:171:U:H2'	1:1:172:A:H8	1.73	0.53
1:1:363:G:H2'	1:1:364:C:C6	2.44	0.53
1:1:481:G:H1'	1:1:506:G:N2	2.23	0.53
1:1:528:A:H3'	1:1:528:A:C8	2.42	0.53
1:1:2294:G:N1	1:1:2339:C:N3	2.57	0.53
1:1:2530:A:N6	11:F:156:PRO:HG3	2.23	0.53
1:1:2666:C:N4	11:F:108:GLY:O	2.40	0.53
2:2:1180:A:OP1	43:n:105:THR:OG1	2.22	0.53
7:B:180:GLU:OE2	7:B:267:ILE:HD12	2.09	0.53
10:E:135:GLN:CD	10:E:150:ARG:H	2.16	0.53
37:h:201:TRP:CD1	37:h:201:TRP:N	2.76	0.53
41:l:5:ARG:NH1	41:l:6:VAL:HG22	2.23	0.53
1:1:935:C:C2	1:1:936:A:C8	2.96	0.53
1:1:1044:C:N4	57:1:3353:HOH:O	2.39	0.53
1:1:1236:G:O2'	1:1:1237:A:O5'	2.25	0.53
1:1:1874:C:H2'	1:1:1875:G:O4'	2.08	0.53
1:1:2339:C:H2'	1:1:2340:A:H8	1.73	0.53
2:2:41:G:H2'	2:2:42:G:C8	2.44	0.53
2:2:75:G:H2'	2:2:76:G:H8	1.72	0.53
2:2:592:G:H2'	2:2:593:U:C6	2.44	0.53
3:3:8:C:O3'	18:O:25:ARG:NH1	2.38	0.53
15:L:20:GLY:O	15:L:21:ARG:HD2	2.08	0.53
18:O:63:LYS:HG3	18:O:64:TYR:N	2.24	0.53
1:1:1592:C:H2'	1:1:1593:A:H8	1.73	0.53
1:1:2802:G:C4'	57:1:3608:HOH:O	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:107:G:H1	54:y:6:SER:HG	1.53	0.53
2:2:1031:C:H5'	2:2:1032:G:N1	2.24	0.53
14:K:63:VAL:HG12	14:K:107:LEU:HD11	1.90	0.53
23:T:2:ILE:HB	23:T:7:LEU:HD11	1.90	0.53
43:n:59:GLU:OE1	43:n:59:GLU:N	2.34	0.53
53:x:10:PHE:O	53:x:39:THR:HG22	2.08	0.53
55:z:28:VAL:O	55:z:32:VAL:HG23	2.09	0.53
1:1:1045:C:H1'	1:1:1047:G:C2	2.44	0.53
1:1:1528:A:OP2	1:1:1543:G:N2	2.42	0.53
1:1:1796:U:H2'	1:1:1797:G:C8	2.42	0.53
1:1:1842:G:H2'	1:1:1843:C:H6	1.74	0.53
1:1:1857:G:H1'	1:1:1885:A:H62	1.74	0.53
2:2:382:A:H2'	2:2:383:A:C8	2.43	0.53
39:j:13:GLU:OE2	39:j:68:ARG:NH1	2.42	0.53
45:p:23:ILE:HD13	45:p:96:THR:OG1	2.09	0.53
1:1:1104:C:C5'	57:1:3501:HOH:O	2.57	0.53
1:1:2680:U:H5'	8:C:194:PRO:HA	1.90	0.53
2:2:727:G:N2	2:2:730:G:OP2	2.41	0.53
2:2:1240:U:OP2	41:l:116:MET:N	2.24	0.53
39:j:13:GLU:CB	39:j:39:VAL:HG12	2.39	0.53
1:1:1441:G:H2'	1:1:1442:U:C6	2.44	0.53
9:D:3:LEU:O	9:D:12:LEU:N	2.42	0.53
18:O:94:ARG:NH2	18:O:97:PHE:O	2.37	0.53
42:m:78:VAL:HG23	42:m:79:SER:H	1.74	0.53
1:1:281:C:H42	1:1:359:G:H1	1.58	0.52
1:1:622:G:H2'	1:1:623:C:C6	2.44	0.52
2:2:662:U:H2'	2:2:663:A:C8	2.45	0.52
11:F:73:ASN:O	11:F:77:ILE:HG12	2.09	0.52
1:1:1416:G:O2'	1:1:1417:C:O5'	2.27	0.52
1:1:1478:G:H1	1:1:1513:U:H3	1.56	0.52
2:2:221:C:H2'	2:2:222:C:H6	1.74	0.52
2:2:373:A:C2	2:2:374:A:C8	2.97	0.52
2:2:689:C:O2'	2:2:705:G:O2'	2.23	0.52
5:5:52:G:H2'	5:5:53:G:H8	1.73	0.52
7:B:82:GLU:OE1	7:B:103:TYR:OH	2.25	0.52
8:C:25:THR:HG21	8:C:193:VAL:HG22	1.91	0.52
16:M:50:ARG:O	16:M:54:THR:HG23	2.09	0.52
36:g:57:LEU:HD23	36:g:217:VAL:HG23	1.92	0.52
47:r:29:ARG:HD2	47:r:63:PHE:CE2	2.44	0.52
53:x:35:SER:O	53:x:35:SER:OG	2.25	0.52
1:1:144:A:H2'	1:1:145:C:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:364:C:H2'	1:1:365:U:C6	2.45	0.52
1:1:458:G:O2'	1:1:459:U:P	2.68	0.52
2:2:1033:G:C2	2:2:1034:G:H1'	2.45	0.52
10:E:37:ASN:OD1	10:E:38:MET:N	2.42	0.52
21:R:37:GLU:HG3	21:R:53:PHE:CG	2.44	0.52
46:q:21:VAL:HG13	46:q:95:TYR:CE1	2.45	0.52
51:v:26:GLU:N	51:v:26:GLU:OE1	2.43	0.52
1:1:319:G:H1	1:1:323:C:H5	1.57	0.52
1:1:1075:C:N4	1:1:1076:C:N3	2.58	0.52
2:2:618:C:O2'	50:u:14:ARG:NH2	2.43	0.52
2:2:676:A:H2'	2:2:677:U:H6	1.74	0.52
34:e:32:ILE:CG2	34:e:35:LYS:HE3	2.40	0.52
1:1:1857:G:O2'	1:1:1858:A:H8	1.92	0.52
1:1:2387:U:O4'	26:W:41:ARG:NH1	2.42	0.52
6:6:66:ASP:O	6:6:118:TRP:HA	2.09	0.52
18:O:43:ASN:ND2	18:O:45:SER:H	2.07	0.52
42:m:11:LEU:HG	42:m:75:ILE:HG12	1.91	0.52
1:1:134:G:H2'	1:1:135:U:C6	2.44	0.52
1:1:460:A:H2'	1:1:461:C:O4'	2.09	0.52
1:1:1098:A:H2'	1:1:1099:G:H5'	1.91	0.52
3:3:42:C:C6	10:E:66:LEU:HB2	2.44	0.52
1:1:1485:U:H2'	1:1:1486:U:C6	2.44	0.52
1:1:2405:G:O2'	1:1:2411:A:N6	2.43	0.52
1:1:2585:U:O2'	1:1:2586:U:OP2	2.25	0.52
4:4:13:A:N1	6:6:146:THR:HG22	2.25	0.52
12:G:2:GLN:HE22	12:G:20:ASN:HB2	1.74	0.52
36:g:115:LYS:O	36:g:119:THR:HG23	2.09	0.52
1:1:729:G:C5	7:B:207:LYS:HB2	2.44	0.52
1:1:2261:C:OP1	26:W:19:LYS:NZ	2.36	0.52
1:1:2682:A:H5'	8:C:11:MET:HB2	1.92	0.52
2:2:78:A:H2'	2:2:79:G:C8	2.42	0.52
3:3:44:G:N2	3:3:48:U:C2	2.77	0.52
32:c:40:ASP:OD1	32:c:42:VAL:HG12	2.10	0.52
52:w:41:PRO:HD2	52:w:44:ILE:HD13	1.92	0.52
1:1:367:G:C4	1:1:368:A:C8	2.98	0.52
1:1:396:G:C6	1:1:397:U:C4	2.98	0.52
1:1:593:U:H2'	1:1:594:U:C6	2.45	0.52
1:1:848:C:H2'	1:1:849:A:H8	1.75	0.52
1:1:1055:G:H1	1:1:1104:C:N4	2.08	0.52
1:1:1801:A:H5'	1:1:1801:A:H8	1.75	0.52
2:2:868:C:H2'	2:2:869:G:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1186:G:N2	48:s:101:TRP:OXT	2.25	0.52
12:G:15:LEU:HD22	12:G:55:GLU:OE1	2.09	0.52
12:G:66:ASN:ND2	12:G:135:HIS:HB2	2.25	0.52
16:M:14:LYS:O	16:M:71:LYS:NZ	2.32	0.52
17:N:86:ARG:NH1	17:N:117:ASP:O	2.42	0.52
1:1:351:C:H2'	1:1:352:A:H8	1.75	0.52
1:1:936:A:H2'	1:1:937:C:C6	2.45	0.52
1:1:2098:U:H2'	1:1:2099:U:C6	2.45	0.52
1:1:2780:G:H1	13:J:102:GLU:CD	2.18	0.52
2:2:1272:G:H2'	2:2:1273:C:C6	2.45	0.52
2:2:1309:G:C6	2:2:1329:A:C2	2.98	0.52
2:2:1461:G:N2	57:2:1816:HOH:O	2.32	0.52
14:K:75:SER:HB2	19:P:73:VAL:O	2.10	0.52
24:U:81:ASP:OD2	24:U:82:ARG:N	2.43	0.52
1:1:565:C:H2'	1:1:566:U:O4'	2.10	0.51
1:1:898:C:H2'	1:1:899:A:O4'	2.10	0.51
2:2:35:G:H2'	2:2:36:C:H6	1.74	0.51
2:2:757:U:O2'	2:2:879:C:O2	2.28	0.51
16:M:49:ALA:O	16:M:53:MET:HG2	2.10	0.51
25:V:45:ASP:N	25:V:45:ASP:OD1	2.43	0.51
26:W:56:ASP:OD1	26:W:58:THR:HG23	2.10	0.51
1:1:1378:A:O2'	1:1:1380:G:OP2	2.28	0.51
1:1:2801:G:H2'	1:1:2802:G:H8	1.75	0.51
2:2:476:U:H2'	2:2:477:C:C6	2.45	0.51
40:k:9:MET:O	40:k:85:ILE:N	2.34	0.51
49:t:35:GLN:HG2	49:t:59:MET:HE1	1.92	0.51
2:2:528:C:H41	46:q:46:ASN:ND2	2.09	0.51
50:u:18:GLN:OE1	50:u:35:ARG:NE	2.32	0.51
1:1:138:U:H5''	23:T:1:MET:HE1	1.91	0.51
1:1:299:A:H2'	1:1:300:A:C8	2.45	0.51
1:1:2557:G:H2'	1:1:2558:C:C6	2.45	0.51
2:2:338:A:H2'	2:2:339:C:H6	1.75	0.51
2:2:1062:U:H2'	2:2:1063:C:C6	2.46	0.51
2:2:1241:G:H2'	2:2:1242:G:H8	1.75	0.51
9:D:48:THR:C	9:D:50:ALA:H	2.19	0.51
10:E:17:MET:HE1	10:E:25:VAL:HA	1.92	0.51
11:F:27:LYS:HG2	11:F:32:GLU:HG2	1.91	0.51
15:L:91:ASP:OD1	15:L:92:LEU:N	2.42	0.51
1:1:171:U:H2'	1:1:172:A:C8	2.45	0.51
1:1:746:U:HO2'	1:1:747:C:P	2.31	0.51
2:2:215:C:H2'	2:2:216:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:264:C:O3'	51:v:65:ARG:NH2	2.43	0.51
10:E:34:ILE:HG23	10:E:156:ILE:HD13	1.93	0.51
10:E:42:GLU:OE1	10:E:148:ARG:NH1	2.44	0.51
13:J:41:LYS:HD2	13:J:50:THR:HG22	1.92	0.51
14:K:58:LEU:HA	14:K:89:ASN:ND2	2.25	0.51
40:k:9:MET:HE3	40:k:86:ARG:HB3	1.92	0.51
1:1:379:G:N1	1:1:396:G:C6	2.79	0.51
1:1:415:A:H2'	1:1:416:U:C6	2.46	0.51
1:1:1411:U:H2'	1:1:1412:U:C6	2.45	0.51
1:1:1799:G:H8	7:B:180:GLU:OE1	1.94	0.51
1:1:2788:C:O2'	1:1:2809:A:N3	2.37	0.51
6:6:5:TYR:HB2	6:6:8:ASP:OD1	2.10	0.51
8:C:152:PRO:HG3	8:C:156:PHE:CZ	2.45	0.51
21:R:27:ILE:HB	21:R:63:VAL:HG21	1.93	0.51
36:g:64:LYS:HA	36:g:225:ARG:HH12	1.74	0.51
1:1:1103:A:H2'	1:1:1103:A:N3	2.26	0.51
2:2:950:U:H2'	2:2:951:G:H8	1.74	0.51
2:2:1391:U:H2'	2:2:1392:G:C8	2.46	0.51
5:5:63:U:H2'	5:5:64:C:C6	2.46	0.51
12:G:86:ASP:HB3	40:k:24:ARG:CZ	2.40	0.51
13:J:6:ALA:HB3	13:J:48:VAL:HG21	1.92	0.51
14:K:76:VAL:H	19:P:73:VAL:HG22	1.76	0.51
26:W:39:ARG:HG2	26:W:58:THR:HG22	1.93	0.51
40:k:12:PRO:O	40:k:15:SER:OG	2.26	0.51
40:k:18:VAL:HG21	40:k:58:HIS:CD2	2.46	0.51
44:o:6:ILE:HG23	44:o:76:ILE:HB	1.92	0.51
1:1:538:A:H4'	13:J:7:LYS:HG2	1.93	0.51
1:1:1592:C:H2'	1:1:1593:A:C8	2.46	0.51
1:1:2070:A:H2'	1:1:2071:A:C8	2.46	0.51
1:1:2515:C:H2'	1:1:2516:A:H8	1.75	0.51
2:2:71:A:N1	2:2:99:C:O2'	2.43	0.51
2:2:110:C:O2'	50:u:25:ARG:O	2.27	0.51
2:2:844:G:C8	57:2:1817:HOH:O	2.44	0.51
2:2:845:A:O4'	52:w:15:ALA:HB2	2.11	0.51
9:D:80:SER:O	9:D:80:SER:OG	2.27	0.51
12:G:90:LEU:HD11	12:G:146:VAL:HG11	1.91	0.51
36:g:127:ASP:OD1	36:g:127:ASP:N	2.41	0.51
1:1:1083:U:O2'	1:1:1085:A:N7	2.32	0.51
1:1:2743:U:OP1	35:f:34:LYS:NZ	2.37	0.51
2:2:1314:C:H2'	2:2:1315:U:C6	2.43	0.51
2:2:1469:C:H5	57:2:2014:HOH:O	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:111:U:H2'	3:3:112:G:H8	1.75	0.51
25:V:55:GLU:O	25:V:59:GLU:HG2	2.11	0.51
30:a:16:CYS:SG	30:a:17:SER:N	2.84	0.51
36:g:208:ARG:HA	36:g:211:THR:HG22	1.93	0.51
1:1:1693:U:O2'	7:B:14:ARG:NH2	2.44	0.51
1:1:1808:A:H3'	1:1:1809:A:C8	2.46	0.51
1:1:1842:G:H2'	1:1:1843:C:C6	2.45	0.51
1:1:1857:G:H1'	1:1:1885:A:N6	2.26	0.51
1:1:2191:A:O2'	1:1:2192:U:O4'	2.13	0.51
21:R:14:VAL:HG21	21:R:98:ILE:HG13	1.91	0.51
23:T:53:VAL:HG21	23:T:93:LEU:HD13	1.93	0.51
38:i:49:SER:OG	38:i:50:ASP:N	2.41	0.51
1:1:726:G:O2'	1:1:727:A:OP2	2.29	0.50
1:1:871:U:H2'	1:1:872:U:C6	2.46	0.50
1:1:1320:C:H4'	1:1:1321:A:O5'	2.11	0.50
1:1:1930:G:H1'	1:1:1931:U:OP2	2.11	0.50
2:2:1014:A:H2	2:2:1219:A:H1'	1.76	0.50
2:2:1129:C:H4'	43:n:18:ARG:HH22	1.76	0.50
17:N:55:ALA:HA	17:N:80:PHE:CE1	2.46	0.50
26:W:15:ASP:OD1	26:W:16:SER:N	2.41	0.50
36:g:48:PRO:O	36:g:52:GLU:HG3	2.11	0.50
47:r:33:ILE:HD11	47:r:63:PHE:CD2	2.46	0.50
47:r:34:LEU:HD12	47:r:41:GLU:HG3	1.93	0.50
47:r:100:GLN:OE1	47:r:100:GLN:N	2.42	0.50
1:1:10:A:C6	1:1:2800:A:C2	2.99	0.50
1:1:24:G:H2'	1:1:25:U:C6	2.46	0.50
1:1:71:A:H4'	1:1:72:U:H5''	1.93	0.50
1:1:996:A:OP2	20:Q:93:LYS:NZ	2.43	0.50
1:1:1236:G:HO2'	1:1:1237:A:P	2.34	0.50
1:1:2748:A:C2	1:1:2757:A:C5	2.99	0.50
1:1:2900:A:H2'	1:1:2901:C:H6	1.75	0.50
2:2:628:G:H2'	2:2:629:A:C8	2.46	0.50
2:2:707:U:H2'	2:2:708:C:C6	2.45	0.50
2:2:974:A:OP1	48:s:69:ARG:NH1	2.43	0.50
15:L:40:SER:O	15:L:40:SER:OG	2.24	0.50
36:g:4:VAL:HG21	36:g:212:LEU:HD21	1.93	0.50
37:h:65:ARG:HG2	37:h:100:GLN:HB2	1.94	0.50
53:x:33:THR:OG1	53:x:34:TRP:N	2.44	0.50
1:1:1283:G:N2	1:1:1285:A:H3'	2.26	0.50
1:1:2192:U:O2'	1:1:2193:G:H2'	2.11	0.50
1:1:2193:G:O2'	1:1:2194:U:H6	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2900:A:H2'	1:1:2901:C:C6	2.46	0.50
2:2:24:U:O2'	2:2:524:G:O2'	2.27	0.50
2:2:965:U:H5''	2:2:966:2MG:OP1	2.12	0.50
2:2:1034:G:H3'	2:2:1035:A:C8	2.45	0.50
2:2:1145:A:HO2'	2:2:1146:A:P	2.34	0.50
33:d:24:THR:O	33:d:28:ARG:NH1	2.44	0.50
37:h:36:ASP:OD2	37:h:59:ARG:NH2	2.44	0.50
48:s:27:LEU:O	48:s:30:ILE:HG22	2.11	0.50
48:s:34:VAL:HG13	48:s:35:ASN:OD1	2.11	0.50
1:1:455:C:O2'	1:1:456:C:OP1	2.28	0.50
1:1:881:G:N2	1:1:897:C:N3	2.60	0.50
2:2:1143:G:H2'	2:2:1144:G:C8	2.46	0.50
12:G:122:LEU:HD11	12:G:128:HIS:CG	2.46	0.50
28:Y:10:SER:OG	28:Y:12:GLU:OE1	2.27	0.50
47:r:47:GLU:O	47:r:48:LEU:HD12	2.11	0.50
1:1:1032:A:O2'	1:1:1033:U:H5'	2.11	0.50
1:1:2064:C:H2'	1:1:2065:C:C6	2.46	0.50
1:1:2329:U:H2'	1:1:2330:G:H8	1.76	0.50
2:2:481:G:O2'	2:2:483:C:N4	2.44	0.50
2:2:878:A:OP1	42:m:80:ARG:NH1	2.43	0.50
2:2:1021:A:C4'	57:2:1885:HOH:O	2.59	0.50
2:2:1030:U:O2'	2:2:1031:C:H5''	2.11	0.50
2:2:1435:G:H2'	2:2:1436:U:C6	2.47	0.50
7:B:53:HIS:CE1	7:B:219:THR:HA	2.47	0.50
9:D:5:LEU:HD23	9:D:122:GLU:HB3	1.92	0.50
18:O:95:SER:O	18:O:95:SER:OG	2.26	0.50
1:1:243:U:OP2	1:1:254:G:N1	2.45	0.50
1:1:849:A:H2'	1:1:850:U:C6	2.46	0.50
1:1:894:U:H2'	1:1:895:U:O4'	2.12	0.50
1:1:1432:G:H2'	1:1:1433:A:C8	2.46	0.50
2:2:999:C:H2'	2:2:1000:A:C8	2.46	0.50
3:3:119:A:H3'	3:3:120:U:C6	2.47	0.50
12:G:95:GLY:O	12:G:99:ILE:HG13	2.11	0.50
38:i:146:ARG:HG2	38:i:148:LYS:HG2	1.94	0.50
1:1:773:U:O2	1:1:778:G:O2'	2.30	0.50
2:2:1412:C:H2'	2:2:1413:A:C8	2.47	0.50
23:T:11:LEU:O	28:Y:29:ARG:NH1	2.44	0.50
30:a:18:CYS:SG	30:a:40:CYS:HB3	2.50	0.50
36:g:31:ILE:HG21	36:g:39:HIS:HD2	1.77	0.50
1:1:117:G:C6	1:1:119:A:N6	2.80	0.50
1:1:244:A:OP2	34:e:8:ARG:NH2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1076:C:H2'	1:1:1077:A:C4	2.46	0.50
1:1:1093:G:H1'	1:1:1098:A:H62	1.76	0.50
1:1:1734:G:C2	1:1:1735:A:C5	3.00	0.50
2:2:78:A:H1'	57:2:1912:HOH:O	2.10	0.50
2:2:216:U:H2'	2:2:217:C:H6	1.77	0.50
2:2:1296:C:H4'	2:2:1302:C:N4	2.27	0.50
2:2:1477:U:H2'	2:2:1478:U:C6	2.46	0.50
3:3:49:C:H2'	3:3:50:A:H8	1.77	0.50
6:6:3:THR:HA	6:6:63:GLU:HA	1.93	0.50
1:1:413:C:H2'	1:1:414:C:H6	1.76	0.50
1:1:532:A:N1	1:1:2020:A:H1'	2.27	0.50
1:1:1255:U:C5	9:D:68:ALA:HA	2.47	0.50
1:1:2749:A:OP1	11:F:2:SER:N	2.44	0.50
1:1:2896:C:H2'	1:1:2897:U:C6	2.47	0.50
2:2:1321:U:OP2	2:2:1322:C:O2'	2.28	0.50
12:G:5:LEU:O	12:G:6:LEU:HD23	2.12	0.50
25:V:21:ARG:HH21	25:V:87:GLN:C	2.19	0.50
42:m:6:PRO:HB2	42:m:33:LYS:HE3	1.94	0.50
43:n:42:GLU:OE2	43:n:45:ARG:NH1	2.43	0.50
53:x:12:ASP:OD1	53:x:37:ARG:NH2	2.45	0.50
55:z:69:ARG:CZ	57:z:101:HOH:O	2.60	0.50
1:1:30:G:O2'	1:1:1214:A:N3	2.41	0.49
1:1:197:A:H62	1:1:2430:A:H2'	1.77	0.49
1:1:273:G:N2	1:1:365:U:C2	2.79	0.49
1:1:382:A:C2	1:1:393:C:N3	2.80	0.49
1:1:614:A:O2'	1:1:615:U:H5'	2.12	0.49
1:1:746:U:O2'	1:1:747:C:P	2.70	0.49
1:1:817:C:H2'	1:1:818:G:O4'	2.12	0.49
1:1:927:A:H2'	1:1:928:A:C8	2.47	0.49
1:1:1176:U:C5'	57:1:3356:HOH:O	2.59	0.49
2:2:128:G:P	51:v:6:ARG:HH12	2.34	0.49
2:2:1095:U:P	2:2:1108:G:H1	2.35	0.49
2:2:1219:A:H2'	2:2:1220:G:H8	1.76	0.49
2:2:1347:G:O6	43:n:12:ARG:NH2	2.30	0.49
8:C:136:ASN:ND2	8:C:139:SER:O	2.39	0.49
13:J:125:TYR:HH	13:J:132:HIS:HE2	1.54	0.49
23:T:34:VAL:HG21	23:T:43:ILE:HD11	1.94	0.49
32:c:36:LEU:O	32:c:49:TYR:N	2.40	0.49
51:v:21:ILE:HG22	57:v:102:HOH:O	2.11	0.49
1:1:624:C:O2'	1:1:657:U:OP1	2.26	0.49
1:1:1013:C:H2'	1:1:1014:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1411:U:H2'	1:1:1412:U:H6	1.77	0.49
1:1:1881:C:H2'	1:1:1882:U:O4'	2.12	0.49
1:1:2086:U:H2'	1:1:2087:G:C8	2.47	0.49
2:2:765:G:N1	2:2:812:G:O2'	2.36	0.49
3:3:118:C:C2	3:3:119:A:C8	3.00	0.49
30:a:53:THR:OG1	30:a:54:GLY:N	2.45	0.49
1:1:372:G:O2'	1:1:373:U:P	2.70	0.49
2:2:767:A:H2'	2:2:768:A:O4'	2.11	0.49
2:2:1521:C:H2'	2:2:1522:U:H6	1.77	0.49
8:C:156:PHE:CE1	13:J:81:ILE:HD13	2.48	0.49
30:a:49:ARG:NH2	47:r:63:PHE:O	2.45	0.49
38:i:67:VAL:HG21	38:i:72:PHE:HD2	1.76	0.49
44:o:26:VAL:HG23	44:o:36:VAL:HG11	1.94	0.49
1:1:18:U:P	20:Q:30:ARG:HH22	2.34	0.49
1:1:404:A:H1'	1:1:406:G:C4	2.48	0.49
1:1:729:G:H5''	1:1:730:A:H5''	1.93	0.49
2:2:461:A:H2'	2:2:462:G:H8	1.77	0.49
2:2:545:C:H5'	38:i:69:GLU:HB2	1.94	0.49
3:3:29:A:H2'	3:3:30:C:H6	1.78	0.49
9:D:176:ASP:OD1	9:D:179:SER:N	2.28	0.49
22:S:51:LEU:HD13	22:S:105:VAL:HG11	1.95	0.49
41:l:32:VAL:HG22	41:l:33:ASP:OD1	2.12	0.49
1:1:1223:G:C6	1:1:1227:G:C6	3.00	0.49
1:1:1913:A:N1	2:2:1492:A:C8	2.81	0.49
1:1:2230:G:H2'	1:1:2231:U:C6	2.47	0.49
1:1:2512:C:H2'	1:1:2513:A:O4'	2.11	0.49
2:2:215:C:H2'	2:2:216:U:H6	1.78	0.49
2:2:1521:C:H2'	2:2:1522:U:C6	2.47	0.49
6:6:15:ILE:HG22	6:6:16:MET:N	2.27	0.49
10:E:42:GLU:H	10:E:42:GLU:CD	2.20	0.49
10:E:108:VAL:O	10:E:111:ILE:HG22	2.11	0.49
14:K:80:ASP:OD1	19:P:62:ARG:NH1	2.34	0.49
18:O:52:SER:OG	18:O:53:THR:N	2.43	0.49
36:g:60:ILE:HD13	36:g:63:ARG:HD2	1.94	0.49
52:w:22:ASP:OD2	52:w:24:LYS:N	2.34	0.49
1:1:1114:C:H2'	1:1:1115:G:C8	2.48	0.49
1:1:1709:U:H2'	1:1:1710:G:H8	1.78	0.49
1:1:2037:A:H2'	1:1:2038:G:C8	2.48	0.49
1:1:2233:U:H2'	1:1:2234:G:H8	1.76	0.49
1:1:2353:G:N2	26:W:34:GLY:O	2.39	0.49
1:1:2814:A:H2'	1:1:2815:C:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:299:G:N2	2:2:565:U:O2	2.46	0.49
2:2:315:A:O2'	2:2:330:C:O2'	2.28	0.49
2:2:404:G:N7	38:i:2:ALA:HB3	2.28	0.49
2:2:509:A:N3	2:2:543:U:O2'	2.37	0.49
2:2:1052:U:C5	57:2:1883:HOH:O	2.53	0.49
16:M:70:ASP:OD1	16:M:70:ASP:N	2.36	0.49
1:1:358:U:H2'	1:1:359:G:C8	2.48	0.49
1:1:1591:A:H2'	1:1:1592:C:C6	2.47	0.49
1:1:2064:C:H2'	1:1:2065:C:H6	1.77	0.49
2:2:542:G:H5'	38:i:39:GLY:HA3	1.95	0.49
41:l:15:ASP:OD1	41:l:20:SER:N	2.28	0.49
41:l:30:LEU:HD11	41:l:116:MET:HE2	1.94	0.49
50:u:20:VAL:HG23	50:u:35:ARG:HA	1.94	0.49
1:1:894:U:H3'	1:1:895:U:C6	2.47	0.49
1:1:1591:A:H2'	1:1:1592:C:H6	1.77	0.49
1:1:2788:C:H2'	1:1:2789:C:C6	2.47	0.49
1:1:2895:G:H2'	1:1:2896:C:H6	1.77	0.49
2:2:407:U:H2'	2:2:408:A:H8	1.78	0.49
2:2:418:C:H2'	2:2:419:C:C6	2.47	0.49
2:2:950:U:H2'	2:2:951:G:C8	2.48	0.49
3:3:74:U:H3	25:V:37:PRO:HD2	1.77	0.49
12:G:87:GLU:OE2	40:k:17:GLN:HG3	2.13	0.49
30:a:48:GLN:HA	30:a:51:VAL:HG22	1.93	0.49
31:b:29:SER:OG	31:b:38:HIS:NE2	2.46	0.49
37:h:156:ARG:NH1	37:h:160:ALA:O	2.46	0.49
38:i:60:LYS:O	38:i:64:ILE:HG13	2.13	0.49
42:m:90:ASP:OD1	42:m:90:ASP:N	2.44	0.49
1:1:173:A:H2'	1:1:174:U:C6	2.48	0.49
1:1:538:A:H5''	13:J:7:LYS:HE3	1.95	0.49
1:1:851:C:H2'	1:1:852:U:C6	2.48	0.49
1:1:2330:G:C2	1:1:2386:A:C2	3.01	0.49
1:1:2822:G:O2'	1:1:2824:C:OP2	2.29	0.49
2:2:475:C:H2'	2:2:476:U:C6	2.48	0.49
29:Z:48:ILE:HD13	29:Z:57:VAL:HG11	1.94	0.49
53:x:36:ARG:HH11	53:x:53:ASN:HA	1.78	0.49
1:1:44:A:H2'	1:1:45:G:O4'	2.13	0.49
1:1:77:G:OP1	28:Y:52:ARG:NH2	2.46	0.49
1:1:475:C:O2	1:1:479:A:N6	2.46	0.49
1:1:517:C:OP2	31:b:10:ARG:NH2	2.46	0.49
1:1:721:A:H2'	1:1:722:A:C8	2.48	0.49
1:1:774:G:HO2'	1:1:775:G:P	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:882:G:H3'	1:1:883:G:H8	1.78	0.49
1:1:1096:A:H3'	1:1:1097:U:H5''	1.94	0.49
1:1:2543:G:H2'	1:1:2544:G:H8	1.77	0.49
1:1:2745:C:H2'	1:1:2746:U:C6	2.47	0.49
1:1:2756:U:OP2	35:f:19:ARG:NE	2.28	0.49
2:2:339:C:H2'	2:2:340:U:C6	2.48	0.49
5:5:44:G:H2'	5:5:45:G:O4'	2.13	0.49
6:6:69:ASP:HA	6:6:115:VAL:O	2.12	0.49
21:R:68:ARG:HH11	21:R:90:ARG:HB2	1.78	0.49
22:S:40:ASN:O	22:S:41:LYS:HG2	2.13	0.49
26:W:37:ILE:HG21	26:W:80:ILE:HG21	1.95	0.49
29:Z:8:THR:HA	29:Z:34:HIS:O	2.13	0.49
37:h:77:ILE:HG13	37:h:84:VAL:HG21	1.95	0.49
43:n:80:ARG:NH1	43:n:103:PHE:HD2	2.10	0.49
44:o:71:LEU:O	44:o:72:ARG:NH1	2.32	0.49
51:v:10:GLY:HA3	51:v:25:ILE:HD13	1.95	0.49
53:x:51:VAL:HG11	53:x:71:LEU:HD23	1.94	0.49
53:x:71:LEU:H	53:x:71:LEU:HD12	1.77	0.49
1:1:421:C:O2'	1:1:422:A:P	2.70	0.48
1:1:958:U:H2'	3:3:89:U:C2	2.48	0.48
2:2:33:A:H2'	2:2:34:C:H6	1.75	0.48
2:2:62:U:O2'	2:2:379:C:O2	2.30	0.48
2:2:1012:A:N6	2:2:1018:G:O6	2.46	0.48
6:6:167:PHE:CE2	6:6:186:ARG:HD3	2.48	0.48
21:R:27:ILE:HG22	21:R:31:GLU:HB2	1.95	0.48
49:t:29:VAL:O	49:t:33:THR:HG23	2.13	0.48
1:1:172:A:H2'	1:1:173:A:C8	2.44	0.48
1:1:2655:G:O2'	1:1:2656:U:P	2.72	0.48
2:2:263:A:P	54:y:74:ARG:HH11	2.36	0.48
2:2:568:G:O6	46:q:2:ALA:HB2	2.13	0.48
2:2:696:A:H2'	2:2:697:U:H6	1.77	0.48
2:2:794:A:H2'	2:2:795:C:C6	2.48	0.48
2:2:861:G:HO2'	2:2:874:G:HO2'	1.60	0.48
2:2:1016:A:H2'	2:2:1017:U:H5'	1.94	0.48
2:2:1174:G:C2'	2:2:1175:G:H5'	2.43	0.48
5:5:23:C:H2'	5:5:24:G:H8	1.77	0.48
20:Q:43:GLY:HA3	21:R:75:VAL:HG11	1.96	0.48
32:c:53:LYS:CB	32:c:55:LYS:HE3	2.43	0.48
42:m:50:LYS:NZ	42:m:52:GLU:OE1	2.31	0.48
1:1:549:G:O2'	1:1:550:C:OP1	2.28	0.48
2:2:16:A:O2'	39:j:21:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:108:G:H5'	2:2:109:A:C5'	2.43	0.48
2:2:713:G:H2'	2:2:714:G:C8	2.48	0.48
2:2:714:G:H2'	2:2:715:A:C8	2.48	0.48
2:2:976:G:C2	2:2:1363:A:C2	3.01	0.48
2:2:1033:G:N3	2:2:1034:G:H1'	2.28	0.48
2:2:1307:U:H2'	2:2:1308:U:C6	2.48	0.48
2:2:1451:U:H5''	2:2:1452:C:C5	2.45	0.48
3:3:30:C:H1'	3:3:57:A:H61	1.79	0.48
9:D:112:LEU:HD13	9:D:186:VAL:HG11	1.96	0.48
10:E:8:TYR:HB2	10:E:173:PHE:HZ	1.78	0.48
12:G:145:ASN:HD22	12:G:147:VAL:HG13	1.78	0.48
17:N:106:ASP:O	17:N:107:ASN:C	2.56	0.48
25:V:6:ALA:HB2	25:V:42:LEU:HD23	1.95	0.48
38:i:95:GLU:CD	38:i:100:ASN:HD21	2.21	0.48
49:t:17:ARG:NH1	49:t:18:ASP:HB3	2.28	0.48
53:x:3:ARG:NH1	53:x:8:GLY:O	2.46	0.48
1:1:1007:C:OP1	13:J:37:ARG:NH2	2.44	0.48
1:1:1047:G:O2'	1:1:1048:A:H8	1.96	0.48
1:1:1080:A:H2'	1:1:1081:U:C6	2.49	0.48
1:1:1141:U:H4'	1:1:1142:A:O4'	2.14	0.48
1:1:2303:G:H1'	10:E:123:ASP:OD1	2.14	0.48
1:1:2339:C:H2'	1:1:2340:A:C8	2.47	0.48
1:1:2469:A:H4'	16:M:55:ARG:CD	2.42	0.48
2:2:375:U:OP1	50:u:70:ARG:NH1	2.44	0.48
2:2:647:C:H2'	2:2:648:A:H8	1.77	0.48
2:2:1201:A:H4'	2:2:1202:U:H5''	1.94	0.48
15:L:78:ARG:HG2	15:L:113:ALA:HB3	1.96	0.48
22:S:83:LYS:HB3	22:S:95:ARG:HD3	1.95	0.48
23:T:53:VAL:HG11	23:T:87:LEU:HD22	1.95	0.48
40:k:95:ALA:O	40:k:97:THR:HG23	2.13	0.48
45:p:64:GLN:O	45:p:68:GLU:HG3	2.13	0.48
49:t:80:GLN:NE2	57:t:103:HOH:O	2.45	0.48
55:z:13:ASP:O	55:z:17:ARG:HG2	2.13	0.48
1:1:367:G:P	57:1:3425:HOH:O	2.71	0.48
1:1:1204:A:H4'	1:1:1205:A:H5''	1.95	0.48
1:1:1220:G:C2	1:1:1230:A:C2	3.01	0.48
1:1:2373:G:H2'	1:1:2374:C:C6	2.49	0.48
2:2:407:U:H2'	2:2:408:A:C8	2.48	0.48
2:2:1003:G:N2	2:2:1005:A:O5'	2.45	0.48
2:2:1061:G:H2'	2:2:1062:U:C6	2.49	0.48
2:2:1226:C:P	47:r:90:ARG:HH22	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:18:G:O2'	5:5:19:G:H5'	2.14	0.48
10:E:32:GLU:OE2	10:E:159:THR:HB	2.13	0.48
42:m:72:VAL:HG23	42:m:72:VAL:O	2.13	0.48
1:1:163:C:H2'	1:1:164:C:C6	2.49	0.48
1:1:613:A:H5''	1:1:614:A:C8	2.48	0.48
1:1:1536:C:H5''	1:1:1537:G:C4	2.49	0.48
2:2:158:G:H2'	2:2:159:G:O4'	2.13	0.48
2:2:707:U:H2'	2:2:708:C:H6	1.79	0.48
2:2:983:A:H5'	2:2:984:C:OP2	2.14	0.48
2:2:1005:A:H3'	2:2:1006:G:H8	1.78	0.48
2:2:1189:U:OP1	48:s:98:LYS:NZ	2.47	0.48
45:p:29:ASN:HB2	45:p:57:LYS:HE3	1.95	0.48
51:v:46:VAL:HG12	51:v:73:TRP:HB2	1.95	0.48
1:1:282:A:H2'	1:1:283:G:C8	2.48	0.48
1:1:871:U:H2'	1:1:872:U:H6	1.79	0.48
1:1:1587:G:C2	1:1:1588:G:C8	3.02	0.48
1:1:1636:U:H2'	1:1:1637:A:C8	2.49	0.48
1:1:2192:U:O2'	1:1:2193:G:OP2	2.26	0.48
1:1:2812:G:H2'	1:1:2813:A:C8	2.49	0.48
2:2:377:G:N2	57:2:1849:HOH:O	2.46	0.48
2:2:662:U:O2'	2:2:836:G:OP1	2.32	0.48
5:5:49:G:H1	5:5:65:U:H3	1.61	0.48
8:C:15:PHE:H	19:P:12:GLN:HE22	1.62	0.48
21:R:55:ASP:OD1	21:R:55:ASP:N	2.45	0.48
37:h:200:VAL:C	37:h:201:TRP:CD1	2.87	0.48
44:o:32:THR:HG21	44:o:83:THR:HA	1.96	0.48
1:1:1104:C:H5'	57:1:3501:HOH:O	2.14	0.48
1:1:1248:G:OP1	9:D:44:ARG:NH2	2.47	0.48
2:2:454:G:N2	2:2:479:U:O2	2.46	0.48
2:2:1422:G:O3'	14:K:49:ARG:NH1	2.37	0.48
10:E:72:LYS:HG2	10:E:73:SER:H	1.78	0.48
29:Z:3:LYS:NZ	57:Z:201:HOH:O	2.42	0.48
30:a:35:ASP:OD2	30:a:36:VAL:N	2.46	0.48
50:u:14:ARG:HD3	50:u:42:ILE:HD11	1.95	0.48
1:1:1007:C:OP1	13:J:39:LYS:HD2	2.14	0.48
1:1:1042:G:H1	1:1:1113:U:H3	1.62	0.48
1:1:1558:C:H4'	1:1:1559:U:O5'	2.14	0.48
2:2:451:A:H61	2:2:481:G:H5'	1.79	0.48
2:2:483:C:H5''	2:2:484:G:OP2	2.14	0.48
2:2:635:A:H2'	2:2:636:U:H6	1.78	0.48
2:2:1095:U:OP1	2:2:1108:G:N2	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1130:A:H2'	2:2:1131:G:H8	1.77	0.48
13:J:102:GLU:HG3	13:J:124:VAL:HG11	1.96	0.48
14:K:13:ASN:OD1	14:K:98:ARG:N	2.47	0.48
37:h:144:LEU:HD23	37:h:144:LEU:HA	1.64	0.48
40:k:101:PRO:HD2	52:w:24:LYS:HE3	1.96	0.48
1:1:232:G:OP2	1:1:232:G:H8	1.95	0.48
1:1:733:G:O6	1:1:761:A:C8	2.67	0.48
1:1:760:G:H2'	1:1:761:A:O4'	2.14	0.48
1:1:1141:U:OP2	13:J:65:THR:OG1	2.32	0.48
1:1:2457:U:H5	1:1:2494:G:H1	1.61	0.48
1:1:2884:U:O2'	1:1:2885:G:O5'	2.28	0.48
2:2:223:A:H2'	2:2:224:U:C6	2.49	0.48
2:2:381:C:H2'	2:2:382:A:O4'	2.14	0.48
9:D:119:ILE:HB	9:D:187:VAL:HG12	1.96	0.48
9:D:152:GLU:N	9:D:152:GLU:OE2	2.47	0.48
18:O:69:ASP:OD1	18:O:70:ALA:N	2.47	0.48
43:n:30:ILE:HG12	43:n:65:ILE:HB	1.96	0.48
1:1:181:A:H2'	1:1:182:A:C8	2.49	0.47
1:1:1089:A:O2'	1:1:1090:A:N7	2.44	0.47
1:1:1149:G:H2'	1:1:1150:C:H6	1.78	0.47
1:1:1636:U:H2'	1:1:1637:A:H8	1.78	0.47
1:1:1727:C:H2'	1:1:1728:C:O4'	2.14	0.47
1:1:2513:A:C5	1:1:2574:G:N1	2.81	0.47
1:1:2607:G:H2'	1:1:2608:G:O4'	2.14	0.47
1:1:2861:U:H2'	1:1:2862:G:C8	2.48	0.47
2:2:131:A:H2'	2:2:132:C:C6	2.48	0.47
2:2:337:G:C6	2:2:338:A:N6	2.82	0.47
2:2:1166:G:N1	2:2:1169:A:OP2	2.47	0.47
6:6:5:TYR:HB2	6:6:8:ASP:CG	2.39	0.47
15:L:57:LEU:HD22	34:e:54:ASP:HB3	1.96	0.47
19:P:31:TRP:NE1	19:P:82:ASP:OD1	2.47	0.47
24:U:25:VAL:HA	24:U:36:VAL:HA	1.96	0.47
37:h:11:ARG:O	37:h:13:GLY:N	2.46	0.47
46:q:67:ILE:HG12	46:q:97:THR:HG21	1.95	0.47
46:q:67:ILE:HA	46:q:97:THR:HG22	1.95	0.47
49:t:26:GLU:HG3	49:t:81:LEU:HD22	1.95	0.47
50:u:16:PHE:HE1	50:u:18:GLN:NE2	2.11	0.47
53:x:25:SER:OG	53:x:27:ASP:OD1	2.32	0.47
1:1:851:C:H2'	1:1:852:U:H6	1.80	0.47
1:1:1115:G:H2'	1:1:1116:G:H8	1.79	0.47
1:1:2285:C:OP2	32:c:6:ARG:NH2	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2901:C:C2	1:1:2902:C:C5	3.02	0.47
2:2:202:G:N2	2:2:466:A:H61	2.09	0.47
2:2:593:U:H2'	2:2:594:U:C6	2.50	0.47
2:2:864:A:O2'	2:2:1078:U:O4	2.28	0.47
2:2:1179:A:H2'	2:2:1180:A:O4'	2.14	0.47
5:5:58:A:H1'	5:5:60:U:OP2	2.13	0.47
16:M:111:GLU:HG2	16:M:112:LEU:N	2.27	0.47
23:T:63:VAL:O	23:T:79:ASP:HB2	2.14	0.47
36:g:214:LEU:HA	36:g:217:VAL:HG12	1.96	0.47
37:h:142:MET:HE1	37:h:148:GLY:HA2	1.94	0.47
1:1:62:U:O2'	1:1:63:A:C8	2.64	0.47
1:1:351:C:H2'	1:1:352:A:C8	2.48	0.47
1:1:2415:G:H2'	1:1:2416:C:H6	1.79	0.47
1:1:2455:G:H2'	1:1:2456:C:H6	1.79	0.47
1:1:2731:G:O2'	1:1:2732:G:H5'	2.15	0.47
2:2:261:U:OP2	54:y:71:LYS:NZ	2.46	0.47
2:2:263:A:H2'	2:2:264:C:C5	2.49	0.47
2:2:958:A:H1'	2:2:985:C:O2'	2.15	0.47
2:2:1204:A:H2'	2:2:1205:U:O4'	2.14	0.47
2:2:1432:G:OP1	19:P:106:LYS:N	2.42	0.47
2:2:1486:G:H2'	2:2:1487:G:O4'	2.14	0.47
6:6:103:ASN:HD22	6:6:125:VAL:HG23	1.79	0.47
10:E:23:ASN:OD1	10:E:27:GLN:NE2	2.47	0.47
10:E:31:VAL:HG12	10:E:158:THR:HG22	1.96	0.47
10:E:122:PHE:O	10:E:124:GLY:N	2.46	0.47
38:i:116:GLN:HE21	38:i:120:HIS:CG	2.31	0.47
46:q:7:LEU:HD22	46:q:12:ARG:HD3	1.96	0.47
1:1:878:A:H5'	1:1:879:G:OP2	2.14	0.47
1:1:880:G:H2'	1:1:881:G:O4'	2.14	0.47
1:1:1399:C:H2'	1:1:1400:U:C6	2.49	0.47
1:1:1957:C:H2'	1:1:1958:C:C6	2.50	0.47
1:1:2737:G:N2	1:1:2768:U:C2	2.83	0.47
2:2:825:A:H2'	2:2:826:C:C6	2.49	0.47
2:2:838:G:H2'	2:2:839:C:C6	2.49	0.47
5:5:75:C:O3'	6:6:34:KEO:N03	2.46	0.47
11:F:83:PHE:CE2	11:F:138:LYS:HB2	2.50	0.47
12:G:132:PHE:N	12:G:140:ALA:O	2.47	0.47
14:K:106:GLU:H	14:K:106:GLU:CD	2.22	0.47
17:N:37:THR:HA	17:N:110:MET:HA	1.95	0.47
36:g:101:LEU:HD13	36:g:179:LEU:HD12	1.95	0.47
37:h:35:SER:O	37:h:39:VAL:HG13	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:29:SER:HB3	42:m:59:LEU:HB2	1.97	0.47
1:1:784:G:C6	7:B:228:VAL:HG21	2.49	0.47
1:1:1055:G:H1'	1:1:1085:A:C2	2.49	0.47
1:1:1224:U:OP2	21:R:68:ARG:NH1	2.41	0.47
1:1:1429:G:H2'	1:1:1430:G:C8	2.50	0.47
1:1:1588:G:H2'	1:1:1589:U:C6	2.50	0.47
1:1:1599:U:H2'	1:1:1600:C:H6	1.79	0.47
1:1:2705:A:H8	1:1:2705:A:O5'	1.97	0.47
2:2:648:A:H2'	2:2:649:A:H8	1.79	0.47
2:2:1232:U:H5''	43:n:126:GLN:HB2	1.97	0.47
9:D:173:THR:HA	9:D:199:MET:HE1	1.95	0.47
13:J:88:THR:OG1	13:J:89:PHE:N	2.46	0.47
17:N:54:LEU:HD23	17:N:66:ALA:HB2	1.95	0.47
37:h:86:LYS:O	37:h:90:VAL:HG23	2.14	0.47
40:k:72:ASP:HA	40:k:75:GLU:HG3	1.96	0.47
1:1:197:A:N6	1:1:2430:A:H2'	2.29	0.47
1:1:627:A:H5''	15:L:78:ARG:NH1	2.29	0.47
1:1:983:A:C6	1:1:984:A:C2	3.03	0.47
1:1:1009:A:N3	1:1:1153:C:O2'	2.43	0.47
1:1:1847:G:O2'	1:1:1848:A:O5'	2.30	0.47
1:1:2834:G:H2'	1:1:2879:A:H61	1.80	0.47
2:2:127:G:O3'	51:v:6:ARG:NH1	2.47	0.47
2:2:167:A:N6	2:2:168:G:O6	2.48	0.47
2:2:600:A:H2'	2:2:601:G:H8	1.80	0.47
2:2:1021:A:H4'	57:2:1885:HOH:O	2.13	0.47
12:G:114:GLU:HG2	12:G:133:GLN:O	2.14	0.47
13:J:35:ARG:HB2	13:J:54:ILE:HD11	1.95	0.47
40:k:21:MET:HE2	40:k:21:MET:HB3	1.83	0.47
41:l:80:VAL:HG23	41:l:81:GLY:H	1.80	0.47
41:l:93:PRO:O	41:l:96:ARG:HG2	2.14	0.47
50:u:73:ALA:O	50:u:77:GLU:HG2	2.14	0.47
1:1:508:A:H5''	57:1:3676:HOH:O	2.13	0.47
1:1:609:A:H2'	1:1:610:C:O4'	2.14	0.47
1:1:2014:A:H2'	1:1:2015:A:C8	2.50	0.47
1:1:2233:U:H2'	1:1:2234:G:C8	2.49	0.47
1:1:2290:G:H2'	1:1:2291:U:C6	2.49	0.47
1:1:2364:C:H2'	1:1:2365:G:O4'	2.14	0.47
1:1:2513:A:C6	1:1:2574:G:C6	3.02	0.47
2:2:338:A:H2'	2:2:339:C:C6	2.49	0.47
2:2:482:A:H2'	2:2:483:C:O4'	2.15	0.47
2:2:1058:G:OP1	37:h:199:LYS:HE3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1326:U:H2'	2:2:1327:C:H6	1.79	0.47
7:B:76:ALA:HB2	7:B:96:TYR:CD1	2.49	0.47
11:F:121:ILE:CD1	11:F:141:ILE:HG22	2.45	0.47
16:M:42:THR:HG22	16:M:93:VAL:HG12	1.96	0.47
17:N:24:MET:HG2	17:N:44:LEU:HD22	1.97	0.47
24:U:14:LEU:HD11	24:U:71:ALA:HB2	1.95	0.47
34:e:54:ASP:O	34:e:58:VAL:HG12	2.14	0.47
36:g:14:VAL:HG12	36:g:209:ALA:HB1	1.97	0.47
37:h:40:ARG:HH21	37:h:57:ILE:HG22	1.80	0.47
37:h:175:LEU:HD21	37:h:201:TRP:CE3	2.50	0.47
37:h:182:ILE:HG22	37:h:203:PHE:HA	1.97	0.47
42:m:13:ARG:HD2	42:m:27:MET:HG2	1.96	0.47
43:n:15:SER:OG	43:n:69:GLY:O	2.23	0.47
50:u:4:ILE:HG12	50:u:21:VAL:HG22	1.97	0.47
1:1:161:A:H3'	1:1:162:U:H5''	1.95	0.47
1:1:752:A:N6	1:1:2609:U:H3	2.12	0.47
1:1:1174:U:O2'	1:1:1176:U:H1'	2.15	0.47
1:1:1486:U:H2'	1:1:1487:U:H6	1.80	0.47
1:1:1790:C:H2'	1:1:1791:A:C8	2.50	0.47
1:1:2455:G:H2'	1:1:2456:C:C6	2.50	0.47
1:1:2547:A:H2'	1:1:2548:U:H6	1.77	0.47
2:2:91:U:C5	57:2:1902:HOH:O	2.63	0.47
2:2:828:U:C4	2:2:859:G:C4	3.03	0.47
2:2:990:C:H2'	2:2:991:U:C6	2.50	0.47
5:5:23:C:H2'	5:5:24:G:C8	2.50	0.47
8:C:15:PHE:H	19:P:12:GLN:NE2	2.13	0.47
14:K:64:ARG:HD3	14:K:102:PRO:O	2.15	0.47
20:Q:62:ILE:HD12	20:Q:76:TYR:OH	2.15	0.47
36:g:20:THR:HA	36:g:39:HIS:CE1	2.50	0.47
36:g:47:VAL:HG23	36:g:48:PRO:HD3	1.96	0.47
38:i:90:LEU:HD23	38:i:94:LEU:HD23	1.97	0.47
40:k:90:MET:HE1	52:w:61:ARG:HD3	1.97	0.47
42:m:96:MET:SD	42:m:130:ALA:HB1	2.55	0.47
44:o:45:ARG:HB3	44:o:69:THR:HG23	1.97	0.47
1:1:366:C:H2'	1:1:367:G:O4'	2.15	0.47
1:1:404:A:H1'	1:1:406:G:N9	2.30	0.47
1:1:2327:A:H2'	1:1:2328:A:H8	1.78	0.47
2:2:718:A:H5''	2:2:719:C:OP2	2.15	0.47
2:2:1193:G:O6	37:h:3:GLN:NE2	2.48	0.47
2:2:1309:G:C6	2:2:1329:A:N1	2.83	0.47
2:2:1401:G:H2'	2:2:1402:4OC:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:51:G:N2	3:3:53:A:H62	2.13	0.47
8:C:142:VAL:HG13	8:C:143:PRO:HD2	1.97	0.47
12:G:3:VAL:CG2	12:G:36:ALA:HB1	2.45	0.47
28:Y:57:LEU:HA	28:Y:57:LEU:HD23	1.67	0.47
39:j:78:ASN:OD1	39:j:79:GLY:N	2.48	0.47
51:v:80:GLU:CD	51:v:82:ALA:H	2.22	0.47
1:1:340:A:H2'	1:1:341:C:O4'	2.14	0.47
1:1:627:A:H5''	15:L:78:ARG:HH11	1.80	0.47
1:1:715:A:H8	1:1:715:A:OP1	1.98	0.47
1:1:813:U:H2'	1:1:814:C:H6	1.80	0.47
1:1:1387:A:C6	1:1:1401:G:N1	2.83	0.47
2:2:593:U:N3	2:2:594:U:C4	2.83	0.47
2:2:720:C:O3'	52:w:52:GLN:NE2	2.48	0.47
2:2:838:G:C4	2:2:849:G:N2	2.83	0.47
2:2:938:A:N6	2:2:939:G:C6	2.83	0.47
2:2:1035:A:H2'	2:2:1036:A:C8	2.49	0.47
2:2:1140:C:O2'	2:2:1141:C:H6	1.98	0.47
2:2:1206:G:C4	2:2:1207:2MG:C8	3.03	0.47
3:3:119:A:H3'	3:3:120:U:H6	1.79	0.47
5:5:75:C:H2'	5:5:76:A:O4'	2.15	0.47
12:G:51:ARG:O	12:G:55:GLU:HG3	2.14	0.47
17:N:35:LYS:HB2	17:N:112:TYR:CE1	2.50	0.47
36:g:111:ILE:CD1	36:g:148:LEU:HD23	2.45	0.47
38:i:117:LEU:HD23	38:i:154:ARG:HH21	1.80	0.47
1:1:1333:G:C2	1:1:1334:G:C8	3.03	0.46
1:1:2391:G:H5''	34:e:32:ILE:HD12	1.97	0.46
1:1:2400:G:N2	1:1:2417:C:C2	2.83	0.46
2:2:263:A:H2'	2:2:264:C:C6	2.50	0.46
2:2:414:A:P	2:2:428:G:H22	2.38	0.46
2:2:838:G:C5	2:2:849:G:N1	2.84	0.46
2:2:1174:G:H2'	2:2:1175:G:H5'	1.97	0.46
6:6:16:MET:HE1	6:6:118:TRP:HZ2	1.79	0.46
7:B:41:GLY:O	7:B:43:ARG:NH1	2.48	0.46
20:Q:49:ASP:HA	20:Q:52:GLN:HB2	1.98	0.46
30:a:56:ARG:HD3	53:x:65:GLU:OE2	2.15	0.46
46:q:54:ARG:HA	46:q:64:THR:HA	1.96	0.46
47:r:56:LEU:O	47:r:60:VAL:HG12	2.14	0.46
1:1:1171:G:N2	1:1:1178:C:C2	2.83	0.46
1:1:1444:G:H2'	1:1:1445:G:H8	1.80	0.46
1:1:1486:U:H2'	1:1:1487:U:C6	2.50	0.46
1:1:1599:U:C2	1:1:1600:C:C5	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2862:G:H2'	1:1:2863:C:C6	2.50	0.46
2:2:501:C:H2'	2:2:502:A:C8	2.50	0.46
2:2:537:G:OP1	46:q:110:ARG:NH2	2.47	0.46
2:2:674:G:H2'	2:2:675:A:C8	2.45	0.46
10:E:71:ARG:O	10:E:81:GLN:HG3	2.15	0.46
10:E:139:PRO:HB2	30:a:32:LEU:HD11	1.96	0.46
13:J:125:TYR:OH	13:J:132:HIS:NE2	2.41	0.46
16:M:19:GLY:O	16:M:38:ARG:NH2	2.48	0.46
22:S:48:LYS:O	22:S:52:GLU:HG3	2.15	0.46
39:j:56:VAL:O	39:j:60:ILE:HG12	2.15	0.46
39:j:156:LYS:NZ	42:m:73:GLU:OE2	2.48	0.46
1:1:1085:A:N7	1:1:1086:A:N6	2.63	0.46
2:2:77:A:H2'	2:2:78:A:C8	2.50	0.46
2:2:269:C:H2'	2:2:270:A:H8	1.78	0.46
2:2:721:G:H4'	2:2:722:G:O4'	2.15	0.46
2:2:1287:A:H2'	2:2:1288:A:C8	2.49	0.46
9:D:127:GLU:OE1	9:D:127:GLU:N	2.39	0.46
17:N:73:ASN:HA	17:N:76:VAL:HG12	1.97	0.46
20:Q:99:ALA:HB2	20:Q:106:PHE:CE1	2.50	0.46
36:g:76:ALA:O	36:g:80:VAL:HG12	2.15	0.46
39:j:19:ASN:N	39:j:19:ASN:OD1	2.47	0.46
48:s:27:LEU:HD23	48:s:48:LEU:HB2	1.97	0.46
1:1:1572:A:H2'	1:1:1573:G:H8	1.79	0.46
1:1:1722:A:N6	1:1:1738:G:H1'	2.31	0.46
1:1:1789:A:H2'	1:1:1790:C:O4'	2.16	0.46
1:1:2388:A:H5'	1:1:2389:G:OP2	2.14	0.46
1:1:2505:G:O2'	1:1:2506:U:O2	2.33	0.46
1:1:2861:U:C2	1:1:2862:G:C8	3.04	0.46
2:2:838:G:C6	2:2:849:G:C6	3.03	0.46
36:g:128:LYS:O	36:g:128:LYS:HD2	2.16	0.46
36:g:191:SER:OG	36:g:192:ASP:N	2.49	0.46
42:m:41:LYS:O	42:m:44:GLY:N	2.49	0.46
43:n:10:GLY:C	43:n:11:ARG:HD3	2.41	0.46
49:t:2:SER:OG	49:t:3:LEU:N	2.47	0.46
1:1:569:U:O2'	1:1:983:A:N1	2.38	0.46
1:1:1024:G:C6	1:1:1025:G:C6	3.03	0.46
1:1:2373:G:H2'	1:1:2374:C:H6	1.80	0.46
2:2:161:A:H2'	2:2:162:A:C8	2.50	0.46
2:2:673:A:H2'	2:2:674:G:H8	1.75	0.46
2:2:818:G:O2'	2:2:819:A:H5'	2.15	0.46
2:2:1208:C:H2'	2:2:1209:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:8:LYS:HB2	8:C:201:LEU:HD11	1.98	0.46
1:1:57:C:H2'	1:1:58:G:O4'	2.16	0.46
1:1:357:C:H2'	1:1:358:U:C6	2.51	0.46
1:1:500:G:N1	1:1:503:A:OP2	2.44	0.46
1:1:592:A:C2	34:e:4:ILE:HD11	2.50	0.46
1:1:1196:C:C2	1:1:1197:G:C8	3.04	0.46
1:1:1370:C:H2'	1:1:1371:G:O4'	2.15	0.46
1:1:2247:A:H2'	1:1:2248:C:H6	1.80	0.46
1:1:2287:A:C5	1:1:2289:G:C8	3.04	0.46
1:1:2302:U:C2	1:1:2303:G:C8	3.03	0.46
1:1:2352:A:N1	26:W:34:GLY:HA3	2.29	0.46
1:1:2725:A:C4	1:1:2727:A:C8	3.03	0.46
2:2:151:A:C4	2:2:152:A:C8	3.03	0.46
2:2:676:A:H2'	2:2:677:U:C6	2.51	0.46
2:2:845:A:C6	57:2:1817:HOH:O	2.56	0.46
2:2:1121:U:H2'	2:2:1122:U:H6	1.79	0.46
2:2:1383:C:O2'	2:2:1384:C:OP1	2.33	0.46
12:G:124:THR:OG1	12:G:125:THR:N	2.48	0.46
19:P:54:GLY:C	19:P:56:HIS:N	2.71	0.46
20:Q:86:ALA:O	20:Q:87:SER:OG	2.30	0.46
46:q:81:LEU:HB3	46:q:98:VAL:HG22	1.98	0.46
51:v:60:GLU:O	51:v:76:VAL:HG22	2.16	0.46
52:w:13:PHE:O	52:w:16:GLU:HG2	2.14	0.46
1:1:6:A:N3	13:J:135:GLN:NE2	2.60	0.46
1:1:493:G:H2'	1:1:494:G:O4'	2.15	0.46
1:1:528:A:C2	1:1:2043:C:H4'	2.50	0.46
1:1:581:C:H2'	1:1:582:A:C8	2.51	0.46
1:1:1172:C:H2'	1:1:1173:U:O4'	2.16	0.46
1:1:1733:G:H2'	1:1:1734:G:H8	1.81	0.46
1:1:2070:A:H2'	1:1:2071:A:H8	1.79	0.46
1:1:2537:U:H2'	1:1:2538:C:C6	2.51	0.46
1:1:2545:G:H2'	1:1:2546:U:O4'	2.15	0.46
2:2:17:U:H2'	2:2:18:C:C6	2.51	0.46
2:2:572:A:N6	57:2:1808:HOH:O	2.26	0.46
7:B:145:GLU:HG2	7:B:151:GLY:C	2.41	0.46
11:F:159:GLY:O	11:F:163:ARG:NH1	2.40	0.46
12:G:41:LYS:HE2	12:G:41:LYS:HB3	1.74	0.46
27:X:31:PRO:HG2	27:X:33:LEU:HD23	1.97	0.46
36:g:57:LEU:HD12	36:g:57:LEU:HA	1.65	0.46
37:h:70:THR:C	37:h:106:VAL:HG12	2.41	0.46
1:1:1083:U:O2	1:1:1085:A:H8	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1103:A:H3'	1:1:1104:C:C6	2.50	0.46
1:1:1321:A:C4	1:1:1322:A:C8	3.04	0.46
1:1:2649:C:H2'	1:1:2650:U:H6	1.81	0.46
2:2:1005:A:C2	2:2:1006:G:H1'	2.51	0.46
12:G:78:VAL:HG13	12:G:144:VAL:HG23	1.98	0.46
12:G:90:LEU:HB2	12:G:123:ARG:O	2.16	0.46
14:K:76:VAL:HG22	19:P:73:VAL:CG2	2.46	0.46
15:L:19:LEU:CD2	15:L:27:LEU:HD23	2.42	0.46
28:Y:16:THR:O	28:Y:20:ASN:ND2	2.48	0.46
30:a:37:CYS:H	30:a:40:CYS:HG	1.62	0.46
39:j:111:MET:HG3	39:j:140:THR:CG2	2.45	0.46
52:w:11:CYS:SG	52:w:12:ARG:N	2.89	0.46
55:z:58:LYS:O	55:z:62:ARG:HG2	2.16	0.46
1:1:24:G:H2'	1:1:25:U:H6	1.81	0.46
1:1:63:A:H2	23:T:70:HIS:CE1	2.33	0.46
1:1:1079:C:H3'	1:1:1080:A:C8	2.51	0.46
1:1:1198:U:C2	1:1:1199:U:C5	3.03	0.46
1:1:1385:A:O2'	1:1:1396:U:O2	2.33	0.46
1:1:1857:G:HO2'	1:1:1858:A:P	2.39	0.46
1:1:2073:C:H5''	7:B:228:VAL:HG22	1.97	0.46
1:1:2291:U:C2	1:1:2292:U:C5	3.04	0.46
1:1:2530:A:N7	11:F:172:LYS:NZ	2.53	0.46
1:1:2591:C:H2'	1:1:2592:G:H8	1.79	0.46
1:1:2818:U:OP2	17:N:42:LYS:NZ	2.39	0.46
2:2:84:U:H2'	2:2:86:G:N2	2.31	0.46
2:2:144:G:C6	2:2:179:A:C6	3.04	0.46
2:2:649:A:H2'	2:2:650:G:O4'	2.16	0.46
2:2:1206:G:C6	2:2:1207:2MG:C5	3.04	0.46
5:5:66:C:H2'	5:5:67:G:H8	1.80	0.46
7:B:212:ARG:HA	7:B:212:ARG:HD2	1.59	0.46
9:D:12:LEU:HD12	9:D:12:LEU:HA	1.77	0.46
27:X:6:GLN:O	27:X:71:LEU:HD21	2.15	0.46
35:f:19:ARG:O	35:f:22:VAL:HG12	2.15	0.46
37:h:138:VAL:HG23	37:h:149:ILE:HG23	1.97	0.46
1:1:242:G:H1'	1:1:243:U:OP2	2.16	0.46
1:1:834:G:H5'	34:e:57:LEU:HD11	1.98	0.46
1:1:1562:U:H2'	1:1:1563:U:O4'	2.16	0.46
1:1:1888:G:N7	57:1:3337:HOH:O	2.35	0.46
1:1:2408:U:H2'	1:1:2409:G:C8	2.51	0.46
1:1:2756:U:H1'	1:1:2757:A:H5''	1.97	0.46
2:2:109:A:C6	2:2:326:G:C6	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:245:U:H2'	2:2:246:A:H5''	1.98	0.46
2:2:468:A:H3'	2:2:469:C:H6	1.81	0.46
2:2:1017:U:O2'	2:2:1018:G:H8	1.99	0.46
9:D:192:ALA:O	9:D:196:VAL:HG23	2.16	0.46
40:k:5:GLU:N	40:k:90:MET:O	2.38	0.46
46:q:56:ARG:HB2	46:q:62:GLU:HG2	1.97	0.46
1:1:659:G:H21	9:D:30:GLN:CD	2.24	0.45
1:1:1906:G:C2	1:1:1907:G:C8	3.04	0.45
1:1:2051:A:H8	1:1:2051:A:OP2	1.98	0.45
1:1:2532:G:N2	1:1:2663:G:O2'	2.49	0.45
1:1:2537:U:H2'	1:1:2538:C:H6	1.81	0.45
2:2:1118:U:H1'	2:2:1179:A:C5	2.51	0.45
2:2:1217:C:P	48:s:9:ARG:HH21	2.39	0.45
2:2:1246:A:N1	2:2:1292:G:C6	2.84	0.45
23:T:1:MET:SD	23:T:1:MET:N	2.74	0.45
25:V:13:GLY:O	25:V:17:SER:OG	2.25	0.45
26:W:33:ALA:N	26:W:64:ASP:OD1	2.49	0.45
41:l:80:VAL:HG21	41:l:85:TYR:CZ	2.51	0.45
1:1:454:A:H4'	1:1:455:C:OP2	2.16	0.45
1:1:581:C:H2'	1:1:582:A:H8	1.81	0.45
1:1:2314:A:H2'	1:1:2315:G:H8	1.82	0.45
2:2:178:C:H2'	2:2:179:A:H8	1.81	0.45
2:2:265:G:N2	2:2:267:C:H5'	2.31	0.45
2:2:496:A:H2'	2:2:496:A:N3	2.31	0.45
2:2:1026:G:H2'	2:2:1026:G:N3	2.31	0.45
2:2:1039:G:H2'	2:2:1040:U:H6	1.81	0.45
12:G:75:LEU:HD23	12:G:75:LEU:H	1.81	0.45
16:M:21:ALA:HB2	16:M:97:GLN:HB2	1.97	0.45
17:N:12:ARG:O	17:N:17:ARG:NH2	2.48	0.45
21:R:25:LEU:HD12	21:R:94:THR:HG21	1.98	0.45
45:p:79:ILE:HG23	45:p:105:PHE:HE1	1.80	0.45
1:1:2650:U:H2'	1:1:2651:C:H6	1.80	0.45
2:2:121:U:C1'	57:2:1893:HOH:O	2.52	0.45
2:2:586:C:OP1	51:v:36:LYS:NZ	2.49	0.45
2:2:1140:C:HO2'	2:2:1141:C:H6	1.62	0.45
7:B:258:ARG:NH2	7:B:264:ASP:OD2	2.33	0.45
8:C:156:PHE:CD1	13:J:81:ILE:HD13	2.50	0.45
13:J:36:LEU:HD11	13:J:122:LEU:HB2	1.98	0.45
15:L:84:LYS:HB2	15:L:84:LYS:HE3	1.64	0.45
23:T:8:LEU:HD13	28:Y:22:LEU:HB3	1.98	0.45
43:n:81:HIS:HE1	43:n:85:ARG:HH21	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:q:79:VAL:O	46:q:103:ASP:HB2	2.16	0.45
47:r:44:LYS:HE2	47:r:44:LYS:HB3	1.81	0.45
1:1:10:A:C2	1:1:2800:A:C4	3.04	0.45
1:1:368:A:C5'	57:1:3731:HOH:O	2.55	0.45
1:1:1263:U:O2'	31:b:8:PRO:HD2	2.16	0.45
1:1:1386:C:H2'	1:1:1387:A:C8	2.51	0.45
1:1:1645:G:H5''	1:1:1646:C:H5'	1.99	0.45
1:1:2024:G:H2'	1:1:2025:C:O4'	2.16	0.45
1:1:2801:G:H2'	1:1:2802:G:C8	2.50	0.45
2:2:414:A:OP2	2:2:428:G:N2	2.48	0.45
7:B:7:LYS:O	7:B:9:THR:N	2.45	0.45
22:S:19:LEU:HD23	22:S:19:LEU:HA	1.71	0.45
24:U:7:ARG:O	24:U:25:VAL:HG13	2.17	0.45
30:a:55:GLY:O	30:a:59:ARG:HG2	2.17	0.45
46:q:99:ARG:NH1	46:q:105:SER:O	2.49	0.45
51:v:80:GLU:OE2	51:v:82:ALA:N	2.48	0.45
54:y:79:LEU:HA	54:y:79:LEU:HD23	1.70	0.45
1:1:372:G:H1'	1:1:373:U:H5	1.82	0.45
1:1:659:G:H4'	9:D:95:LYS:HD3	1.99	0.45
1:1:1039:A:H2'	1:1:1040:A:O4'	2.16	0.45
1:1:1095:A:H3'	1:1:1096:A:C8	2.52	0.45
1:1:2572:A:H5''	1:1:2574:G:H4'	1.97	0.45
2:2:76:G:H22	2:2:93:U:H3	1.62	0.45
2:2:323:U:H2'	2:2:324:G:O4'	2.17	0.45
2:2:501:C:H2'	2:2:502:A:H8	1.82	0.45
24:U:41:LEU:HD23	24:U:41:LEU:HA	1.78	0.45
43:n:116:VAL:HG11	44:o:62:ARG:HG3	1.97	0.45
50:u:54:LEU:O	50:u:57:ILE:HG22	2.17	0.45
52:w:21:ILE:CG2	52:w:54:GLN:HB3	2.45	0.45
1:1:271:G:O2'	1:1:272:A:H5''	2.17	0.45
1:1:704:G:C2'	1:1:726:G:H22	2.27	0.45
1:1:704:G:C2	1:1:726:G:C2	3.04	0.45
1:1:863:A:O2'	3:3:100:G:N3	2.44	0.45
1:1:1199:U:H2'	1:1:1200:C:C6	2.52	0.45
1:1:1315:C:C2	1:1:1338:G:N2	2.84	0.45
1:1:2414:G:C2	1:1:2415:G:C8	3.05	0.45
1:1:2896:C:H2'	1:1:2897:U:H6	1.80	0.45
2:2:113:G:N3	2:2:353:A:O2'	2.50	0.45
7:B:222:GLY:HA2	7:B:225:MET:HE3	1.98	0.45
30:a:46:GLY:O	30:a:50:ASP:CB	2.63	0.45
44:o:40:ILE:HB	44:o:73:LEU:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:s:6:MET:SD	48:s:9:ARG:NH1	2.90	0.45
49:t:22:THR:HA	49:t:27:VAL:HG11	1.98	0.45
1:1:62:U:O2'	1:1:63:A:H8	2.00	0.45
1:1:181:A:H2'	1:1:182:A:H8	1.82	0.45
1:1:528:A:C8	1:1:528:A:C3'	3.00	0.45
1:1:1159:U:C2	1:1:1160:G:C8	3.04	0.45
1:1:2376:A:N3	18:O:111:ARG:NH1	2.65	0.45
2:2:174:A:C5	2:2:175:C:C5	3.05	0.45
2:2:628:G:H2'	2:2:629:A:H8	1.80	0.45
2:2:666:G:H5'	2:2:726:C:H1'	1.98	0.45
2:2:952:U:H4'	2:2:964:A:H61	1.81	0.45
2:2:1034:G:N3	2:2:1034:G:H2'	2.31	0.45
2:2:1039:G:H2'	2:2:1040:U:C6	2.52	0.45
2:2:1191:A:OP1	37:h:3:GLN:HB3	2.17	0.45
2:2:1326:U:H2'	2:2:1327:C:C6	2.51	0.45
21:R:2:TYR:CD1	21:R:13:ARG:HD3	2.52	0.45
21:R:15:SER:O	21:R:18:GLN:HB2	2.16	0.45
29:Z:16:ARG:HA	29:Z:16:ARG:HD3	1.84	0.45
32:c:8:LYS:HA	32:c:24:THR:HA	1.97	0.45
36:g:61:ALA:HB3	36:g:224:GLY:HA3	1.97	0.45
37:h:130:PHE:CE1	37:h:157:LEU:HD23	2.52	0.45
49:t:17:ARG:HH12	49:t:18:ASP:HB3	1.81	0.45
53:x:49:ILE:O	53:x:60:VAL:HG12	2.17	0.45
55:z:55:ARG:O	55:z:59:LYS:HG2	2.17	0.45
1:1:613:A:H5''	1:1:614:A:N7	2.32	0.45
1:1:632:A:H2'	1:1:633:A:C8	2.51	0.45
1:1:640:C:H2'	1:1:641:U:C6	2.52	0.45
1:1:645:C:O2'	1:1:646:U:H5'	2.16	0.45
1:1:1112:G:H2'	1:1:1113:U:C6	2.50	0.45
1:1:1198:U:H2'	1:1:1199:U:C6	2.51	0.45
1:1:1470:A:H2'	1:1:1471:G:O4'	2.16	0.45
1:1:1627:G:C2	1:1:1628:G:C8	3.05	0.45
6:6:186:ARG:HE	6:6:186:ARG:HB2	1.44	0.45
7:B:13:ARG:HD2	7:B:13:ARG:HA	1.79	0.45
21:R:76:LYS:HD2	21:R:85:LYS:HE3	1.99	0.45
28:Y:17:GLU:HA	28:Y:20:ASN:HD22	1.81	0.45
36:g:43:LEU:HA	36:g:46:THR:HG22	1.98	0.45
39:j:149:SER:H	39:j:152:MET:HE2	1.82	0.45
54:y:25:ARG:HD2	54:y:29:ARG:NH2	2.32	0.45
1:1:34:U:O5'	57:1:3303:HOH:O	2.21	0.45
1:1:1028:A:N6	1:1:1125:G:H2'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1075:C:C4	1:1:1076:C:N3	2.85	0.45
1:1:1316:U:H2'	1:1:1317:G:H8	1.82	0.45
1:1:1794:A:H2'	1:1:1795:C:H6	1.82	0.45
2:2:107:G:N1	54:y:6:SER:OG	2.43	0.45
2:2:222:C:H2'	2:2:223:A:H8	1.82	0.45
2:2:297:G:N2	2:2:300:A:OP2	2.45	0.45
2:2:1299:A:H5'	57:2:1882:HOH:O	2.16	0.45
11:F:124:GLU:O	11:F:126:PRO:HD3	2.16	0.45
22:S:29:VAL:HB	22:S:55:ILE:HD11	1.99	0.45
36:g:50:PHE:O	36:g:54:LEU:HD13	2.16	0.45
44:o:32:THR:HG23	44:o:33:GLY:H	1.81	0.45
48:s:6:MET:O	48:s:10:GLU:HG2	2.17	0.45
51:v:44:LEU:HA	51:v:44:LEU:HD12	1.64	0.45
51:v:53:CYS:HA	51:v:81:LYS:NZ	2.31	0.45
1:1:217:A:H2'	1:1:218:A:C8	2.52	0.45
1:1:578:G:OP1	1:1:1255:U:O2'	2.31	0.45
1:1:587:C:O2'	15:L:19:LEU:HD12	2.17	0.45
1:1:1069:A:N3	1:1:1096:A:H5'	2.31	0.45
1:1:1073:A:H2'	1:1:1074:G:C8	2.52	0.45
1:1:1114:C:H2'	1:1:1115:G:H8	1.82	0.45
1:1:1343:G:C2	1:1:1344:U:C4	3.05	0.45
1:1:1914:C:O2'	57:1:3301:HOH:O	2.21	0.45
1:1:2323:G:H2'	1:1:2324:U:O4'	2.17	0.45
2:2:648:A:H2'	2:2:649:A:C8	2.53	0.45
3:3:6:G:O2'	3:3:7:G:H5'	2.18	0.45
5:5:68:U:C6	57:5:103:HOH:O	2.54	0.45
19:P:14:LYS:HD2	19:P:77:HIS:HA	1.99	0.45
28:Y:46:VAL:O	28:Y:50:VAL:HG12	2.17	0.45
36:g:23:TRP:HA	36:g:189:THR:O	2.16	0.45
38:i:170:TRP:O	38:i:183:LYS:HB3	2.17	0.45
44:o:9:ARG:HG3	44:o:73:LEU:HD13	1.98	0.45
48:s:83:LYS:HD3	48:s:83:LYS:HA	1.65	0.45
55:z:20:LYS:HE2	55:z:20:LYS:HB3	1.59	0.45
1:1:375:G:O6	1:1:400:G:N2	2.49	0.44
1:1:1240:U:O2'	1:1:1241:A:O5'	2.34	0.44
1:1:2236:U:H2'	1:1:2237:G:O4'	2.17	0.44
1:1:2480:C:H2'	1:1:2481:G:O4'	2.17	0.44
1:1:2516:A:C6	1:1:2569:G:C2	3.05	0.44
1:1:2519:U:C5	1:1:2541:A:C6	3.06	0.44
2:2:71:A:C6	2:2:72:A:C8	3.05	0.44
2:2:836:G:C6	2:2:851:G:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1316:G:N2	2:2:1318:A:H3'	2.32	0.44
9:D:84:THR:HG23	9:D:85:PHE:N	2.32	0.44
11:F:76:VAL:O	11:F:80:THR:HG22	2.18	0.44
11:F:84:THR:HG22	11:F:134:LYS:HG2	1.97	0.44
15:L:85:VAL:HG22	15:L:86:GLU:H	1.81	0.44
16:M:135:VAL:HG13	25:V:57:TYR:CD2	2.52	0.44
24:U:25:VAL:HA	24:U:36:VAL:HG12	1.99	0.44
36:g:133:GLU:HA	36:g:136:MET:HG2	1.99	0.44
37:h:19:ASN:OD1	37:h:40:ARG:NH1	2.50	0.44
42:m:5:ASP:OD2	42:m:81:PRO:HD3	2.16	0.44
49:t:3:LEU:HA	49:t:3:LEU:HD12	1.76	0.44
1:1:367:G:C6	1:1:368:A:C5	3.06	0.44
1:1:876:C:H2'	1:1:877:A:O4'	2.17	0.44
1:1:886:A:N3	1:1:891:G:N2	2.64	0.44
1:1:981:A:N1	1:1:2027:G:O2'	2.43	0.44
1:1:1819:A:H5''	7:B:160:THR:HG21	1.99	0.44
1:1:2322:A:N6	1:1:2333:A:H62	2.16	0.44
1:1:2847:U:H2'	1:1:2848:G:O4'	2.17	0.44
2:2:482:A:H8	2:2:482:A:O5'	2.00	0.44
2:2:492:C:H2'	2:2:493:A:C8	2.51	0.44
2:2:622:A:C8	2:2:623:C:C6	3.06	0.44
9:D:23:PHE:HA	9:D:107:SER:OG	2.17	0.44
19:P:8:LEU:O	19:P:11:GLU:HG2	2.16	0.44
23:T:6:ARG:HA	23:T:6:ARG:HD2	1.56	0.44
37:h:112:ASP:O	37:h:116:VAL:HG12	2.18	0.44
37:h:175:LEU:HD21	37:h:201:TRP:CZ3	2.52	0.44
50:u:76:LYS:HD2	50:u:76:LYS:HA	1.70	0.44
52:w:34:THR:HG23	52:w:36:SER:N	2.32	0.44
1:1:634:C:O5'	1:1:634:C:H6	2.00	0.44
1:1:1378:A:O2'	1:1:1379:U:OP2	2.32	0.44
2:2:68:G:N7	2:2:69:G:C8	2.86	0.44
2:2:74:A:O2'	2:2:75:G:H8	2.00	0.44
2:2:270:A:H2'	2:2:271:C:C6	2.52	0.44
2:2:352:C:O2'	2:2:354:G:OP1	2.23	0.44
2:2:811:C:O2'	2:2:901:A:N1	2.51	0.44
2:2:921:U:O2	39:j:24:THR:OG1	2.36	0.44
2:2:963:G:C2	2:2:964:A:C8	3.05	0.44
2:2:1107:C:C4	2:2:1108:G:C8	3.05	0.44
2:2:1141:C:O2'	2:2:1142:G:H8	2.00	0.44
7:B:80:ARG:NE	7:B:82:GLU:OE2	2.49	0.44
20:Q:44:GLN:NE2	21:R:77:PHE:HB3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:V:60:VAL:C	25:V:61:LEU:HD12	2.42	0.44
36:g:132:LYS:HD2	36:g:133:GLU:N	2.32	0.44
36:g:188:ASP:C	36:g:190:ASN:H	2.24	0.44
43:n:7:TYR:CG	43:n:8:GLY:N	2.85	0.44
44:o:35:GLN:HG2	44:o:77:VAL:HB	1.99	0.44
49:t:39:LEU:HD23	49:t:43:PHE:HE2	1.81	0.44
1:1:3:U:H2'	1:1:4:U:H6	1.81	0.44
1:1:919:U:H2'	1:1:920:A:O4'	2.18	0.44
1:1:1048:A:H2'	1:1:1048:A:N3	2.32	0.44
1:1:1679:A:H2'	1:1:1680:U:H6	1.82	0.44
1:1:2053:G:H5'	8:C:150:GLN:H	1.81	0.44
1:1:2273:A:H2'	1:1:2274:A:C8	2.53	0.44
1:1:2335:A:N7	1:1:2337:G:C5	2.85	0.44
2:2:73:C:C2'	2:2:74:A:H5'	2.47	0.44
2:2:105:G:H2'	2:2:106:C:C6	2.53	0.44
2:2:339:C:H2'	2:2:340:U:H6	1.83	0.44
3:3:1:U:H2'	3:3:2:G:H8	1.81	0.44
3:3:77:U:O2'	3:3:78:A:OP2	2.35	0.44
8:C:142:VAL:HG12	8:C:144:GLY:H	1.82	0.44
12:G:51:ARG:HA	12:G:51:ARG:HD2	1.74	0.44
44:o:7:ARG:NH1	44:o:73:LEU:HD21	2.33	0.44
44:o:24:GLU:CD	44:o:24:GLU:C	2.86	0.44
1:1:227:A:HO2'	1:1:228:C:P	2.39	0.44
1:1:483:A:H4'	24:U:46:GLN:O	2.17	0.44
1:1:600:G:N2	1:1:605:G:O3'	2.50	0.44
1:1:910:A:H2	1:1:2264:C:O2	2.00	0.44
1:1:1093:G:H22	1:1:1097:U:H5'	1.82	0.44
1:1:1199:U:H2'	1:1:1200:C:H6	1.83	0.44
1:1:1779:U:C2	1:1:1783:A:N7	2.86	0.44
1:1:2327:A:C5	1:1:2388:A:N1	2.86	0.44
2:2:208:U:H2'	2:2:210:C:N3	2.32	0.44
2:2:247:G:C6	2:2:278:G:C2	3.04	0.44
2:2:664:G:H22	2:2:741:G:H1	1.66	0.44
5:5:72:G:H1'	5:5:73:A:H5'	2.00	0.44
7:B:30:PHE:CE2	7:B:32:PRO:HD2	2.53	0.44
9:D:105:LEU:HD23	9:D:105:LEU:HA	1.74	0.44
10:E:159:THR:O	10:E:159:THR:OG1	2.28	0.44
14:K:64:ARG:NE	19:P:68:GLU:OE1	2.48	0.44
24:U:100:SER:O	24:U:100:SER:OG	2.31	0.44
39:j:23:LYS:HE3	39:j:30:ILE:HD11	1.99	0.44
39:j:82:GLN:OE1	39:j:149:SER:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:o:21:ALA:HB1	44:o:92:LEU:HD12	2.00	0.44
1:1:363:G:H2'	1:1:364:C:H6	1.82	0.44
1:1:419:U:H2'	1:1:420:C:H6	1.83	0.44
1:1:752:A:H3'	33:d:1:MET:SD	2.58	0.44
1:1:911:A:H5''	1:1:912:C:H5''	2.00	0.44
1:1:980:A:N7	1:1:1136:G:H5'	2.32	0.44
1:1:1102:C:H2'	1:1:1103:A:C8	2.53	0.44
1:1:1675:C:C4	8:C:134:HIS:CE1	3.05	0.44
1:1:1831:G:C6	1:1:1832:C:N4	2.85	0.44
1:1:2803:G:H2'	1:1:2804:U:H6	1.83	0.44
1:1:2867:G:O2'	1:1:2868:A:P	2.76	0.44
2:2:71:A:C6	2:2:100:G:N7	2.86	0.44
2:2:464:U:O2'	2:2:466:A:N7	2.50	0.44
2:2:838:G:H2'	2:2:839:C:H6	1.83	0.44
6:6:73:THR:HA	6:6:112:GLU:HA	1.98	0.44
8:C:91:THR:HG23	8:C:94:GLN:HB2	2.00	0.44
14:K:64:ARG:O	14:K:82:ASN:HA	2.17	0.44
20:Q:83:LEU:HD23	20:Q:83:LEU:HA	1.77	0.44
26:W:38:VAL:HG22	26:W:59:LEU:HB2	1.99	0.44
37:h:156:ARG:NH1	37:h:161:GLU:HA	2.33	0.44
38:i:65:TYR:CG	38:i:94:LEU:HD12	2.53	0.44
39:j:149:SER:N	39:j:152:MET:HE2	2.33	0.44
46:q:99:ARG:HG2	46:q:104:CYS:SG	2.58	0.44
1:1:1797:G:C6	1:1:1798:U:C4	3.05	0.44
1:1:2271:G:OP1	26:W:18:ALA:HB1	2.17	0.44
1:1:2331:G:N2	1:1:2385:C:C2	2.86	0.44
1:1:2478:A:H5'	35:f:32:LYS:HE2	1.99	0.44
1:1:2846:G:H2'	1:1:2847:U:C6	2.53	0.44
2:2:6:G:H4'	2:2:298:A:H4'	2.00	0.44
2:2:884:U:H4'	2:2:885:G:H5''	2.00	0.44
2:2:1119:C:H2'	2:2:1120:C:H6	1.83	0.44
3:3:18:G:H2'	3:3:19:C:C6	2.52	0.44
10:E:42:GLU:CG	10:E:148:ARG:HH12	2.31	0.44
12:G:51:ARG:O	12:G:53:GLU:N	2.51	0.44
12:G:97:ARG:HH21	12:G:101:ASP:N	2.16	0.44
17:N:24:MET:HE3	17:N:24:MET:HB2	1.77	0.44
17:N:92:GLY:HA2	17:N:94:TYR:CZ	2.52	0.44
23:T:26:LYS:HE2	23:T:26:LYS:HB2	1.83	0.44
37:h:12:LEU:HD12	37:h:12:LEU:HA	1.82	0.44
37:h:184:TYR:CE2	57:h:304:HOH:O	2.56	0.44
44:o:8:ILE:HD13	44:o:100:ILE:HA	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:t:25:THR:HG21	49:t:69:TYR:HE2	1.83	0.44
55:z:55:ARG:HD2	55:z:55:ARG:HA	1.75	0.44
1:1:744:U:H2'	1:1:745:G:O4'	2.18	0.44
1:1:927:A:H2'	1:1:928:A:H8	1.83	0.44
1:1:929:U:H4'	29:Z:38:ARG:NH2	2.33	0.44
1:1:1307:A:H2'	1:1:1308:A:O4'	2.18	0.44
2:2:414:A:C4	2:2:415:A:C8	3.06	0.44
2:2:949:A:C5	2:2:1233:G:C2	3.06	0.44
2:2:1026:G:H5''	2:2:1027:C:OP1	2.18	0.44
2:2:1177:G:H2'	2:2:1178:G:O4'	2.18	0.44
8:C:149:ASN:C	8:C:151:THR:H	2.26	0.44
12:G:3:VAL:HG21	12:G:36:ALA:HB1	1.99	0.44
37:h:24:ALA:HB1	37:h:28:GLU:HG2	1.99	0.44
37:h:131:ARG:HD2	37:h:135:LYS:HZ1	1.83	0.44
39:j:20:ARG:NH2	39:j:31:PHE:CD1	2.84	0.44
39:j:41:ASP:OD1	39:j:41:ASP:N	2.51	0.44
41:l:126:ASP:HA	41:l:129:GLU:HG2	1.99	0.44
46:q:80:ILE:HA	46:q:80:ILE:HD13	1.69	0.44
1:1:131:A:H2'	1:1:132:G:C8	2.53	0.44
1:1:289:G:H2'	1:1:290:U:C6	2.53	0.44
1:1:607:U:O2	1:1:608:A:C8	2.71	0.44
1:1:1532:A:N1	1:1:1540:G:C6	2.85	0.44
1:1:1766:G:C6	1:1:1987:A:C6	3.06	0.44
1:1:2478:A:C8	1:1:2529:G:C5	3.06	0.44
1:1:2589:A:N1	1:1:2605:U:H5	2.15	0.44
1:1:2862:G:H2'	1:1:2863:C:H6	1.83	0.44
2:2:313:A:H2'	2:2:314:C:C6	2.53	0.44
2:2:687:A:C2	2:2:704:A:C5	3.06	0.44
2:2:1161:C:H5''	57:2:1917:HOH:O	2.17	0.44
10:E:49:LEU:HD23	10:E:148:ARG:NH1	2.32	0.44
11:F:87:LEU:HB2	11:F:131:ILE:HB	1.99	0.44
19:P:52:ASN:C	19:P:53:ARG:HG2	2.42	0.44
25:V:66:ASP:HB2	25:V:68:LYS:HE2	2.00	0.44
35:f:25:VAL:O	35:f:26:ILE:HD13	2.17	0.44
36:g:16:PHE:HB2	36:g:203:ASN:HD22	1.83	0.44
37:h:79:LYS:HB3	37:h:82:GLU:OE1	2.18	0.44
47:r:76:SER:O	47:r:80:LEU:HD23	2.18	0.44
48:s:64:CYS:SG	48:s:80:SER:N	2.85	0.44
54:y:78:ASN:O	54:y:82:GLN:HG2	2.17	0.44
1:1:138:U:H5''	23:T:1:MET:CE	2.48	0.43
1:1:300:A:OP2	24:U:97:LYS:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:638:G:C5	1:1:651:G:C2	3.06	0.43
1:1:1275:A:OP2	1:1:1646:C:N4	2.47	0.43
1:1:1580:A:C8	1:1:1581:G:C8	3.06	0.43
1:1:1619:G:C2	1:1:1620:G:C8	3.06	0.43
1:1:2545:G:C2	1:1:2546:U:O2	2.71	0.43
1:1:2733:A:C4	1:1:2734:A:C8	3.06	0.43
2:2:784:A:C6	2:2:799:G:N1	2.86	0.43
2:2:1276:G:H2'	2:2:1277:C:O4'	2.18	0.43
8:C:32:ASN:OD1	8:C:52:THR:OG1	2.36	0.43
12:G:24:GLY:O	12:G:28:ASN:ND2	2.51	0.43
31:b:54:VAL:HG23	31:b:55:ILE:HG22	2.00	0.43
36:g:202:GLY:HA3	36:g:213:TYR:OH	2.18	0.43
44:o:7:ARG:HH12	44:o:73:LEU:HD21	1.83	0.43
45:p:18:ASP:OD1	45:p:18:ASP:N	2.50	0.43
45:p:79:ILE:HG23	45:p:105:PHE:CE1	2.53	0.43
46:q:27:CYS:SG	46:q:30:LYS:NZ	2.91	0.43
49:t:38:HIS:ND1	49:t:38:HIS:O	2.50	0.43
54:y:9:LYS:HE2	54:y:13:GLN:NE2	2.31	0.43
1:1:106:C:O2'	1:1:294:A:O2'	2.30	0.43
1:1:365:U:H2'	1:1:366:C:C6	2.53	0.43
1:1:463:G:N2	1:1:466:A:OP2	2.47	0.43
1:1:532:A:H2'	1:1:532:A:N3	2.33	0.43
1:1:988:A:P	29:Z:12:SER:HB3	2.57	0.43
1:1:1857:G:H2'	1:1:1884:G:H22	1.83	0.43
2:2:92:U:H2'	2:2:93:U:C6	2.53	0.43
2:2:224:U:H2'	2:2:225:C:C6	2.53	0.43
2:2:632:U:H5''	2:2:633:G:C8	2.54	0.43
2:2:634:C:H2'	2:2:635:A:H8	1.82	0.43
2:2:1480:A:H2'	2:2:1481:U:O4'	2.18	0.43
5:5:53:G:H1	5:5:61:C:H42	1.65	0.43
6:6:23:ALA:HB2	6:6:46:LEU:HD11	1.99	0.43
9:D:139:LYS:HE2	9:D:139:LYS:HB2	1.79	0.43
9:D:148:ILE:HB	9:D:169:VAL:HA	1.98	0.43
13:J:12:LYS:O	13:J:41:LYS:NZ	2.51	0.43
15:L:95:LEU:HD23	15:L:100:ILE:HD12	2.00	0.43
16:M:36:VAL:HG13	25:V:82:TYR:CD1	2.53	0.43
28:Y:6:LEU:HB3	28:Y:56:LEU:HD12	2.00	0.43
33:d:9:VAL:HG12	33:d:12:ARG:NH1	2.27	0.43
42:m:10:MET:HE1	42:m:36:ILE:HB	1.99	0.43
45:p:123:PRO:HD2	55:z:38:TYR:HD1	1.83	0.43
48:s:41:ARG:NH2	53:x:6:LYS:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:z:60:LEU:O	55:z:64:ASN:ND2	2.51	0.43
1:1:151:C:H2'	1:1:152:A:H8	1.83	0.43
1:1:153:U:H2'	1:1:154:U:H6	1.83	0.43
1:1:173:A:H2'	1:1:174:U:H6	1.84	0.43
1:1:607:U:N3	1:1:608:A:N7	2.65	0.43
1:1:813:U:O2'	1:1:1225:G:H1'	2.18	0.43
1:1:1055:G:H22	1:1:1104:C:N4	2.15	0.43
1:1:1196:C:H2'	1:1:1197:G:H8	1.83	0.43
1:1:1409:U:H2'	1:1:1410:G:H8	1.83	0.43
1:1:1779:U:H5	1:1:1784:A:N7	2.16	0.43
1:1:2728:U:HO2'	1:1:2729:G:C5'	2.28	0.43
2:2:820:U:H4'	2:2:821:G:OP2	2.19	0.43
8:C:5:VAL:HG12	8:C:32:ASN:ND2	2.33	0.43
12:G:80:ILE:HG12	12:G:94:ILE:HD12	2.00	0.43
16:M:53:MET:HG2	16:M:53:MET:H	1.64	0.43
21:R:40:MET:HE2	21:R:40:MET:HB3	1.91	0.43
39:j:22:SER:OG	39:j:23:LYS:N	2.52	0.43
44:o:18:ILE:HD12	44:o:96:VAL:HG23	2.01	0.43
45:p:82:LEU:HD12	45:p:82:LEU:HA	1.78	0.43
48:s:37:SER:O	48:s:41:ARG:HG3	2.18	0.43
50:u:54:LEU:HA	50:u:57:ILE:HG22	2.00	0.43
1:1:139:U:H2'	1:1:140:C:C5	2.52	0.43
1:1:153:U:H2'	1:1:154:U:C6	2.53	0.43
1:1:276:U:O2'	1:1:278:A:N7	2.43	0.43
1:1:607:U:H5	1:1:620:G:C4	2.36	0.43
1:1:886:A:N1	1:1:890:C:N4	2.66	0.43
1:1:1087:G:C6	1:1:1089:A:C2	3.06	0.43
1:1:1196:C:H2'	1:1:1197:G:C8	2.54	0.43
1:1:2350:C:OP2	34:e:45:ARG:NH1	2.51	0.43
1:1:2737:G:C2	1:1:2768:U:C2	3.06	0.43
2:2:83:C:O2'	2:2:86:G:N1	2.49	0.43
2:2:94:G:H4'	2:2:95:C:O5'	2.18	0.43
2:2:173:U:C2	2:2:197:A:N1	2.86	0.43
2:2:212:G:C2	2:2:213:G:C8	3.07	0.43
2:2:996:A:C4	2:2:997:U:C5	3.07	0.43
2:2:1141:C:C2	2:2:1142:G:C8	3.07	0.43
2:2:1169:A:H2'	2:2:1170:A:C8	2.54	0.43
23:T:29:THR:HG22	23:T:86:THR:HA	2.00	0.43
32:c:39:PHE:HE2	32:c:41:PRO:HA	1.83	0.43
36:g:56:GLU:HG3	36:g:198:PHE:CZ	2.54	0.43
36:g:60:ILE:HA	36:g:63:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:i:50:ASP:O	38:i:53:VAL:HG12	2.19	0.43
44:o:57:VAL:O	44:o:57:VAL:HG23	2.19	0.43
46:q:7:LEU:HD23	46:q:7:LEU:HA	1.64	0.43
50:u:9:HIS:O	50:u:16:PHE:N	2.42	0.43
52:w:63:ARG:HB3	52:w:70:TYR:CE2	2.53	0.43
53:x:51:VAL:CG2	53:x:75:ALA:HB2	2.48	0.43
1:1:62:U:O2	1:1:62:U:H2'	2.17	0.43
1:1:1422:G:C6	1:1:1577:C:N3	2.86	0.43
1:1:2640:G:OP1	13:J:96:ARG:NH2	2.50	0.43
1:1:2804:U:H2'	1:1:2805:C:H6	1.84	0.43
2:2:211:G:C6	2:2:212:G:H1'	2.53	0.43
2:2:1001:C:C5	57:2:1881:HOH:O	2.66	0.43
2:2:1043:G:O6	2:2:1044:A:N6	2.52	0.43
9:D:48:THR:C	9:D:50:ALA:N	2.75	0.43
11:F:102:VAL:HG12	11:F:116:GLN:HA	1.99	0.43
12:G:57:LYS:HD3	12:G:57:LYS:C	2.43	0.43
12:G:101:ASP:HA	12:G:104:THR:HG22	2.00	0.43
15:L:92:LEU:HD23	15:L:92:LEU:HA	1.88	0.43
21:R:39:LEU:HD23	21:R:53:PHE:HB3	1.99	0.43
25:V:35:GLU:OE1	25:V:35:GLU:N	2.42	0.43
36:g:42:ASN:HB3	36:g:45:LYS:HB2	2.00	0.43
36:g:130:THR:O	36:g:133:GLU:HG3	2.18	0.43
37:h:83:ASP:OD1	37:h:84:VAL:N	2.51	0.43
39:j:96:MET:HE3	39:j:96:MET:HB2	1.76	0.43
40:k:3:HIS:NE2	40:k:65:GLU:OE2	2.50	0.43
47:r:117:LYS:HD3	47:r:117:LYS:HA	1.78	0.43
1:1:54:G:C6	1:1:117:G:N2	2.86	0.43
1:1:225:C:H2'	1:1:226:A:O4'	2.19	0.43
1:1:811:U:H2'	15:L:21:ARG:HA	2.00	0.43
1:1:1060:U:H4'	1:1:1062:G:H5'	2.01	0.43
1:1:1268:A:H2'	1:1:1269:A:O4'	2.19	0.43
1:1:1357:C:H2'	1:1:1358:G:O4'	2.17	0.43
1:1:1490:A:C8	7:B:98:ASP:HB3	2.53	0.43
1:1:1494:A:H2'	1:1:1495:A:C8	2.54	0.43
1:1:1509:A:H2'	1:1:1510:G:H8	1.83	0.43
1:1:2531:A:C2	1:1:2532:G:C8	3.07	0.43
1:1:2595:G:H1	7:B:239:ASN:ND2	2.17	0.43
1:1:2756:U:H5''	35:f:19:ARG:HG2	2.01	0.43
2:2:149:A:C6	2:2:150:U:C4	3.07	0.43
2:2:455:G:C2	2:2:478:A:C2	3.07	0.43
2:2:493:A:H2'	2:2:494:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:496:A:O2'	2:2:497:G:C8	2.72	0.43
2:2:827:U:C2	2:2:874:G:N2	2.87	0.43
2:2:1372:U:C4	2:2:1373:G:C5	3.07	0.43
2:2:1374:A:C2	2:2:1375:A:C4	3.06	0.43
3:3:8:C:O2'	18:O:40:ILE:HD13	2.19	0.43
3:3:74:U:H3'	3:3:75:G:H8	1.84	0.43
11:F:120:GLY:O	11:F:121:ILE:HD13	2.19	0.43
11:F:133:LEU:HD13	11:F:144:VAL:HG23	2.00	0.43
13:J:88:THR:HG23	13:J:91:GLU:H	1.83	0.43
22:S:13:SER:HB3	22:S:16:LYS:HD2	2.00	0.43
36:g:113:ARG:HH12	36:g:117:LEU:HB2	1.81	0.43
37:h:19:ASN:CG	37:h:40:ARG:HH12	2.26	0.43
37:h:57:ILE:CG1	37:h:64:ILE:HD11	2.48	0.43
39:j:44:GLY:HA2	39:j:74:VAL:HB	1.99	0.43
41:l:39:ALA:O	41:l:43:VAL:HG12	2.18	0.43
47:r:29:ARG:HD2	47:r:63:PHE:CZ	2.53	0.43
1:1:279:A:H2'	1:1:280:U:O4'	2.18	0.43
1:1:419:U:H2'	1:1:420:C:C6	2.54	0.43
1:1:882:G:H22	1:1:895:U:H1'	1.82	0.43
1:1:2295:C:O2'	1:1:2296:U:H5'	2.17	0.43
1:1:2574:G:C2	1:1:2575:C:O2	2.72	0.43
2:2:420:U:O2'	2:2:423:G:O6	2.20	0.43
2:2:1310:G:N1	2:2:1328:C:N3	2.66	0.43
2:2:1439:G:OP1	54:y:33:LYS:NZ	2.47	0.43
6:6:132:GLU:O	6:6:133:LEU:HD23	2.19	0.43
6:6:173:VAL:O	6:6:187:VAL:HB	2.19	0.43
10:E:63:GLN:HA	30:a:6:HIS:ND1	2.34	0.43
12:G:4:ILE:HD11	12:G:47:PHE:CD2	2.54	0.43
12:G:66:ASN:CG	12:G:135:HIS:HB2	2.43	0.43
28:Y:9:LYS:NZ	57:Y:102:HOH:O	2.51	0.43
40:k:53:LYS:HE2	40:k:53:LYS:HB2	1.76	0.43
47:r:16:VAL:HG13	47:r:34:LEU:HD12	2.01	0.43
55:z:57:ALA:O	55:z:60:LEU:HG	2.19	0.43
1:1:131:A:H2'	1:1:132:G:H8	1.81	0.43
1:1:664:G:C5	1:1:665:U:C5	3.07	0.43
1:1:1085:A:H3'	1:1:1086:A:C2	2.53	0.43
1:1:1496:A:H2'	1:1:1498:C:C5	2.54	0.43
1:1:1598:A:C5	1:1:1599:U:C5	3.07	0.43
1:1:1682:G:H2'	1:1:1683:U:C6	2.53	0.43
1:1:1928:A:H2'	1:1:1929:G:O4'	2.19	0.43
1:1:2305:U:H2'	1:1:2306:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2313:C:C2	1:1:2314:A:C8	3.07	0.43
1:1:2723:C:H2'	1:1:2724:U:O4'	2.19	0.43
1:1:2856:A:C6	1:1:2862:G:C6	3.07	0.43
1:1:2895:G:H2'	1:1:2896:C:C6	2.54	0.43
2:2:162:A:H8	2:2:162:A:O5'	2.02	0.43
2:2:1324:A:H2'	2:2:1325:C:O4'	2.19	0.43
12:G:104:THR:HA	12:G:108:VAL:O	2.19	0.43
38:i:198:HIS:HA	38:i:201:VAL:HG12	2.00	0.43
39:j:66:LYS:HD3	39:j:69:ARG:NH1	2.34	0.43
52:w:29:LEU:HD12	52:w:59:ILE:CG1	2.49	0.43
52:w:32:TYR:O	52:w:40:VAL:HG22	2.19	0.43
1:1:1309:G:OP1	33:d:9:VAL:HG22	2.19	0.43
1:1:1583:A:H5'	57:1:3616:HOH:O	2.19	0.43
1:1:2867:G:HO2'	1:1:2868:A:P	2.42	0.43
2:2:515:G:H2'	2:2:516:PSU:O4	2.18	0.43
2:2:563:A:H2	46:q:12:ARG:HH21	1.65	0.43
2:2:602:A:H2'	2:2:603:U:C6	2.54	0.43
2:2:894:G:C6	2:2:895:G:N7	2.87	0.43
11:F:18:LYS:HE3	11:F:18:LYS:HB3	1.92	0.43
12:G:31:VAL:HG22	12:G:32:PRO:HD3	2.00	0.43
15:L:56:PRO:HG2	15:L:59:ARG:HG3	1.99	0.43
22:S:36:LEU:HB3	22:S:48:LYS:HB2	2.01	0.43
23:T:5:GLU:O	23:T:9:LYS:HG2	2.18	0.43
28:Y:19:LEU:HB3	28:Y:23:ARG:NH2	2.34	0.43
36:g:6:MET:HE2	36:g:6:MET:HB3	1.83	0.43
41:l:101:MET:O	41:l:105:VAL:HG12	2.19	0.43
44:o:50:THR:OG1	44:o:64:GLN:NE2	2.48	0.43
47:r:11:ASP:HB3	47:r:46:SER:OG	2.19	0.43
50:u:34:GLU:OE1	50:u:60:TRP:NE1	2.46	0.43
54:y:59:ASP:OD1	54:y:76:LYS:NZ	2.51	0.43
1:1:2:G:H2'	1:1:3:U:C6	2.54	0.43
1:1:272:A:H2'	1:1:273:G:C8	2.54	0.43
1:1:628:G:C6	1:1:636:G:C2	3.07	0.43
1:1:733:G:H8	1:1:733:G:O5'	2.02	0.43
1:1:1005:C:C2	1:1:1006:C:C5	3.07	0.43
1:1:1425:G:N2	1:1:1574:C:N4	2.67	0.43
1:1:1569:A:C6	1:1:1570:A:C6	3.07	0.43
1:1:1840:G:C2	1:1:1841:U:C2	3.07	0.43
1:1:2415:G:H2'	1:1:2416:C:C6	2.54	0.43
1:1:2516:A:O2'	1:1:2517:C:H5'	2.19	0.43
2:2:131:A:H2'	2:2:132:C:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:172:A:N7	2:2:174:A:N7	2.67	0.43
2:2:227:G:H2'	2:2:228:A:O4'	2.19	0.43
2:2:438:U:H3	2:2:496:A:H62	1.67	0.43
2:2:1026:G:C2	2:2:1027:C:N4	2.87	0.43
26:W:37:ILE:HD11	26:W:61:ALA:HB2	2.00	0.43
27:X:69:ALA:HA	27:X:72:ARG:CZ	2.49	0.43
31:b:38:HIS:CB	31:b:44:THR:HG22	2.49	0.43
36:g:131:LYS:O	36:g:135:LEU:HG	2.19	0.43
38:i:124:MET:HA	38:i:129:VAL:HA	2.01	0.43
39:j:110:ALA:O	39:j:114:VAL:HG12	2.19	0.43
1:1:161:A:H2	1:1:2217:G:N3	2.16	0.42
1:1:367:G:C5	1:1:368:A:N7	2.87	0.42
1:1:379:G:C6	1:1:396:G:O6	2.72	0.42
1:1:571:U:C4	1:1:575:A:C5	3.07	0.42
1:1:587:C:H3'	1:1:588:U:H5'	2.01	0.42
1:1:866:A:C2	1:1:867:C:C6	3.06	0.42
1:1:948:C:H2'	1:1:949:G:H8	1.84	0.42
1:1:1026:G:C2	1:1:1027:A:C8	3.07	0.42
1:1:1210:G:H4'	1:1:1211:C:H5''	2.01	0.42
1:1:1430:G:H2'	1:1:1431:A:O4'	2.19	0.42
1:1:1590:A:C2	1:1:1591:A:C5	3.07	0.42
1:1:1736:U:O2'	1:1:1737:G:H5'	2.19	0.42
1:1:1798:U:OP2	7:B:271:ARG:NH2	2.44	0.42
6:6:9:PHE:HE1	6:6:41:VAL:HG11	1.82	0.42
21:R:4:VAL:HA	21:R:12:HIS:O	2.19	0.42
27:X:56:MET:HE2	27:X:56:MET:HB2	1.86	0.42
39:j:107:ALA:HB2	39:j:125:ALA:HB3	2.01	0.42
42:m:92:LEU:HD23	42:m:92:LEU:HA	1.83	0.42
49:t:17:ARG:NH2	49:t:18:ASP:HB3	2.34	0.42
49:t:29:VAL:CG1	49:t:81:LEU:HD21	2.47	0.42
52:w:21:ILE:HG12	52:w:55:LEU:CD2	2.49	0.42
1:1:335:C:O2	24:U:68:SER:OG	2.36	0.42
1:1:388:G:N7	1:1:390:U:H2'	2.35	0.42
1:1:518:G:H2'	1:1:519:U:C6	2.54	0.42
1:1:519:U:C2	1:1:520:G:C8	3.07	0.42
1:1:743:A:OP1	8:C:135:GLY:HA2	2.19	0.42
1:1:2297:A:C8	1:1:2297:A:OP2	2.72	0.42
2:2:110:C:H2'	2:2:111:G:O4'	2.19	0.42
2:2:475:C:H2'	2:2:476:U:H6	1.83	0.42
2:2:522:C:H41	46:q:50:ARG:HH12	1.66	0.42
2:2:539:A:H2'	2:2:540:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:960:U:C2	2:2:1225:A:N7	2.87	0.42
2:2:1055:A:H5''	57:2:2060:HOH:O	2.19	0.42
3:3:5:U:H2'	3:3:6:G:C8	2.52	0.42
6:6:45:ARG:HD2	6:6:48:THR:OG1	2.19	0.42
12:G:116:ARG:HG3	12:G:133:GLN:HB2	2.01	0.42
15:L:127:VAL:HG11	15:L:142:ILE:HG21	2.01	0.42
24:U:38:GLY:O	24:U:39:ILE:HD13	2.19	0.42
34:e:16:LYS:HE3	34:e:20:GLY:HA2	2.01	0.42
39:j:92:SER:OG	39:j:136:VAL:HG12	2.19	0.42
43:n:39:PHE:O	43:n:45:ARG:NE	2.52	0.42
50:u:21:VAL:O	50:u:33:ILE:HG22	2.19	0.42
54:y:25:ARG:HG3	54:y:66:LEU:HD12	2.01	0.42
1:1:301:G:C4	1:1:302:C:C5	3.07	0.42
1:1:404:A:H1'	1:1:406:G:C8	2.54	0.42
1:1:970:U:N3	1:1:971:G:N7	2.67	0.42
1:1:2025:C:H2'	1:1:2026:U:C6	2.54	0.42
1:1:2751:G:C8	11:F:3:ARG:HD2	2.53	0.42
1:1:2807:U:O5'	1:1:2807:U:H6	2.02	0.42
1:1:2836:U:N3	1:1:2837:A:N7	2.66	0.42
1:1:2897:U:H2'	1:1:2898:U:C6	2.54	0.42
2:2:489:C:H2'	2:2:490:C:H6	1.84	0.42
2:2:757:U:OP1	2:2:822:U:O2'	2.37	0.42
12:G:67:ALA:HB1	12:G:71:LYS:NZ	2.35	0.42
25:V:26:PHE:CE1	25:V:42:LEU:HB2	2.54	0.42
32:c:6:ARG:HA	32:c:6:ARG:HD3	1.85	0.42
32:c:37:LYS:HB2	32:c:37:LYS:HE2	1.85	0.42
48:s:62:ASN:OD1	48:s:62:ASN:N	2.51	0.42
1:1:64:A:H2'	1:1:65:U:C6	2.54	0.42
1:1:100:U:H4'	1:1:101:A:O4'	2.19	0.42
1:1:133:U:O2'	1:1:134:G:H5'	2.20	0.42
1:1:815:C:C2	1:1:1193:G:N2	2.88	0.42
1:1:848:C:H2'	1:1:849:A:C8	2.53	0.42
1:1:1509:A:H2'	1:1:1510:G:C8	2.54	0.42
1:1:2298:A:H2'	1:1:2299:U:O4'	2.19	0.42
2:2:144:G:H2'	2:2:145:G:H8	1.85	0.42
2:2:320:A:H2'	2:2:321:A:O4'	2.19	0.42
2:2:401:C:H2'	2:2:402:G:H8	1.84	0.42
2:2:1118:U:H1'	2:2:1179:A:C4	2.54	0.42
2:2:1130:A:H2'	2:2:1131:G:C8	2.53	0.42
2:2:1130:A:OP1	43:n:18:ARG:NH2	2.51	0.42
8:C:176:ASP:OD1	8:C:190:LYS:HB3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:64:LYS:HD2	30:a:5:ILE:CG1	2.48	0.42
11:F:9:VAL:HG22	11:F:50:LEU:HB2	2.01	0.42
30:a:8:LYS:HB2	57:a:101:HOH:O	2.17	0.42
30:a:34:LEU:HD23	30:a:35:ASP:N	2.34	0.42
37:h:62:LYS:HE3	37:h:62:LYS:HB2	1.79	0.42
38:i:48:LEU:HD12	38:i:48:LEU:HA	1.74	0.42
40:k:45:ARG:HD3	40:k:59:TYR:CD1	2.53	0.42
1:1:261:G:C2	1:1:262:A:C8	3.08	0.42
1:1:396:G:C5	1:1:397:U:C4	3.07	0.42
1:1:1856:U:H2'	1:1:1857:G:O4'	2.19	0.42
1:1:1923:U:OP1	5:5:24:G:O2'	2.37	0.42
1:1:2078:C:H2'	1:1:2079:U:C6	2.54	0.42
1:1:2337:G:C6	1:1:2338:C:N4	2.88	0.42
1:1:2349:G:OP1	34:e:45:ARG:NH2	2.51	0.42
1:1:2425:A:H4'	1:1:2426:A:H5''	2.02	0.42
2:2:617:G:H4'	50:u:47:GLU:OE2	2.19	0.42
2:2:947:G:H2'	2:2:948:C:C6	2.54	0.42
2:2:1518:MA6:H103	2:2:1519:MA6:H102	2.01	0.42
6:6:137:ASP:HB3	6:6:155:THR:HB	2.00	0.42
6:6:140:PRO:O	41:l:84:THR:HG21	2.20	0.42
8:C:5:VAL:N	8:C:32:ASN:HD21	2.15	0.42
13:J:50:THR:HG22	13:J:50:THR:O	2.20	0.42
16:M:69:PRO:HA	16:M:94:ALA:HB2	2.00	0.42
33:d:18:PHE:HB2	33:d:43:THR:HG21	2.02	0.42
45:p:20:VAL:HA	45:p:83:GLU:O	2.20	0.42
45:p:58:SER:O	45:p:91:PRO:HG2	2.19	0.42
46:q:74:LEU:HD23	46:q:74:LEU:HA	1.72	0.42
53:x:40:ILE:HD12	53:x:69:HIS:O	2.19	0.42
1:1:458:G:H2'	1:1:469:G:O6	2.20	0.42
1:1:640:C:H2'	1:1:641:U:H6	1.83	0.42
1:1:1437:C:O2'	1:1:1516:G:O2'	2.22	0.42
1:1:1676:A:H8	1:1:1676:A:O5'	2.02	0.42
1:1:1841:U:C4	1:1:1842:G:N7	2.88	0.42
1:1:2297:A:OP2	1:1:2297:A:H8	2.03	0.42
1:1:2314:A:H2'	1:1:2315:G:C8	2.55	0.42
1:1:2365:G:N7	34:e:39:LYS:NZ	2.56	0.42
1:1:2595:G:H1	7:B:239:ASN:HD22	1.66	0.42
1:1:2803:G:H2'	1:1:2804:U:C6	2.54	0.42
2:2:191:G:H5'	57:2:1896:HOH:O	2.19	0.42
2:2:606:G:N2	2:2:632:U:OP1	2.46	0.42
2:2:634:C:H2'	2:2:635:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1053:G:H4'	2:2:1054:C:H3'	2.01	0.42
2:2:1140:C:O2'	2:2:1141:C:O5'	2.37	0.42
2:2:1320:C:C2	53:x:72:GLY:HA3	2.54	0.42
3:3:24:G:N2	3:3:28:C:C2	2.87	0.42
6:6:6:SER:HB3	6:6:56:PHE:HB3	2.01	0.42
8:C:32:ASN:O	8:C:96:ILE:N	2.45	0.42
10:E:8:TYR:HB2	10:E:173:PHE:CZ	2.54	0.42
21:R:4:VAL:HG12	21:R:13:ARG:HA	2.01	0.42
24:U:36:VAL:HG23	24:U:39:ILE:HB	2.02	0.42
25:V:72:VAL:HG12	25:V:93:ARG:HA	2.01	0.42
29:Z:8:THR:HG22	29:Z:35:THR:HG23	2.02	0.42
37:h:88:ARG:O	37:h:91:VAL:HG12	2.19	0.42
38:i:7:PRO:HB2	38:i:10:LYS:HB3	2.00	0.42
39:j:111:MET:SD	39:j:125:ALA:HB1	2.60	0.42
45:p:13:ARG:HB3	45:p:14:LYS:H	1.59	0.42
47:r:17:ILE:HD12	47:r:17:ILE:H	1.84	0.42
49:t:66:LEU:HA	49:t:66:LEU:HD23	1.69	0.42
50:u:80:LYS:HE3	50:u:80:LYS:HB3	1.84	0.42
55:z:40:LYS:O	55:z:43:THR:OG1	2.33	0.42
1:1:67:U:C2	1:1:68:G:C8	3.07	0.42
1:1:332:A:N6	57:1:3315:HOH:O	2.26	0.42
1:1:885:C:C2	1:1:892:A:C2	3.07	0.42
1:1:936:A:H2'	1:1:937:C:H6	1.83	0.42
1:1:974:G:H8	1:1:990:A:H62	1.66	0.42
1:1:1094:U:H1'	1:1:1097:U:H5	1.84	0.42
1:1:1538:G:H2'	1:1:1539:U:C6	2.55	0.42
1:1:2848:G:O2'	1:1:2849:U:O5'	2.35	0.42
2:2:973:G:OP2	2:2:974:A:O2'	2.36	0.42
2:2:998:C:H5'	57:2:2064:HOH:O	2.19	0.42
2:2:1391:U:H2'	2:2:1392:G:H8	1.85	0.42
5:5:46:G:H2'	5:5:47:U:H4'	2.01	0.42
8:C:1:MET:HE1	8:C:100:LEU:HD21	2.00	0.42
13:J:57:LEU:HD23	13:J:57:LEU:H	1.85	0.42
17:N:18:GLN:HE21	17:N:22:ARG:NH1	2.18	0.42
20:Q:94:ILE:HG21	21:R:4:VAL:HG11	2.00	0.42
25:V:38:LEU:HD12	25:V:38:LEU:HA	1.87	0.42
26:W:45:PHE:O	26:W:59:LEU:HD11	2.20	0.42
29:Z:37:GLU:O	29:Z:38:ARG:HD3	2.20	0.42
31:b:38:HIS:CG	31:b:44:THR:HG22	2.55	0.42
40:k:18:VAL:HB	40:k:19:PRO:HD3	2.01	0.42
47:r:20:THR:HA	47:r:25:VAL:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:v:61:ILE:HA	51:v:75:LEU:HA	2.02	0.42
53:x:29:LYS:HE2	53:x:29:LYS:HB3	1.87	0.42
1:1:280:U:C4	1:1:361:G:N2	2.88	0.42
1:1:1419:A:C8	1:1:1579:A:N6	2.88	0.42
1:1:2831:G:P	8:C:56:LYS:NZ	2.93	0.42
2:2:829:G:C6	2:2:858:G:N2	2.88	0.42
2:2:1241:G:C2	2:2:1242:G:C5	3.08	0.42
6:6:142:LEU:HD22	41:l:77:SER:CB	2.46	0.42
8:C:1:MET:HE2	8:C:1:MET:HB3	1.89	0.42
8:C:20:VAL:HG12	14:K:72:PRO:HB3	2.01	0.42
8:C:56:LYS:HB2	8:C:59:ARG:HG2	2.00	0.42
11:F:175:LYS:HD2	11:F:175:LYS:HA	1.76	0.42
12:G:96:THR:HG23	12:G:115:VAL:CG1	2.49	0.42
18:O:63:LYS:HE2	18:O:63:LYS:HB2	1.91	0.42
22:S:12:SER:OG	22:S:13:SER:N	2.51	0.42
37:h:83:ASP:OD1	37:h:83:ASP:N	2.52	0.42
39:j:39:VAL:HG22	39:j:67:ALA:HB1	2.00	0.42
42:m:18:GLN:OE1	42:m:63:LEU:HD23	2.20	0.42
43:n:18:ARG:HG3	43:n:66:THR:HG23	2.02	0.42
45:p:89:PRO:HD3	55:z:32:VAL:HG11	2.02	0.42
50:u:57:ILE:O	50:u:61:VAL:HG23	2.20	0.42
1:1:429:A:H2'	1:1:430:A:C8	2.55	0.42
1:1:686:U:H2'	1:1:788:A:N1	2.35	0.42
1:1:1458:U:H1'	1:1:1459:G:C6	2.54	0.42
1:1:1918:A:O2'	1:1:1920:C:N4	2.53	0.42
1:1:2898:U:H2'	1:1:2899:A:C8	2.54	0.42
2:2:457:G:C6	2:2:458:U:C4	3.08	0.42
2:2:791:G:C5	2:2:792:A:N7	2.88	0.42
2:2:825:A:H2'	2:2:826:C:H6	1.83	0.42
11:F:46:ALA:C	11:F:48:ASN:H	2.28	0.42
20:Q:95:LEU:HA	20:Q:95:LEU:HD23	1.69	0.42
21:R:24:LYS:HD3	21:R:92:TRP:HB3	2.01	0.42
25:V:65:VAL:O	25:V:68:LYS:N	2.48	0.42
30:a:61:ASN:HA	30:a:64:PHE:O	2.19	0.42
32:c:32:GLU:H	32:c:32:GLU:HG3	1.60	0.42
34:e:63:PRO:HG2	34:e:64:TYR:CD2	2.55	0.42
36:g:78:GLU:H	36:g:78:GLU:CD	2.26	0.42
47:r:69:LEU:HD12	47:r:69:LEU:HA	1.82	0.42
54:y:10:ARG:HD2	54:y:10:ARG:HA	1.72	0.42
54:y:44:LYS:HB2	54:y:86:LEU:HD22	2.02	0.42
1:1:37:C:H4'	1:1:451:U:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:279:A:N6	1:1:361:G:O2'	2.49	0.42
1:1:543:G:H2'	1:1:544:C:O4'	2.20	0.42
1:1:608:A:H2'	1:1:609:A:C8	2.55	0.42
1:1:807:U:H1'	1:1:2445:G:OP1	2.20	0.42
1:1:811:U:O4	15:L:21:ARG:NH1	2.53	0.42
2:2:75:G:C4	2:2:76:G:C8	3.08	0.42
2:2:976:G:OP2	2:2:1358:U:O2'	2.38	0.42
2:2:1036:A:H2'	2:2:1037:C:O4'	2.19	0.42
6:6:86:ASN:HB2	6:6:90:PHE:H	1.85	0.42
13:J:88:THR:HG22	13:J:91:GLU:OE1	2.20	0.42
34:e:54:ASP:OD1	34:e:54:ASP:N	2.53	0.42
34:e:55:LEU:HA	34:e:55:LEU:HD23	1.77	0.42
38:i:44:ARG:HB2	38:i:44:ARG:NH1	2.35	0.42
50:u:20:VAL:HG21	50:u:32:PHE:CG	2.54	0.42
55:z:40:LYS:HB3	55:z:42:THR:HG22	2.01	0.42
1:1:684:G:OP1	33:d:16:HIS:HD2	2.03	0.41
1:1:1080:A:H8	1:1:1080:A:O5'	2.02	0.41
1:1:1091:G:H22	1:1:1101:U:H1'	1.85	0.41
1:1:1653:G:OP1	1:1:2822:G:N2	2.44	0.41
1:1:1724:G:H2'	1:1:1725:U:H6	1.84	0.41
1:1:1735:A:C6	1:1:1736:U:C4	3.08	0.41
1:1:2092:U:OP1	1:1:2199:A:O2'	2.29	0.41
2:2:58:C:O2	2:2:58:C:H2'	2.19	0.41
2:2:166:U:H2'	2:2:167:A:C8	2.55	0.41
2:2:415:A:C4	2:2:416:G:C8	3.08	0.41
2:2:636:U:H2'	2:2:637:C:C6	2.55	0.41
2:2:1305:G:C4	2:2:1331:G:N2	2.88	0.41
2:2:1452:C:H4'	2:2:1453:G:H5''	2.02	0.41
2:2:1532:U:H3'	57:2:1937:HOH:O	2.20	0.41
10:E:10:ASP:O	10:E:14:LYS:HE3	2.20	0.41
10:E:30:ARG:O	10:E:159:THR:HG22	2.20	0.41
10:E:72:LYS:C	10:E:81:GLN:HB2	2.44	0.41
16:M:26:VAL:HG23	16:M:104:GLU:CD	2.45	0.41
16:M:81:ARG:HD3	16:M:81:ARG:HA	1.86	0.41
18:O:79:ALA:HB3	18:O:113:ALA:HB3	2.02	0.41
21:R:61:ALA:HB2	21:R:98:ILE:HD13	2.01	0.41
24:U:4:LYS:HB3	24:U:83:VAL:HG11	2.01	0.41
28:Y:4:LYS:HE3	28:Y:4:LYS:HB3	1.86	0.41
38:i:99:ASP:OD1	38:i:100:ASN:N	2.53	0.41
43:n:107:ASP:OD1	43:n:109:ARG:HG3	2.20	0.41
1:1:9:G:C6	1:1:2629:U:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:188:G:O2'	1:1:1365:A:N6	2.53	0.41
1:1:590:A:H2'	1:1:591:U:O4'	2.21	0.41
1:1:918:A:H4'	3:3:97:C:O2	2.19	0.41
1:1:1070:A:H4'	1:1:1071:G:H5''	2.02	0.41
1:1:1224:U:H2'	1:1:1225:G:C8	2.54	0.41
1:1:1794:A:H2'	1:1:1795:C:C6	2.56	0.41
1:1:1884:G:OP2	1:1:1884:G:H8	2.03	0.41
1:1:2455:G:C4	1:1:2456:C:C5	3.08	0.41
1:1:2884:U:C6	31:b:50:ARG:HG2	2.55	0.41
2:2:4:U:H2'	2:2:5:U:H2'	2.02	0.41
2:2:1018:G:C2	2:2:1019:A:C4	3.08	0.41
3:3:75:G:H21	25:V:29:ILE:HD13	1.85	0.41
6:6:63:GLU:CD	6:6:63:GLU:H	2.27	0.41
10:E:65:PRO:HA	10:E:89:VAL:HG22	2.01	0.41
12:G:6:LEU:HD12	12:G:34:GLY:O	2.20	0.41
17:N:22:ARG:HE	17:N:22:ARG:HB2	1.56	0.41
17:N:97:ILE:HD13	17:N:97:ILE:HA	1.93	0.41
36:g:94:HIS:O	36:g:95:ARG:C	2.63	0.41
42:m:55:THR:OG1	42:m:56:LYS:N	2.53	0.41
49:t:4:SER:O	49:t:8:THR:HG23	2.20	0.41
50:u:42:ILE:O	50:u:42:ILE:HG13	2.20	0.41
50:u:57:ILE:HD13	50:u:75:ILE:HD11	2.02	0.41
1:1:585:G:N7	20:Q:6:ARG:NH1	2.54	0.41
1:1:598:U:H2'	1:1:599:A:C8	2.55	0.41
1:1:613:A:H2'	1:1:613:A:N3	2.35	0.41
1:1:1565:C:O2'	1:1:1566:A:H8	2.02	0.41
1:1:1964:G:O2'	1:1:1967:C:OP2	2.34	0.41
1:1:2328:A:H2'	1:1:2329:U:H6	1.80	0.41
1:1:2854:G:C6	1:1:2864:G:C6	3.08	0.41
2:2:126:G:H5'	2:2:633:G:N2	2.36	0.41
2:2:262:A:H2'	2:2:263:A:C8	2.55	0.41
2:2:373:A:N3	2:2:374:A:C8	2.88	0.41
2:2:461:A:H2'	2:2:462:G:C8	2.54	0.41
2:2:502:A:H2'	2:2:503:C:O4'	2.20	0.41
2:2:715:A:H8	2:2:715:A:O5'	2.03	0.41
2:2:908:A:C2	2:2:909:A:C5	3.08	0.41
2:2:1032:G:H3'	2:2:1032:G:N3	2.35	0.41
2:2:1255:G:OP2	44:o:45:ARG:NH1	2.52	0.41
2:2:1299:A:O2'	2:2:1300:G:H4'	2.20	0.41
3:3:109:A:H5'	57:3:306:HOH:O	2.20	0.41
11:F:89:LEU:HD13	11:F:94:TYR:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:V:67:GLY:O	25:V:68:LYS:HD3	2.21	0.41
36:g:100:MET:HE3	36:g:100:MET:HB2	1.74	0.41
37:h:109:PRO:C	37:h:111:LEU:H	2.28	0.41
38:i:160:GLU:O	38:i:163:GLU:HB2	2.20	0.41
45:p:119:ASN:HD21	55:z:35:ARG:HH22	1.66	0.41
48:s:98:LYS:HB3	48:s:98:LYS:HE2	1.86	0.41
50:u:8:ARG:CZ	50:u:15:PRO:HB3	2.50	0.41
1:1:83:A:OP1	24:U:2:ALA:N	2.53	0.41
1:1:172:A:C2	1:1:173:A:C5	3.08	0.41
1:1:381:G:N2	1:1:394:C:C2	2.88	0.41
1:1:413:C:H2'	1:1:414:C:C6	2.53	0.41
1:1:572:A:C2	1:1:2033:A:C2	3.08	0.41
1:1:873:C:H2'	1:1:874:G:C8	2.56	0.41
1:1:890:C:H6	1:1:890:C:P	2.44	0.41
1:1:892:A:H2'	1:1:893:C:C6	2.56	0.41
1:1:1084:A:C6	1:1:1085:A:N1	2.89	0.41
1:1:1263:U:H2'	1:1:1264:A:C8	2.56	0.41
1:1:1326:U:C2	1:1:1327:A:C8	3.08	0.41
1:1:1507:C:H2'	1:1:1508:A:H1'	2.03	0.41
1:1:2487:G:H2'	1:1:2488:G:H8	1.85	0.41
1:1:2850:A:H2'	1:1:2851:A:H8	1.86	0.41
1:1:2898:U:H2'	1:1:2899:A:H8	1.85	0.41
2:2:1021:A:H2'	2:2:1021:A:N3	2.35	0.41
2:2:1118:U:OP1	43:n:11:ARG:NH1	2.54	0.41
2:2:1208:C:C2	2:2:1209:C:C6	3.09	0.41
8:C:159:LYS:HD2	8:C:160:LYS:H	1.86	0.41
12:G:74:ALA:HA	12:G:76:GLU:OE2	2.20	0.41
12:G:132:PHE:O	12:G:139:PHE:HA	2.21	0.41
14:K:1:MET:SD	14:K:67:LYS:HE3	2.61	0.41
15:L:28:GLY:HA3	21:R:82:HIS:NE2	2.34	0.41
21:R:14:VAL:CG2	21:R:98:ILE:HG13	2.50	0.41
22:S:66:ILE:H	22:S:66:ILE:HD12	1.85	0.41
22:S:85:ILE:HG12	22:S:95:ARG:HH21	1.85	0.41
31:b:34:SER:OG	31:b:36:GLU:HG2	2.20	0.41
39:j:83:HIS:CE1	42:m:96:MET:HE3	2.55	0.41
40:k:68:GLN:H	40:k:68:GLN:HG3	1.70	0.41
46:q:57:LEU:HD23	46:q:57:LEU:HA	1.86	0.41
1:1:150:U:H2'	1:1:151:C:C6	2.56	0.41
1:1:362:A:H8	1:1:362:A:OP2	2.03	0.41
1:1:818:G:N1	1:1:1188:U:OP2	2.31	0.41
1:1:930:G:C2	1:1:933:A:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1107:G:H2'	1:1:1108:U:C6	2.55	0.41
1:1:1203:U:OP2	1:1:1204:A:O2'	2.26	0.41
1:1:1533:C:O3'	57:1:3304:HOH:O	2.22	0.41
1:1:1915:U:H2'	1:1:1916:A:H8	1.85	0.41
1:1:2024:G:C4	1:1:2040:G:N2	2.87	0.41
1:1:2198:A:C4	12:G:29:PHE:HB2	2.56	0.41
1:1:2408:U:H2'	1:1:2409:G:H8	1.86	0.41
1:1:2556:C:H2'	1:1:2557:G:O4'	2.20	0.41
2:2:148:G:C2	2:2:149:A:C8	3.09	0.41
2:2:191:G:H2'	2:2:192:A:C8	2.50	0.41
2:2:263:A:OP2	54:y:74:ARG:NH1	2.53	0.41
2:2:620:C:C2	38:i:132:ILE:HG13	2.56	0.41
2:2:946:A:C2	2:2:947:G:C5	3.09	0.41
10:E:62:GLY:O	30:a:7:PRO:HD2	2.20	0.41
13:J:4:PHE:CD1	20:Q:100:VAL:HG11	2.56	0.41
15:L:90:VAL:HG22	15:L:122:VAL:HA	2.02	0.41
20:Q:50:ARG:O	20:Q:54:LYS:NZ	2.53	0.41
31:b:33:THR:HG23	31:b:51:GLY:HA2	2.03	0.41
36:g:169:GLU:O	36:g:171:ILE:N	2.53	0.41
37:h:73:PRO:O	37:h:77:ILE:HB	2.21	0.41
38:i:17:THR:HG22	38:i:18:ASP:O	2.20	0.41
41:l:26:PHE:HE2	41:l:120:LEU:HD21	1.86	0.41
44:o:37:ARG:HA	44:o:37:ARG:HD2	1.69	0.41
45:p:84:VAL:HG13	45:p:110:ILE:HG23	2.02	0.41
47:r:85:CYS:HB2	53:x:73:GLU:HB3	2.02	0.41
51:v:21:ILE:CG2	57:v:102:HOH:O	2.67	0.41
1:1:742:A:H2'	1:1:743:A:C8	2.56	0.41
1:1:772:C:C2	1:1:773:U:C5	3.09	0.41
1:1:813:U:H2'	1:1:814:C:C6	2.55	0.41
1:1:1326:U:O2'	1:1:2010:G:O2'	2.28	0.41
1:1:1637:A:H5'	1:1:1760:C:O2'	2.20	0.41
1:1:1715:G:O2'	1:1:1716:U:H6	2.03	0.41
1:1:2563:U:O2	1:1:2565:A:H8	2.03	0.41
1:1:2578:G:H21	8:C:130:GLN:NE2	2.18	0.41
1:1:2684:U:H2'	1:1:2685:G:O4'	2.20	0.41
1:1:2726:A:O2'	1:1:2727:A:O5'	2.30	0.41
1:1:2747:G:O6	1:1:2755:C:H5''	2.21	0.41
2:2:642:A:H2'	2:2:643:C:H6	1.85	0.41
2:2:836:G:C5	2:2:851:G:C6	3.09	0.41
2:2:909:A:N3	2:2:1413:A:O2'	2.45	0.41
2:2:1038:C:C2	2:2:1039:G:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:60:ASP:O	11:F:64:GLN:HG2	2.21	0.41
12:G:29:PHE:C	12:G:32:PRO:HD2	2.46	0.41
37:h:70:THR:O	37:h:106:VAL:HG12	2.21	0.41
38:i:13:ARG:NH2	38:i:38:PRO:HA	2.36	0.41
1:1:84:A:H62	1:1:101:A:H2	1.65	0.41
1:1:217:A:H2'	1:1:218:A:H8	1.85	0.41
1:1:245:G:O2'	1:1:384:A:N1	2.44	0.41
1:1:1318:U:C2	1:1:1319:C:C5	3.09	0.41
1:1:1482:G:C2	1:1:1483:G:C8	3.09	0.41
1:1:1742:U:H2'	1:1:1743:G:C8	2.55	0.41
1:1:1900:A:H1'	1:1:1970:A:H2'	2.01	0.41
1:1:2262:U:H2'	1:1:2263:C:H6	1.85	0.41
1:1:2378:A:H1'	18:O:91:SER:OG	2.20	0.41
1:1:2529:G:O6	35:f:32:LYS:NZ	2.53	0.41
2:2:1:A:C2'	2:2:2:A:H5'	2.50	0.41
2:2:152:A:N6	2:2:170:U:C2	2.89	0.41
2:2:474:G:C6	2:2:475:C:C4	3.08	0.41
2:2:1277:C:HO2'	2:2:1279:G:H8	1.66	0.41
2:2:1315:U:O2	2:2:1360:A:H2	2.04	0.41
2:2:1330:U:C5	2:2:1331:G:C5	3.09	0.41
8:C:5:VAL:HG12	8:C:32:ASN:HD21	1.86	0.41
10:E:122:PHE:CE1	10:E:128:TYR:HD1	2.39	0.41
11:F:38:ASN:C	11:F:40:ALA:H	2.27	0.41
18:O:21:LEU:HD23	18:O:21:LEU:HA	1.88	0.41
21:R:4:VAL:HG23	21:R:39:LEU:HB2	2.02	0.41
35:f:11:CYS:HB3	35:f:33:HIS:HE1	1.85	0.41
36:g:73:LYS:C	36:g:75:ALA:H	2.29	0.41
36:g:74:ARG:HE	36:g:74:ARG:HB3	1.75	0.41
36:g:97:LEU:HD11	36:g:147:SER:HB3	2.03	0.41
39:j:76:LEU:O	39:j:82:GLN:NE2	2.54	0.41
39:j:104:GLY:O	39:j:122:ASN:HA	2.21	0.41
41:l:103:TRP:CE2	41:l:137:LYS:HD3	2.55	0.41
45:p:34:ILE:HG13	45:p:70:CYS:SG	2.61	0.41
47:r:53:ILE:O	47:r:57:ARG:HG3	2.21	0.41
50:u:1:MET:HE2	50:u:1:MET:HB3	1.86	0.41
1:1:216:A:C8	1:1:432:A:N6	2.89	0.41
1:1:242:G:O2'	1:1:254:G:O6	2.25	0.41
1:1:254:G:N2	34:e:8:ARG:HH12	2.18	0.41
1:1:570:G:H2'	1:1:2030:A:N7	2.36	0.41
1:1:781:A:OP1	7:B:217:ARG:NH2	2.43	0.41
1:1:1055:G:H2'	1:1:1056:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:3:A:H5''	2:2:4:U:O4'	2.21	0.41
2:2:128:G:O2'	2:2:129:A:H5'	2.21	0.41
2:2:373:A:C2	2:2:482:A:C6	3.09	0.41
2:2:1270:G:HO2'	2:2:1313:U:HO2'	1.67	0.41
3:3:68:C:H2'	3:3:69:G:O4'	2.20	0.41
9:D:24:ASN:O	9:D:28:VAL:HG23	2.21	0.41
16:M:111:GLU:O	16:M:114:ARG:HB2	2.20	0.41
25:V:4:ILE:HD11	25:V:63:ILE:HG12	2.02	0.41
36:g:167:ASP:HB3	36:g:191:SER:HB2	2.02	0.41
50:u:14:ARG:HG3	50:u:14:ARG:O	2.21	0.41
1:1:30:G:H2'	1:1:31:C:H6	1.86	0.41
1:1:131:A:C2	1:1:132:G:C5	3.09	0.41
1:1:163:C:H2'	1:1:164:C:H6	1.84	0.41
1:1:228:C:O2'	1:1:229:C:H5''	2.21	0.41
1:1:276:U:H2'	1:1:277:G:O4'	2.20	0.41
1:1:377:G:C6	1:1:398:C:N3	2.88	0.41
1:1:387:U:OP1	27:X:22:LEU:HD21	2.21	0.41
1:1:481:G:H2'	1:1:507:A:N1	2.36	0.41
1:1:560:C:H2'	1:1:561:G:O4'	2.20	0.41
1:1:598:U:H2'	1:1:599:A:H8	1.86	0.41
1:1:770:G:H5''	33:d:10:LEU:HD22	2.03	0.41
1:1:807:U:O2'	1:1:2060:A:N1	2.53	0.41
1:1:1407:G:C2	1:1:1408:G:C5	3.09	0.41
1:1:1582:C:H2'	1:1:1583:A:O4'	2.20	0.41
1:1:1737:G:H8	1:1:1737:G:O5'	2.03	0.41
1:1:1914:C:C1'	57:1:3301:HOH:O	2.65	0.41
1:1:2225:A:H4'	1:1:2226:C:H6	1.86	0.41
1:1:2447:G:C8	1:1:2501:C:C6	3.09	0.41
1:1:2514:U:C2	1:1:2515:C:C5	3.09	0.41
1:1:2574:G:H2'	1:1:2575:C:O4'	2.21	0.41
1:1:2845:U:H5''	19:P:52:ASN:O	2.20	0.41
1:1:2850:A:H2'	1:1:2851:A:C8	2.56	0.41
2:2:64:G:C5	2:2:99:C:N4	2.89	0.41
2:2:687:A:C2	2:2:704:A:C6	3.08	0.41
2:2:705:G:C5	2:2:706:A:C8	3.09	0.41
2:2:1144:G:N2	2:2:1146:A:H62	2.19	0.41
2:2:1522:U:H2'	2:2:1523:G:H8	1.86	0.41
3:3:18:G:H2'	3:3:19:C:H6	1.86	0.41
3:3:111:U:H2'	3:3:112:G:C8	2.56	0.41
6:6:107:LEU:HD13	6:6:107:LEU:HA	1.78	0.41
8:C:116:LYS:H	8:C:116:LYS:HG2	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:146:ILE:HD13	8:C:146:ILE:HG21	1.86	0.41
10:E:30:ARG:H	10:E:159:THR:HG22	1.86	0.41
11:F:29:LYS:HE2	11:F:29:LYS:HB2	1.92	0.41
13:J:43:GLU:OE1	13:J:43:GLU:N	2.49	0.41
13:J:84:ILE:HG23	13:J:84:ILE:O	2.20	0.41
15:L:76:GLU:C	15:L:77:ILE:HG13	2.45	0.41
16:M:12:MET:HE3	16:M:12:MET:HB2	1.78	0.41
18:O:62:LEU:HD23	18:O:62:LEU:HA	1.72	0.41
24:U:6:ARG:O	24:U:25:VAL:HG11	2.21	0.41
36:g:47:VAL:N	36:g:48:PRO:HD2	2.36	0.41
37:h:64:ILE:HD12	37:h:64:ILE:HA	1.90	0.41
37:h:180:ALA:HA	37:h:206:GLU:HA	2.03	0.41
37:h:188:GLU:OE2	37:h:190:HIS:HB2	2.21	0.41
42:m:50:LYS:NZ	42:m:52:GLU:HB2	2.36	0.41
42:m:102:ALA:HB3	42:m:113:ASP:HB3	2.02	0.41
51:v:57:ASP:O	51:v:59:VAL:HG13	2.21	0.41
52:w:22:ASP:OD2	52:w:23:TYR:N	2.54	0.41
1:1:175:G:H2'	1:1:176:A:C8	2.56	0.41
1:1:216:A:C8	1:1:432:A:C6	3.09	0.41
1:1:642:U:O4	57:1:3302:HOH:O	2.21	0.41
1:1:901:C:H2'	1:1:902:C:H6	1.85	0.41
1:1:1220:G:C6	1:1:1230:A:N1	2.89	0.41
1:1:1324:G:O2'	1:1:1326:U:OP2	2.38	0.41
1:1:1957:C:H2'	1:1:1958:C:H6	1.86	0.41
1:1:2646:C:OP2	1:1:2732:G:O2'	2.39	0.41
2:2:401:C:O2'	2:2:621:A:N3	2.54	0.41
2:2:539:A:H2'	2:2:540:G:C8	2.56	0.41
2:2:986:U:H2'	2:2:987:G:O4'	2.21	0.41
2:2:1004:A:OP1	2:2:1024:G:N1	2.44	0.41
2:2:1026:G:H1	2:2:1035:A:H2	1.65	0.41
2:2:1513:A:H2'	2:2:1514:G:C8	2.56	0.41
10:E:143:TYR:HA	10:E:146:VAL:CG1	2.51	0.41
19:P:78:SER:OG	19:P:80:VAL:HG22	2.21	0.41
20:Q:47:TYR:OH	21:R:76:LYS:NZ	2.53	0.41
22:S:11:ARG:HA	22:S:11:ARG:HD2	1.73	0.41
24:U:9:ASP:O	24:U:25:VAL:HG12	2.21	0.41
30:a:41:HIS:O	30:a:43:PHE:N	2.47	0.41
42:m:10:MET:HG3	42:m:27:MET:CE	2.49	0.41
1:1:141:G:OP2	1:1:141:G:N2	2.53	0.40
1:1:528:A:C2	1:1:2042:A:H2'	2.56	0.40
1:1:608:A:H2'	1:1:609:A:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:782:A:N7	7:B:220:VAL:HG21	2.36	0.40
1:1:1419:A:H4'	1:1:1420:A:OP1	2.21	0.40
1:1:2192:U:O2'	1:1:2193:G:H8	2.03	0.40
1:1:2674:G:H2'	1:1:2675:A:H8	1.85	0.40
1:1:2723:C:OP1	8:C:114:LYS:NZ	2.44	0.40
2:2:203:G:N2	2:2:215:C:C2	2.89	0.40
2:2:280:C:N3	51:v:41:THR:HG22	2.36	0.40
2:2:430:A:OP1	38:i:9:LEU:HB2	2.20	0.40
2:2:748:G:C6	2:2:749:A:C5	3.09	0.40
2:2:883:C:O2'	2:2:884:U:H5'	2.21	0.40
2:2:949:A:H2'	2:2:950:U:C6	2.56	0.40
2:2:1145:A:O2'	2:2:1146:A:H8	2.03	0.40
2:2:1243:C:H2'	2:2:1244:G:H8	1.86	0.40
2:2:1244:G:C6	2:2:1294:G:N1	2.89	0.40
3:3:44:G:N2	3:3:48:U:O2	2.54	0.40
8:C:175:LEU:HA	8:C:175:LEU:HD23	1.84	0.40
26:W:42:GLY:O	26:W:44:LYS:N	2.48	0.40
34:e:37:ALA:O	34:e:41:LYS:HG3	2.21	0.40
38:i:105:MET:SD	38:i:173:VAL:HG22	2.61	0.40
40:k:50:PRO:HB3	40:k:55:HIS:CD2	2.56	0.40
41:l:14:PRO:HB2	41:l:19:GLY:HA2	2.03	0.40
52:w:45:THR:HG23	52:w:47:THR:HG23	2.02	0.40
1:1:492:A:H2'	1:1:493:G:O4'	2.20	0.40
1:1:689:A:H2'	1:1:690:G:C8	2.57	0.40
1:1:894:U:H3'	1:1:895:U:H6	1.85	0.40
1:1:974:G:C6	1:1:1186:G:C6	3.08	0.40
1:1:1020:A:C2	1:1:1141:U:C2	3.10	0.40
1:1:1295:C:C2	1:1:1296:G:C8	3.10	0.40
1:1:1328:A:H2'	1:1:1330:C:C4	2.56	0.40
1:1:2287:A:N7	1:1:2289:G:C8	2.89	0.40
1:1:2400:G:H2'	1:1:2401:U:O4'	2.21	0.40
1:1:2542:A:H5''	1:1:2766:A:O2'	2.21	0.40
1:1:2680:U:O2'	1:1:2681:C:H5'	2.20	0.40
2:2:165:G:H2'	2:2:166:U:C6	2.56	0.40
2:2:540:G:C6	2:2:541:G:C5	3.10	0.40
2:2:1028:C:H2'	2:2:1029:U:C6	2.55	0.40
2:2:1057:G:C5	2:2:1204:A:C2	3.10	0.40
2:2:1140:C:C2	2:2:1141:C:C5	3.09	0.40
2:2:1226:C:H4'	2:2:1227:A:OP1	2.21	0.40
2:2:1251:A:H2'	2:2:1252:A:C8	2.56	0.40
7:B:251:GLN:HG3	7:B:252:THR:N	2.34	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:133:THR:O	8:C:134:HIS:HB2	2.21	0.40
10:E:30:ARG:H	10:E:159:THR:CG2	2.34	0.40
12:G:2:GLN:HB3	12:G:18:GLN:OE1	2.20	0.40
17:N:13:ASN:OD1	17:N:13:ASN:N	2.53	0.40
17:N:38:LEU:HB3	17:N:39:PRO:HD3	2.03	0.40
22:S:23:LEU:HD22	31:b:22:LEU:HD23	2.04	0.40
26:W:37:ILE:HG22	26:W:38:VAL:HG13	2.03	0.40
36:g:72:THR:C	36:g:74:ARG:H	2.28	0.40
37:h:190:HIS:HD2	37:h:191:THR:N	2.19	0.40
38:i:58:LYS:HD3	38:i:203:LEU:HD22	2.03	0.40
40:k:3:HIS:NE2	40:k:95:ALA:HB2	2.37	0.40
40:k:4:TYR:CD1	40:k:71:ILE:HG13	2.56	0.40
40:k:6:ILE:CD1	40:k:89:VAL:HG23	2.51	0.40
43:n:120:LYS:HE2	43:n:120:LYS:HB3	1.72	0.40
52:w:72:ASP:OD1	52:w:73:ARG:N	2.54	0.40
53:x:71:LEU:HD12	53:x:71:LEU:N	2.36	0.40
1:1:17:G:H2'	1:1:18:U:C6	2.56	0.40
1:1:26:G:H1'	1:1:514:A:N6	2.35	0.40
1:1:401:A:C6	1:1:402:A:C6	3.09	0.40
1:1:607:U:O2	1:1:607:U:H2'	2.22	0.40
1:1:772:C:N3	1:1:773:U:C5	2.90	0.40
1:1:893:C:H2'	1:1:894:U:H6	1.85	0.40
1:1:1054:A:C6	1:1:1055:G:C6	3.09	0.40
1:1:1096:A:H8	1:1:1096:A:OP2	2.05	0.40
1:1:1366:A:H2'	1:1:1367:A:O4'	2.22	0.40
1:1:1496:A:N3	1:1:1577:C:O2'	2.49	0.40
1:1:1551:A:H2'	1:1:1552:A:O4'	2.21	0.40
1:1:1735:A:C2	1:1:1736:U:C2	3.10	0.40
1:1:2038:G:H2'	1:1:2039:U:O4'	2.21	0.40
1:1:2391:G:O2'	1:1:2392:A:H8	2.04	0.40
1:1:2798:U:H2'	57:1:3727:HOH:O	2.21	0.40
2:2:130:A:O2'	2:2:131:A:O5'	2.36	0.40
2:2:592:G:C6	2:2:648:A:C6	3.09	0.40
2:2:600:A:H2'	2:2:601:G:C8	2.56	0.40
2:2:704:A:C5	2:2:705:G:C8	3.09	0.40
2:2:842:U:H3'	2:2:843:U:H5''	2.03	0.40
2:2:1004:A:P	2:2:1024:G:H22	2.44	0.40
2:2:1309:G:C5	2:2:1329:A:C2	3.10	0.40
2:2:1354:U:H2'	2:2:1355:G:H8	1.87	0.40
2:2:1363:A:C5	2:2:1365:G:C6	3.10	0.40
8:C:204:LYS:HE2	8:C:204:LYS:HB3	1.76	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:191:ASP:O	9:D:195:GLN:HG2	2.21	0.40
12:G:115:VAL:O	12:G:116:ARG:NH1	2.54	0.40
37:h:20:SER:OG	48:s:92:GLU:O	2.38	0.40
38:i:155:VAL:O	38:i:159:LEU:HD23	2.21	0.40
43:n:11:ARG:HG3	43:n:16:ALA:HA	2.03	0.40
43:n:87:LEU:HA	43:n:87:LEU:HD23	1.77	0.40
48:s:10:GLU:O	48:s:14:VAL:HG12	2.21	0.40
1:1:100:U:H1'	1:1:101:A:C6	2.56	0.40
1:1:322:A:OP2	9:D:163:ASN:HB2	2.21	0.40
1:1:929:U:H1'	29:Z:26:GLY:O	2.21	0.40
1:1:1056:G:H4'	1:1:1086:A:C8	2.56	0.40
1:1:1111:A:O2'	1:1:1112:G:P	2.79	0.40
1:1:1342:A:O2'	1:1:1344:U:OP2	2.29	0.40
1:1:1651:G:C4	1:1:1652:A:C8	3.09	0.40
1:1:2411:A:H2'	1:1:2412:A:H8	1.86	0.40
1:1:2552:U:C5	1:1:2554:U:H5'	2.56	0.40
2:2:212:G:C4	2:2:213:G:C8	3.10	0.40
2:2:745:G:H2'	2:2:746:A:C8	2.57	0.40
2:2:845:A:H5''	2:2:846:G:H8	1.86	0.40
2:2:1172:C:H2'	2:2:1173:U:H6	1.85	0.40
6:6:83:HIS:CE1	6:6:92:GLN:HG3	2.57	0.40
10:E:135:GLN:OE1	10:E:150:ARG:N	2.54	0.40
15:L:129:LYS:HG3	15:L:130:GLY:H	1.86	0.40
16:M:136:MET:HE3	16:M:136:MET:HB2	1.89	0.40
22:S:88:ARG:HA	22:S:88:ARG:HD2	1.67	0.40
23:T:80:TRP:CZ3	23:T:82:LYS:HB2	2.57	0.40
32:c:27:LYS:HB3	32:c:28:ARG:HH21	1.87	0.40
36:g:133:GLU:O	36:g:136:MET:HG2	2.22	0.40
37:h:140:ASN:ND2	37:h:143:ARG:HH12	2.19	0.40
38:i:27:ALA:HB3	38:i:30:THR:CG2	2.51	0.40
38:i:155:VAL:HG13	38:i:156:LYS:HD2	2.02	0.40
40:k:4:TYR:CE1	40:k:71:ILE:HG13	2.56	0.40
40:k:16:GLU:H	40:k:16:GLU:CD	2.30	0.40
44:o:42:LEU:HD23	44:o:42:LEU:HA	1.96	0.40
45:p:13:ARG:HA	45:p:13:ARG:NE	2.36	0.40
45:p:72:ASP:O	45:p:75:LYS:HG2	2.21	0.40
46:q:37:VAL:HG11	46:q:75:GLN:HA	2.03	0.40
49:t:23:GLY:O	49:t:28:GLN:NE2	2.51	0.40
49:t:33:THR:HG22	49:t:63:ARG:NH1	2.25	0.40
1:1:150:U:H2'	1:1:151:C:H6	1.87	0.40
1:1:167:A:H2'	1:1:168:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:866:A:N7	1:1:914:G:C5	2.89	0.40
1:1:1074:G:C6	1:1:1075:C:N4	2.89	0.40
1:1:1183:U:H2'	1:1:1184:U:C6	2.56	0.40
1:1:1537:G:C5	1:1:1538:G:H1'	2.57	0.40
1:1:1797:G:C5	1:1:1798:U:C5	3.10	0.40
1:1:1862:G:C2	1:1:1863:G:C8	3.09	0.40
1:1:2281:A:C2	1:1:2282:G:C5	3.10	0.40
1:1:2505:G:O2'	1:1:2506:U:O5'	2.39	0.40
1:1:2674:G:H2'	1:1:2675:A:C8	2.57	0.40
1:1:2683:C:C2	1:1:2684:U:C5	3.10	0.40
1:1:2683:C:H2'	14:K:70:ARG:HH22	1.86	0.40
2:2:455:G:C2	2:2:478:A:N1	2.89	0.40
2:2:978:A:C6	2:2:1318:A:C6	3.10	0.40
2:2:1015:G:H2'	2:2:1016:A:C8	2.56	0.40
2:2:1034:G:H3'	2:2:1035:A:N7	2.37	0.40
2:2:1175:G:O2'	2:2:1176:A:P	2.80	0.40
6:6:75:LEU:HD12	6:6:92:GLN:HE22	1.87	0.40
10:E:170:LEU:HB3	10:E:175:PHE:HB2	2.04	0.40
11:F:127:THR:HG22	11:F:128:GLN:N	2.32	0.40
17:N:65:LEU:HD23	17:N:65:LEU:HA	1.86	0.40
37:h:7:PRO:O	37:h:11:ARG:HD2	2.22	0.40
42:m:29:SER:OG	42:m:57:PRO:HG2	2.22	0.40
43:n:24:GLY:HA3	43:n:62:ASP:CG	2.47	0.40
46:q:24:LEU:HD23	46:q:24:LEU:HA	1.79	0.40
49:t:8:THR:O	49:t:12:VAL:HG12	2.21	0.40
52:w:29:LEU:HD12	52:w:59:ILE:HG12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
6	6	185/188 (98%)	167 (90%)	16 (9%)	2 (1%)	11	43
7	B	269/273 (98%)	243 (90%)	26 (10%)	0	100	100
8	C	207/209 (99%)	184 (89%)	23 (11%)	0	100	100
9	D	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
10	E	175/179 (98%)	161 (92%)	14 (8%)	0	100	100
11	F	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
12	G	147/149 (99%)	133 (90%)	14 (10%)	0	100	100
13	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
14	K	121/123 (98%)	110 (91%)	11 (9%)	0	100	100
15	L	142/144 (99%)	127 (89%)	15 (11%)	0	100	100
16	M	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
17	N	117/127 (92%)	108 (92%)	9 (8%)	0	100	100
18	O	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
19	P	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
20	Q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
21	R	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
22	S	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
23	T	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
24	U	101/104 (97%)	95 (94%)	6 (6%)	0	100	100
25	V	92/94 (98%)	82 (89%)	10 (11%)	0	100	100
26	W	74/84 (88%)	67 (90%)	7 (10%)	0	100	100
27	X	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
28	Y	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
29	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
30	a	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
31	b	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
32	c	50/55 (91%)	45 (90%)	5 (10%)	0	100	100
33	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
34	e	62/65 (95%)	53 (86%)	9 (14%)	0	100	100
35	f	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
36	g	223/241 (92%)	198 (89%)	24 (11%)	1 (0%)	30	62
37	h	206/233 (88%)	189 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	i	203/206 (98%)	191 (94%)	12 (6%)	0	100	100
39	j	154/167 (92%)	144 (94%)	10 (6%)	0	100	100
40	k	102/135 (76%)	96 (94%)	6 (6%)	0	100	100
41	l	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
42	m	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
43	n	125/130 (96%)	116 (93%)	9 (7%)	0	100	100
44	o	97/103 (94%)	86 (89%)	11 (11%)	0	100	100
45	p	115/129 (89%)	106 (92%)	9 (8%)	0	100	100
46	q	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
47	r	114/118 (97%)	103 (90%)	11 (10%)	0	100	100
48	s	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
49	t	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
50	u	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
51	v	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
52	w	64/75 (85%)	59 (92%)	5 (8%)	0	100	100
53	x	81/92 (88%)	75 (93%)	6 (7%)	0	100	100
54	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
55	z	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
All	All	5793/6100 (95%)	5374 (93%)	416 (7%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	6	165	PRO
6	6	187	VAL
36	g	128	LYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
6	6	154/154 (100%)	139 (90%)	15 (10%)	8	32
7	B	216/218 (99%)	215 (100%)	1 (0%)	81	85
8	C	164/164 (100%)	164 (100%)	0	100	100
9	D	165/165 (100%)	164 (99%)	1 (1%)	78	84
10	E	148/150 (99%)	147 (99%)	1 (1%)	76	83
11	F	136/138 (99%)	134 (98%)	2 (2%)	57	76
12	G	114/114 (100%)	114 (100%)	0	100	100
13	J	116/116 (100%)	115 (99%)	1 (1%)	70	81
14	K	104/104 (100%)	104 (100%)	0	100	100
15	L	103/103 (100%)	101 (98%)	2 (2%)	50	73
16	M	109/109 (100%)	108 (99%)	1 (1%)	70	81
17	N	99/103 (96%)	98 (99%)	1 (1%)	68	80
18	O	86/87 (99%)	85 (99%)	1 (1%)	63	79
19	P	99/100 (99%)	95 (96%)	4 (4%)	28	61
20	Q	89/90 (99%)	87 (98%)	2 (2%)	45	71
21	R	84/84 (100%)	84 (100%)	0	100	100
22	S	93/93 (100%)	93 (100%)	0	100	100
23	T	81/84 (96%)	81 (100%)	0	100	100
24	U	84/85 (99%)	83 (99%)	1 (1%)	63	79
25	V	78/78 (100%)	77 (99%)	1 (1%)	61	78
26	W	58/62 (94%)	57 (98%)	1 (2%)	53	75
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	54/55 (98%)	54 (100%)	0	100	100
29	Z	48/49 (98%)	48 (100%)	0	100	100
30	a	59/62 (95%)	58 (98%)	1 (2%)	53	75
31	b	47/48 (98%)	46 (98%)	1 (2%)	47	71
32	c	47/49 (96%)	47 (100%)	0	100	100
33	d	38/38 (100%)	38 (100%)	0	100	100
34	e	51/52 (98%)	50 (98%)	1 (2%)	48	72
35	f	34/34 (100%)	33 (97%)	1 (3%)	37	67
36	g	187/199 (94%)	186 (100%)	1 (0%)	81	85
37	h	171/190 (90%)	168 (98%)	3 (2%)	51	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	i	172/173 (99%)	171 (99%)	1 (1%)	78	84
39	j	119/126 (94%)	119 (100%)	0	100	100
40	k	91/116 (78%)	91 (100%)	0	100	100
41	l	124/147 (84%)	121 (98%)	3 (2%)	43	70
42	m	104/105 (99%)	104 (100%)	0	100	100
43	n	105/107 (98%)	103 (98%)	2 (2%)	50	73
44	o	86/90 (96%)	86 (100%)	0	100	100
45	p	90/99 (91%)	90 (100%)	0	100	100
46	q	102/103 (99%)	101 (99%)	1 (1%)	68	80
47	r	94/96 (98%)	91 (97%)	3 (3%)	34	65
48	s	83/84 (99%)	82 (99%)	1 (1%)	63	79
49	t	76/77 (99%)	76 (100%)	0	100	100
50	u	65/65 (100%)	65 (100%)	0	100	100
51	v	74/78 (95%)	74 (100%)	0	100	100
52	w	57/65 (88%)	57 (100%)	0	100	100
53	x	72/79 (91%)	72 (100%)	0	100	100
54	y	65/66 (98%)	64 (98%)	1 (2%)	57	76
55	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4822/4982 (97%)	4767 (99%)	55 (1%)	63	79

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	6	51	ARG
6	6	59	THR
6	6	60	ASP
6	6	68	VAL
6	6	69	ASP
6	6	89	THR
6	6	90	PHE
6	6	107	LEU
6	6	109	ASP
6	6	149	THR
6	6	152	LYS
6	6	170	ILE
6	6	173	VAL

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Mol	Chain	Res	Type
6	6	174	ILE
6	6	186	ARG
7	B	16	VAL
9	D	7	ASP
10	E	153	ASP
11	F	72	LEU
11	F	141	ILE
13	J	30	THR
15	L	30	THR
15	L	99	ASN
16	M	74	THR
17	N	50	PRO
18	O	47	VAL
19	P	30	VAL
19	P	32	VAL
19	P	53	ARG
19	P	60	THR
20	Q	4	VAL
20	Q	53	ARG
24	U	70	VAL
25	V	48	MET
26	W	10	THR
30	a	28	VAL
31	b	55	ILE
34	e	6	THR
35	f	3	VAL
36	g	130	THR
37	h	52	VAL
37	h	116	VAL
37	h	201	TRP
38	i	21	LEU
41	l	6	VAL
41	l	27	VAL
41	l	60	GLU
43	n	9	THR
43	n	66	THR
46	q	80	ILE
47	r	9	ILE
47	r	16	VAL
47	r	68	ASP
48	s	27	LEU
54	y	30	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (88) such sidechains are listed below:

Mol	Chain	Res	Type
6	6	77	ASN
6	6	92	GLN
6	6	103	ASN
6	6	169	GLN
7	B	21	ASN
7	B	53	HIS
7	B	143	ASN
7	B	197	ASN
9	D	92	HIS
9	D	136	GLN
10	E	27	GLN
11	F	73	ASN
12	G	2	GLN
12	G	28	ASN
12	G	119	ASN
14	K	89	ASN
15	L	4	ASN
16	M	13	HIS
17	N	18	GLN
18	O	34	HIS
18	O	43	ASN
19	P	12	GLN
19	P	52	ASN
22	S	15	GLN
22	S	60	HIS
22	S	61	ASN
23	T	70	HIS
24	U	40	ASN
24	U	74	ASN
25	V	49	ASN
26	W	12	ASN
27	X	16	ASN
27	X	17	ASN
28	Y	15	ASN
28	Y	20	ASN
28	Y	31	GLN
28	Y	36	GLN
28	Y	58	ASN
29	Z	49	ASN
30	a	33	ASN
31	b	6	ASN

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Mol	Chain	Res	Type
33	d	13	ASN
33	d	16	HIS
33	d	26	ASN
34	e	43	HIS
36	g	39	HIS
36	g	51	ASN
36	g	89	GLN
37	h	41	GLN
37	h	100	GLN
37	h	123	GLN
37	h	140	ASN
37	h	190	HIS
38	i	36	GLN
38	i	40	GLN
38	i	54	GLN
38	i	59	GLN
38	i	74	ASN
38	i	116	GLN
38	i	152	GLN
40	k	68	GLN
41	l	86	GLN
42	m	18	GLN
42	m	21	ASN
42	m	76	GLN
43	n	75	GLN
43	n	81	HIS
44	o	35	GLN
44	o	58	ASN
45	p	15	GLN
45	p	118	HIS
46	q	29	GLN
46	q	46	ASN
47	r	8	ASN
47	r	105	ASN
48	s	49	GLN
50	u	9	HIS
50	u	26	ASN
50	u	40	ASN
51	v	50	ASN
52	w	19	GLN
52	w	54	GLN
53	x	69	HIS

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Mol	Chain	Res	Type
54	y	13	GLN
54	y	48	GLN
54	y	52	ASN
54	y	78	ASN
55	z	9	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2811/2904 (96%)	522 (18%)	46 (1%)
2	2	1530/1540 (99%)	260 (16%)	6 (0%)
3	3	119/120 (99%)	22 (18%)	0
4	4	5/18 (27%)	1 (20%)	0
5	5	76/77 (98%)	24 (31%)	4 (5%)
All	All	4541/4659 (97%)	829 (18%)	56 (1%)

All (829) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	36	G
1	1	46	G
1	1	50	U
1	1	51	G
1	1	63	A
1	1	71	A
1	1	74	A
1	1	75	G
1	1	84	A
1	1	102	U
1	1	103	A
1	1	118	A
1	1	119	A
1	1	120	U
1	1	125	A
1	1	135	U
1	1	139	U
1	1	140	C

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Mol	Chain	Res	Type
1	1	141	G
1	1	142	A
1	1	144	A
1	1	149	A
1	1	162	U
1	1	163	C
1	1	181	A
1	1	196	A
1	1	199	A
1	1	215	G
1	1	216	A
1	1	218	A
1	1	221	A
1	1	222	A
1	1	228	C
1	1	229	C
1	1	242	G
1	1	243	U
1	1	248	G
1	1	255	A
1	1	265	A
1	1	267	C
1	1	276	U
1	1	279	A
1	1	281	C
1	1	285	G
1	1	311	A
1	1	323	C
1	1	329	G
1	1	330	A
1	1	331	C
1	1	345	A
1	1	361	G
1	1	362	A
1	1	367	G
1	1	369	U
1	1	370	G
1	1	371	A
1	1	372	G
1	1	373	U
1	1	386	G
1	1	387	U

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Mol	Chain	Res	Type
1	1	388	G
1	1	395	U
1	1	396	G
1	1	403	U
1	1	404	A
1	1	405	U
1	1	406	G
1	1	411	G
1	1	417	C
1	1	421	C
1	1	422	A
1	1	423	A
1	1	424	G
1	1	435	C
1	1	448	U
1	1	455	C
1	1	456	C
1	1	458	G
1	1	459	U
1	1	465	G
1	1	481	G
1	1	482	A
1	1	489	G
1	1	491	G
1	1	494	G
1	1	505	A
1	1	509	C
1	1	510	C
1	1	530	G
1	1	532	A
1	1	533	G
1	1	545	U
1	1	546	U
1	1	547	A
1	1	548	G
1	1	549	G
1	1	550	C
1	1	556	A
1	1	563	A
1	1	573	U
1	1	575	A
1	1	586	A

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Mol	Chain	Res	Type
1	1	603	A
1	1	614	A
1	1	615	U
1	1	616	A
1	1	622	G
1	1	627	A
1	1	637	A
1	1	645	C
1	1	646	U
1	1	647	G
1	1	654	A
1	1	655	A
1	1	659	G
1	1	669	G
1	1	685	A
1	1	686	U
1	1	694	U
1	1	695	G
1	1	711	G
1	1	717	C
1	1	726	G
1	1	730	A
1	1	747	C
1	1	752	A
1	1	762	U
1	1	764	A
1	1	765	C
1	1	775	G
1	1	776	G
1	1	782	A
1	1	783	A
1	1	784	G
1	1	785	G
1	1	789	A
1	1	805	G
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	844	A
1	1	845	A
1	1	846	U

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Mol	Chain	Res	Type
1	1	847	U
1	1	858	G
1	1	859	G
1	1	877	A
1	1	878	A
1	1	879	G
1	1	882	G
1	1	885	C
1	1	886	A
1	1	891	G
1	1	892	A
1	1	897	C
1	1	907	G
1	1	910	A
1	1	933	A
1	1	938	G
1	1	941	A
1	1	945	A
1	1	946	C
1	1	961	C
1	1	973	A
1	1	974	G
1	1	975	A
1	1	983	A
1	1	995	C
1	1	996	A
1	1	997	G
1	1	999	U
1	1	1006	C
1	1	1012	U
1	1	1013	C
1	1	1021	A
1	1	1022	G
1	1	1023	U
1	1	1026	G
1	1	1033	U
1	1	1040	A
1	1	1045	C
1	1	1046	A
1	1	1047	G
1	1	1057	A
1	1	1059	G

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Mol	Chain	Res	Type
1	1	1060	U
1	1	1061	U
1	1	1062	G
1	1	1064	C
1	1	1065	U
1	1	1066	U
1	1	1067	A
1	1	1068	G
1	1	1069	A
1	1	1070	A
1	1	1071	G
1	1	1072	C
1	1	1073	A
1	1	1076	C
1	1	1078	U
1	1	1079	C
1	1	1081	U
1	1	1085	A
1	1	1086	A
1	1	1087	G
1	1	1088	A
1	1	1089	A
1	1	1090	A
1	1	1095	A
1	1	1096	A
1	1	1097	U
1	1	1098	A
1	1	1099	G
1	1	1100	C
1	1	1103	A
1	1	1104	C
1	1	1106	G
1	1	1111	A
1	1	1112	G
1	1	1130	U
1	1	1132	U
1	1	1133	A
1	1	1134	A
1	1	1135	C
1	1	1139	G
1	1	1142	A
1	1	1172	C

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Mol	Chain	Res	Type
1	1	1173	U
1	1	1174	U
1	1	1175	A
1	1	1176	U
1	1	1177	G
1	1	1180	U
1	1	1205	A
1	1	1206	G
1	1	1211	C
1	1	1212	G
1	1	1237	A
1	1	1241	A
1	1	1247	A
1	1	1248	G
1	1	1250	G
1	1	1253	A
1	1	1256	G
1	1	1265	A
1	1	1271	G
1	1	1272	A
1	1	1300	G
1	1	1301	A
1	1	1302	A
1	1	1306	C
1	1	1321	A
1	1	1329	U
1	1	1330	C
1	1	1341	G
1	1	1345	C
1	1	1352	U
1	1	1359	A
1	1	1365	A
1	1	1368	G
1	1	1379	U
1	1	1383	A
1	1	1395	A
1	1	1397	U
1	1	1416	G
1	1	1420	A
1	1	1421	G
1	1	1428	C
1	1	1434	A

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Mol	Chain	Res	Type
1	1	1437	C
1	1	1453	A
1	1	1458	U
1	1	1459	G
1	1	1461	C
1	1	1482	G
1	1	1488	C
1	1	1489	C
1	1	1490	A
1	1	1491	G
1	1	1497	U
1	1	1504	A
1	1	1509	A
1	1	1515	A
1	1	1523	U
1	1	1524	G
1	1	1529	G
1	1	1532	A
1	1	1534	U
1	1	1535	A
1	1	1536	C
1	1	1537	G
1	1	1542	U
1	1	1558	C
1	1	1559	U
1	1	1560	G
1	1	1569	A
1	1	1578	U
1	1	1583	A
1	1	1584	U
1	1	1585	C
1	1	1608	A
1	1	1618	A
1	1	1647	U
1	1	1648	U
1	1	1651	G
1	1	1665	A
1	1	1667	G
1	1	1674	G
1	1	1675	C
1	1	1694	C
1	1	1695	G

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Mol	Chain	Res	Type
1	1	1698	A
1	1	1699	G
1	1	1715	G
1	1	1729	U
1	1	1730	C
1	1	1731	G
1	1	1733	G
1	1	1735	A
1	1	1738	G
1	1	1756	G
1	1	1758	U
1	1	1764	C
1	1	1773	A
1	1	1776	G
1	1	1780	A
1	1	1787	A
1	1	1800	C
1	1	1801	A
1	1	1802	A
1	1	1808	A
1	1	1809	A
1	1	1816	C
1	1	1818	U
1	1	1819	A
1	1	1826	G
1	1	1829	A
1	1	1833	C
1	1	1848	A
1	1	1858	A
1	1	1870	C
1	1	1871	A
1	1	1872	A
1	1	1882	U
1	1	1896	G
1	1	1901	A
1	1	1906	G
1	1	1913	A
1	1	1914	C
1	1	1917	U
1	1	1929	G
1	1	1930	G
1	1	1931	U

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Mol	Chain	Res	Type
1	1	1937	A
1	1	1938	A
1	1	1940	U
1	1	1941	C
1	1	1955	U
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1991	U
1	1	1993	U
1	1	1996	C
1	1	1997	C
1	1	2022	U
1	1	2023	C
1	1	2030	A
1	1	2031	A
1	1	2033	A
1	1	2043	C
1	1	2055	C
1	1	2056	G
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	A
1	1	2072	C
1	1	2093	G
1	1	2096	C
1	1	2098	U
1	1	2102	G
1	1	2103	C
1	1	2104	C
1	1	2190	G
1	1	2191	A
1	1	2193	G
1	1	2194	U
1	1	2198	A
1	1	2203	U
1	1	2204	G
1	1	2211	A
1	1	2213	U
1	1	2214	C

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Mol	Chain	Res	Type
1	1	2225	A
1	1	2226	C
1	1	2238	G
1	1	2239	G
1	1	2250	G
1	1	2251	G
1	1	2278	A
1	1	2279	G
1	1	2283	C
1	1	2287	A
1	1	2288	A
1	1	2297	A
1	1	2305	U
1	1	2309	A
1	1	2320	U
1	1	2321	U
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2334	U
1	1	2345	G
1	1	2350	C
1	1	2361	G
1	1	2382	G
1	1	2383	G
1	1	2385	C
1	1	2391	G
1	1	2392	A
1	1	2402	U
1	1	2403	C
1	1	2406	A
1	1	2418	A
1	1	2422	C
1	1	2424	C
1	1	2425	A
1	1	2426	A
1	1	2429	G
1	1	2430	A
1	1	2431	U
1	1	2435	A
1	1	2441	U
1	1	2448	A

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Mol	Chain	Res	Type
1	1	2449	U
1	1	2470	G
1	1	2475	C
1	1	2476	A
1	1	2492	U
1	1	2502	G
1	1	2503	A
1	1	2504	U
1	1	2505	G
1	1	2506	U
1	1	2507	C
1	1	2518	A
1	1	2529	G
1	1	2535	G
1	1	2547	A
1	1	2554	U
1	1	2566	A
1	1	2567	G
1	1	2572	A
1	1	2573	C
1	1	2576	G
1	1	2582	G
1	1	2585	U
1	1	2586	U
1	1	2602	A
1	1	2604	U
1	1	2609	U
1	1	2613	U
1	1	2615	U
1	1	2629	U
1	1	2630	G
1	1	2639	A
1	1	2646	C
1	1	2654	A
1	1	2655	G
1	1	2656	U
1	1	2661	G
1	1	2682	A
1	1	2689	U
1	1	2690	U
1	1	2707	U
1	1	2713	U

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Mol	Chain	Res	Type
1	1	2714	G
1	1	2718	G
1	1	2722	G
1	1	2726	A
1	1	2727	A
1	1	2732	G
1	1	2733	A
1	1	2744	G
1	1	2748	A
1	1	2764	A
1	1	2765	A
1	1	2769	U
1	1	2778	A
1	1	2779	U
1	1	2791	G
1	1	2793	C
1	1	2798	U
1	1	2799	A
1	1	2800	A
1	1	2807	U
1	1	2808	G
1	1	2809	A
1	1	2818	U
1	1	2820	A
1	1	2821	A
1	1	2833	U
1	1	2843	G
1	1	2849	U
1	1	2861	U
1	1	2867	G
1	1	2868	A
1	1	2872	A
1	1	2873	A
1	1	2880	C
1	1	2884	U
1	1	2885	G
1	1	2887	A
1	1	2893	A
2	2	2	A
2	2	4	U
2	2	6	G
2	2	9	G

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Mol	Chain	Res	Type
2	2	22	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	50	A
2	2	51	A
2	2	52	C
2	2	70	U
2	2	72	A
2	2	73	C
2	2	74	A
2	2	79	G
2	2	82	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	87	C
2	2	88	U
2	2	92	U
2	2	94	G
2	2	120	A
2	2	121	U
2	2	130	A
2	2	131	A
2	2	141	G
2	2	163	C
2	2	183	C
2	2	184	G
2	2	189	A
2	2	197	A
2	2	204	G
2	2	208	U
2	2	209	U
2	2	210	C
2	2	211	G
2	2	212	G
2	2	226	G
2	2	246	A
2	2	247	G
2	2	251	G
2	2	266	G

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Mol	Chain	Res	Type
2	2	267	C
2	2	279	A
2	2	280	C
2	2	289	G
2	2	299	G
2	2	316	C
2	2	321	A
2	2	326	G
2	2	328	C
2	2	330	C
2	2	332	G
2	2	347	G
2	2	351	G
2	2	352	C
2	2	353	A
2	2	354	G
2	2	365	U
2	2	367	U
2	2	372	C
2	2	382	A
2	2	384	G
2	2	392	C
2	2	397	A
2	2	406	G
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	424	G
2	2	428	G
2	2	429	U
2	2	458	U
2	2	463	U
2	2	464	U
2	2	465	A
2	2	467	U
2	2	468	A
2	2	474	G
2	2	481	G
2	2	482	A
2	2	484	G

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Mol	Chain	Res	Type
2	2	486	U
2	2	496	A
2	2	511	C
2	2	517	G
2	2	518	C
2	2	521	G
2	2	527	G7M
2	2	531	U
2	2	532	A
2	2	533	A
2	2	536	C
2	2	547	A
2	2	559	A
2	2	564	C
2	2	568	G
2	2	570	G
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	579	A
2	2	588	G
2	2	596	A
2	2	639	G
2	2	650	G
2	2	653	U
2	2	665	A
2	2	687	A
2	2	703	G
2	2	718	A
2	2	721	G
2	2	723	U
2	2	724	G
2	2	731	G
2	2	734	G
2	2	747	A
2	2	748	G
2	2	755	G
2	2	777	A
2	2	793	U
2	2	794	A
2	2	813	U

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Mol	Chain	Res	Type
2	2	815	A
2	2	817	C
2	2	828	U
2	2	829	G
2	2	836	G
2	2	841	C
2	2	843	U
2	2	844	G
2	2	845	A
2	2	846	G
2	2	900	A
2	2	914	A
2	2	926	G
2	2	934	C
2	2	935	A
2	2	960	U
2	2	966	2MG
2	2	967	5MC
2	2	968	A
2	2	969	A
2	2	971	G
2	2	974	A
2	2	975	A
2	2	976	G
2	2	977	A
2	2	982	U
2	2	992	U
2	2	993	G
2	2	994	A
2	2	996	A
2	2	1004	A
2	2	1008	U
2	2	1009	U
2	2	1018	G
2	2	1022	A
2	2	1026	G
2	2	1027	C
2	2	1028	C
2	2	1029	U
2	2	1030	U
2	2	1031	C
2	2	1034	G

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Mol	Chain	Res	Type
2	2	1035	A
2	2	1037	C
2	2	1043	G
2	2	1065	U
2	2	1084	G
2	2	1085	U
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1108	G
2	2	1124	G
2	2	1131	G
2	2	1133	G
2	2	1136	C
2	2	1137	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1143	G
2	2	1145	A
2	2	1146	A
2	2	1151	A
2	2	1158	C
2	2	1159	U
2	2	1167	A
2	2	1168	U
2	2	1171	A
2	2	1175	G
2	2	1176	A
2	2	1184	G
2	2	1196	A
2	2	1197	A
2	2	1213	A
2	2	1214	C
2	2	1227	A
2	2	1228	C
2	2	1236	A
2	2	1238	A
2	2	1239	A
2	2	1240	U
2	2	1241	G
2	2	1257	A

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Mol	Chain	Res	Type
2	2	1260	G
2	2	1275	A
2	2	1280	A
2	2	1281	C
2	2	1285	A
2	2	1286	U
2	2	1287	A
2	2	1289	A
2	2	1299	A
2	2	1300	G
2	2	1302	C
2	2	1305	G
2	2	1317	C
2	2	1320	C
2	2	1322	C
2	2	1323	G
2	2	1332	A
2	2	1338	G
2	2	1346	A
2	2	1363	A
2	2	1370	G
2	2	1379	G
2	2	1381	U
2	2	1384	C
2	2	1398	A
2	2	1399	C
2	2	1419	G
2	2	1429	A
2	2	1441	A
2	2	1442	G
2	2	1446	A
2	2	1452	C
2	2	1453	G
2	2	1475	G
2	2	1487	G
2	2	1492	A
2	2	1493	A
2	2	1495	U
2	2	1497	G
2	2	1499	A
2	2	1503	A
2	2	1506	U

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Mol	Chain	Res	Type
2	2	1517	G
2	2	1519	MA6
2	2	1529	G
2	2	1530	G
3	3	8	C
3	3	24	G
3	3	35	C
3	3	45	A
3	3	48	U
3	3	49	C
3	3	56	G
3	3	67	G
3	3	73	A
3	3	74	U
3	3	77	U
3	3	78	A
3	3	79	G
3	3	88	C
3	3	89	U
3	3	90	C
3	3	108	A
3	3	109	A
3	3	116	G
3	3	117	G
3	3	118	C
3	3	119	A
4	4	15	G
5	5	2	G
5	5	3	G
5	5	4	C
5	5	5	A
5	5	6	C
5	5	10	G
5	5	14	A
5	5	17	C
5	5	18	G
5	5	19	G
5	5	20	U
5	5	21	A
5	5	22	G
5	5	43	G
5	5	46	G

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Mol	Chain	Res	Type
5	5	47	U
5	5	48	C
5	5	49	G
5	5	61	C
5	5	68	U
5	5	69	G
5	5	72	G
5	5	73	A
5	5	76	A

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	227	A
1	1	228	C
1	1	242	G
1	1	323	C
1	1	369	U
1	1	372	G
1	1	404	A
1	1	421	C
1	1	455	C
1	1	458	G
1	1	481	G
1	1	546	U
1	1	549	G
1	1	555	G
1	1	746	U
1	1	774	G
1	1	784	G
1	1	858	G
1	1	1020	A
1	1	1022	G
1	1	1070	A
1	1	1111	A
1	1	1236	G
1	1	1240	U
1	1	1320	C
1	1	1329	U
1	1	1396	U
1	1	1730	C
1	1	1801	A

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Mol	Chain	Res	Type
1	1	1818	U
1	1	1847	G
1	1	1857	G
1	1	1913	A
1	1	1930	G
1	1	1940	U
1	1	2190	G
1	1	2286	G
1	1	2308	G
1	1	2319	G
1	1	2326	C
1	1	2391	G
1	1	2405	G
1	1	2609	U
1	1	2655	G
1	1	2808	G
1	1	2867	G
2	2	516	PSU
2	2	575	G
2	2	966	2MG
2	2	1109	C
2	2	1145	A
2	2	1383	C
5	5	2	G
5	5	3	G
5	5	18	G
5	5	72	G

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

13 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
2	PSU	2	516	2	18,21,22	1.06	1 (5%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	4OC	2	1402	2	20,23,24	2.92	8 (40%)	25,32,35	1.14	3 (12%)
2	2MG	2	1207	2	23,26,27	2.74	8 (34%)	33,38,41	2.14	10 (30%)
2	2MG	2	1516	2	23,26,27	2.60	8 (34%)	33,38,41	2.45	11 (33%)
2	MA6	2	1519	2	23,26,27	1.74	6 (26%)	33,38,41	3.01	12 (36%)
2	G7M	2	527	2	23,26,27	3.51	11 (47%)	34,39,42	1.86	7 (20%)
2	MA6	2	1518	2	23,26,27	1.70	5 (21%)	33,38,41	2.93	12 (36%)
2	5MC	2	967	2	19,22,23	3.45	8 (42%)	26,32,35	1.07	2 (7%)
6	KEO	6	34	6	16,18,19	0.74	0	15,21,23	1.54	1 (6%)
46	0TD	q	89	46	8,9,10	2.55	2 (25%)	6,11,13	1.24	0
2	5MC	2	1407	2	19,22,23	3.29	8 (42%)	26,32,35	1.06	1 (3%)
2	2MG	2	966	2	23,26,27	2.82	8 (34%)	33,38,41	2.17	7 (21%)
2	UR3	2	1498	2	19,22,23	2.48	5 (26%)	26,32,35	1.58	3 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
6	KEO	6	34	6	-	8/19/20/22	-
46	0TD	q	89	46	-	2/7/12/14	-
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2

All (78) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	527	G7M	C8-N7	10.30	1.50	1.33
2	2	967	5MC	C6-C5	8.49	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1407	5MC	C6-C5	8.37	1.48	1.34
2	2	966	2MG	C2-N3	7.26	1.45	1.32
2	2	1207	2MG	C2-N3	6.82	1.45	1.32
2	2	1402	4OC	C4-N3	6.43	1.43	1.32
2	2	966	2MG	C4-N3	6.34	1.48	1.34
2	2	1207	2MG	C4-N3	6.19	1.48	1.34
2	2	967	5MC	C4-N3	6.16	1.44	1.34
46	q	89	0TD	CB-CA	-6.08	1.52	1.54
2	2	1516	2MG	C2-N3	5.97	1.43	1.32
2	2	1402	4OC	C6-C5	5.95	1.48	1.35
2	2	1498	UR3	C2-N1	5.91	1.46	1.38
2	2	527	G7M	C2-N3	5.86	1.47	1.33
2	2	1407	5MC	C4-N3	5.86	1.43	1.34
2	2	1498	UR3	C6-C5	5.84	1.48	1.35
2	2	967	5MC	C2-N3	5.66	1.47	1.36
2	2	966	2MG	C2-N2	5.66	1.45	1.33
2	2	1402	4OC	C2-N3	5.56	1.47	1.36
2	2	1407	5MC	C2-N3	5.55	1.47	1.36
2	2	1516	2MG	C4-N3	5.52	1.46	1.34
2	2	527	G7M	C8-N9	5.51	1.50	1.35
2	2	1207	2MG	C2-N2	5.45	1.44	1.33
2	2	967	5MC	C5-C4	5.28	1.48	1.44
2	2	1516	2MG	C2-N2	5.24	1.44	1.33
2	2	527	G7M	C4-N3	5.19	1.46	1.34
2	2	527	G7M	C5-N7	4.70	1.44	1.39
2	2	1407	5MC	C5-C4	4.29	1.47	1.44
2	2	967	5MC	C4-N4	4.23	1.44	1.34
2	2	1207	2MG	C2-N1	4.09	1.43	1.36
2	2	1407	5MC	C4-N4	4.02	1.44	1.34
2	2	1402	4OC	C4-N4	4.02	1.44	1.36
2	2	966	2MG	C2-N1	3.98	1.43	1.36
2	2	1498	UR3	C2-N3	3.96	1.46	1.39
2	2	1516	2MG	C2-N1	3.90	1.42	1.36
2	2	1519	MA6	C5-C4	-3.82	1.32	1.39
2	2	967	5MC	C6-N1	3.76	1.44	1.38
2	2	966	2MG	C5-N7	-3.74	1.31	1.39
2	2	1407	5MC	C6-N1	3.73	1.44	1.38
2	2	1518	MA6	C5-C4	-3.65	1.32	1.39
2	2	1519	MA6	C5-N7	-3.63	1.32	1.39
2	2	527	G7M	O6-C6	-3.61	1.16	1.23
2	2	1516	2MG	C5-N7	-3.55	1.31	1.39
2	2	1207	2MG	C5-N7	-3.53	1.32	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1402	4OC	O2-C2	-3.51	1.17	1.23
2	2	1402	4OC	C2-N1	3.48	1.47	1.40
2	2	1518	MA6	C5-N7	-3.46	1.32	1.39
2	2	967	5MC	C2-N1	3.40	1.47	1.40
2	2	1518	MA6	C6-N6	3.38	1.46	1.36
2	2	1402	4OC	C5-C4	3.38	1.48	1.41
2	2	1498	UR3	O2-C2	-3.30	1.16	1.22
2	2	1519	MA6	C6-N6	3.21	1.45	1.36
2	2	1498	UR3	O4-C4	-3.13	1.16	1.23
2	2	967	5MC	O2-C2	-3.11	1.17	1.23
2	2	1407	5MC	O2-C2	-3.10	1.17	1.23
2	2	1407	5MC	C2-N1	3.07	1.46	1.40
2	2	1516	2MG	C4-N9	-3.05	1.30	1.38
2	2	1519	MA6	C8-N9	-3.03	1.32	1.37
2	2	527	G7M	C2-N2	3.02	1.41	1.34
2	2	1207	2MG	O6-C6	-3.01	1.17	1.23
2	2	527	G7M	C2-N1	3.01	1.44	1.37
2	2	966	2MG	O6-C6	-2.99	1.17	1.23
2	2	1516	2MG	O6-C6	-2.96	1.17	1.23
2	2	1518	MA6	C4-N9	-2.94	1.31	1.37
2	2	527	G7M	C6-N1	2.92	1.44	1.38
2	2	527	G7M	C5-C6	2.83	1.51	1.43
2	2	527	G7M	C4-N9	2.80	1.45	1.38
2	2	516	PSU	C6-C5	2.79	1.38	1.35
2	2	1519	MA6	C4-N9	-2.73	1.32	1.37
2	2	1402	4OC	C6-N1	2.67	1.44	1.38
2	2	1518	MA6	C8-N9	-2.64	1.33	1.37
2	2	1207	2MG	C4-N9	-2.57	1.31	1.38
2	2	966	2MG	C4-N9	-2.42	1.31	1.38
2	2	1516	2MG	C5-C6	2.18	1.52	1.44
2	2	1207	2MG	C5-C6	2.12	1.52	1.44
2	2	966	2MG	C5-C6	2.03	1.52	1.44
2	2	1519	MA6	C5-C6	-2.03	1.36	1.41
46	q	89	0TD	CSB-SB	-2.01	1.75	1.79

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	N1-C6-N6	-10.22	104.41	116.86
2	2	1518	MA6	N1-C6-N6	-10.08	104.58	116.86
2	2	1516	2MG	C2-N3-C4	6.63	120.29	112.00
2	2	1518	MA6	C5-C6-N6	6.54	135.69	125.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	C5-C6-N6	6.50	135.62	125.33
2	2	966	2MG	C2-N3-C4	6.26	119.83	112.00
2	2	1516	2MG	N1-C2-N2	6.02	122.70	116.56
2	2	1207	2MG	C2-N3-C4	6.00	119.51	112.00
2	2	966	2MG	C5-C4-N3	-5.68	119.35	128.39
2	2	1519	MA6	N1-C2-N3	-5.67	120.00	128.58
2	2	1518	MA6	N1-C2-N3	-5.62	120.08	128.58
2	2	1498	UR3	C4-N3-C2	-5.35	120.28	124.58
2	2	1519	MA6	C5-C4-N3	-5.19	119.57	126.72
2	2	1207	2MG	C5-C4-N3	-5.15	120.19	128.39
2	2	516	PSU	C4-N3-C2	-5.09	119.37	126.37
2	2	516	PSU	N1-C2-N3	5.01	120.45	115.17
2	2	1516	2MG	C5-C4-N3	-4.85	120.67	128.39
2	2	527	G7M	C2-N3-C4	4.84	120.64	112.30
2	2	1516	2MG	C2-N1-C6	-4.77	118.78	124.55
2	2	966	2MG	C2-N1-C6	-4.74	118.81	124.55
2	2	1519	MA6	C4-C5-C6	4.69	120.76	115.91
2	2	1518	MA6	C5-C4-N3	-4.62	120.35	126.72
2	2	1207	2MG	C2-N1-C6	-4.58	119.02	124.55
2	2	527	G7M	C5-C4-N3	-4.55	119.56	128.15
6	6	34	KEO	CB-CA-C	-4.37	104.26	110.99
2	2	527	G7M	C5-C6-N1	4.28	120.70	111.84
2	2	1518	MA6	C4-C5-C6	4.15	120.20	115.91
2	2	1518	MA6	N9-C8-N7	-3.94	108.35	113.94
2	2	1516	2MG	CM2-N2-C2	-3.81	115.47	123.65
2	2	1498	UR3	C5-C4-N3	3.76	119.99	115.04
2	2	966	2MG	N9-C4-N3	3.75	133.45	125.95
2	2	1519	MA6	N9-C8-N7	-3.70	108.69	113.94
2	2	967	5MC	C5-C6-N1	-3.66	119.34	123.31
2	2	527	G7M	C2-N1-C6	-3.59	118.60	125.11
2	2	527	G7M	O6-C6-C5	-3.45	120.31	128.01
2	2	1518	MA6	C2-N1-C6	3.40	120.13	111.83
2	2	1407	5MC	C5-C6-N1	-3.38	119.64	123.31
2	2	1519	MA6	C2-N3-C4	3.36	120.03	111.83
2	2	1207	2MG	N1-C2-N2	3.31	119.94	116.56
2	2	1519	MA6	C2-N1-C6	3.21	119.66	111.83
2	2	1518	MA6	C2-N3-C4	3.14	119.50	111.83
2	2	1207	2MG	N9-C8-N7	-3.05	107.74	113.40
2	2	1516	2MG	N2-C2-N3	-3.00	116.69	120.51
2	2	1402	4OC	CM4-N4-C4	-2.99	116.61	122.45
2	2	1519	MA6	N3-C4-N9	2.95	132.19	127.17
2	2	1516	2MG	N9-C8-N7	-2.94	107.95	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	966	2MG	N9-C8-N7	-2.89	108.05	113.40
2	2	1207	2MG	N9-C4-N3	2.88	131.72	125.95
2	2	966	2MG	C5-C6-N1	2.83	120.45	113.25
2	2	1516	2MG	C5-C6-N1	2.74	120.24	113.25
2	2	1207	2MG	C5-C6-N1	2.74	120.23	113.25
2	2	527	G7M	N9-C8-N7	-2.62	106.13	112.48
2	2	1518	MA6	N3-C4-N9	2.61	131.61	127.17
2	2	516	PSU	C6-N1-C2	-2.58	120.30	122.69
2	2	1207	2MG	CM2-N2-C2	-2.57	118.13	123.65
2	2	1519	MA6	C5-N7-C8	2.55	107.46	103.45
2	2	1518	MA6	C5-N7-C8	2.47	107.33	103.45
2	2	966	2MG	O6-C6-C5	-2.43	120.12	126.53
2	2	1207	2MG	O6-C6-C5	-2.39	120.22	126.53
2	2	1516	2MG	O6-C6-C5	-2.39	120.24	126.53
2	2	967	5MC	CM5-C5-C6	-2.23	119.83	122.85
2	2	1519	MA6	C5-C4-N9	2.23	108.24	105.81
2	2	1402	4OC	C6-C5-C4	2.23	119.69	117.00
2	2	516	PSU	O2-C2-N1	-2.21	120.51	122.79
2	2	527	G7M	N9-C4-N3	2.19	130.34	125.95
2	2	1402	4OC	O2-C2-N3	-2.19	118.88	122.33
2	2	1519	MA6	C4-C5-N7	-2.15	108.13	110.58
2	2	1498	UR3	C1'-N1-C2	2.13	120.53	117.04
2	2	1207	2MG	C8-N7-C5	2.12	108.04	104.26
2	2	1516	2MG	C5-C4-N9	2.08	109.38	105.66
2	2	1516	2MG	C4-C5-N7	-2.07	107.39	110.67
2	2	1518	MA6	C4-N9-C8	2.07	107.91	105.74
2	2	1518	MA6	C5-C4-N9	2.04	108.03	105.81

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	967	5MC	C3'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
6	6	34	KEO	CE-CD-CG-CB
6	6	34	KEO	CE-CD-CG-O01
6	6	34	KEO	CG-CD-CE-NZ
6	6	34	KEO	C05-C06-C07-C08
6	6	34	KEO	C05-C06-C07-N02

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Mol	Chain	Res	Type	Atoms
6	6	34	KEO	C06-C07-C08-C09
6	6	34	KEO	C06-C05-NZ-CE
2	2	527	G7M	C3'-C4'-C5'-O5'
6	6	34	KEO	O02-C05-NZ-CE
2	2	527	G7M	O4'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
2	2	1402	4OC	O4'-C4'-C5'-O5'
46	q	89	0TD	CG-CB-SB-CSB
46	q	89	0TD	SB-CB-CG-OD1
2	2	1402	4OC	C3'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	516	PSU	1	0
2	2	1402	4OC	1	0
2	2	1207	2MG	2	0
2	2	1519	MA6	1	0
2	2	1518	MA6	2	0
6	6	34	KEO	3	0
2	2	966	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 481 ligands modelled in this entry, 481 are monoatomic - leaving 0 for Mogul analysis.

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.

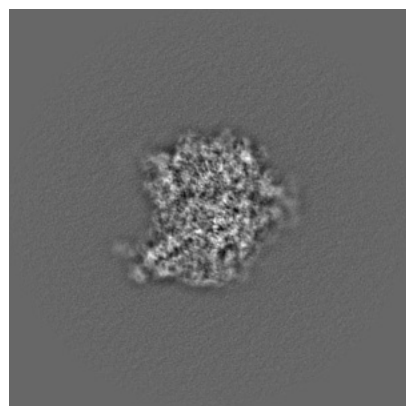
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43752. These allow visual inspection of the internal detail of the map and identification of artifacts.

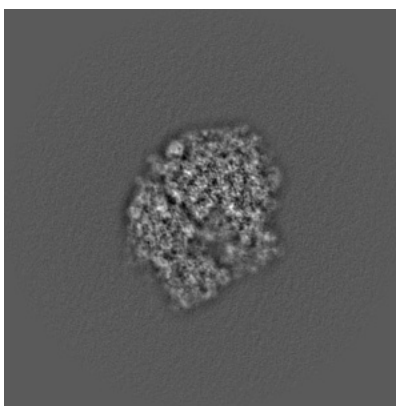
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

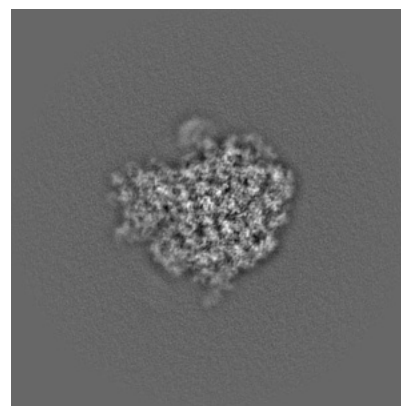
6.1.1 Primary map



X

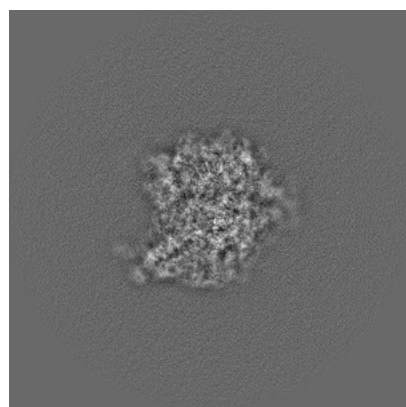


Y

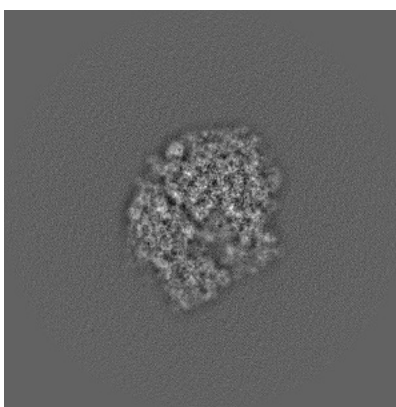


Z

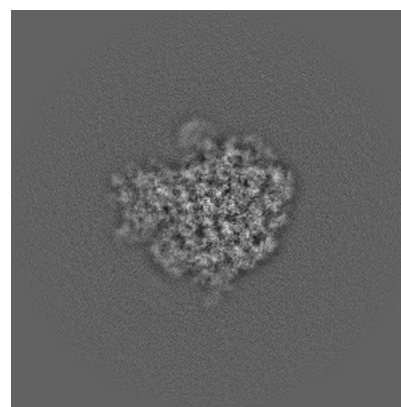
6.1.2 Raw map



X



Y

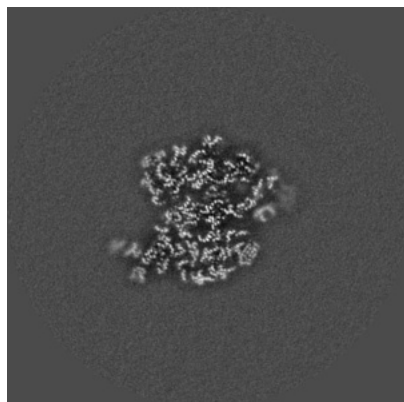


Z

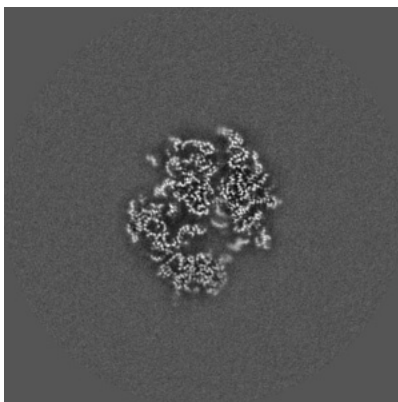
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

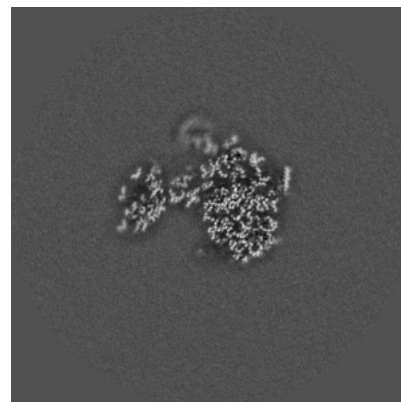
6.2.1 Primary map



X Index: 256

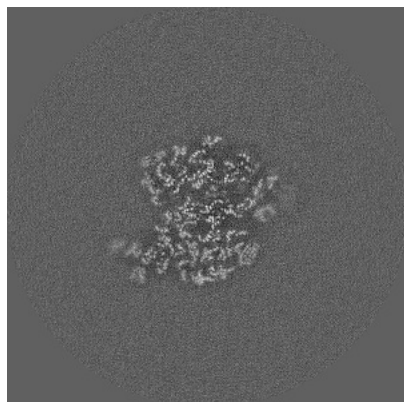


Y Index: 256

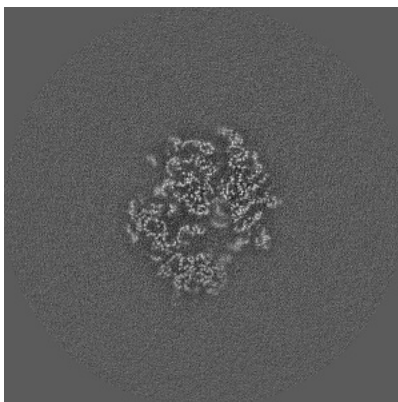


Z Index: 256

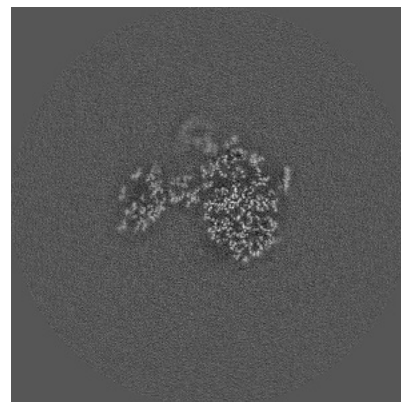
6.2.2 Raw map



X Index: 256



Y Index: 256

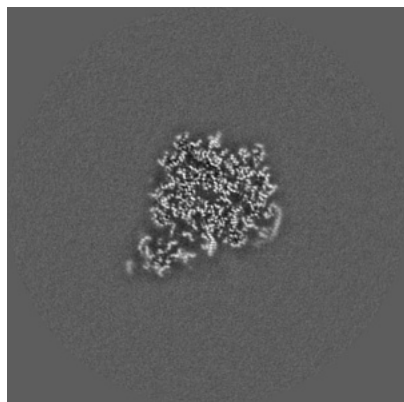


Z Index: 256

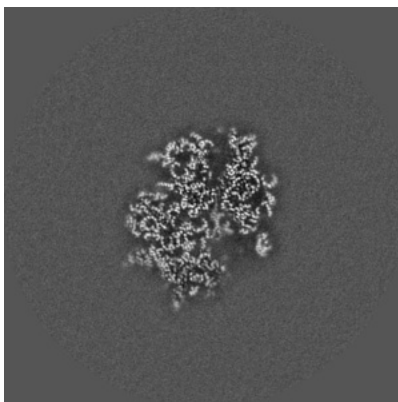
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

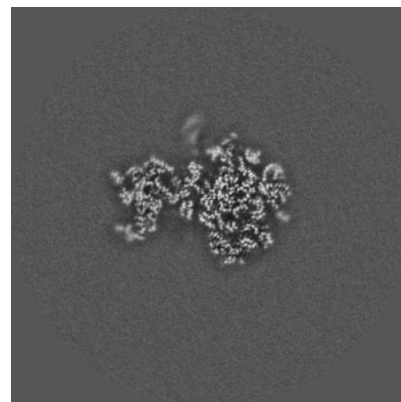
6.3.1 Primary map



X Index: 283

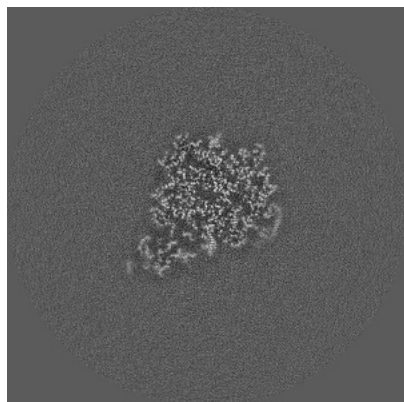


Y Index: 263

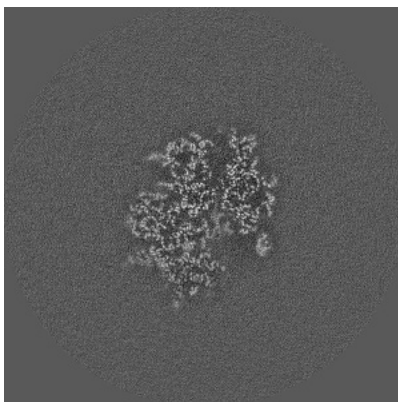


Z Index: 241

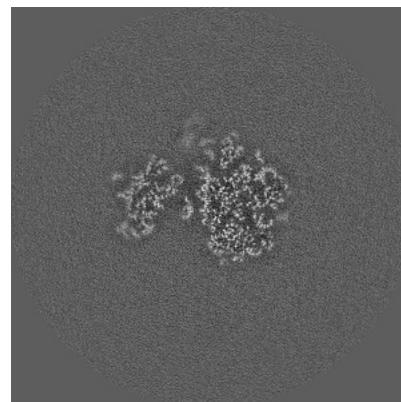
6.3.2 Raw map



X Index: 283



Y Index: 263

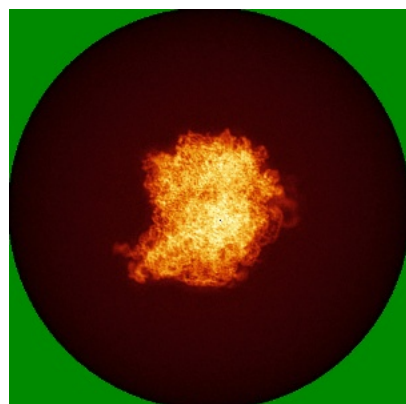


Z Index: 247

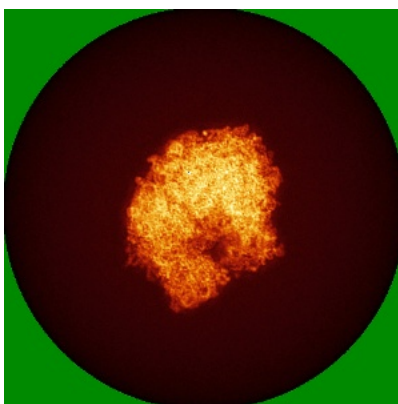
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

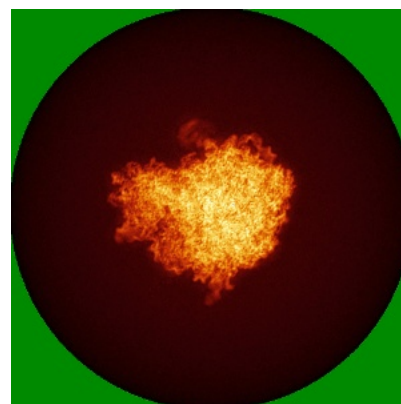
6.4.1 Primary map



X

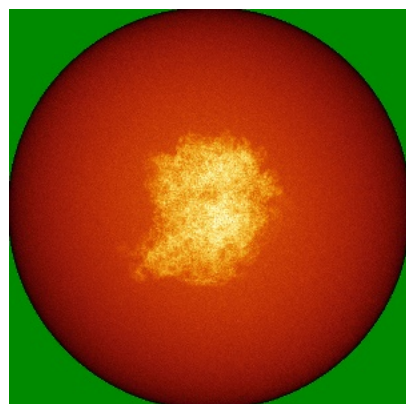


Y

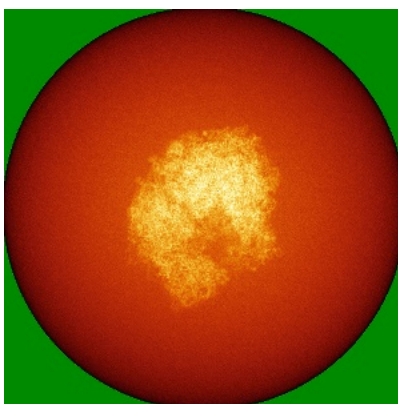


Z

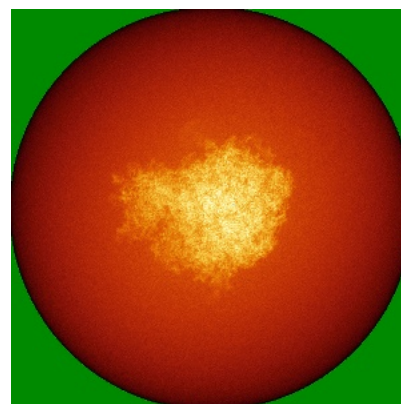
6.4.2 Raw map



X



Y

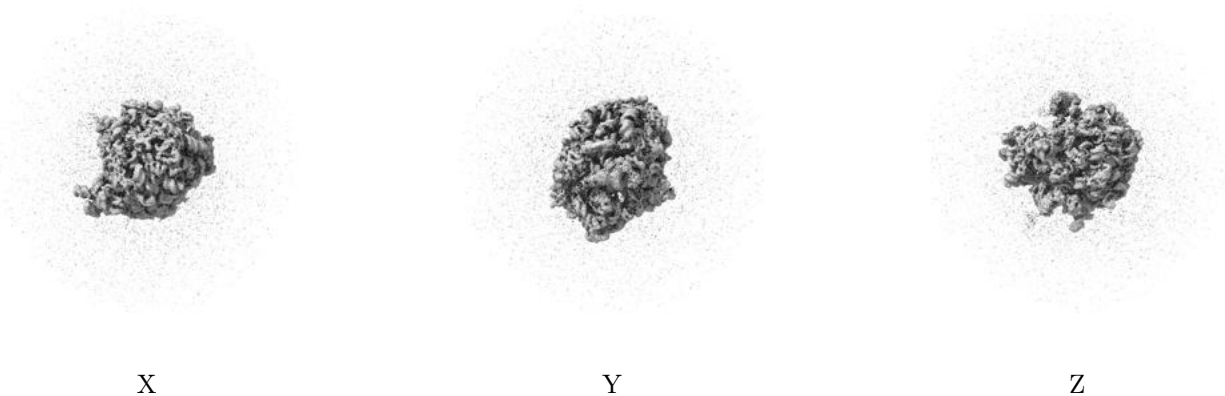


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

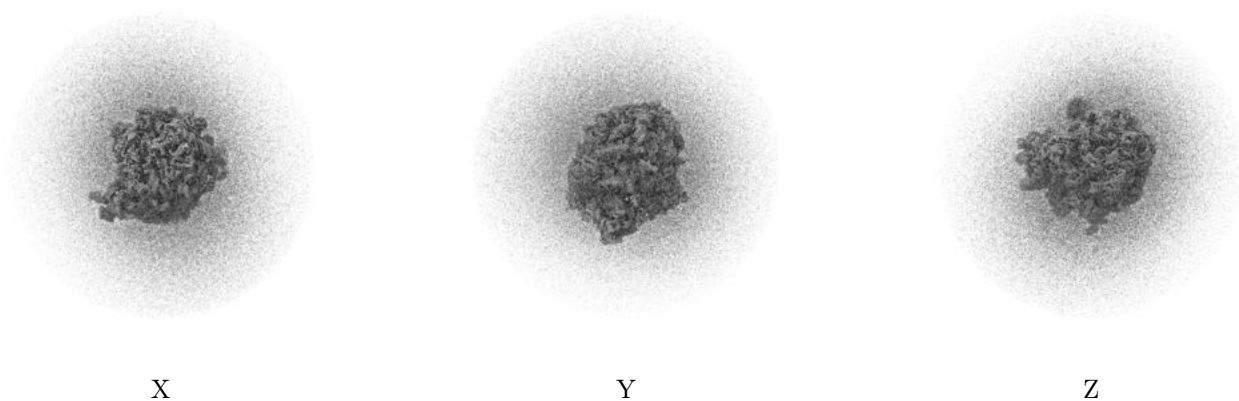
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00251. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

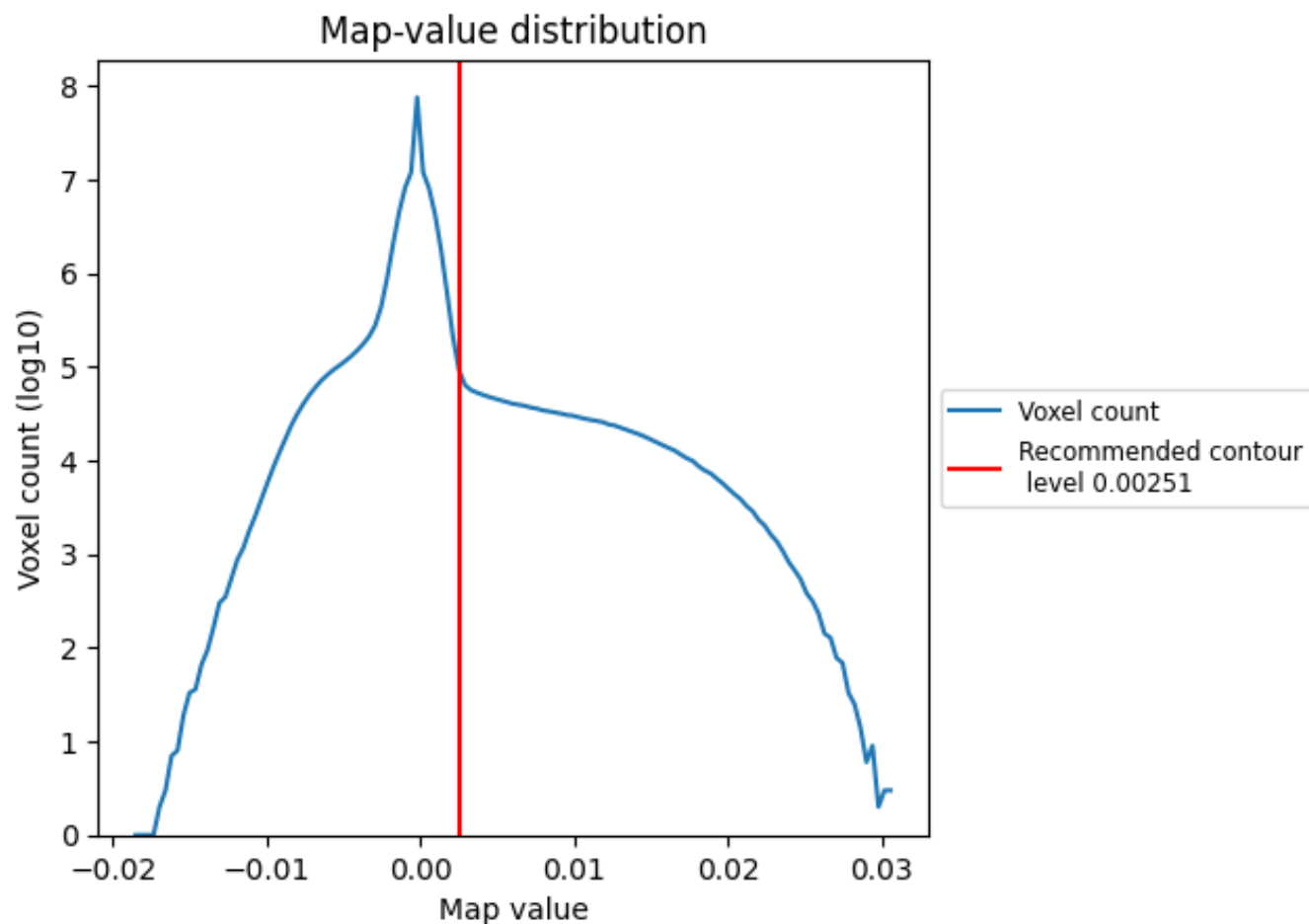
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

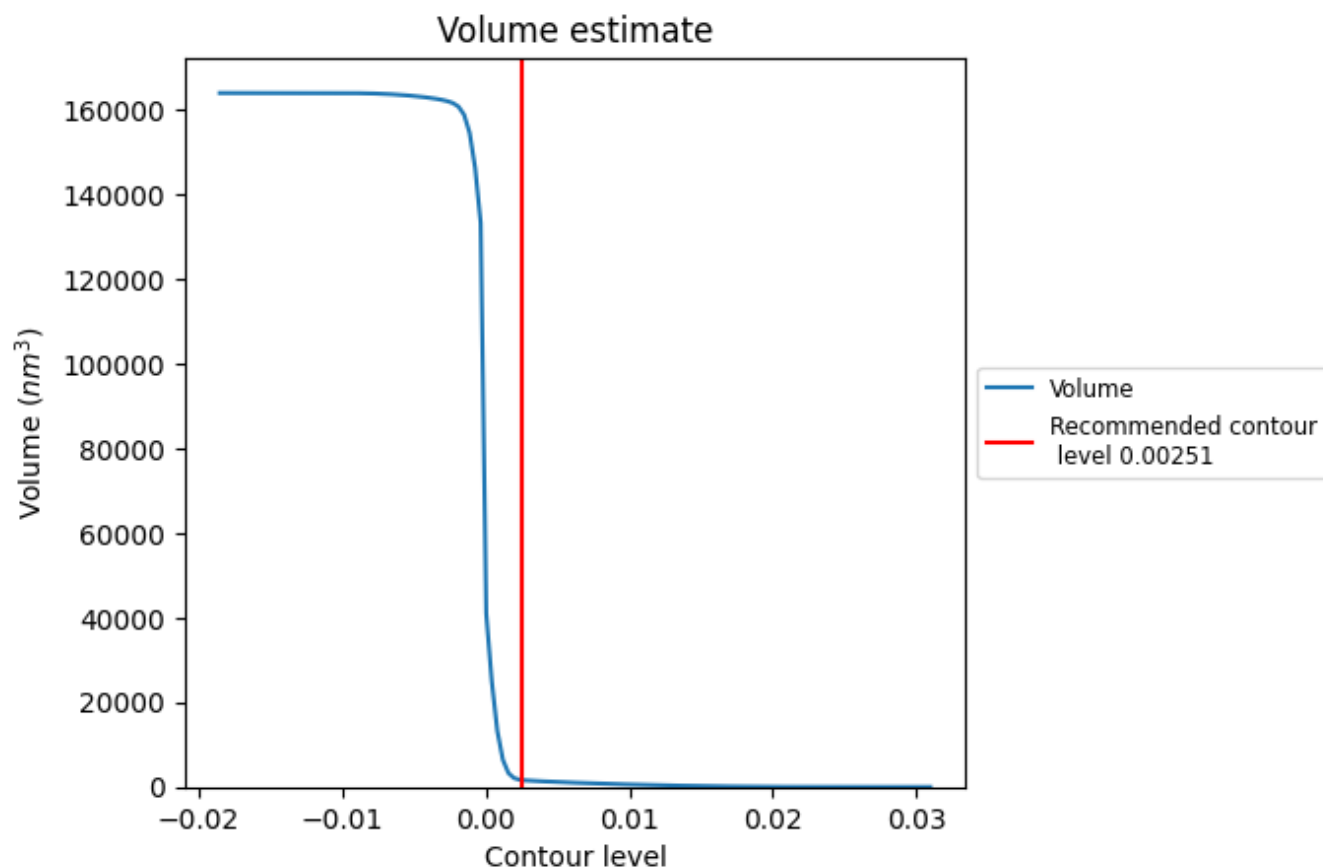
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

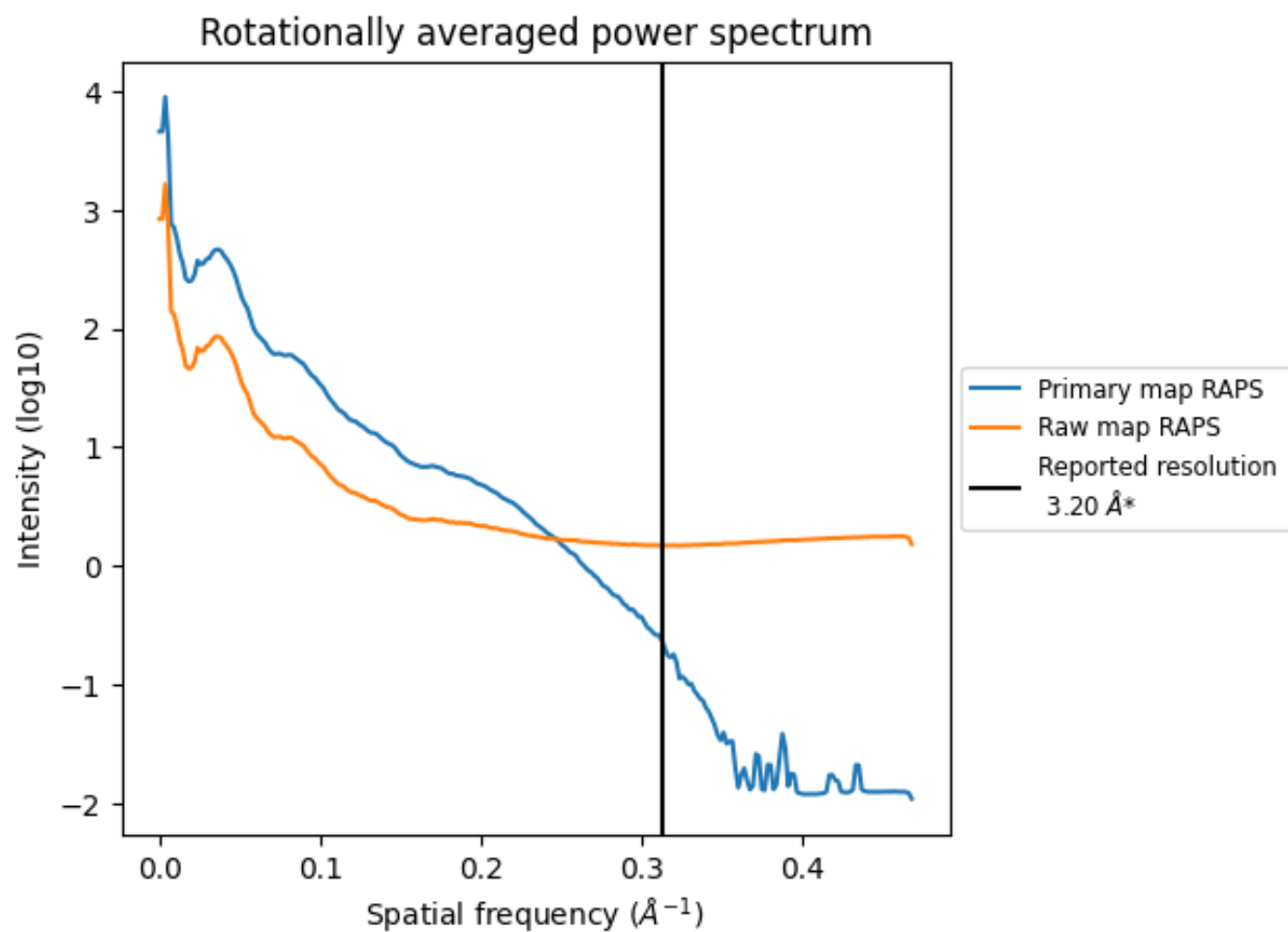
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1650 nm³; this corresponds to an approximate mass of 1491 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

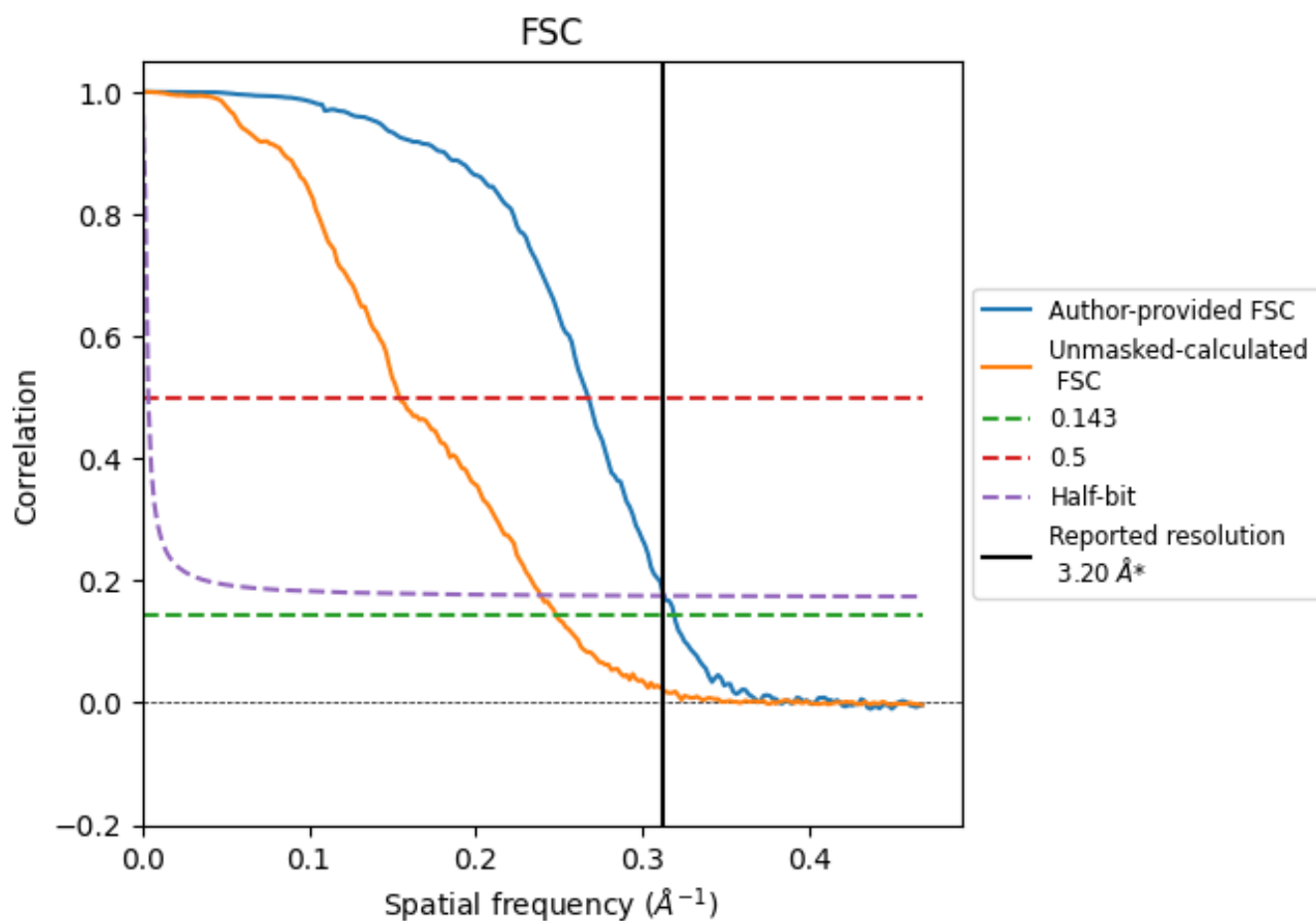


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

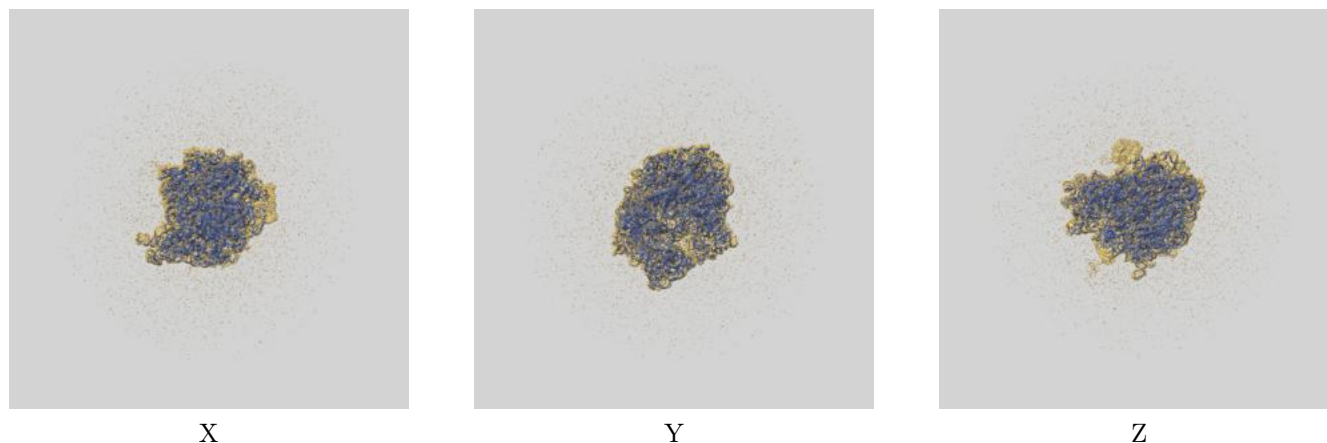
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.13	3.74	3.20
Unmasked-calculated*	4.03	6.48	4.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

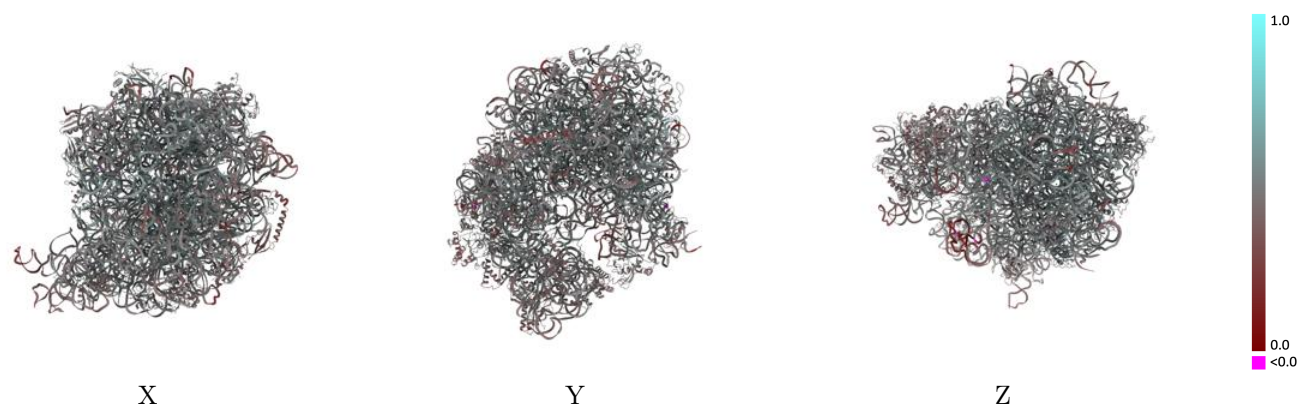
This section contains information regarding the fit between EMDB map EMD-43752 and PDB model 8W2N. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

9.1 Map-model overlay [i](#)



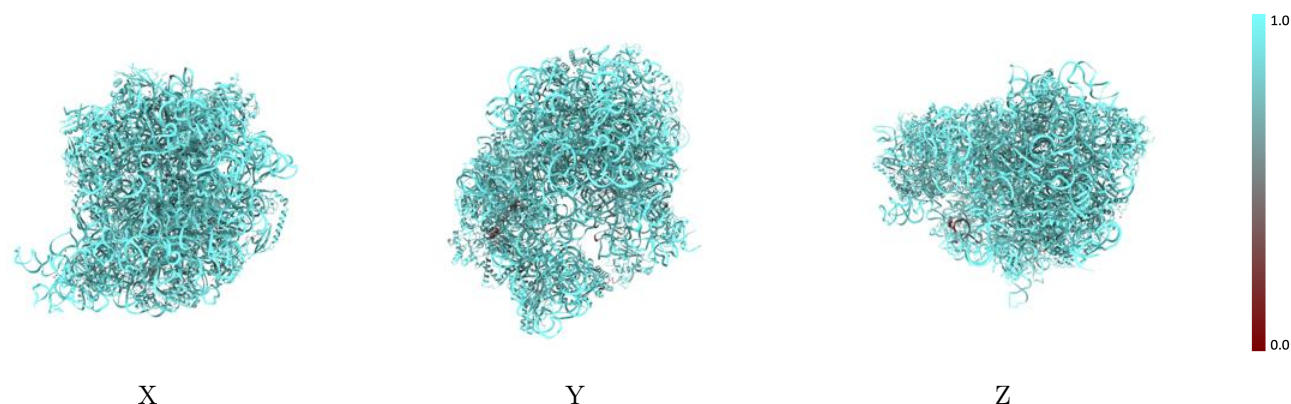
The images above show the 3D surface view of the map at the recommended contour level 0.00251 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



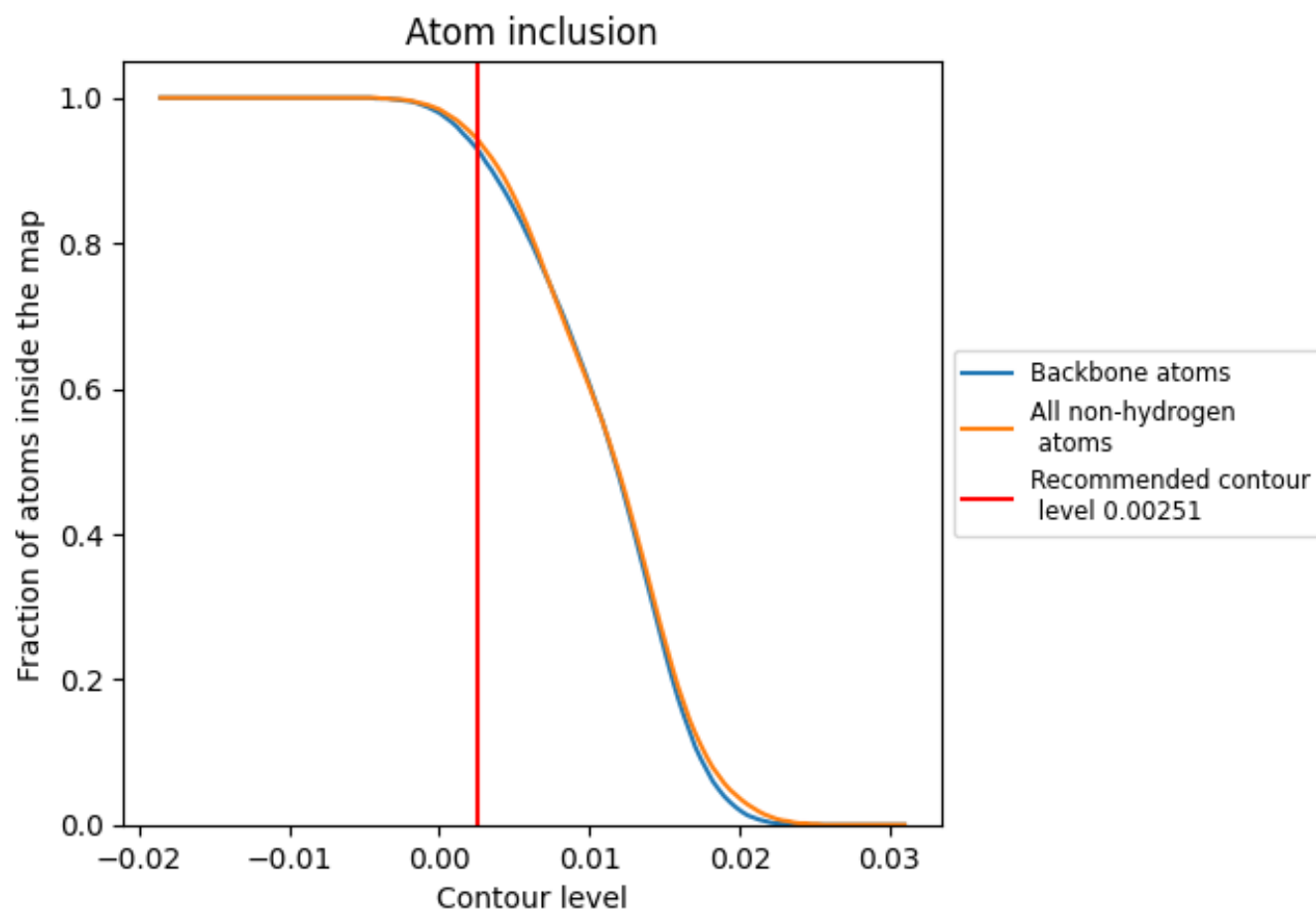
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00251).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.00251) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4770
1	 0.9800	 0.4850
2	 0.9850	 0.4700
3	 0.9820	 0.4600
4	 0.9200	 0.5050
5	 0.9730	 0.4610
6	 0.7960	 0.4400
B	 0.8890	 0.5260
C	 0.8960	 0.5140
D	 0.8940	 0.4920
E	 0.8710	 0.4300
F	 0.9260	 0.4540
G	 0.9110	 0.3870
J	 0.8950	 0.5020
K	 0.8860	 0.5130
L	 0.8790	 0.5070
M	 0.8990	 0.5090
N	 0.8840	 0.5100
O	 0.8970	 0.4590
P	 0.8940	 0.5130
Q	 0.8750	 0.4930
R	 0.9120	 0.5100
S	 0.8730	 0.5020
T	 0.8500	 0.4830
U	 0.8940	 0.4790
V	 0.9240	 0.4850
W	 0.8780	 0.5180
X	 0.8770	 0.5010
Y	 0.8900	 0.4320
Z	 0.9130	 0.4980
a	 0.7460	 0.4060
b	 0.8880	 0.5120
c	 0.8900	 0.4850
d	 0.8510	 0.5170
e	 0.8460	 0.5240



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Chain	Atom inclusion	Q-score
f	 0.8060	 0.4940
g	 0.8260	 0.4160
h	 0.8930	 0.4670
i	 0.8450	 0.4480
j	 0.8820	 0.4830
k	 0.9010	 0.4470
l	 0.8820	 0.4350
m	 0.8930	 0.4880
n	 0.8650	 0.4510
o	 0.8560	 0.4480
p	 0.8990	 0.4700
q	 0.8730	 0.4960
r	 0.8840	 0.4410
s	 0.8540	 0.4580
t	 0.8850	 0.4520
u	 0.8770	 0.4890
v	 0.8860	 0.4620
w	 0.8130	 0.4280
x	 0.8810	 0.4530
y	 0.8440	 0.4250
z	 0.5600	 0.4060