



Full wwPDB EM Validation Report ⓘ

Apr 5, 2026 – 09:49 PM UTC

PDB ID : 9ZTL / pdb_00009ztl
EMDB ID : EMD-74757
Title : Single Particle Cryo EM Analysis of a Ribosome Nascent Globin Complex
Authors : Masse, M.M.; Millan, N.; Morgan, C.; Cavagnero, S.
Deposited on : 2025-12-23
Resolution : 2.91 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

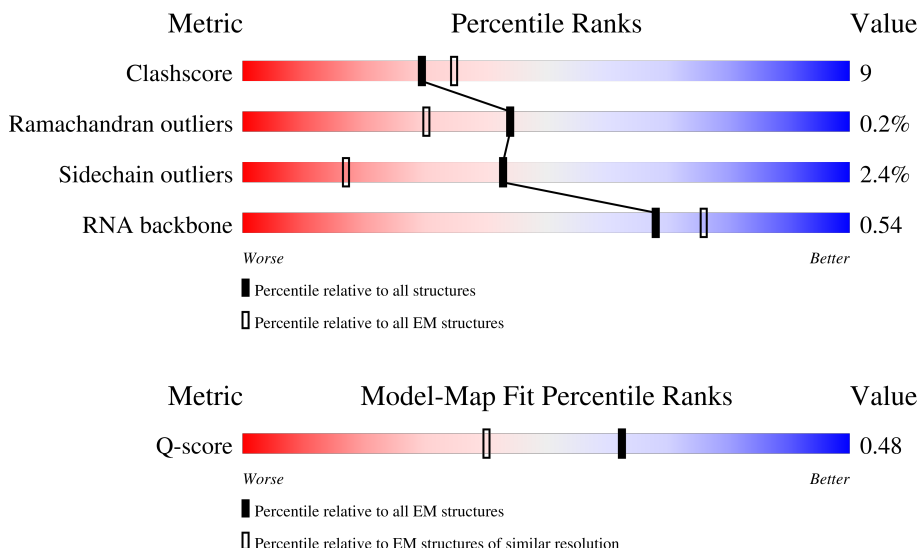
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.91 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	12972 (2.41 - 3.41)

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	0	55	
2	1	46	
3	2	65	

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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	5	75	
7	A	1542	
8	B	241	
9	C	233	
10	D	206	
11	E	167	
12	F	135	
13	G	179	
14	H	130	
15	I	130	
16	J	103	
17	K	129	
18	L	124	
19	M	118	
20	N	101	
21	O	89	
22	P	82	
23	Q	84	
24	R	75	
25	S	92	
26	T	87	
27	U	71	
28	X	6	

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Mol	Chain	Length	Quality of chain
29	Y	34	 12% 100%
30	a	2753	 57% 39% 5%
31	b	120	 63% 33% ..
32	c	273	 86% 13% .
33	d	209	 82% 16% .
34	e	201	 85% 15%
35	f	179	 71% 27% ..
36	g	177	 86% 13% ..
37	h	149	 22% 5% 72%
38	i	142	 85% 15%
39	j	123	 79% 18% .
40	k	144	 81% 18% .
41	l	136	 73% 26% .
42	m	127	 69% 24% 7%
43	n	117	 81% 17% ..
44	o	115	 77% 21% ..
45	p	118	 81% 19% .
46	q	103	 79% 21%
47	r	110	 82% 17% .
48	s	100	 81% 15% ..
49	t	104	 80% 18% .
50	u	94	 76% 24%
51	v	85	 74% 16% 8%
52	w	78	 71% 27% ..
53	x	63	 81% 16% .

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Mol	Chain	Length	Quality of chain
54	y	59	<div><div></div><div>81%</div><div>17%</div><div></div></div>
55	z	57	<div><div></div><div>65%</div><div>33%</div><div></div></div>

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 139790 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 protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 4 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	75	Total	C	N	O	P	0	0
			1586	710	270	531	75		

- Molecule 7 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	1519	Total	C	N	O	P	0	0
			32612	14552	5986	10555	1519		

- Molecule 8 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 9 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 10 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	195	Total	C	N	O	S	0	0
			1563	977	300	283	3		

- Molecule 11 is a protein called 30S ribosomal protein S5.

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

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 14 is a protein called 30S ribosomal protein S8.

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

- Molecule 15 is a protein called 30S ribosomal protein S9.

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

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 17 is a protein called 30S ribosomal protein S11.

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

- Molecule 18 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 19 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 20 is a protein called 30S ribosomal protein S14.

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

- Molecule 21 is a protein called 30S ribosomal protein S15.

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

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 23 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 24 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	R	54	Total	C	N	O		
			446	283	85	78	0	0

- Molecule 25 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 26 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 27 is a protein called 30S ribosomal protein S21.

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

- Molecule 28 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	6	Total	C	N	O	P	0	0
			131	58	25	42	6		

- Molecule 29 is a protein called apoMyoglobin nascent polypeptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	34	Total	C	N	O		0	0
			170	102	34	34			

- Molecule 30 is a RNA chain called 23s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2753	Total	C	N	O	P	0	0
			59129	26383	10897	19096	2753		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 32 is a protein called 50S ribosomal protein L2.

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

- Molecule 33 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 34 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 35 is a protein called 50S ribosomal protein L5.

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

- Molecule 36 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 37 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 38 is a protein called 50S ribosomal protein L13.

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

- Molecule 39 is a protein called 50S ribosomal protein L14.

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

- Molecule 40 is a protein called 50S ribosomal protein L15.

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

- Molecule 41 is a protein called 50S ribosomal protein L16.

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

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 43 is a protein called 50S ribosomal protein L18.

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

- Molecule 44 is a protein called 50S ribosomal protein L19.

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

- Molecule 45 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 46 is a protein called 50S ribosomal protein L21.

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

- Molecule 47 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 48 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	97	Total	C	N	O	S	0	0
			768	486	143	137	2		

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	t	102	Total	C	N	O		
			779	492	146	141	0	0

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

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

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	v	78	Total	C	N	O	S	
			586	362	116	107	1	0

- Molecule 52 is a protein called 50S ribosomal protein L28.

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

- Molecule 53 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	x	61	Total	C	N	O	S	
			495	305	97	92	1	0

- Molecule 54 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	y	58	Total	C	N	O	S	
			449	281	87	79	2	0

- Molecule 55 is a protein called 50S ribosomal protein L32.

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

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total 1	Zn 1	0
56	4	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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: 50S ribosomal protein L33

Chain 0: 




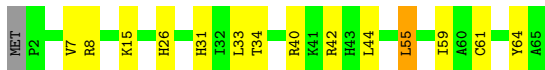
- Molecule 2: 50S ribosomal protein L34

Chain 1: 



- Molecule 3: 50S ribosomal protein L35

Chain 2: 



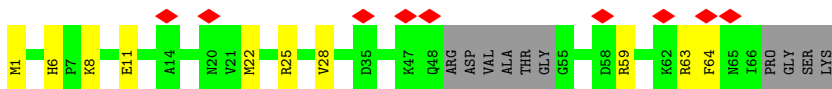
- Molecule 4: 50S ribosomal protein L36

Chain 3: 



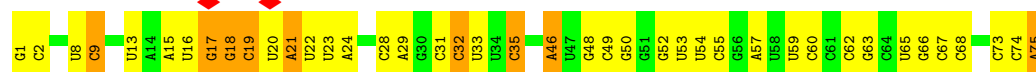
- Molecule 5: 50S ribosomal protein L31

Chain 4: 



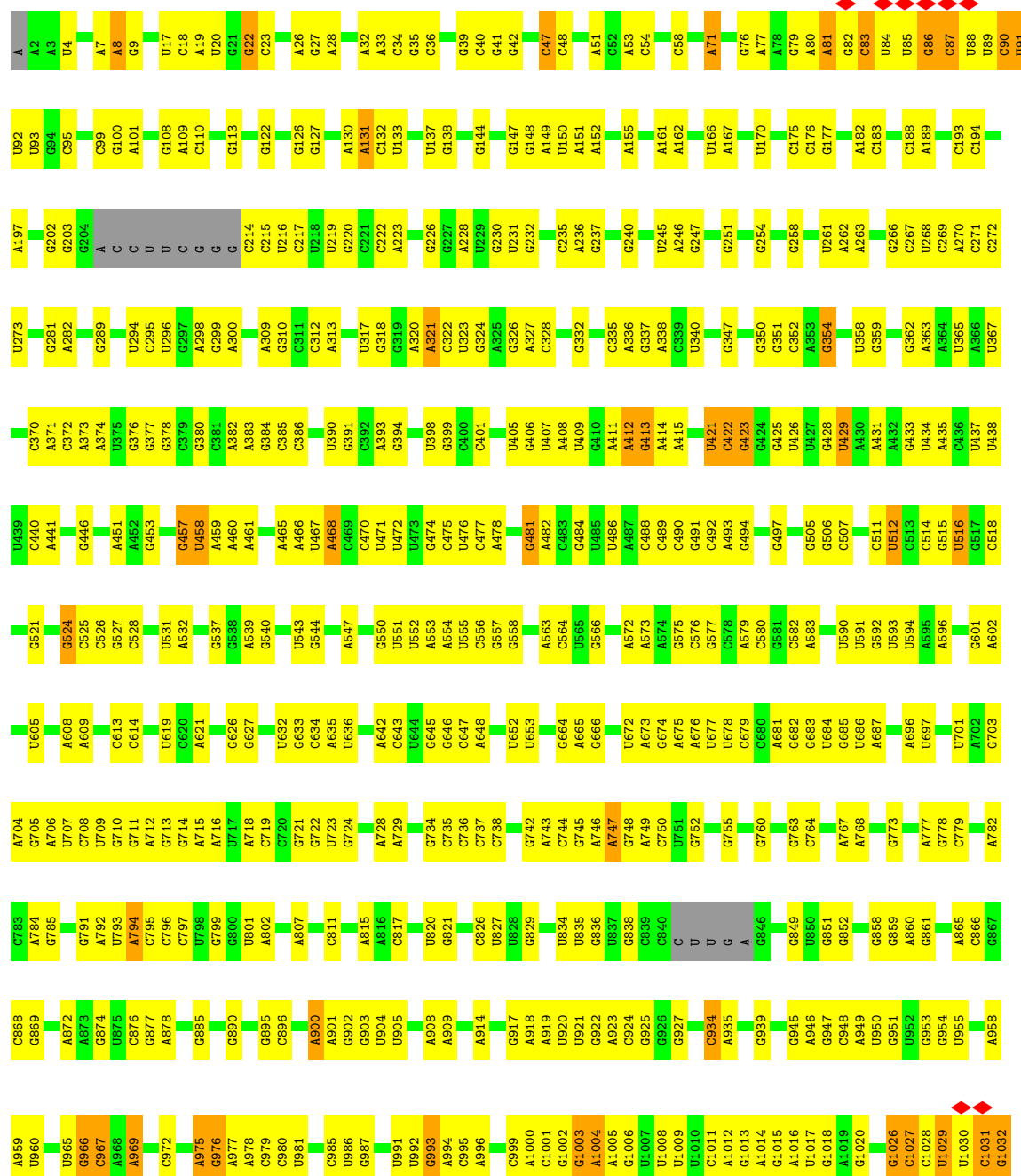
- Molecule 6: P-site tRNA

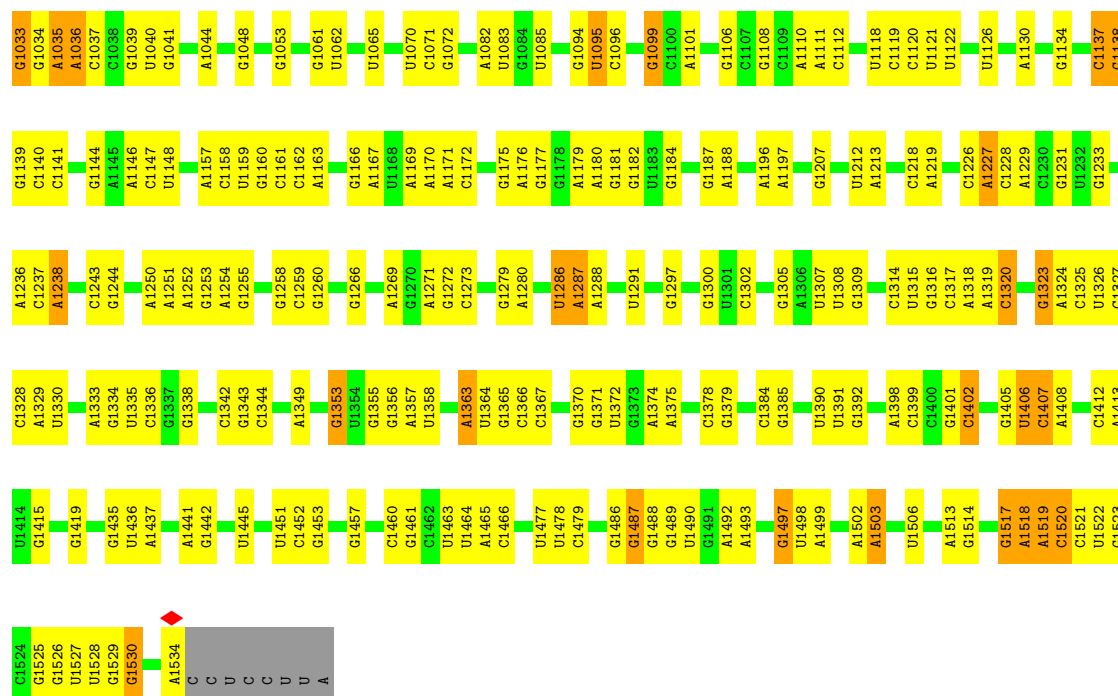
Chain 5: 



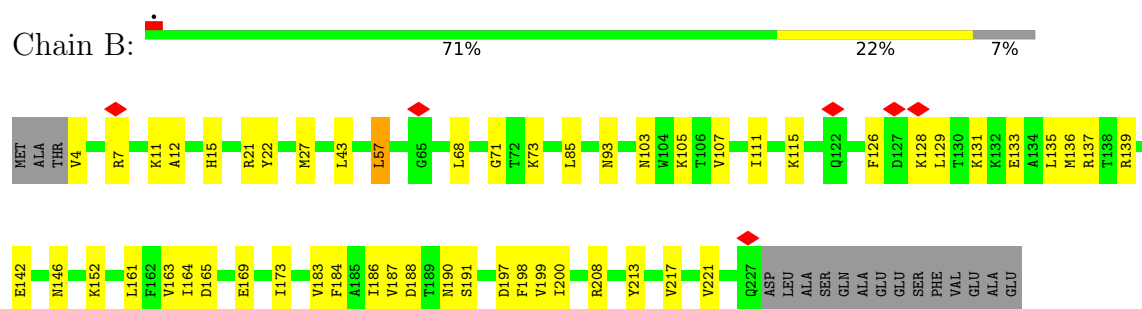
• Molecule 7: 16S rRNA

Chain A: 

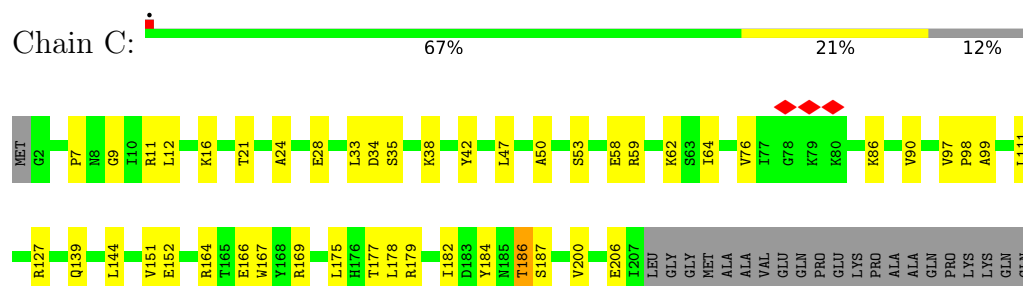




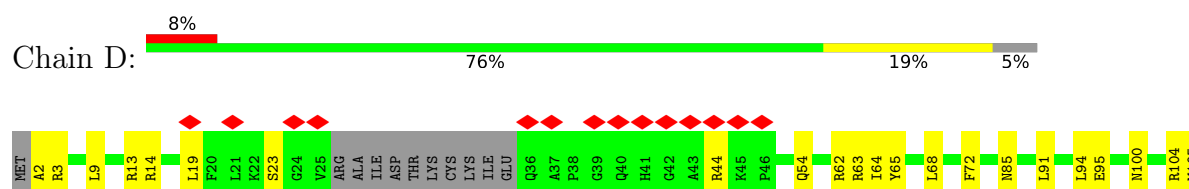
• Molecule 8: 30S ribosomal protein S2

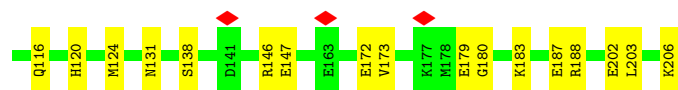


• Molecule 9: 30S ribosomal protein S3



• Molecule 10: 30S ribosomal protein S4





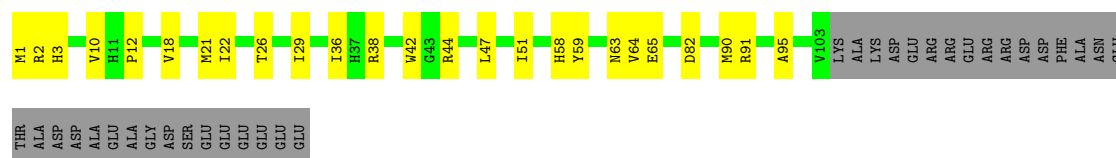
- Molecule 11: 30S ribosomal protein S5

Chain E: 68% 25% 7%



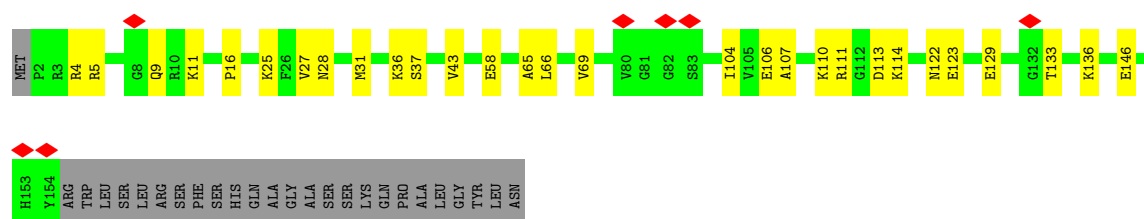
- Molecule 12: 30S ribosomal protein S6

Chain F: 58% 19% 24%



- Molecule 13: 30S ribosomal protein S7

Chain G: 69% 16% 15%



- Molecule 14: 30S ribosomal protein S8

Chain H: 81% 18% ..



- Molecule 15: 30S ribosomal protein S9

Chain I: 71% 27% .





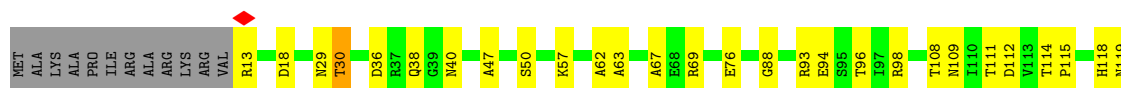
- Molecule 16: 30S ribosomal protein S10

Chain J: 65% 28% 5%



- Molecule 17: 30S ribosomal protein S11

Chain K: 68% 22% 9%



- Molecule 18: 30S ribosomal protein S12

Chain L: 73% 23% 2%



- Molecule 19: 30S ribosomal protein S13

Chain M: 73% 25% 2%



- Molecule 20: 30S ribosomal protein S14

Chain N: 75% 24% 1%

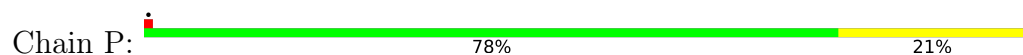


- Molecule 21: 30S ribosomal protein S15

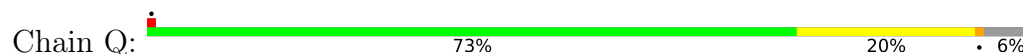
Chain O: 81% 18% 1%



- Molecule 22: 30S ribosomal protein S16



- Molecule 23: 30S ribosomal protein S17



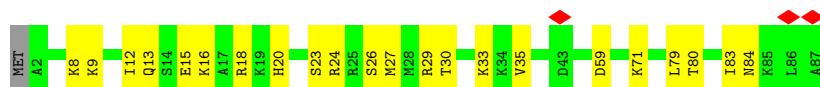
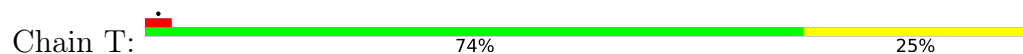
- Molecule 24: 30S ribosomal protein S18



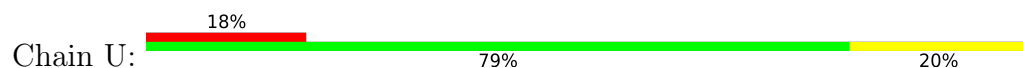
- Molecule 25: 30S ribosomal protein S19



- Molecule 26: 30S ribosomal protein S20



- Molecule 27: 30S ribosomal protein S21



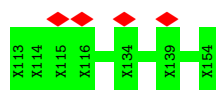
- Molecule 28: mRNA

Chain X:  50% 50%



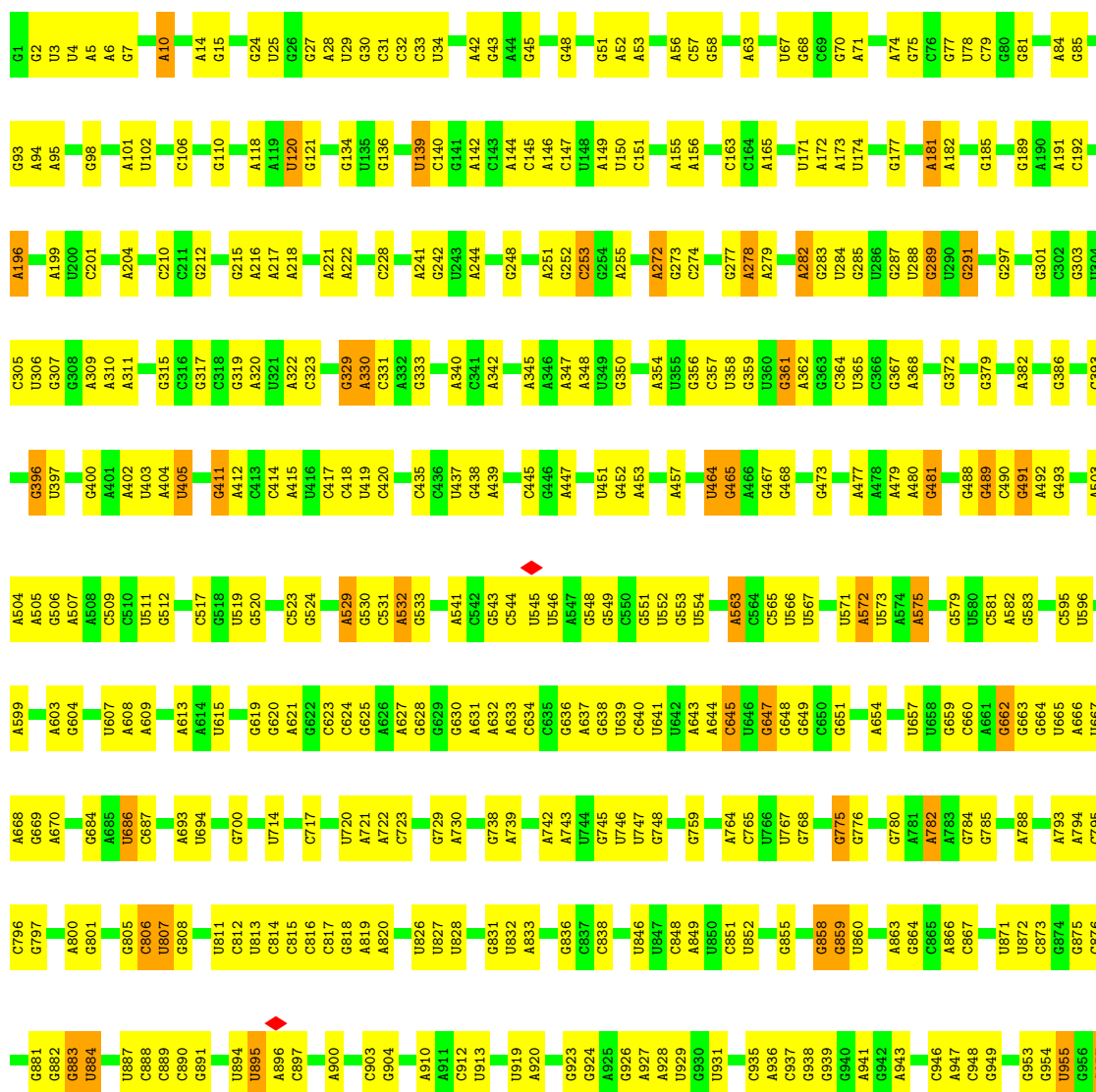
- Molecule 29: apoMyoglobin nascent polypeptide

Chain Y:  12% 100%

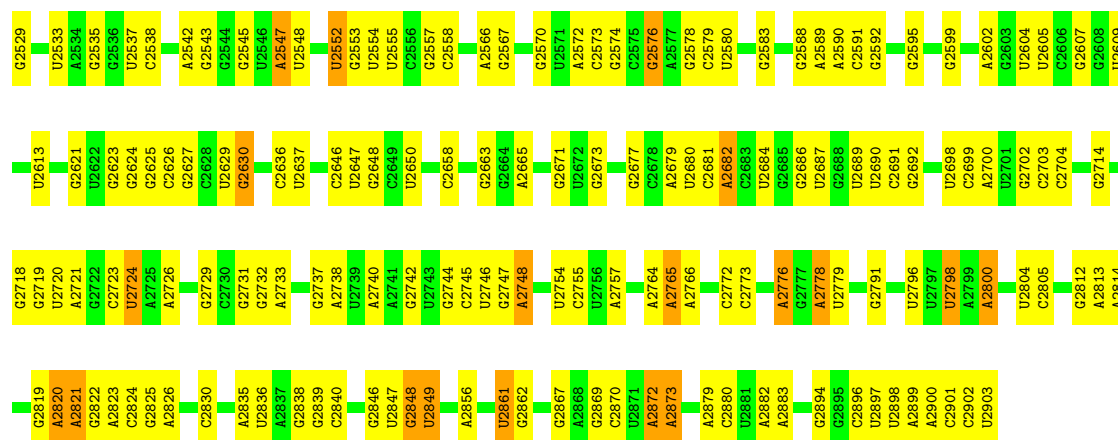


- Molecule 30: 23s rRNA

Chain a:  57% 39% 5%



G2437	G2360	U2249	A2062	G1972	C1881	A1791	G1899	A1608	G1529	A1419	U1316	C1221	G1047	U958
U2438	G2361	G2250	C2063	G1975	A1889	U1796	G1703	A1609	G1530	A1420	G1317	U1222	G1110	A959
A2439	C2362	G2251	C2064	G1976	G1797	U1797	G1704	A1618	G1531	G1421	G1324	U1223	A1111	A960
C2440	G2365	C2258	C2065	G1983	G1896	U1798	G1705	A1619	A1532	G1422	G1325	U1224	A1112	C961
C2441	C2366	U2259	G2066	G1984	G1897	U1799	G1706	G1620	G1533	G1423	U1326	U1225	G1113	C962
A2469	A2369	C2260	U2068	A1987	U1898	C1800	G1707	G1621	G1534	G1424	A1327	U1226	U1114	U963
G2444	G2370	C2261	G2069	G1988	A1899	A1801	C1708	G1622	A1535	G1425	A1328	G1227	C1114	C964
	A2476	A2267	A2070	U1991	G1904	A1802	U1709	U1624	A1536	A1426		G1228		
	A2477	A2268	A2071	U1992	G1905	A1803	U1710	U1625	G1537	A1427			G1120	G969
	A2478	A2269	C2072	U1993	G1906	A1804	U1711	U1626	G1538	G1428		U1234	G1124	U970
	A2479	A2270	C2073	U1994	G1907	A1805	U1712	G1627	G1539	G1429		U1235	G1125	A972
A2480	G2375	A2281	A2082	C1996	G1908	A1806	U1713	A1632	U1540	G1430		G1239	G1126	G974
	A2376	G2282		C1997	G1909	A1807	U1714	G1633	A1541	G1431				
	A2377	C2283	G2093	A1998	U1911	A1808	U1715	A1634	A1542	G1432		A1247	U1132	G977
		A2284	C2094	A1999	U1912	A1809	U1716	G1635	A1543	A1433		G1248	A1133	G978
		C2285	G2095	U1999	A1913	A1810	G1724	A1636	G1544	A1434			C1134	
		G2286	C2096	G2002	A1914	G1813	U1729	A1637	G1545	G1435		G1252	C1135	A983
		A2287	A2097	C2003	C1914	G1814	C1730	A1641	A1546	U1436		A1253	G1140	
		A2288	U2098	C2004	U1915	G1815	G1731	G1642	A1547	U1437		A1254		G989
		A2289	U2099	C2005	A1916	G1816	G1732	G1643	A1548	U1438		U1255	U1141	A990
		G2290	U2100	U1917	G1917	G1817	G1733	G1644	A1549	U1439		G1256	A1142	
		U2192	G2101	A1918	U1918	U1818	A1735	G1645	C1550	U1440		G1257	A1143	
		G2193	G2102	A1919	U1919	U1819	U1736	G1646	A1551	U1441			A1144	
		U2292	G2103	G1921	G1921	G1820	G1737	U1647	A1552	G1442		G1259	C1145	G993
		G2293	A2013	G1922	G1922	G1821	G1738	U1648	A1553	G1443		A1262		C995
		U2197	U2016	C1924	C1924	G1822	G1739	U1649	A1554	U1444		U1263	C1153	A996
		A2198	U2017	U1925	U1925	U1823	C1741	G1650	A1555	U1445		U1264	G1154	
		A2199	G2018	G1926	G1926	U1824	U1742	G1651	A1556	U1446		U1265	A1155	
		U2203	U2019	G1927	G1927	G1825	G1743	U1652	A1557	U1447		G1266	A1156	A1000
		G2204	A2020	G1928	G1928	G1826	A1745	U1653	A1558	U1448		U1267		
		C2307	C2021	A1830	G1830	U1827	U1747	A1654	U1575	U1449		U1268	G1164	C1005
		G2308	U2022	G1831	C1831	G1828	U1748	A1655	U1576	G1450		U1269	C1165	C1006
		U2312	C2023	G1832	G1832	U1829	G1750	G1656	U1577	U1451		G1270	A1166	C1007
		C2313	G2024	A1936	A1936	G1833	A1751	U1657	A1580	U1452		U1271	A1008	
		A2314	A2030	A1937	G1834	G1834	G1752	G1658	U1581	U1453		U1272	A1009	
		G2315	A2031	U1938	C1835	U1841	G1753	G1659	C1582	U1454		U1273	G1179	U1012
		U2316	G2032	U1939	G1836	G1842	U1754	A1664	U1583	G1473		C1278	U1180	C1013
		A2317	A2033	U1940	C1837	C1843	U1755	A1665	U1584			G1279	A1014	
			C2034	C1941	G1838	G1844	C1761	G1666	C1585	G1482		G1280	U1183	
			U2039	C1942	G1839	C1845	G1762	G1667	A1586	G1483		U1281	G1185	A1021
			G2041	G1945	U1841	G1846	U1763	A1668	G1587	U1484		U1282	G1186	G1022
			A2042	G1946	C1842	U1847	G1764	A1669	G1588	U1485		G1288	U1187	U1023
			C2043	U1955	G1843	A1847	G1765	C1670	U1589				U1188	
			G2044	G1956	U1844		G1766	U1671	A1590	C1493				G1026
			C2045	G1957	G1845		G1767	G1672	A1591	U1395		G1296	C1196	A1027
			G2046	G1958	A1847			G1673	C1592	G1499		C1297	G1197	U1028
			C2047	G1959	U1848			G1674	A1593	U1397		C1298	U1198	A1029
			G2048	G1960	A1849			G1675	U1594	G1500		U1299	U1199	
			U2049	C1961	U1850			G1684	A1595	A1509		G1300	C1200	U1033
			G2050	G1962	A1851			G1685	U1596	G1510		A1301		
			A2052	G1963	U1852			G1686	A1597	G1511		C1306	A1204	G1036
			U2053	G1964	A1853			C1687	U1598	G1512		A1307	G1208	G1037
			C2054	C1965	U1854			G1688	A1599	G1513		G1307	U1209	G1038
			G2055	A1966	G1870			G1689	U1600	G1514		C1308	U1210	A1039
			U2056	G1967	A1871			C1690		G1515		A1309	G1212	A1040
			G2057	G1968	U1872			G1691		G1516		G1310	G1213	G1041
			A2060	A1969	G1873			C1692		G1517		U1313	G1220	G1042
			G2061	U1971	U1874			G1693		G1518				
					G1875			G1694		G1519				
					U1876			G1695		G1520				
					G1877			G1696		G1521				
					A1878			G1697		G1522				
					U1879			G1698		G1523				
					C1790			A1698		G1524				



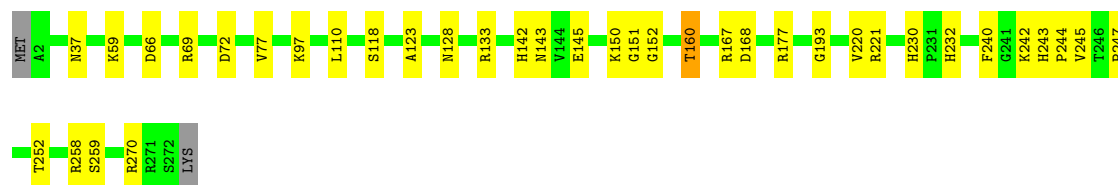
• Molecule 31: 5S rRNA

Chain b: 63% 33% ..



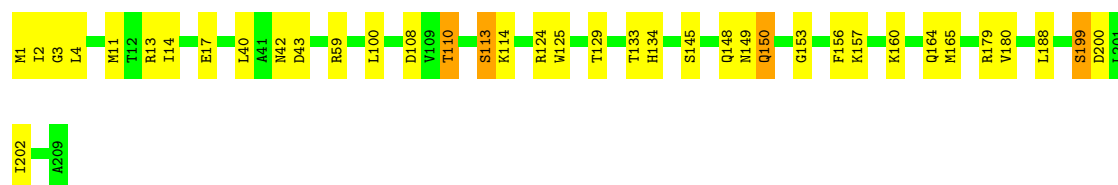
• Molecule 32: 50S ribosomal protein L2

Chain c: 86% 13% .



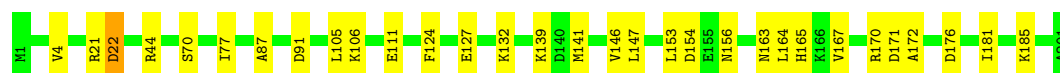
• Molecule 33: 50S ribosomal protein L3

Chain d: 82% 16% .

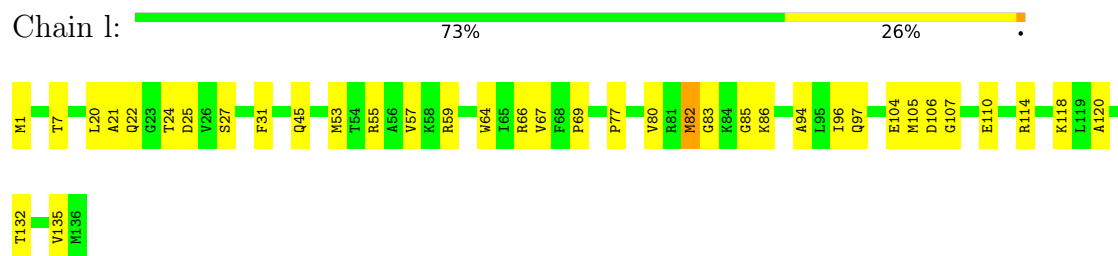


• Molecule 34: Large ribosomal subunit protein uL4

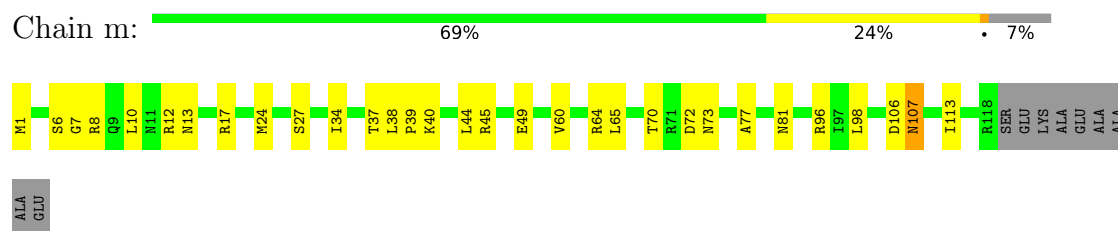
Chain e: 85% 15%



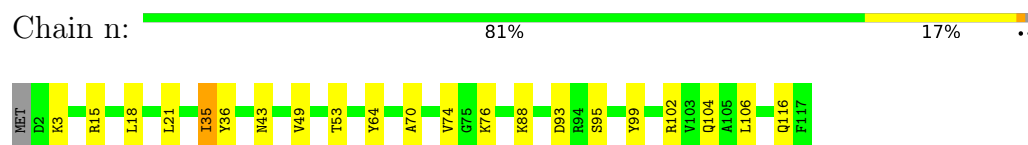
- Molecule 41: 50S ribosomal protein L16



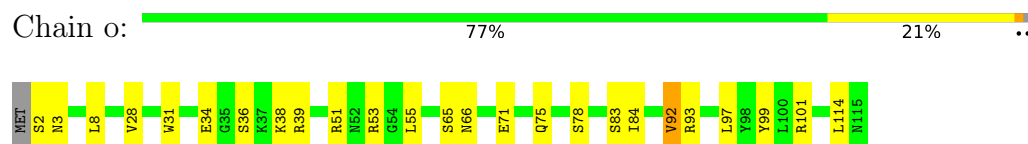
- Molecule 42: 50S ribosomal protein L17



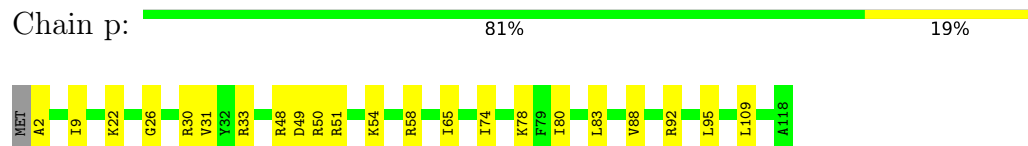
- Molecule 43: 50S ribosomal protein L18



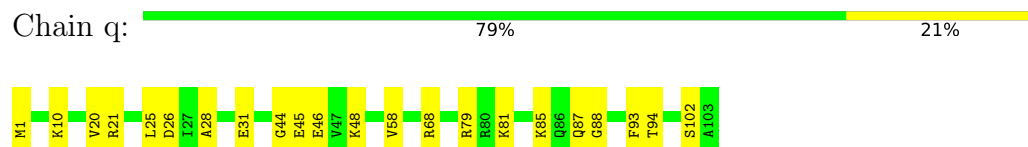
- Molecule 44: 50S ribosomal protein L19




- Molecule 45: 50S ribosomal protein L20



- Molecule 46: 50S ribosomal protein L21




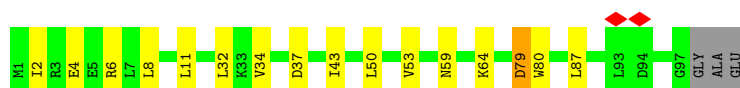
- Molecule 47: Large ribosomal subunit protein uL22

Chain r:  82% 17%




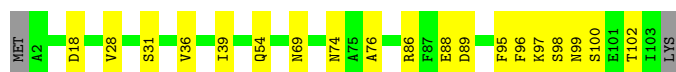
- Molecule 48: 50S ribosomal protein L23

Chain s:  81% 15%




- Molecule 49: 50S ribosomal protein L24

Chain t:  80% 18%



- Molecule 50: 50S ribosomal protein L25

Chain u:  76% 24%



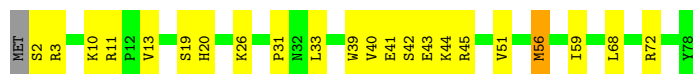
- Molecule 51: 50S ribosomal protein L27

Chain v:  74% 16% 8%




- Molecule 52: 50S ribosomal protein L28

Chain w:  71% 27%

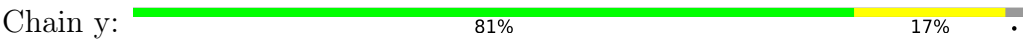


- Molecule 53: 50S ribosomal protein L29

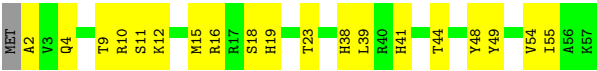
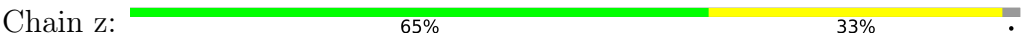
Chain x:  81% 16%



- Molecule 54: Large ribosomal subunit protein uL30



• Molecule 55: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	213770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	2.310	Depositor
Minimum map value	-1.552	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.087	Depositor
Recommended contour level	0.2	Depositor
Map size (\AA)	484.864, 484.864, 484.864	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.947, 0.947, 0.947	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, 6MZ, 4OC, UR3, 5MC, H2U, 2MG, 5MU, OMC, OMG, G7M, MA6, OMU, 2MA, PSU, ZN, MEQ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.43	0/424	0.51	0/565
2	1	0.53	0/380	0.71	0/498
3	2	0.51	0/513	0.60	0/676
4	3	0.49	0/303	0.50	0/397
5	4	0.15	0/488	0.38	0/649
6	5	0.22	0/1697	0.31	0/2638
7	A	0.32	0/36236	0.34	2/56520 (0.0%)
8	B	0.24	0/1784	0.43	0/2403
9	C	0.26	0/1651	0.40	0/2225
10	D	0.22	0/1584	0.34	0/2118
11	E	0.34	0/1165	0.47	0/1568
12	F	0.30	0/858	0.48	0/1160
13	G	0.19	0/1219	0.40	0/1635
14	H	0.32	0/989	0.43	0/1326
15	I	0.22	0/1034	0.34	0/1375
16	J	0.24	0/796	0.38	0/1077
17	K	0.35	0/893	0.48	0/1205
18	L	0.29	0/969	0.41	0/1300
19	M	0.21	0/900	0.36	0/1204
20	N	0.27	0/817	0.36	0/1088
21	O	0.27	0/722	0.41	0/964
22	P	0.28	0/653	0.40	0/877
23	Q	0.26	0/650	0.39	0/871
24	R	0.29	0/453	0.42	0/609
25	S	0.20	0/685	0.37	0/922
26	T	0.26	0/676	0.38	0/895
27	U	0.19	0/597	0.26	0/792
28	X	0.32	0/146	0.29	0/226
30	a	0.49	0/65674	0.42	5/102451 (0.0%)
31	b	0.39	0/2850	0.33	0/4444
32	c	0.49	0/2121	0.55	0/2852

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.50	0/1576	0.54	0/2119
34	e	0.47	1/1571 (0.1%)	0.50	0/2113
35	f	0.27	0/1434	0.46	0/1926
36	g	0.34	0/1343	0.46	0/1816
37	h	0.38	0/306	0.56	0/413
38	i	0.50	0/1152	0.47	0/1551
39	j	0.49	0/955	0.50	0/1279
40	k	0.47	0/1062	0.48	0/1413
41	l	0.48	0/1093	0.50	0/1460
42	m	0.51	0/958	0.60	0/1281
43	n	0.36	0/902	0.53	0/1209
44	o	0.49	0/929	0.58	0/1242
45	p	0.56	0/960	0.59	0/1278
46	q	0.45	0/829	0.56	0/1107
47	r	0.46	0/864	0.59	0/1156
48	s	0.46	0/775	0.61	0/1036
49	t	0.43	0/787	0.58	0/1051
50	u	0.44	0/766	0.56	0/1025
51	v	0.48	0/593	0.48	0/785
52	w	0.45	0/635	0.54	0/848
53	x	0.36	0/496	0.49	0/660
54	y	0.48	0/453	0.60	0/605
55	z	0.47	0/450	0.56	0/599
All	All	0.42	1/150816 (0.0%)	0.42	7/225502 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	e	87	ALA	C-N	-6.22	1.22	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	1915	U	P-O3'-C3'	-7.88	108.38	120.20
30	a	2251	OMG	P-O3'-C3'	-7.84	108.44	120.20
30	a	1914	C	P-O3'-C3'	-6.71	110.14	120.20
7	A	1207	2MG	P-O3'-C3'	-6.54	110.39	120.20
30	a	1835	2MG	P-O3'-C3'	-6.17	110.94	120.20
7	A	1407	5MC	P-O3'-C3'	-6.07	111.10	120.20
30	a	2498	OMC	P-O3'-C3'	-5.23	112.35	120.20

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	0	417	0	451	9	0
2	1	377	0	418	13	0
3	2	504	0	572	11	0
4	3	302	0	340	9	0
5	4	480	0	478	9	0
6	5	1586	0	813	33	0
7	A	32612	0	16432	550	0
8	B	1753	0	1780	38	0
9	C	1624	0	1696	30	0
10	D	1563	0	1618	33	0
11	E	1152	0	1196	28	0
12	F	839	0	833	18	0
13	G	1203	0	1254	28	0
14	H	979	0	1031	18	0
15	I	1022	0	1070	26	0
16	J	786	0	828	23	0
17	K	877	0	887	25	0
18	L	955	0	1016	18	0
19	M	891	0	952	24	0
20	N	805	0	844	22	0
21	O	714	0	734	11	0
22	P	643	0	661	15	0
23	Q	641	0	682	13	0
24	R	446	0	472	16	0
25	S	668	0	693	11	0
26	T	670	0	719	13	0
27	U	589	0	629	11	0
28	X	131	0	66	2	0
29	Y	170	0	47	0	0
30	a	59129	0	29767	796	0
31	b	2549	0	1291	30	0
32	c	2082	0	2154	27	0
33	d	1566	0	1618	28	0
34	e	1552	0	1619	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	f	1410	0	1444	43	0
36	g	1323	0	1371	20	0
37	h	303	0	327	6	0
38	i	1129	0	1162	16	0
39	j	946	0	1023	18	0
40	k	1053	0	1129	22	0
41	l	1074	0	1157	23	0
42	m	945	0	989	20	0
43	n	892	0	923	17	0
44	o	917	0	962	19	0
45	p	947	0	1019	18	0
46	q	816	0	839	15	0
47	r	857	0	922	13	0
48	s	768	0	832	11	0
49	t	779	0	831	13	0
50	u	753	0	780	16	0
51	v	586	0	596	9	0
52	w	625	0	652	14	0
53	x	495	0	526	10	0
54	y	449	0	488	9	0
55	z	444	0	458	13	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
All	All	139790	0	94091	2118	0

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

All (2118) 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)
7:A:409:U:H3	7:A:433:G:H1	1.04	0.98
7:A:1009:U:H3	7:A:1020:G:H1	1.16	0.93
30:a:1047:G:HO2'	30:a:1110:G:H1	0.98	0.92
17:K:98:ARG:HH21	27:U:16:LEU:HD23	1.33	0.92
30:a:1962:5MC:H4'	30:a:1963:U:OP1	1.71	0.87
24:R:68:LEU:HD12	24:R:69:PRO:HD2	1.59	0.83
7:A:269:C:H2'	7:A:270:A:H8	1.43	0.82
2:1:37:LYS:NZ	30:a:468:G:OP2	2.13	0.81
7:A:421:U:O2	9:C:127:ARG:NH1	2.13	0.81
7:A:552:U:H2'	7:A:553:A:H8	1.43	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:864:G:OP2	41:l:22:GLN:NE2	2.14	0.81
2:1:24:THR:HG23	2:1:27:GLY:H	1.45	0.81
12:F:29:ILE:HD13	12:F:64:VAL:HG11	1.60	0.80
35:f:80:ARG:HG3	35:f:83:TYR:HE2	1.45	0.80
7:A:1026:G:O6	7:A:1035:A:N1	2.15	0.79
26:T:9:LYS:NZ	26:T:13:GLN:OE1	2.15	0.79
30:a:2588:G:C5	30:a:2607:G:N2	2.51	0.79
7:A:137:U:H3	7:A:226:G:H1	1.30	0.79
7:A:674:G:H2'	7:A:675:A:H8	1.47	0.78
47:r:29:VAL:HG21	47:r:55:ILE:HD11	1.63	0.78
1:0:6:ARG:NH1	30:a:2285:C:OP2	2.16	0.78
7:A:673:A:H2'	7:A:674:G:C8	2.19	0.78
30:a:881:G:H1	30:a:895:U:H3	1.29	0.78
30:a:1140:C:OP2	38:i:68:LYS:NZ	2.17	0.78
13:G:133:THR:HB	13:G:136:LYS:HZ2	1.47	0.77
30:a:1602:U:OP2	48:s:64:LYS:NZ	2.18	0.76
25:S:41:PHE:H	25:S:44:MET:HE2	1.48	0.76
24:R:37:GLY:O	24:R:63:ARG:NH2	2.18	0.76
7:A:673:A:H2'	7:A:674:G:H8	1.51	0.76
42:m:37:THR:HG22	42:m:39:PRO:HD2	1.67	0.76
35:f:80:ARG:HG3	35:f:83:TYR:CE2	2.20	0.76
13:G:16:PRO:HA	15:I:46:MET:HE1	1.65	0.75
43:n:35:ILE:HD11	43:n:106:LEU:HD12	1.67	0.75
11:E:88:VAL:HG22	11:E:93:ARG:HG2	1.69	0.75
7:A:1356:G:H2'	7:A:1357:A:C8	2.21	0.75
30:a:396:G:OP2	52:w:10:LYS:NZ	2.19	0.75
30:a:1264:A:OP1	55:z:16:ARG:NH2	2.18	0.75
9:C:35:SER:OG	9:C:59:ARG:NH2	2.20	0.75
34:e:111:GLU:HG2	40:k:1:MET:HG3	1.68	0.74
30:a:1306:C:H2'	30:a:1307:A:H8	1.49	0.74
7:A:528:C:N4	18:L:46:ASN:OD1	2.19	0.74
30:a:1434:A:H2'	30:a:1435:G:H8	1.52	0.74
41:l:53:MET:HG3	41:l:120:ALA:HB2	1.69	0.73
53:x:12:GLU:N	53:x:12:GLU:OE2	2.22	0.73
10:D:95:GLU:OE2	10:D:100:ASN:ND2	2.19	0.73
30:a:1466:U:HO2'	30:a:1546:G:HO2'	1.34	0.73
30:a:2588:G:C6	30:a:2607:G:C2	2.77	0.73
30:a:882:G:H1	30:a:894:U:H3	1.36	0.73
48:s:11:LEU:HD11	48:s:32:LEU:HD13	1.70	0.72
41:l:66:ARG:NH1	41:l:104:GLU:OE1	2.22	0.72
7:A:950:U:H2'	7:A:951:G:H8	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:T:15:GLU:OE1	26:T:18:ARG:NH2	2.22	0.72
49:t:98:SER:O	49:t:99:ASN:HB3	1.89	0.72
30:a:284:U:H3	30:a:356:G:H1	1.38	0.71
30:a:955:PSU:OP1	41:l:86:LYS:NZ	2.23	0.71
30:a:2849:U:OP1	44:o:93:ARG:NH2	2.23	0.71
12:F:10:VAL:HG12	12:F:58:HIS:HB3	1.72	0.71
35:f:116:GLY:HA3	35:f:178:ARG:HB2	1.72	0.71
41:l:20:LEU:HD23	50:u:81:PRO:HG2	1.71	0.71
48:s:4:GLU:O	48:s:8:LEU:HD12	1.90	0.71
7:A:337:G:H2'	7:A:338:A:H8	1.54	0.71
30:a:994:C:O2	46:q:10:LYS:NZ	2.22	0.71
30:a:1651:G:OP1	42:m:40:LYS:NZ	2.23	0.71
30:a:1842:G:H2'	30:a:1843:C:H6	1.56	0.71
34:e:127:GLU:OE1	34:e:127:GLU:N	2.18	0.70
48:s:53:VAL:HG11	48:s:87:LEU:HD22	1.72	0.70
30:a:191:A:H2'	30:a:192:C:H6	1.57	0.70
50:u:35:GLU:N	50:u:35:GLU:OE2	2.25	0.70
13:G:9:GLN:O	13:G:11:LYS:NZ	2.24	0.70
7:A:1356:G:H2'	7:A:1357:A:H8	1.53	0.70
38:i:43:GLU:OE1	38:i:43:GLU:N	2.24	0.70
30:a:1196:C:H2'	30:a:1197:G:H8	1.55	0.69
35:f:29:PRO:HB2	35:f:169:LEU:HD12	1.74	0.69
41:l:69:PRO:HA	41:l:94:ALA:HB2	1.74	0.69
30:a:532:A:N7	30:a:2021:C:O2'	2.22	0.69
38:i:31:GLU:HG2	38:i:142:ILE:HG12	1.74	0.69
7:A:405:U:O4	10:D:2:ALA:N	2.26	0.69
7:A:1297:G:O2'	13:G:114:LYS:NZ	2.26	0.69
7:A:1323:G:H2'	7:A:1324:A:H8	1.58	0.69
44:o:92:VAL:HG21	44:o:97:LEU:HD11	1.75	0.69
35:f:134:GLU:N	35:f:134:GLU:OE2	2.26	0.69
7:A:1517:G:H2'	7:A:1518:MA6:C8	2.23	0.68
31:b:114:C:H2'	31:b:115:A:H8	1.57	0.68
33:d:133:THR:OG1	33:d:134:HIS:N	2.26	0.68
30:a:2011:U:OP2	47:r:16:LYS:NZ	2.24	0.68
33:d:199:SER:OG	33:d:200:ASP:N	2.22	0.68
30:a:1187:G:OP1	46:q:85:LYS:NZ	2.26	0.68
7:A:1218:C:H2'	7:A:1219:A:H8	1.59	0.68
32:c:142:HIS:ND1	32:c:193:GLY:O	2.26	0.68
30:a:1590:A:H2'	30:a:1591:A:H8	1.59	0.68
31:b:1:U:H2'	31:b:2:G:H8	1.59	0.67
5:4:1:MET:N	31:b:40:U:O4	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:946:A:H2'	7:A:947:G:H8	1.58	0.67
52:w:41:GLU:OE1	52:w:44:LYS:NZ	2.27	0.67
15:I:88:MET:HE3	15:I:98:LEU:HD12	1.77	0.67
4:3:4:ARG:HG3	4:3:6:SER:H	1.59	0.67
7:A:1227:A:C8	19:M:116:ILE:HD11	2.30	0.67
30:a:2848:G:O2'	30:a:2867:G:N2	2.27	0.67
7:A:1130:A:H61	7:A:1144:G:H1'	1.58	0.67
14:H:10:MET:HB2	14:H:27:MET:HE1	1.77	0.67
7:A:477:C:H2'	7:A:478:A:C8	2.30	0.67
10:D:202:GLU:OE1	11:E:112:ARG:NH1	2.28	0.67
11:E:151:GLU:OE1	11:E:151:GLU:N	2.26	0.67
31:b:95:U:H2'	31:b:96:G:H8	1.60	0.67
17:K:50:SER:HA	17:K:69:ARG:HH12	1.60	0.66
2:1:25:LYS:NZ	30:a:210:C:OP1	2.25	0.66
34:e:171:ASP:OD1	34:e:172:ALA:N	2.28	0.66
30:a:2250:G:O2'	30:a:2496:C:OP1	2.12	0.66
30:a:358:U:H2'	30:a:359:G:H8	1.60	0.66
6:5:55:C:N3	35:f:80:ARG:NH2	2.43	0.66
10:D:124:MET:SD	10:D:146:ARG:HG2	2.36	0.66
50:u:55:GLU:N	50:u:55:GLU:OE1	2.28	0.66
24:R:28:THR:HA	24:R:31:ASN:ND2	2.11	0.66
30:a:2646:C:OP2	30:a:2732:G:O2'	2.14	0.66
33:d:148:GLN:OE1	33:d:148:GLN:N	2.29	0.66
7:A:1445:U:H3	7:A:1457:G:H1	1.42	0.65
30:a:2246:G:H2'	30:a:2247:A:H8	1.62	0.65
30:a:2304:G:H22	30:a:2312:U:H3	1.44	0.65
7:A:1412:C:H2'	7:A:1413:A:C8	2.31	0.65
53:x:26:PHE:CZ	53:x:30:MET:HE1	2.32	0.65
7:A:269:C:H2'	7:A:270:A:C8	2.28	0.65
7:A:337:G:H2'	7:A:338:A:C8	2.32	0.65
7:A:1218:C:H2'	7:A:1219:A:C8	2.31	0.65
20:N:90:ARG:NH2	20:N:92:GLU:OE2	2.29	0.65
30:a:1801:A:OP2	32:c:150:LYS:NZ	2.27	0.65
7:A:390:U:H4'	22:P:28:ARG:HH21	1.62	0.65
26:T:29:ARG:O	26:T:33:LYS:HG2	1.97	0.65
30:a:2576:G:O2'	30:a:2579:C:OP2	2.13	0.65
10:D:64:ILE:HG22	10:D:65:TYR:CD1	2.31	0.65
12:F:42:TRP:HB2	12:F:59:TYR:HB2	1.79	0.65
30:a:1842:G:H2'	30:a:1843:C:C6	2.31	0.65
36:g:19:ILE:HG22	36:g:24:ILE:HD13	1.77	0.65
12:F:26:THR:HG23	12:F:36:ILE:HG13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:x:26:PHE:CE1	53:x:30:MET:HE1	2.32	0.65
7:A:1323:G:H2'	7:A:1324:A:C8	2.32	0.64
45:p:26:GLY:O	45:p:30:ARG:NH1	2.30	0.64
30:a:2861:U:H2'	30:a:2862:G:H8	1.62	0.64
6:5:62:C:H2'	6:5:63:G:C8	2.33	0.64
30:a:820:A:H4'	30:a:836:G:H22	1.63	0.64
19:M:65:VAL:HG12	19:M:66:GLU:HG2	1.78	0.64
25:S:35:SER:HG	25:S:38:SER:HG	1.45	0.64
6:5:21:A:O2'	6:5:46:A:N6	2.31	0.64
30:a:2328:A:H2'	30:a:2329:U:C6	2.33	0.64
30:a:2533:U:OP1	30:a:2665:A:O2'	2.15	0.64
43:n:70:ALA:O	43:n:74:VAL:HG23	1.97	0.64
3:2:8:ARG:NH2	30:a:244:A:OP2	2.31	0.64
13:G:69:VAL:HG21	13:G:104:ILE:HD11	1.80	0.64
30:a:1433:A:H2'	30:a:1434:A:C8	2.33	0.64
30:a:2498:OMC:HM23	30:a:2498:OMC:O3'	1.97	0.64
25:S:3:ARG:HH21	25:S:7:LYS:HD3	1.63	0.64
30:a:2376:A:C4	43:n:99:TYR:HE2	2.15	0.64
35:f:62:GLY:O	35:f:95:ARG:NH2	2.31	0.64
52:w:20:HIS:ND1	52:w:20:HIS:O	2.30	0.64
4:3:11:CYS:HB3	4:3:33:HIS:CE1	2.33	0.64
9:C:53:SER:HB3	9:C:115:LEU:HD21	1.80	0.64
21:O:88:ARG:NH2	30:a:714:U:OP2	2.31	0.64
30:a:1664:A:H61	30:a:1996:C:N4	1.96	0.64
41:l:106:ASP:OD1	41:l:107:GLY:N	2.31	0.64
17:K:50:SER:HA	17:K:69:ARG:NH1	2.13	0.64
36:g:60:ASP:OD1	36:g:60:ASP:N	2.22	0.64
30:a:1570:A:H2'	30:a:1571:A:C8	2.34	0.63
30:a:2291:U:H2'	30:a:2292:U:C6	2.34	0.63
30:a:2439:A:H4'	30:a:2440:C:H5''	1.80	0.63
41:l:67:VAL:HG11	41:l:96:ILE:HD11	1.80	0.63
7:A:71:A:H61	7:A:99:C:H1'	1.63	0.63
7:A:634:C:H2'	7:A:635:A:H8	1.62	0.63
7:A:1147:C:O2'	15:I:7:TYR:OH	2.15	0.63
30:a:272:A:H2'	30:a:273:G:H8	1.61	0.63
30:a:1248:G:OP1	34:e:44:ARG:NH1	2.26	0.63
4:3:11:CYS:HB3	4:3:33:HIS:HE1	1.64	0.63
7:A:222:C:H2'	7:A:223:A:H8	1.64	0.63
7:A:1391:U:H2'	7:A:1392:G:H8	1.63	0.63
27:U:4:ILE:HD13	27:U:19:PHE:HD1	1.63	0.63
30:a:5:A:H2'	30:a:6:A:H8	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3:2:LYS:NZ	4:3:32:LYS:O	2.32	0.63
30:a:989:G:C8	54:y:14:ILE:HD11	2.34	0.63
48:s:79:ASP:OD1	48:s:79:ASP:N	2.30	0.63
11:E:13:GLU:OE1	11:E:68:ARG:NH1	2.30	0.63
11:E:107:ALA:O	11:E:112:ARG:NH2	2.32	0.63
7:A:235:C:H2'	7:A:236:A:H8	1.64	0.63
25:S:50:ALA:HB1	25:S:57:HIS:HB3	1.80	0.63
23:Q:68:SER:OG	23:Q:69:LYS:N	2.32	0.63
30:a:445:C:OP1	45:p:2:ALA:N	2.32	0.63
7:A:76:G:H1	7:A:93:U:H3	1.47	0.62
50:u:77:VAL:HG23	50:u:89:ILE:HG12	1.81	0.62
15:I:92:GLU:OE1	15:I:92:GLU:N	2.31	0.62
17:K:29:ASN:OD1	17:K:57:LYS:HD3	1.99	0.62
6:5:8:U:O2'	6:5:21:A:N1	2.29	0.62
2:1:34:ARG:NE	2:1:42:LEU:O	2.32	0.62
7:A:946:A:H2'	7:A:947:G:C8	2.34	0.62
35:f:14:LYS:O	35:f:18:THR:HG23	2.00	0.62
36:g:86:LYS:HG3	36:g:165:ALA:HB2	1.80	0.62
47:r:86:MET:HE3	47:r:96:ILE:HG12	1.82	0.62
30:a:155:A:H2'	30:a:156:A:H8	1.64	0.62
16:J:35:GLN:HG2	16:J:77:VAL:HB	1.82	0.62
5:4:28:VAL:HG12	35:f:140:GLU:HA	1.82	0.62
30:a:2192:U:H2'	30:a:2193:G:H8	1.64	0.62
47:r:7:HIS:ND1	47:r:7:HIS:O	2.32	0.62
7:A:1513:A:H2'	7:A:1514:G:H8	1.65	0.61
7:A:1412:C:H2'	7:A:1413:A:H8	1.64	0.61
10:D:116:GLN:HE21	10:D:120:HIS:CE1	2.18	0.61
13:G:16:PRO:HG3	15:I:43:THR:HG22	1.82	0.61
30:a:1548:A:H2'	30:a:1549:A:H8	1.65	0.61
7:A:1112:C:N3	9:C:178:LEU:HD12	2.15	0.61
30:a:1799:G:OP1	32:c:258:ARG:NH1	2.32	0.61
53:x:10:SER:OG	53:x:13:GLU:OE2	2.18	0.61
7:A:41:G:H2'	7:A:42:G:H8	1.66	0.61
7:A:90:C:H2'	7:A:91:U:C6	2.35	0.61
30:a:820:A:C2	30:a:943:A:H4'	2.35	0.61
30:a:1154:G:OP2	45:p:58:ARG:NH2	2.28	0.61
39:j:98:ARG:HH21	39:j:100:PHE:HE1	1.47	0.61
7:A:47:C:N3	7:A:362:G:N2	2.48	0.61
7:A:87:C:H2'	7:A:88:U:H6	1.65	0.61
7:A:745:G:H2'	7:A:746:A:H8	1.66	0.61
30:a:1041:G:H2'	30:a:1042:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1597:A:H5''	30:a:1598:A:H5'	1.81	0.61
7:A:701:U:O2	7:A:703:G:N1	2.34	0.61
30:a:1047:G:O2'	30:a:1110:G:N1	2.14	0.61
30:a:1654:A:OP2	42:m:1:MET:N	2.33	0.61
8:B:184:PHE:HD1	8:B:198:PHE:HB2	1.66	0.61
14:H:18:GLN:HG2	14:H:63:LEU:HD13	1.83	0.61
52:w:43:GLU:OE2	52:w:45:ARG:NH2	2.33	0.61
7:A:137:U:O2	7:A:226:G:N2	2.29	0.60
6:5:62:C:H2'	6:5:63:G:H8	1.66	0.60
7:A:459:A:H2'	7:A:460:A:H8	1.65	0.60
30:a:2812:G:H2'	30:a:2813:A:H8	1.66	0.60
39:j:1:MET:SD	39:j:67:LYS:NZ	2.74	0.60
7:A:674:G:H2'	7:A:675:A:C8	2.33	0.60
30:a:24:G:H2'	30:a:25:U:C6	2.36	0.60
32:c:230:HIS:CE1	32:c:232:HIS:HD2	2.19	0.60
7:A:216:U:H2'	7:A:217:C:C6	2.37	0.60
30:a:1724:G:O6	30:a:1737:G:N2	2.34	0.60
7:A:965:U:H1'	7:A:969:A:C2	2.37	0.60
7:A:1391:U:H2'	7:A:1392:G:C8	2.36	0.60
16:J:32:THR:HG21	16:J:83:THR:HA	1.82	0.60
19:M:14:HIS:HB2	19:M:17:ILE:HD12	1.83	0.60
49:t:74:ASN:O	49:t:76:ALA:N	2.34	0.60
7:A:999:C:H2'	7:A:1000:A:H8	1.66	0.60
30:a:970:U:H2'	30:a:971:G:H8	1.65	0.60
52:w:19:SER:OG	52:w:20:HIS:N	2.32	0.60
30:a:989:G:N7	54:y:14:ILE:HD11	2.17	0.60
2:1:11:LYS:O	2:1:15:SER:OG	2.19	0.60
7:A:26:A:H61	7:A:558:G:H1'	1.66	0.60
30:a:1779:U:OP2	30:a:1784:A:N6	2.33	0.60
30:a:1987:A:H2'	30:a:1988:G:H8	1.65	0.60
30:a:2514:U:H2'	30:a:2515:C:H6	1.66	0.60
32:c:232:HIS:HE1	32:c:244:PRO:HA	1.67	0.60
7:A:405:U:OP2	10:D:3:ARG:NH2	2.29	0.60
8:B:128:LYS:H	8:B:128:LYS:HD2	1.67	0.59
20:N:89:MET:HA	20:N:89:MET:HE2	1.84	0.59
27:U:63:GLU:OE1	27:U:66:ARG:NH2	2.35	0.59
30:a:2064:C:H2'	30:a:2065:C:C6	2.37	0.59
33:d:42:ASN:ND2	33:d:43:ASP:OD1	2.34	0.59
7:A:236:A:H2'	7:A:237:G:H8	1.67	0.59
7:A:945:G:C2	7:A:946:A:C8	2.90	0.59
30:a:993:G:OP2	45:p:51:ARG:NH2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:p:83:LEU:HD22	45:p:88:VAL:HB	1.85	0.59
8:B:15:HIS:HB3	8:B:43:LEU:HD21	1.83	0.59
14:H:90:ASP:OD1	14:H:90:ASP:N	2.35	0.59
43:n:15:ARG:NH2	43:n:95:SER:OG	2.31	0.59
7:A:460:A:H2'	7:A:461:A:H8	1.67	0.59
7:A:686:U:O2'	7:A:703:G:N2	2.35	0.59
7:A:1032:G:H2'	7:A:1033:G:H4'	1.84	0.59
30:a:414:C:H2'	30:a:415:A:H8	1.66	0.59
7:A:87:C:H2'	7:A:88:U:C6	2.37	0.59
13:G:133:THR:HA	13:G:136:LYS:HD3	1.84	0.59
41:l:25:ASP:N	41:l:25:ASP:OD1	2.32	0.59
3:2:15:LYS:NZ	30:a:630:G:OP2	2.34	0.59
7:A:459:A:H2'	7:A:460:A:C8	2.38	0.59
7:A:514:C:H2'	7:A:515:G:H8	1.68	0.59
7:A:619:U:N3	10:D:131:ASN:OD1	2.35	0.59
8:B:68:LEU:HB3	8:B:161:LEU:HD23	1.84	0.59
30:a:155:A:H2'	30:a:156:A:C8	2.37	0.59
7:A:382:A:H2'	7:A:383:A:H8	1.67	0.59
30:a:819:A:OP2	30:a:1187:G:N2	2.28	0.59
30:a:1434:A:H2'	30:a:1435:G:C8	2.37	0.59
33:d:124:ARG:HA	33:d:165:MET:SD	2.43	0.59
10:D:14:ARG:HG2	10:D:63:ARG:HH12	1.67	0.59
12:F:38:ARG:NE	12:F:63:ASN:OD1	2.33	0.59
30:a:139:U:H5''	30:a:140:C:H5	1.67	0.59
30:a:619:G:OP2	30:a:620:G:N2	2.35	0.59
30:a:1853:A:N7	30:a:1889:A:N6	2.50	0.59
7:A:792:A:H1'	7:A:794:A:N7	2.17	0.59
21:O:10:LYS:HZ1	21:O:14:GLU:HB2	1.66	0.59
31:b:36:C:N4	31:b:49:C:O2	2.36	0.59
19:M:77:ILE:HG22	19:M:81:MET:HE2	1.84	0.59
30:a:720:U:H2'	30:a:721:A:C8	2.38	0.59
30:a:720:U:H2'	30:a:721:A:H8	1.68	0.59
8:B:115:LYS:NZ	8:B:152:LYS:O	2.33	0.58
30:a:1196:C:H2'	30:a:1197:G:C8	2.37	0.58
30:a:2291:U:H2'	30:a:2292:U:H6	1.67	0.58
30:a:2824:C:OP2	30:a:2825:G:N2	2.35	0.58
6:5:65:U:H2'	6:5:66:G:H8	1.67	0.58
30:a:1799:G:OP2	32:c:270:ARG:NH2	2.36	0.58
35:f:57:LEU:HA	35:f:60:ILE:HD12	1.84	0.58
7:A:674:G:H21	17:K:118:HIS:HB2	1.68	0.58
7:A:714:G:H2'	7:A:715:A:C8	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:65:TYR:CD2	10:D:94:LEU:HB3	2.39	0.58
10:D:85:ASN:OD1	11:E:102:GLY:HA3	2.03	0.58
30:a:2016:U:O2	55:z:4:GLN:NE2	2.32	0.58
30:a:2328:A:H2'	30:a:2329:U:H6	1.68	0.58
6:5:8:U:O2	6:5:15:A:N6	2.36	0.58
7:A:1279:G:OP2	16:J:11:LYS:NZ	2.29	0.58
30:a:832:U:H2'	30:a:833:A:H8	1.68	0.58
51:v:21:LEU:HD11	51:v:41:ARG:HH12	1.68	0.58
7:A:27:G:H2'	7:A:28:A:H8	1.68	0.58
7:A:1493:A:OP1	30:a:1913:A:N6	2.37	0.58
30:a:24:G:H2'	30:a:25:U:H6	1.67	0.58
15:I:84:THR:HG23	15:I:98:LEU:HD13	1.86	0.58
7:A:407:U:H2'	7:A:408:A:H8	1.68	0.58
14:H:3:MET:HE2	14:H:9:ASP:HB2	1.85	0.58
24:R:26:ILE:O	24:R:30:LYS:HG3	2.02	0.58
46:q:46:GLU:OE2	46:q:48:LYS:NZ	2.26	0.58
52:w:68:LEU:HD12	52:w:72:ARG:NH1	2.18	0.58
7:A:231:U:H2'	7:A:232:G:H8	1.69	0.58
7:A:1147:C:H4'	15:I:7:TYR:CE2	2.38	0.58
7:A:1167:A:O2'	7:A:1169:A:N7	2.34	0.58
30:a:1589:U:H2'	30:a:1590:A:H8	1.68	0.58
7:A:645:G:C2	7:A:646:G:C8	2.92	0.58
7:A:744:C:H2'	7:A:745:G:H8	1.67	0.58
7:A:1095:U:OP1	7:A:1108:G:N2	2.29	0.58
10:D:62:ARG:HG2	10:D:72:PHE:HD2	1.67	0.58
30:a:27:G:O2'	30:a:28:A:OP2	2.22	0.58
30:a:742:A:H2'	30:a:743:A:H8	1.68	0.58
30:a:1837:C:N4	30:a:1899:A:N7	2.52	0.58
50:u:80:HIS:ND1	50:u:83:LYS:HB2	2.18	0.58
54:y:27:LEU:HD22	54:y:47:MET:HE3	1.86	0.58
7:A:382:A:H2'	7:A:383:A:C8	2.39	0.58
9:C:28:GLU:N	9:C:28:GLU:OE1	2.36	0.58
16:J:66:GLU:HB2	20:N:99:ALA:HB2	1.86	0.58
30:a:196:A:H61	30:a:831:G:H21	1.51	0.58
30:a:814:C:H1'	30:a:1225:G:H21	1.69	0.58
31:b:114:C:H2'	31:b:115:A:C8	2.37	0.58
33:d:157:LYS:HD2	38:i:80:HIS:CD2	2.39	0.58
7:A:492:C:H2'	7:A:493:A:C8	2.39	0.57
6:5:31:C:H2'	6:5:32:4OC:H6	1.86	0.57
7:A:918:A:H2'	7:A:919:A:C8	2.39	0.57
8:B:163:VAL:HG11	8:B:173:ILE:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:113:ASP:OD2	13:G:122:ASN:ND2	2.36	0.57
16:J:88:MET:HA	16:J:88:MET:HE3	1.86	0.57
30:a:2302:U:O2'	35:f:123:ASP:O	2.22	0.57
7:A:1048:G:P	20:N:4:GLN:HE22	2.26	0.57
8:B:213:TYR:O	8:B:217:VAL:HG12	2.03	0.57
30:a:1432:G:H2'	30:a:1433:A:C8	2.39	0.57
35:f:8:TYR:HB2	35:f:173:PHE:HZ	1.67	0.57
41:l:77:PRO:HG2	41:l:80:VAL:HG21	1.87	0.57
43:n:99:TYR:HE1	43:n:104:GLN:HG3	1.69	0.57
17:K:111:THR:HG23	27:U:3:VAL:HG12	1.87	0.57
20:N:66:GLN:HG3	20:N:79:LEU:HD22	1.86	0.57
30:a:307:G:N1	30:a:310:A:OP2	2.35	0.57
30:a:859:G:O2'	30:a:860:U:OP2	2.22	0.57
30:a:2591:C:H2'	30:a:2592:G:H8	1.69	0.57
34:e:176:ASP:OD1	34:e:176:ASP:N	2.35	0.57
38:i:11:VAL:HG11	38:i:50:THR:HG22	1.85	0.57
13:G:27:VAL:HG22	13:G:43:VAL:HG11	1.86	0.57
30:a:5:A:H2'	30:a:6:A:C8	2.38	0.57
42:m:34:ILE:HG12	42:m:113:ILE:HG22	1.87	0.57
15:I:7:TYR:HD1	15:I:8:GLY:N	2.01	0.57
4:3:24:ARG:HH22	30:a:2742:G:P	2.27	0.57
7:A:709:U:H2'	7:A:710:G:H8	1.69	0.57
22:P:18:GLN:OE1	22:P:35:ARG:NH1	2.34	0.57
30:a:171:U:H2'	30:a:172:A:H8	1.70	0.57
30:a:189:G:OP2	52:w:26:LYS:NZ	2.37	0.57
30:a:2515:C:H2'	30:a:2516:A:H8	1.70	0.57
13:G:111:ARG:NH1	13:G:123:GLU:OE1	2.38	0.57
30:a:1433:A:H2'	30:a:1434:A:H8	1.67	0.57
30:a:2812:G:H2'	30:a:2813:A:C8	2.40	0.57
7:A:1144:G:N2	7:A:1146:A:H62	2.03	0.57
17:K:36:ASP:OD1	17:K:38:GLN:N	2.35	0.57
35:f:162:SER:OG	35:f:165:GLU:OE1	2.21	0.57
7:A:451:A:H61	7:A:481:G:H5'	1.69	0.57
7:A:552:U:H2'	7:A:553:A:C8	2.33	0.57
30:a:2030:6MZ:H4'	30:a:2031:A:O5'	2.04	0.57
30:a:48:G:N2	30:a:177:G:OP2	2.38	0.56
30:a:2246:G:H2'	30:a:2247:A:C8	2.39	0.56
30:a:2898:U:H2'	30:a:2899:A:H8	1.70	0.56
6:5:19:C:H42	35:f:80:ARG:NH2	2.04	0.56
7:A:166:U:H2'	7:A:167:A:H8	1.70	0.56
8:B:126:PHE:HE1	8:B:137:ARG:HH11	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2682:A:C8	33:d:11:MET:HE3	2.40	0.56
7:A:335:C:H2'	7:A:336:A:H8	1.69	0.56
7:A:1253:G:H2'	7:A:1254:A:H8	1.70	0.56
30:a:948:C:H2'	30:a:949:G:H8	1.70	0.56
30:a:1301:A:H62	30:a:1641:A:H61	1.53	0.56
30:a:1306:C:H2'	30:a:1307:A:C8	2.36	0.56
30:a:2327:A:H2'	30:a:2328:A:C8	2.41	0.56
30:a:2485:G:OP1	41:l:45:GLN:NE2	2.30	0.56
36:g:52:PHE:CE2	36:g:69:ARG:HA	2.40	0.56
36:g:52:PHE:CZ	36:g:72:LEU:HD12	2.40	0.56
51:v:64:ASP:N	51:v:64:ASP:OD1	2.33	0.56
6:5:17:G:H4'	6:5:18:G:O5'	2.06	0.56
7:A:19:A:H2'	7:A:20:U:C6	2.40	0.56
8:B:183:VAL:HG23	8:B:197:ASP:H	1.70	0.56
30:a:172:A:H2'	30:a:173:A:H8	1.70	0.56
49:t:54:GLN:N	49:t:54:GLN:OE1	2.36	0.56
10:D:65:TYR:HD2	10:D:94:LEU:HD22	1.70	0.56
36:g:127:THR:HG22	36:g:128:GLN:H	1.69	0.56
42:m:70:THR:O	42:m:72:ASP:N	2.38	0.56
42:m:106:ASP:O	42:m:107:ASN:C	2.48	0.56
9:C:7:PRO:HD2	9:C:184:TYR:CD2	2.41	0.56
12:F:82:ASP:OD1	12:F:82:ASP:N	2.33	0.56
30:a:319:G:OP2	34:e:132:LYS:NZ	2.31	0.56
30:a:2082:A:C4	30:a:2239:G:N2	2.74	0.56
31:b:1:U:H2'	31:b:2:G:C8	2.38	0.56
47:r:92:ARG:HG2	47:r:92:ARG:HH11	1.70	0.56
7:A:1266:G:N2	7:A:1269:A:OP2	2.29	0.56
7:A:422:C:O2	7:A:423:G:N1	2.39	0.56
8:B:142:GLU:O	8:B:146:ASN:ND2	2.36	0.56
9:C:62:LYS:NZ	9:C:98:PRO:HD2	2.21	0.56
30:a:1437:C:HO2'	30:a:1516:G:HO2'	1.50	0.56
30:a:1843:C:H2'	30:a:1844:C:H6	1.71	0.56
35:f:42:GLU:HB2	35:f:49:LEU:HD23	1.88	0.56
8:B:217:VAL:O	8:B:221:VAL:HG12	2.06	0.56
30:a:927:A:H2'	30:a:928:A:H8	1.70	0.56
30:a:1824:G:H2'	30:a:1825:U:H6	1.71	0.56
31:b:60:C:H2'	31:b:61:G:H8	1.70	0.56
7:A:312:C:H2'	7:A:313:A:C8	2.41	0.56
7:A:512:U:OP1	10:D:44:ARG:NH1	2.39	0.56
7:A:1137:C:O2	7:A:1138:G:N2	2.39	0.56
30:a:48:G:N2	30:a:177:G:H21	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:851:C:H2'	30:a:852:U:C6	2.40	0.56
7:A:1001:C:H2'	7:A:1002:G:H8	1.70	0.55
8:B:12:ALA:HA	8:B:208:ARG:HD2	1.87	0.55
30:a:452:G:H2'	30:a:453:A:H8	1.71	0.55
30:a:1590:A:H2'	30:a:1591:A:C8	2.40	0.55
54:y:14:ILE:O	54:y:14:ILE:HG23	2.06	0.55
7:A:999:C:H2'	7:A:1000:A:C8	2.40	0.55
30:a:2243:U:H2'	30:a:2244:U:C6	2.41	0.55
7:A:1004:A:H2'	7:A:1005:A:O4'	2.07	0.55
30:a:1365:A:O2'	52:w:11:ARG:NH1	2.40	0.55
30:a:2455:G:H2'	30:a:2456:C:H6	1.72	0.55
53:x:44:LYS:HD2	53:x:48:ARG:NH1	2.21	0.55
7:A:591:U:OP2	14:H:31:LYS:NZ	2.39	0.55
7:A:1488:G:H2'	7:A:1489:G:H8	1.72	0.55
7:A:1521:C:H2'	7:A:1522:U:H6	1.71	0.55
32:c:230:HIS:HE1	32:c:232:HIS:HD2	1.53	0.55
40:k:82:LEU:HD22	40:k:90:VAL:HG21	1.88	0.55
7:A:1363:A:O2'	7:A:1365:G:N7	2.31	0.55
30:a:1353:A:N7	30:a:1378:A:N6	2.54	0.55
30:a:1837:C:C2	30:a:1904:G:N2	2.74	0.55
30:a:2376:A:C4	43:n:99:TYR:CE2	2.94	0.55
44:o:2:SER:OG	44:o:3:ASN:N	2.37	0.55
7:A:91:U:H2'	7:A:92:U:C6	2.42	0.55
7:A:1003:G:N2	7:A:1005:A:H5'	2.21	0.55
11:E:149:SER:OG	11:E:152:MET:HE3	2.06	0.55
6:5:23:U:H2'	6:5:24:A:C8	2.42	0.55
7:A:794:A:H2'	7:A:795:C:H6	1.72	0.55
13:G:28:ASN:O	13:G:31:MET:HB3	2.06	0.55
30:a:252:G:O2'	30:a:253:C:OP1	2.21	0.55
30:a:581:C:H2'	30:a:582:A:H8	1.71	0.55
7:A:203:G:O2'	7:A:465:A:N1	2.40	0.55
7:A:1226:C:O2	25:S:83:HIS:HE1	1.90	0.55
30:a:572:A:H61	30:a:2029:G:H21	1.55	0.55
30:a:1664:A:H61	30:a:1996:C:H42	1.54	0.55
7:A:378:G:O6	7:A:386:C:N4	2.39	0.55
7:A:505:G:H2'	7:A:506:G:H8	1.72	0.55
30:a:935:C:H2'	30:a:936:A:H8	1.72	0.55
30:a:1668:A:N3	30:a:1670:C:N4	2.54	0.55
7:A:676:A:H5''	17:K:115:PRO:HB3	1.88	0.55
7:A:746:A:H2'	7:A:747:A:C8	2.42	0.55
7:A:1157:A:N7	7:A:1180:A:N6	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1343:G:H2'	7:A:1344:C:C6	2.42	0.55
10:D:64:ILE:HG22	10:D:65:TYR:HD1	1.67	0.55
12:F:3:HIS:CD2	12:F:95:ALA:HB2	2.42	0.55
30:a:2591:C:H2'	30:a:2592:G:C8	2.42	0.55
51:v:25:ARG:HD2	51:v:31:VAL:HG12	1.89	0.55
7:A:796:C:O3'	17:K:127:ARG:NH1	2.40	0.54
9:C:151:VAL:HG22	9:C:200:VAL:HG23	1.90	0.54
17:K:88:GLY:H	17:K:114:THR:HB	1.72	0.54
30:a:272:A:H2'	30:a:273:G:C8	2.41	0.54
30:a:288:U:H2'	30:a:289:G:C8	2.42	0.54
30:a:517:C:OP2	55:z:10:ARG:NH1	2.39	0.54
7:A:736:C:H2'	7:A:737:C:H6	1.72	0.54
8:B:190:ASN:OD1	8:B:191:SER:N	2.41	0.54
14:H:41:LYS:NZ	14:H:48:ASP:OD1	2.39	0.54
30:a:1252:G:N2	45:p:33:ARG:O	2.40	0.54
41:l:97:GLN:OE1	41:l:97:GLN:N	2.40	0.54
7:A:1355:G:H2'	7:A:1356:G:H8	1.72	0.54
8:B:73:LYS:HD2	8:B:165:ASP:OD2	2.08	0.54
30:a:742:A:H2'	30:a:743:A:C8	2.42	0.54
7:A:1406:U:H2'	7:A:1407:5MC:O4'	2.06	0.54
8:B:188:ASP:OD1	8:B:188:ASP:N	2.35	0.54
24:R:26:ILE:HD11	24:R:67:LEU:HD23	1.89	0.54
33:d:133:THR:O	33:d:134:HIS:HB2	2.07	0.54
35:f:38:MET:HE3	35:f:53:ALA:HB1	1.89	0.54
7:A:1158:C:C5	7:A:1160:G:H1'	2.42	0.54
3:2:33:LEU:HD23	30:a:2419:U:OP2	2.07	0.54
7:A:34:C:H2'	7:A:35:G:H8	1.72	0.54
7:A:950:U:H2'	7:A:951:G:C8	2.39	0.54
30:a:2901:C:H2'	30:a:2902:C:C6	2.43	0.54
7:A:1349:A:H1'	7:A:1374:A:N6	2.23	0.54
30:a:947:A:C6	30:a:971:G:C6	2.96	0.54
49:t:99:ASN:OD1	49:t:99:ASN:O	2.26	0.54
6:5:28:C:H2'	6:5:29:A:H8	1.72	0.54
6:5:55:C:C4	35:f:80:ARG:NH2	2.76	0.54
7:A:1287:A:H2	7:A:1353:G:H1'	1.73	0.54
7:A:1513:A:H2'	7:A:1514:G:C8	2.42	0.54
17:K:36:ASP:OD1	17:K:38:GLN:NE2	2.40	0.54
30:a:604:G:C6	30:a:625:G:N1	2.76	0.54
30:a:851:C:H2'	30:a:852:U:H6	1.71	0.54
30:a:903:C:H2'	30:a:904:G:H8	1.73	0.54
35:f:123:ASP:OD1	35:f:124:GLY:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:43:VAL:HG12	36:g:52:PHE:CE1	2.43	0.54
44:o:28:VAL:HG12	44:o:84:ILE:HG23	1.90	0.54
7:A:713:G:H2'	7:A:714:G:C8	2.43	0.54
10:D:172:GLU:OE1	10:D:183:LYS:NZ	2.35	0.54
14:H:11:LEU:HD12	14:H:75:ILE:HG12	1.89	0.54
18:L:5:ASN:O	18:L:9:ARG:HG3	2.08	0.54
19:M:12:HIS:O	19:M:44:LYS:NZ	2.28	0.54
30:a:85:G:C5	30:a:98:G:N2	2.76	0.54
32:c:160:THR:HB	32:c:177:ARG:HG3	1.90	0.54
45:p:50:ARG:O	45:p:54:LYS:NZ	2.41	0.54
49:t:36:VAL:HB	49:t:39:ILE:HG13	1.89	0.54
10:D:65:TYR:CE2	10:D:94:LEU:HB3	2.43	0.54
13:G:4:ARG:HA	13:G:4:ARG:NH1	2.23	0.54
27:U:14:VAL:HG22	27:U:17:ARG:HH12	1.73	0.54
30:a:833:A:OP2	40:k:39:LYS:NZ	2.40	0.54
30:a:1278:C:H2'	30:a:1279:G:H8	1.73	0.54
30:a:1364:G:OP2	52:w:2:SER:N	2.41	0.54
31:b:66:A:H61	31:b:107:G:H2'	1.72	0.54
49:t:97:LYS:O	49:t:98:SER:OG	2.23	0.54
5:4:11:GLU:HA	5:4:25:ARG:HA	1.89	0.53
7:A:728:A:H2'	7:A:729:A:C8	2.43	0.53
7:A:728:A:H2'	7:A:729:A:H8	1.73	0.53
6:5:32:4OC:HM22	6:5:33:U:H5'	1.89	0.53
7:A:40:C:H2'	7:A:41:G:H8	1.74	0.53
7:A:1015:G:H2'	7:A:1016:A:C8	2.44	0.53
8:B:136:MET:N	8:B:139:ARG:HH21	2.06	0.53
30:a:2192:U:H2'	30:a:2193:G:C8	2.44	0.53
35:f:119:ALA:O	35:f:167:ARG:NH2	2.36	0.53
44:o:34:GLU:OE2	44:o:39:ARG:NH2	2.31	0.53
7:A:460:A:H2'	7:A:461:A:C8	2.43	0.53
7:A:918:A:H2'	7:A:919:A:H8	1.72	0.53
30:a:309:A:N7	30:a:330:A:N6	2.55	0.53
30:a:452:G:H2'	30:a:453:A:C8	2.44	0.53
30:a:989:G:C5	54:y:14:ILE:HD11	2.43	0.53
30:a:1548:A:H2'	30:a:1549:A:C8	2.42	0.53
30:a:1746:A:H2'	30:a:1747:U:C6	2.43	0.53
30:a:1773:A:N7	30:a:1829:A:H1'	2.23	0.53
7:A:270:A:H2'	7:A:271:C:C6	2.42	0.53
30:a:2494:G:C2	30:a:2495:G:C8	2.96	0.53
7:A:429:U:H3	7:A:431:A:H62	1.55	0.53
7:A:934:C:H5	7:A:1344:C:H2'	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:571:U:N3	30:a:575:A:N7	2.57	0.53
30:a:807:U:OP2	40:k:41:ARG:NH2	2.41	0.53
30:a:848:C:H2'	30:a:849:A:H8	1.73	0.53
30:a:1197:G:C2	30:a:1198:U:C5	2.96	0.53
7:A:437:U:O2'	10:D:120:HIS:ND1	2.41	0.53
9:C:64:ILE:HG22	9:C:97:VAL:HG23	1.90	0.53
30:a:2745:C:H2'	30:a:2746:U:C6	2.44	0.53
33:d:156:PHE:CE1	38:i:81:ILE:HD13	2.43	0.53
7:A:1126:U:OP1	16:J:7:ARG:NH2	2.33	0.53
7:A:1286:U:H2'	7:A:1287:A:H5'	1.91	0.53
27:U:7:ARG:HG3	27:U:18:ARG:HH22	1.74	0.53
30:a:694:U:OP2	32:c:59:LYS:NZ	2.34	0.53
30:a:887:U:O2'	30:a:889:C:OP2	2.24	0.53
30:a:1746:A:H2'	30:a:1747:U:H6	1.73	0.53
30:a:2588:G:C6	30:a:2607:G:N1	2.77	0.53
48:s:53:VAL:CG1	48:s:87:LEU:HD22	2.38	0.53
7:A:131:A:H2'	7:A:132:C:C6	2.44	0.53
7:A:161:A:H2'	7:A:162:A:C8	2.43	0.53
30:a:721:A:H2'	30:a:722:A:C8	2.44	0.53
30:a:721:A:H2'	30:a:722:A:H8	1.72	0.53
30:a:2588:G:C5	30:a:2607:G:C2	2.95	0.53
30:a:2591:C:C2	30:a:2592:G:N7	2.77	0.53
13:G:5:ARG:HG3	13:G:5:ARG:O	2.08	0.53
30:a:145:C:H2'	30:a:146:A:C8	2.44	0.53
30:a:191:A:H2'	30:a:192:C:C6	2.41	0.53
38:i:19:ASP:OD1	38:i:20:ALA:N	2.42	0.53
7:A:216:U:H2'	7:A:217:C:H6	1.72	0.53
7:A:261:U:OP2	26:T:71:LYS:NZ	2.31	0.53
12:F:10:VAL:HG21	12:F:21:MET:HE1	1.91	0.53
19:M:4:ILE:HG23	19:M:57:ARG:HG2	1.91	0.53
30:a:2415:G:C4	30:a:2416:C:C5	2.97	0.53
34:e:146:VAL:HG13	34:e:167:VAL:HG13	1.89	0.53
7:A:1407:5MC:H2'	7:A:1408:A:H8	1.74	0.52
11:E:54:ARG:HG2	11:E:54:ARG:HH11	1.74	0.52
23:Q:46:VAL:HG21	23:Q:61:ILE:HG21	1.91	0.52
30:a:1142:A:C4	30:a:1144:A:N7	2.77	0.52
30:a:1153:C:OP1	45:p:92:ARG:NH2	2.41	0.52
31:b:39:A:C2	31:b:44:G:C2	2.97	0.52
42:m:24:MET:HE2	42:m:44:LEU:HD13	1.90	0.52
4:3:37:GLN:OE1	30:a:1124:G:H1'	2.08	0.52
7:A:440:C:C2	7:A:441:A:C8	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:5:ILE:HD13	23:Q:62:ARG:HE	1.75	0.52
30:a:1870:C:O2'	30:a:1871:A:O4'	2.26	0.52
30:a:2443:C:H2'	30:a:2444:G:H8	1.73	0.52
30:a:2521:C:C2	30:a:2545:G:N2	2.77	0.52
7:A:370:C:H2'	7:A:371:A:C8	2.44	0.52
7:A:1176:A:H2'	7:A:1177:G:C8	2.45	0.52
15:I:106:ARG:NH1	15:I:107:ASP:O	2.42	0.52
30:a:973:A:OP2	46:q:81:LYS:NZ	2.31	0.52
30:a:2064:C:H2'	30:a:2065:C:H6	1.74	0.52
30:a:2414:G:C2	30:a:2415:G:C8	2.98	0.52
7:A:28:A:O2'	7:A:296:U:OP1	2.27	0.52
14:H:10:MET:HE3	14:H:33:LYS:HG2	1.90	0.52
1:0:35:GLU:HG2	1:0:50:LYS:HG2	1.90	0.52
7:A:147:G:H2'	7:A:148:G:C8	2.44	0.52
7:A:579:A:H2'	7:A:580:C:C6	2.45	0.52
23:Q:30:LYS:HB2	23:Q:37:PHE:HE1	1.74	0.52
30:a:2357:G:N2	30:a:2361:G:N7	2.57	0.52
33:d:1:MET:HE3	33:d:100:LEU:HD21	1.92	0.52
6:5:23:U:H2'	6:5:24:A:H8	1.75	0.52
7:A:312:C:H2'	7:A:313:A:H8	1.75	0.52
7:A:413:G:H1'	7:A:428:G:H21	1.74	0.52
7:A:1477:U:H2'	7:A:1478:U:C6	2.44	0.52
30:a:1509:A:HO2'	30:a:1510:G:H8	1.57	0.52
30:a:2514:U:H2'	30:a:2515:C:C6	2.44	0.52
30:a:2578:G:N7	33:d:145:SER:OG	2.41	0.52
32:c:259:SER:O	32:c:259:SER:OG	2.28	0.52
34:e:147:LEU:HD11	34:e:170:ARG:HG3	1.91	0.52
35:f:56:ASP:OD2	35:f:150:ARG:NH1	2.41	0.52
6:5:65:U:H2'	6:5:66:G:C8	2.45	0.52
7:A:270:A:H2'	7:A:271:C:H6	1.74	0.52
7:A:922:G:H2'	7:A:923:A:C8	2.45	0.52
7:A:965:U:H5''	7:A:966:2MG:OP1	2.10	0.52
7:A:1302:C:OP2	19:M:13:LYS:NZ	2.43	0.52
30:a:1827:U:OP2	32:c:221:ARG:NH1	2.43	0.52
35:f:119:ALA:HB1	35:f:167:ARG:HH12	1.75	0.52
6:5:35:C:H42	28:X:17:G:H1	1.57	0.52
7:A:634:C:H2'	7:A:635:A:C8	2.44	0.52
7:A:1477:U:H2'	7:A:1478:U:H6	1.74	0.52
19:M:22:ILE:HD11	19:M:65:VAL:HG11	1.92	0.52
21:O:80:GLN:OE1	21:O:80:GLN:HA	2.09	0.52
30:a:1484:U:H2'	30:a:1485:U:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2290:G:H2'	30:a:2291:U:C6	2.45	0.52
7:A:175:C:H2'	7:A:176:C:H6	1.75	0.52
7:A:408:A:O3'	10:D:23:SER:OG	2.27	0.52
7:A:705:G:C5	7:A:706:A:C8	2.98	0.52
7:A:1243:C:H2'	7:A:1244:G:H8	1.74	0.52
7:A:1530:G:O6	27:U:46:LYS:NZ	2.27	0.52
30:a:172:A:H2'	30:a:173:A:C8	2.45	0.52
30:a:832:U:H2'	30:a:833:A:C8	2.44	0.52
30:a:1532:A:C6	30:a:1540:G:C6	2.97	0.52
30:a:2068:U:H3	30:a:2430:A:H62	1.57	0.52
30:a:2215:C:H2'	30:a:2216:G:H8	1.74	0.52
7:A:246:A:C2	7:A:282:A:C5	2.97	0.52
7:A:1171:A:H2'	7:A:1172:C:H6	1.75	0.52
7:A:1314:C:H2'	7:A:1315:U:C6	2.45	0.52
8:B:133:GLU:OE2	8:B:133:GLU:N	2.22	0.52
26:T:35:VAL:HG11	26:T:79:LEU:HD13	1.91	0.52
30:a:848:C:H2'	30:a:849:A:C8	2.45	0.52
31:b:14:U:OP2	31:b:70:C:O2'	2.28	0.52
34:e:165:HIS:H	34:e:165:HIS:CD2	2.28	0.52
38:i:12:LYS:O	38:i:41:LYS:NZ	2.43	0.52
7:A:1517:G:H2'	7:A:1518:MA6:H8	1.92	0.51
21:O:10:LYS:NZ	21:O:14:GLU:HB2	2.24	0.51
30:a:644:A:H2'	30:a:645:C:O4'	2.10	0.51
30:a:814:C:H1'	30:a:1225:G:N2	2.25	0.51
30:a:1907:G:O6	30:a:1924:C:N4	2.42	0.51
30:a:2013:A:H2	47:r:88:ARG:HH22	1.58	0.51
30:a:2316:G:H2'	30:a:2317:A:H8	1.75	0.51
31:b:83:G:O6	31:b:94:A:N6	2.43	0.51
46:q:87:GLN:HG2	46:q:88:GLY:H	1.74	0.51
7:A:539:A:H2'	7:A:540:G:H8	1.76	0.51
7:A:1030:U:H5'	7:A:1031:C:H5''	1.92	0.51
9:C:21:THR:O	9:C:58:GLU:HG2	2.10	0.51
11:E:41:ASP:OD1	11:E:43:ASN:N	2.41	0.51
21:O:8:THR:O	21:O:12:VAL:HG12	2.11	0.51
30:a:1582:C:H42	30:a:1583:A:H62	1.58	0.51
30:a:1587:G:H2'	30:a:1588:G:H8	1.75	0.51
33:d:125:TRP:CD1	33:d:160:LYS:HB3	2.44	0.51
38:i:72:LYS:HE3	38:i:74:TYR:HE1	1.75	0.51
7:A:980:C:O2'	20:N:13:ARG:NH1	2.43	0.51
7:A:1029:U:O2'	7:A:1032:G:O6	2.24	0.51
12:F:3:HIS:HD2	12:F:95:ALA:HB2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1463:C:H2'	30:a:1464:G:H8	1.75	0.51
30:a:1707:G:C5	30:a:1756:G:C6	2.98	0.51
30:a:1844:C:C2	30:a:1897:G:N2	2.78	0.51
7:A:17:U:H2'	7:A:18:C:H6	1.74	0.51
7:A:1328:C:C2	7:A:1329:A:C8	2.99	0.51
15:I:28:ILE:HG23	15:I:63:LEU:HD12	1.92	0.51
18:L:24:LEU:HD23	18:L:27:CYS:O	2.11	0.51
24:R:33:ILE:HD12	24:R:68:LEU:HD21	1.93	0.51
30:a:309:A:C5	30:a:330:A:C6	2.99	0.51
30:a:1684:G:O6	30:a:1705:A:N6	2.43	0.51
30:a:2626:C:H2'	30:a:2627:G:C8	2.45	0.51
30:a:2720:U:C4	30:a:2872:A:N1	2.78	0.51
39:j:12:ASP:OD1	39:j:14:SER:OG	2.28	0.51
7:A:126:G:OP1	7:A:605:U:O2'	2.22	0.51
7:A:1162:C:H2'	7:A:1163:A:H8	1.74	0.51
7:A:1287:A:H2'	7:A:1288:A:C8	2.45	0.51
30:a:2070:A:H2'	30:a:2071:A:H8	1.74	0.51
34:e:22:ASP:OD1	34:e:22:ASP:N	2.29	0.51
39:j:93:GLN:HA	39:j:93:GLN:NE2	2.24	0.51
7:A:54:C:OP1	7:A:351:G:N2	2.40	0.51
30:a:414:C:H2'	30:a:415:A:C8	2.46	0.51
30:a:937:C:H2'	30:a:938:G:H8	1.75	0.51
33:d:156:PHE:CD1	38:i:81:ILE:HD13	2.46	0.51
44:o:71:GLU:OE2	44:o:101:ARG:NE	2.41	0.51
7:A:137:U:H2'	7:A:138:G:H8	1.75	0.51
7:A:1014:A:C2	7:A:1219:A:H1'	2.46	0.51
20:N:73:PHE:HE1	20:N:75:ARG:HA	1.76	0.51
7:A:53:A:C6	7:A:359:G:C6	2.99	0.51
7:A:476:U:H2'	7:A:477:C:C6	2.46	0.51
7:A:1521:C:H2'	7:A:1522:U:C6	2.46	0.51
20:N:6:MET:HB3	20:N:63:ARG:NH2	2.26	0.51
7:A:373:A:C2	7:A:374:A:C8	2.99	0.51
7:A:1229:A:P	19:M:113:ARG:HH21	2.34	0.51
30:a:329:G:C2	30:a:477:A:C2	2.99	0.51
30:a:858:G:C5	30:a:2268:A:H2	2.29	0.51
30:a:1395:A:O2'	30:a:1396:U:H5''	2.09	0.51
51:v:23:VAL:HG23	51:v:38:VAL:HB	1.91	0.51
9:C:186:THR:OG1	9:C:187:SER:N	2.44	0.51
30:a:196:A:N6	30:a:831:G:H21	2.08	0.51
30:a:882:G:N2	30:a:894:U:O2	2.37	0.51
30:a:1538:G:H2'	30:a:1539:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2071:A:H2'	30:a:2072:C:C6	2.46	0.51
30:a:2302:U:C2	30:a:2303:G:C8	2.99	0.51
30:a:2449:H2U:H4'	30:a:2450:A:OP1	2.09	0.51
31:b:116:G:H2'	31:b:117:G:H8	1.76	0.51
7:A:323:U:H3	7:A:327:A:H62	1.59	0.50
30:a:402:A:H2'	30:a:403:U:O4'	2.10	0.50
30:a:668:A:C4	30:a:670:A:N7	2.79	0.50
30:a:2345:G:N3	30:a:2381:A:H2'	2.26	0.50
30:a:2682:A:N7	33:d:11:MET:HE3	2.26	0.50
39:j:63:VAL:HG12	39:j:107:LEU:HD11	1.93	0.50
39:j:73:ASP:OD2	44:o:78:SER:OG	2.27	0.50
7:A:90:C:H2'	7:A:91:U:C5	2.45	0.50
7:A:556:C:H2'	7:A:557:G:H8	1.76	0.50
7:A:1317:C:OP1	20:N:56:SER:OG	2.27	0.50
30:a:1853:A:N6	30:a:1889:A:C5	2.79	0.50
1:0:17:THR:OG1	1:0:18:GLY:N	2.43	0.50
7:A:358:U:H2'	7:A:359:G:H8	1.76	0.50
7:A:1465:A:H2'	7:A:1466:C:H6	1.76	0.50
8:B:21:ARG:HG3	8:B:22:TYR:CD1	2.45	0.50
15:I:33:ARG:HH21	15:I:38:TYR:HA	1.77	0.50
17:K:98:ARG:NH2	27:U:16:LEU:HD23	2.13	0.50
31:b:95:U:H2'	31:b:96:G:C8	2.43	0.50
39:j:12:ASP:CG	39:j:14:SER:HG	2.18	0.50
48:s:50:LEU:HD23	53:x:26:PHE:CZ	2.46	0.50
7:A:91:U:H2'	7:A:92:U:H6	1.75	0.50
7:A:236:A:H2'	7:A:237:G:C8	2.46	0.50
7:A:872:A:C4	7:A:874:G:N7	2.79	0.50
7:A:1166:G:N1	7:A:1169:A:OP2	2.45	0.50
17:K:94:GLU:HB2	27:U:20:LYS:HZ1	1.75	0.50
30:a:1208:C:C2	30:a:1239:G:N2	2.79	0.50
30:a:1629:U:O4	30:a:1630:A:N6	2.44	0.50
30:a:2415:G:H2'	30:a:2416:C:C6	2.47	0.50
30:a:2537:U:H2'	30:a:2538:C:H6	1.76	0.50
51:v:42:GLY:O	51:v:44:LYS:N	2.44	0.50
7:A:526:C:OP2	18:L:88:LYS:NZ	2.25	0.50
7:A:696:A:H2'	7:A:697:U:H6	1.75	0.50
1:0:7:GLU:OE1	1:0:27:LYS:NZ	2.36	0.50
7:A:131:A:H2'	7:A:132:C:H6	1.76	0.50
7:A:745:G:H2'	7:A:746:A:C8	2.46	0.50
7:A:1436:U:H2'	7:A:1437:A:H8	1.76	0.50
8:B:129:LEU:HB3	8:B:133:GLU:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:I:23:PRO:HA	15:I:61:LEU:HD23	1.93	0.50
30:a:666:A:H4'	40:k:48:ARG:HD3	1.94	0.50
30:a:927:A:H2'	30:a:928:A:C8	2.46	0.50
30:a:1707:G:C8	30:a:1756:G:C5	2.99	0.50
30:a:2008:C:H2'	30:a:2009:A:H8	1.75	0.50
36:g:27:LYS:HZ3	36:g:32:GLU:HB2	1.76	0.50
41:l:21:ALA:HB2	41:l:97:GLN:HB2	1.94	0.50
44:o:36:SER:O	44:o:36:SER:OG	2.29	0.50
46:q:58:VAL:H	46:q:102:SER:HG	1.53	0.50
30:a:807:U:C2	30:a:808:G:C8	2.99	0.50
30:a:2233:U:H2'	30:a:2234:G:H8	1.77	0.50
7:A:1017:U:H2'	7:A:1018:G:H8	1.77	0.50
30:a:251:A:OP1	40:k:58:TYR:OH	2.25	0.50
30:a:928:A:H2'	30:a:929:U:H6	1.77	0.50
31:b:44:G:N2	31:b:48:U:C2	2.80	0.50
6:5:21:A:N6	6:5:46:A:H2'	2.26	0.50
7:A:219:U:H2'	7:A:220:G:H8	1.77	0.50
18:L:68:GLY:O	18:L:99:ARG:NH1	2.45	0.50
30:a:464:U:C4	30:a:788:A:C5	3.00	0.50
30:a:1009:A:N3	30:a:1153:C:O2'	2.45	0.50
30:a:1196:C:C2	30:a:1197:G:C8	3.00	0.50
31:b:52:A:N7	43:n:64:TYR:OH	2.44	0.50
37:h:9:VAL:HG22	37:h:12:LEU:HB2	1.93	0.50
6:5:67:C:H2'	6:5:68:C:H6	1.77	0.49
7:A:33:A:H2'	7:A:34:C:C6	2.47	0.49
30:a:974:G:C6	30:a:989:G:C5	3.00	0.49
30:a:1288:G:C2	30:a:1327:A:C2	2.99	0.49
30:a:1770:G:C6	30:a:1983:G:C6	3.00	0.49
6:5:1:G:H2'	6:5:2:C:H6	1.77	0.49
7:A:193:C:H2'	7:A:194:C:C6	2.46	0.49
7:A:337:G:C2	7:A:338:A:C5	3.00	0.49
7:A:676:A:H2'	7:A:677:U:H6	1.77	0.49
7:A:923:A:O2'	7:A:1399:C:OP2	2.28	0.49
16:J:31:ARG:HH22	16:J:82:LYS:HE2	1.77	0.49
30:a:379:G:N1	30:a:396:G:C6	2.81	0.49
30:a:447:A:C6	30:a:473:G:C4	3.00	0.49
30:a:960:A:H2	30:a:2495:G:N3	2.10	0.49
30:a:2291:U:OP1	30:a:2380:C:O2'	2.28	0.49
3:2:7:VAL:HG21	3:2:61:CYS:HB3	1.94	0.49
7:A:90:C:O2'	7:A:91:U:OP1	2.26	0.49
7:A:1271:A:H2'	7:A:1272:G:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:103:ASN:O	8:B:107:VAL:HG23	2.12	0.49
17:K:112:ASP:OD1	17:K:114:THR:HG22	2.12	0.49
30:a:145:C:H2'	30:a:146:A:H8	1.77	0.49
30:a:201:C:O2	30:a:251:A:H2	1.95	0.49
30:a:511:U:H5	30:a:512:G:C5	2.29	0.49
7:A:991:U:C4	7:A:1212:U:H1'	2.48	0.49
7:A:1147:C:H2'	7:A:1148:U:C6	2.47	0.49
16:J:53:ILE:HD11	16:J:61:ALA:HB1	1.92	0.49
22:P:61:VAL:HG22	22:P:67:ILE:HD11	1.95	0.49
43:n:99:TYR:CE1	43:n:104:GLN:HG3	2.47	0.49
49:t:96:PHE:O	49:t:100:SER:HA	2.12	0.49
7:A:268:U:H2'	7:A:269:C:C6	2.47	0.49
7:A:458:U:H2'	7:A:459:A:C8	2.47	0.49
7:A:593:U:H2'	7:A:594:U:C6	2.48	0.49
7:A:1118:U:H2'	7:A:1119:C:H6	1.78	0.49
30:a:277:G:H4'	30:a:278:A:O5'	2.11	0.49
42:m:70:THR:O	42:m:70:THR:OG1	2.28	0.49
7:A:370:C:H2'	7:A:371:A:H8	1.77	0.49
7:A:865:A:H2'	7:A:866:C:C6	2.47	0.49
30:a:252:G:H2'	30:a:253:C:H6	1.78	0.49
30:a:541:A:N6	30:a:553:G:O6	2.46	0.49
30:a:621:A:OP2	40:k:99:ASN:ND2	2.41	0.49
30:a:894:U:H2'	30:a:895:U:O4'	2.12	0.49
30:a:2507:C:C2	30:a:2583:G:C2	3.00	0.49
33:d:3:GLY:O	33:d:4:LEU:HD23	2.13	0.49
42:m:10:LEU:O	42:m:12:ARG:NH1	2.46	0.49
7:A:76:G:H2'	7:A:77:A:C8	2.48	0.49
7:A:235:C:H2'	7:A:236:A:C8	2.46	0.49
7:A:652:U:O4	7:A:752:G:O2'	2.27	0.49
7:A:1071:C:H2'	7:A:1072:G:H8	1.77	0.49
7:A:1355:G:H2'	7:A:1356:G:C8	2.47	0.49
21:O:75:VAL:O	21:O:79:THR:HG23	2.12	0.49
30:a:644:A:N1	30:a:2369:A:H1'	2.28	0.49
30:a:1709:U:C2	30:a:1750:G:N2	2.80	0.49
30:a:2720:U:C2	30:a:2721:A:C8	3.00	0.49
40:k:91:ASP:H	40:k:94:THR:CG2	2.25	0.49
55:z:11:SER:O	55:z:15:MET:HG3	2.12	0.49
7:A:175:C:H2'	7:A:176:C:C6	2.48	0.49
7:A:425:G:H2'	7:A:426:U:C6	2.47	0.49
7:A:1333:A:H2'	7:A:1334:G:O4'	2.13	0.49
10:D:95:GLU:O	10:D:100:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:150:PRO:HA	11:E:153:VAL:HG12	1.95	0.49
22:P:8:ARG:HB3	22:P:28:ARG:NH1	2.28	0.49
30:a:668:A:C5	30:a:670:A:N7	2.81	0.49
30:a:775:G:C5	30:a:794:A:C8	3.00	0.49
30:a:813:U:H2'	30:a:814:C:H6	1.78	0.49
30:a:1143:A:N7	38:i:27:ARG:NH1	2.61	0.49
30:a:1341:G:OP2	30:a:1394:U:O2'	2.21	0.49
30:a:2097:A:H2'	30:a:2098:U:C6	2.48	0.49
30:a:2896:C:H2'	30:a:2897:U:C6	2.48	0.49
7:A:309:A:H2'	7:A:310:G:H8	1.78	0.49
7:A:340:U:C2	7:A:350:G:N2	2.81	0.49
7:A:861:G:O6	7:A:869:G:N2	2.46	0.49
7:A:1014:A:H2	7:A:1219:A:H1'	1.78	0.49
7:A:1436:U:C2	7:A:1437:A:C8	3.00	0.49
11:E:115:LEU:HD13	11:E:123:VAL:HG11	1.95	0.49
23:Q:30:LYS:HB2	23:Q:37:PHE:CE1	2.47	0.49
30:a:582:A:C6	30:a:1259:G:N1	2.81	0.49
30:a:820:A:H2	30:a:943:A:H4'	1.76	0.49
30:a:1473:G:C6	30:a:1519:G:C6	3.00	0.49
30:a:1802:A:H2'	30:a:1803:A:C8	2.48	0.49
30:a:1831:G:C4	30:a:1975:G:N2	2.81	0.49
30:a:1838:C:N4	30:a:1899:A:C4	2.80	0.49
30:a:2684:U:O4'	39:j:70:ARG:NH1	2.46	0.49
37:h:6:LEU:O	37:h:6:LEU:HD23	2.12	0.49
3:2:40:ARG:NH2	30:a:2362:C:OP1	2.40	0.49
7:A:794:A:H2'	7:A:795:C:C6	2.47	0.49
7:A:811:C:O2'	7:A:901:A:N1	2.46	0.49
18:L:59:ASN:OD1	18:L:61:PHE:HD1	1.96	0.49
30:a:52:A:H2'	30:a:53:A:H8	1.77	0.49
30:a:2070:A:H2'	30:a:2071:A:C8	2.48	0.49
35:f:8:TYR:HB2	35:f:173:PHE:CZ	2.47	0.49
35:f:49:LEU:HD12	35:f:150:ARG:HH21	1.78	0.49
7:A:150:U:H2'	7:A:151:A:H8	1.78	0.48
7:A:539:A:H2'	7:A:540:G:C8	2.48	0.48
7:A:563:A:O2'	7:A:566:G:O2'	2.27	0.48
11:E:41:ASP:OD1	11:E:41:ASP:C	2.56	0.48
20:N:34:VAL:O	20:N:41:ARG:NH2	2.43	0.48
22:P:48:GLU:HA	22:P:48:GLU:OE1	2.12	0.48
30:a:282:A:H2'	30:a:283:G:C8	2.48	0.48
30:a:971:G:O2'	30:a:983:A:N3	2.43	0.48
30:a:1266:G:N2	30:a:2013:A:OP2	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1387:A:C6	30:a:1401:G:N1	2.80	0.48
30:a:2901:C:H2'	30:a:2902:C:H6	1.78	0.48
35:f:30:ARG:O	35:f:159:THR:HG22	2.12	0.48
49:t:99:ASN:O	49:t:100:SER:C	2.57	0.48
50:u:1:MET:HE2	50:u:1:MET:HA	1.95	0.48
3:2:55:LEU:O	3:2:59:ILE:HG12	2.12	0.48
15:I:19:VAL:HG11	15:I:83:ILE:HD13	1.93	0.48
30:a:2067:G:N1	30:a:2444:G:C6	2.81	0.48
35:f:77:PHE:O	35:f:78:LYS:HG2	2.13	0.48
39:j:98:ARG:O	39:j:99:ILE:HD13	2.13	0.48
41:l:110:GLU:O	41:l:114:ARG:HG3	2.12	0.48
49:t:86:ARG:NH2	49:t:102:THR:OG1	2.46	0.48
7:A:17:U:H2'	7:A:18:C:C6	2.48	0.48
7:A:1157:A:C2	7:A:1181:G:C4	3.01	0.48
11:E:65:GLU:HA	11:E:65:GLU:OE2	2.13	0.48
30:a:780:G:C2	30:a:782:A:C2	3.01	0.48
30:a:1342:A:O2'	30:a:1344:U:OP2	2.24	0.48
30:a:2056:G:N2	55:z:2:ALA:HA	2.28	0.48
30:a:2289:G:C2	30:a:2290:G:C8	3.00	0.48
30:a:2547:A:H2'	30:a:2548:U:C6	2.48	0.48
7:A:26:A:N6	7:A:558:G:H1'	2.29	0.48
7:A:859:G:H2'	7:A:860:A:C8	2.48	0.48
7:A:859:G:H2'	7:A:860:A:H8	1.78	0.48
7:A:1254:A:H2'	7:A:1255:G:H8	1.78	0.48
30:a:361:G:H8	30:a:361:G:OP2	1.96	0.48
30:a:960:A:C8	30:a:962:G:C8	3.01	0.48
30:a:1270:C:H5''	30:a:1271:G:H5'	1.94	0.48
30:a:1426:G:C8	30:a:1427:A:C8	3.02	0.48
7:A:975:A:H8	7:A:1357:A:HO2'	1.60	0.48
7:A:993:G:O2'	7:A:995:C:N4	2.46	0.48
12:F:12:PRO:O	12:F:44:ARG:NH2	2.46	0.48
12:F:22:ILE:O	12:F:26:THR:OG1	2.29	0.48
30:a:1838:C:C2	30:a:1898:U:C5	3.02	0.48
30:a:2830:C:OP2	33:d:59:ARG:NH1	2.46	0.48
45:p:48:ARG:NH2	45:p:49:ASP:OD1	2.38	0.48
7:A:320:A:H2'	7:A:321:A:C8	2.48	0.48
7:A:543:U:H2'	7:A:544:G:H8	1.77	0.48
7:A:1415:G:C6	7:A:1486:G:C6	3.02	0.48
14:H:7:ILE:HD12	14:H:7:ILE:H	1.78	0.48
30:a:1484:U:H2'	30:a:1485:U:C6	2.48	0.48
30:a:1645:G:H5''	30:a:1646:C:H5'	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1837:C:C2	30:a:1904:G:C2	3.02	0.48
30:a:2056:G:H21	55:z:2:ALA:HA	1.79	0.48
30:a:2487:G:H2'	30:a:2488:G:H8	1.77	0.48
7:A:83:C:H1'	7:A:86:G:H1	1.78	0.48
7:A:707:U:H2'	7:A:708:C:C6	2.48	0.48
7:A:939:G:N3	7:A:1375:A:H2	2.12	0.48
30:a:358:U:H2'	30:a:359:G:C8	2.44	0.48
30:a:648:G:C2	30:a:649:G:C5	3.01	0.48
30:a:1632:A:N1	30:a:1633:G:N2	2.61	0.48
30:a:1827:U:C2	30:a:1828:G:C8	3.02	0.48
30:a:2804:U:H2'	30:a:2805:C:C6	2.48	0.48
7:A:166:U:H2'	7:A:167:A:C8	2.47	0.48
7:A:687:A:C2	7:A:704:A:C5	3.02	0.48
7:A:917:G:H2'	7:A:918:A:C8	2.49	0.48
30:a:347:A:H2'	30:a:348:A:C8	2.48	0.48
30:a:1198:U:C2	30:a:1199:U:C5	3.02	0.48
30:a:1386:C:H2'	30:a:1387:A:C8	2.48	0.48
30:a:1831:G:C6	30:a:1832:C:N4	2.82	0.48
30:a:2748:A:C2	30:a:2757:A:C5	3.01	0.48
30:a:2898:U:H2'	30:a:2899:A:C8	2.48	0.48
51:v:66:LYS:NZ	51:v:85:GLU:OXT	2.44	0.48
7:A:215:C:H2'	7:A:216:U:H6	1.77	0.48
9:C:42:TYR:OH	9:C:90:VAL:HG11	2.14	0.48
9:C:62:LYS:HZ1	9:C:98:PRO:HD2	1.78	0.48
11:E:74:VAL:HG11	11:E:144:LEU:HB3	1.95	0.48
30:a:282:A:N6	30:a:359:G:O6	2.47	0.48
30:a:287:G:C6	30:a:354:A:C6	3.02	0.48
30:a:464:U:C4	30:a:788:A:C6	3.02	0.48
30:a:782:A:C8	32:c:220:VAL:HG11	2.48	0.48
48:s:59:ASN:N	48:s:59:ASN:OD1	2.47	0.48
6:5:49:C:H2'	6:5:50:G:H8	1.79	0.48
7:A:927:G:O2'	7:A:1503:A:N7	2.43	0.48
7:A:1013:G:N2	7:A:1016:A:OP2	2.32	0.48
7:A:1027:C:H2'	7:A:1028:C:C6	2.49	0.48
19:M:85:CYS:O	19:M:88:GLY:N	2.47	0.48
30:a:85:G:C4	30:a:98:G:N2	2.82	0.48
30:a:1361:G:H2'	30:a:1362:C:H6	1.79	0.48
30:a:1630:A:N6	30:a:1637:A:N6	2.61	0.48
30:a:1910:G:N2	30:a:1921:G:C4	2.81	0.48
31:b:99:A:C4	31:b:100:G:C8	3.01	0.48
32:c:143:ASN:OD1	32:c:152:GLY:HA3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:c:145:GLU:HG2	32:c:151:GLY:C	2.39	0.48
7:A:41:G:H2'	7:A:42:G:C8	2.45	0.47
7:A:1316:G:N1	7:A:1319:A:OP2	2.47	0.47
30:a:1734:G:H2'	30:a:1735:A:H8	1.79	0.47
30:a:2650:U:C2	30:a:2671:G:N2	2.82	0.47
7:A:317:U:N3	7:A:318:G:N7	2.62	0.47
7:A:390:U:H4'	22:P:28:ARG:NH2	2.29	0.47
7:A:674:G:N2	17:K:118:HIS:HB2	2.29	0.47
7:A:1520:C:H2'	7:A:1521:C:H6	1.79	0.47
10:D:54:GLN:HB3	10:D:203:LEU:HB2	1.97	0.47
13:G:133:THR:HB	13:G:136:LYS:NZ	2.25	0.47
30:a:1406:U:H2'	30:a:1407:G:H8	1.79	0.47
35:f:108:VAL:HG11	35:f:176:PRO:HG2	1.97	0.47
44:o:65:SER:OG	44:o:66:ASN:OD1	2.27	0.47
48:s:2:ILE:H	48:s:2:ILE:HD12	1.79	0.47
7:A:524:G:H2'	7:A:525:C:C6	2.49	0.47
7:A:979:C:O2	20:N:59:ARG:NH1	2.46	0.47
7:A:1326:U:H2'	7:A:1327:C:H6	1.79	0.47
13:G:31:MET:HE2	13:G:31:MET:HB2	1.68	0.47
22:P:51:ARG:C	22:P:52:LEU:HD12	2.39	0.47
30:a:552:U:H2'	30:a:553:G:H8	1.79	0.47
30:a:881:G:O6	30:a:895:U:O4	2.32	0.47
30:a:1036:G:C6	30:a:1120:G:C6	3.02	0.47
30:a:2387:U:H4'	51:v:41:ARG:HH21	1.78	0.47
33:d:110:THR:HG23	33:d:202:ILE:HB	1.95	0.47
7:A:82:G:H1	7:A:86:G:N2	2.12	0.47
7:A:707:U:H2'	7:A:708:C:H6	1.79	0.47
7:A:838:G:C6	7:A:849:G:C6	3.02	0.47
7:A:1028:C:H2'	7:A:1029:U:O4'	2.14	0.47
7:A:1489:G:H2'	7:A:1490:U:C6	2.50	0.47
9:C:118:ASP:O	9:C:121:THR:HG22	2.15	0.47
10:D:147:GLU:OE1	10:D:147:GLU:N	2.47	0.47
30:a:581:C:H2'	30:a:582:A:C8	2.48	0.47
30:a:595:C:H2'	30:a:596:U:H6	1.80	0.47
30:a:638:G:C5	30:a:651:G:N2	2.83	0.47
30:a:669:G:C2	30:a:801:G:N1	2.82	0.47
30:a:2723:C:H2'	30:a:2724:U:O4'	2.14	0.47
31:b:30:C:H1'	31:b:57:A:H61	1.79	0.47
34:e:146:VAL:HA	34:e:185:LYS:O	2.15	0.47
51:v:47:ALA:HB1	51:v:51:VAL:HG12	1.94	0.47
55:z:41:HIS:HA	55:z:49:TYR:OH	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:5:19:C:H42	35:f:80:ARG:CZ	2.28	0.47
7:A:954:G:H2'	7:A:955:U:C6	2.50	0.47
17:K:30:THR:HG21	17:K:63:ALA:HB2	1.95	0.47
30:a:608:A:C6	30:a:609:A:C5	3.03	0.47
30:a:645:C:H2'	30:a:647:G:C8	2.50	0.47
30:a:722:A:H2'	30:a:723:C:C6	2.49	0.47
30:a:1013:C:H2'	30:a:1014:A:H8	1.79	0.47
44:o:55:LEU:O	44:o:55:LEU:HD23	2.15	0.47
55:z:38:HIS:HB3	55:z:44:THR:HG22	1.96	0.47
7:A:1314:C:H2'	7:A:1315:U:H6	1.79	0.47
7:A:1463:U:H2'	7:A:1464:U:H6	1.79	0.47
7:A:1465:A:H2'	7:A:1466:C:C6	2.50	0.47
8:B:133:GLU:O	8:B:136:MET:HG3	2.14	0.47
11:E:107:ALA:HB2	11:E:125:ALA:HB3	1.96	0.47
11:E:108:GLY:O	11:E:112:ARG:HB2	2.15	0.47
12:F:2:ARG:HD3	12:F:91:ARG:CZ	2.44	0.47
30:a:1582:C:H42	30:a:1583:A:N6	2.11	0.47
30:a:1594:U:H2'	30:a:1595:C:C6	2.49	0.47
30:a:2041:U:C2	30:a:2042:A:C8	3.03	0.47
30:a:2052:A:H4'	33:d:148:GLN:O	2.13	0.47
33:d:113:SER:OG	33:d:114:LYS:N	2.46	0.47
41:l:82:MET:HE3	41:l:82:MET:HB3	1.61	0.47
6:5:1:G:H2'	6:5:2:C:C6	2.50	0.47
7:A:543:U:H2'	7:A:544:G:C8	2.49	0.47
7:A:632:U:H5''	7:A:633:G:C8	2.50	0.47
7:A:1160:G:C2	7:A:1161:C:C6	3.03	0.47
7:A:1291:U:OP1	13:G:37:SER:OG	2.29	0.47
7:A:1315:U:H2'	7:A:1316:G:O4'	2.15	0.47
7:A:1478:U:H2'	7:A:1479:C:H6	1.78	0.47
8:B:105:LYS:H	8:B:105:LYS:HD2	1.79	0.47
9:C:11:ARG:NH2	9:C:177:THR:O	2.41	0.47
12:F:18:VAL:HA	12:F:21:MET:HE2	1.97	0.47
23:Q:17:MET:HE2	23:Q:20:SER:HB2	1.96	0.47
30:a:78:U:H2'	30:a:79:C:H6	1.79	0.47
30:a:277:G:H1'	30:a:278:A:C5	2.50	0.47
30:a:624:C:O2'	30:a:657:U:OP1	2.32	0.47
30:a:1666:G:HO2'	39:j:6:THR:HG1	1.55	0.47
30:a:2466:C:C2	30:a:2467:C:C5	3.03	0.47
30:a:2747:G:N1	30:a:2754:U:O2	2.47	0.47
51:v:21:LEU:HD11	51:v:41:ARG:NH1	2.29	0.47
7:A:127:G:O2'	23:Q:6:ARG:NH1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:493:A:H2'	7:A:494:G:C8	2.50	0.47
7:A:953:G:C6	7:A:1229:A:C6	3.03	0.47
7:A:1032:G:H3'	7:A:1032:G:N3	2.30	0.47
7:A:1366:C:H2'	7:A:1367:C:C6	2.50	0.47
8:B:187:VAL:HB	8:B:199:VAL:HG23	1.96	0.47
15:I:27:LYS:N	15:I:62:ASP:OD1	2.45	0.47
30:a:608:A:C6	30:a:609:A:C6	3.03	0.47
30:a:963:U:C2	30:a:964:C:C5	3.03	0.47
30:a:1824:G:H2'	30:a:1825:U:C6	2.48	0.47
1:O:10:LYS:HG2	1:O:54:ILE:HD12	1.97	0.47
7:A:299:G:C6	7:A:300:A:C6	3.03	0.47
7:A:1324:A:H2'	7:A:1325:C:H6	1.80	0.47
19:M:77:ILE:HG22	19:M:81:MET:CE	2.45	0.47
30:a:150:U:H2'	30:a:151:C:H6	1.80	0.47
30:a:947:A:N6	30:a:971:G:O6	2.48	0.47
30:a:1353:A:C8	30:a:1378:A:N6	2.83	0.47
30:a:1659:G:C6	30:a:2002:G:N1	2.83	0.47
30:a:2702:G:C4	30:a:2703:C:C5	3.03	0.47
35:f:140:GLU:OE1	35:f:140:GLU:N	2.34	0.47
36:g:27:LYS:NZ	36:g:32:GLU:HB2	2.30	0.47
38:i:90:GLU:HA	38:i:93:ILE:HG22	1.96	0.47
6:5:28:C:H2'	6:5:29:A:C8	2.50	0.47
7:A:215:C:H2'	7:A:216:U:C6	2.49	0.47
7:A:457:G:H5'	7:A:458:U:OP2	2.14	0.47
7:A:1040:U:H2'	7:A:1041:G:C8	2.50	0.47
7:A:1120:C:H2'	7:A:1121:U:H6	1.80	0.47
12:F:90:MET:HE2	12:F:90:MET:HB3	1.66	0.47
19:M:59:GLU:OE1	19:M:59:GLU:HA	2.13	0.47
30:a:185:G:C4	30:a:212:G:N2	2.83	0.47
30:a:287:G:H2'	30:a:288:U:C6	2.49	0.47
30:a:1936:A:N7	30:a:1945:G:C8	2.83	0.47
30:a:2698:U:H2'	30:a:2699:C:C6	2.50	0.47
33:d:13:ARG:O	33:d:14:ILE:HD13	2.15	0.47
48:s:34:VAL:HG21	48:s:43:ILE:HD11	1.97	0.47
6:5:59:U:H5''	6:5:60:C:OP2	2.15	0.46
7:A:27:G:H2'	7:A:28:A:C8	2.49	0.46
7:A:390:U:H2'	7:A:391:G:C8	2.50	0.46
8:B:139:ARG:HA	8:B:142:GLU:OE2	2.15	0.46
11:E:92:SER:OG	11:E:130:SER:O	2.29	0.46
30:a:669:G:C2	30:a:801:G:C6	3.03	0.46
30:a:2513:A:C6	30:a:2574:G:C6	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:b:16:G:N2	31:b:69:G:H1'	2.30	0.46
32:c:123:ALA:O	32:c:128:ASN:ND2	2.47	0.46
7:A:904:U:C2	7:A:905:U:C5	3.04	0.46
7:A:1522:U:O2	7:A:1523:G:C8	2.69	0.46
7:A:1527:U:H2'	7:A:1528:U:C6	2.49	0.46
18:L:89:ASP:OD1	18:L:89:ASP:N	2.45	0.46
24:R:34:THR:HG23	24:R:40:VAL:HG13	1.98	0.46
30:a:306:U:H2'	30:a:307:G:O4'	2.15	0.46
30:a:411:G:OP2	30:a:2406:A:O2'	2.33	0.46
30:a:2698:U:H2'	30:a:2699:C:H6	1.80	0.46
37:h:30:LEU:HB3	37:h:36:ALA:HB3	1.96	0.46
2:1:16:HIS:CD2	30:a:465:G:H5'	2.51	0.46
7:A:22:G:H2'	7:A:23:C:C6	2.50	0.46
7:A:408:A:C6	7:A:435:A:N1	2.83	0.46
7:A:475:C:H2'	7:A:476:U:H6	1.81	0.46
7:A:601:G:H2'	7:A:602:A:H8	1.81	0.46
7:A:976:G:OP2	7:A:1358:U:O2'	2.31	0.46
7:A:1012:A:N6	7:A:1018:G:O6	2.48	0.46
17:K:13:ARG:N	17:K:76:GLU:OE2	2.48	0.46
30:a:962:G:H2'	30:a:963:U:H6	1.80	0.46
30:a:2313:C:H2'	30:a:2314:A:H8	1.80	0.46
30:a:2681:C:C4	30:a:2724:U:H5	2.34	0.46
30:a:2718:G:O2'	30:a:2847:U:OP1	2.25	0.46
40:k:100:ILE:HD13	40:k:100:ILE:N	2.30	0.46
42:m:6:SER:OG	42:m:7:GLY:N	2.48	0.46
5:4:64:PHE:CD1	25:S:9:PRO:HD3	2.49	0.46
7:A:537:G:H5''	18:L:110:ARG:NH2	2.31	0.46
7:A:1486:G:H2'	7:A:1487:G:O4'	2.14	0.46
8:B:131:LYS:C	8:B:131:LYS:HD2	2.40	0.46
12:F:44:ARG:HB2	12:F:44:ARG:NH1	2.31	0.46
30:a:873:C:H4'	41:l:64:TRP:HE1	1.81	0.46
30:a:947:A:N1	30:a:971:G:C6	2.83	0.46
30:a:2623:G:C2	30:a:2624:G:C8	3.04	0.46
30:a:2677:G:C4	30:a:2731:G:N2	2.83	0.46
30:a:2804:U:H2'	30:a:2805:C:H6	1.80	0.46
30:a:2813:A:H2'	30:a:2814:A:H8	1.81	0.46
31:b:29:A:H2'	31:b:30:C:O4'	2.15	0.46
7:A:515:G:H2'	7:A:516:PSU:H6	1.80	0.46
7:A:735:C:H2'	7:A:736:C:H6	1.80	0.46
10:D:19:LEU:HD22	10:D:64:ILE:HG13	1.97	0.46
20:N:79:LEU:HB2	20:N:84:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:P:4:ILE:HG12	22:P:21:VAL:HG22	1.98	0.46
30:a:52:A:H2'	30:a:53:A:C8	2.49	0.46
30:a:858:G:C4	30:a:2268:A:C2	3.04	0.46
30:a:1254:A:N1	34:e:77:ILE:HD11	2.31	0.46
42:m:65:LEU:HA	42:m:65:LEU:HD23	1.69	0.46
42:m:72:ASP:OD1	42:m:73:ASN:N	2.48	0.46
44:o:114:LEU:HD23	44:o:114:LEU:HA	1.77	0.46
54:y:12:SER:OG	54:y:13:ALA:N	2.48	0.46
7:A:393:A:C2	7:A:394:G:C8	3.03	0.46
7:A:505:G:C2	7:A:506:G:C5	3.04	0.46
7:A:900:A:H2'	7:A:901:A:C8	2.51	0.46
7:A:1489:G:H2'	7:A:1490:U:H6	1.81	0.46
8:B:7:ARG:O	8:B:11:LYS:HE2	2.15	0.46
30:a:6:A:H2'	30:a:7:G:H8	1.81	0.46
30:a:32:C:O2'	30:a:33:C:H5'	2.15	0.46
30:a:217:A:C4	30:a:218:A:C8	3.03	0.46
30:a:572:A:N1	30:a:2033:A:C2	2.84	0.46
30:a:1268:A:H1'	30:a:2013:A:H61	1.80	0.46
30:a:2882:A:OP1	42:m:96:ARG:NH1	2.49	0.46
7:A:672:U:H2'	7:A:673:A:H8	1.81	0.46
7:A:744:C:H2'	7:A:745:G:C8	2.49	0.46
7:A:791:G:C6	7:A:792:A:N7	2.84	0.46
7:A:981:U:OP1	20:N:9:ARG:NH1	2.48	0.46
7:A:1036:A:H2'	7:A:1037:C:O4'	2.15	0.46
15:I:79:ILE:O	15:I:83:ILE:HG12	2.16	0.46
30:a:553:G:H2'	30:a:554:U:H6	1.80	0.46
30:a:1361:G:H2'	30:a:1362:C:C6	2.51	0.46
30:a:1419:A:C8	30:a:1579:A:N6	2.84	0.46
30:a:1422:G:C6	30:a:1577:C:N3	2.84	0.46
30:a:1509:A:N3	30:a:1510:G:C8	2.84	0.46
30:a:1605:C:H2'	30:a:1606:C:O4'	2.16	0.46
30:a:2443:C:O2'	30:a:2444:G:H5'	2.16	0.46
38:i:125:TYR:OH	38:i:132:HIS:NE2	2.44	0.46
6:5:49:C:H2'	6:5:50:G:C8	2.51	0.46
7:A:471:U:H2'	7:A:472:U:C6	2.50	0.46
7:A:1147:C:H2'	7:A:1148:U:H6	1.80	0.46
7:A:1175:G:H2'	7:A:1176:A:H8	1.81	0.46
7:A:1436:U:H2'	7:A:1437:A:C8	2.50	0.46
9:C:16:LYS:NZ	9:C:182:ILE:O	2.42	0.46
11:E:52:LYS:HB2	11:E:52:LYS:HE3	1.72	0.46
16:J:35:GLN:CD	16:J:35:GLN:H	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:974:G:C6	30:a:989:G:C6	3.04	0.46
30:a:1691:C:N4	30:a:1697:G:N2	2.64	0.46
32:c:232:HIS:CE1	32:c:244:PRO:HA	2.49	0.46
40:k:5:THR:O	40:k:5:THR:OG1	2.28	0.46
30:a:273:G:C6	30:a:274:C:N4	2.84	0.46
30:a:543:G:C6	30:a:551:G:C6	3.04	0.46
30:a:2292:U:H2'	30:a:2293:G:H8	1.80	0.46
30:a:2305:U:H2'	30:a:2306:C:C6	2.51	0.46
30:a:2822:G:OP1	33:d:164:GLN:NE2	2.49	0.46
36:g:52:PHE:HZ	36:g:72:LEU:HD12	1.78	0.46
44:o:8:LEU:HD23	44:o:8:LEU:HA	1.74	0.46
2:l:46:LYS:HA	2:l:46:LYS:HE2	1.97	0.46
7:A:1171:A:H2'	7:A:1172:C:C6	2.50	0.46
11:E:86:LYS:HB2	11:E:86:LYS:HE2	1.70	0.46
24:R:32:TYR:O	24:R:40:VAL:HG22	2.16	0.46
24:R:35:GLU:OE2	24:R:35:GLU:N	2.42	0.46
30:a:1197:G:H2'	30:a:1198:U:H6	1.80	0.46
30:a:1843:C:H2'	30:a:1844:C:C6	2.51	0.46
30:a:2330:G:C2	30:a:2386:A:C2	3.04	0.46
30:a:2902:C:H2'	30:a:2903:U:O4'	2.15	0.46
34:e:181:ILE:HG12	40:k:1:MET:SD	2.56	0.46
36:g:45:HIS:HA	36:g:50:LEU:HD23	1.97	0.46
39:j:19:VAL:HB	39:j:41:ILE:HD12	1.98	0.46
26:T:16:LYS:NZ	26:T:20:HIS:HB2	2.31	0.45
28:X:13:C:H2'	28:X:14:A:O4'	2.16	0.45
30:a:382:A:C2	30:a:393:C:C2	3.03	0.45
30:a:418:C:H2'	30:a:419:U:C6	2.51	0.45
7:A:1169:A:H2'	7:A:1170:A:C8	2.51	0.45
22:P:6:LEU:HD13	22:P:17:TYR:CG	2.51	0.45
24:R:65:LEU:HA	24:R:65:LEU:HD23	1.72	0.45
30:a:465:G:N2	30:a:684:G:H1'	2.31	0.45
30:a:2399:G:C6	30:a:2418:A:C6	3.04	0.45
30:a:2469:A:H4'	41:l:55:ARG:HD3	1.98	0.45
31:b:115:A:H2'	31:b:116:G:H8	1.81	0.45
37:h:32:PRO:HA	52:w:39:TRP:CD1	2.52	0.45
40:k:28:GLY:O	40:k:31:GLY:N	2.49	0.45
49:t:86:ARG:HG3	49:t:95:PHE:CD1	2.51	0.45
7:A:324:G:N2	7:A:327:A:C8	2.84	0.45
7:A:608:A:C2	7:A:609:A:H1'	2.51	0.45
7:A:678:U:H2'	7:A:679:C:H6	1.82	0.45
7:A:749:A:H2'	7:A:750:C:H6	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:24:ALA:HB1	9:C:28:GLU:HG2	1.99	0.45
14:H:29:SER:HB2	14:H:59:LEU:HB2	1.99	0.45
30:a:81:G:C2	30:a:106:C:C2	3.04	0.45
30:a:1000:A:C6	30:a:1155:A:C5	3.04	0.45
30:a:1199:U:H2'	30:a:1200:C:H6	1.80	0.45
40:k:28:GLY:O	40:k:30:THR:N	2.49	0.45
45:p:80:ILE:HA	45:p:80:ILE:HD13	1.69	0.45
54:y:24:LEU:HD23	54:y:24:LEU:HA	1.70	0.45
6:5:22:U:H2'	6:5:23:U:C6	2.52	0.45
7:A:947:G:H2'	7:A:948:C:H6	1.82	0.45
7:A:951:G:C6	7:A:1231:G:C6	3.04	0.45
7:A:972:C:OP2	16:J:59:LYS:NZ	2.49	0.45
16:J:86:ALA:HA	16:J:89:ARG:HG2	1.99	0.45
30:a:2:G:H2'	30:a:3:U:C6	2.51	0.45
30:a:419:U:H2'	30:a:420:C:C6	2.52	0.45
30:a:563:A:C4	30:a:2018:G:C2	3.05	0.45
30:a:1113:U:H2'	30:a:1114:C:C6	2.52	0.45
30:a:1545:A:H2'	30:a:1546:G:O4'	2.15	0.45
30:a:2071:A:H2'	30:a:2072:C:H6	1.82	0.45
30:a:2267:A:H5''	30:a:2268:A:H5'	1.98	0.45
30:a:2686:G:H2'	30:a:2687:U:C6	2.51	0.45
32:c:252:THR:O	32:c:252:THR:OG1	2.22	0.45
34:e:124:PHE:HE2	34:e:141:MET:HE1	1.81	0.45
44:o:34:GLU:CD	44:o:39:ARG:HH21	2.22	0.45
45:p:22:LYS:HB2	45:p:22:LYS:HE3	1.75	0.45
50:u:90:ASP:OD1	50:u:90:ASP:N	2.48	0.45
3:2:8:ARG:HA	3:2:8:ARG:HD2	1.73	0.45
7:A:110:C:O2'	22:P:25:ARG:O	2.35	0.45
7:A:1026:G:O2'	7:A:1027:C:OP1	2.31	0.45
7:A:1435:G:H2'	7:A:1436:U:C6	2.51	0.45
30:a:94:A:C6	30:a:95:A:C6	3.05	0.45
30:a:1499:C:C2	30:a:1500:G:C8	3.05	0.45
30:a:1788:C:H2'	30:a:1789:A:H8	1.82	0.45
30:a:2456:C:N3	30:a:2457:PSU:N1	2.65	0.45
31:b:77:U:OP1	50:u:21:ARG:NH2	2.49	0.45
38:i:74:TYR:CD2	38:i:92:MET:HG3	2.51	0.45
40:k:3:LEU:HA	40:k:3:LEU:HD23	1.67	0.45
45:p:65:ILE:HD11	45:p:95:LEU:HB3	1.99	0.45
5:4:64:PHE:CG	25:S:9:PRO:HD3	2.51	0.45
17:K:94:GLU:OE1	17:K:98:ARG:NH1	2.49	0.45
30:a:417:C:H2'	30:a:418:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:503:A:C6	30:a:506:G:C6	3.05	0.45
30:a:782:A:N7	32:c:220:VAL:HG21	2.32	0.45
30:a:866:A:C2	30:a:867:C:C6	3.05	0.45
30:a:1463:C:H2'	30:a:1464:G:C8	2.51	0.45
30:a:1670:C:O5'	30:a:1670:C:H6	2.00	0.45
30:a:2554:U:H2'	30:a:2555:U:C6	2.51	0.45
30:a:2625:G:H2'	30:a:2626:C:C6	2.52	0.45
30:a:2813:A:C4	30:a:2814:A:C8	3.04	0.45
7:A:188:C:H2'	7:A:189:A:O4'	2.17	0.45
7:A:380:G:N1	7:A:384:G:O6	2.49	0.45
7:A:407:U:H2'	7:A:408:A:C8	2.49	0.45
7:A:554:A:H2'	7:A:555:U:C6	2.51	0.45
7:A:1253:G:H2'	7:A:1254:A:C8	2.50	0.45
7:A:1356:G:C2	7:A:1357:A:C5	3.04	0.45
15:I:52:LEU:HD11	15:I:63:LEU:HD11	1.98	0.45
16:J:57:VAL:HG23	16:J:58:ASN:OD1	2.17	0.45
18:L:52:VAL:HG12	18:L:66:TYR:HA	1.99	0.45
18:L:114:ARG:HB3	18:L:119:VAL:HB	1.98	0.45
30:a:285:G:C6	30:a:356:G:C6	3.04	0.45
30:a:693:A:O2'	30:a:1353:A:N3	2.47	0.45
30:a:1164:C:H2'	30:a:1165:A:H8	1.81	0.45
30:a:2048:G:C5	30:a:2049:G:C8	3.04	0.45
30:a:2287:A:C4	30:a:2289:G:N7	2.85	0.45
46:q:20:VAL:HG12	46:q:21:ARG:H	1.80	0.45
7:A:408:A:H2'	7:A:409:U:H6	1.82	0.45
7:A:490:C:C2	7:A:491:G:C8	3.05	0.45
7:A:505:G:H2'	7:A:506:G:C8	2.52	0.45
7:A:696:A:H2'	7:A:697:U:C6	2.52	0.45
7:A:820:U:H4'	7:A:821:G:OP2	2.17	0.45
30:a:287:G:H2'	30:a:288:U:H6	1.80	0.45
30:a:1534:U:O3'	30:a:1535:A:H2'	2.17	0.45
30:a:1589:U:C2	30:a:1590:A:C8	3.04	0.45
30:a:1796:U:H2'	30:a:1797:G:C8	2.52	0.45
30:a:2543:G:C6	30:a:2765:A:C5	3.05	0.45
32:c:72:ASP:OD1	32:c:72:ASP:N	2.38	0.45
34:e:91:ASP:C	34:e:91:ASP:OD1	2.60	0.45
39:j:69:VAL:HG21	39:j:106:GLU:CD	2.42	0.45
41:l:83:GLY:C	41:l:85:GLY:H	2.24	0.45
49:t:89:ASP:OD1	49:t:89:ASP:O	2.35	0.45
7:A:335:C:C2	7:A:336:A:C8	3.05	0.45
8:B:57:LEU:HD13	8:B:217:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:J:57:VAL:HG23	16:J:58:ASN:N	2.31	0.45
17:K:18:ASP:OD1	17:K:18:ASP:N	2.47	0.45
26:T:24:ARG:HH11	26:T:27:MET:HE1	1.81	0.45
27:U:7:ARG:HG3	27:U:18:ARG:NH2	2.31	0.45
30:a:364:C:H2'	30:a:365:U:C6	2.51	0.45
30:a:977:G:C6	30:a:978:G:N7	2.84	0.45
30:a:1482:G:H2'	30:a:1483:G:H8	1.82	0.45
30:a:2869:G:H2'	30:a:2870:C:C6	2.52	0.45
33:d:150:MEQ:O	33:d:153:GLY:N	2.50	0.45
40:k:1:MET:HE3	40:k:1:MET:HB3	1.91	0.45
45:p:83:LEU:HA	45:p:83:LEU:HD23	1.78	0.45
47:r:4:ILE:HG22	47:r:106:VAL:HB	1.99	0.45
1:0:51:GLU:HG2	1:0:52:ALA:N	2.31	0.45
3:2:34:THR:OG1	30:a:2420:C:OP1	2.29	0.45
7:A:490:C:H2'	7:A:491:G:H8	1.82	0.45
7:A:590:U:H2'	7:A:591:U:H6	1.82	0.45
7:A:664:G:P	24:R:53:ARG:HH21	2.40	0.45
7:A:900:A:H8	7:A:900:A:O5'	2.00	0.45
7:A:1187:G:H2'	7:A:1188:A:H8	1.82	0.45
7:A:1258:G:H2'	7:A:1259:C:C6	2.52	0.45
10:D:68:LEU:HD23	10:D:68:LEU:HA	1.79	0.45
10:D:187:GLU:CD	10:D:188:ARG:H	2.24	0.45
19:M:78:LYS:O	19:M:78:LYS:HD3	2.17	0.45
30:a:150:U:H2'	30:a:151:C:C6	2.52	0.45
30:a:305:C:H2'	30:a:306:U:C6	2.52	0.45
30:a:329:G:OP2	49:t:69:ASN:ND2	2.49	0.45
30:a:767:U:H2'	30:a:768:G:H8	1.81	0.45
30:a:1227:G:C2	30:a:1228:G:C8	3.05	0.45
30:a:2630:G:C5	30:a:2894:G:C6	3.05	0.45
31:b:100:G:C4	31:b:101:A:C8	3.04	0.45
7:A:413:G:H21	7:A:428:G:H1'	1.81	0.44
7:A:737:C:C2	7:A:738:C:C5	3.06	0.44
7:A:950:U:OP2	19:M:101:ARG:HD2	2.17	0.44
7:A:985:C:H2'	7:A:986:U:C6	2.52	0.44
7:A:1254:A:H2'	7:A:1255:G:C8	2.52	0.44
7:A:1415:G:C4	7:A:1486:G:C2	3.05	0.44
17:K:108:THR:HG22	17:K:109:ASN:CG	2.41	0.44
30:a:347:A:H2'	30:a:348:A:H8	1.82	0.44
30:a:871:U:H2'	30:a:872:U:C6	2.51	0.44
30:a:1268:A:N3	30:a:2013:A:C6	2.85	0.44
30:a:1281:G:H2'	30:a:1282:U:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1385:A:C4	30:a:1403:A:C2	3.06	0.44
30:a:1407:G:C2	30:a:1596:A:C2	3.05	0.44
30:a:1853:A:H2'	30:a:1854:A:C8	2.52	0.44
30:a:2196:C:C2	30:a:2197:U:C5	3.04	0.44
30:a:2698:U:C2	30:a:2699:C:C5	3.05	0.44
30:a:2737:G:H2'	30:a:2738:A:C8	2.52	0.44
34:e:21:ARG:HD3	34:e:106:LYS:HB3	1.99	0.44
36:g:72:LEU:HA	36:g:72:LEU:HD23	1.67	0.44
46:q:21:ARG:HG3	46:q:93:PHE:HD2	1.82	0.44
7:A:133:U:H1'	7:A:230:G:N2	2.32	0.44
7:A:148:G:H2'	7:A:149:A:O4'	2.17	0.44
7:A:593:U:H2'	7:A:594:U:H6	1.81	0.44
7:A:1236:A:H2'	7:A:1237:C:C6	2.53	0.44
18:L:40:THR:OG1	18:L:41:THR:N	2.50	0.44
20:N:56:SER:HB3	20:N:59:ARG:HG2	1.99	0.44
30:a:28:A:H2'	30:a:29:U:H6	1.82	0.44
30:a:529:A:C5	30:a:2042:A:C2	3.06	0.44
30:a:579:G:C5	30:a:1262:A:N6	2.84	0.44
30:a:838:C:C4	30:a:941:A:N6	2.86	0.44
30:a:1941:C:C4	30:a:1942:C:N4	2.85	0.44
30:a:2588:G:O6	30:a:2607:G:N1	2.51	0.44
50:u:58:SER:O	50:u:58:SER:OG	2.32	0.44
4:3:15:LYS:HE2	4:3:15:LYS:HB3	1.76	0.44
7:A:84:U:O4	7:A:88:U:H1'	2.18	0.44
7:A:272:C:H2'	7:A:273:U:H6	1.81	0.44
7:A:851:G:C2	7:A:852:G:C8	3.06	0.44
7:A:1011:C:H2'	7:A:1012:A:H8	1.82	0.44
7:A:1061:G:H2'	7:A:1062:U:C6	2.53	0.44
7:A:1399:C:C4	7:A:1401:G:C2	3.05	0.44
7:A:1497:G:H1'	7:A:1518:MA6:H2	1.99	0.44
14:H:118:GLN:OE1	14:H:118:GLN:HA	2.17	0.44
30:a:447:A:C5	30:a:473:G:C5	3.05	0.44
30:a:816:C:H2'	30:a:817:C:H6	1.82	0.44
30:a:1026:G:OP2	30:a:1134:A:O2'	2.30	0.44
30:a:1550:C:H2'	30:a:1551:A:H8	1.82	0.44
30:a:2747:G:O6	30:a:2755:C:H5''	2.17	0.44
39:j:40:LYS:HE3	39:j:57:VAL:HG12	1.98	0.44
47:r:3:THR:OG1	47:r:58:ALA:HB2	2.18	0.44
7:A:35:G:H2'	7:A:36:C:C6	2.52	0.44
7:A:76:G:H2'	7:A:77:A:H8	1.81	0.44
7:A:773:G:O6	7:A:807:A:N6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1106:G:O2'	9:C:169:ARG:NH1	2.49	0.44
8:B:186:ILE:HD13	8:B:200:ILE:HG13	2.00	0.44
13:G:58:GLU:H	13:G:58:GLU:CD	2.25	0.44
22:P:66:THR:C	22:P:67:ILE:HD12	2.42	0.44
30:a:372:G:O2'	30:a:400:G:O6	2.31	0.44
30:a:565:C:H2'	30:a:566:U:C6	2.53	0.44
30:a:623:C:C2	30:a:624:C:C5	3.05	0.44
30:a:912:C:O2'	30:a:913:U:H5'	2.17	0.44
30:a:953:G:C2	30:a:954:G:N7	2.86	0.44
30:a:1038:G:H2'	30:a:1039:A:C8	2.52	0.44
30:a:1657:U:C2	30:a:1658:C:C5	3.06	0.44
30:a:1741:C:H2'	30:a:1742:U:C6	2.53	0.44
30:a:1805:A:C6	30:a:1813:G:C6	3.05	0.44
30:a:1914:C:O5'	30:a:1914:C:H6	2.01	0.44
53:x:22:LEU:HD23	53:x:22:LEU:HA	1.79	0.44
3:2:42:ARG:NH1	30:a:2349:G:OP2	2.50	0.44
7:A:100:G:C4	7:A:101:A:C8	3.06	0.44
7:A:591:U:C2	7:A:592:G:C8	3.06	0.44
7:A:745:G:C2	7:A:746:A:C5	3.05	0.44
7:A:1238:A:OP1	7:A:1335:U:O2'	2.27	0.44
7:A:1307:U:H2'	7:A:1308:U:C6	2.53	0.44
7:A:1324:A:H2'	7:A:1325:C:C6	2.52	0.44
12:F:18:VAL:O	12:F:22:ILE:HG13	2.17	0.44
17:K:47:ALA:HB1	17:K:62:ALA:HB1	1.98	0.44
30:a:662:G:C2	30:a:663:G:N7	2.86	0.44
30:a:1656:C:H2'	30:a:1657:U:H6	1.82	0.44
30:a:1663:G:C6	30:a:1992:G:N7	2.86	0.44
30:a:1685:C:H2'	30:a:1686:C:C6	2.53	0.44
30:a:1741:C:H2'	30:a:1742:U:H6	1.82	0.44
30:a:1917:PSU:O2	30:a:1918:A:N6	2.50	0.44
30:a:2290:G:H2'	30:a:2291:U:H6	1.82	0.44
30:a:2428:G:N2	40:k:54:GLN:OE1	2.50	0.44
33:d:124:ARG:HD3	33:d:125:TRP:CD1	2.52	0.44
35:f:159:THR:O	35:f:159:THR:OG1	2.29	0.44
47:r:109:ASP:C	47:r:109:ASP:OD1	2.60	0.44
7:A:550:G:C6	7:A:551:U:C4	3.06	0.44
7:A:784:A:N6	7:A:799:G:C6	2.86	0.44
7:A:1120:C:C2	7:A:1121:U:C5	3.05	0.44
8:B:111:ILE:HD13	8:B:111:ILE:HA	1.85	0.44
30:a:974:G:C8	30:a:1186:G:N2	2.85	0.44
30:a:1332:G:C6	30:a:1609:A:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2636:C:H2'	30:a:2637:U:C6	2.52	0.44
30:a:2839:G:H4'	42:m:49:GLU:OE1	2.18	0.44
7:A:409:U:O4	7:A:433:G:O6	2.36	0.44
7:A:553:A:H2'	7:A:554:A:C8	2.53	0.44
7:A:685:G:C2	7:A:686:U:C4	3.06	0.44
7:A:718:A:H5'	17:K:119:ASN:ND2	2.33	0.44
7:A:985:C:H2'	7:A:986:U:H6	1.82	0.44
7:A:1307:U:H2'	7:A:1308:U:H6	1.83	0.44
30:a:644:A:C2	30:a:2369:A:H1'	2.52	0.44
30:a:957:C:N4	30:a:959:A:C6	2.85	0.44
30:a:1156:A:C8	45:p:51:ARG:HD3	2.52	0.44
30:a:1948:G:C6	30:a:1959:G:C6	3.06	0.44
30:a:2073:C:C2	30:a:2437:G:C2	3.05	0.44
30:a:2721:A:C4	30:a:2873:A:N7	2.85	0.44
32:c:110:LEU:HA	32:c:110:LEU:HD12	1.64	0.44
36:g:19:ILE:HG22	36:g:24:ILE:CD1	2.46	0.44
7:A:81:A:H2	7:A:88:U:H3	1.65	0.44
7:A:470:C:H2'	7:A:471:U:C6	2.53	0.44
7:A:632:U:H5''	7:A:633:G:H8	1.82	0.44
7:A:715:A:H2'	7:A:716:A:C8	2.53	0.44
7:A:1371:G:O3'	15:I:71:GLY:HA3	2.18	0.44
11:E:76:LEU:HD23	11:E:76:LEU:HA	1.80	0.44
30:a:6:A:H2'	30:a:7:G:C8	2.53	0.44
30:a:78:U:H2'	30:a:79:C:C6	2.52	0.44
30:a:417:C:H2'	30:a:418:C:H6	1.83	0.44
30:a:1208:C:C2	30:a:1239:G:C2	3.06	0.44
30:a:1589:U:H2'	30:a:1590:A:C8	2.49	0.44
30:a:2199:A:C4	30:a:2225:A:C2	3.05	0.44
30:a:2415:G:H2'	30:a:2416:C:H6	1.82	0.44
30:a:2699:C:H2'	30:a:2700:A:H8	1.82	0.44
34:e:139:LYS:HB2	34:e:139:LYS:HE3	1.90	0.44
43:n:93:ASP:OD1	43:n:93:ASP:C	2.60	0.44
44:o:31:TRP:CZ3	44:o:38:LYS:HB3	2.53	0.44
55:z:18:SER:OG	55:z:19:HIS:N	2.51	0.44
7:A:682:G:C2	7:A:683:G:C8	3.06	0.44
7:A:736:C:OP1	24:R:61:ARG:NH1	2.51	0.44
7:A:1121:U:H2'	7:A:1122:U:H6	1.83	0.44
8:B:85:LEU:HD23	8:B:85:LEU:HA	1.78	0.44
9:C:64:ILE:HG23	9:C:99:ALA:HA	2.00	0.44
13:G:31:MET:HE1	13:G:36:LYS:HA	1.99	0.44
22:P:40:ASN:C	22:P:40:ASN:OD1	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:367:G:H2'	30:a:368:A:H8	1.82	0.44
30:a:639:U:H2'	30:a:640:C:C6	2.53	0.44
30:a:687:C:O5'	30:a:687:C:H6	2.00	0.44
30:a:882:G:H2'	30:a:883:G:H1'	1.99	0.44
30:a:2209:G:C5	30:a:2210:U:C4	3.06	0.44
30:a:2515:C:C2	30:a:2570:G:N1	2.86	0.44
35:f:36:LEU:HD22	35:f:154:ILE:HG12	2.00	0.44
7:A:53:A:N6	7:A:359:G:O6	2.51	0.43
7:A:262:A:H2'	7:A:263:A:H8	1.83	0.43
7:A:489:C:H2'	7:A:490:C:H6	1.81	0.43
8:B:71:GLY:O	8:B:93:ASN:HA	2.18	0.43
10:D:105:MET:SD	10:D:180:GLY:HA3	2.58	0.43
16:J:25:ILE:HA	16:J:90:LEU:HD21	2.00	0.43
16:J:59:LYS:O	16:J:62:ARG:NH1	2.51	0.43
26:T:15:GLU:OE1	26:T:15:GLU:HA	2.17	0.43
30:a:858:G:C4	30:a:2268:A:H2	2.36	0.43
30:a:1005:C:C2	30:a:1006:C:C5	3.06	0.43
30:a:1734:G:C2	30:a:1735:A:C5	3.06	0.43
30:a:2393:U:H2'	30:a:2394:C:H6	1.82	0.43
33:d:179:ARG:HB3	33:d:188:LEU:HD13	1.99	0.43
34:e:154:ASP:OD1	34:e:156:ASN:N	2.49	0.43
35:f:120:LYS:HA	35:f:120:LYS:HE3	1.99	0.43
40:k:104:GLN:HE21	40:k:104:GLN:HB3	1.57	0.43
47:r:53:SER:O	47:r:57:ASN:HB2	2.18	0.43
52:w:56:MET:HE2	52:w:56:MET:HB2	1.82	0.43
55:z:12:LYS:HD3	55:z:12:LYS:HA	1.79	0.43
2:1:31:LEU:HA	2:1:31:LEU:HD23	1.84	0.43
7:A:895:G:C6	7:A:896:C:C4	3.05	0.43
7:A:978:A:C5	7:A:1318:A:C6	3.06	0.43
7:A:1226:C:O2'	19:M:110:LYS:NZ	2.52	0.43
9:C:164:ARG:NH1	9:C:166:GLU:OE2	2.39	0.43
10:D:9:LEU:HD12	10:D:9:LEU:HA	1.76	0.43
11:E:45:ARG:HG2	11:E:73:ASN:OD1	2.17	0.43
24:R:21:ILE:HD13	24:R:21:ILE:HA	1.84	0.43
26:T:8:LYS:O	26:T:12:ILE:HG13	2.18	0.43
30:a:291:G:C6	30:a:350:G:C6	3.06	0.43
30:a:582:A:N6	30:a:1259:G:O6	2.51	0.43
30:a:1571:A:H2'	30:a:1572:A:H8	1.83	0.43
30:a:1823:G:C2	30:a:1824:G:C8	3.06	0.43
30:a:1831:G:C6	30:a:1975:G:N1	2.86	0.43
30:a:2044:C:N3	30:a:2625:G:C2	2.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2428:G:H5''	30:a:2429:G:OP1	2.19	0.43
30:a:2557:G:H2'	30:a:2558:C:C6	2.53	0.43
31:b:45:A:C4	31:b:46:A:C8	3.06	0.43
33:d:180:VAL:HG13	33:d:180:VAL:O	2.19	0.43
43:n:76:LYS:HE2	43:n:76:LYS:HB2	1.78	0.43
7:A:778:G:C6	7:A:779:C:C4	3.07	0.43
7:A:904:U:H2'	7:A:905:U:H6	1.83	0.43
7:A:924:C:H2'	7:A:925:G:H8	1.84	0.43
7:A:1342:C:H2'	7:A:1343:G:C8	2.53	0.43
8:B:161:LEU:HB2	8:B:183:VAL:HG12	2.00	0.43
9:C:47:LEU:HB3	9:C:50:ALA:HB3	2.00	0.43
9:C:179:ARG:NE	9:C:206:GLU:OE2	2.51	0.43
13:G:106:GLU:O	13:G:110:LYS:HG2	2.18	0.43
14:H:48:ASP:OD1	14:H:49:PHE:N	2.51	0.43
16:J:56:HIS:ND1	16:J:57:VAL:HG13	2.33	0.43
18:L:31:ARG:HA	18:L:81:LEU:HD12	1.99	0.43
20:N:19:LYS:HG2	20:N:20:TYR:CE1	2.53	0.43
30:a:81:G:N1	30:a:106:C:N3	2.65	0.43
30:a:938:G:C2	30:a:939:G:N7	2.86	0.43
30:a:1324:G:O2'	30:a:1326:U:OP2	2.24	0.43
30:a:2072:C:H2'	30:a:2073:C:H6	1.82	0.43
35:f:42:GLU:H	35:f:42:GLU:CD	2.27	0.43
37:h:9:VAL:CG2	37:h:12:LEU:HB2	2.48	0.43
7:A:294:U:C2	7:A:295:C:C5	3.07	0.43
7:A:1243:C:H2'	7:A:1244:G:C8	2.52	0.43
11:E:94:VAL:HB	11:E:111:MET:HE1	2.01	0.43
30:a:519:U:C2	30:a:520:G:C8	3.06	0.43
30:a:815:C:C2	30:a:816:C:C5	3.06	0.43
30:a:1529:G:H2'	30:a:1530:G:H8	1.82	0.43
30:a:2373:G:H2'	30:a:2374:C:C6	2.53	0.43
38:i:60:ASP:C	38:i:60:ASP:OD1	2.61	0.43
46:q:26:ASP:CG	46:q:26:ASP:O	2.61	0.43
50:u:20:LEU:HD12	50:u:20:LEU:HA	1.80	0.43
6:5:52:G:O2'	6:5:53:5MU:H5''	2.18	0.43
10:D:104:ARG:HG2	10:D:104:ARG:HH11	1.83	0.43
13:G:129:GLU:N	13:G:129:GLU:OE2	2.51	0.43
17:K:88:GLY:O	17:K:93:ARG:HD2	2.19	0.43
30:a:134:G:C6	30:a:146:A:C6	3.07	0.43
30:a:357:C:H2'	30:a:358:U:C6	2.53	0.43
30:a:937:C:C2	30:a:938:G:C8	3.06	0.43
30:a:1028:A:H2'	30:a:1029:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1380:G:C2	30:a:1381:G:C8	3.06	0.43
30:a:1570:A:H2'	30:a:1571:A:H8	1.81	0.43
30:a:1747:U:H2'	30:a:1748:C:C6	2.54	0.43
30:a:1964:G:C6	30:a:1967:C:N4	2.87	0.43
30:a:2681:C:C4	30:a:2724:U:C5	3.06	0.43
30:a:2691:C:C4	30:a:2719:G:N2	2.86	0.43
30:a:2820:A:N3	30:a:2820:A:H2'	2.34	0.43
30:a:2838:G:C4	30:a:2839:G:C8	3.05	0.43
48:s:6:ARG:NH2	48:s:37:ASP:O	2.49	0.43
7:A:152:A:N6	7:A:170:U:C2	2.87	0.43
7:A:1012:A:C6	7:A:1018:G:C6	3.06	0.43
7:A:1442:G:H1'	44:o:114:LEU:HD13	2.00	0.43
8:B:169:GLU:N	8:B:169:GLU:OE2	2.52	0.43
18:L:98:VAL:HG13	18:L:101:ALA:HB2	2.00	0.43
30:a:30:G:H2'	30:a:31:C:H6	1.83	0.43
30:a:491:G:C6	30:a:492:A:C5	3.07	0.43
30:a:563:A:C5	30:a:2018:G:C2	3.07	0.43
30:a:806:C:C2	30:a:807:U:C5	3.06	0.43
30:a:1233:C:C2	30:a:1234:U:C5	3.07	0.43
30:a:1442:U:H2'	30:a:1443:U:C6	2.54	0.43
30:a:1670:C:H2'	30:a:1671:U:O4'	2.18	0.43
30:a:1747:U:H2'	30:a:1748:C:H6	1.84	0.43
42:m:13:ASN:O	42:m:17:ARG:HG3	2.19	0.43
45:p:74:ILE:HG13	45:p:78:LYS:HB2	1.99	0.43
7:A:681:A:C6	7:A:710:G:C6	3.07	0.43
7:A:721:G:H4'	7:A:722:G:O4'	2.19	0.43
7:A:736:C:H2'	7:A:737:C:C6	2.51	0.43
7:A:836:G:C6	7:A:851:G:C5	3.07	0.43
7:A:876:C:H2'	7:A:877:G:H8	1.84	0.43
7:A:1001:C:H2'	7:A:1002:G:C8	2.53	0.43
7:A:1003:G:H21	7:A:1005:A:H5'	1.83	0.43
7:A:1250:A:H4'	15:I:70:GLY:H	1.83	0.43
10:D:188:ARG:O	10:D:188:ARG:HD3	2.17	0.43
12:F:1:MET:HE2	12:F:65:GLU:HG2	2.01	0.43
26:T:80:THR:O	26:T:84:ASN:ND2	2.38	0.43
30:a:1171:G:C6	30:a:1179:G:C6	3.07	0.43
30:a:1424:G:N1	30:a:1575:C:N3	2.67	0.43
30:a:1447:C:H2'	30:a:1448:G:H8	1.84	0.43
30:a:1532:A:N6	30:a:1540:G:O6	2.52	0.43
30:a:1796:U:H2'	30:a:1797:G:H8	1.84	0.43
30:a:2041:U:H2'	30:a:2042:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:2215:C:H2'	30:a:2216:G:C8	2.54	0.43
30:a:2658:C:OP1	36:g:160:LYS:NZ	2.52	0.43
30:a:2819:G:H2'	30:a:2821:A:N7	2.33	0.43
30:a:2839:G:H2'	30:a:2840:C:H6	1.83	0.43
7:A:476:U:H2'	7:A:477:C:H6	1.83	0.43
7:A:601:G:H2'	7:A:602:A:C8	2.54	0.43
7:A:784:A:H2'	7:A:785:G:H8	1.83	0.43
7:A:923:A:H2'	7:A:924:C:H6	1.84	0.43
7:A:1095:U:H2'	7:A:1096:C:C6	2.54	0.43
7:A:1121:U:H2'	7:A:1122:U:C6	2.54	0.43
11:E:54:ARG:HG2	11:E:54:ARG:NH1	2.33	0.43
13:G:146:GLU:OE1	13:G:146:GLU:HA	2.19	0.43
14:H:54:ASP:OD1	14:H:54:ASP:N	2.51	0.43
16:J:6:ILE:HB	16:J:76:ILE:HB	2.00	0.43
18:L:94:ARG:HB2	18:L:95:TYR:CE1	2.54	0.43
19:M:95:LEU:HB3	19:M:96:PRO:HD2	2.00	0.43
30:a:185:G:C6	30:a:212:G:N1	2.86	0.43
30:a:465:G:H21	30:a:684:G:H1'	1.83	0.43
30:a:722:A:H2'	30:a:723:C:H6	1.83	0.43
30:a:1208:C:C4	30:a:1209:U:C4	3.07	0.43
30:a:2303:G:C4	30:a:2304:G:C8	3.06	0.43
30:a:2357:G:N2	30:a:2360:G:OP2	2.48	0.43
30:a:2846:G:H2'	30:a:2847:U:C6	2.54	0.43
32:c:243:HIS:O	32:c:245:VAL:HG13	2.19	0.43
35:f:30:ARG:H	35:f:159:THR:CG2	2.32	0.43
36:g:121:ILE:HD13	36:g:121:ILE:N	2.34	0.43
7:A:109:A:N1	7:A:326:G:C6	2.87	0.43
7:A:363:A:C2	18:L:28:PRO:HD2	2.54	0.43
7:A:488:C:H2'	7:A:489:C:H6	1.83	0.43
7:A:635:A:H2'	7:A:636:U:C6	2.54	0.43
7:A:672:U:H2'	7:A:673:A:C8	2.54	0.43
7:A:687:A:H2	7:A:704:A:C5	2.37	0.43
7:A:1070:U:H2'	7:A:1071:C:C6	2.54	0.43
8:B:111:ILE:HD12	8:B:152:LYS:HA	2.00	0.43
21:O:14:GLU:HG3	21:O:15:PHE:CD1	2.53	0.43
30:a:667:U:H2'	30:a:668:A:O4'	2.18	0.43
30:a:1299:G:H5''	30:a:1300:G:OP1	2.18	0.43
30:a:1837:C:C2	30:a:1899:A:N6	2.86	0.43
30:a:2856:A:C6	30:a:2862:G:C6	3.06	0.43
32:c:66:ASP:OD1	32:c:66:ASP:C	2.61	0.43
41:l:31:PHE:HD1	41:l:132:THR:HG22	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:z:54:VAL:HG12	55:z:55:ILE:HG23	2.00	0.43
5:4:22:MET:HE3	5:4:22:MET:HB2	1.87	0.43
6:5:67:C:H2'	6:5:68:C:C6	2.54	0.43
7:A:82:G:H2'	7:A:82:G:N3	2.33	0.43
7:A:438:U:C4	7:A:494:G:C5	3.07	0.43
11:E:106:ILE:HB	11:E:124:LEU:HD23	2.00	0.43
30:a:241:A:H2	30:a:242:G:H21	1.66	0.43
30:a:479:A:H4'	30:a:480:A:OP1	2.18	0.43
30:a:608:A:H2'	30:a:609:A:C8	2.54	0.43
30:a:818:G:N1	30:a:1188:U:OP2	2.50	0.43
30:a:883:G:H5'	30:a:884:U:OP2	2.19	0.43
30:a:919:U:C2	30:a:920:A:C8	3.06	0.43
30:a:1585:C:H2'	30:a:1586:A:O4'	2.18	0.43
30:a:1629:U:C4	30:a:1630:A:N7	2.87	0.43
30:a:2740:A:N6	30:a:2764:A:C8	2.87	0.43
42:m:38:LEU:HB3	42:m:39:PRO:HD3	1.99	0.43
43:n:88:LYS:HE3	43:n:116:GLN:OE1	2.19	0.43
7:A:1525:G:C2	7:A:1526:G:C8	3.07	0.42
14:H:7:ILE:O	14:H:11:LEU:HD23	2.19	0.42
16:J:23:ALA:O	16:J:27:GLU:HG2	2.19	0.42
30:a:860:U:C2	30:a:2268:A:C8	3.07	0.42
30:a:1128:G:C6	30:a:2518:A:C6	3.07	0.42
30:a:2258:C:O2'	30:a:2427:C:OP2	2.33	0.42
30:a:2455:G:H2'	30:a:2456:C:C6	2.52	0.42
30:a:2703:C:C2	30:a:2704:C:C5	3.07	0.42
30:a:2900:A:H2'	30:a:2901:C:C6	2.54	0.42
49:t:86:ARG:NH2	49:t:88:GLU:OE1	2.51	0.42
7:A:8:A:N7	10:D:206:LYS:HA	2.33	0.42
7:A:33:A:H2'	7:A:34:C:H6	1.82	0.42
7:A:271:C:C2	7:A:272:C:C5	3.07	0.42
7:A:298:A:H8	7:A:298:A:OP1	2.02	0.42
7:A:317:U:C2	7:A:318:G:C8	3.06	0.42
15:I:55:VAL:HG11	15:I:87:LEU:HD11	2.00	0.42
15:I:120:LYS:HE2	15:I:120:LYS:HB3	1.58	0.42
17:K:67:ALA:HB2	17:K:96:THR:HG23	2.00	0.42
19:M:80:LEU:HD23	19:M:80:LEU:HA	1.78	0.42
30:a:2349:G:C6	30:a:2369:A:C6	3.08	0.42
30:a:2776:A:C6	30:a:2778:A:C6	3.08	0.42
40:k:28:GLY:O	40:k:29:LYS:C	2.62	0.42
1:0:44:ARG:NH2	30:a:643:A:C4	2.88	0.42
3:2:26:HIS:HB3	3:2:44:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:763:G:H2'	7:A:764:C:C6	2.54	0.42
7:A:908:A:H2'	7:A:909:A:H8	1.84	0.42
7:A:1011:C:H2'	7:A:1012:A:C8	2.55	0.42
7:A:1460:C:C2	7:A:1461:G:C8	3.07	0.42
16:J:67:ILE:HG13	20:N:96:LEU:HD13	2.01	0.42
30:a:67:U:C2	30:a:68:G:C8	3.08	0.42
30:a:1356:G:C6	30:a:1357:C:C4	3.07	0.42
30:a:1443:U:C2	30:a:1444:G:C8	3.07	0.42
30:a:1482:G:N3	30:a:1483:G:C8	2.88	0.42
30:a:1735:A:C6	30:a:1736:U:C4	3.08	0.42
30:a:2281:A:O2'	30:a:2282:G:H5'	2.19	0.42
30:a:2589:A:H2'	30:a:2590:A:H8	1.84	0.42
31:b:83:G:C6	31:b:94:A:C6	3.07	0.42
36:g:128:GLN:OE1	36:g:128:GLN:HA	2.18	0.42
7:A:254:G:OP1	23:Q:68:SER:OG	2.35	0.42
7:A:1140:C:H2'	7:A:1141:C:C6	2.55	0.42
7:A:1287:A:C6	7:A:1288:A:C6	3.06	0.42
7:A:1520:C:H2'	7:A:1521:C:C6	2.54	0.42
20:N:93:ILE:HG21	20:N:96:LEU:HD22	2.01	0.42
21:O:26:GLU:HG2	21:O:81:LEU:HD22	2.02	0.42
22:P:6:LEU:HD23	22:P:6:LEU:HA	1.84	0.42
30:a:1386:C:H2'	30:a:1387:A:H8	1.83	0.42
30:a:1707:G:H2'	30:a:1708:C:H6	1.84	0.42
30:a:1715:G:O2'	30:a:1716:U:OP2	2.38	0.42
30:a:1770:G:C5	30:a:1983:G:C6	3.07	0.42
30:a:1964:G:C2	30:a:1967:C:C5	3.07	0.42
30:a:2018:G:C6	30:a:2019:A:C6	3.07	0.42
30:a:2679:A:H2'	30:a:2680:U:H6	1.84	0.42
32:c:69:ARG:HA	32:c:69:ARG:HD2	1.74	0.42
35:f:85:ILE:HG13	35:f:85:ILE:O	2.19	0.42
3:2:31:HIS:HE1	30:a:2392:A:OP2	2.02	0.42
6:5:74:C:H5''	6:5:75:A:OP2	2.19	0.42
7:A:1317:C:H5'	20:N:24:ARG:HH21	1.85	0.42
14:H:101:ILE:O	14:H:101:ILE:HG13	2.19	0.42
30:a:43:G:N1	30:a:437:U:C4	2.88	0.42
30:a:252:G:HO2'	30:a:253:C:P	2.42	0.42
30:a:488:G:C2	30:a:493:G:O6	2.72	0.42
30:a:1220:G:C6	30:a:1221:C:C4	3.07	0.42
30:a:1297:C:H2'	30:a:1298:C:H6	1.84	0.42
30:a:1342:A:C6	30:a:1397:U:C5	3.08	0.42
36:g:103:ILE:HD11	36:g:131:ILE:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:35:ILE:H	43:n:53:THR:CG2	2.32	0.42
7:A:79:G:H2'	7:A:80:A:C8	2.54	0.42
7:A:176:C:C2	7:A:177:G:C2	3.08	0.42
7:A:258:G:H1	7:A:268:U:H3	1.66	0.42
7:A:380:G:C2	7:A:384:G:C6	3.07	0.42
7:A:1009:U:O2	7:A:1020:G:N2	2.38	0.42
7:A:1162:C:C2	7:A:1163:A:C8	3.08	0.42
8:B:27:MET:HE2	8:B:187:VAL:HG12	2.02	0.42
9:C:86:LYS:O	9:C:90:VAL:HG12	2.18	0.42
13:G:66:LEU:HD23	13:G:66:LEU:HA	1.87	0.42
14:H:77:ARG:NH1	14:H:79:SER:O	2.53	0.42
30:a:171:U:H2'	30:a:172:A:C8	2.54	0.42
30:a:1026:G:H2'	30:a:1027:A:H8	1.84	0.42
30:a:1686:C:C2	30:a:1703:G:N2	2.88	0.42
30:a:1766:G:C2	30:a:1767:G:C8	3.08	0.42
30:a:1846:G:O2'	30:a:1847:A:H5'	2.20	0.42
30:a:1967:C:N4	30:a:1968:G:C6	2.88	0.42
30:a:2039:U:H2'	30:a:2040:G:C8	2.54	0.42
30:a:2692:G:C6	30:a:2718:G:C6	3.06	0.42
7:A:127:G:H4'	23:Q:6:ARG:HH12	1.84	0.42
7:A:322:C:N3	7:A:332:G:N2	2.68	0.42
7:A:335:C:H2'	7:A:336:A:C8	2.52	0.42
7:A:797:C:OP1	17:K:127:ARG:HD2	2.19	0.42
7:A:958:A:H2'	7:A:959:A:C8	2.55	0.42
7:A:1070:U:H2'	7:A:1071:C:H6	1.84	0.42
7:A:1272:G:H2'	7:A:1273:C:C6	2.54	0.42
30:a:29:U:C2	30:a:30:G:C8	3.08	0.42
30:a:599:A:N6	30:a:659:G:O6	2.53	0.42
30:a:631:A:N3	30:a:2415:G:O2'	2.48	0.42
30:a:1298:C:C2	30:a:1643:G:N2	2.88	0.42
30:a:1343:G:C2	30:a:1344:U:C4	3.08	0.42
30:a:2370:G:C6	30:a:2371:G:C6	3.07	0.42
30:a:2396:G:C2	30:a:2421:G:C2	3.08	0.42
40:k:18:ARG:HG2	40:k:18:ARG:HH11	1.84	0.42
2:1:12:ARG:NE	2:1:44:VAL:HG21	2.35	0.42
7:A:84:U:H6	7:A:86:G:H21	1.66	0.42
7:A:271:C:H2'	7:A:272:C:H6	1.85	0.42
7:A:384:G:H2'	7:A:385:C:C6	2.55	0.42
7:A:412:A:H62	7:A:431:A:H61	1.67	0.42
7:A:458:U:H2'	7:A:459:A:H8	1.84	0.42
7:A:742:G:C2	7:A:743:A:C8	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:47:LEU:HD13	12:F:51:ILE:HD12	2.02	0.42
15:I:38:TYR:HD1	15:I:39:PHE:CD1	2.38	0.42
23:Q:13:VAL:HG22	23:Q:22:VAL:HG23	2.01	0.42
30:a:572:A:H5'	46:q:79:ARG:HH21	1.84	0.42
30:a:1649:G:C2	30:a:1650:A:C8	3.08	0.42
30:a:2247:A:H2'	30:a:2248:C:C6	2.55	0.42
30:a:2303:G:O2'	35:f:121:SER:O	2.32	0.42
32:c:240:PHE:O	32:c:242:LYS:HD3	2.20	0.42
46:q:44:GLY:O	46:q:46:GLU:N	2.53	0.42
47:r:86:MET:HE3	47:r:96:ILE:CG1	2.49	0.42
52:w:41:GLU:HA	52:w:41:GLU:OE2	2.20	0.42
2:1:12:ARG:HB2	30:a:686:U:O4	2.19	0.42
7:A:477:C:H2'	7:A:478:A:H8	1.81	0.42
7:A:579:A:H2'	7:A:580:C:H6	1.82	0.42
7:A:920:U:H2'	7:A:921:U:H6	1.85	0.42
7:A:1099:G:H4'	27:U:69:ARG:NH2	2.35	0.42
7:A:1320:C:H42	25:S:36:ARG:HB2	1.85	0.42
7:A:1415:G:C5	7:A:1486:G:N1	2.88	0.42
8:B:7:ARG:HB3	8:B:11:LYS:NZ	2.35	0.42
9:C:11:ARG:NH2	9:C:175:LEU:O	2.37	0.42
9:C:34:ASP:O	9:C:38:LYS:HG3	2.20	0.42
16:J:47:GLU:OE1	20:N:76:LYS:NZ	2.53	0.42
30:a:58:G:C2	30:a:70:G:C2	3.08	0.42
30:a:301:G:C6	30:a:317:G:C6	3.08	0.42
30:a:481:G:C4	30:a:507:A:C2	3.08	0.42
30:a:1223:G:OP1	46:q:68:ARG:NH1	2.53	0.42
30:a:1365:A:OP1	52:w:3:ARG:NH1	2.53	0.42
30:a:1473:G:N1	30:a:1519:G:C6	2.88	0.42
30:a:1519:G:C5	30:a:1520:U:C4	3.07	0.42
30:a:1619:G:C2	30:a:1620:G:C8	3.07	0.42
30:a:1870:C:O2'	30:a:1871:A:O5'	2.38	0.42
30:a:2217:G:C2	30:a:2218:G:C8	3.08	0.42
30:a:2525:G:C2	30:a:2526:G:N7	2.88	0.42
30:a:2552:OMU:H6	30:a:2552:OMU:H3'	2.02	0.42
30:a:2856:A:N6	30:a:2862:G:O6	2.53	0.42
31:b:116:G:H2'	31:b:117:G:C8	2.55	0.42
32:c:97:LYS:HE2	32:c:97:LYS:HB2	1.81	0.42
35:f:127:ASN:OD1	35:f:127:ASN:N	2.52	0.42
43:n:43:ASN:C	43:n:43:ASN:OD1	2.62	0.42
7:A:613:C:H2'	7:A:614:C:C6	2.55	0.42
7:A:782:A:C6	7:A:801:U:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:N:96:LEU:HD12	20:N:96:LEU:HA	1.87	0.42
25:S:80:TYR:CZ	25:S:82:GLY:HA2	2.55	0.42
30:a:173:A:H2'	30:a:174:U:C6	2.54	0.42
30:a:396:G:C6	30:a:397:U:C4	3.07	0.42
30:a:794:A:C4	30:a:795:C:C5	3.08	0.42
30:a:953:G:C2	30:a:954:G:C8	3.08	0.42
30:a:2849:U:P	44:o:93:ARG:HH21	2.42	0.42
31:b:39:A:C2	31:b:44:G:N3	2.87	0.42
35:f:111:ILE:HD12	35:f:137:ILE:HG21	2.02	0.42
39:j:38:ILE:HD11	39:j:112:PHE:HZ	1.85	0.42
43:n:35:ILE:H	43:n:53:THR:HG22	1.85	0.42
50:u:21:ARG:NH1	50:u:87:GLN:O	2.53	0.42
5:4:6:HIS:CE1	35:f:64:LYS:H	2.37	0.41
7:A:272:C:C2	7:A:273:U:C5	3.08	0.41
7:A:466:A:H2'	7:A:468:A:C8	2.55	0.41
7:A:470:C:H2'	7:A:471:U:H6	1.85	0.41
7:A:482:A:H8	7:A:482:A:O5'	2.03	0.41
7:A:902:G:H2'	7:A:903:G:H8	1.85	0.41
7:A:1399:C:O2	7:A:1502:A:N6	2.53	0.41
7:A:1464:U:C2	7:A:1465:A:C8	3.08	0.41
16:J:73:LEU:HD12	16:J:74:VAL:N	2.34	0.41
25:S:11:ILE:HD11	25:S:15:LEU:HB3	2.01	0.41
30:a:404:A:H1'	30:a:405:U:OP2	2.20	0.41
30:a:511:U:C5	30:a:512:G:C5	3.07	0.41
30:a:1144:A:C4	30:a:1145:C:C5	3.08	0.41
33:d:4:LEU:HD23	33:d:4:LEU:HA	1.86	0.41
44:o:51:ARG:HH21	44:o:53:ARG:NH1	2.18	0.41
5:4:59:ARG:O	5:4:63:ARG:HG2	2.21	0.41
7:A:222:C:H2'	7:A:223:A:C8	2.49	0.41
7:A:376:G:H2'	7:A:377:G:H8	1.84	0.41
7:A:380:G:N2	7:A:383:A:OP2	2.46	0.41
7:A:922:G:C2	7:A:923:A:C4	3.08	0.41
7:A:1040:U:H2'	7:A:1041:G:H8	1.83	0.41
13:G:106:GLU:OE2	13:G:107:ALA:N	2.54	0.41
19:M:85:CYS:O	19:M:89:LEU:HD12	2.21	0.41
19:M:116:ILE:HD12	19:M:116:ILE:HA	1.89	0.41
30:a:24:G:C4	30:a:25:U:C5	3.07	0.41
30:a:523:C:H2'	30:a:524:G:H8	1.86	0.41
31:b:49:C:OP1	43:n:102:ARG:HG3	2.20	0.41
32:c:133:ARG:O	32:c:167:ARG:NH1	2.53	0.41
40:k:89:VAL:HG21	40:k:123:ARG:NH2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:18:LEU:HD23	43:n:18:LEU:HA	1.87	0.41
50:u:51:GLN:OE1	50:u:57:TYR:OH	2.34	0.41
50:u:72:VAL:HB	50:u:91:PHE:HB3	2.02	0.41
7:A:401:C:O2'	7:A:621:A:N3	2.49	0.41
7:A:920:U:C2	7:A:921:U:C5	3.08	0.41
7:A:923:A:H2'	7:A:924:C:C6	2.55	0.41
7:A:1110:A:C4	7:A:1111:A:C8	3.09	0.41
7:A:1161:C:C2	7:A:1162:C:C5	3.07	0.41
9:C:152:GLU:HG3	9:C:167:TRP:HB3	2.03	0.41
15:I:34:SER:HB3	15:I:37:GLN:CD	2.45	0.41
15:I:59:GLU:H	15:I:59:GLU:CD	2.27	0.41
19:M:27:LYS:HE2	19:M:27:LYS:HB2	1.92	0.41
30:a:93:G:H2'	30:a:94:A:H8	1.85	0.41
30:a:146:A:H2'	30:a:147:C:C6	2.54	0.41
30:a:659:G:C6	30:a:660:C:C4	3.08	0.41
30:a:1425:G:N2	30:a:1574:C:N4	2.68	0.41
30:a:2046:G:H1'	55:z:19:HIS:CE1	2.55	0.41
30:a:2228:G:H2'	30:a:2229:U:H6	1.85	0.41
30:a:2648:G:C4	30:a:2673:G:C2	3.09	0.41
34:e:105:LEU:HD23	34:e:105:LEU:HA	1.65	0.41
37:h:41:LYS:HE2	37:h:41:LYS:HB3	1.91	0.41
55:z:44:THR:OG1	55:z:48:TYR:N	2.53	0.41
7:A:459:A:C6	7:A:474:G:C6	3.08	0.41
7:A:1082:A:C4	7:A:1083:U:C5	3.08	0.41
7:A:1326:U:C2	7:A:1327:C:C5	3.08	0.41
7:A:1327:C:H2'	7:A:1328:C:H6	1.85	0.41
13:G:4:ARG:HA	13:G:4:ARG:HH11	1.86	0.41
14:H:32:LEU:HA	14:H:32:LEU:HD12	1.80	0.41
21:O:6:GLU:H	21:O:6:GLU:CD	2.28	0.41
23:Q:71:LYS:HE2	23:Q:71:LYS:HB3	1.77	0.41
26:T:80:THR:O	26:T:83:ILE:HG12	2.20	0.41
30:a:826:U:O2'	40:k:53:GLY:HA3	2.20	0.41
30:a:926:G:H2'	30:a:927:A:H8	1.85	0.41
30:a:1179:G:H2'	30:a:1180:U:C6	2.56	0.41
30:a:1233:C:H2'	30:a:1234:U:H6	1.86	0.41
30:a:1324:G:N3	30:a:1328:A:N6	2.68	0.41
30:a:1623:G:C2	30:a:1624:U:C6	3.08	0.41
30:a:1797:G:C6	30:a:1823:G:C6	3.08	0.41
34:e:163:ASN:N	34:e:163:ASN:HD22	2.17	0.41
35:f:17:MET:HE2	35:f:17:MET:HB2	1.86	0.41
7:A:228:A:H5'	22:P:63:GLN:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:767:A:C4	7:A:768:A:C8	3.08	0.41
7:A:834:U:H2'	7:A:835:U:C6	2.56	0.41
7:A:868:C:H2'	7:A:869:G:O4'	2.20	0.41
7:A:903:G:H2'	7:A:904:U:H6	1.86	0.41
7:A:1226:C:N4	19:M:103:LYS:HG2	2.35	0.41
8:B:164:ILE:HD13	8:B:186:ILE:HG13	2.03	0.41
30:a:639:U:H2'	30:a:640:C:H6	1.85	0.41
30:a:1000:A:C5	30:a:1155:A:C6	3.08	0.41
30:a:1443:U:H2'	30:a:1444:G:H8	1.86	0.41
30:a:1519:G:C6	30:a:1520:U:C4	3.09	0.41
30:a:1592:C:H2'	30:a:1593:A:H8	1.86	0.41
30:a:2048:G:C6	30:a:2621:G:N1	2.88	0.41
30:a:2283:C:C5	30:a:2389:G:C4	3.09	0.41
35:f:80:ARG:NH1	35:f:80:ARG:HG2	2.36	0.41
38:i:140:LEU:CD2	38:i:142:ILE:HG13	2.50	0.41
41:l:59:ARG:N	41:l:59:ARG:HD2	2.36	0.41
44:o:99:TYR:C	44:o:101:ARG:H	2.28	0.41
47:r:70:LYS:NZ	47:r:70:LYS:HB3	2.34	0.41
52:w:31:PRO:HG2	52:w:33:LEU:CD1	2.50	0.41
53:x:19:LEU:HD23	53:x:19:LEU:HA	1.84	0.41
6:5:9:C:O2	6:5:9:C:H2'	2.20	0.41
7:A:434:U:O4	7:A:435:A:N6	2.54	0.41
7:A:719:C:O2'	24:R:38:LYS:HB3	2.21	0.41
7:A:1181:G:O2'	7:A:1182:G:N7	2.47	0.41
7:A:1463:U:H2'	7:A:1464:U:C6	2.55	0.41
9:C:7:PRO:HD2	9:C:184:TYR:HD2	1.86	0.41
10:D:91:LEU:HD23	10:D:91:LEU:HA	1.88	0.41
30:a:541:A:C6	30:a:553:G:C6	3.09	0.41
30:a:1297:C:H2'	30:a:1298:C:C6	2.56	0.41
30:a:1437:C:H2'	30:a:1438:U:C6	2.56	0.41
30:a:1871:A:H2'	30:a:1872:A:C8	2.55	0.41
30:a:2590:A:C2	30:a:2591:C:C5	3.09	0.41
31:b:66:A:N6	31:b:107:G:H2'	2.34	0.41
35:f:48:LYS:HE2	35:f:48:LYS:HA	2.02	0.41
39:j:7:MET:SD	39:j:20:MET:HB2	2.59	0.41
42:m:8:ARG:HB3	42:m:10:LEU:HD13	2.02	0.41
53:x:30:MET:HE2	53:x:30:MET:HB2	1.69	0.41
2:1:16:HIS:HB2	2:1:44:VAL:HG11	2.02	0.41
2:1:44:VAL:O	2:1:45:SER:C	2.63	0.41
7:A:113:G:H1'	7:A:354:G:H5'	2.02	0.41
7:A:214:C:C2	7:A:215:C:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:647:C:C2	7:A:648:A:C8	3.09	0.41
7:A:743:A:H2'	7:A:744:C:H6	1.85	0.41
7:A:1002:G:H2'	7:A:1003:G:O4'	2.21	0.41
7:A:1017:U:H2'	7:A:1018:G:C8	2.55	0.41
7:A:1134:G:N2	7:A:1141:C:C2	2.89	0.41
13:G:25:LYS:HD2	13:G:25:LYS:HA	1.95	0.41
13:G:133:THR:C	13:G:136:LYS:HZ3	2.28	0.41
18:L:110:ARG:NH1	18:L:112:GLN:O	2.54	0.41
22:P:6:LEU:HD22	22:P:17:TYR:HB3	2.03	0.41
30:a:322:A:C2	30:a:340:A:C6	3.09	0.41
30:a:438:G:H2'	30:a:439:A:H8	1.86	0.41
30:a:567:U:O3'	40:k:36:LYS:NZ	2.53	0.41
30:a:665:U:H2'	30:a:666:A:H8	1.86	0.41
30:a:1418:G:N2	30:a:1579:A:C8	2.89	0.41
30:a:1668:A:H4'	30:a:1669:A:O5'	2.21	0.41
30:a:2031:A:N3	30:a:2455:G:O2'	2.51	0.41
30:a:2823:A:C6	30:a:2824:C:C4	3.08	0.41
35:f:133:ARG:HB2	35:f:134:GLU:OE2	2.20	0.41
45:p:48:ARG:O	45:p:48:ARG:HG2	2.21	0.41
46:q:79:ARG:O	46:q:81:LYS:HG2	2.20	0.41
50:u:68:LYS:HB2	50:u:68:LYS:HE2	1.85	0.41
7:A:986:U:H2'	7:A:987:G:C8	2.56	0.41
7:A:1390:U:H2'	7:A:1391:U:H6	1.86	0.41
8:B:135:LEU:HB3	8:B:139:ARG:NH2	2.36	0.41
30:a:56:A:H2'	30:a:57:C:C6	2.56	0.41
30:a:120:U:H4'	30:a:121:G:H5''	2.02	0.41
30:a:467:G:C4	30:a:468:G:C8	3.09	0.41
30:a:1734:G:H2'	30:a:1735:A:C8	2.55	0.41
30:a:1765:U:H2'	30:a:1766:G:H8	1.85	0.41
30:a:1797:G:C5	30:a:1798:U:C4	3.09	0.41
30:a:1880:U:H2'	30:a:1881:C:H6	1.85	0.41
30:a:2259:U:H2'	30:a:2260:C:H6	1.85	0.41
30:a:2766:A:H2'	30:a:2766:A:N3	2.36	0.41
33:d:2:ILE:HD11	33:d:100:LEU:HD11	2.02	0.41
2:1:23:ALA:O	2:1:24:THR:HB	2.21	0.41
5:4:8:LYS:HE3	5:4:8:LYS:HB3	1.92	0.41
7:A:553:A:H2'	7:A:554:A:H8	1.86	0.41
7:A:683:G:C6	7:A:684:U:C4	3.09	0.41
7:A:878:A:OP2	14:H:80:ARG:NH1	2.53	0.41
7:A:1004:A:N6	7:A:1026:G:H1'	2.35	0.41
7:A:1157:A:H4'	7:A:1158:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1162:C:H2'	7:A:1163:A:C8	2.54	0.41
7:A:1329:A:C5	7:A:1330:U:C5	3.09	0.41
10:D:104:ARG:HG2	10:D:104:ARG:NH1	2.36	0.41
11:E:14:LYS:HE3	11:E:14:LYS:HB2	1.65	0.41
11:E:126:LYS:HG2	11:E:128:TYR:CZ	2.55	0.41
13:G:31:MET:HE1	13:G:36:LYS:HB2	2.03	0.41
13:G:65:ALA:O	13:G:69:VAL:HG23	2.20	0.41
18:L:42:PRO:HD3	18:L:48:ALA:O	2.20	0.41
18:L:79:VAL:O	18:L:103:ASP:HB3	2.21	0.41
19:M:11:ASP:OD1	19:M:11:ASP:N	2.54	0.41
19:M:19:LEU:HD23	19:M:19:LEU:HA	1.84	0.41
24:R:65:LEU:HB3	24:R:67:LEU:HD13	2.03	0.41
25:S:40:ILE:HA	25:S:44:MET:HE1	2.03	0.41
26:T:16:LYS:HZ1	26:T:20:HIS:HB2	1.86	0.41
30:a:4:U:H2'	30:a:5:A:H8	1.86	0.41
30:a:134:G:N1	30:a:146:A:C6	2.89	0.41
30:a:319:G:H2'	30:a:320:A:O4'	2.20	0.41
30:a:738:G:C2	30:a:759:G:C6	3.08	0.41
30:a:855:G:C6	30:a:923:G:C6	3.08	0.41
30:a:863:A:H2'	30:a:864:G:H8	1.86	0.41
30:a:923:G:C2	30:a:924:G:C8	3.09	0.41
30:a:1000:A:H2'	30:a:1001:A:C8	2.56	0.41
30:a:1845:G:C6	30:a:1896:G:C6	3.08	0.41
30:a:1935:G:N2	30:a:1964:G:C4	2.89	0.41
30:a:2096:C:H2'	30:a:2097:A:C8	2.56	0.41
30:a:2204:G:C5	30:a:2221:G:C2	3.09	0.41
30:a:2228:G:H2'	30:a:2229:U:C6	2.56	0.41
30:a:2626:C:H2'	30:a:2627:G:H8	1.85	0.41
30:a:2686:G:H2'	30:a:2687:U:H6	1.85	0.41
30:a:2772:C:H2'	30:a:2773:C:C6	2.56	0.41
32:c:230:HIS:CD2	32:c:247:PRO:HB3	2.55	0.41
35:f:128:TYR:HE2	35:f:130:MET:HE2	1.86	0.41
39:j:7:MET:HA	39:j:19:VAL:O	2.21	0.41
42:m:45:ARG:HE	42:m:45:ARG:HB2	1.57	0.41
43:n:21:LEU:HD23	43:n:21:LEU:HA	1.80	0.41
46:q:28:ALA:CB	46:q:31:GLU:HG2	2.51	0.41
54:y:24:LEU:HD11	54:y:54:MET:SD	2.61	0.41
7:A:506:G:C6	7:A:507:C:N4	2.89	0.41
7:A:1384:C:C2	7:A:1385:G:C8	3.09	0.41
9:C:9:GLY:HA3	20:N:89:MET:SD	2.61	0.41
9:C:21:THR:O	9:C:21:THR:HG23	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:9:LEU:O	10:D:13:ARG:HG3	2.21	0.41
11:E:19:ASN:OD1	11:E:20:ARG:N	2.53	0.41
15:I:100:LYS:HB3	15:I:100:LYS:HE3	1.77	0.41
16:J:59:LYS:HG3	16:J:62:ARG:HH12	1.86	0.41
30:a:241:A:H2	30:a:242:G:N2	2.19	0.41
30:a:297:G:C6	30:a:342:A:N1	2.89	0.41
30:a:489:G:C6	30:a:491:G:C2	3.09	0.41
30:a:599:A:C6	30:a:659:G:O6	2.74	0.41
30:a:669:G:N2	30:a:801:G:H1	2.18	0.41
30:a:738:G:C6	30:a:739:A:C2	3.08	0.41
30:a:859:G:HO2'	30:a:860:U:P	2.44	0.41
30:a:1197:G:N3	30:a:1198:U:C5	2.89	0.41
30:a:1361:G:C6	30:a:1371:G:N2	2.89	0.41
30:a:1817:G:C6	30:a:1818:U:C5	3.08	0.41
30:a:1827:U:H2'	30:a:1828:G:O4'	2.21	0.41
30:a:2096:C:H2'	30:a:2097:A:H8	1.86	0.41
30:a:2412:A:H2'	30:a:2413:G:O4'	2.20	0.41
33:d:40:LEU:HD23	33:d:40:LEU:HA	1.77	0.41
34:e:164:LEU:HD23	34:e:164:LEU:HA	1.84	0.41
36:g:38:ASN:ND2	36:g:64:GLN:OE1	2.54	0.41
36:g:134:LYS:HB3	36:g:134:LYS:HE3	1.81	0.41
39:j:116:ILE:HD12	39:j:116:ILE:HA	1.89	0.41
41:l:105:MET:HE3	41:l:105:MET:HB2	1.84	0.41
41:l:118:LYS:HE2	41:l:118:LYS:HB2	1.90	0.41
53:x:21:LEU:HA	53:x:21:LEU:HD23	1.71	0.41
7:A:41:G:C2	7:A:42:G:C5	3.09	0.40
7:A:89:U:C4	7:A:90:C:C4	3.09	0.40
7:A:155:A:N6	7:A:167:A:N6	2.69	0.40
7:A:262:A:H2'	7:A:263:A:C8	2.56	0.40
7:A:525:C:H2'	7:A:526:C:C6	2.56	0.40
7:A:626:G:C2	7:A:627:G:C4	3.09	0.40
7:A:642:A:C6	7:A:643:C:C4	3.10	0.40
7:A:711:G:H2'	7:A:712:A:H8	1.86	0.40
7:A:773:G:C6	7:A:807:A:N6	2.89	0.40
7:A:826:C:H2'	7:A:827:U:C6	2.56	0.40
7:A:1005:A:C2	7:A:1006:G:H1'	2.56	0.40
7:A:1118:U:H1'	7:A:1179:A:C4	2.57	0.40
21:O:71:LYS:HG3	21:O:78:TYR:CD2	2.57	0.40
30:a:467:G:C2	30:a:468:G:C8	3.08	0.40
30:a:579:G:C6	30:a:1262:A:N6	2.89	0.40
30:a:632:A:H2'	30:a:633:A:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:700:G:O2'	30:a:1632:A:N3	2.49	0.40
30:a:796:C:H2'	30:a:797:G:H8	1.86	0.40
30:a:974:G:C5	30:a:1186:G:C2	3.08	0.40
30:a:1296:G:H2'	30:a:1297:C:H6	1.87	0.40
30:a:1316:U:H2'	30:a:1317:G:H8	1.85	0.40
30:a:1658:C:H2'	30:a:1659:G:H8	1.86	0.40
30:a:1713:A:N6	30:a:1746:A:N1	2.69	0.40
30:a:1831:G:H2'	30:a:1832:C:C6	2.56	0.40
30:a:1841:U:N3	30:a:1842:G:N7	2.68	0.40
30:a:1844:C:C2	30:a:1845:G:C8	3.09	0.40
30:a:1967:C:C4	30:a:1968:G:C5	3.09	0.40
30:a:2292:U:H2'	30:a:2293:G:C8	2.56	0.40
30:a:2522:U:O2'	30:a:2647:U:OP1	2.25	0.40
42:m:60:VAL:O	42:m:64:ARG:HG3	2.21	0.40
45:p:95:LEU:HD21	45:p:109:LEU:HD13	2.03	0.40
7:A:47:C:O4'	7:A:365:U:N3	2.54	0.40
7:A:582:C:C2	7:A:583:A:C8	3.09	0.40
7:A:681:A:N6	7:A:710:G:O6	2.54	0.40
7:A:1308:U:H2'	7:A:1309:G:H8	1.86	0.40
11:E:146:ASN:OD1	11:E:146:ASN:C	2.63	0.40
20:N:19:LYS:HG2	20:N:20:TYR:CD1	2.55	0.40
23:Q:28:PHE:CE1	23:Q:39:LYS:HE2	2.56	0.40
24:R:33:ILE:HG22	24:R:34:THR:O	2.20	0.40
30:a:181:A:C2	30:a:182:A:C5	3.10	0.40
30:a:244:A:C2	30:a:255:A:C4	3.09	0.40
30:a:1310:G:N2	30:a:1313:U:C4	2.90	0.40
30:a:1571:A:H2'	30:a:1572:A:C8	2.57	0.40
30:a:2068:U:O4	30:a:2430:A:N7	2.54	0.40
30:a:2260:C:C2	30:a:2261:C:C5	3.09	0.40
30:a:2553:G:H5''	30:a:2554:U:OP2	2.21	0.40
30:a:2796:U:C4	30:a:2798:U:C4	3.10	0.40
36:g:43:VAL:HG12	36:g:52:PHE:CD1	2.56	0.40
42:m:77:ALA:O	42:m:81:ASN:ND2	2.54	0.40
44:o:51:ARG:HE	44:o:53:ARG:HH12	1.68	0.40
45:p:9:ILE:HD13	45:p:9:ILE:HA	1.74	0.40
46:q:25:LEU:H	46:q:94:THR:HG21	1.86	0.40
54:y:56:LYS:O	54:y:56:LYS:HG3	2.20	0.40
1:0:34:LEU:HA	1:0:34:LEU:HD23	1.80	0.40
7:A:949:A:C6	7:A:1233:G:N1	2.89	0.40
7:A:1031:C:O2'	7:A:1032:G:N1	2.49	0.40
7:A:1179:A:H2'	7:A:1180:A:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1251:A:H2'	7:A:1252:A:C8	2.56	0.40
15:I:29:VAL:HG13	15:I:64:TYR:HA	2.03	0.40
30:a:607:U:H5	30:a:620:G:C4	2.39	0.40
30:a:628:G:C6	30:a:636:G:C2	3.09	0.40
30:a:640:C:H2'	30:a:641:U:C6	2.56	0.40
30:a:1183:U:H2'	30:a:1184:U:C6	2.56	0.40
30:a:1369:G:N3	30:a:1810:A:H2	2.20	0.40
30:a:1663:G:C6	30:a:1998:A:N6	2.90	0.40
30:a:2191:A:H2'	30:a:2192:U:C6	2.56	0.40
30:a:2557:G:H2'	30:a:2558:C:H6	1.87	0.40
30:a:2595:G:N1	30:a:2599:G:C6	2.90	0.40
39:j:17:ARG:NE	39:j:47:ILE:HD11	2.37	0.40
4:3:24:ARG:NH2	30:a:2742:G:OP2	2.47	0.40
4:3:33:HIS:O	4:3:35:GLN:HG3	2.21	0.40
6:5:17:G:H4'	6:5:18:G:C5'	2.52	0.40
7:A:706:A:C6	7:A:707:U:C4	3.09	0.40
9:C:12:LEU:HA	9:C:12:LEU:HD23	1.78	0.40
23:Q:25:ILE:HD11	23:Q:61:ILE:HD11	2.03	0.40
30:a:10:A:C6	30:a:2800:A:C2	3.09	0.40
30:a:77:G:C5	30:a:110:G:C2	3.09	0.40
30:a:273:G:N1	30:a:365:U:N3	2.69	0.40
30:a:323:C:N4	30:a:333:G:N7	2.68	0.40
30:a:582:A:C4	30:a:583:G:C8	3.10	0.40
30:a:608:A:H2'	30:a:609:A:H8	1.86	0.40
30:a:949:G:C6	30:a:969:G:N1	2.90	0.40
30:a:1419:A:C5	30:a:1579:A:C6	3.09	0.40
30:a:2519:U:C4	30:a:2542:A:C5	3.10	0.40
31:b:109:A:C6	31:b:110:C:C4	3.10	0.40
47:r:73:LYS:O	47:r:106:VAL:HG12	2.21	0.40
1:0:14:SER:OG	1:0:48:ILE:HG22	2.21	0.40
6:5:21:A:H62	6:5:46:A:H2'	1.86	0.40
7:A:214:C:H2'	7:A:215:C:C6	2.57	0.40
7:A:236:A:C2	7:A:237:G:C5	3.10	0.40
7:A:398:U:H2'	7:A:399:G:C8	2.56	0.40
7:A:829:G:C6	7:A:858:G:N2	2.90	0.40
7:A:1372:U:OP1	15:I:73:SER:OG	2.36	0.40
7:A:1384:C:H2'	7:A:1385:G:H8	1.85	0.40
7:A:1405:G:C2	7:A:1406:U:C4	3.09	0.40
7:A:1513:A:C2	7:A:1514:G:C5	3.09	0.40
16:J:7:ARG:HB2	16:J:101:SER:HB3	2.04	0.40
19:M:12:HIS:ND1	19:M:12:HIS:N	2.66	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:O:67:LEU:HD23	21:O:67:LEU:HA	1.89	0.40
26:T:26:SER:O	26:T:30:THR:OG1	2.37	0.40
30:a:136:G:C6	30:a:144:A:C6	3.10	0.40
30:a:303:G:C6	30:a:315:G:N1	2.90	0.40
30:a:875:G:H2'	30:a:876:C:C6	2.56	0.40
30:a:1394:U:C4	30:a:1395:A:C6	3.10	0.40
30:a:1429:G:C2	30:a:1430:G:C5	3.10	0.40
30:a:1462:C:O2'	30:a:2702:G:O2'	2.37	0.40
30:a:1534:U:H1'	30:a:1538:G:N2	2.37	0.40
30:a:1843:C:C2	30:a:1844:C:C5	3.10	0.40
30:a:1933:G:C6	30:a:1934:C:C4	3.10	0.40
30:a:2039:U:H2'	30:a:2040:G:H8	1.86	0.40
30:a:2073:C:N3	30:a:2437:G:N1	2.69	0.40
30:a:2745:C:H2'	30:a:2746:U:H6	1.85	0.40
41:l:1:MET:HB3	41:l:1:MET:HE3	1.74	0.40
50:u:9:ARG:HE	50:u:9:ARG:HB3	1.69	0.40
50:u:24:ASN:OD1	50:u:24:ASN:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
1	0	49/55 (89%)	47 (96%)	2 (4%)	0	100	100
2	1	44/46 (96%)	40 (91%)	3 (7%)	1 (2%)	5	18
3	2	62/65 (95%)	51 (82%)	11 (18%)	0	100	100
4	3	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
5	4	56/70 (80%)	54 (96%)	2 (4%)	0	100	100
8	B	222/241 (92%)	210 (95%)	12 (5%)	0	100	100
9	C	204/233 (88%)	200 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	D	191/206 (93%)	189 (99%)	2 (1%)	0	100	100
11	E	154/167 (92%)	152 (99%)	2 (1%)	0	100	100
12	F	101/135 (75%)	100 (99%)	1 (1%)	0	100	100
13	G	151/179 (84%)	144 (95%)	7 (5%)	0	100	100
14	H	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
15	I	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
16	J	96/103 (93%)	92 (96%)	3 (3%)	1 (1%)	12	37
17	K	115/129 (89%)	110 (96%)	5 (4%)	0	100	100
18	L	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
19	M	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
20	N	98/101 (97%)	98 (100%)	0	0	100	100
21	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
22	P	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
23	Q	77/84 (92%)	74 (96%)	3 (4%)	0	100	100
24	R	52/75 (69%)	50 (96%)	1 (2%)	1 (2%)	6	22
25	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
26	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
27	U	68/71 (96%)	68 (100%)	0	0	100	100
32	c	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
33	d	206/209 (99%)	189 (92%)	16 (8%)	1 (0%)	24	53
34	e	199/201 (99%)	183 (92%)	16 (8%)	0	100	100
35	f	175/179 (98%)	164 (94%)	11 (6%)	0	100	100
36	g	174/177 (98%)	162 (93%)	11 (6%)	1 (1%)	21	50
37	h	39/149 (26%)	31 (80%)	8 (20%)	0	100	100
38	i	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
39	j	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
40	k	142/144 (99%)	132 (93%)	9 (6%)	1 (1%)	18	46
41	l	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
42	m	116/127 (91%)	108 (93%)	7 (6%)	1 (1%)	14	40
43	n	114/117 (97%)	103 (90%)	10 (9%)	1 (1%)	14	40
44	o	112/115 (97%)	98 (88%)	14 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	p	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
46	q	101/103 (98%)	88 (87%)	12 (12%)	1 (1%)	12	37
47	r	108/110 (98%)	101 (94%)	7 (6%)	0	100	100
48	s	95/100 (95%)	86 (90%)	9 (10%)	0	100	100
49	t	100/104 (96%)	86 (86%)	14 (14%)	0	100	100
50	u	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
51	v	76/85 (89%)	74 (97%)	2 (3%)	0	100	100
52	w	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
53	x	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
54	y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
55	z	54/57 (95%)	48 (89%)	6 (11%)	0	100	100
All	All	5465/5913 (92%)	5163 (94%)	293 (5%)	9 (0%)	44	71

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	45	SER
40	k	29	LYS
16	J	57	VAL
33	d	149	ASN
46	q	45	GLU
36	g	118	PRO
24	R	22	ASP
42	m	107	ASN
43	n	3	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	
1	0	46/49 (94%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	38/38 (100%)	35 (92%)	3 (8%)	11	33
3	2	51/52 (98%)	49 (96%)	2 (4%)	28	61
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	55 (100%)	0	100	100
8	B	186/199 (94%)	184 (99%)	2 (1%)	65	86
9	C	170/190 (90%)	164 (96%)	6 (4%)	32	64
10	D	163/173 (94%)	160 (98%)	3 (2%)	51	79
11	E	119/126 (94%)	116 (98%)	3 (2%)	42	73
12	F	90/116 (78%)	90 (100%)	0	100	100
13	G	126/147 (86%)	126 (100%)	0	100	100
14	H	104/105 (99%)	103 (99%)	1 (1%)	68	87
15	I	105/107 (98%)	105 (100%)	0	100	100
16	J	86/90 (96%)	84 (98%)	2 (2%)	44	74
17	K	90/99 (91%)	88 (98%)	2 (2%)	45	75
18	L	103/104 (99%)	97 (94%)	6 (6%)	18	47
19	M	93/96 (97%)	92 (99%)	1 (1%)	65	86
20	N	83/84 (99%)	83 (100%)	0	100	100
21	O	76/77 (99%)	75 (99%)	1 (1%)	61	84
22	P	65/65 (100%)	65 (100%)	0	100	100
23	Q	73/78 (94%)	71 (97%)	2 (3%)	39	71
24	R	47/65 (72%)	47 (100%)	0	100	100
25	S	72/79 (91%)	70 (97%)	2 (3%)	38	70
26	T	65/66 (98%)	63 (97%)	2 (3%)	35	67
27	U	60/61 (98%)	59 (98%)	1 (2%)	53	80
32	c	216/218 (99%)	211 (98%)	5 (2%)	44	74
33	d	163/163 (100%)	157 (96%)	6 (4%)	30	63
34	e	165/165 (100%)	161 (98%)	4 (2%)	43	73
35	f	148/150 (99%)	144 (97%)	4 (3%)	39	71
36	g	137/138 (99%)	135 (98%)	2 (2%)	57	82
37	h	32/114 (28%)	30 (94%)	2 (6%)	16	43
38	i	116/116 (100%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	j	104/104 (100%)	100 (96%)	4 (4%)	29	62
40	k	103/103 (100%)	100 (97%)	3 (3%)	37	69
41	l	109/109 (100%)	103 (94%)	6 (6%)	19	49
42	m	98/103 (95%)	96 (98%)	2 (2%)	48	77
43	n	86/87 (99%)	83 (96%)	3 (4%)	32	64
44	o	99/100 (99%)	96 (97%)	3 (3%)	36	68
45	p	89/90 (99%)	88 (99%)	1 (1%)	65	86
46	q	84/84 (100%)	83 (99%)	1 (1%)	63	85
47	r	93/93 (100%)	89 (96%)	4 (4%)	26	58
48	s	83/84 (99%)	81 (98%)	2 (2%)	43	73
49	t	83/85 (98%)	80 (96%)	3 (4%)	31	63
50	u	78/78 (100%)	75 (96%)	3 (4%)	29	62
51	v	58/63 (92%)	55 (95%)	3 (5%)	21	50
52	w	67/68 (98%)	61 (91%)	6 (9%)	9	27
53	x	54/55 (98%)	54 (100%)	0	100	100
54	y	48/49 (98%)	46 (96%)	2 (4%)	26	59
55	z	47/48 (98%)	44 (94%)	3 (6%)	16	43
All	All	4560/4829 (94%)	4449 (98%)	111 (2%)	43	73

All (111) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	1	4	THR
2	1	12	ARG
2	1	43	THR
3	2	55	LEU
3	2	64	TYR
8	B	4	VAL
8	B	57	LEU
9	C	33	LEU
9	C	76	VAL
9	C	111	LEU
9	C	139	GLN
9	C	144	LEU
9	C	186	THR
10	D	138	SER

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Mol	Chain	Res	Type
10	D	173	VAL
10	D	179	GLU
11	E	16	ILE
11	E	24	THR
11	E	164	ILE
14	H	27	MET
16	J	36	VAL
16	J	90	LEU
17	K	30	THR
17	K	40	ASN
18	L	3	THR
18	L	5	ASN
18	L	39	THR
18	L	40	THR
18	L	89	ASP
18	L	98	VAL
19	M	45	ILE
21	O	11	ILE
23	Q	13	VAL
23	Q	78	VAL
25	S	28	LYS
25	S	79	THR
26	T	23	SER
26	T	59	ASP
27	U	42	THR
32	c	37	ASN
32	c	77	VAL
32	c	118	SER
32	c	160	THR
32	c	168	ASP
33	d	17	GLU
33	d	108	ASP
33	d	110	THR
33	d	113	SER
33	d	129	THR
33	d	199	SER
34	e	4	VAL
34	e	22	ASP
34	e	70	SER
34	e	153	LEU
35	f	66	LEU
35	f	69	LYS

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Mol	Chain	Res	Type
35	f	137	ILE
35	f	165	GLU
36	g	36	THR
36	g	60	ASP
37	h	9	VAL
37	h	28	ASN
39	j	14	SER
39	j	47	ILE
39	j	73	ASP
39	j	93	GLN
40	k	46	VAL
40	k	74	THR
40	k	118	THR
41	l	7	THR
41	l	24	THR
41	l	27	SER
41	l	57	VAL
41	l	82	MET
41	l	135	VAL
42	m	27	SER
42	m	98	LEU
43	n	35	ILE
43	n	36	TYR
43	n	49	VAL
44	o	75	GLN
44	o	83	SER
44	o	92	VAL
45	p	31	VAL
46	q	1	MET
47	r	66	ILE
47	r	74	ILE
47	r	85	ILE
47	r	86	MET
48	s	79	ASP
48	s	80	TRP
49	t	18	ASP
49	t	28	VAL
49	t	31	SER
50	u	3	THR
50	u	62	THR
50	u	65	VAL
51	v	53	CYS

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Mol	Chain	Res	Type
51	v	64	ASP
51	v	71	VAL
52	w	13	VAL
52	w	40	VAL
52	w	42	SER
52	w	51	VAL
52	w	56	MET
52	w	59	ILE
54	y	41	THR
54	y	55	VAL
55	z	9	THR
55	z	23	THR
55	z	39	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
5	4	20	ASN
5	4	65	ASN
10	D	116	GLN
12	F	3	HIS
16	J	70	HIS
17	K	38	GLN
20	N	4	GLN
20	N	71	HIS
24	R	31	ASN
26	T	55	GLN
26	T	68	HIS
26	T	78	ASN
32	c	232	HIS
33	d	32	ASN
34	e	46	GLN
34	e	90	GLN
36	g	38	ASN
36	g	139	GLN
38	i	80	HIS
39	j	29	HIS
39	j	82	ASN
40	k	104	GLN
42	m	13	ASN
42	m	81	ASN
45	p	20	GLN

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Mol	Chain	Res	Type
47	r	9	HIS
47	r	15	GLN
47	r	60	HIS
49	t	53	ASN
49	t	99	ASN
51	v	46	HIS
52	w	36	HIS
54	y	34	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	X	5/6 (83%)	0	0
30	a	2749/2753 (99%)	347 (12%)	0
31	b	118/120 (98%)	10 (8%)	0
6	5	74/75 (98%)	14 (18%)	1 (1%)
7	A	1516/1542 (98%)	177 (11%)	3 (0%)
All	All	4462/4496 (99%)	548 (12%)	4 (0%)

All (548) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	5	9	C
6	5	13	U
6	5	16	U
6	5	17	G
6	5	18	G
6	5	19	C
6	5	20	U
6	5	21	A
6	5	35	C
6	5	46	A
6	5	48	G
6	5	57	A
6	5	73	C
6	5	75	A
7	A	4	U
7	A	7	A
7	A	8	A
7	A	9	G
7	A	22	G

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Mol	Chain	Res	Type
7	A	32	A
7	A	39	G
7	A	47	C
7	A	48	C
7	A	51	A
7	A	58	C
7	A	71	A
7	A	81	A
7	A	83	C
7	A	85	U
7	A	86	G
7	A	87	C
7	A	91	U
7	A	95	C
7	A	108	G
7	A	122	G
7	A	130	A
7	A	131	A
7	A	144	G
7	A	182	A
7	A	183	C
7	A	197	A
7	A	202	G
7	A	240	G
7	A	245	U
7	A	247	G
7	A	251	G
7	A	266	G
7	A	267	C
7	A	281	G
7	A	289	G
7	A	321	A
7	A	328	C
7	A	347	G
7	A	352	C
7	A	354	G
7	A	367	U
7	A	372	C
7	A	406	G
7	A	411	A
7	A	412	A
7	A	413	G

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Mol	Chain	Res	Type
7	A	414	A
7	A	415	A
7	A	421	U
7	A	422	C
7	A	423	G
7	A	429	U
7	A	446	G
7	A	453	G
7	A	457	G
7	A	458	U
7	A	467	U
7	A	468	A
7	A	481	G
7	A	484	G
7	A	486	U
7	A	497	G
7	A	511	C
7	A	512	U
7	A	518	C
7	A	521	G
7	A	524	G
7	A	531	U
7	A	532	A
7	A	547	A
7	A	564	C
7	A	572	A
7	A	573	A
7	A	575	G
7	A	576	C
7	A	577	G
7	A	596	A
7	A	653	U
7	A	665	A
7	A	666	G
7	A	723	U
7	A	724	G
7	A	734	G
7	A	747	A
7	A	748	G
7	A	755	G
7	A	760	G
7	A	777	A

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Mol	Chain	Res	Type
7	A	793	U
7	A	794	A
7	A	802	A
7	A	815	A
7	A	817	C
7	A	885	G
7	A	890	G
7	A	900	A
7	A	914	A
7	A	934	C
7	A	935	A
7	A	960	U
7	A	966	2MG
7	A	967	5MC
7	A	969	A
7	A	975	A
7	A	976	G
7	A	977	A
7	A	992	U
7	A	993	G
7	A	994	A
7	A	996	A
7	A	1003	G
7	A	1004	A
7	A	1008	U
7	A	1027	C
7	A	1029	U
7	A	1031	C
7	A	1032	G
7	A	1033	G
7	A	1034	G
7	A	1036	A
7	A	1039	G
7	A	1044	A
7	A	1053	G
7	A	1065	U
7	A	1085	U
7	A	1094	G
7	A	1095	U
7	A	1099	G
7	A	1101	A
7	A	1137	C

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Mol	Chain	Res	Type
7	A	1138	G
7	A	1139	G
7	A	1159	U
7	A	1184	G
7	A	1196	A
7	A	1197	A
7	A	1213	A
7	A	1227	A
7	A	1228	C
7	A	1238	A
7	A	1260	G
7	A	1280	A
7	A	1286	U
7	A	1287	A
7	A	1300	G
7	A	1305	G
7	A	1320	C
7	A	1323	G
7	A	1336	C
7	A	1338	G
7	A	1353	G
7	A	1363	A
7	A	1364	U
7	A	1370	G
7	A	1378	C
7	A	1379	G
7	A	1398	A
7	A	1402	4OC
7	A	1406	U
7	A	1419	G
7	A	1441	A
7	A	1451	U
7	A	1452	C
7	A	1453	G
7	A	1487	G
7	A	1492	A
7	A	1497	G
7	A	1499	A
7	A	1503	A
7	A	1506	U
7	A	1517	G
7	A	1519	MA6

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Mol	Chain	Res	Type
7	A	1520	C
7	A	1529	G
7	A	1530	G
7	A	1534	A
30	a	10	A
30	a	14	A
30	a	15	G
30	a	34	U
30	a	42	A
30	a	45	G
30	a	51	G
30	a	63	A
30	a	71	A
30	a	74	A
30	a	75	G
30	a	84	A
30	a	101	A
30	a	102	U
30	a	118	A
30	a	120	U
30	a	139	U
30	a	142	A
30	a	149	A
30	a	163	C
30	a	165	A
30	a	181	A
30	a	196	A
30	a	199	A
30	a	204	A
30	a	215	G
30	a	216	A
30	a	221	A
30	a	222	A
30	a	228	C
30	a	248	G
30	a	253	C
30	a	272	A
30	a	278	A
30	a	279	A
30	a	282	A
30	a	289	G
30	a	291	G

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Mol	Chain	Res	Type
30	a	311	A
30	a	329	G
30	a	330	A
30	a	331	C
30	a	345	A
30	a	361	G
30	a	362	A
30	a	386	G
30	a	396	G
30	a	405	U
30	a	411	G
30	a	412	A
30	a	435	C
30	a	451	U
30	a	457	A
30	a	464	U
30	a	465	G
30	a	481	G
30	a	489	G
30	a	490	C
30	a	491	G
30	a	504	A
30	a	505	A
30	a	509	C
30	a	529	A
30	a	530	G
30	a	531	C
30	a	532	A
30	a	533	G
30	a	544	C
30	a	545	U
30	a	546	U
30	a	548	G
30	a	549	G
30	a	563	A
30	a	572	A
30	a	573	U
30	a	575	A
30	a	603	A
30	a	613	A
30	a	615	U
30	a	627	A

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Mol	Chain	Res	Type
30	a	634	C
30	a	637	A
30	a	645	C
30	a	647	G
30	a	654	A
30	a	662	G
30	a	664	G
30	a	686	U
30	a	717	C
30	a	729	G
30	a	730	A
30	a	747	5MU
30	a	748	G
30	a	764	A
30	a	765	C
30	a	775	G
30	a	776	G
30	a	782	A
30	a	784	G
30	a	785	G
30	a	793	A
30	a	800	A
30	a	805	G
30	a	806	C
30	a	807	U
30	a	811	U
30	a	812	C
30	a	827	U
30	a	828	U
30	a	846	U
30	a	858	G
30	a	859	G
30	a	883	G
30	a	884	U
30	a	888	C
30	a	890	C
30	a	891	G
30	a	895	U
30	a	896	A
30	a	897	C
30	a	900	A
30	a	910	A

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Mol	Chain	Res	Type
30	a	931	U
30	a	946	C
30	a	957	C
30	a	961	C
30	a	973	A
30	a	974	G
30	a	983	A
30	a	989	G
30	a	990	A
30	a	996	A
30	a	1005	C
30	a	1008	A
30	a	1012	U
30	a	1013	C
30	a	1021	A
30	a	1022	G
30	a	1023	U
30	a	1026	G
30	a	1027	A
30	a	1033	U
30	a	1047	G
30	a	1111	A
30	a	1112	G
30	a	1132	U
30	a	1133	A
30	a	1135	C
30	a	1142	A
30	a	1204	A
30	a	1212	G
30	a	1247	A
30	a	1248	G
30	a	1253	A
30	a	1255	U
30	a	1256	G
30	a	1271	G
30	a	1272	A
30	a	1273	U
30	a	1300	G
30	a	1301	A
30	a	1346	G
30	a	1352	U
30	a	1364	G

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Mol	Chain	Res	Type
30	a	1365	A
30	a	1379	U
30	a	1383	A
30	a	1395	A
30	a	1416	G
30	a	1417	C
30	a	1419	A
30	a	1420	A
30	a	1427	A
30	a	1428	C
30	a	1452	G
30	a	1460	U
30	a	1482	G
30	a	1493	C
30	a	1509	A
30	a	1510	G
30	a	1515	A
30	a	1524	G
30	a	1535	A
30	a	1536	C
30	a	1537	G
30	a	1566	A
30	a	1569	A
30	a	1578	U
30	a	1581	G
30	a	1583	A
30	a	1584	U
30	a	1585	C
30	a	1608	A
30	a	1647	U
30	a	1648	U
30	a	1664	A
30	a	1674	G
30	a	1675	C
30	a	1694	C
30	a	1698	A
30	a	1699	G
30	a	1715	G
30	a	1729	U
30	a	1730	C
30	a	1733	G
30	a	1738	G

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Mol	Chain	Res	Type
30	a	1756	G
30	a	1758	U
30	a	1761	C
30	a	1764	C
30	a	1773	A
30	a	1781	U
30	a	1784	A
30	a	1791	A
30	a	1800	C
30	a	1801	A
30	a	1808	A
30	a	1816	C
30	a	1819	A
30	a	1828	G
30	a	1829	A
30	a	1836	C
30	a	1839	G
30	a	1847	A
30	a	1858	A
30	a	1870	C
30	a	1871	A
30	a	1873	G
30	a	1905	C
30	a	1906	G
30	a	1913	A
30	a	1929	G
30	a	1930	G
30	a	1936	A
30	a	1938	A
30	a	1939	5MU
30	a	1940	U
30	a	1955	U
30	a	1963	U
30	a	1966	A
30	a	1967	C
30	a	1970	A
30	a	1971	U
30	a	1972	G
30	a	1991	U
30	a	1993	U
30	a	2023	C
30	a	2030	6MZ

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Mol	Chain	Res	Type
30	a	2031	A
30	a	2033	A
30	a	2043	C
30	a	2055	C
30	a	2056	G
30	a	2060	A
30	a	2061	G
30	a	2062	A
30	a	2069	G7M
30	a	2093	G
30	a	2198	A
30	a	2203	U
30	a	2204	G
30	a	2211	A
30	a	2225	A
30	a	2238	G
30	a	2239	G
30	a	2283	C
30	a	2284	A
30	a	2287	A
30	a	2288	A
30	a	2305	U
30	a	2308	G
30	a	2322	A
30	a	2325	G
30	a	2333	A
30	a	2345	G
30	a	2347	C
30	a	2361	G
30	a	2365	G
30	a	2377	A
30	a	2383	G
30	a	2385	C
30	a	2402	U
30	a	2403	C
30	a	2425	A
30	a	2428	G
30	a	2429	G
30	a	2435	A
30	a	2440	C
30	a	2441	U
30	a	2448	A

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Mol	Chain	Res	Type
30	a	2450	A
30	a	2457	PSU
30	a	2476	A
30	a	2491	U
30	a	2492	U
30	a	2498	OMC
30	a	2502	G
30	a	2503	2MA
30	a	2504	PSU
30	a	2505	G
30	a	2518	A
30	a	2520	C
30	a	2525	G
30	a	2529	G
30	a	2535	G
30	a	2547	A
30	a	2566	A
30	a	2567	G
30	a	2572	A
30	a	2573	C
30	a	2576	G
30	a	2602	A
30	a	2609	U
30	a	2613	U
30	a	2629	U
30	a	2630	G
30	a	2663	G
30	a	2682	A
30	a	2689	U
30	a	2690	U
30	a	2714	G
30	a	2724	U
30	a	2726	A
30	a	2729	G
30	a	2733	A
30	a	2744	G
30	a	2748	A
30	a	2765	A
30	a	2776	A
30	a	2778	A
30	a	2779	U
30	a	2791	G

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Mol	Chain	Res	Type
30	a	2798	U
30	a	2800	A
30	a	2820	A
30	a	2821	A
30	a	2826	A
30	a	2835	A
30	a	2836	U
30	a	2848	G
30	a	2849	U
30	a	2861	U
30	a	2872	A
30	a	2873	A
30	a	2879	A
30	a	2880	C
30	a	2883	A
31	b	13	G
31	b	35	C
31	b	36	C
31	b	56	G
31	b	67	G
31	b	89	U
31	b	90	C
31	b	99	A
31	b	105	G
31	b	109	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	5	17	G
7	A	90	C
7	A	1026	G
7	A	1035	A

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

38 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
7	MA6	A	1519	7	23,26,27	1.53	5 (21%)	33,38,41	2.55	15 (45%)
30	5MU	a	1939	30	19,22,23	0.33	0	27,32,35	0.34	0
30	6MZ	a	2030	30	22,25,26	3.88	10 (45%)	29,36,39	2.76	14 (48%)
30	PSU	a	2504	30	18,21,22	1.11	3 (16%)	21,30,33	1.96	4 (19%)
30	PSU	a	746	30	18,21,22	1.05	3 (16%)	21,30,33	1.81	5 (23%)
30	OMG	a	2251	30,6	23,26,27	0.38	0	32,38,41	0.83	2 (6%)
30	OMU	a	2552	30	19,22,23	3.00	8 (42%)	25,31,34	1.91	5 (20%)
6	PSU	5	54	6	18,21,22	1.09	2 (11%)	21,30,33	1.93	5 (23%)
33	MEQ	d	150	33	8,9,10	0.96	0	5,10,12	1.05	1 (20%)
7	2MG	A	1207	7	23,26,27	0.35	0	33,38,41	0.42	0
7	UR3	A	1498	7	19,22,23	2.60	5 (26%)	26,32,35	1.64	4 (15%)
30	5MC	a	1962	30	19,22,23	0.94	1 (5%)	26,32,35	0.67	0
30	PSU	a	1911	30	18,21,22	1.07	2 (11%)	21,30,33	1.96	4 (19%)
30	PSU	a	2457	30	18,21,22	1.02	3 (16%)	21,30,33	1.83	4 (19%)
30	OMC	a	2498	30	19,22,23	0.39	0	25,31,34	0.75	0
7	2MG	A	1516	7	23,26,27	0.34	0	33,38,41	0.46	0
30	5MU	a	747	30	19,22,23	0.28	0	27,32,35	0.49	0
30	2MG	a	1835	30	23,26,27	0.35	0	33,38,41	0.59	0
30	H2U	a	2449	30	18,21,22	0.73	1 (5%)	19,30,33	0.85	1 (5%)
30	PSU	a	2580	30	18,21,22	1.13	3 (16%)	21,30,33	2.11	5 (23%)
6	4OC	5	32	6	20,23,24	3.40	8 (40%)	25,32,35	0.97	1 (4%)
30	2MG	a	2445	30	23,26,27	0.34	0	33,38,41	0.64	1 (3%)
30	G7M	a	2069	30	23,26,27	2.98	9 (39%)	34,39,42	2.20	10 (29%)
30	1MG	a	745	30	23,26,27	2.86	8 (34%)	33,39,42	1.74	6 (18%)
7	2MG	A	966	7	23,26,27	0.35	0	33,38,41	0.48	0
30	PSU	a	2604	30	18,21,22	1.08	3 (16%)	21,30,33	2.03	5 (23%)
7	4OC	A	1402	7	20,23,24	3.33	8 (40%)	25,32,35	0.86	1 (4%)
7	5MC	A	1407	7	19,22,23	0.93	1 (5%)	26,32,35	0.59	0
7	5MC	A	967	7	19,22,23	0.86	1 (5%)	26,32,35	0.53	0
30	PSU	a	2605	30	18,21,22	1.10	2 (11%)	21,30,33	2.14	5 (23%)
6	5MU	5	53	6	19,22,23	0.24	0	27,32,35	0.39	0
7	PSU	A	516	7	18,21,22	1.06	3 (16%)	21,30,33	1.86	5 (23%)
30	2MA	a	2503	30	22,25,26	0.83	1 (4%)	32,37,40	1.19	3 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
30	PSU	a	955	30	18,21,22	1.07	3 (16%)	21,30,33	1.87	4 (19%)
7	MA6	A	1518	7	23,26,27	1.52	4 (17%)	33,38,41	2.65	14 (42%)
30	6MZ	a	1618	30	22,25,26	2.40	6 (27%)	29,36,39	2.58	12 (41%)
7	G7M	A	527	7	23,26,27	2.91	9 (39%)	34,39,42	2.26	10 (29%)
30	PSU	a	1917	30	18,21,22	1.04	2 (11%)	21,30,33	1.89	4 (19%)

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
7	MA6	A	1519	7	-	6/11/29/30	0/3/3/3
30	5MU	a	1939	30	-	1/7/25/26	0/2/2/2
30	6MZ	a	2030	30	-	3/9/27/28	0/3/3/3
30	PSU	a	2504	30	-	0/7/25/26	0/2/2/2
30	PSU	a	746	30	-	0/7/25/26	0/2/2/2
30	OMG	a	2251	30,6	-	2/9/27/28	0/3/3/3
30	OMU	a	2552	30	-	1/9/27/28	0/2/2/2
6	PSU	5	54	6	-	2/7/25/26	0/2/2/2
33	MEQ	d	150	33	-	4/8/9/11	-
7	2MG	A	1207	7	-	0/9/27/28	0/3/3/3
7	UR3	A	1498	7	-	0/7/25/26	0/2/2/2
30	5MC	a	1962	30	-	4/7/25/26	0/2/2/2
30	PSU	a	1911	30	-	4/7/25/26	0/2/2/2
30	PSU	a	2457	30	-	2/7/25/26	0/2/2/2
30	OMC	a	2498	30	-	5/9/27/28	0/2/2/2
7	2MG	A	1516	7	-	0/9/27/28	0/3/3/3
30	5MU	a	747	30	-	0/7/25/26	0/2/2/2
30	2MG	a	1835	30	-	1/9/27/28	0/3/3/3
30	H2U	a	2449	30	-	0/7/38/39	0/2/2/2
30	PSU	a	2580	30	-	0/7/25/26	0/2/2/2
6	4OC	5	32	6	-	0/9/29/30	0/2/2/2
30	2MG	a	2445	30	-	2/9/27/28	0/3/3/3
30	G7M	a	2069	30	-	1/7/25/26	0/3/3/3
30	1MG	a	745	30	-	0/7/25/26	0/3/3/3
7	2MG	A	966	7	-	0/9/27/28	0/3/3/3
30	PSU	a	2604	30	-	2/7/25/26	0/2/2/2
7	4OC	A	1402	7	-	2/9/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	5MC	A	1407	7	-	0/7/25/26	0/2/2/2
7	5MC	A	967	7	-	2/7/25/26	0/2/2/2
30	PSU	a	2605	30	-	1/7/25/26	0/2/2/2
6	5MU	5	53	6	-	0/7/25/26	0/2/2/2
7	PSU	A	516	7	-	0/7/25/26	0/2/2/2
30	2MA	a	2503	30	-	3/7/25/26	0/3/3/3
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2
7	MA6	A	1518	7	-	2/11/29/30	0/3/3/3
30	6MZ	a	1618	30	-	2/9/27/28	0/3/3/3
7	G7M	A	527	7	-	0/7/25/26	0/3/3/3
30	PSU	a	1917	30	-	1/7/25/26	0/2/2/2

All (114) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2030	6MZ	C6-N6	9.71	1.45	1.34
30	a	2030	6MZ	C3'-C4'	-8.93	1.30	1.53
30	a	1618	6MZ	C6-N6	8.77	1.44	1.34
30	a	2069	G7M	C5-N7	-8.47	1.29	1.39
30	a	745	1MG	C2-N3	7.92	1.46	1.33
6	5	32	4OC	C4-N3	7.22	1.44	1.32
30	a	2552	OMU	C2-N3	7.12	1.50	1.38
7	A	1402	4OC	C4-N3	7.12	1.44	1.32
7	A	527	G7M	C5-N7	-6.97	1.31	1.39
30	a	2030	6MZ	C2'-C1'	-6.79	1.32	1.53
7	A	1498	UR3	C2-N1	6.75	1.47	1.38
7	A	527	G7M	C4-N3	6.66	1.49	1.34
6	5	32	4OC	C4-N4	6.60	1.49	1.36
6	5	32	4OC	C2-N3	6.58	1.49	1.36
7	A	1402	4OC	C4-N4	6.50	1.49	1.36
30	a	2552	OMU	C2-N1	6.42	1.48	1.38
7	A	1402	4OC	C2-N3	6.32	1.48	1.36
6	5	32	4OC	C6-C5	6.28	1.49	1.35
30	a	745	1MG	C4-N3	6.24	1.48	1.34
7	A	1402	4OC	C6-C5	6.22	1.49	1.35
30	a	745	1MG	C2-N2	6.12	1.44	1.34
30	a	2069	G7M	C4-N3	6.03	1.48	1.34
7	A	1498	UR3	C6-C5	6.02	1.49	1.35
30	a	2552	OMU	C6-C5	6.00	1.49	1.35
30	a	2030	6MZ	O4'-C4'	5.72	1.57	1.45
7	A	527	G7M	C2-N3	5.20	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2069	G7M	C2-N3	4.83	1.44	1.33
7	A	1518	MA6	C5-C4	4.52	1.47	1.39
7	A	1519	MA6	C5-C4	4.47	1.47	1.39
30	a	2030	6MZ	O4'-C1'	4.37	1.52	1.42
7	A	527	G7M	C2-N2	4.33	1.44	1.34
6	5	32	4OC	C2-N1	4.28	1.49	1.40
30	a	2069	G7M	C2-N2	4.03	1.43	1.34
7	A	1402	4OC	C2-N1	3.93	1.48	1.40
30	a	2552	OMU	C4-N3	3.88	1.45	1.38
30	a	745	1MG	C5-N7	-3.83	1.31	1.39
7	A	1498	UR3	C2-N3	3.80	1.46	1.39
7	A	1407	5MC	C5-C4	-3.79	1.41	1.44
30	a	1962	5MC	C5-C4	-3.78	1.41	1.44
6	5	32	4OC	C5-C4	3.73	1.49	1.41
7	A	1402	4OC	C5-C4	3.62	1.49	1.41
7	A	1498	UR3	O2-C2	-3.58	1.15	1.22
30	a	1618	6MZ	C5-N7	-3.54	1.32	1.39
30	a	2069	G7M	O6-C6	-3.49	1.16	1.23
7	A	527	G7M	C5-C6	3.48	1.53	1.43
7	A	967	5MC	C5-C4	-3.47	1.41	1.44
7	A	527	G7M	O6-C6	-3.44	1.17	1.23
6	5	54	PSU	C6-C5	3.38	1.39	1.35
30	a	2030	6MZ	C3'-C2'	3.35	1.62	1.53
30	a	1618	6MZ	C5-C4	-3.34	1.33	1.39
30	a	2030	6MZ	C5-C4	-3.30	1.33	1.39
7	A	1498	UR3	O4-C4	-3.22	1.16	1.23
7	A	527	G7M	C2-N1	3.21	1.45	1.37
6	5	32	4OC	C6-N1	3.20	1.45	1.38
30	a	2069	G7M	CN7-N7	-3.18	1.41	1.46
7	A	1402	4OC	C6-N1	3.16	1.45	1.38
30	a	1911	PSU	C6-C5	3.12	1.38	1.35
30	a	2069	G7M	C2-N1	3.08	1.45	1.37
7	A	516	PSU	C6-C5	3.06	1.38	1.35
7	A	527	G7M	CN7-N7	-3.02	1.41	1.46
30	a	2030	6MZ	C5-N7	-3.02	1.33	1.39
30	a	1917	PSU	C6-C5	2.94	1.38	1.35
7	A	1402	4OC	O2-C2	-2.94	1.18	1.23
30	a	745	1MG	C2-N1	2.91	1.42	1.37
30	a	2069	G7M	C5-C6	2.91	1.51	1.43
30	a	2552	OMU	O4-C4	-2.86	1.18	1.24
30	a	2069	G7M	C4-N9	-2.85	1.30	1.38
30	a	745	1MG	O6-C6	-2.83	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	1618	6MZ	C8-N9	-2.81	1.32	1.37
30	a	2605	PSU	C6-C5	2.79	1.38	1.35
7	A	1518	MA6	C5-N7	-2.76	1.34	1.39
6	5	32	4OC	O2-C2	-2.70	1.18	1.23
30	a	2552	OMU	O2-C2	-2.68	1.18	1.23
30	a	746	PSU	C6-C5	2.65	1.38	1.35
30	a	2604	PSU	C4-C5	-2.63	1.37	1.44
7	A	1519	MA6	C5-C6	2.62	1.48	1.41
30	a	955	PSU	C6-C5	2.61	1.38	1.35
30	a	2030	6MZ	C8-N9	-2.59	1.33	1.37
30	a	1618	6MZ	C6-N1	-2.59	1.30	1.35
30	a	2580	PSU	C6-C5	2.55	1.38	1.35
30	a	2504	PSU	C6-C5	2.54	1.38	1.35
7	A	1519	MA6	C5-N7	-2.51	1.34	1.39
30	a	2580	PSU	O4'-C1'	-2.50	1.40	1.43
30	a	2580	PSU	C4-C5	-2.48	1.37	1.44
30	a	2503	2MA	C6-N6	-2.44	1.28	1.34
30	a	2605	PSU	C4-C5	-2.44	1.37	1.44
30	a	745	1MG	C5-C6	2.38	1.51	1.45
30	a	2457	PSU	C4-C5	-2.35	1.37	1.44
30	a	2030	6MZ	O3'-C3'	2.34	1.48	1.43
7	A	1519	MA6	C8-N7	2.34	1.36	1.31
30	a	2504	PSU	C4-C5	-2.33	1.37	1.44
30	a	746	PSU	C4-C5	-2.32	1.37	1.44
30	a	2504	PSU	O4'-C1'	-2.31	1.40	1.43
30	a	2552	OMU	C6-N1	2.30	1.43	1.38
30	a	2449	H2U	C2-N3	-2.27	1.34	1.38
7	A	1518	MA6	C5-C6	2.25	1.47	1.41
7	A	527	G7M	C4-N9	-2.23	1.32	1.38
30	a	2457	PSU	O4'-C1'	-2.23	1.40	1.43
30	a	2604	PSU	O4'-C1'	-2.19	1.40	1.43
7	A	1519	MA6	C4-N9	-2.18	1.33	1.37
30	a	1618	6MZ	C5-C6	-2.17	1.36	1.41
7	A	1518	MA6	C4-N9	-2.15	1.33	1.37
30	a	2552	OMU	C5-C4	2.13	1.48	1.43
30	a	2457	PSU	C6-C5	2.12	1.37	1.35
30	a	955	PSU	O4'-C1'	-2.12	1.40	1.43
30	a	745	1MG	C4-N9	-2.12	1.32	1.38
30	a	1911	PSU	C4-C5	-2.08	1.38	1.44
30	a	955	PSU	C4-C5	-2.06	1.38	1.44
6	5	54	PSU	C4-C5	-2.06	1.38	1.44
7	A	516	PSU	O4'-C1'	-2.06	1.41	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	1917	PSU	C4-C5	-2.04	1.38	1.44
7	A	516	PSU	C4-C5	-2.04	1.38	1.44
30	a	746	PSU	O4'-C1'	-2.03	1.41	1.43
30	a	2604	PSU	C6-C5	2.01	1.37	1.35

All (150) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	1618	6MZ	C5-C4-N3	-6.03	118.41	126.72
30	a	2552	OMU	C4-N3-C2	-5.90	119.28	126.61
7	A	1518	MA6	C5-C4-N3	-5.82	118.71	126.72
30	a	745	1MG	C5-C4-N3	-5.81	119.14	128.39
7	A	1518	MA6	N1-C6-N6	5.72	123.82	116.86
7	A	1519	MA6	C5-C4-N3	-5.62	118.98	126.72
30	a	2030	6MZ	N1-C2-N3	-5.56	120.16	128.58
30	a	2604	PSU	C4-N3-C2	-5.41	118.92	126.37
30	a	2605	PSU	C4-N3-C2	-5.35	119.01	126.37
7	A	1498	UR3	C4-N3-C2	-5.32	120.30	124.58
30	a	2605	PSU	N1-C2-N3	5.27	120.73	115.17
30	a	1618	6MZ	C9-N6-C6	-5.21	118.02	122.85
30	a	2030	6MZ	C4-N9-C1'	-5.13	114.62	126.63
7	A	527	G7M	CN7-N7-C5	5.13	133.19	126.80
30	a	1618	6MZ	N1-C2-N3	-5.13	120.82	128.58
30	a	2580	PSU	N1-C2-N3	5.01	120.46	115.17
30	a	1911	PSU	C4-N3-C2	-5.01	119.47	126.37
7	A	1518	MA6	N3-C4-N9	4.99	135.66	127.17
30	a	2580	PSU	C4-N3-C2	-4.99	119.50	126.37
30	a	1917	PSU	C4-N3-C2	-4.97	119.52	126.37
30	a	1618	6MZ	C4-C5-C6	4.97	120.91	116.78
30	a	2504	PSU	C4-N3-C2	-4.94	119.57	126.37
30	a	746	PSU	C4-N3-C2	-4.92	119.60	126.37
30	a	2030	6MZ	C5-C4-N3	-4.91	119.96	126.72
7	A	1519	MA6	C10-N6-C6	-4.89	108.07	120.52
30	a	1911	PSU	N1-C2-N3	4.86	120.30	115.17
6	5	54	PSU	C4-N3-C2	-4.79	119.77	126.37
7	A	1519	MA6	C9-N6-C6	-4.75	108.44	120.52
30	a	955	PSU	C4-N3-C2	-4.74	119.84	126.37
30	a	2604	PSU	N1-C2-N3	4.73	120.16	115.17
7	A	527	G7M	C2-N3-C4	4.68	120.36	112.30
6	5	54	PSU	N1-C2-N3	4.67	120.09	115.17
30	a	2504	PSU	N1-C2-N3	4.63	120.05	115.17
30	a	1917	PSU	N1-C2-N3	4.61	120.03	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	527	G7M	C5-C4-N3	-4.56	119.53	128.15
7	A	516	PSU	C4-N3-C2	-4.56	120.09	126.37
30	a	2069	G7M	CN7-N7-C5	4.53	132.45	126.80
30	a	955	PSU	N1-C2-N3	4.50	119.92	115.17
30	a	2030	6MZ	N9-C8-N7	-4.49	107.56	113.94
30	a	2457	PSU	C4-N3-C2	-4.49	120.19	126.37
30	a	2030	6MZ	C1'-N9-C8	4.45	136.96	127.09
30	a	2069	G7M	C1'-N9-C4	-4.42	113.43	126.49
7	A	516	PSU	N1-C2-N3	4.41	119.82	115.17
7	A	1519	MA6	N3-C4-N9	4.37	134.61	127.17
30	a	2069	G7M	C2-N3-C4	4.35	119.80	112.30
30	a	2069	G7M	C5-C4-N3	-4.34	119.94	128.15
30	a	2457	PSU	N1-C2-N3	4.34	119.74	115.17
7	A	1518	MA6	C5-C6-N6	-4.27	118.57	125.33
30	a	746	PSU	N1-C2-N3	4.23	119.63	115.17
30	a	2030	6MZ	C4-C5-C6	4.22	120.29	116.78
30	a	2552	OMU	N3-C2-N1	4.22	120.38	114.89
7	A	527	G7M	CN7-N7-C8	-4.19	118.45	124.79
7	A	527	G7M	C5-C6-N1	4.09	120.29	111.84
30	a	2069	G7M	C5-C6-N1	4.06	120.23	111.84
7	A	1518	MA6	C9-N6-C6	-4.04	110.23	120.52
7	A	1519	MA6	C2-N1-C6	4.03	121.68	111.83
7	A	527	G7M	C1'-N9-C4	-3.99	114.71	126.49
7	A	1518	MA6	C10-N6-C6	-3.87	110.68	120.52
7	A	1498	UR3	C5-C4-N3	3.85	120.11	115.04
7	A	1518	MA6	C2-N1-C6	3.85	121.22	111.83
30	a	2605	PSU	O2-C2-N1	-3.81	118.86	122.79
30	a	2069	G7M	O6-C6-C5	-3.74	119.66	128.01
7	A	1518	MA6	C2'-C1'-N9	-3.71	104.09	113.30
30	a	2580	PSU	O2-C2-N1	-3.64	119.03	122.79
30	a	1618	6MZ	N3-C4-N9	3.62	133.32	127.17
30	a	2552	OMU	C5-C4-N3	3.61	119.85	114.80
30	a	2069	G7M	C1'-N9-C8	3.61	138.91	126.74
7	A	1519	MA6	C2-N3-C4	3.59	120.61	111.83
30	a	745	1MG	C2-N3-C4	3.59	120.05	111.98
30	a	1618	6MZ	C2-N3-C4	3.57	120.54	111.83
30	a	2504	PSU	O2-C2-N1	-3.56	119.12	122.79
30	a	745	1MG	N9-C4-N3	3.52	133.00	125.95
30	a	2457	PSU	O2-C2-N1	-3.50	119.18	122.79
30	a	2069	G7M	C2-N1-C6	-3.49	118.79	125.11
7	A	527	G7M	O6-C6-C5	-3.45	120.30	128.01
7	A	1519	MA6	C2'-C1'-N9	-3.45	104.73	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	527	G7M	N9-C4-N3	3.42	132.79	125.95
7	A	1518	MA6	C2-N3-C4	3.41	120.16	111.83
7	A	1519	MA6	C4-C5-N7	-3.40	106.69	110.58
30	a	955	PSU	O2-C2-N1	-3.39	119.29	122.79
30	a	2030	6MZ	C9-N6-C6	-3.35	119.75	122.85
30	a	2503	2MA	C5-C4-N3	-3.34	123.66	127.18
30	a	746	PSU	O2-C2-N1	-3.27	119.42	122.79
30	a	2030	6MZ	C2-N3-C4	3.26	119.79	111.83
30	a	1618	6MZ	N9-C8-N7	-3.23	109.36	113.94
30	a	2069	G7M	CN7-N7-C8	-3.22	119.91	124.79
30	a	2552	OMU	O2-C2-N1	-3.21	118.62	122.80
30	a	745	1MG	C5-C6-N1	3.20	120.93	115.02
7	A	516	PSU	O2-C2-N1	-3.17	119.52	122.79
7	A	1519	MA6	N1-C2-N3	-3.17	123.79	128.58
7	A	527	G7M	C2-N1-C6	-3.14	119.42	125.11
30	a	2580	PSU	C6-N1-C2	-3.13	119.79	122.69
30	a	2030	6MZ	C5-N7-C8	3.10	108.32	103.45
7	A	527	G7M	C1'-N9-C8	3.02	136.93	126.74
7	A	1519	MA6	N1-C6-N6	3.00	120.51	116.86
30	a	2069	G7M	N9-C4-N3	2.99	131.93	125.95
30	a	1911	PSU	O2-C2-N1	-2.98	119.71	122.79
6	5	54	PSU	O2-C2-N1	-2.98	119.72	122.79
30	a	2552	OMU	O4-C4-C5	-2.97	120.03	125.16
30	a	2030	6MZ	N3-C4-N9	2.97	132.22	127.17
30	a	2605	PSU	C6-N1-C2	-2.94	119.97	122.69
7	A	1518	MA6	N1-C2-N3	-2.81	124.33	128.58
7	A	1498	UR3	C6-N1-C2	-2.81	119.50	121.80
7	A	1518	MA6	C4-C5-N7	-2.76	107.42	110.58
30	a	1917	PSU	O2-C2-N1	-2.76	119.94	122.79
30	a	1618	6MZ	C4-N9-C1'	-2.71	120.29	126.63
30	a	2604	PSU	O2-C2-N1	-2.70	120.00	122.79
7	A	1518	MA6	C4-N9-C8	2.70	108.57	105.74
7	A	1519	MA6	C10-N6-C9	-2.70	107.51	116.18
30	a	2457	PSU	C6-N1-C2	-2.69	120.20	122.69
7	A	1519	MA6	C4-N9-C8	2.67	108.54	105.74
30	a	1618	6MZ	C1'-N9-C8	2.63	132.94	127.09
30	a	2580	PSU	O4'-C1'-C2'	2.62	108.77	105.15
30	a	2503	2MA	C2-N1-C6	2.60	122.10	118.10
30	a	2504	PSU	C6-N1-C2	-2.58	120.30	122.69
30	a	2030	6MZ	C4-N9-C8	2.55	108.41	105.74
7	A	516	PSU	C6-N1-C2	-2.54	120.34	122.69
30	a	1911	PSU	C6-N1-C2	-2.46	120.41	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2251	OMG	O2'-C2'-C1'	2.43	113.61	108.99
7	A	1519	MA6	C5-N7-C8	2.43	107.27	103.45
30	a	955	PSU	C6-N1-C2	-2.42	120.45	122.69
30	a	745	1MG	C2-N1-C6	-2.41	118.97	120.99
30	a	1618	6MZ	C5-N7-C8	2.40	107.22	103.45
30	a	2030	6MZ	C4-C5-N7	-2.36	107.88	110.58
7	A	1519	MA6	C5-C6-N6	-2.36	121.60	125.33
6	5	54	PSU	C6-N1-C2	-2.35	120.51	122.69
30	a	2449	H2U	O2-C2-N1	-2.33	120.31	123.10
30	a	2251	OMG	O3'-C3'-C4'	2.31	117.72	111.08
30	a	1618	6MZ	C5-C6-N1	2.31	120.63	118.15
30	a	2503	2MA	N3-C2-N1	-2.26	121.78	125.77
30	a	1618	6MZ	C5-C4-N9	2.26	108.27	105.81
30	a	745	1MG	N9-C8-N7	-2.24	109.25	113.40
33	d	150	MEQ	CB-CG-CD	-2.24	108.07	113.06
30	a	2030	6MZ	C5'-C4'-C3'	-2.24	107.16	115.21
6	5	54	PSU	C6-C5-C4	2.21	119.67	118.17
30	a	2445	2MG	CM2-N2-C2	-2.21	118.90	123.65
30	a	1917	PSU	C6-N1-C2	-2.21	120.64	122.69
7	A	516	PSU	O4'-C1'-C2'	2.21	108.20	105.15
30	a	2030	6MZ	C4'-O4'-C1'	-2.16	104.69	109.47
7	A	1498	UR3	C1'-N1-C2	2.12	120.52	117.04
6	5	32	4OC	C6-C5-C4	2.10	119.53	117.00
7	A	1402	4OC	C6-C5-C4	2.09	119.52	117.00
30	a	746	PSU	O4-C4-C5	-2.08	118.84	124.01
30	a	2605	PSU	O4-C4-C5	-2.08	118.85	124.01
30	a	2604	PSU	O4-C4-C5	-2.07	118.87	124.01
30	a	2604	PSU	O4'-C1'-C2'	2.07	108.01	105.15
7	A	1518	MA6	C4-C5-C6	2.03	118.01	115.91
7	A	1519	MA6	N9-C8-N7	-2.01	111.08	113.94
7	A	1518	MA6	C5-N7-C8	2.01	106.61	103.45
30	a	746	PSU	C6-N1-C2	-2.01	120.83	122.69

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	967	5MC	O4'-C4'-C5'-O5'
7	A	1518	MA6	C5-C6-N6-C9
7	A	1519	MA6	C5-C6-N6-C9
7	A	1519	MA6	C5-C6-N6-C10
7	A	1519	MA6	N1-C6-N6-C9

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Mol	Chain	Res	Type	Atoms
33	d	150	MEQ	C-CA-CB-CG
30	a	1618	6MZ	C5-C6-N6-C9
30	a	1618	6MZ	N1-C6-N6-C9
30	a	1835	2MG	N3-C2-N2-CM2
30	a	1911	PSU	C2'-C1'-C5-C4
30	a	2030	6MZ	C5-C6-N6-C9
30	a	2030	6MZ	N1-C6-N6-C9
30	a	2251	OMG	C1'-C2'-O2'-CM2
30	a	2445	2MG	N1-C2-N2-CM2
30	a	2445	2MG	N3-C2-N2-CM2
30	a	2457	PSU	O4'-C4'-C5'-O5'
30	a	2498	OMC	C3'-C2'-O2'-CM2
7	A	1402	4OC	O4'-C4'-C5'-O5'
7	A	1519	MA6	O4'-C4'-C5'-O5'
6	5	54	PSU	C3'-C4'-C5'-O5'
6	5	54	PSU	O4'-C4'-C5'-O5'
7	A	1519	MA6	N1-C6-N6-C10
30	a	1962	5MC	C2'-C1'-N1-C6
7	A	967	5MC	C3'-C4'-C5'-O5'
30	a	2457	PSU	C3'-C4'-C5'-O5'
30	a	2498	OMC	O4'-C4'-C5'-O5'
33	d	150	MEQ	CA-CB-CG-CD
33	d	150	MEQ	NE2-CD-CG-CB
33	d	150	MEQ	OE1-CD-CG-CB
30	a	1962	5MC	C2'-C1'-N1-C2
7	A	1402	4OC	C3'-C4'-C5'-O5'
7	A	1519	MA6	C3'-C4'-C5'-O5'
30	a	1911	PSU	O4'-C4'-C5'-O5'
30	a	1962	5MC	O4'-C1'-N1-C6
30	a	1962	5MC	O4'-C1'-N1-C2
7	A	1518	MA6	N1-C6-N6-C9
30	a	2498	OMC	C2'-C1'-N1-C2
30	a	2251	OMG	C4'-C5'-O5'-P
30	a	1911	PSU	O4'-C1'-C5-C4
30	a	2604	PSU	O4'-C1'-C5-C4
30	a	2605	PSU	O4'-C1'-C5-C4
30	a	2503	2MA	O4'-C1'-N9-C8
30	a	2503	2MA	O4'-C1'-N9-C4
30	a	2498	OMC	C2'-C1'-N1-C6
30	a	1917	PSU	O4'-C4'-C5'-O5'
30	a	1939	5MU	O4'-C4'-C5'-O5'
30	a	2604	PSU	O4'-C1'-C5-C6

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Mol	Chain	Res	Type	Atoms
30	a	2552	OMU	C3'-C2'-O2'-CM2
30	a	2069	G7M	O4'-C4'-C5'-O5'
30	a	2503	2MA	O4'-C4'-C5'-O5'
30	a	1911	PSU	C3'-C4'-C5'-O5'
30	a	2498	OMC	C3'-C4'-C5'-O5'
30	a	2030	6MZ	C2'-C1'-N9-C8

There are no ring outliers.

15 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	a	2030	6MZ	1	0
30	a	2552	OMU	1	0
33	d	150	MEQ	1	0
30	a	1962	5MC	1	0
30	a	2457	PSU	1	0
30	a	2498	OMC	1	0
30	a	2449	H2U	1	0
6	5	32	4OC	2	0
7	A	966	2MG	1	0
7	A	1407	5MC	2	0
6	5	53	5MU	1	0
7	A	516	PSU	1	0
30	a	955	PSU	1	0
7	A	1518	MA6	3	0
30	a	1917	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	a	3
29	Y	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Y	118:UNK	C	124:UNK	N	22.94
1	a	1052:C	O3'	1107:G	P	17.39
1	a	2098:U	O3'	2191:A	P	16.58
1	a	1172:C	O3'	1177:G	P	15.99
1	Y	127:UNK	C	131:UNK	N	10.74

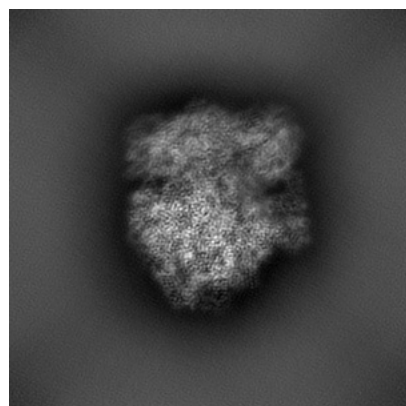
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74757. These allow visual inspection of the internal detail of the map and identification of artifacts.

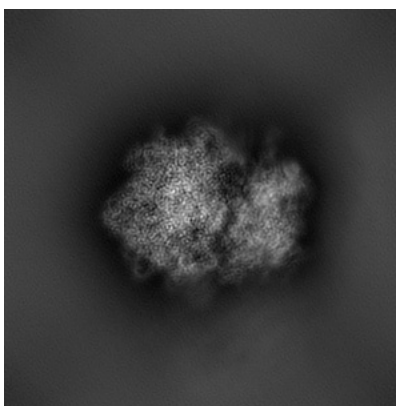
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

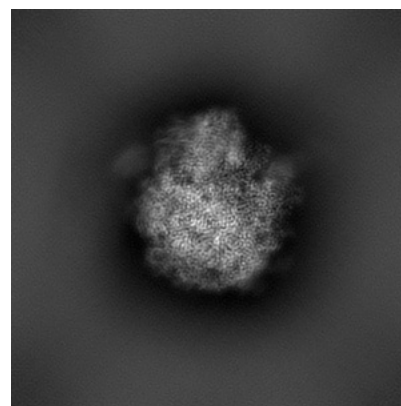
6.1.1 Primary map



X

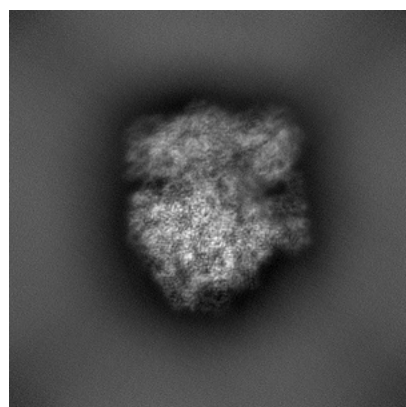


Y

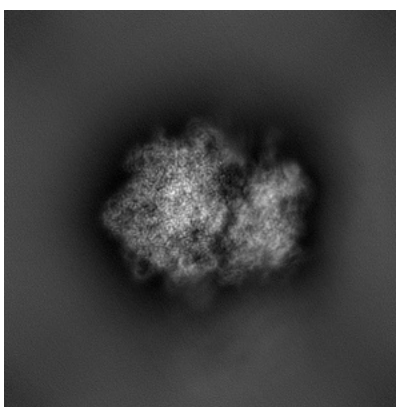


Z

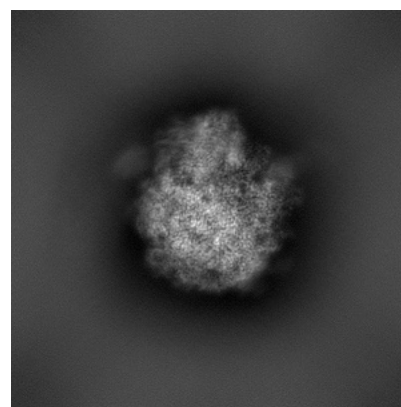
6.1.2 Raw map



X



Y

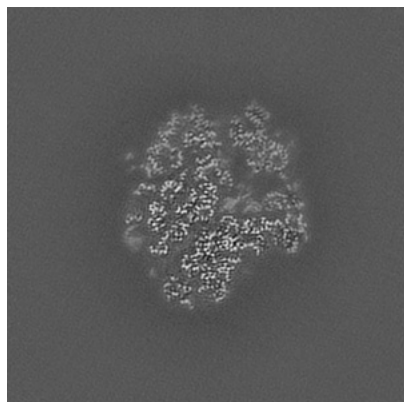


Z

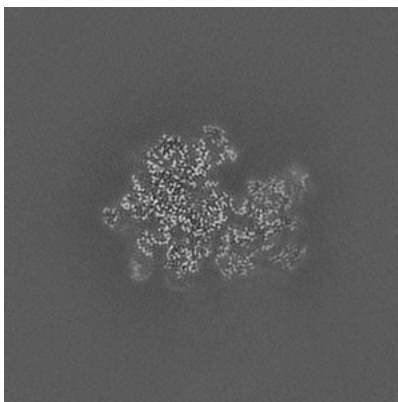
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

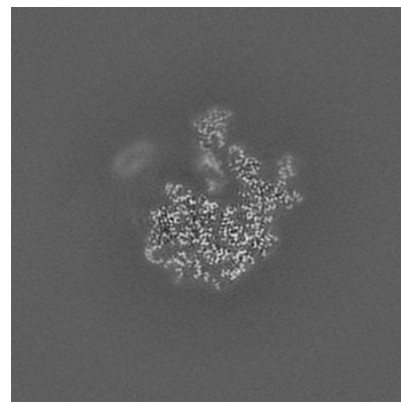
6.2.1 Primary map



X Index: 256

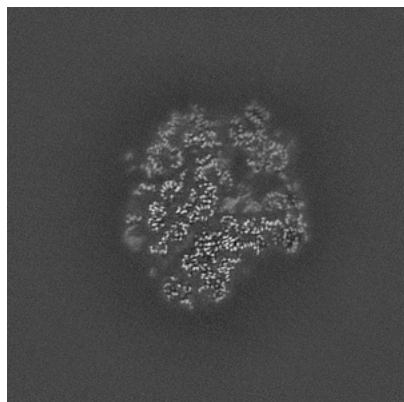


Y Index: 256

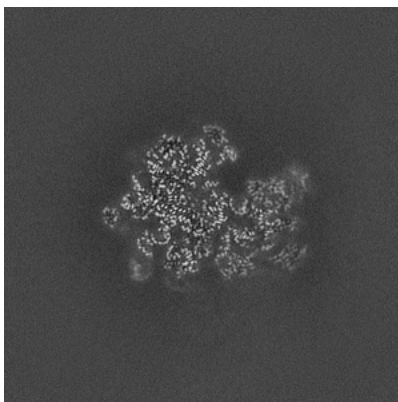


Z Index: 256

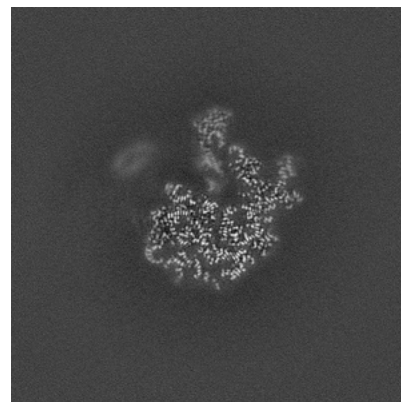
6.2.2 Raw map



X Index: 256



Y Index: 256

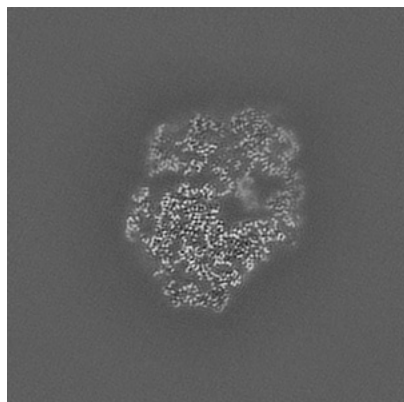


Z Index: 256

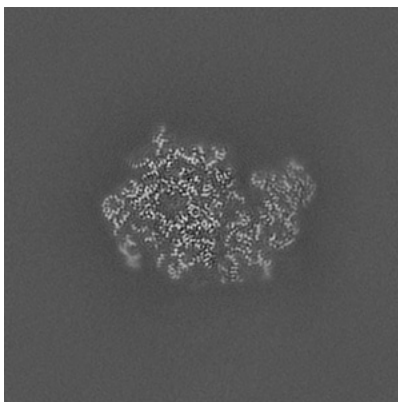
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

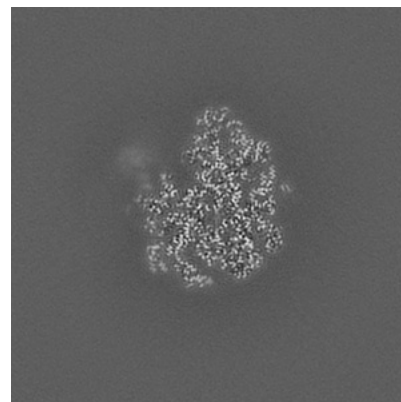
6.3.1 Primary map



X Index: 243

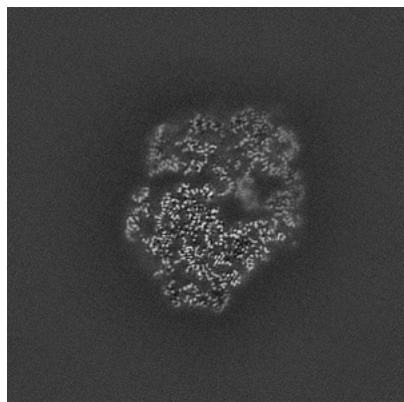


Y Index: 235

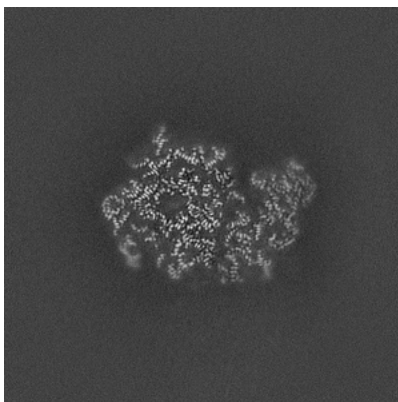


Z Index: 230

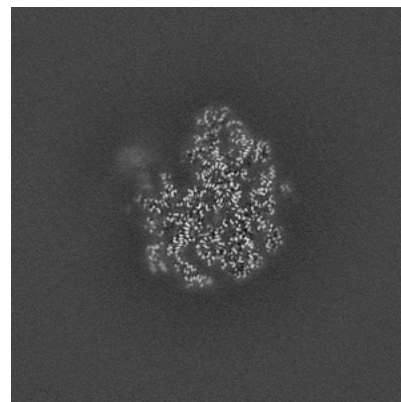
6.3.2 Raw map



X Index: 243



Y Index: 235

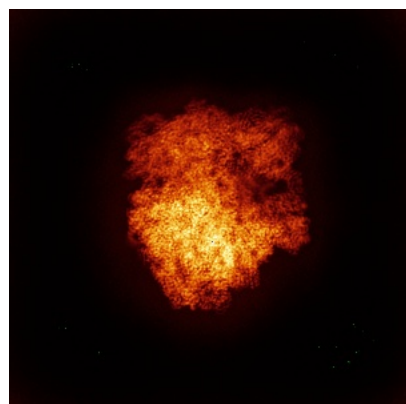


Z Index: 230

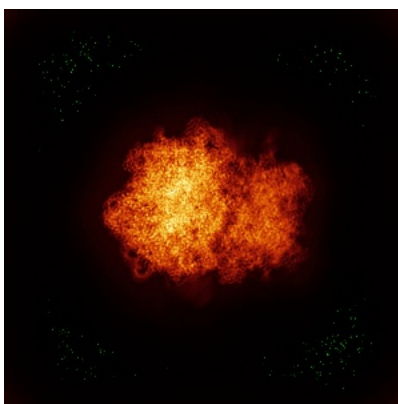
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

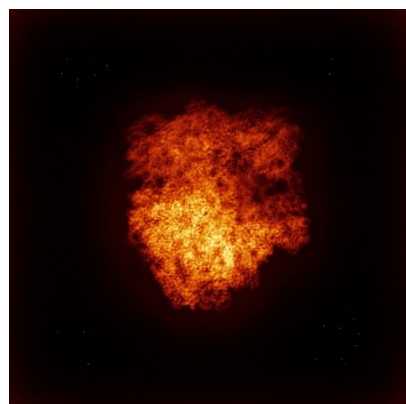


Y

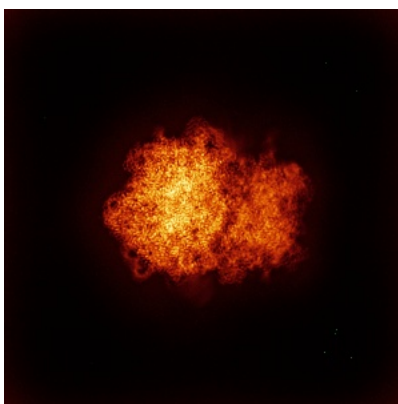


Z

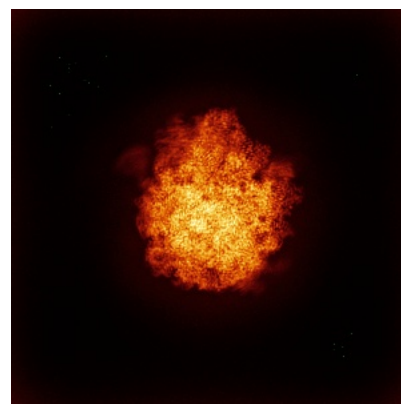
6.4.2 Raw map



X



Y

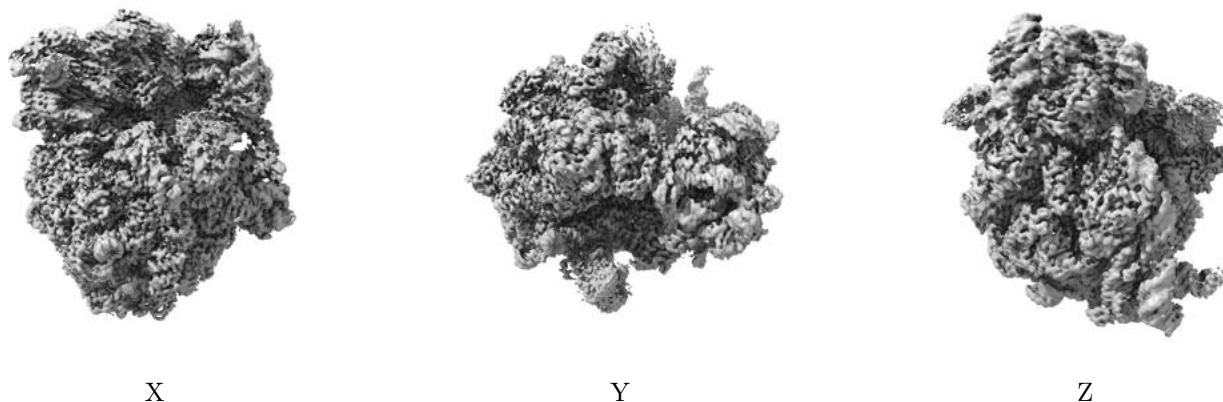


Z

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.

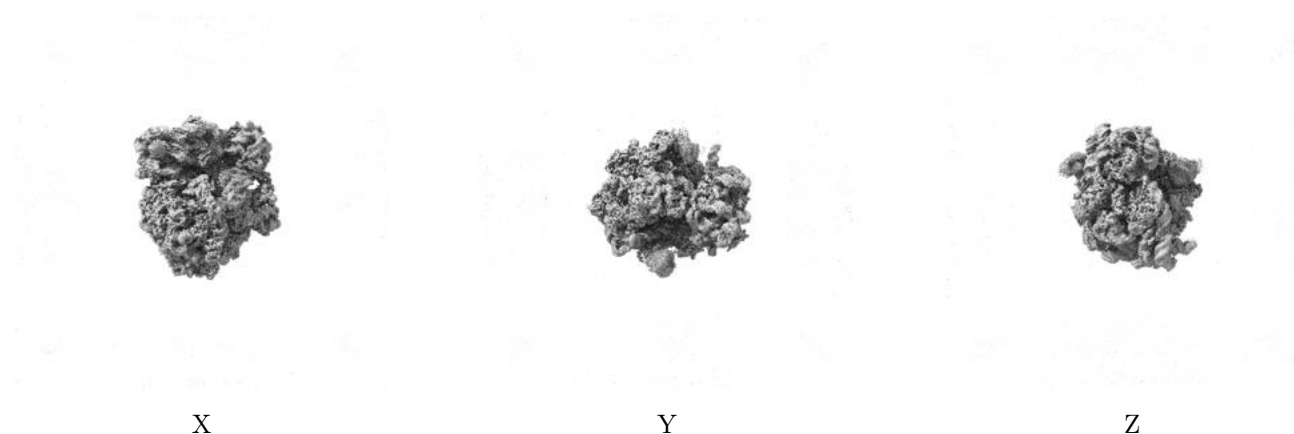
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. 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.

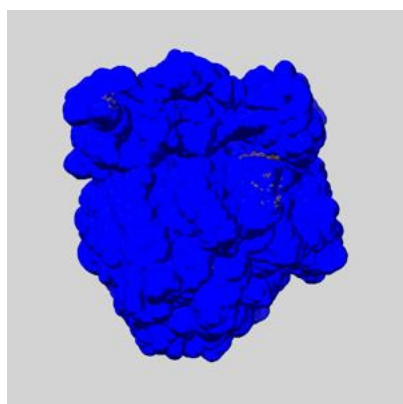
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

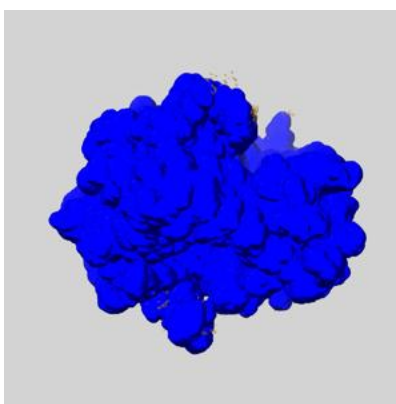
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

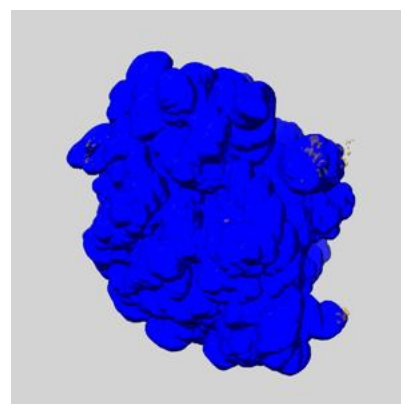
6.6.1 emd_74757_msk_1.map [i](#)



X



Y

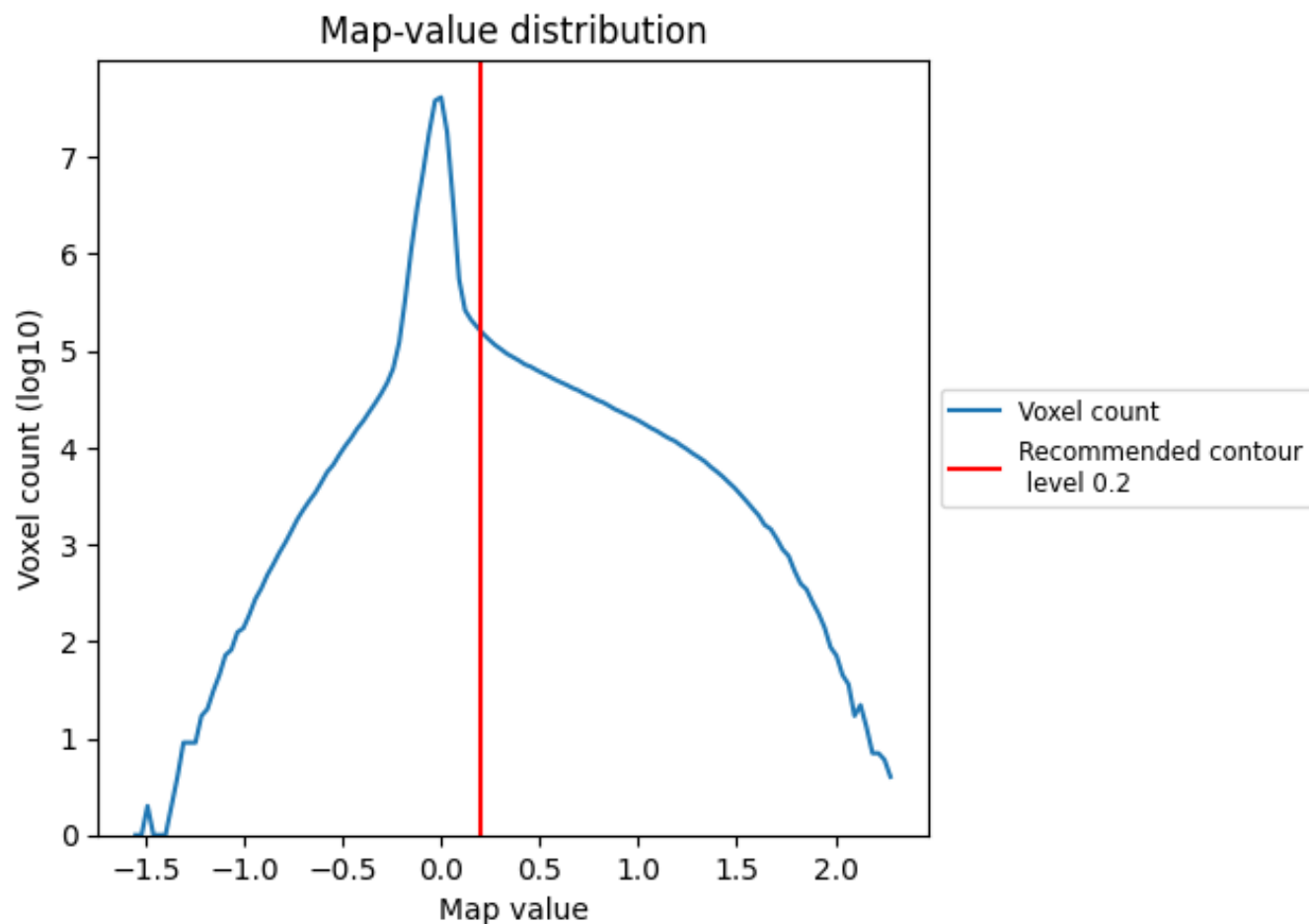


Z

7 Map analysis [i](#)

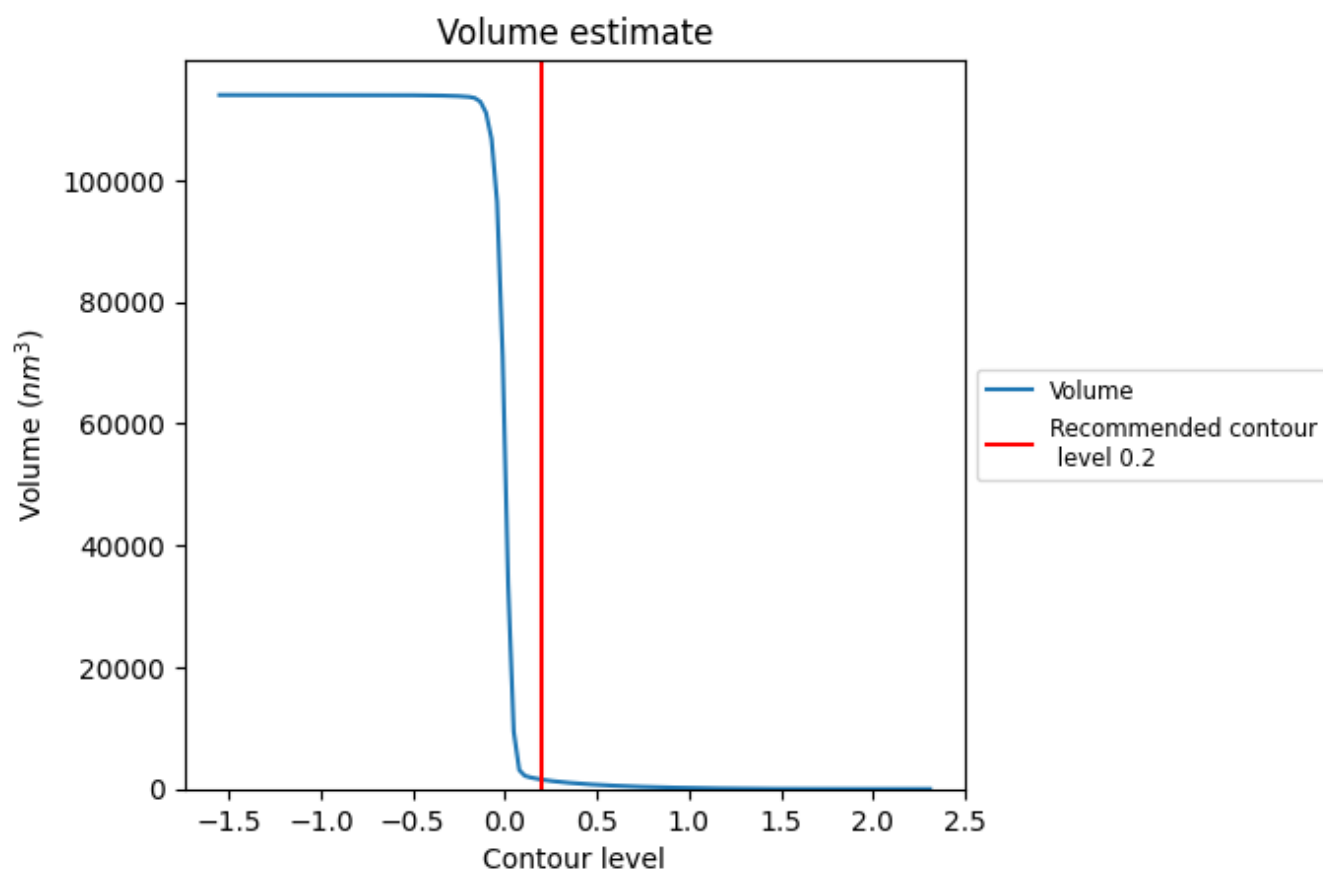
This section contains the results of statistical analysis of the map.

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.

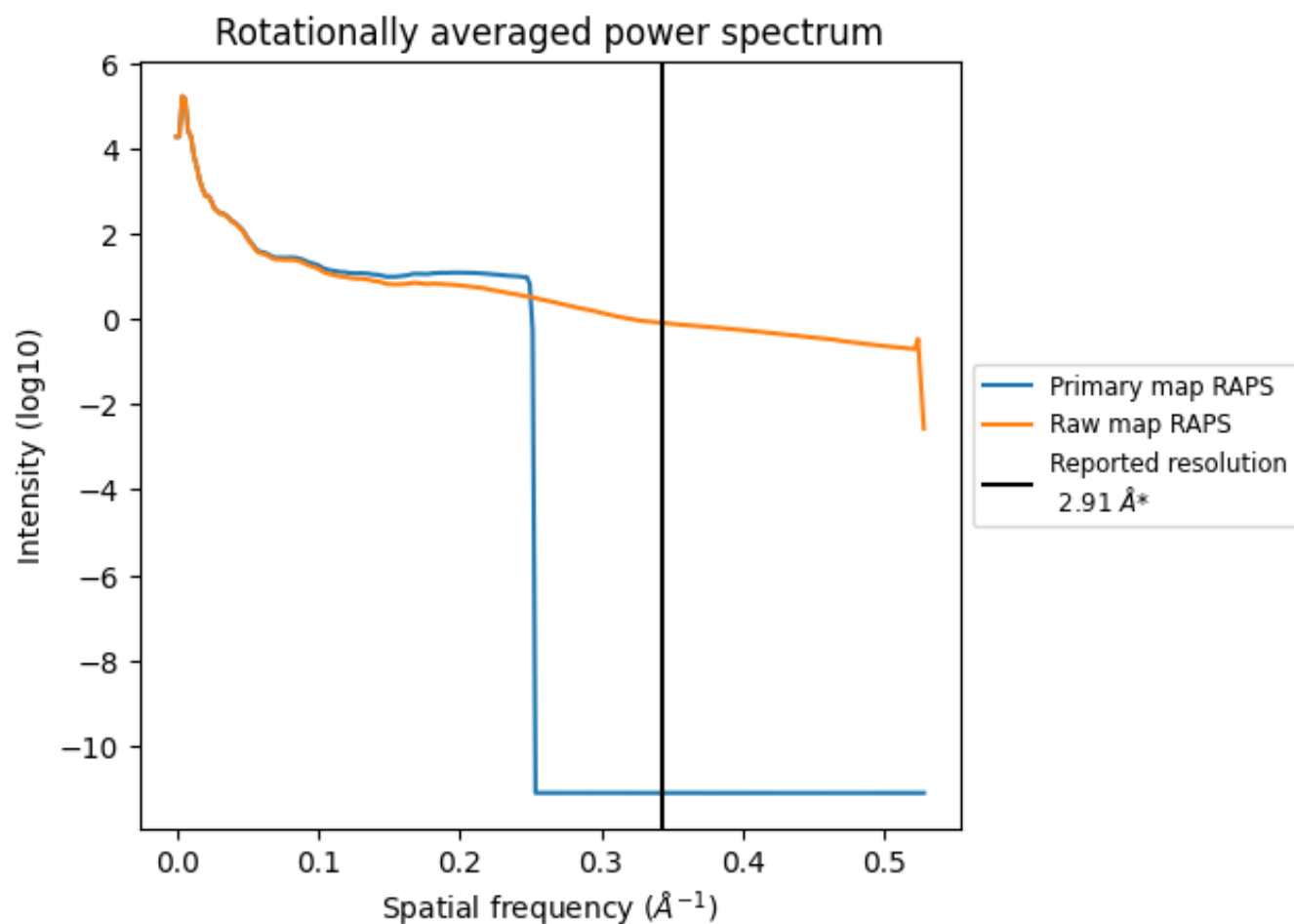
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1534 nm³; this corresponds to an approximate mass of 1385 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 ⓘ

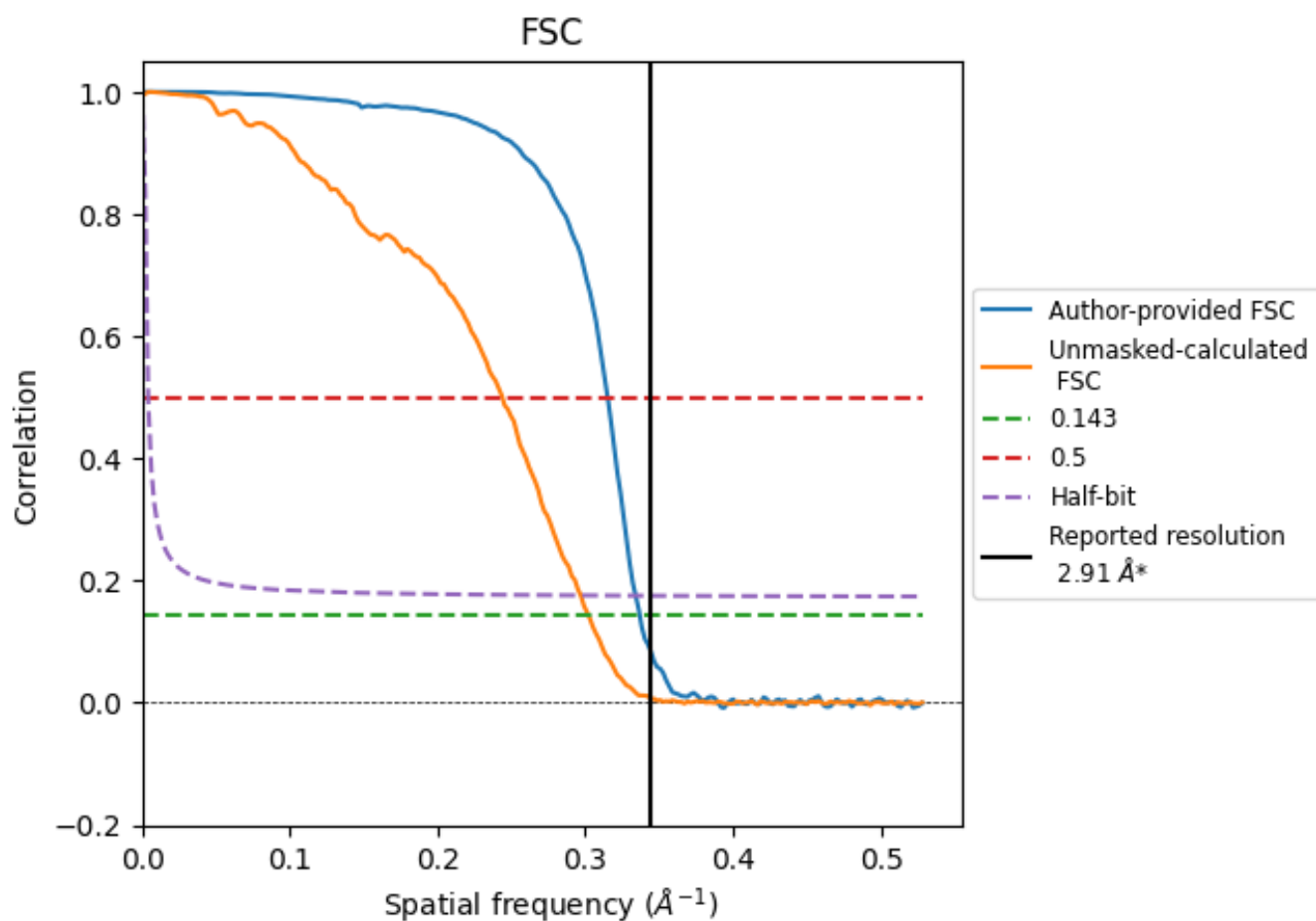


*Reported resolution corresponds to spatial frequency of 0.344 \AA^{-1}

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 0.344 \AA^{-1}

8.2 Resolution estimates [i](#)

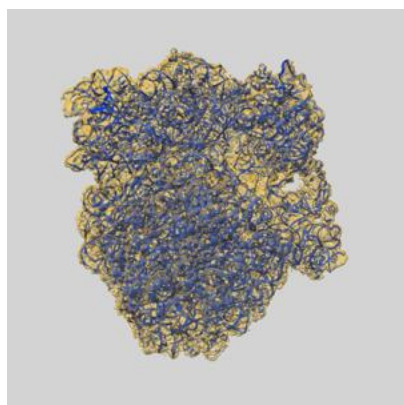
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	2.97	3.17	2.99
Unmasked-calculated*	3.31	4.10	3.37

*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 3.31 differs from the reported value 2.91 by more than 10 %

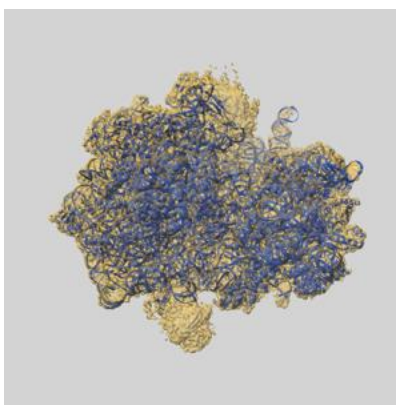
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74757 and PDB model 9ZTL. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

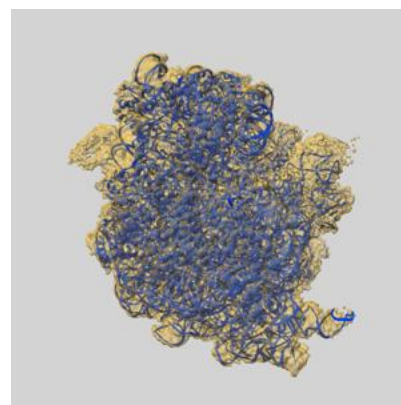
9.1 Map-model overlay [i](#)



X



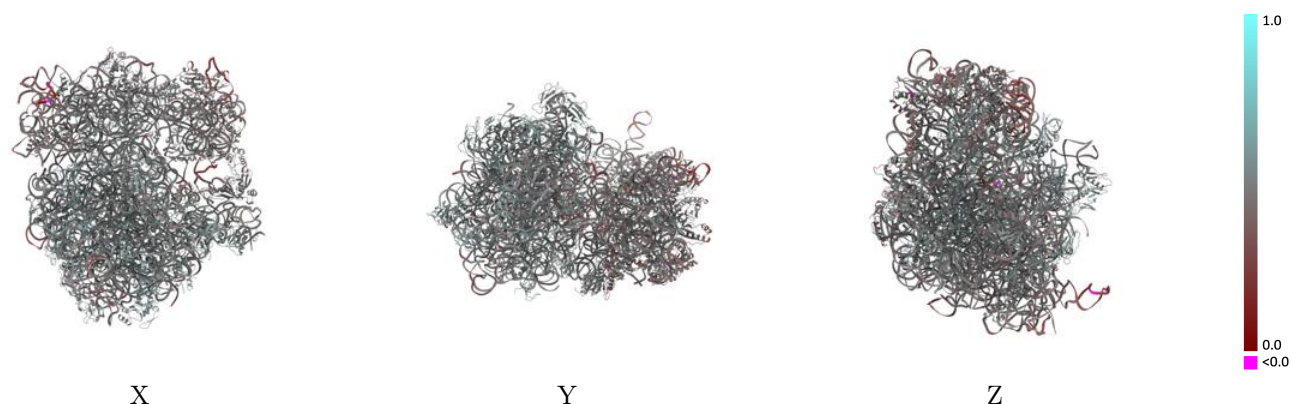
Y



Z

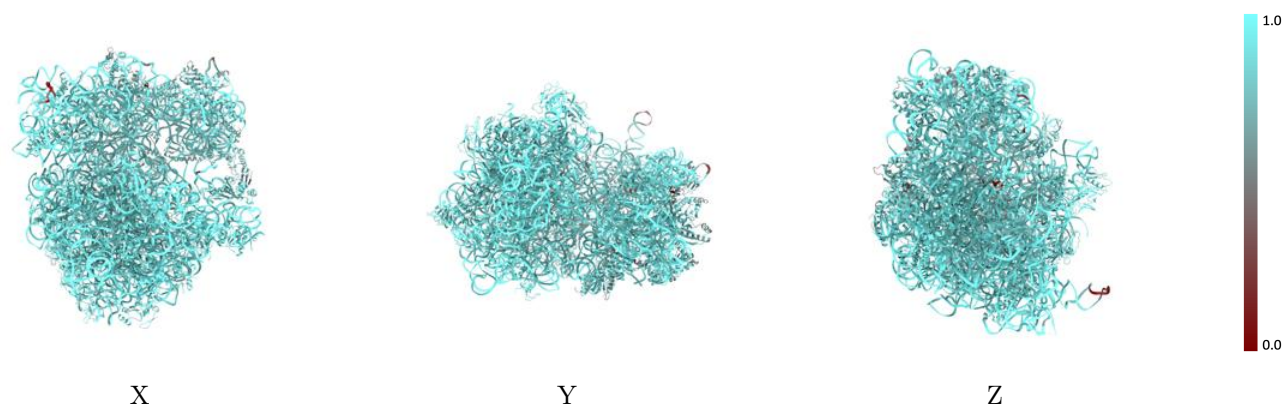
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



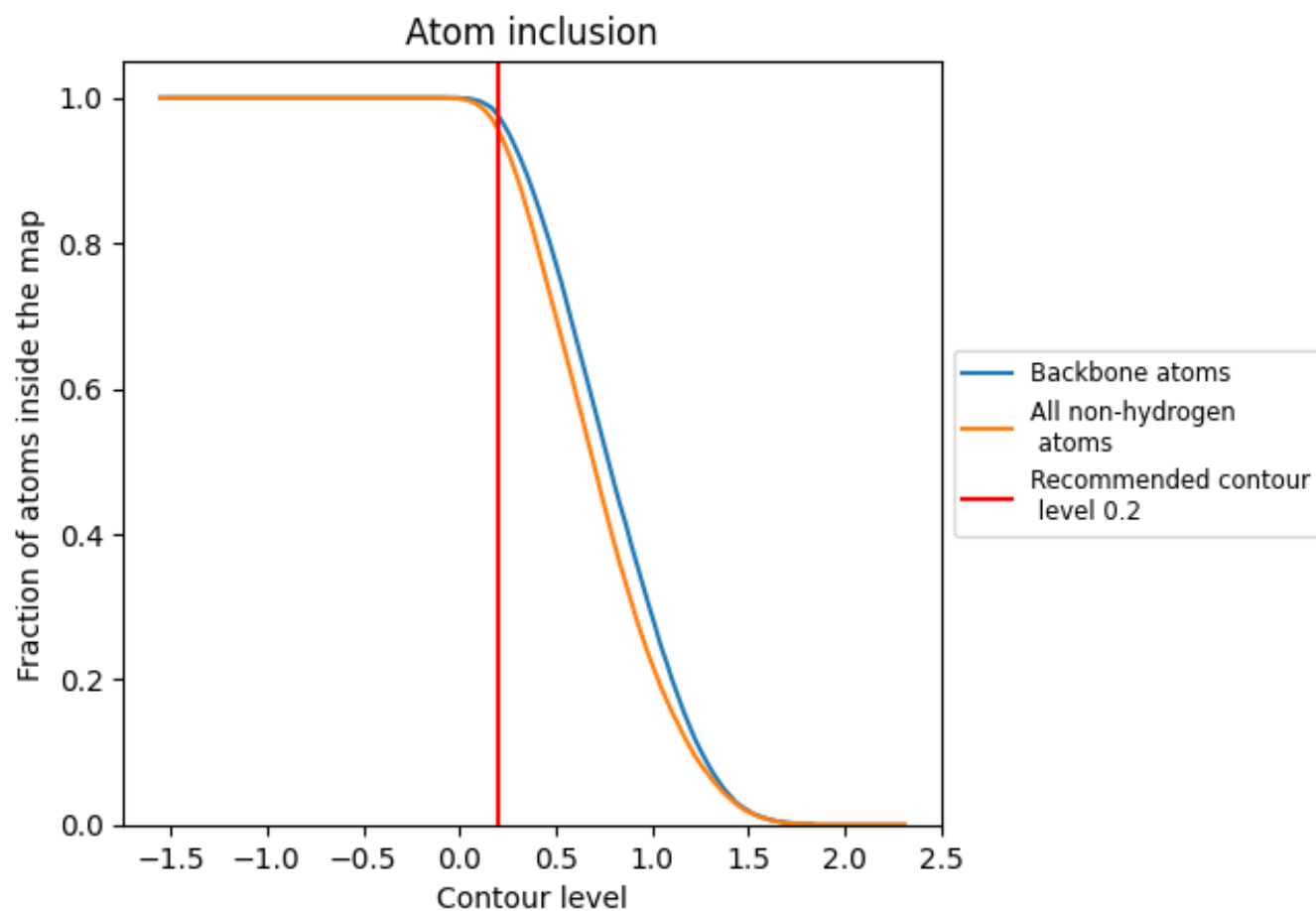
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.4800
0	 0.9580	 0.5380
1	 0.9580	 0.5410
2	 0.9880	 0.5490
3	 0.9760	 0.5520
4	 0.6480	 0.4350
5	 0.9530	 0.4080
A	 0.9730	 0.4500
B	 0.7920	 0.4670
C	 0.8560	 0.4940
D	 0.7590	 0.4660
E	 0.9260	 0.5060
F	 0.8800	 0.4860
G	 0.7900	 0.4240
H	 0.9240	 0.5120
I	 0.8730	 0.4540
J	 0.7910	 0.4410
K	 0.8780	 0.4970
L	 0.9160	 0.5070
M	 0.8630	 0.4660
N	 0.9100	 0.4780
O	 0.9490	 0.4920
P	 0.9030	 0.5090
Q	 0.8960	 0.4920
R	 0.9370	 0.5050
S	 0.8470	 0.4570
T	 0.8840	 0.4660
U	 0.6830	 0.4290
X	 0.9160	 0.4320
Y	 0.7530	 0.4470
a	 0.9820	 0.4800
b	 0.9920	 0.4680
c	 0.9640	 0.5410
d	 0.9710	 0.5430
e	 0.9430	 0.5330



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Chain	Atom inclusion	Q-score
f	 0.8940	 0.4700
g	 0.9310	 0.5070
h	 0.9100	 0.5050
i	 0.9660	 0.5400
j	 0.9400	 0.5430
k	 0.9610	 0.5370
l	 0.9660	 0.5380
m	 0.9670	 0.5410
n	 0.9620	 0.5200
o	 0.9380	 0.5470
p	 0.9730	 0.5350
q	 0.9620	 0.5510
r	 0.9450	 0.5430
s	 0.9330	 0.5270
t	 0.9320	 0.5210
u	 0.9550	 0.5370
v	 0.9770	 0.5520
w	 0.9680	 0.5340
x	 0.9320	 0.5130
y	 0.9520	 0.5410
z	 0.9770	 0.5440