



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 12:19 AM UTC

PDB ID : 9V1I / pdb_00009v1i
EMDB ID : EMD-64694
Title : Cryo- EM structure of ribosomal large subunit (LSU) from Entamoeba histolytica at 2.8 angstrom resolution
Authors : Sharma, S.; Mishra, S.; Gourinath, S.; Kaushal, P.S.
Deposited on : 2025-05-19
Resolution : 2.80 Å (reported)
Based on initial models : 4UG0, 5XXB

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
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

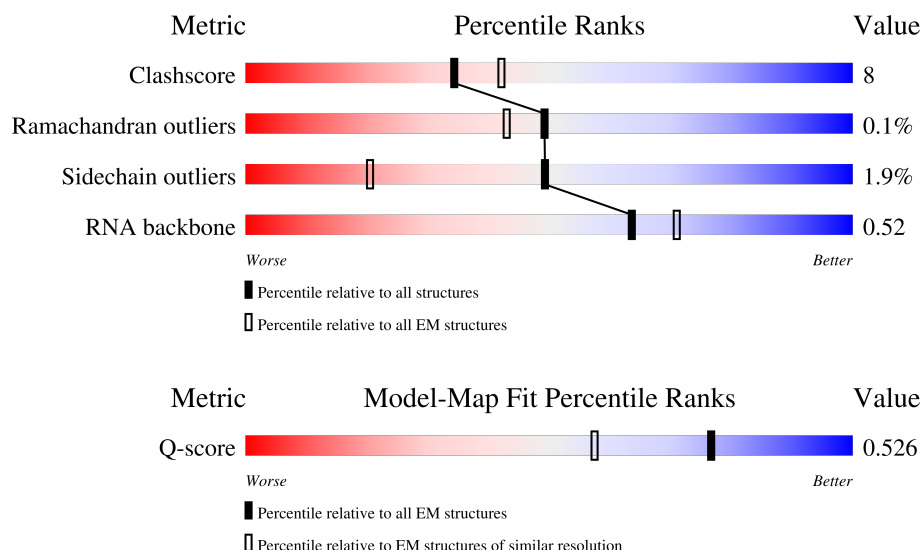
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

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



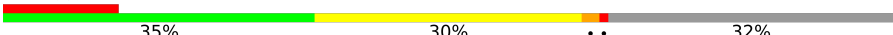
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	1A	3503	
2	1B	155	
3	1C	117	

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Mol	Chain	Length	Quality of chain
4	ID	257	
5	IE	402	
6	IF	431	
7	IG	286	
8	IH	204	
9	II	230	
10	IJ	286	
11	IK	197	
12	IL	210	
13	IM	174	
14	IN	291	
15	IO	205	
16	IP	135	
17	IQ	205	
18	IR	179	
19	IS	168	
20	IT	173	
21	IU	198	
22	IV	166	
23	IW	137	
24	IX	140	
25	IY	121	
26	IZ	163	
27	la	213	
28	lb	139	

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Mol	Chain	Length	Quality of chain
29	lc	149	 86% 13% ..
30	ld	64	 88% 6% 6%
31	le	109	 15% 72% 22% 6%
32	lf	150	 13% 79% 17% ..
33	lg	134	 81% 16% .
34	lh	137	 64% 12% 23%
35	li	122	 87% 13%
36	lj	108	 86% 12% .
37	lk	104	 70% 15% 14%
38	ll	77	 71% 21% . 6%
39	lm	93	 78% 18% .
40	ln	84	 10% 63% 23% . 13%
41	lo	51	 86% 10% ..
42	lp	56	 59% 32% . 5%
43	lq	98	 81% 13% 6%
44	lr	13	 100%

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 121291 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA (3068-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3067	Total	C	N	O	P	0	0
			65572	29397	11934	21174	3067		

- Molecule 2 is a RNA chain called 5.8S rRNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	145	Total	C	N	O	P	0	0
			3097	1390	560	1002	145		

- Molecule 3 is a RNA chain called 5S rRNA (117-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	117	Total	C	N	O	P	0	0
			2477	1108	425	827	117		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	246	Total	C	N	O	S	0	0
			1881	1165	382	326	8		

- Molecule 5 is a protein called 60S ribosomal protein L3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	387	Total	C	N	O	S	0	0
			3076	1956	578	527	15		

- Molecule 6 is a protein called 60S ribosomal protein L4, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	424	Total	C	N	O	S	0	0
			3272	2085	622	551	14		

- Molecule 7 is a protein called 60S ribosomal protein L5, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	lG	279	Total	C	N	O	S	0	0
			2222	1421	400	393	8		

- Molecule 8 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	lH	203	Total	C	N	O	S	0	0
			1607	1053	272	278	4		

- Molecule 9 is a protein called 60S ribosomal protein L7, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	lI	210	Total	C	N	O	S	0	0
			1658	1067	301	282	8		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	lJ	213	Total	C	N	O	S	0	0
			1727	1114	317	291	5		

- Molecule 11 is a protein called 60S ribosomal protein L9, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	lK	193	Total	C	N	O	S	0	0
			1538	974	279	279	6		

- Molecule 12 is a protein called Ribosomal protein L10, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	lL	200	Total	C	N	O	S	0	0
			1597	1017	302	264	14		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	lM	170	Total	C	N	O	S	0	0
			1350	857	243	245	5		

- Molecule 14 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	lN	232	Total	C	N	O	S	0	0
			1872	1186	369	309	8		

- Molecule 15 is a protein called 60S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	lO	204	Total	C	N	O	S	0	0
			1616	1030	302	275	9		

- Molecule 16 is a protein called 60S ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	lP	132	Total	C	N	O	S	0	0
			1039	666	192	177	4		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	lQ	204	Total	C	N	O	S	0	0
			1676	1051	356	264	5		

- Molecule 18 is a protein called 60S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	lR	158	Total	C	N	O	S	0	0
			1232	779	238	210	5		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	lS	167	Total	C	N	O	S	0	0
			1321	835	258	219	9		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	lT	173	Total	C	N	O	S	0	0
			1413	910	259	235	9		

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	IU	150	Total	C	N	O	S	0	0
			1235	787	246	197	5		

- Molecule 22 is a protein called 60S ribosomal protein L21, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	IV	165	Total	C	N	O	S	0	0
			1320	846	254	217	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	IW	93	Total	C	N	O	S	0	0
			763	493	132	133	5		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	IX	133	Total	C	N	O	S	0	0
			1015	629	196	182	8		

- Molecule 25 is a protein called Ribosomal protein L23A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	IY	116	Total	C	N	O	S	0	0
			926	597	166	159	4		

- Molecule 26 is a protein called 60S ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	IZ	57	Total	C	N	O	S	0	0
			481	318	88	73	2		

- Molecule 27 is a protein called 60S ribosomal protein L26, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	la	210	Total	C	N	O	S	0	0
			1651	1055	304	285	7		

- Molecule 28 is a protein called 60S ribosomal protein L27, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	lb	137	Total	C	N	O	S	0	0
			1094	707	196	187	4		

- Molecule 29 is a protein called Large ribosomal subunit protein uL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	lc	148	Total	C	N	O	S	0	0
			1192	757	236	194	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ld	60	Total	C	N	O	S	0	0
			478	297	97	82	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	le	103	Total	C	N	O	S	0	0
			768	486	131	149	2		

- Molecule 32 is a protein called 60S ribosomal protein L31, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	lf	146	Total	C	N	O	S	0	0
			1184	759	219	200	6		

- Molecule 33 is a protein called 60S ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	lg	129	Total	C	N	O	S	0	0
			1058	672	209	172	5		

- Molecule 34 is a protein called 60S ribosomal protein L34, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	lh	105	Total	C	N	O	S	0	0
			820	512	169	133	6		

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	li	122	Total	C	N	O	S	0	0
			974	620	188	162	4		

- Molecule 36 is a protein called 60S ribosomal protein L35a, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	lj	106	Total	C	N	O	S	0	0
			841	545	158	135	3		

- Molecule 37 is a protein called 60S ribosomal protein L36, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	lk	89	Total	C	N	O	S	0	0
			712	447	144	116	5		

- Molecule 38 is a protein called 60S ribosomal protein L37-A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ll	72	Total	C	N	O	S	0	0
			591	361	132	91	7		

- Molecule 39 is a protein called 60S ribosomal protein L37A, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	lm	90	Total	C	N	O	S	0	0
			688	428	135	119	6		

- Molecule 40 is a protein called 60S ribosomal protein L38, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ln	73	Total	C	N	O	S	0	0
			584	378	104	100	2		

- Molecule 41 is a protein called Ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	lo	50	Total	C	N	O	S	0	0
			432	275	91	63	3		

- Molecule 42 is a protein called 60S ribosomal protein L40, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	lp	53	Total	C	N	O	S	0	0
			420	259	86	69	6		

- Molecule 43 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	lq	92	Total	C	N	O	S	0	0
			756	480	148	122	6		

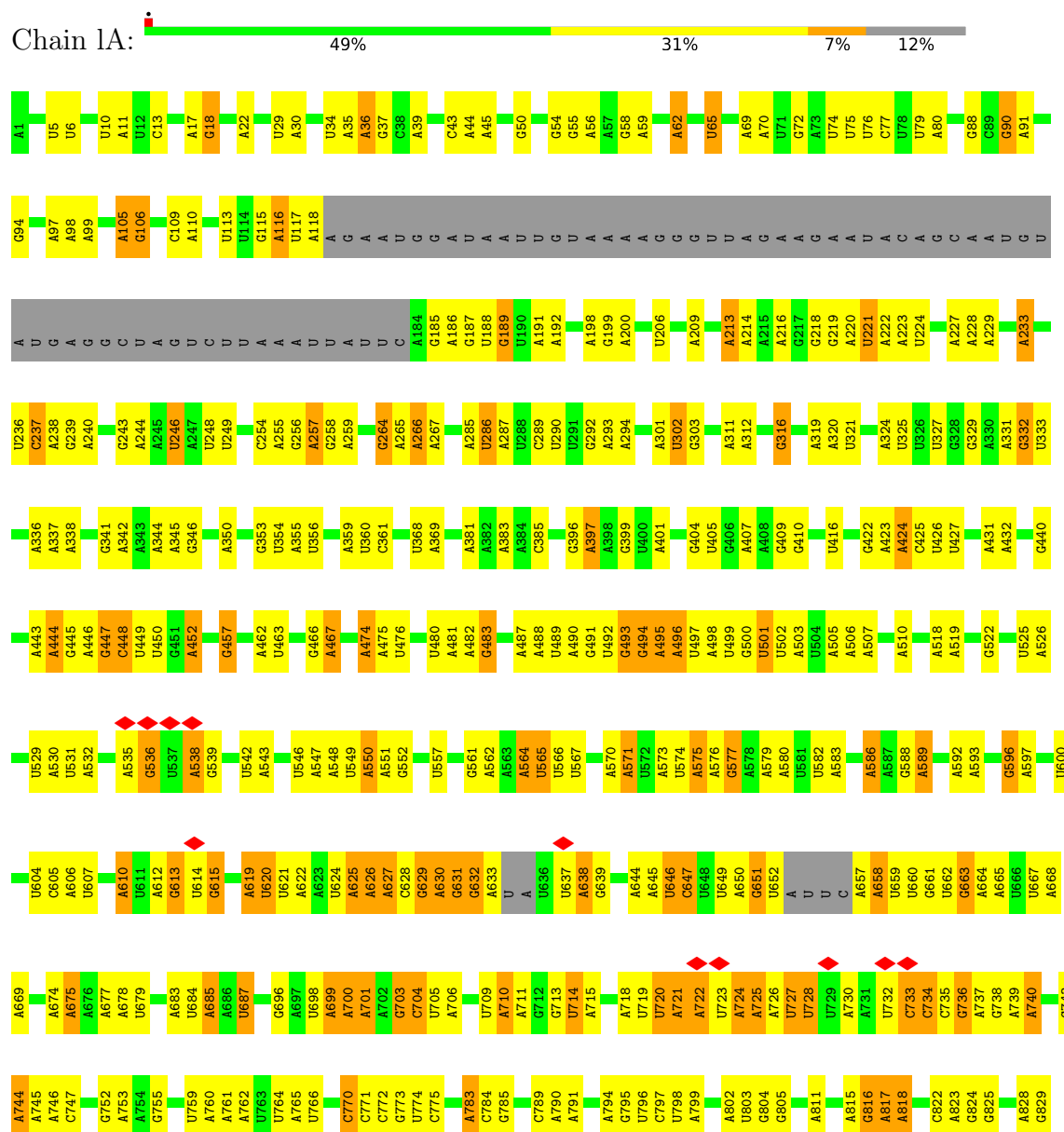
- Molecule 44 is a protein called Unknown peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	lr	13	Total	C	N	O	0	0
			65	39	13	13		

3 Residue-property plots

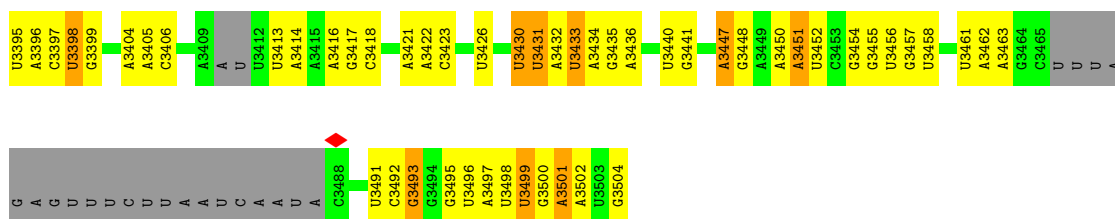
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 25S rRNA (3068-MER)



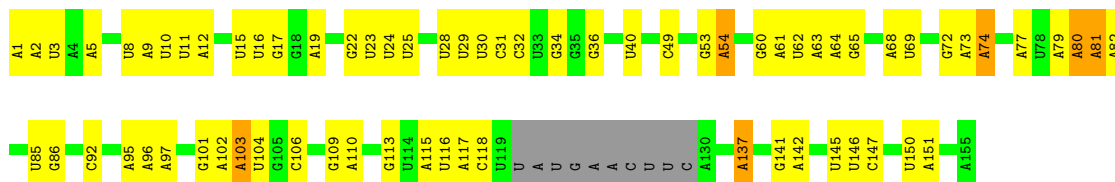
G2025	G1956	U1870	U	G1601	U1508	C1399	A1326	A1204	U1130	G1035	G934	A832
G2034	U1959	U1876	C	A1602	A1509	U1400	A1327	C1205	G1131	A1036	A935	U833
U2035	U1960	A1877	U	A1603	A1610	A1328	A1328	C1207	U1132	C1042	A936	A834
A2036	G1961	A1878	A	A1604	G1511	A1402	U1334	U1208	A	G1043	U938	A835
A2040	U1962	A1882	A	A1605	A1516	G1409	U1335	C1210	U	A1044	A939	C836
U2041	G1963	A1883	G	A1606	C1517	A1410	G1336	A1211	G	U1047	U940	A837
A2042	G1964	A1884	U	A1607	A1518	A1411	A1337	U1217	G	A1048	A941	A841
A2043	U1965	A1885	C	A1615	A1519	A1417	U1338	U1218	G	G1053	C942	A846
C2044	U1966	A1886	A	G1621	A1520	G1417	U1342	U1219	U	G1056	C948	A847
C2050	U1967	A1887	A	A1622	A1521	G1430	A1343	A1219	A	C1057	C949	A851
A2051	U1968	A1888	U	A1623	G1522	G1431	U1344	A1220	G	U1058	U953	A852
G2052	A1974	U1890	A	A1624	A1524	A1432	U1345	A1221	U	C1063	G954	A853
A2062	G1975	C1991	U	A1631	A1527	U1433	A1347	U1222	A	U1079	A954	A854
A2063	U1978	U1892	A	A1632	A1728	A1437	C1356	A1225	U	A1071	G960	A855
A2064	U1979	G1729	A	G1633	G1730	A1440	G	G1240	U	U1072	A961	A858
A2067	A1982	A1735	U	U1634	U1533	U1441	U	G1241	C	A1073	A	G864
U2072	A1983	A1736	C	A1635	A1535	U1447	G	C1243	C	C1078	A	A868
A2079	A1984	A1737	A	U1639	G1538	C1447	G	G1247	U	U1079	A	G869
A2080	A1985	A1738	G	A1640	U1539	A1456	U	U1248	A	G1086	A	A870
U2081	A1986	G1739	A	A1641	A1540	U1456	G	C1249	U	U1087	C	A871
U2082	A1987	A1740	U	A1642	A1541	U1459	C	G1256	A	U1088	U	U872
A2083	U1988	A1741	A	U1648	A1545	G1454	A	U1263	A	U1089	A	U873
G2084	A1989	U1742	U	A1649	G1546	U1456	U	G1277	A	A1090	C	A874
A2085	U1990	U1743	U	U1652	A1547	U1459	A	A1278	A	A1091	U	C875
G2095	U1991	A1744	G	G1661	U1549	U1465	A	U1289	A	A1092	G	G881
A2098	U1992	A1745	U	U1667	G1550	U1466	G	G1270	A	G1093	G	A886
G2099	U1993	U1752	U	C1668	A1551	U1467	U	C1271	A	U1094	G	A887
G2100	U1994	A1753	U	G1669	A1552	A1468	C	G1277	A	U1095	G	A889
G2101	U1995	G1754	U	U1674	C1553	A1468	G	A1278	A	U1096	A	U892
G2108	U1996	U1755	U	A1675	U1554	A1469	A	G1282	A	U1097	U	U893
C2109	U1997	U1756	U	A1676	G1556	A1474	A	A1284	A	A1098	C	A896
U2112	U1998	A1757	U	A1677	U1557	A1475	A	A1290	A	U1100	G	A897
A2113	U1999	U1758	U	U1681	C1558	G1476	C	G1291	A	U1103	U	U898
U2114	U2000	C1763	U	A1688	A1562	A1477	C	A1292	A	U1104	U	U899
U2122	U2001	A1764	U	A1689	G1563	A1478	G	U1293	A	U1105	A	A899
A2123	U2002	A1765	U	A1690	U1564	U1480	C	A1305	A	U1106	A	A904
A2124	U2003	G1768	U	G1698	G1568	A1484	U	A1306	A	G1107	A	A905
A2128	U2004	A	A	A1701	A1569	A1485	A	A1310	A	U1112	A	A908
G2129	U2005	A	U	U	U1570	C1486	A	C1311	A	A1115	A	A909
C2130	U2006	U	U	U	C1571	A1495	A	G1312	A	U1118	A	A910
A2131	U2007	U	U	U	A1580	A1496	A	U1313	A	U1119	A	G918
A2132	U2008	U	U	U	G1581	A1496	A	A1314	A	G1027	A	G919
A2133	U2009	U	U	U	G1584	G1499	A	A1315	A	A1120	A	A920
A2134	U2010	U	U	U	U1589	A1501	A	G1316	A	A1121	A	A925
G2142	U2011	U	U	U	U1592	A1502	A	A1324	A	U1126	A	A926
C2143	U2012	U	U	U	A1593	G1503	A	C1325	A	A1127	A	A1033
	U2013	U	U	U	U	G1504	A		A		A	A1034
	U2014	U	U	U	U	G1505	A		A		A	
	U2015	U	U	U	U		A		A		A	
	U2016	U	U	U	U		A		A		A	
	U2017	U	U	U	U		A		A		A	
	U2018	U	U	U	U		A		A		A	
	U2019	U	U	U	U		A		A		A	
	U2020	U	U	U	U		A		A		A	
	U2021	U	U	U	U		A		A		A	
	U2022	U	U	U	U		A		A		A	
	U2023	U	U	U	U		A		A		A	
	U2024	U	U	U	U		A		A		A	
	U2025	U	U	U	U		A		A		A	
	U2026	U	U	U	U		A		A		A	
	U2027	U	U	U	U		A		A		A	
	U2028	U	U	U	U		A		A		A	
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	U2030	U	U	U	U		A		A		A	
	U2031	U	U	U	U		A		A		A	
	U2032	U	U	U	U		A		A		A	
	U2033	U	U	U	U		A		A		A	
	U2034	U	U	U	U		A		A		A	
	U2035	U	U	U	U		A		A		A	
	U2036	U	U	U	U		A		A		A	
	U2037	U	U	U	U		A		A		A	
	U2038	U	U	U	U		A		A		A	
	U2039	U	U	U	U		A		A		A	
	U2040	U	U	U	U		A		A		A	
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	U2043	U	U	U	U		A		A		A	
	U2044	U	U	U	U		A		A		A	
	U2045	U	U	U	U		A		A		A	
	U2046	U	U	U	U		A		A		A	
	U2047	U	U	U	U		A		A		A	
	U2048	U	U	U	U		A		A		A	
	U2049	U	U	U	U		A		A		A	
	U2050	U	U	U	U		A		A		A	
	U2051	U	U	U	U		A		A		A	
	U2052	U	U	U	U		A		A		A	
	U2053	U	U	U	U		A		A		A	
	U2054	U	U	U	U		A		A		A	
	U2055	U	U	U	U		A		A		A	
	U2056	U	U	U	U		A		A		A	
	U2057	U	U	U	U		A		A		A	
	U2058	U	U	U	U		A		A		A	
	U2059	U	U	U	U		A		A		A	
	U2060	U	U	U	U		A		A		A	
	U2061	U	U	U	U		A		A		A	
	U2062	U	U	U	U		A		A		A	
	U2063	U	U	U	U		A		A		A	
	U2064	U	U	U	U		A		A		A	
	U2065	U	U	U	U		A		A		A	
	U2066	U	U	U	U		A		A		A	
	U2067	U	U	U	U		A		A		A	
	U2068	U	U	U	U		A		A		A	
	U2069	U	U	U	U		A		A		A	
	U2070	U	U	U	U		A		A		A	
	U2071	U	U	U	U		A		A		A	
	U2072	U	U	U	U		A		A		A	
	U2073	U	U	U	U		A		A		A	
	U2074	U	U	U	U		A		A		A	
	U2075	U	U	U	U		A		A		A	
	U2076	U	U	U	U		A		A		A	
	U2077	U	U	U	U		A		A		A	
	U2078	U	U	U	U		A		A		A	
	U2079	U	U	U	U		A		A		A	
	U2080	U	U	U	U		A		A		A	
	U2081	U	U	U	U		A		A		A	
	U2082	U	U	U	U		A		A		A	
	U2083	U	U	U	U		A		A		A	
	U2084	U	U	U	U		A		A		A	
	U2085	U	U	U	U		A		A		A	
	U2086	U	U	U	U		A		A		A	
	U2087	U	U	U	U		A		A		A	
	U2088	U	U	U	U		A		A		A	
	U2089	U	U	U	U		A		A		A	
	U2090	U	U	U	U		A		A		A	
	U2091	U	U	U	U		A		A		A	
	U2092	U	U	U	U		A		A		A	
	U2093	U	U	U	U		A		A		A	
	U2094	U	U	U	U		A		A		A	
	U2095	U	U	U	U		A		A		A	
	U2096	U	U	U	U		A		A		A	
	U2097	U	U	U	U		A		A		A	
	U2098	U	U	U	U		A		A		A	
	U2099	U	U	U	U		A		A		A	
	U2100	U	U	U	U		A		A		A	
	U2101	U	U	U	U		A		A		A	
	U2102	U	U	U	U		A		A		A	
	U2103	U	U	U	U		A		A		A	
	U2104	U	U	U	U		A		A		A	
	U2105	U	U	U	U		A		A		A	
	U2106	U	U	U	U		A		A		A	
	U2107	U	U	U	U		A		A		A	





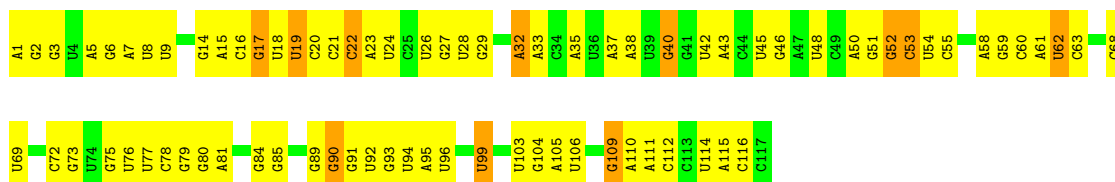
• Molecule 2: 5.8S rRNA (145-MER)

Chain IB: 48% 41% 6%



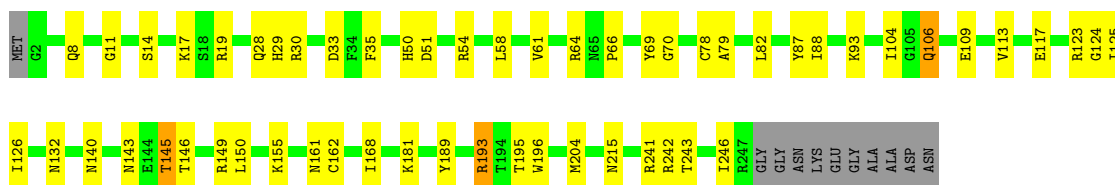
• Molecule 3: 5S rRNA (117-MER)

Chain IC: 32% 58% 9%



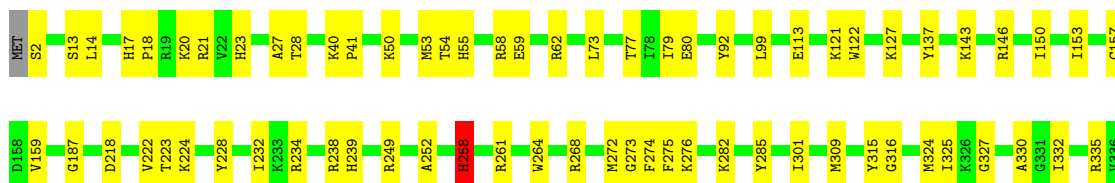
• Molecule 4: Large ribosomal subunit protein uL2

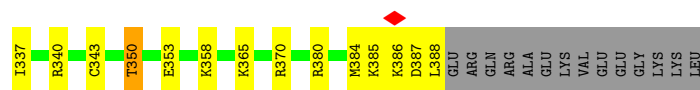
Chain ID: 74% 21%



• Molecule 5: 60S ribosomal protein L3, putative

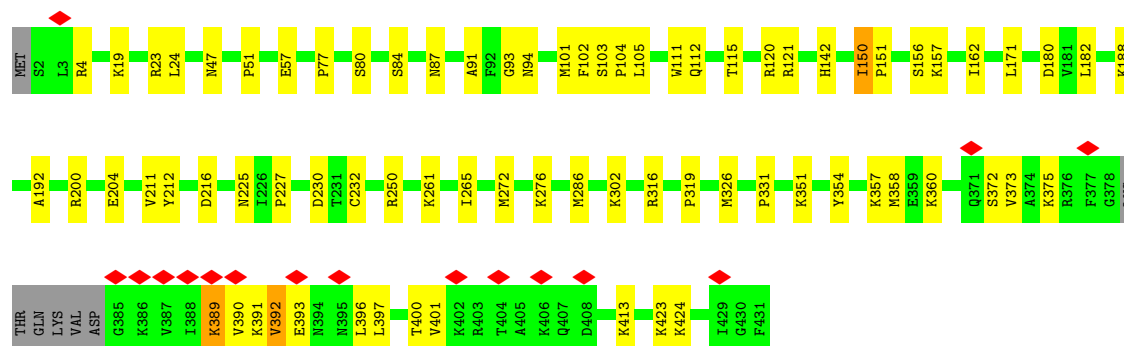
Chain IE: 76% 20%





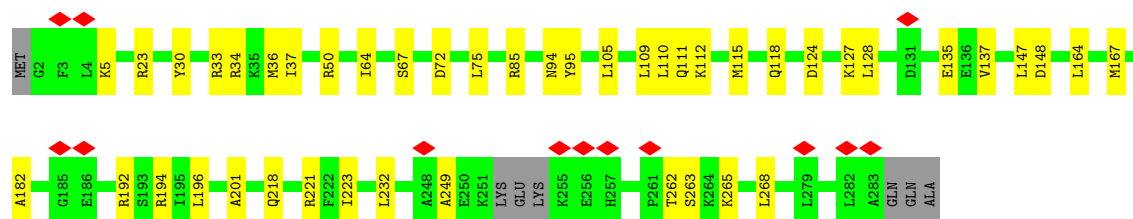
- Molecule 6: 60S ribosomal protein L4, putative

Chain IF: 81% 17% ..



- Molecule 7: 60S ribosomal protein L5, putative

Chain IG: 5% 82% 16% .



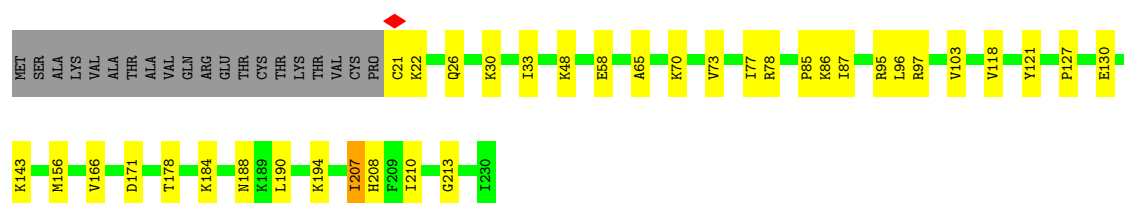
- Molecule 8: 60S ribosomal protein L6, putative

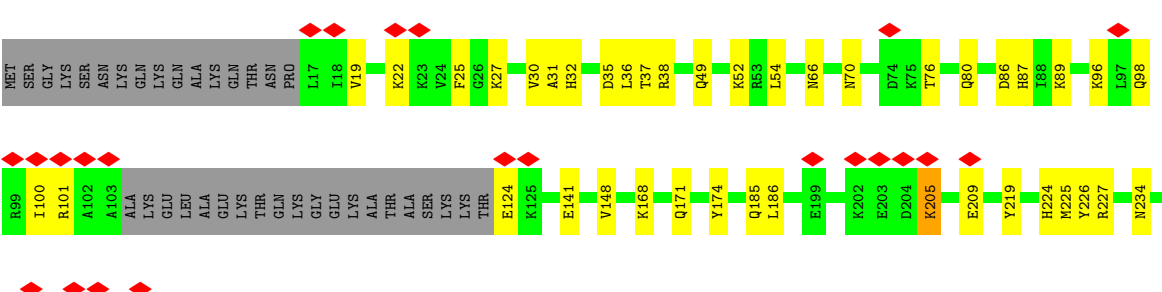
Chain IH: 78% 21%



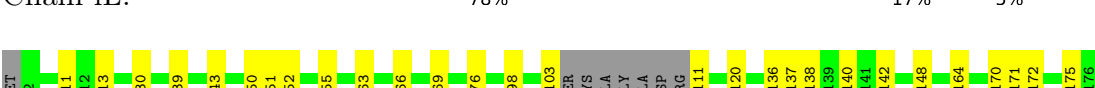
- Molecule 9: 60S ribosomal protein L7, putative

Chain II: 76% 15% 9%

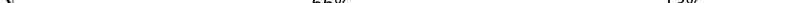


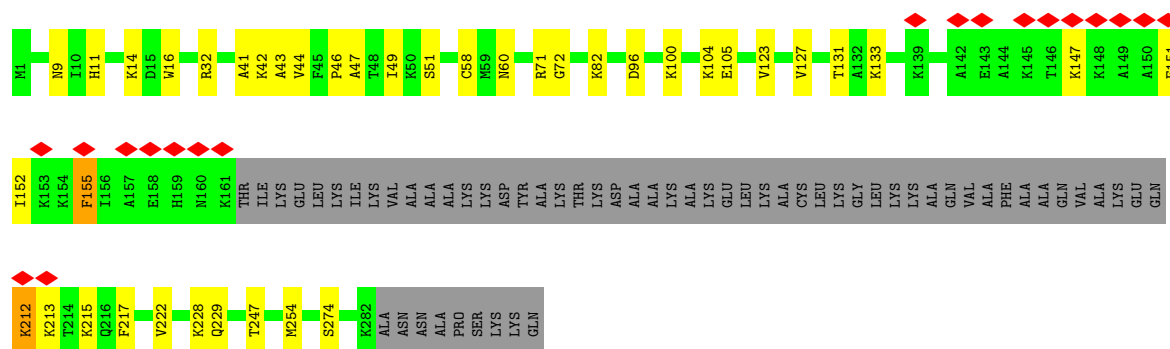
- Chain 1J: 
- 
- | Position | Amino Acid | Frequency (bits) |
|----------|------------|------------------|
| 1 | Met | 0.00 |
| 2 | Ser | 0.00 |
| 3 | Gly | 0.00 |
| 4 | Lys | 0.00 |
| 5 | Ser | 0.00 |
| 6 | Asn | 0.00 |
| 7 | Gln | 0.00 |
| 8 | Lys | 0.00 |
| 9 | Gln | 0.00 |
| 10 | Ala | 0.00 |
| 11 | Lys | 0.00 |
| 12 | Gln | 0.00 |
| 13 | Thr | 0.00 |
| 14 | Asn | 0.00 |
| 15 | Pro | 0.00 |
| 16 | Lys | 0.00 |
| 17 | Lys | 0.00 |
| 18 | Lys | 0.00 |
| 19 | Lys | 0.00 |
| 20 | Lys | 0.00 |
| 21 | Lys | 0.00 |
| 22 | Lys | 0.00 |
| 23 | Lys | 0.00 |
| 24 | Lys | 0.00 |
| 25 | Lys | 0.00 |
| 26 | Lys | 0.00 |
| 27 | Lys | 0.00 |
| 28 | Lys | 0.00 |
| 29 | Lys | 0.00 |
| 30 | Lys | 0.00 |
| 31 | Lys | 0.00 |
| 32 | Lys | 0.00 |
| 33 | Lys | 0.00 |
| 34 | Lys | 0.00 |
| 35 | Lys | 0.00 |
| 36 | Lys | 0.00 |
| 37 | Lys | 0.00 |
| 38 | Lys | 0.00 |
| 39 | Lys | 0.00 |
| 40 | Lys | 0.00 |
| 41 | Lys | 0.00 |
| 42 | Lys | 0.00 |
| 43 | Lys | 0.00 |
| 44 | Lys | 0.00 |
| 45 | Lys | 0.00 |
| 46 | Lys | 0.00 |
| 47 | Lys | 0.00 |
| 48 | Lys | 0.00 |
| 49 | Lys | 0.00 |
| 50 | Lys | 0.00 |
| 51 | Lys | 0.00 |
| 52 | Lys | 0.00 |
| 53 | Lys | 0.00 |
| 54 | Lys | 0.00 |
| 55 | Lys | 0.00 |
| 56 | Lys | 0.00 |
| 57 | Lys | 0.00 |
| 58 | Lys | 0.00 |
| 59 | Lys | 0.00 |
| 60 | Lys | 0.00 |
| 61 | Lys | 0.00 |
| 62 | Lys | 0.00 |
| 63 | Lys | 0.00 |
| 64 | Lys | 0.00 |
| 65 | Lys | 0.00 |
| 66 | Lys | 0.00 |
| 67 | Lys | 0.00 |
| 68 | Lys | 0.00 |
| 69 | Lys | 0.00 |
| 70 | Lys | 0.00 |
| 71 | Lys | 0.00 |
| 72 | Lys | 0.00 |
| 73 | Lys | 0.00 |
| 74 | Lys | 0.00 |
| 75 | Lys | 0.00 |
| 76 | Lys | 0.00 |
| 77 | Lys | 0.00 |
| 78 | Lys | 0.00 |
| 79 | Lys | 0.00 |
| 80 | Lys | 0.00 |
| 81 | Lys | 0.00 |
| 82 | Lys | 0.00 |
| 83 | Lys | 0.00 |
| 84 | Lys | 0.00 |
| 85 | Lys | 0.00 |
| 86 | Lys | 0.00 |
| 87 | Lys | 0.00 |
| 88 | Lys | 0.00 |
| 89 | Lys | 0.00 |
| 90 | Lys | 0.00 |
| 91 | Lys | 0.00 |
| 92 | Lys | 0.00 |
| 93 | Lys | 0.00 |
| 94 | Lys | 0.00 |
| 95 | Lys | 0.00 |
| 96 | Lys | 0.00 |
| 97 | Lys | 0.00 |
| 98 | Lys | 0.00 |
| 99 | Lys | 0.00 |
| 100 | Lys | 0.00 |
| 101 | Lys | 0.00 |
| 102 | Lys | 0.00 |
| 103 | Lys | 0.00 |
| 104 | Lys | 0.00 |
| 105 | Lys | 0.00 |
| 106 | Lys | 0.00 |
| 107 | Lys | 0.00 |
| 108 | Lys | 0.00 |
| 109 | Lys | 0.00 |
| 110 | Lys | 0.00 |
| 111 | Lys | 0.00 |
| 112 | Lys | 0.00 |
| 113 | Lys | 0.00 |
| 114 | Lys | 0.00 |
| 115 | Lys | 0.00 |
| 116 | Lys | 0.00 |
| 117 | Lys | 0.00 |
| 118 | Lys | 0.00 |
| 119 | Lys | 0.00 |
| 120 | Lys | 0.00 |
| 121 | Lys | 0.00 |
| 122 | Lys | 0.00 |
| 123 | Lys | 0.00 |
| 124 | Lys | 0.00 |
| 125 | Lys | 0.00 |
| 126 | Lys | 0.00 |
| 127 | Lys | 0.00 |
| 128 | Lys | 0.00 |
| 129 | Lys | 0.00 |
| 130 | Lys | 0.00 |
| 131 | Lys | 0.00 |
| 132 | Lys | 0.00 |
| 133 | Lys | 0.00 |
| 134 | Lys | 0.00 |
| 135 | Lys | 0.00 |
| 136 | Lys | 0.00 |
| 137 | Lys | 0.00 |
| 138 | Lys | 0.00 |
| 139 | Lys | 0.00 |
| 140 | Lys | 0.00 |
| 141 | Lys | 0.00 |
| 142 | Lys | 0.00 |
| 143 | Lys | |

- Chain 1K: 

- Chain 1L: 
- 

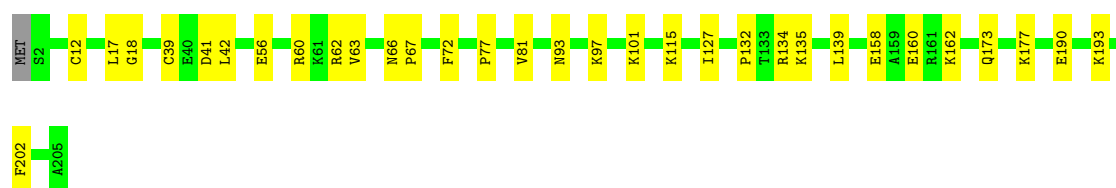
- Chain IM: 

- Chain IN: 



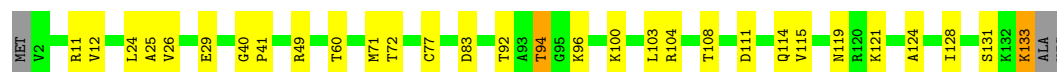
- Molecule 15: 60S ribosomal protein L13, putative

Chain IO: 84% 16%



- Molecule 16: 60S ribosomal protein L14, putative

Chain IP: 76% 21% ..



- Molecule 17: Ribosomal protein L15

Chain IQ: 89% 10%



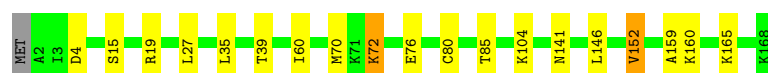
- Molecule 18: 60S ribosomal protein L17, putative

Chain IR: 79% 8% 12%



- Molecule 19: 60S ribosomal protein L18, putative

Chain IS: 88% 10% ..



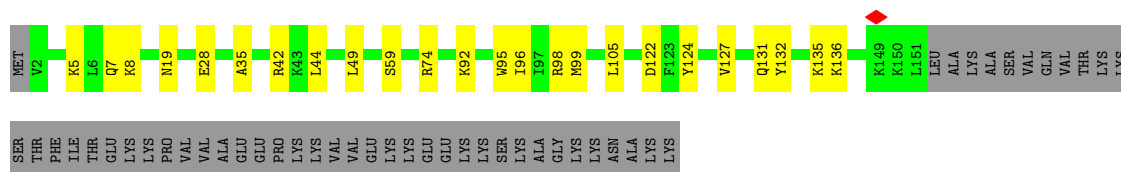
- Molecule 20: 60S ribosomal protein L18a

Chain 1T:  86% 13% .



- Molecule 21: Ribosomal protein L19

Chain 1U:  64% 12% 24%

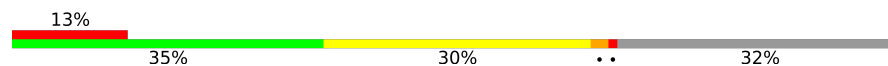


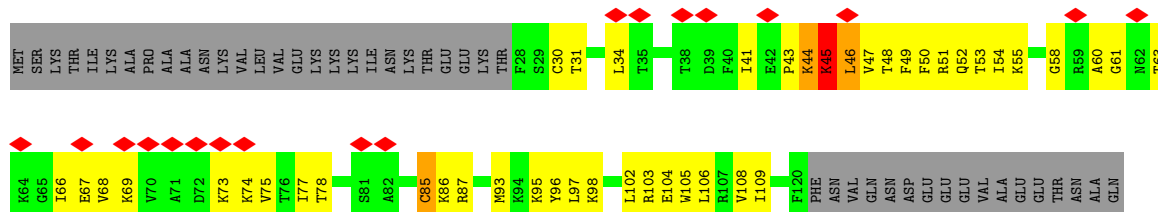
- Molecule 22: 60S ribosomal protein L21, putative

Chain 1V:  86% 13% ..



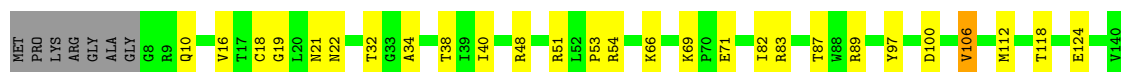
- Molecule 23: Large ribosomal subunit protein eL22

Chain 1W:  13% 35% 30% .. 32%



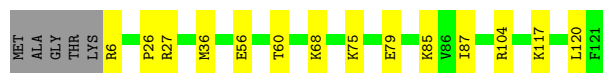
- Molecule 24: 60S ribosomal protein L23, putative

Chain 1X:  76% 19% . 5%

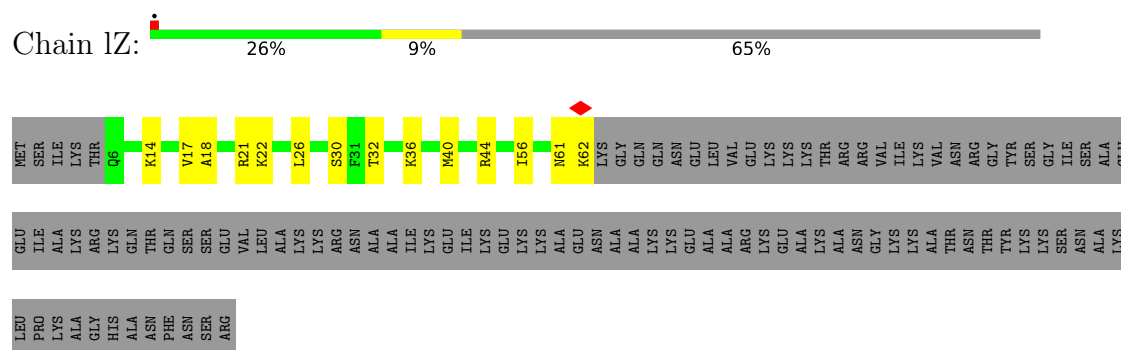


- Molecule 25: Ribosomal protein L23A, putative

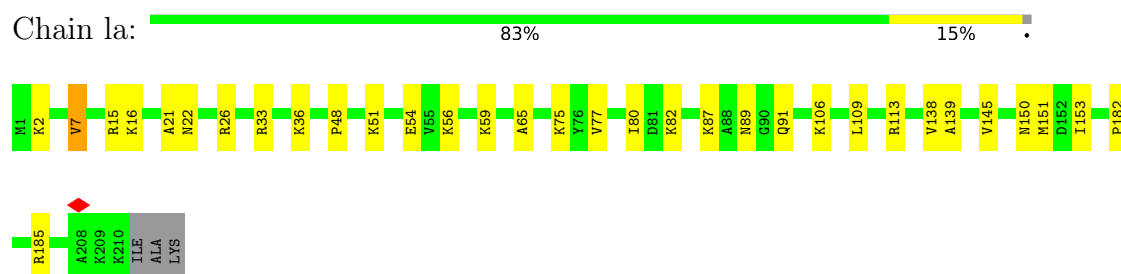
Chain 1Y:  84% 12% .



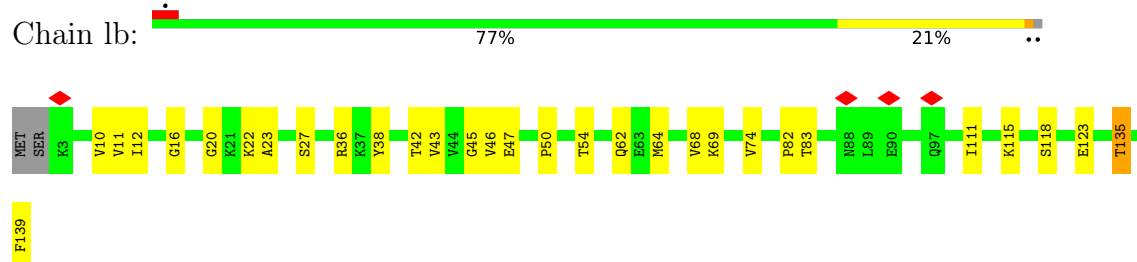
- Molecule 26: 60S ribosomal protein L24, putative



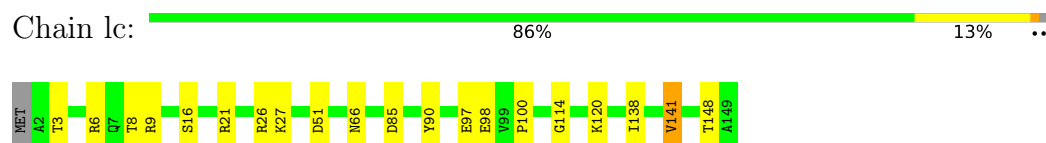
- Molecule 27: 60S ribosomal protein L26, putative



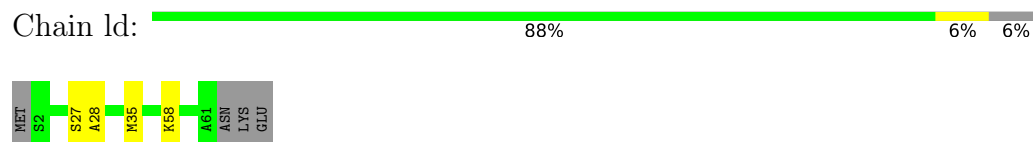
- Molecule 28: 60S ribosomal protein L27, putative



- Molecule 29: Large ribosomal subunit protein uL15A

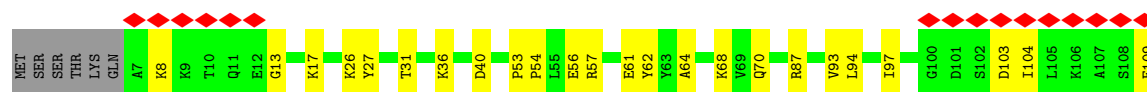


- Molecule 30: 60S ribosomal protein L29

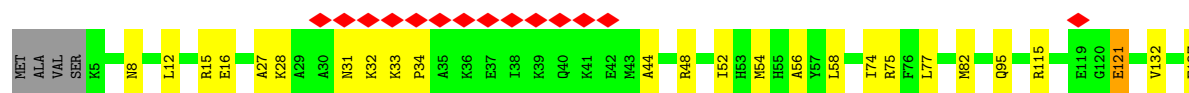
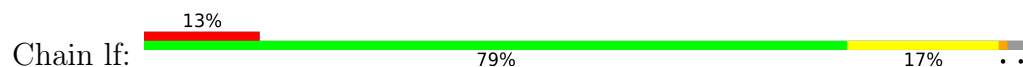


- Molecule 31: 60S ribosomal protein L30, putative

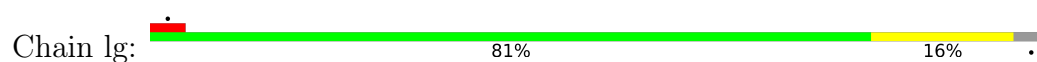




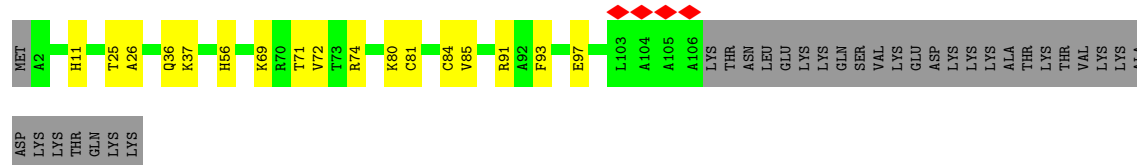
- Molecule 32: 60S ribosomal protein L31, putative



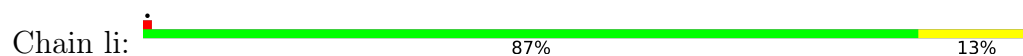
- Molecule 33: 60S ribosomal protein L32, putative



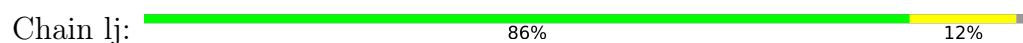
- Molecule 34: 60S ribosomal protein L34, putative



- Molecule 35: uL29

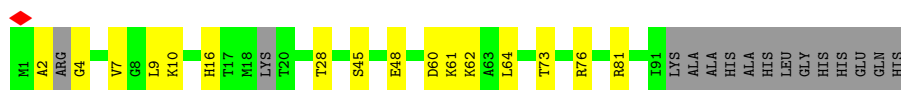


- Molecule 36: 60S ribosomal protein L35a, putative



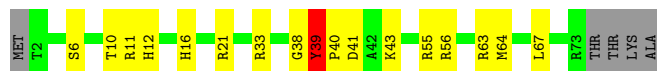
- Molecule 37: 60S ribosomal protein L36, putative





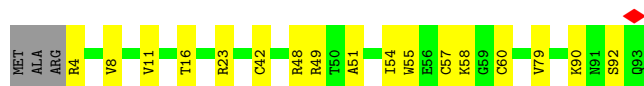
- Molecule 38: 60S ribosomal protein L37-A, putative

Chain II: 71% 21% 6%



- Molecule 39: 60S ribosomal protein L37A, putative

Chain Im: 78% 18% 4%



- Molecule 40: 60S ribosomal protein L38, putative

Chain In: 10% 63% 23% 2%



- Molecule 41: Ribosomal protein L39, putative

Chain Io: 86% 10% 4%



- Molecule 42: 60S ribosomal protein L40, putative

Chain Ip: 59% 32% 9%



- Molecule 43: 60S ribosomal protein L44, putative

Chain Iq: 81% 13% 6%



- Molecule 44: Unknown peptide

Chain lr:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	378061	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	18.211	Depositor
Minimum map value	-6.837	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	321.00003, 321.00003, 321.00003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1A	0.19	0/73480	0.30	0/114456
2	1B	0.19	0/3470	0.30	0/5401
3	1C	0.20	0/2765	0.37	2/4303 (0.0%)
4	1D	0.18	0/1920	0.29	0/2582
5	1E	0.18	0/3140	0.33	0/4216
6	1F	0.19	0/3330	0.30	1/4468 (0.0%)
7	1G	0.14	0/2261	0.29	0/3028
8	1H	0.14	0/1639	0.31	0/2203
9	1I	0.16	0/1680	0.29	0/2252
10	1J	0.12	0/1757	0.28	0/2360
11	1K	0.13	0/1562	0.23	0/2103
12	1L	0.16	0/1633	0.31	0/2184
13	1M	0.11	0/1369	0.26	0/1834
14	1N	0.16	0/1900	0.29	0/2534
15	1O	0.17	0/1646	0.28	0/2209
16	1P	0.23	0/1051	0.34	1/1411 (0.1%)
17	1Q	0.18	0/1707	0.24	0/2276
18	1R	0.18	0/1251	0.26	0/1675
19	1S	0.16	0/1342	0.25	0/1796
20	1T	0.16	0/1445	0.26	0/1946
21	1U	0.14	0/1253	0.24	0/1666
22	1V	0.17	0/1351	0.27	0/1819
23	1W	0.27	0/774	0.67	1/1031 (0.1%)
24	1X	0.17	0/1030	0.29	0/1384
25	1Y	0.14	0/941	0.22	0/1262
26	1Z	0.12	0/492	0.24	0/656
27	1a	0.14	0/1673	0.23	0/2236
28	1b	0.13	0/1112	0.26	0/1489
29	1c	0.19	0/1223	0.27	0/1636
30	1d	0.18	0/485	0.31	0/639
31	1e	0.13	0/776	0.29	0/1044
32	1f	0.15	0/1205	0.28	0/1609
33	1g	0.18	0/1075	0.26	0/1434
34	1h	0.16	0/833	0.23	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	li	0.14	0/984	0.23	0/1310
36	lj	0.19	0/862	0.29	0/1163
37	lk	0.11	0/721	0.22	0/955
38	ll	0.20	0/602	0.33	0/797
39	lm	0.16	0/696	0.33	0/928
40	ln	0.15	0/592	0.29	0/789
41	lo	0.19	0/444	0.23	0/587
42	lp	0.17	0/425	0.54	2/563 (0.4%)
43	lq	0.16	0/770	0.24	0/1019
All	All	0.18	0/130667	0.30	7/192368 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	lE	0	1
20	lT	0	1
23	lW	0	1
38	ll	0	1
All	All	0	4

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	lC	62	U	OP2-P-O3'	-8.80	81.60	108.00
3	lC	62	U	OP1-P-O3'	-8.53	82.40	108.00
42	lp	24	CYS	CA-CB-SG	6.31	128.92	114.40
42	lp	35	CYS	CA-CB-SG	5.99	128.18	114.40
6	lF	389	LYS	CA-CB-CG	5.92	125.94	114.10
16	lP	133	LYS	CA-CB-CG	5.82	125.74	114.10
23	lW	45	LYS	CA-CB-CG	5.32	124.73	114.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	lE	258	HIS	Peptide
20	lT	172	LEU	Peptide

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Mol	Chain	Res	Type	Group
23	IW	44	LYS	Peptide
38	II	39	TYR	Peptide

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	IA	65572	0	32902	942	0
2	IB	3097	0	1552	41	0
3	IC	2477	0	1252	95	0
4	ID	1881	0	1928	40	0
5	IE	3076	0	3209	62	0
6	IF	3272	0	3500	63	0
7	IG	2222	0	2304	35	0
8	IH	1607	0	1726	31	0
9	II	1658	0	1802	29	0
10	IJ	1727	0	1849	25	0
11	IK	1538	0	1598	28	0
12	IL	1597	0	1654	23	0
13	IM	1350	0	1390	28	0
14	IN	1872	0	2034	37	0
15	IO	1616	0	1700	21	0
16	IP	1039	0	1133	23	0
17	IQ	1676	0	1777	16	0
18	IR	1232	0	1307	12	0
19	IS	1321	0	1427	14	0
20	IT	1413	0	1479	17	0
21	IU	1235	0	1369	21	0
22	IV	1320	0	1406	18	0
23	IW	763	0	818	38	0
24	IX	1015	0	1054	24	0
25	IY	926	0	997	11	0
26	IZ	481	0	518	10	0
27	la	1651	0	1822	23	0
28	lb	1094	0	1174	22	0
29	lc	1192	0	1205	18	0
30	ld	478	0	507	3	0
31	le	768	0	810	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	lf	1184	0	1270	18	0
33	lg	1058	0	1140	15	0
34	lh	820	0	864	13	0
35	li	974	0	1093	14	0
36	lj	841	0	878	9	0
37	lk	712	0	755	11	0
38	ll	591	0	617	13	0
39	lm	688	0	728	14	0
40	ln	584	0	643	13	0
41	lo	432	0	444	6	0
42	lp	420	0	450	15	0
43	lq	756	0	821	10	0
44	lr	65	0	16	0	0
All	All	121291	0	88922	1660	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (1660) 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)
3:IC:79:G:N1	3:IC:95:A:C2	2.13	1.17
3:IC:79:G:N1	3:IC:95:A:H2	1.41	1.15
3:IC:81:A:H2	3:IC:93:G:N1	1.44	1.13
1:1A:3454:G:N1	1:1A:3502:A:H2	1.50	1.09
1:1A:3454:G:N1	1:1A:3502:A:C2	2.20	1.05
3:IC:27:G:H1	3:IC:50:A:N6	1.55	1.03
5:IE:17:HIS:HD2	5:IE:18:PRO:HA	1.23	1.03
1:1A:638:A:N6	1:1A:651:G:H1	1.64	0.95
1:1A:869:G:H21	1:1A:872:A:N6	1.64	0.94
3:IC:81:A:C2	3:IC:93:G:N1	2.24	0.94
1:1A:638:A:H61	1:1A:651:G:H1	0.98	0.94
2:1B:49:C:HO2'	2:1B:63:A:HO2'	1.06	0.92
1:1A:869:G:N2	1:1A:872:A:N6	2.17	0.91
3:IC:18:U:H3	3:IC:58:A:H61	1.20	0.90
3:IC:27:G:H1	3:IC:50:A:H61	0.91	0.89
23:1W:52:GLN:HA	23:1W:61:GLY:HA2	1.54	0.89
23:1W:45:LYS:O	23:1W:49:PHE:N	2.07	0.87
1:1A:631:G:H1	1:1A:659:U:H3	1.16	0.86
1:1A:3457:G:H1	1:1A:3496:U:H3	1.18	0.86
3:IC:52:G:N2	3:IC:54:U:O4	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:774:U:OP1	29:lc:21:ARG:NH2	2.09	0.85
1:1A:737:A:H3'	1:1A:738:G:H21	1.40	0.85
3:1C:26:U:H3	3:1C:51:G:H22	1.26	0.83
3:1C:81:A:N1	3:1C:93:G:O6	2.11	0.83
1:1A:2269:U:H5'	1:1A:2270:G:H5'	1.59	0.83
1:1A:17:A:H2	2:1B:137:A:H61	1.25	0.83
3:1C:75:G:H1	3:1C:99:U:H5	1.22	0.83
1:1A:3146:U:H4'	1:1A:3147:U:H5''	1.61	0.81
3:1C:27:G:N2	3:1C:50:A:N1	2.28	0.81
1:1A:1118:A:H2	1:1A:1165:A:H62	1.27	0.81
13:1M:110:ILE:HD12	13:1M:111:ASP:H	1.44	0.81
1:1A:3455:G:H22	1:1A:3501:A:H2	1.30	0.80
6:1F:389:LYS:HD2	6:1F:389:LYS:O	1.81	0.79
1:1A:493:G:H21	1:1A:580:A:H61	1.31	0.79
1:1A:1841:G:H22	1:1A:1975:G:H1	1.27	0.79
1:1A:869:G:N2	1:1A:872:A:H62	1.78	0.79
1:1A:1818:C:OP2	34:lh:74:ARG:NH2	2.16	0.78
1:1A:869:G:N2	1:1A:872:A:C6	2.51	0.78
3:1C:69:U:H3	3:1C:104:G:H1	1.28	0.78
3:1C:79:G:O6	3:1C:95:A:N1	2.16	0.78
5:1E:17:HIS:CD2	5:1E:18:PRO:HA	2.15	0.77
23:1W:45:LYS:HB2	23:1W:45:LYS:HZ2	1.48	0.77
1:1A:1605:A:H2	1:1A:3430:U:H3	1.33	0.76
1:1A:409:G:OP2	38:ll:56:ARG:NH2	2.19	0.76
1:1A:3211:A:H2	1:1A:3239:G:H21	1.32	0.75
1:1A:3454:G:O6	1:1A:3502:A:N1	2.18	0.75
3:1C:68:C:H42	3:1C:105:A:H61	1.31	0.75
1:1A:3498:U:H4'	1:1A:3499:U:H5'	1.69	0.75
1:1A:2721:G:H1	1:1A:2941:C:H5	1.34	0.75
6:1F:375:LYS:HB2	6:1F:390:VAL:HG11	1.69	0.75
9:1I:30:LYS:H	9:1I:30:LYS:HD2	1.51	0.74
17:1Q:14:LYS:O	17:1Q:23:ARG:NH2	2.19	0.73
1:1A:869:G:N2	1:1A:872:A:C5	2.56	0.73
25:1Y:60:THR:HG22	25:1Y:104:ARG:HG3	1.71	0.73
35:li:-7:LEU:HD22	35:li:42:ASP:HB3	1.70	0.73
1:1A:816:G:N2	1:1A:829:G:OP2	2.21	0.73
6:1F:101:MET:HE3	6:1F:104:PRO:HA	1.71	0.73
25:1Y:56:GLU:OE2	25:1Y:56:GLU:N	2.18	0.72
42:lp:21:CYS:HB3	42:lp:24:CYS:HB2	1.71	0.72
1:1A:1086:G:H1	1:1A:1240:C:H5	1.38	0.72
8:1H:56:ARG:NH1	36:lj:108:ILE:O	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1661:G:O2'	1:1A:1751:A:N6	2.22	0.72
1:1A:631:G:N2	1:1A:659:U:O2	2.22	0.72
39:1m:8:VAL:HG13	39:1m:11:VAL:HG23	1.72	0.71
12:1L:179:GLU:OE2	12:1L:179:GLU:N	2.21	0.71
13:1M:108:GLU:HG2	13:1M:122:ILE:HD11	1.72	0.71
33:1g:41:ASN:HB3	33:1g:44:ARG:HG2	1.72	0.71
20:1T:5:TYR:HB2	20:1T:60:ILE:HD11	1.73	0.71
7:1G:50:ARG:NH2	7:1G:72:ASP:OD2	2.23	0.71
1:1A:1883:A:H62	1:1A:1931:U:H3	1.36	0.71
3:1C:6:G:H1	3:1C:111:A:H2	1.39	0.71
3:1C:59:G:H5'	7:1G:265:LYS:HG2	1.71	0.71
28:1b:68:VAL:O	28:1b:118:SER:OG	2.08	0.71
1:1A:1502:A:N6	19:1S:15:SER:OG	2.24	0.70
1:1A:1247:G:H1	3:1C:92:U:H5	1.37	0.70
1:1A:3456:U:H3	1:1A:3497:A:H2	1.38	0.70
23:1W:45:LYS:HB2	23:1W:45:LYS:NZ	2.01	0.70
3:1C:3:G:H1	3:1C:114:U:H3	1.37	0.70
9:1I:130:GLU:N	9:1I:130:GLU:OE2	2.25	0.70
1:1A:50:G:HO2'	1:1A:1688:A:HO2'	1.39	0.69
3:1C:84:G:H22	3:1C:91:G:N2	1.91	0.69
1:1A:3302:U:H2'	1:1A:3303:A:H8	1.56	0.69
1:1A:804:G:H22	1:1A:911:U:H3	1.39	0.69
4:1D:117:GLU:HG2	4:1D:124:GLY:H	1.58	0.69
32:1f:27:ALA:O	32:1f:31:ASN:ND2	2.25	0.69
16:1P:25:ALA:HA	16:1P:40:GLY:HA3	1.73	0.69
14:1N:82:LYS:NZ	14:1N:215:LYS:O	2.26	0.69
22:1V:88:ARG:NH2	30:1d:28:ALA:O	2.25	0.69
1:1A:920:A:OP1	29:1c:27:LYS:NZ	2.25	0.69
40:1n:31:ARG:HG3	40:1n:42:LYS:HB2	1.75	0.69
37:1k:45:SER:HB2	37:1k:48:GLU:HG3	1.75	0.69
1:1A:1187:A:H62	1:1A:1217:U:H3	1.41	0.68
3:1C:22:C:H2'	3:1C:23:A:H8	1.58	0.68
12:1L:170:LYS:HA	12:1L:177:THR:HA	1.74	0.68
1:1A:2416:U:O2'	1:1A:3246:A:N1	2.22	0.68
1:1A:3204:C:O2	24:1X:89:ARG:NH1	2.26	0.68
1:1A:1864:C:OP1	23:1W:98:LYS:NZ	2.27	0.68
1:1A:3246:A:O2'	24:1X:54:ARG:NH2	2.27	0.68
1:1A:3458:U:H3	1:1A:3495:G:H1	1.41	0.68
3:1C:79:G:C6	3:1C:95:A:N1	2.61	0.68
6:1F:230:ASP:OD2	6:1F:250:ARG:NH2	2.24	0.68
1:1A:638:A:N1	1:1A:651:G:N2	2.36	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:IC:26:U:O2	3:IC:52:G:N2	2.27	0.67
11:IK:112:VAL:HB	11:IK:121:GLN:HB2	1.75	0.67
34:lh:81:CYS:SG	34:lh:84:CYS:N	2.64	0.67
3:IC:17:G:H1	3:IC:59:G:H1	1.42	0.67
1:IA:2906:U:H2'	1:IA:2907:C:H6	1.60	0.67
1:IA:3336:G:O2'	15:IO:115:LYS:O	2.12	0.67
1:IA:3454:G:H1	1:IA:3502:A:H2	0.74	0.67
4:ID:106:GLN:O	39:lm:90:LYS:NZ	2.28	0.67
1:IA:1127:A:H4'	12:IL:39:ARG:HD2	1.77	0.67
1:IA:2688:G:O2'	1:IA:3008:U:OP1	2.11	0.67
1:IA:2261:G:O2'	1:IA:2390:U:OP2	2.13	0.66
6:IF:77:PRO:HB2	6:IF:91:ALA:HB3	1.77	0.66
1:IA:331:A:OP2	43:lq:39:ARG:NH1	2.28	0.66
1:IA:610:A:N6	1:IA:687:U:O4	2.28	0.66
33:lg:91:ARG:HG3	33:lg:91:ARG:HH11	1.60	0.66
1:IA:43:C:H5''	14:IN:14:LYS:HG3	1.78	0.66
1:IA:1763:C:H2'	1:IA:1764:A:H8	1.60	0.66
1:IA:1841:G:N2	1:IA:1975:G:H22	1.94	0.66
1:IA:993:U:OP2	1:IA:2109:C:O2'	2.12	0.66
3:IC:79:G:C2	3:IC:95:A:H2	2.10	0.66
1:IA:2906:U:H2'	1:IA:2907:C:C6	2.31	0.66
2:IB:60:G:O6	38:ll:63:ARG:NH2	2.28	0.66
1:IA:2466:G:N2	5:IE:228:TYR:OH	2.24	0.66
1:IA:116:A:N6	10:IJ:124:GLU:O	2.30	0.65
1:IA:1744:A:H2'	1:IA:1745:A:C8	2.32	0.65
9:II:95:ARG:NH2	9:II:190:LEU:O	2.29	0.65
1:IA:189:G:OP1	17:IQ:4:TYR:OH	2.12	0.65
1:IA:1749:U:OP2	21:IU:42:ARG:NH2	2.30	0.65
4:ID:126:ILE:HG21	4:ID:150:LEU:HD22	1.77	0.65
5:IE:370:ARG:HH22	5:IE:380:ARG:HH21	1.45	0.65
9:II:87:ILE:HG23	9:II:118:VAL:HG12	1.79	0.65
1:IA:2213:U:OP2	1:IA:2218:A:N6	2.23	0.65
10:IJ:76:THR:O	10:IJ:80:GLN:NE2	2.28	0.65
10:IJ:89:LYS:HE2	10:IJ:186:LEU:HD23	1.78	0.65
1:IA:1763:C:H2'	1:IA:1764:A:C8	2.32	0.65
1:IA:2178:A:HO2'	1:IA:2179:U:H6	1.42	0.65
8:IH:56:ARG:NH2	8:IH:107:GLN:O	2.30	0.65
1:IA:1356:C:N4	1:IA:1386:G:OP2	2.30	0.65
3:IC:94:U:H2'	3:IC:95:A:C8	2.32	0.65
8:IH:98:ASN:ND2	8:IH:187:MET:O	2.29	0.65
12:IL:171:TRP:CD1	12:IL:172:GLY:H	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:218:G:H1	1:1A:290:U:H3	1.45	0.64
1:1A:597:A:N3	8:1H:51:ASN:ND2	2.44	0.64
1:1A:732:U:O2'	1:1A:733:C:O5'	2.13	0.64
3:1C:17:G:H22	3:1C:59:G:H22	1.44	0.64
1:1A:570:A:H2'	1:1A:571:A:C8	2.33	0.64
1:1A:3107:G:N2	1:1A:3110:A:OP2	2.26	0.64
1:1A:3454:G:C6	1:1A:3502:A:N1	2.65	0.64
20:1T:39:MET:HE2	20:1T:43:LYS:HE2	1.78	0.64
14:1N:104:LYS:HB2	37:1k:16:HIS:HB2	1.79	0.64
32:1f:48:ARG:HG2	32:1f:48:ARG:HH11	1.63	0.64
1:1A:1648:U:OP2	1:1A:2081:A:O2'	2.14	0.64
3:1C:14:G:H2'	3:1C:15:A:H8	1.61	0.64
10:1J:66:ASN:OD1	10:1J:70:ASN:ND2	2.30	0.64
13:1M:32:ARG:NH1	13:1M:119:GLN:O	2.31	0.64
38:1l:39:TYR:O	38:1l:41:ASP:N	2.30	0.64
1:1A:118:A:N6	1:1A:189:G:O2'	2.28	0.64
9:1I:65:ALA:HB1	22:1V:142:ARG:HH12	1.62	0.64
1:1A:341:G:OP2	17:1Q:15:GLN:NE2	2.31	0.64
1:1A:1293:U:O4	1:1A:1454:G:O2'	2.14	0.64
24:1X:71:GLU:OE1	24:1X:71:GLU:N	2.20	0.64
1:1A:2114:U:N3	1:1A:2198:G:OP2	2.31	0.64
20:1T:19:GLU:OE1	22:1V:153:LYS:NZ	2.31	0.64
1:1A:457:G:N2	18:1R:5:CYS:SG	2.71	0.64
34:1h:25:THR:HG22	34:1h:26:ALA:H	1.63	0.64
1:1A:621:U:OP1	6:1F:372:SER:OG	2.12	0.63
1:1A:896:A:O2'	1:1A:2790:U:OP1	2.13	0.63
1:1A:1892:C:H2'	1:1A:1893:A:H8	1.63	0.63
1:1A:220:A:H2'	1:1A:221:U:H6	1.61	0.63
1:1A:919:G:H22	6:1F:103:SER:HB2	1.64	0.63
14:1N:47:ALA:HB2	35:1i:109:PHE:HA	1.80	0.63
28:1b:10:VAL:O	28:1b:83:THR:OG1	2.16	0.63
36:1j:5:ARG:NH1	36:1j:7:HIS:O	2.30	0.63
1:1A:440:G:N1	1:1A:443:A:OP2	2.28	0.63
18:1R:18:ARG:NH1	18:1R:20:ASP:OD1	2.32	0.63
37:1k:2:ALA:O	37:1k:4:GLY:N	2.32	0.63
1:1A:2381:G:OP2	1:1A:2381:G:N2	2.26	0.63
1:1A:2958:G:O2'	1:1A:2959:G:OP1	2.16	0.63
1:1A:58:G:H22	1:1A:75:U:H4'	1.63	0.63
1:1A:626:A:OP1	1:1A:664:A:N6	2.32	0.63
1:1A:3306:U:HO2'	1:1A:3322:A:HO2'	1.45	0.63
1:1A:536:G:O6	14:1N:212:LYS:N	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:IG:85:ARG:NH1	7:IG:249:ALA:O	2.30	0.62
12:IL:76:MET:HE1	12:IL:148:MET:HG2	1.81	0.62
1:IA:897:A:H8	1:IA:898:U:HO2'	1.46	0.62
10:IJ:98:GLN:HA	10:IJ:101:ARG:HD2	1.81	0.62
1:IA:626:A:HO2'	1:IA:627:A:H8	1.46	0.62
6:IF:84:SER:OG	6:IF:87:ASN:OD1	2.16	0.62
22:IV:80:VAL:HG12	22:IV:81:ASN:H	1.65	0.62
28:lb:54:THR:O	28:lb:62:GLN:NE2	2.32	0.62
28:lb:27:SER:HG	28:lb:42:THR:HG1	1.45	0.62
33:lg:36:PRO:HG2	33:lg:44:ARG:HB3	1.81	0.62
1:IA:2991:G:OP1	42:lp:25:TYR:OH	2.18	0.62
2:IB:101:G:OP2	2:IB:103:A:O2'	2.16	0.62
1:IA:3462:A:H2'	1:IA:3463:A:C8	2.34	0.62
3:IC:84:G:H1	3:IC:91:G:H22	1.45	0.62
1:IA:589:A:OP1	8:IH:35:ARG:NH2	2.33	0.62
1:IA:628:C:H2'	1:IA:629:G:C8	2.34	0.62
1:IA:871:A:H2'	1:IA:872:A:C8	2.34	0.62
7:IG:50:ARG:NH1	7:IG:148:ASP:OD2	2.33	0.62
35:li:71:GLU:OE2	35:li:71:GLU:N	2.32	0.62
5:IE:50:LYS:HB2	5:IE:337:ILE:HD11	1.82	0.62
7:IG:64:ILE:HG13	7:IG:105:LEU:HD21	1.81	0.62
13:IM:41:THR:O	13:IM:75:LYS:NZ	2.32	0.62
24:IX:22:ASN:ND2	24:IX:40:ILE:O	2.33	0.62
17:IQ:31:ARG:NH1	17:IQ:124:ASP:OD2	2.32	0.62
1:IA:881:G:OP1	19:IS:72:LYS:NZ	2.30	0.61
1:IA:3367:U:H2'	1:IA:3368:G:C8	2.35	0.61
5:IE:80:GLU:OE1	5:IE:315:TYR:OH	2.14	0.61
1:IA:625:A:O2'	1:IA:664:A:N6	2.34	0.61
1:IA:897:A:O2'	1:IA:899:A:N1	2.29	0.61
4:ID:109:GLU:CD	4:ID:109:GLU:H	2.08	0.61
13:IM:110:ILE:HD12	13:IM:111:ASP:N	2.15	0.61
1:IA:815:A:H4'	1:IA:817:A:OP1	2.01	0.61
5:IE:222:VAL:O	5:IE:335:ARG:NH1	2.34	0.61
6:IF:319:PRO:HB2	6:IF:326:MET:HE2	1.82	0.61
33:lg:130:GLN:HA	33:lg:134:GLN:HB3	1.82	0.61
1:IA:570:A:H2'	1:IA:571:A:H8	1.66	0.61
1:IA:1555:U:H2'	1:IA:1556:G:H8	1.66	0.61
24:IX:83:ARG:NH2	24:IX:118:THR:O	2.34	0.61
27:la:138:VAL:HG12	27:la:151:MET:HE1	1.81	0.61
1:IA:490:A:N1	1:IA:583:A:N6	2.49	0.61
1:IA:698:U:O2'	1:IA:699:A:N3	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3170:A:H2'	1:1A:3171:A:H8	1.66	0.61
3:1C:22:C:H2'	3:1C:23:A:C8	2.36	0.61
9:1I:21:CYS:SG	9:1I:22:LYS:N	2.73	0.61
1:1A:1209:U:OP1	1:1A:1211:A:O2'	2.19	0.61
1:1A:2767:A:H2'	1:1A:2768:G:C8	2.36	0.61
3:1C:80:G:H1	3:1C:94:U:H3	1.47	0.60
1:1A:1605:A:O2'	1:1A:1607:A:OP2	2.17	0.60
1:1A:2908:U:H2'	1:1A:2909:A:C8	2.36	0.60
1:1A:3372:U:O2'	1:1A:3374:C:OP2	2.19	0.60
3:1C:75:G:N1	3:1C:99:U:H5	1.98	0.60
5:1E:17:HIS:HD2	5:1E:18:PRO:CA	2.08	0.60
13:1M:18:VAL:HG13	13:1M:70:THR:HG22	1.83	0.60
23:1W:104:GLU:OE2	23:1W:104:GLU:N	2.26	0.60
1:1A:191:A:H2'	1:1A:192:A:C8	2.37	0.60
1:1A:209:A:O3'	14:1N:215:LYS:NZ	2.34	0.60
1:1A:1476:G:O2'	1:1A:1477:A:H5'	2.01	0.60
1:1A:2429:G:H5''	18:1R:86:LYS:HB2	1.82	0.60
1:1A:893:U:H3	1:1A:897:A:H2	1.47	0.60
1:1A:495:A:N6	1:1A:577:G:O2'	2.31	0.60
1:1A:1269:U:OP2	33:1g:44:ARG:NH2	2.33	0.60
1:1A:1737:A:OP2	34:1h:11:HIS:ND1	2.32	0.60
1:1A:2461:G:O2'	1:1A:2462:G:OP2	2.17	0.60
1:1A:3044:G:O2'	1:1A:3178:A:N1	2.34	0.60
1:1A:1523:U:OP1	33:1g:105:LYS:NZ	2.32	0.60
1:1A:2101:G:O2'	1:1A:2410:U:O4	2.15	0.60
1:1A:2944:A:O2'	1:1A:2945:A:H2'	2.02	0.60
1:1A:3352:G:H4'	1:1A:3353:U:H5''	1.84	0.60
28:1b:42:THR:HG22	28:1b:74:VAL:HG22	1.83	0.60
1:1A:2414:C:OP1	5:1E:238:ARG:NH1	2.31	0.60
14:1N:9:ASN:HB2	19:1S:165:LYS:HB2	1.84	0.60
1:1A:725:A:OP2	6:1F:413:LYS:NZ	2.34	0.60
1:1A:822:C:H2'	1:1A:823:A:C8	2.37	0.60
1:1A:873:U:H2'	1:1A:874:A:C8	2.37	0.59
1:1A:1327:A:H2'	1:1A:1328:A:C8	2.37	0.59
16:1P:49:ARG:NH2	16:1P:71:MET:O	2.28	0.59
1:1A:1912:A:H61	39:1m:42:CYS:HA	1.67	0.59
1:1A:2062:A:O2'	1:1A:3220:U:OP1	2.16	0.59
10:1J:35:ASP:OD1	25:1Y:6:ARG:N	2.35	0.59
11:1K:43:LYS:HE3	15:1O:132:PRO:HG2	1.84	0.59
1:1A:1208:U:C4	1:1A:1211:A:H5''	2.38	0.59
3:1C:17:G:H22	3:1C:59:G:N2	2.00	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:11:U:H2'	2:1B:12:A:H8	1.67	0.59
15:1O:127:ILE:HD12	20:1T:170:THR:HG23	1.84	0.59
28:1b:20:GLY:HA3	28:1b:139:PHE:CZ	2.37	0.59
1:1A:492:U:O2'	1:1A:493:G:O5'	2.20	0.59
1:1A:705:U:H2'	1:1A:706:A:H8	1.68	0.59
1:1A:796:U:H2'	1:1A:797:C:C6	2.38	0.59
3:1C:29:G:O6	3:1C:46:G:O6	2.20	0.59
4:1D:64:ARG:NH1	4:1D:70:GLY:O	2.35	0.59
1:1A:759:U:H2'	1:1A:760:A:H8	1.66	0.59
1:1A:1277:G:OP2	1:1A:1277:G:N2	2.31	0.59
1:1A:1384:A:O2'	1:1A:1385:G:O4'	2.20	0.59
1:1A:213:A:H5'	14:1N:133:LYS:H	1.68	0.59
1:1A:246:U:N3	1:1A:266:A:OP2	2.34	0.59
1:1A:2632:A:O2'	28:1b:139:PHE:O	2.19	0.59
8:1H:11:LYS:NZ	8:1H:27:ILE:O	2.34	0.59
5:1E:28:THR:O	5:1E:276:LYS:NZ	2.35	0.59
27:1a:48:PRO:O	27:1a:113:ARG:NH2	2.36	0.59
1:1A:639:G:H1	1:1A:650:A:H2	1.50	0.59
1:1A:1290:A:OP1	36:1j:85:ARG:NH2	2.35	0.59
1:1A:220:A:H2'	1:1A:221:U:C6	2.38	0.59
1:1A:663:G:OP2	16:1P:72:THR:OG1	2.12	0.59
1:1A:1846:A:H2'	1:1A:1847:A:H8	1.68	0.59
2:1B:1:A:H2'	2:1B:2:A:C8	2.38	0.59
1:1A:1823:C:H2'	1:1A:1824:A:C4	2.37	0.58
1:1A:3302:U:H2'	1:1A:3303:A:C8	2.37	0.58
3:1C:28:U:H3'	3:1C:29:G:H21	1.67	0.58
3:1C:81:A:N1	3:1C:93:G:C6	2.71	0.58
3:1C:85:G:H22	3:1C:90:G:H1	1.49	0.58
1:1A:424:A:O2'	1:1A:425:C:OP2	2.22	0.58
1:1A:1225:A:H5''	9:1I:95:ARG:HD2	1.84	0.58
1:1A:1992:A:H2'	1:1A:1993:G:H8	1.67	0.58
24:1X:51:ARG:HH21	24:1X:54:ARG:HH12	1.51	0.58
1:1A:547:A:H2'	1:1A:548:A:H8	1.68	0.58
1:1A:550:A:H2'	1:1A:551:A:C8	2.38	0.58
1:1A:789:C:H2'	1:1A:790:A:H8	1.67	0.58
1:1A:2739:U:H2'	1:1A:2740:G:H8	1.66	0.58
1:1A:816:G:H22	1:1A:829:G:P	2.25	0.58
1:1A:3368:G:H2'	1:1A:3369:U:C6	2.37	0.58
1:1A:3454:G:C2	1:1A:3502:A:H2	2.18	0.58
3:1C:79:G:H1	3:1C:95:A:H2	0.67	0.58
6:1F:389:LYS:HD3	6:1F:391:LYS:HE2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:lc:6:ARG:HB3	29:lc:8:THR:HG22	1.86	0.58
1:lA:1877:A:H2'	1:lA:1878:A:C8	2.38	0.58
1:lA:3008:U:O2'	1:lA:3009:C:OP1	2.22	0.58
20:lT:69:LYS:NZ	20:lT:93:VAL:O	2.36	0.58
10:lJ:52:LYS:NZ	17:lQ:29:GLU:OE2	2.29	0.58
1:lA:3336:G:H5'	1:lA:3373:A:H61	1.69	0.58
1:lA:852:A:O2'	1:lA:854:A:OP2	2.22	0.57
1:lA:1846:A:H2'	1:lA:1847:A:C8	2.39	0.57
1:lA:2637:A:H61	1:lA:2649:G:H2'	1.69	0.57
1:lA:3397:C:OP2	1:lA:3398:U:O2'	2.22	0.57
1:lA:227:A:H2'	1:lA:228:A:C8	2.38	0.57
4:lD:193:ARG:HG3	4:lD:195:THR:HG23	1.86	0.57
22:lV:75:MET:SD	22:lV:88:ARG:NH1	2.77	0.57
27:la:21:ALA:O	27:la:26:ARG:NH1	2.36	0.57
1:lA:476:U:OP1	36:lj:66:ARG:NH1	2.37	0.57
3:lC:2:G:O2'	3:lC:24:U:O2	2.21	0.57
6:lF:101:MET:HE1	6:lF:105:LEU:HG	1.85	0.57
1:lA:13:C:OP2	25:lY:27:ARG:NH2	2.35	0.57
1:lA:2346:A:H2'	1:lA:2347:A:C8	2.38	0.57
1:lA:586:A:N6	8:lH:43:THR:O	2.38	0.57
1:lA:1729:G:O2'	1:lA:1730:G:O4'	2.15	0.57
1:lA:191:A:H2'	1:lA:192:A:H8	1.68	0.57
1:lA:1220:A:H2'	1:lA:1220:A:N3	2.19	0.57
1:lA:3368:G:H2'	1:lA:3369:U:H6	1.69	0.57
8:lH:23:THR:H	8:lH:26:MET:HE2	1.70	0.57
13:lM:49:GLU:HA	13:lM:64:GLN:HA	1.87	0.57
1:lA:286:U:H4'	14:lN:43:ALA:HA	1.87	0.57
1:lA:873:U:H2'	1:lA:874:A:H8	1.69	0.57
1:lA:1019:G:H1'	1:lA:1737:A:N6	2.19	0.57
1:lA:1186:G:H21	1:lA:1220:A:N6	2.02	0.57
1:lA:2634:A:OP2	4:lD:64:ARG:NH2	2.36	0.57
1:lA:2767:A:H2'	1:lA:2768:G:H8	1.69	0.57
1:lA:2848:A:N1	1:lA:2911:U:H5	2.02	0.57
1:lA:3129:U:H2'	1:lA:3130:A:H8	1.68	0.57
10:lJ:174:TYR:HH	10:lJ:226:TYR:HH	1.53	0.57
31:le:26:LYS:HG3	31:le:97:ILE:HB	1.87	0.57
1:lA:505:A:H2'	1:lA:506:A:C8	2.39	0.57
1:lA:721:A:H2'	1:lA:722:A:C8	2.39	0.57
1:lA:2236:A:H2'	1:lA:2237:A:C8	2.39	0.57
10:lJ:37:THR:HG22	10:lJ:38:ARG:H	1.70	0.57
23:lW:102:LEU:HD12	23:lW:106:LEU:HD13	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:ln:14:GLU:HG2	40:ln:17:GLN:OE1	2.05	0.57
1:lA:99:A:H5''	14:lN:58:CYS:HB3	1.87	0.57
1:lA:493:G:H1'	1:lA:579:A:H61	1.68	0.57
24:lX:18:CYS:HB2	24:lX:54:ARG:HB3	1.86	0.57
1:lA:785:G:O2'	1:lA:1569:A:OP1	2.23	0.57
1:lA:2236:A:H2'	1:lA:2237:A:H8	1.70	0.57
1:lA:975:G:OP1	21:lU:92:LYS:NZ	2.38	0.56
1:lA:1553:A:OP1	2:lB:22:G:O2'	2.22	0.56
1:lA:1639:U:H2'	1:lA:1640:A:H8	1.69	0.56
2:lB:11:U:H2'	2:lB:12:A:C8	2.39	0.56
29:lc:85:ASP:N	29:lc:85:ASP:OD2	2.38	0.56
1:lA:1115:A:O2'	3:lC:76:U:O2	2.22	0.56
1:lA:2746:A:H5'	1:lA:2747:G:C8	2.40	0.56
1:lA:2751:C:P	13:lM:51:ARG:HE	2.28	0.56
9:lI:30:LYS:HD2	9:lI:30:LYS:N	2.20	0.56
1:lA:737:A:O5'	1:lA:738:G:N2	2.37	0.56
3:lC:85:G:N2	3:lC:90:G:H22	2.03	0.56
1:lA:2979:C:H5	1:lA:2995:C:H42	1.52	0.56
1:lA:3452:U:H3	1:lA:3504:G:H22	1.53	0.56
10:lJ:168:LYS:O	10:lJ:171:GLN:NE2	2.38	0.56
1:lA:605:C:H2'	1:lA:606:A:H8	1.70	0.56
1:lA:721:A:H2'	1:lA:722:A:H8	1.70	0.56
1:lA:1814:G:N2	1:lA:1817:A:OP2	2.36	0.56
8:lH:64:ILE:HD12	8:lH:115:GLN:HB3	1.85	0.56
1:lA:675:A:H5''	6:lF:354:TYR:CE2	2.41	0.56
1:lA:1346:G:H21	1:lA:1410:A:H62	1.54	0.56
1:lA:3139:G:H1'	2:lB:1:A:C2	2.40	0.56
21:lU:95:TRP:CH2	21:lU:99:MET:HE3	2.40	0.56
3:lC:17:G:H1	3:lC:59:G:H22	1.53	0.56
12:lL:140:CYS:SG	12:lL:148:MET:HG3	2.46	0.56
1:lA:502:U:H2'	1:lA:503:A:C8	2.41	0.56
1:lA:624:U:H2'	1:lA:625:A:O4'	2.06	0.56
1:lA:1764:A:H2'	1:lA:1765:A:C8	2.41	0.56
1:lA:1847:A:H2'	1:lA:1848:A:C8	2.41	0.56
15:lO:12:CYS:HB3	15:lO:42:LEU:HG	1.88	0.56
23:lW:53:THR:HA	23:lW:60:ALA:HB1	1.87	0.56
1:lA:227:A:H2'	1:lA:228:A:H8	1.71	0.56
1:lA:2468:C:O2'	5:lE:268:ARG:NH1	2.39	0.56
5:lE:27:ALA:HB1	5:lE:276:LYS:HD2	1.88	0.56
1:lA:760:A:H2'	1:lA:761:A:H8	1.71	0.55
1:lA:797:C:H2'	1:lA:798:U:H6	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:IM:64:GLN:N	13:IM:64:GLN:OE1	2.38	0.55
1:IA:2632:A:OP2	4:ID:87:TYR:OH	2.20	0.55
27:la:80:ILE:HG22	27:la:82:LYS:H	1.71	0.55
1:IA:941:A:H2'	1:IA:942:C:C6	2.41	0.55
1:IA:2745:C:H42	13:IM:22:SER:HB3	1.72	0.55
5:IE:223:THR:OG1	5:IE:273:GLY:O	2.23	0.55
31:le:17:LYS:NZ	31:le:103:ASP:OD1	2.40	0.55
1:IA:265:A:H1'	1:IA:266:A:H2	1.71	0.55
1:IA:918:G:O2'	14:IN:16:TRP:NE1	2.32	0.55
3:IC:109:G:H2'	3:IC:110:A:C8	2.41	0.55
1:IA:1095:A:H2	1:IA:1099:A:H2	1.54	0.55
1:IA:2732:A:H2'	1:IA:2733:A:H8	1.71	0.55
22:IV:129:LEU:HD23	22:IV:129:LEU:H	1.71	0.55
1:IA:665:A:OP1	20:IT:64:ASN:ND2	2.39	0.55
1:IA:1476:G:N3	1:IA:1476:G:H2'	2.21	0.55
1:IA:1640:A:H2'	1:IA:1641:A:C8	2.41	0.55
1:IA:2485:G:H3'	1:IA:2486:U:H4'	1.88	0.55
1:IA:3038:C:O2'	42:lp:25:TYR:O	2.24	0.55
1:IA:3450:A:H2'	1:IA:3451:A:C8	2.42	0.55
1:IA:447:G:N2	2:IB:17:G:OP2	2.40	0.55
1:IA:1327:A:H2'	1:IA:1328:A:H8	1.71	0.55
1:IA:2499:U:H2'	1:IA:2500:A:H8	1.72	0.55
1:IA:2730:U:H2'	1:IA:2731:G:H8	1.71	0.55
5:IE:384:MET:O	5:IE:388:LEU:N	2.36	0.55
1:IA:1558:C:H4'	27:la:182:PRO:HG2	1.89	0.55
1:IA:2721:G:H5''	1:IA:2722:U:O4'	2.07	0.55
1:IA:674:A:OP1	6:IF:357:LYS:NZ	2.40	0.55
1:IA:1841:G:H22	1:IA:1975:G:H22	1.55	0.55
11:IK:182:LEU:HB3	42:lp:11:ALA:HB1	1.89	0.55
22:IV:8:ASN:O	22:IV:11:THR:OG1	2.25	0.55
24:IX:106:VAL:HG12	24:IX:112:MET:HG2	1.89	0.55
1:IA:462:A:H2'	1:IA:463:U:C6	2.42	0.55
1:IA:1027:G:H4'	1:IA:1028:G:O5'	2.07	0.55
3:IC:17:G:N2	3:IC:59:G:H22	2.05	0.55
1:IA:1562:A:H2'	29:lc:3:THR:HG21	1.89	0.54
1:IA:3413:U:O2'	36:lj:58:LYS:NZ	2.36	0.54
1:IA:3457:G:N2	1:IA:3496:U:O2	2.30	0.54
1:IA:450:U:H4'	1:IA:1550:G:H4'	1.89	0.54
1:IA:774:U:H2'	1:IA:775:C:C6	2.42	0.54
1:IA:1639:U:H2'	1:IA:1640:A:C8	2.41	0.54
1:IA:3139:G:H1'	2:IB:1:A:H2	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:76:U:H2'	1:1A:77:C:H6	1.73	0.54
1:1A:401:A:N1	6:1F:84:SER:HB3	2.22	0.54
1:1A:502:U:H2'	1:1A:503:A:H8	1.73	0.54
1:1A:1177:A:H2'	1:1A:1178:A:C8	2.43	0.54
1:1A:1912:A:N6	39:1m:42:CYS:HA	2.23	0.54
3:1C:78:C:H2'	3:1C:79:G:H8	1.72	0.54
1:1A:720:U:O2'	1:1A:721:A:OP1	2.25	0.54
1:1A:886:A:H4'	30:1d:27:SER:HB2	1.89	0.54
1:1A:2908:U:H2'	1:1A:2909:A:H8	1.73	0.54
2:1B:25:U:OP2	27:1a:15:ARG:NH1	2.41	0.54
1:1A:1090:A:H2'	1:1A:1091:A:C8	2.41	0.54
1:1A:1886:A:H2'	1:1A:1887:A:C8	2.43	0.54
2:1B:25:U:H4'	27:1a:16:LYS:HB2	1.90	0.54
6:1F:4:ARG:HD2	6:1F:24:LEU:O	2.06	0.54
42:1p:11:ALA:O	42:1p:15:ASN:ND2	2.35	0.54
1:1A:10:U:H2'	1:1A:11:A:H8	1.73	0.54
1:1A:106:G:OP2	14:1N:71:ARG:NH2	2.40	0.54
1:1A:632:G:H2'	1:1A:633:A:C8	2.43	0.54
1:1A:1401:C:H2'	1:1A:1402:A:H8	1.72	0.54
1:1A:2981:A:N6	1:1A:2993:G:O2'	2.39	0.54
1:1A:3393:A:H2'	1:1A:3394:A:C8	2.42	0.54
3:1C:84:G:H22	3:1C:91:G:H22	1.56	0.54
5:1E:21:ARG:HB2	5:1E:274:PHE:HB3	1.90	0.54
5:1E:59:GLU:HG2	5:1E:358:LYS:HD2	1.89	0.54
1:1A:667:U:H2'	1:1A:668:A:N3	2.23	0.54
1:1A:1071:A:H4'	1:1A:1087:G:N2	2.22	0.54
1:1A:1538:G:N2	1:1A:1541:A:OP2	2.34	0.54
1:1A:1848:A:H2'	1:1A:1849:A:C8	2.41	0.54
1:1A:2985:C:OP1	1:1A:2987:C:N4	2.40	0.54
3:1C:84:G:N2	3:1C:91:G:H22	2.05	0.54
14:1N:46:PRO:HB2	35:1i:109:PHE:HB3	1.90	0.54
16:1P:11:ARG:NH1	16:1P:60:THR:O	2.36	0.54
21:1U:95:TRP:CZ2	21:1U:99:MET:HE3	2.43	0.54
31:1e:62:TYR:HE2	34:1h:97:GLU:HG2	1.72	0.54
33:1g:95:ALA:HB3	33:1g:120:VAL:HG22	1.89	0.54
1:1A:501:U:H2'	1:1A:502:U:H6	1.72	0.54
1:1A:2272:C:O2'	1:1A:2346:A:N3	2.38	0.54
1:1A:2732:A:H2'	1:1A:2733:A:C8	2.42	0.54
1:1A:244:A:N3	1:1A:264:G:O2'	2.39	0.54
1:1A:699:A:H2'	1:1A:700:A:C8	2.42	0.54
1:1A:1006:A:H2'	1:1A:1007:C:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3023:U:H1'	5:1E:252:ALA:HB3	1.90	0.54
19:1S:152:VAL:HA	19:1S:159:ALA:H	1.73	0.54
1:1A:789:C:H2'	1:1A:790:A:C8	2.43	0.53
1:1A:1459:U:H5''	9:1I:194:LYS:HB3	1.91	0.53
15:1O:63:VAL:HG12	15:1O:66:ASN:H	1.72	0.53
1:1A:660:U:H2'	1:1A:661:G:H8	1.74	0.53
1:1A:804:G:H2'	1:1A:805:G:C8	2.44	0.53
1:1A:1103:U:H2'	1:1A:1104:A:H8	1.73	0.53
1:1A:1305:A:H1'	1:1A:1306:A:C8	2.44	0.53
1:1A:2489:A:H2'	1:1A:2490:G:H8	1.72	0.53
3:1C:78:C:H2'	3:1C:79:G:C8	2.44	0.53
5:1E:232:ILE:HG13	5:1E:249:ARG:HB3	1.90	0.53
13:1M:92:LYS:HA	13:1M:172:LEU:HB3	1.90	0.53
32:1f:48:ARG:HG2	32:1f:48:ARG:NH1	2.23	0.53
35:1i:-9:ALA:HA	35:1i:38:VAL:HG13	1.90	0.53
1:1A:500:G:O6	1:1A:573:A:N6	2.41	0.53
1:1A:675:A:H2'	6:1F:354:TYR:CD2	2.43	0.53
1:1A:765:A:N3	36:1j:92:PRO:HG2	2.24	0.53
1:1A:2099:G:O2'	24:1X:19:GLY:O	2.26	0.53
5:1E:92:TYR:HB3	5:1E:99:LEU:HD22	1.90	0.53
25:1Y:26:PRO:HD2	35:1i:69:PRO:HG3	1.89	0.53
1:1A:759:U:H2'	1:1A:760:A:C8	2.43	0.53
1:1A:1545:A:H4'	33:1g:122:ASN:HD21	1.73	0.53
1:1A:3024:C:H2'	1:1A:3025:U:C6	2.43	0.53
23:1W:85:CYS:SG	23:1W:86:LYS:N	2.81	0.53
1:1A:700:A:H5''	1:1A:745:A:H62	1.73	0.53
1:1A:1206:A:H2'	1:1A:1207:C:C6	2.43	0.53
1:1A:979:G:C5	4:1D:181:LYS:HB3	2.44	0.53
1:1A:2427:U:H2'	1:1A:2428:A:H8	1.74	0.53
1:1A:3250:G:O2'	5:1E:282:LYS:NZ	2.42	0.53
1:1A:646:U:O2'	1:1A:647:C:O5'	2.26	0.53
1:1A:728:U:OP2	9:1I:48:LYS:NZ	2.33	0.53
1:1A:3237:G:O3'	26:1Z:44:ARG:NH2	2.41	0.53
29:1c:3:THR:HA	29:1c:6:ARG:HD3	1.89	0.53
6:1F:372:SER:HB2	6:1F:392:VAL:HG11	1.89	0.53
7:1G:36:MET:HE1	7:1G:148:ASP:CG	2.34	0.53
11:1K:94:LYS:HB3	11:1K:194:GLU:HB2	1.89	0.53
11:1K:101:ARG:HG3	11:1K:188:SER:HB3	1.90	0.53
15:1O:173:GLN:O	15:1O:177:LYS:HD3	2.08	0.53
21:1U:44:LEU:HD22	21:1U:49:LEU:HD12	1.91	0.53
1:1A:3088:G:O2'	1:1A:3091:C:OP2	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IK:67:MET:HE1	11:IK:74:ASP:HB3	1.90	0.53
14:IN:105:GLU:N	14:IN:105:GLU:OE1	2.41	0.53
15:IO:190:GLU:O	15:IO:193:LYS:NZ	2.42	0.53
1:IA:65:U:O2'	1:IA:97:A:O2'	2.22	0.53
1:IA:3103:C:H2'	1:IA:3104:G:H8	1.74	0.53
3:IC:32:A:H2'	3:IC:33:A:C8	2.43	0.53
38:II:21:ARG:NH2	38:II:38:GLY:O	2.42	0.53
3:IC:2:G:H2'	3:IC:3:G:H8	1.73	0.52
3:IC:103:U:H2'	3:IC:104:G:C8	2.44	0.52
36:IJ:40:THR:HG21	36:IJ:75:PRO:HB3	1.91	0.52
1:IA:3198:A:H4'	5:IE:13:SER:HB2	1.90	0.52
28:IB:46:VAL:HG13	28:IB:68:VAL:HG13	1.91	0.52
1:IA:236:U:O4'	27:IA:33:ARG:NH1	2.43	0.52
1:IA:761:A:H2'	1:IA:762:A:C8	2.44	0.52
1:IA:816:G:H5'	1:IA:817:A:OP1	2.09	0.52
1:IA:2041:U:H4'	1:IA:2042:A:H5''	1.91	0.52
1:IA:2308:A:H2'	1:IA:2309:A:C8	2.44	0.52
3:IC:14:G:H2'	3:IC:15:A:C8	2.42	0.52
8:IH:64:ILE:O	8:IH:113:THR:OG1	2.21	0.52
1:IA:1593:A:OP1	32:IF:75:ARG:NH2	2.43	0.52
1:IA:2123:A:H2'	1:IA:2124:A:C8	2.44	0.52
7:IG:128:LEU:HB3	7:IG:192:ARG:HG3	1.91	0.52
8:IH:122:VAL:HG12	8:IH:169:VAL:HG13	1.92	0.52
35:II:85:THR:HG22	35:II:87:ALA:H	1.73	0.52
38:II:64:MET:HE2	38:II:67:LEU:HB3	1.91	0.52
1:IA:622:A:H5''	6:IF:391:LYS:HG3	1.90	0.52
1:IA:772:C:N4	1:IA:773:G:O6	2.43	0.52
2:IB:116:U:H2'	2:IB:117:A:C8	2.44	0.52
6:IF:80:SER:O	6:IF:87:ASN:ND2	2.38	0.52
9:II:166:VAL:HG13	9:II:171:ASP:HB2	1.91	0.52
1:IA:301:A:H2'	1:IA:302:U:C6	2.45	0.52
1:IA:337:A:H2'	1:IA:338:A:H8	1.74	0.52
1:IA:1509:A:H2'	1:IA:1510:A:C8	2.43	0.52
1:IA:1848:A:H2'	1:IA:1849:A:H8	1.74	0.52
11:IK:71:ASN:OD1	11:IK:71:ASN:N	2.40	0.52
19:IS:35:LEU:O	19:IS:39:THR:OG1	2.26	0.52
32:IF:52:ILE:HD13	32:IF:77:LEU:HD12	1.90	0.52
1:IA:361:C:OP1	14:IN:100:LYS:NZ	2.41	0.52
1:IA:452:A:C2	2:IB:19:A:H1'	2.45	0.52
1:IA:2128:A:OP1	39:IM:23:ARG:NH2	2.42	0.52
1:IA:2589:C:OP2	1:IA:2656:G:N2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3148:C:H2'	1:1A:3149:A:H8	1.74	0.52
1:1A:3315:U:O2'	1:1A:3418:C:OP2	2.27	0.52
4:1D:143:ASN:N	4:1D:143:ASN:OD1	2.43	0.52
27:1a:87:LYS:O	27:1a:89:ASN:N	2.43	0.52
35:1i:-6:LYS:O	35:1i:-3:ALA:N	2.39	0.52
1:1A:237:C:H2'	1:1A:238:A:H8	1.74	0.52
1:1A:709:U:O2'	1:1A:710:A:OP1	2.27	0.52
1:1A:941:A:H2'	1:1A:942:C:H6	1.75	0.52
1:1A:1409:G:H5''	11:1K:55:LYS:HE3	1.91	0.52
1:1A:3431:U:H3	1:1A:3441:G:H1	1.58	0.52
12:1L:66:GLU:OE1	12:1L:69:ARG:NH2	2.42	0.52
1:1A:797:C:H2'	1:1A:798:U:C6	2.45	0.52
1:1A:1342:U:H2'	1:1A:1343:A:H4'	1.91	0.52
1:1A:1640:A:H2'	1:1A:1641:A:H8	1.75	0.52
10:1J:30:VAL:HG12	10:1J:31:ALA:H	1.74	0.52
12:1L:55:LEU:HD21	12:1L:164:LYS:HE2	1.92	0.52
1:1A:701:A:C5	1:1A:703:G:H1'	2.45	0.52
1:1A:832:A:O2'	1:1A:833:U:OP1	2.26	0.52
1:1A:835:A:H2'	1:1A:836:C:O4'	2.10	0.52
1:1A:2357:A:H8	1:1A:3117:U:H1'	1.75	0.52
2:1B:74:A:OP2	27:1a:51:LYS:HB2	2.10	0.52
11:1K:101:ARG:NH1	11:1K:149:GLU:OE1	2.43	0.52
39:1m:57:CYS:SG	39:1m:60:CYS:HB3	2.50	0.52
1:1A:678:A:H2'	1:1A:679:U:C6	2.45	0.51
1:1A:1130:U:H2'	1:1A:1131:G:H8	1.75	0.51
1:1A:2730:U:H2'	1:1A:2731:G:C8	2.45	0.51
1:1A:1887:A:H2'	1:1A:1888:A:C8	2.45	0.51
1:1A:1992:A:H2'	1:1A:1993:G:C8	2.44	0.51
2:1B:141:G:H5''	17:1Q:60:VAL:HG11	1.92	0.51
1:1A:1856:G:H2'	1:1A:1857:A:H8	1.75	0.51
1:1A:1956:G:OP2	40:1n:79:LYS:NZ	2.35	0.51
31:1e:27:TYR:OH	31:1e:87:ARG:NH1	2.43	0.51
1:1A:5:U:H2'	1:1A:6:U:C6	2.46	0.51
1:1A:869:G:C5	1:1A:870:A:H1'	2.45	0.51
1:1A:1752:U:H2'	1:1A:1753:A:O4'	2.11	0.51
1:1A:1809:A:C8	28:1b:64:MET:HG2	2.45	0.51
1:1A:255:A:N3	6:1F:225:ASN:ND2	2.55	0.51
1:1A:2483:C:H2'	1:1A:2484:U:H6	1.75	0.51
1:1A:2837:U:H2'	1:1A:2838:A:H8	1.75	0.51
1:1A:3350:U:OP2	1:1A:3351:U:O2'	2.23	0.51
4:1D:19:ARG:NH1	4:1D:189:TYR:O	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:18:G:H5'	38:1L:43:LYS:HG2	1.93	0.51
1:1A:59:A:N3	1:1A:74:U:O2'	2.37	0.51
1:1A:546:U:N3	1:1A:547:A:N7	2.59	0.51
1:1A:2414:C:O2	24:1X:21:ASN:ND2	2.40	0.51
11:1K:13:ILE:HD11	11:1K:63:VAL:HG23	1.93	0.51
23:1W:49:PHE:CD2	23:1W:96:TYR:HD1	2.28	0.51
39:1m:51:ALA:HB3	39:1m:54:ILE:HD12	1.93	0.51
1:1A:575:A:H2'	1:1A:576:A:O4'	2.10	0.51
1:1A:1112:G:O2'	1:1A:1172:G:O6	2.21	0.51
1:1A:2683:U:H5	1:1A:2948:G:N7	2.08	0.51
1:1A:3203:A:H4'	5:1E:365:LYS:HD2	1.92	0.51
14:1N:49:ILE:HG22	14:1N:51:SER:H	1.76	0.51
22:1V:52:LEU:HD12	22:1V:53:PRO:HD2	1.93	0.51
23:1W:55:LYS:HE2	23:1W:58:GLY:HA2	1.92	0.51
23:1W:63:THR:HB	23:1W:66:ILE:HD13	1.93	0.51
1:1A:501:U:H2'	1:1A:502:U:C6	2.46	0.51
1:1A:3285:A:C6	1:1A:3287:U:H1'	2.45	0.51
1:1A:3462:A:H2'	1:1A:3463:A:H8	1.75	0.51
6:1F:115:THR:HB	6:1F:120:ARG:HD2	1.93	0.51
24:1X:87:THR:HA	24:1X:97:TYR:HB3	1.92	0.51
1:1A:482:A:N1	1:1A:752:G:O2'	2.42	0.51
1:1A:1325:C:H42	1:1A:3000:C:H5''	1.76	0.51
1:1A:1635:U:OP1	41:1o:42:ARG:NH2	2.44	0.51
1:1A:1888:A:N1	1:1A:1922:U:H5	2.08	0.51
1:1A:2079:A:H2'	1:1A:2080:A:O4'	2.10	0.51
3:1C:3:G:H22	3:1C:114:U:H3	1.58	0.51
1:1A:592:A:H2'	1:1A:593:A:H8	1.75	0.51
1:1A:2841:A:O2'	1:1A:2842:U:OP2	2.22	0.51
1:1A:3396:A:H5''	16:1P:121:LYS:HD3	1.93	0.51
43:1q:72:CYS:SG	43:1q:75:CYS:N	2.84	0.51
1:1A:312:A:OP2	37:1k:28:THR:OG1	2.22	0.50
1:1A:467:A:N1	1:1A:2438:C:O2'	2.32	0.50
1:1A:1337:A:H2'	1:1A:1338:U:H6	1.76	0.50
1:1A:1430:G:O6	1:1A:2442:C:O2'	2.25	0.50
1:1A:2482:C:H2'	1:1A:2483:C:C6	2.46	0.50
3:1C:8:U:H3	3:1C:109:G:H1	1.58	0.50
11:1K:100:MET:HE1	11:1K:167:ILE:HB	1.92	0.50
22:1V:26:ASN:HB2	22:1V:29:THR:HG23	1.93	0.50
27:1a:54:GLU:HG3	27:1a:106:LYS:HB3	1.93	0.50
1:1A:1107:G:H2'	1:1A:1108:A:C8	2.46	0.50
1:1A:1633:G:H1'	1:1A:2044:C:H5''	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2052:G:O2'	38:1L:6:SER:OG	2.29	0.50
1:1A:2739:U:H2'	1:1A:2740:G:C8	2.46	0.50
1:1A:3222:U:OP1	21:1U:59:SER:N	2.34	0.50
3:1C:85:G:N2	3:1C:90:G:H1	2.10	0.50
5:1E:234:ARG:HG3	5:1E:272:MET:HB3	1.93	0.50
8:1H:93:GLY:O	8:1H:98:ASN:HB2	2.11	0.50
17:1Q:80:VAL:HB	17:1Q:82:ARG:HD2	1.92	0.50
5:1E:224:LYS:HB2	5:1E:332:ILE:HG23	1.93	0.50
23:1W:67:GLU:HB3	23:1W:69:LYS:HE2	1.94	0.50
1:1A:213:A:H2'	14:1N:127:VAL:HG21	1.94	0.50
1:1A:663:G:H5'	16:1P:72:THR:HG23	1.93	0.50
1:1A:1157:A:H4'	7:1G:5:LYS:H	1.77	0.50
1:1A:1479:A:H4'	1:1A:1480:U:O5'	2.11	0.50
1:1A:1524:A:H5''	33:1g:102:SER:HB3	1.92	0.50
1:1A:1974:A:H2'	1:1A:1975:G:C8	2.46	0.50
5:1E:386:LYS:HD3	5:1E:386:LYS:C	2.36	0.50
29:1c:51:ASP:OD1	29:1c:51:ASP:N	2.44	0.50
1:1A:855:A:OP1	30:1d:58:LYS:NZ	2.43	0.50
1:1A:1752:U:H4'	1:1A:2036:A:H4'	1.92	0.50
3:1C:6:G:OP1	7:1G:33:ARG:NH1	2.44	0.50
1:1A:493:G:H21	1:1A:580:A:N6	2.05	0.50
1:1A:1310:A:N3	20:1T:108:SER:OG	2.43	0.50
1:1A:1847:A:H2'	1:1A:1848:A:H8	1.76	0.50
1:1A:1892:C:H2'	1:1A:1893:A:C8	2.46	0.50
1:1A:3154:A:H2'	1:1A:3155:U:C6	2.46	0.50
4:1D:161:ASN:OD1	4:1D:161:ASN:N	2.43	0.50
6:1F:121:ARG:HG2	6:1F:276:LYS:HD3	1.92	0.50
1:1A:10:U:H2'	1:1A:11:A:C8	2.47	0.50
1:1A:823:A:H2'	1:1A:824:G:H2'	1.94	0.50
1:1A:1200:A:H1'	7:1G:115:MET:HE1	1.94	0.50
1:1A:2433:A:H2'	1:1A:2434:A:C8	2.47	0.50
3:1C:81:A:C2	3:1C:93:G:C6	2.97	0.50
26:1Z:36:LYS:O	26:1Z:40:MET:HG2	2.12	0.50
1:1A:802:A:H2'	1:1A:803:U:C6	2.47	0.50
1:1A:1468:A:H2'	1:1A:1469:A:C8	2.47	0.50
1:1A:1555:U:H2'	1:1A:1556:G:C8	2.47	0.50
1:1A:1982:U:H2'	4:1D:50:HIS:CD2	2.46	0.50
3:1C:9:U:OP2	22:1V:26:ASN:ND2	2.41	0.50
1:1A:868:A:H2'	1:1A:869:G:C8	2.47	0.50
1:1A:2504:U:H2'	1:1A:2505:A:H8	1.77	0.50
1:1A:3025:U:H2'	1:1A:3026:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IK:102:VAL:HG21	11:IK:111:LEU:HD11	1.93	0.50
40:ln:18:ILE:O	40:ln:22:LEU:HD12	2.10	0.50
1:IA:213:A:N6	14:IN:131:THR:OG1	2.41	0.49
1:IA:547:A:H2'	1:IA:548:A:C8	2.47	0.49
1:IA:2634:A:OP1	4:ID:69:TYR:OH	2.25	0.49
1:IA:3393:A:H2'	1:IA:3394:A:H8	1.75	0.49
4:ID:168:ILE:HD11	39:lm:79:VAL:HG21	1.93	0.49
1:IA:926:A:N1	1:IA:2487:U:O2'	2.38	0.49
12:IL:138:GLY:C	12:IL:148:MET:HE1	2.37	0.49
28:lb:23:ALA:HA	28:lb:45:GLY:HA2	1.93	0.49
1:IA:316:G:OP1	17:IQ:47:ARG:NE	2.45	0.49
1:IA:466:G:O2'	1:IA:2441:U:OP2	2.20	0.49
1:IA:1130:U:H2'	1:IA:1131:G:C8	2.48	0.49
1:IA:1225:A:OP2	9:II:184:LYS:NZ	2.45	0.49
14:IN:152:ILE:HA	14:IN:155:PHE:HB2	1.94	0.49
21:IU:99:MET:HE1	21:IU:127:VAL:O	2.11	0.49
1:IA:662:U:H2'	1:IA:663:G:O4'	2.11	0.49
1:IA:1198:U:H3	1:IA:1204:A:H62	1.59	0.49
1:IA:1904:U:OP2	21:IU:124:TYR:OH	2.24	0.49
1:IA:2505:A:H2'	1:IA:2506:U:C6	2.47	0.49
1:IA:2839:A:H5''	43:lq:78:LYS:HD2	1.93	0.49
1:IA:3038:C:H5''	42:lp:27:ARG:HH21	1.77	0.49
2:IB:80:A:O2'	2:IB:81:A:OP1	2.29	0.49
26:IZ:61:ASN:OD1	26:IZ:61:ASN:N	2.46	0.49
28:lb:23:ALA:HB1	28:lb:43:VAL:HB	1.92	0.49
28:lb:27:SER:OG	28:lb:42:THR:OG1	2.18	0.49
1:IA:443:A:H4'	1:IA:444:A:OP1	2.12	0.49
1:IA:1631:A:O2'	38:II:12:HIS:O	2.29	0.49
1:IA:2149:U:OP1	21:IU:136:LYS:HE3	2.11	0.49
1:IA:2289:A:H2'	1:IA:2290:A:C8	2.48	0.49
1:IA:2416:U:OP2	5:IE:239:HIS:ND1	2.27	0.49
1:IA:3084:A:H8	1:IA:3084:A:OP2	1.94	0.49
2:IB:2:A:H2'	2:IB:3:U:H6	1.76	0.49
3:IC:7:A:H5''	22:IV:27:THR:OG1	2.12	0.49
12:IL:30:ARG:HG3	12:IL:63:GLU:HG3	1.95	0.49
28:lb:123:GLU:HA	28:lb:123:GLU:OE2	2.12	0.49
1:IA:1026:G:OP1	17:IQ:76:ARG:NH2	2.45	0.49
1:IA:1312:A:H62	1:IA:1441:U:H3	1.60	0.49
1:IA:1855:G:H2'	1:IA:1856:G:O4'	2.12	0.49
1:IA:2084:G:H2'	1:IA:2085:A:H8	1.77	0.49
1:IA:2226:G:O2'	1:IA:2265:U:OP1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3103:C:H2'	1:1A:3104:G:C8	2.48	0.49
3:1C:7:A:OP1	22:1V:27:THR:HG21	2.11	0.49
16:1P:41:PRO:HB3	16:1P:77:CYS:SG	2.53	0.49
23:1W:73:LYS:HG3	23:1W:74:LYS:HD3	1.94	0.49
37:1k:73:THR:HB	37:1k:76:ARG:HB2	1.94	0.49
1:1A:1090:A:H2'	1:1A:1091:A:H8	1.77	0.49
1:1A:2499:U:H2'	1:1A:2500:A:C8	2.48	0.49
2:1B:141:G:H2'	2:1B:142:A:C8	2.47	0.49
3:1C:35:A:H2	3:1C:40:G:H22	1.61	0.49
1:1A:506:A:H2'	1:1A:507:A:C8	2.48	0.49
1:1A:2299:A:H2'	1:1A:2300:A:C8	2.48	0.49
1:1A:3168:A:H2'	1:1A:3169:C:C6	2.48	0.49
3:1C:6:G:H2'	3:1C:7:A:C8	2.47	0.49
1:1A:58:G:N2	1:1A:75:U:H4'	2.28	0.49
1:1A:493:G:H2'	1:1A:494:G:C4	2.48	0.49
1:1A:668:A:H2'	1:1A:669:A:H8	1.77	0.49
1:1A:3170:A:H2'	1:1A:3171:A:C8	2.48	0.49
1:1A:3499:U:H5''	32:1f:56:ALA:HB1	1.93	0.49
2:1B:116:U:H2'	2:1B:117:A:H8	1.77	0.49
3:1C:84:G:H1	3:1C:91:G:N2	2.10	0.49
23:1W:105:TRP:HB2	23:1W:106:LEU:HD12	1.94	0.49
1:1A:239:G:H2'	1:1A:240:A:C8	2.48	0.49
1:1A:764:U:H2'	1:1A:765:A:H8	1.78	0.49
1:1A:1533:U:O2'	1:1A:1534:U:OP1	2.30	0.49
1:1A:1669:G:O2'	1:1A:1736:A:N3	2.42	0.49
1:1A:1897:A:C2	1:1A:1913:G:N2	2.74	0.49
1:1A:3083:A:N7	5:1E:2:SER:N	2.61	0.49
1:1A:3344:U:C5	20:1T:172:LEU:HG	2.48	0.49
6:1F:375:LYS:HB2	6:1F:390:VAL:CG1	2.42	0.49
14:1N:42:LYS:O	14:1N:44:VAL:N	2.45	0.49
1:1A:90:G:H2'	1:1A:91:A:C8	2.48	0.48
1:1A:404:G:N2	1:1A:407:A:OP2	2.34	0.48
3:1C:80:G:H22	3:1C:94:U:H3	1.59	0.48
7:1G:75:LEU:O	7:1G:112:LYS:NZ	2.45	0.48
27:1a:2:LYS:HD3	27:1a:7:VAL:HG22	1.94	0.48
1:1A:897:A:H8	1:1A:898:U:O2'	1.96	0.48
1:1A:3260:A:H2'	1:1A:3261:A:C8	2.47	0.48
5:1E:77:THR:OG1	5:1E:327:GLY:O	2.30	0.48
1:1A:43:C:OP1	14:1N:14:LYS:HD2	2.12	0.48
1:1A:525:U:H2'	1:1A:526:A:C8	2.48	0.48
1:1A:675:A:H8	6:1F:354:TYR:HD2	1.59	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:790:A:H2'	1:1A:791:A:C8	2.48	0.48
1:1A:2780:A:H2'	1:1A:2781:U:C6	2.49	0.48
1:1A:3440:U:O2'	5:1E:23:HIS:O	2.29	0.48
2:1B:145:U:H2'	2:1B:146:U:C6	2.47	0.48
14:1N:247:THR:OG1	29:1c:98:GLU:HB3	2.14	0.48
28:1b:16:GLY:O	34:1h:74:ARG:HG3	2.13	0.48
1:1A:97:A:H2'	1:1A:98:A:O4'	2.13	0.48
1:1A:992:U:H3'	1:1A:993:U:H4'	1.94	0.48
1:1A:2064:G:N1	1:1A:2067:A:OP2	2.46	0.48
4:1D:149:ARG:HG3	4:1D:155:LYS:HD3	1.96	0.48
16:1P:29:GLU:HG2	20:1T:68:VAL:HG21	1.95	0.48
37:1k:60:ASP:O	37:1k:81:ARG:NH1	2.46	0.48
1:1A:113:U:OP2	17:1Q:2:GLY:N	2.47	0.48
1:1A:243:G:O2'	1:1A:264:G:N2	2.47	0.48
1:1A:764:U:H2'	1:1A:765:A:C8	2.49	0.48
1:1A:1073:A:H62	1:1A:1086:G:H21	1.59	0.48
1:1A:1675:A:H2'	1:1A:1676:A:C8	2.49	0.48
1:1A:2230:U:H2'	1:1A:2231:C:C6	2.49	0.48
26:1Z:22:LYS:HE3	26:1Z:30:SER:HB2	1.95	0.48
1:1A:1201:A:H2'	1:1A:1202:A:O4'	2.13	0.48
1:1A:2129:G:C8	39:1m:16:THR:HG22	2.49	0.48
1:1A:2178:A:O2'	1:1A:2179:U:H6	1.95	0.48
1:1A:2492:U:H2'	1:1A:2493:U:C6	2.49	0.48
1:1A:2836:C:O2'	43:1q:31:ASP:OD1	2.31	0.48
1:1A:3426:U:O4	5:1E:121:LYS:NZ	2.44	0.48
1:1A:1431:G:OP2	15:1O:60:ARG:NH1	2.47	0.48
1:1A:1502:A:H3'	1:1A:1502:A:N3	2.29	0.48
1:1A:2503:U:H2'	1:1A:2504:U:C6	2.49	0.48
1:1A:2959:G:N7	1:1A:3013:C:H5'	2.29	0.48
1:1A:3168:A:H2'	1:1A:3169:C:H6	1.79	0.48
5:1E:285:TYR:HB2	5:1E:324:MET:HG2	1.95	0.48
28:1b:50:PRO:HG3	28:1b:68:VAL:HG22	1.96	0.48
1:1A:564:A:H4'	1:1A:565:U:O5'	2.12	0.48
12:1L:142:GLU:OE2	12:1L:142:GLU:HA	2.13	0.48
14:1N:46:PRO:HA	14:1N:229:GLN:HG3	1.95	0.48
18:1R:18:ARG:NH2	18:1R:147:GLU:HG2	2.29	0.48
1:1A:718:A:H2'	1:1A:719:U:C6	2.49	0.48
1:1A:2034:G:O2'	41:1o:3:GLY:O	2.31	0.48
3:1C:54:U:H4'	13:1M:152:HIS:HB2	1.96	0.48
6:1F:286:MET:HE1	19:1S:27:LEU:HD13	1.95	0.48
9:1I:207:ILE:HG13	9:1I:213:GLY:HA3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:IL:98:ARG:HB3	12:IL:120:GLY:HA3	1.95	0.48
20:IT:147:MET:HE2	20:IT:173:CYS:SG	2.54	0.48
23:IW:95:LYS:HB3	23:IW:95:LYS:HE2	1.68	0.48
1:IA:94:G:N7	14:IN:11:HIS:NE2	2.57	0.48
1:IA:494:G:H4'	1:IA:495:A:OP1	2.13	0.48
1:IA:1219:A:H4'	1:IA:1220:A:H5'	1.96	0.48
1:IA:1745:A:H5'	1:IA:1877:A:H1'	1.96	0.48
1:IA:3148:C:H2'	1:IA:3149:A:C8	2.49	0.48
3:IC:55:C:O2'	13:IM:146:ASP:OD2	2.32	0.48
3:IC:60:C:H2'	3:IC:61:A:C8	2.49	0.48
8:IH:23:THR:OG1	8:IH:25:ASP:OD1	2.21	0.48
20:IT:3:GLU:OE2	20:IT:95:ARG:NH1	2.47	0.48
41:IO:46:ARG:HD3	41:IO:46:ARG:HA	1.60	0.48
1:IA:668:A:H2'	1:IA:669:A:C8	2.48	0.47
1:IA:1035:G:H5'	1:IA:1036:A:OP1	2.14	0.47
1:IA:1508:U:H2'	1:IA:1509:A:C8	2.49	0.47
1:IA:3493:G:H4'	5:IE:385:LYS:HD3	1.95	0.47
11:IK:147:LYS:HE3	11:IK:147:LYS:HB3	1.76	0.47
24:IX:48:ARG:HD2	24:IX:51:ARG:NH1	2.29	0.47
40:IN:56:ASP:HB3	40:IN:59:LYS:HG3	1.95	0.47
1:IA:216:A:N6	1:IA:292:G:H1	2.12	0.47
1:IA:255:A:H4'	1:IA:257:A:N7	2.29	0.47
1:IA:724:A:O2'	1:IA:725:A:H5''	2.14	0.47
1:IA:1738:G:C2	1:IA:1739:G:C8	3.02	0.47
1:IA:1869:U:H2'	1:IA:1870:U:C6	2.50	0.47
1:IA:2844:U:H2'	1:IA:2845:U:C6	2.49	0.47
3:IC:89:G:H4'	12:IL:11:LEU:HD22	1.96	0.47
7:IG:167:MET:HE2	7:IG:167:MET:HB3	1.67	0.47
15:IO:158:GLU:O	15:IO:162:LYS:HG2	2.14	0.47
38:IL:33:ARG:NH2	38:IL:41:ASP:OD2	2.44	0.47
1:IA:592:A:H2'	1:IA:593:A:C8	2.48	0.47
1:IA:2123:A:H2'	1:IA:2124:A:H8	1.78	0.47
6:IF:150:ILE:HG22	6:IF:151:PRO:HD3	1.96	0.47
7:IG:37:ILE:HD12	7:IG:67:SER:HB2	1.95	0.47
7:IG:223:ILE:HD12	7:IG:223:ILE:H	1.78	0.47
1:IA:732:U:O2'	1:IA:733:C:H6	1.97	0.47
1:IA:1856:G:H2'	1:IA:1857:A:C8	2.50	0.47
1:IA:2432:A:H61	1:IA:3126:C:H5	1.62	0.47
1:IA:2838:A:H2'	1:IA:2839:A:C8	2.48	0.47
1:IA:3362:U:H2'	1:IA:3363:C:C6	2.49	0.47
6:IF:212:TYR:HB2	6:IF:216:ASP:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1F:357:LYS:HA	6:1F:360:LYS:HE3	1.95	0.47
10:1J:89:LYS:NZ	10:1J:185:GLN:O	2.44	0.47
35:li:-5:ILE:HG12	35:li:45:ARG:HD3	1.96	0.47
1:1A:223:A:H2'	1:1A:224:U:C6	2.49	0.47
1:1A:858:A:O2'	1:1A:1185:A:N7	2.48	0.47
1:1A:871:A:O2'	1:1A:872:A:O5'	2.29	0.47
1:1A:3447:A:H2'	1:1A:3448:G:O4'	2.14	0.47
1:1A:3462:A:O4'	1:1A:3493:G:N2	2.44	0.47
24:1X:22:ASN:HB2	24:1X:53:PRO:HD2	1.97	0.47
27:1a:75:LYS:HB2	27:1a:77:VAL:HG22	1.95	0.47
31:le:36:LYS:HE3	31:le:36:LYS:HB3	1.52	0.47
1:1A:353:G:H2'	1:1A:354:U:C6	2.49	0.47
1:1A:426:U:H2'	1:1A:427:U:C6	2.49	0.47
1:1A:525:U:H2'	1:1A:526:A:H8	1.79	0.47
1:1A:1222:U:O2'	22:1V:136:ARG:O	2.31	0.47
3:1C:2:G:H2'	3:1C:3:G:C8	2.49	0.47
8:1H:158:LYS:HD3	8:1H:158:LYS:N	2.29	0.47
8:1H:165:LYS:HE3	8:1H:165:LYS:HB3	1.63	0.47
13:1M:48:SER:N	13:1M:66:ALA:O	2.48	0.47
20:1T:147:MET:HG3	20:1T:150:CYS:SG	2.55	0.47
31:le:57:ARG:O	31:le:61:GLU:HG3	2.14	0.47
42:lp:8:GLU:O	42:lp:12:ARG:HG3	2.14	0.47
1:1A:43:C:OP2	1:1A:44:A:O2'	2.20	0.47
1:1A:557:U:OP2	6:1F:23:ARG:NH1	2.47	0.47
1:1A:605:C:H2'	1:1A:606:A:C8	2.49	0.47
1:1A:619:A:O2'	1:1A:620:U:O5'	2.28	0.47
1:1A:817:A:H2'	1:1A:818:A:C8	2.49	0.47
1:1A:1086:G:H2'	1:1A:1087:G:H8	1.79	0.47
1:1A:1189:U:H2'	1:1A:1190:U:C6	2.50	0.47
1:1A:1739:G:OP1	34:lh:37:LYS:NZ	2.47	0.47
1:1A:1749:U:P	21:1U:42:ARG:HH22	2.37	0.47
1:1A:1841:G:H22	1:1A:1975:G:N2	2.12	0.47
1:1A:2766:A:H2'	1:1A:2767:A:C8	2.50	0.47
1:1A:2856:G:C8	1:1A:2903:A:N6	2.76	0.47
1:1A:2978:C:H2'	1:1A:2979:C:O2	2.15	0.47
2:1B:10:U:H2'	2:1B:11:U:C6	2.50	0.47
23:1W:63:THR:HB	23:1W:66:ILE:HB	1.96	0.47
33:lg:33:TRP:O	33:lg:34:ARG:NH1	2.48	0.47
1:1A:405:U:OP1	38:ll:11:ARG:NH2	2.48	0.47
1:1A:491:G:C6	1:1A:582:U:C2	3.02	0.47
1:1A:685:A:O4'	1:1A:1450:A:N6	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:700:A:H5''	1:1A:745:A:N6	2.28	0.47
1:1A:892:U:H2'	1:1A:893:U:C6	2.49	0.47
1:1A:1605:A:H2	1:1A:3430:U:N3	2.08	0.47
5:1E:40:LYS:HA	5:1E:40:LYS:HD3	1.70	0.47
6:1F:47:ASN:HA	6:1F:112:GLN:HG3	1.97	0.47
28:1b:36:ARG:HG3	28:1b:38:TYR:CZ	2.50	0.47
1:1A:727:U:H2'	9:1I:48:LYS:HE2	1.96	0.47
1:1A:1985:A:H2'	1:1A:1986:A:C8	2.49	0.47
7:1G:262:THR:OG1	7:1G:263:SER:N	2.47	0.47
11:1K:157:VAL:O	11:1K:161:SER:OG	2.21	0.47
13:1M:111:ASP:HB3	13:1M:112:LEU:H	1.52	0.47
23:1W:48:THR:O	23:1W:49:PHE:C	2.58	0.47
1:1A:221:U:H2'	1:1A:222:A:H8	1.80	0.47
1:1A:631:G:N1	1:1A:659:U:N3	2.36	0.47
1:1A:701:A:C4	1:1A:703:G:H1'	2.50	0.47
1:1A:2637:A:H2'	1:1A:2638:A:H8	1.79	0.47
2:1B:28:U:H2'	2:1B:29:U:C6	2.50	0.47
5:1E:79:ILE:HD12	5:1E:325:ILE:HG13	1.97	0.47
7:1G:182:ALA:HB1	7:1G:194:ARG:HD2	1.97	0.47
14:1N:215:LYS:NZ	14:1N:217:PHE:O	2.46	0.47
1:1A:2112:C:C2	1:1A:2113:A:C8	3.03	0.46
1:1A:2142:G:H2'	1:1A:2143:C:C6	2.50	0.46
1:1A:2209:U:O4	1:1A:2223:A:H2	1.98	0.46
1:1A:2433:A:H2'	1:1A:2434:A:H8	1.80	0.46
1:1A:3370:A:H2'	1:1A:3371:U:C6	2.50	0.46
1:1A:3404:A:H2'	8:1H:95:PHE:CZ	2.49	0.46
2:1B:115:A:H2'	2:1B:116:U:C6	2.49	0.46
6:1F:112:GLN:HB3	17:1Q:203:TYR:CE2	2.51	0.46
10:1J:205:LYS:O	10:1J:209:GLU:HG2	2.16	0.46
12:1L:50:VAL:HG22	12:1L:148:MET:HE3	1.97	0.46
14:1N:47:ALA:C	14:1N:49:ILE:H	2.23	0.46
16:1P:100:LYS:O	16:1P:104:ARG:HG2	2.16	0.46
27:1a:2:LYS:HB3	27:1a:2:LYS:HE3	1.63	0.46
1:1A:187:G:H5''	1:1A:188:U:H3'	1.96	0.46
1:1A:228:A:H2'	1:1A:229:A:C8	2.49	0.46
1:1A:677:A:OP1	6:1F:351:LYS:NZ	2.36	0.46
1:1A:1103:U:H2'	1:1A:1104:A:C8	2.50	0.46
1:1A:1621:G:O2'	1:1A:2072:U:O4	2.21	0.46
1:1A:1883:A:N6	1:1A:1931:U:H3	2.11	0.46
1:1A:3395:U:H2'	1:1A:3396:A:C8	2.51	0.46
11:1K:35:LEU:HD13	11:1K:88:MET:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:IR:126:ARG:NH1	18:IR:140:SER:OG	2.47	0.46
24:IX:32:THR:O	24:IX:34:ALA:N	2.48	0.46
1:IA:631:G:H2'	1:IA:631:G:N3	2.30	0.46
1:IA:1189:U:H2'	1:IA:1190:U:H6	1.79	0.46
1:IA:1270:G:O2'	33:lg:46:LYS:O	2.31	0.46
1:IA:2262:U:H2'	1:IA:2263:G:O4'	2.14	0.46
1:IA:2486:U:H5	1:IA:2944:A:N1	2.13	0.46
31:le:62:TYR:CE2	34:lh:97:GLU:HG2	2.50	0.46
1:IA:410:G:O6	38:ll:56:ARG:HD3	2.15	0.46
1:IA:573:A:H2'	1:IA:574:U:C6	2.50	0.46
1:IA:735:C:H2'	1:IA:736:G:O4'	2.15	0.46
1:IA:953:U:H2'	1:IA:954:G:O4'	2.15	0.46
1:IA:1961:G:H2'	1:IA:1962:U:O4'	2.16	0.46
8:IH:72:TYR:CD2	8:IH:103:MET:HE1	2.50	0.46
1:IA:355:A:H2'	1:IA:356:U:C6	2.50	0.46
1:IA:2904:U:H2'	1:IA:2905:U:H6	1.80	0.46
1:IA:3254:U:H4'	1:IA:3255:G:H5'	1.97	0.46
1:IA:3286:A:C2	1:IA:3287:U:H5'	2.51	0.46
2:IB:15:U:H5'	18:IR:2:VAL:HG13	1.98	0.46
3:IC:38:A:C2	13:IM:70:THR:HG23	2.50	0.46
12:IL:51:HIS:ND1	12:IL:137:SER:OG	2.39	0.46
15:IO:202:PHE:CZ	16:IP:111:ASP:HB3	2.51	0.46
16:IP:108:THR:OG1	16:IP:111:ASP:OD1	2.32	0.46
32:lf:28:LYS:O	32:lf:32:LYS:HB2	2.16	0.46
1:IA:795:G:H4'	1:IA:796:U:H6	1.81	0.46
1:IA:798:U:C2	1:IA:799:A:C8	3.03	0.46
1:IA:1876:U:H2'	1:IA:1936:A:N6	2.31	0.46
1:IA:1889:U:H2'	1:IA:1890:U:C6	2.50	0.46
1:IA:3136:U:H2'	1:IA:3137:C:C6	2.50	0.46
1:IA:3349:G:OP1	16:IP:94:THR:OG1	2.29	0.46
3:IC:21:C:H4'	3:IC:22:C:C5	2.51	0.46
23:IW:85:CYS:SG	23:IW:87:ARG:N	2.86	0.46
32:lf:8:ASN:O	32:lf:12:LEU:HG	2.15	0.46
32:lf:82:MET:HE3	32:lf:115:ARG:HB2	1.97	0.46
1:IA:258:G:C8	6:IF:227:PRO:HG3	2.51	0.46
1:IA:474:A:H2'	1:IA:475:A:H8	1.81	0.46
1:IA:760:A:H2'	1:IA:761:A:C8	2.49	0.46
1:IA:836:C:H2'	1:IA:837:A:C8	2.51	0.46
1:IA:1509:A:H2'	1:IA:1510:A:H8	1.80	0.46
1:IA:2445:G:H2'	1:IA:2446:G:C8	2.50	0.46
1:IA:2504:U:H2'	1:IA:2505:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2753:U:H2'	1:1A:2754:C:C6	2.51	0.46
1:1A:3262:U:OP1	42:lp:39:LYS:HE2	2.16	0.46
12:1L:190:ILE:HG23	12:1L:197:PHE:HB2	1.98	0.46
13:1M:21:ILE:HG13	13:1M:125:MET:HG3	1.97	0.46
23:1W:45:LYS:NZ	23:1W:96:TYR:OH	2.24	0.46
1:1A:105:A:N1	1:1A:368:U:O2'	2.43	0.46
1:1A:337:A:H2'	1:1A:338:A:C8	2.51	0.46
1:1A:565:U:H2'	1:1A:566:U:C6	2.50	0.46
1:1A:668:A:C8	1:1A:669:A:C8	3.04	0.46
1:1A:1764:A:H2'	1:1A:1765:A:H8	1.77	0.46
1:1A:2427:U:H2'	1:1A:2428:A:C8	2.50	0.46
1:1A:3311:U:H2'	1:1A:3312:U:C6	2.51	0.46
3:1C:16:C:H2'	3:1C:17:G:O4'	2.15	0.46
4:1D:79:ALA:HB3	4:1D:82:LEU:HD13	1.98	0.46
6:1F:360:LYS:NZ	6:1F:400:THR:OG1	2.48	0.46
1:1A:474:A:H2'	1:1A:475:A:C8	2.51	0.46
1:1A:564:A:H1'	1:1A:565:U:OP2	2.15	0.46
1:1A:1086:G:H2'	1:1A:1087:G:C8	2.51	0.46
1:1A:1968:U:H2'	1:1A:1969:U:C6	2.51	0.46
1:1A:2818:A:N3	7:1G:36:MET:HG2	2.31	0.46
1:1A:2903:A:H2'	1:1A:2904:U:O4'	2.16	0.46
2:1B:141:G:H2'	2:1B:142:A:H8	1.80	0.46
23:1W:43:PRO:O	23:1W:47:VAL:HG23	2.15	0.46
23:1W:48:THR:O	23:1W:51:ARG:N	2.49	0.46
32:1f:48:ARG:NH1	32:1f:144:THR:OG1	2.48	0.46
33:1g:91:ARG:HG3	33:1g:91:ARG:NH1	2.27	0.46
36:1j:48:VAL:HG22	36:1j:101:VAL:HG22	1.98	0.46
1:1A:1520:A:H4'	1:1A:1521:A:O5'	2.15	0.46
1:1A:3207:G:H2'	1:1A:3208:A:C8	2.51	0.46
3:1C:1:A:H61	3:1C:116:C:H42	1.64	0.46
3:1C:76:U:H2'	3:1C:77:U:O4'	2.16	0.46
20:1T:78:VAL:HG22	20:1T:83:ILE:HG12	1.98	0.46
24:1X:10:GLN:HA	24:1X:10:GLN:OE1	2.15	0.46
42:lp:29:PRO:HG2	42:lp:32:ALA:HB2	1.97	0.46
1:1A:480:U:H2'	1:1A:481:A:O4'	2.16	0.45
1:1A:2273:C:H4'	1:1A:2274:A:O5'	2.15	0.45
1:1A:3312:U:H2'	1:1A:3313:U:H6	1.80	0.45
1:1A:3501:A:H2'	1:1A:3502:A:H8	1.81	0.45
2:1B:15:U:C2	2:1B:16:U:C5	3.05	0.45
6:1F:272:MET:HE1	19:1S:104:LYS:HE3	1.99	0.45
16:1P:124:ALA:O	16:1P:128:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:lf:33:LYS:N	32:lf:34:PRO:HD3	2.31	0.45
1:lA:489:U:H2'	1:lA:490:A:C8	2.51	0.45
1:lA:745:A:H4'	8:lH:50:TRP:HB2	1.99	0.45
1:lA:1741:A:N3	1:lA:1763:C:O2'	2.47	0.45
5:lE:223:THR:HG22	5:lE:330:ALA:HB1	1.99	0.45
8:lH:113:THR:HG22	8:lH:204:PHE:HB3	1.98	0.45
1:lA:828:A:OP1	17:lQ:202:ARG:NH2	2.48	0.45
1:lA:1688:A:H2'	1:lA:1689:A:C8	2.52	0.45
5:lE:137:TYR:O	5:lE:146:ARG:NH1	2.49	0.45
1:lA:1389:U:H2'	1:lA:1390:G:C8	2.52	0.45
1:lA:1391:U:H2'	1:lA:1392:G:O4'	2.17	0.45
1:lA:2495:A:H2'	1:lA:2496:C:C6	2.51	0.45
1:lA:2835:C:O3'	43:lq:37:GLY:HA3	2.16	0.45
1:lA:2847:A:H2'	1:lA:2848:A:C8	2.52	0.45
4:lD:140:ASN:HB3	4:lD:145:THR:HG22	1.98	0.45
5:lE:58:ARG:NH1	5:lE:353:GLU:OE2	2.50	0.45
10:lJ:219:TYR:CD1	10:lJ:225:MET:HE1	2.52	0.45
15:lO:77:PRO:O	15:lO:81:VAL:HG23	2.17	0.45
39:lm:92:SER:O	39:lm:92:SER:OG	2.34	0.45
1:lA:961:A:H5'	21:lU:131:GLN:NE2	2.31	0.45
1:lA:996:C:O2'	1:lA:999:G:O2'	2.30	0.45
1:lA:1337:A:H2'	1:lA:1338:U:C6	2.51	0.45
1:lA:1729:G:H2'	1:lA:1730:G:C8	2.52	0.45
1:lA:1934:G:O3'	40:ln:51:THR:HG21	2.16	0.45
1:lA:2297:G:N7	37:lk:61:LYS:NZ	2.63	0.45
1:lA:3396:A:H2'	1:lA:3397:C:C6	2.52	0.45
2:lB:1:A:H2'	2:lB:2:A:H8	1.80	0.45
6:lF:162:ILE:HD11	6:lF:171:LEU:HD13	1.97	0.45
9:lI:70:LYS:NZ	9:lI:178:THR:O	2.44	0.45
9:lI:73:VAL:HG12	9:lI:127:PRO:HD3	1.97	0.45
35:li:-9:ALA:HB3	35:li:45:ARG:HH22	1.82	0.45
1:lA:1033:A:C2	4:lD:204:MET:HG2	2.52	0.45
1:lA:1078:C:O2'	1:lA:2486:U:O4	2.34	0.45
1:lA:1183:G:H5'	1:lA:1187:A:OP1	2.17	0.45
1:lA:3188:C:H42	11:lK:129:LYS:HG2	1.82	0.45
4:lD:35:PHE:CD1	4:lD:66:PRO:HB2	2.51	0.45
4:lD:189:TYR:CD2	4:lD:196:TRP:HB2	2.51	0.45
13:lM:12:ILE:HD12	13:lM:154:LEU:HD21	1.98	0.45
19:lS:160:LYS:HD3	19:lS:160:LYS:HA	1.59	0.45
1:lA:327:U:O2'	1:lA:329:G:N7	2.40	0.45
1:lA:960:G:H2'	1:lA:961:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2851:A:H2'	1:1A:2852:G:C8	2.52	0.45
1:1A:2979:C:H5	1:1A:2995:C:N4	2.13	0.45
6:1F:102:PHE:O	6:1F:103:SER:C	2.59	0.45
7:1G:95:TYR:CG	7:1G:194:ARG:HG2	2.52	0.45
18:1R:61:ARG:O	18:1R:64:ASN:ND2	2.50	0.45
28:1b:47:GLU:HB3	28:1b:69:LYS:HG2	1.99	0.45
29:1c:148:THR:HA	37:1k:2:ALA:HB3	1.99	0.45
32:1f:54:MET:HG3	32:1f:58:LEU:HG	1.98	0.45
1:1A:34:U:H2'	1:1A:35:A:O4'	2.17	0.45
1:1A:770:C:O2	1:1A:2453:G:O2'	2.26	0.45
1:1A:1105:U:H2'	1:1A:1106:U:C6	2.52	0.45
1:1A:1476:G:O2'	1:1A:1477:A:N3	2.45	0.45
1:1A:1921:A:H2'	1:1A:1922:U:O2	2.17	0.45
1:1A:2482:C:H2'	1:1A:2483:C:H6	1.81	0.45
1:1A:3262:U:H2'	1:1A:3263:G:C8	2.52	0.45
3:1C:48:U:OP1	7:1G:221:ARG:HB2	2.17	0.45
5:1E:73:LEU:HD22	26:1Z:18:ALA:HB1	1.99	0.45
5:1E:387:ASP:C	5:1E:387:ASP:OD2	2.59	0.45
6:1F:358:MET:HE3	6:1F:358:MET:HB3	1.81	0.45
6:1F:393:GLU:HB3	6:1F:396:LEU:HG	1.99	0.45
12:1L:175:LYS:HD2	12:1L:175:LYS:HA	1.66	0.45
23:1W:77:ILE:HD12	23:1W:78:THR:N	2.31	0.45
1:1A:1844:U:H2'	1:1A:1845:G:H8	1.82	0.45
1:1A:1876:U:H2'	1:1A:1936:A:H61	1.82	0.45
1:1A:1989:U:H2'	1:1A:1990:A:C8	2.52	0.45
3:1C:104:G:H2'	3:1C:105:A:C8	2.51	0.45
4:1D:51:ASP:HB2	4:1D:58:LEU:HD22	1.99	0.45
5:1E:153:ILE:O	5:1E:157:CYS:HB2	2.16	0.45
5:1E:218:ASP:OD2	5:1E:340:ARG:NH2	2.48	0.45
5:1E:273:GLY:O	5:1E:275:PHE:N	2.49	0.45
23:1W:44:LYS:O	23:1W:45:LYS:HG3	2.17	0.45
39:1m:16:THR:O	39:1m:16:THR:OG1	2.35	0.45
42:1p:17:ASP:HB3	42:1p:30:LEU:HD11	1.98	0.45
1:1A:223:A:H2'	1:1A:224:U:H6	1.81	0.45
1:1A:498:A:N1	1:1A:575:A:N6	2.64	0.45
1:1A:551:A:H2'	1:1A:552:G:O4'	2.16	0.45
1:1A:732:U:O2'	1:1A:733:C:O4'	2.35	0.45
1:1A:1606:A:H5''	18:1R:53:ILE:HB	1.98	0.45
1:1A:2720:U:O2'	1:1A:2721:G:H5'	2.17	0.45
1:1A:3150:A:H2'	1:1A:3151:A:H8	1.82	0.45
5:1E:122:TRP:CZ2	5:1E:127:LYS:HG2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:lZ:40:MET:O	26:lZ:44:ARG:HG3	2.17	0.45
1:lA:610:A:N6	1:lA:687:U:C4	2.85	0.44
1:lA:1882:A:H1'	1:lA:1883:A:H2	1.82	0.44
1:lA:2632:A:C8	34:lh:91:ARG:HD2	2.52	0.44
1:lA:3344:U:OP1	11:lK:24:LYS:NZ	2.45	0.44
3:lC:26:U:H2'	3:lC:27:G:C8	2.52	0.44
7:lG:201:ALA:HB2	7:lG:232:LEU:HD12	2.00	0.44
14:lN:147:LYS:H	14:lN:147:LYS:HD2	1.81	0.44
28:lb:22:LYS:NZ	28:lb:135:THR:HG23	2.32	0.44
33:lg:50:THR:O	33:lg:50:THR:OG1	2.28	0.44
42:lp:45:ASP:O	42:lp:46:LEU:HD23	2.17	0.44
1:lA:548:A:H2'	1:lA:549:U:C6	2.53	0.44
1:lA:596:G:C2	1:lA:597:A:C8	3.05	0.44
1:lA:713:G:H3'	1:lA:714:U:C5'	2.47	0.44
1:lA:720:U:H2'	1:lA:721:A:C8	2.53	0.44
1:lA:2320:A:O4'	4:lD:243:THR:HG21	2.18	0.44
1:lA:3033:C:H2'	1:lA:3034:A:C8	2.52	0.44
1:lA:3090:G:C2	5:lE:252:ALA:HB1	2.52	0.44
4:lD:104:ILE:HD11	4:lD:113:VAL:HG21	2.00	0.44
6:lF:372:SER:HB3	6:lF:396:LEU:HD13	1.98	0.44
9:lI:143:LYS:HE3	9:lI:143:LYS:HB2	1.72	0.44
20:lT:93:VAL:HG23	20:lT:94:THR:HG23	1.99	0.44
1:lA:467:A:C2	1:lA:2439:A:H4'	2.52	0.44
1:lA:542:U:H2'	1:lA:543:A:C8	2.52	0.44
1:lA:700:A:O2'	1:lA:701:A:OP1	2.31	0.44
1:lA:1263:U:O3'	9:lI:85:PRO:HD3	2.17	0.44
1:lA:1392:G:H21	1:lA:1397:A:H62	1.65	0.44
1:lA:1534:U:H2'	1:lA:1535:A:C8	2.52	0.44
1:lA:2633:C:H2'	1:lA:2634:A:O4'	2.18	0.44
1:lA:2903:A:O5'	1:lA:2903:A:H8	1.98	0.44
24:lX:38:THR:HG21	24:lX:66:LYS:HD2	2.00	0.44
1:lA:1057:C:OP2	29:lc:26:ARG:NH1	2.51	0.44
1:lA:1093:G:OP1	19:lS:19:ARG:NH1	2.44	0.44
1:lA:1744:A:H2'	1:lA:1745:A:H8	1.80	0.44
1:lA:2851:A:H2'	1:lA:2852:G:H8	1.81	0.44
3:lC:84:G:N3	3:lC:84:G:H2'	2.33	0.44
3:lC:85:G:H1	3:lC:90:G:H1	1.65	0.44
4:lD:93:LYS:HB3	4:lD:93:LYS:HE3	1.84	0.44
5:lE:53:MET:HE2	5:lE:53:MET:HB3	1.77	0.44
6:lF:4:ARG:HA	6:lF:4:ARG:HD3	1.73	0.44
6:lF:157:LYS:HE2	27:la:145:VAL:HG12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:lb:83:THR:HG22	34:lh:93:PHE:CZ	2.53	0.44
1:1A:336:A:H5''	17:lQ:97:SER:HB3	1.98	0.44
1:1A:490:A:C6	1:1A:583:A:N6	2.85	0.44
1:1A:2303:U:H2'	1:1A:2304:A:H8	1.82	0.44
9:II:26:GLN:OE1	9:II:30:LYS:NZ	2.45	0.44
11:IK:35:LEU:HD23	11:IK:35:LEU:HA	1.90	0.44
19:IS:70:MET:HE3	19:IS:70:MET:HB3	1.80	0.44
23:IW:68:VAL:HG22	23:IW:77:ILE:HG22	2.00	0.44
1:1A:630:A:C4	1:1A:631:G:C8	3.06	0.44
1:1A:632:G:H2'	1:1A:633:A:N9	2.32	0.44
1:1A:2230:U:H2'	1:1A:2231:C:H6	1.82	0.44
1:1A:2910:G:H2'	1:1A:2911:U:O4'	2.17	0.44
1:1A:3141:A:N6	1:1A:3151:A:OP1	2.46	0.44
1:1A:3337:A:C5	15:IO:115:LYS:HG2	2.53	0.44
1:1A:3432:A:O2'	1:1A:3433:U:OP1	2.34	0.44
2:IB:23:U:O2'	2:IB:24:U:H5'	2.17	0.44
12:IL:43:CYS:O	12:IL:171:TRP:NE1	2.48	0.44
14:IN:228:LYS:HA	14:IN:228:LYS:HD3	1.90	0.44
19:IS:60:ILE:HD12	19:IS:85:THR:HG21	2.00	0.44
35:li:79:LYS:O	35:li:83:GLN:HG2	2.17	0.44
40:ln:47:LYS:HD3	40:ln:48:TYR:CE2	2.53	0.44
1:1A:237:C:H2'	1:1A:238:A:C8	2.52	0.44
1:1A:431:A:H2'	1:1A:432:A:C8	2.52	0.44
1:1A:1667:U:O2	1:1A:1743:U:H5'	2.18	0.44
1:1A:1841:G:N2	1:1A:1975:G:H1	2.05	0.44
1:1A:3314:U:O2'	1:1A:3417:G:OP2	2.33	0.44
2:IB:29:U:H2'	2:IB:30:U:C6	2.53	0.44
9:II:96:LEU:HD21	9:II:103:VAL:HG22	1.99	0.44
10:IJ:141:GLU:OE2	17:IQ:6:TYR:OH	2.27	0.44
11:IK:133:HIS:CD2	11:IK:133:HIS:O	2.71	0.44
21:IU:122:ASP:N	21:IU:122:ASP:OD1	2.50	0.44
27:la:139:ALA:HA	27:la:151:MET:SD	2.58	0.44
31:le:70:GLN:HE22	31:le:109:GLU:H	1.66	0.44
1:1A:625:A:O2'	1:1A:626:A:OP1	2.35	0.44
1:1A:1095:A:C2	1:1A:1099:A:H2	2.34	0.44
1:1A:1904:U:O2'	1:1A:1906:A:N7	2.41	0.44
1:1A:1922:U:H2'	1:1A:1923:U:C6	2.52	0.44
1:1A:2207:A:C8	1:1A:2264:A:C8	3.06	0.44
1:1A:2303:U:H2'	1:1A:2304:A:C8	2.52	0.44
2:IB:8:U:H2'	2:IB:9:A:H8	1.82	0.44
3:IC:45:U:H2'	3:IC:46:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IE:41:PRO:HA	5:IE:187:GLY:HA3	1.99	0.44
8:IH:155:TYR:O	8:IH:159:LYS:HG2	2.17	0.44
28:lb:11:VAL:HG12	28:lb:82:PRO:HA	2.00	0.44
1:IA:219:G:H2'	1:IA:220:A:H8	1.83	0.44
1:IA:246:U:OP1	27:la:59:LYS:NZ	2.47	0.44
1:IA:743:G:H2'	1:IA:744:A:C4	2.53	0.44
1:IA:765:A:H2'	1:IA:766:U:C6	2.53	0.44
1:IA:2122:U:O2'	1:IA:2134:A:N7	2.44	0.44
1:IA:2483:C:H2'	1:IA:2484:U:C6	2.52	0.44
2:IB:79:A:O2'	2:IB:80:A:OP1	2.29	0.44
14:IN:72:GLY:HA3	14:IN:96:ASP:HB2	1.99	0.44
16:IP:92:THR:O	16:IP:96:LYS:HG3	2.18	0.44
1:IA:13:C:P	25:IY:27:ARG:HH22	2.41	0.43
1:IA:62:A:N6	1:IA:72:G:H1'	2.33	0.43
1:IA:908:A:H2'	1:IA:909:A:C8	2.53	0.43
1:IA:1485:A:H2'	1:IA:1486:C:O4'	2.18	0.43
1:IA:1592:U:H2'	1:IA:1593:A:H8	1.82	0.43
1:IA:3163:G:O2'	5:IE:14:LEU:O	2.31	0.43
1:IA:3169:C:H2'	1:IA:3170:A:H8	1.83	0.43
3:IC:45:U:H2'	3:IC:46:G:C8	2.53	0.43
7:IG:118:GLN:HB2	7:IG:137:VAL:HG11	1.99	0.43
21:IU:5:LYS:HB3	21:IU:5:LYS:HE3	1.71	0.43
23:IW:45:LYS:HZ2	23:IW:46:LEU:H	1.66	0.43
29:lc:97:GLU:OE1	29:lc:97:GLU:N	2.40	0.43
31:le:64:ALA:O	31:le:68:LYS:N	2.51	0.43
1:IA:426:U:H2'	1:IA:427:U:H6	1.82	0.43
1:IA:909:A:H2'	1:IA:910:A:H8	1.82	0.43
1:IA:2744:A:C2	13:IM:124:GLY:HA3	2.53	0.43
1:IA:3149:A:H2'	1:IA:3150:A:C8	2.53	0.43
1:IA:3501:A:H2'	1:IA:3502:A:C8	2.52	0.43
7:IG:127:LYS:HB2	7:IG:127:LYS:HE3	1.75	0.43
12:IL:52:ILE:HD12	12:IL:136:ILE:HB	2.00	0.43
23:IW:49:PHE:CE2	23:IW:96:TYR:HD1	2.35	0.43
34:lh:80:LYS:HB3	34:lh:85:VAL:HG23	2.00	0.43
1:IA:797:C:C2	1:IA:798:U:C5	3.06	0.43
3:IC:5:A:H61	3:IC:112:C:H42	1.65	0.43
6:IF:354:TYR:HD1	6:IF:354:TYR:O	2.01	0.43
14:IN:60:ASN:OD1	29:lc:66:ASN:HB3	2.19	0.43
1:IA:399:G:O6	38:ll:55:ARG:NH2	2.44	0.43
1:IA:496:A:H2'	1:IA:497:U:O4'	2.18	0.43
1:IA:606:A:H2'	1:IA:607:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:996:C:HO2'	1:1A:999:G:HO2'	1.64	0.43
1:1A:1207:C:H2'	1:1A:1208:U:O4'	2.18	0.43
1:1A:2639:A:H2'	1:1A:2640:A:C8	2.53	0.43
1:1A:3262:U:H2'	1:1A:3263:G:H8	1.83	0.43
1:1A:3455:G:N2	1:1A:3501:A:H2	2.07	0.43
11:1K:97:GLN:HE21	11:1K:99:LYS:HD2	1.83	0.43
13:1M:91:LEU:HD23	13:1M:91:LEU:HA	1.84	0.43
16:1P:103:LEU:HD12	16:1P:103:LEU:HA	1.82	0.43
21:1U:105:LEU:HD13	21:1U:135:LYS:HE2	2.01	0.43
26:1Z:14:LYS:HE2	26:1Z:14:LYS:HB2	1.78	0.43
27:1a:87:LYS:N	27:1a:91:GLN:O	2.39	0.43
32:1f:54:MET:HE1	32:1f:74:ILE:HG13	2.00	0.43
34:1h:69:LYS:HE3	34:1h:69:LYS:HB3	1.83	0.43
1:1A:582:U:H2'	1:1A:583:A:C8	2.54	0.43
1:1A:619:A:H2'	1:1A:619:A:N3	2.33	0.43
1:1A:632:G:C2	1:1A:657:A:C2	3.06	0.43
1:1A:703:G:C8	1:1A:704:C:C6	3.07	0.43
1:1A:790:A:H2'	1:1A:791:A:H8	1.82	0.43
1:1A:1495:A:H2'	1:1A:1496:A:H8	1.83	0.43
1:1A:1592:U:H2'	1:1A:1593:A:C8	2.54	0.43
1:1A:2254:A:H5''	4:1D:132:ASN:OD1	2.18	0.43
1:1A:3142:G:N3	1:1A:3143:A:N6	2.65	0.43
3:1C:35:A:O5'	3:1C:35:A:H8	2.02	0.43
6:1F:91:ALA:O	6:1F:93:GLY:N	2.52	0.43
7:1G:147:LEU:HD22	7:1G:164:LEU:HD13	2.00	0.43
10:1J:37:THR:HG22	10:1J:38:ARG:N	2.32	0.43
12:1L:191:ILE:HD11	12:1L:200:ALA:HB2	1.99	0.43
19:1S:141:ASN:HA	19:1S:146:LEU:HD12	1.99	0.43
32:1f:121:GLU:N	32:1f:121:GLU:OE1	2.51	0.43
1:1A:333:U:O2'	17:1Q:180:ARG:O	2.34	0.43
1:1A:491:G:C5	1:1A:492:U:C4	3.06	0.43
1:1A:529:U:H2'	1:1A:530:A:H8	1.84	0.43
1:1A:1030:C:OP1	4:1D:14:SER:OG	2.36	0.43
1:1A:2815:G:N2	1:1A:2818:A:OP2	2.39	0.43
1:1A:2958:G:N2	1:1A:2961:U:O2	2.48	0.43
1:1A:3291:G:C5	1:1A:3292:U:C5	3.07	0.43
1:1A:3311:U:H2'	1:1A:3312:U:H6	1.84	0.43
16:1P:108:THR:N	16:1P:111:ASP:OD1	2.44	0.43
25:1Y:85:LYS:HD2	25:1Y:85:LYS:HA	1.71	0.43
1:1A:2835:C:H2'	1:1A:2836:C:H6	1.83	0.43
1:1A:2848:A:H2'	1:1A:2849:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2979:C:H2'	1:1A:2980:A:O4'	2.19	0.43
1:1A:3303:A:H2'	1:1A:3304:C:C6	2.53	0.43
1:1A:3346:U:C2	1:1A:3347:A:C8	3.06	0.43
3:1C:85:G:H22	3:1C:90:G:N2	2.17	0.43
3:1C:114:U:H2'	3:1C:115:A:N3	2.34	0.43
6:1F:424:LYS:NZ	9:1I:58:GLU:OE1	2.52	0.43
41:1o:29:MET:HE2	41:1o:29:MET:HB2	1.87	0.43
1:1A:360:U:H2'	1:1A:361:C:H6	1.84	0.43
1:1A:1058:U:O2'	1:1A:2478:A:N1	2.48	0.43
1:1A:1187:A:N6	1:1A:1217:U:H3	2.13	0.43
1:1A:2721:G:N1	1:1A:2941:C:H5	2.09	0.43
1:1A:2744:A:H1'	13:1M:107:GLU:OE2	2.18	0.43
1:1A:3312:U:H2'	1:1A:3313:U:C6	2.54	0.43
1:1A:3328:G:H2'	1:1A:3329:U:O4'	2.19	0.43
1:1A:3332:A:H2'	1:1A:3333:A:C8	2.53	0.43
1:1A:3370:A:H2'	1:1A:3371:U:H6	1.84	0.43
1:1A:3452:U:H3	1:1A:3504:G:H1	1.66	0.43
4:1D:17:LYS:HE3	4:1D:17:LYS:HB2	1.73	0.43
7:1G:110:LEU:HD22	7:1G:115:MET:HG3	2.01	0.43
16:1P:133:LYS:HD2	16:1P:133:LYS:O	2.18	0.43
23:1W:50:PHE:O	23:1W:54:ILE:HD12	2.19	0.43
37:1k:10:LYS:HB3	37:1k:10:LYS:HE2	1.87	0.43
1:1A:324:A:H2'	1:1A:325:U:C6	2.53	0.43
1:1A:498:A:H2'	1:1A:499:U:C6	2.53	0.43
1:1A:739:A:H2'	1:1A:740:A:C8	2.53	0.43
1:1A:836:C:H2'	1:1A:837:A:H8	1.84	0.43
1:1A:2432:A:H2	18:1R:131:ARG:HH22	1.66	0.43
1:1A:2937:G:O2'	1:1A:2938:U:OP2	2.33	0.43
1:1A:3130:A:O2'	5:1E:261:ARG:HB3	2.19	0.43
1:1A:3195:G:H2'	1:1A:3196:U:C6	2.53	0.43
1:1A:3292:U:N3	1:1A:3293:C:C5	2.87	0.43
1:1A:3392:G:H2'	1:1A:3393:A:H8	1.83	0.43
3:1C:46:G:N3	7:1G:218:GLN:NE2	2.66	0.43
4:1D:61:VAL:HG11	4:1D:88:ILE:HD11	2.01	0.43
4:1D:246:ILE:HD12	4:1D:246:ILE:H	1.84	0.43
6:1F:51:PRO:HA	6:1F:111:TRP:CE2	2.54	0.43
6:1F:286:MET:HE1	19:1S:27:LEU:HB3	2.00	0.43
7:1G:111:GLN:HE21	7:1G:111:GLN:HB2	1.62	0.43
11:1K:54:LYS:HB3	11:1K:57:GLY:H	1.84	0.43
36:1j:43:TYR:HA	36:1j:46:LYS:HG3	2.01	0.43
1:1A:332:G:C6	43:1q:43:ARG:HD3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:lA:359:A:H2'	1:lA:360:U:C6	2.54	0.43
1:lA:632:G:H2'	1:lA:633:A:C4	2.53	0.43
1:lA:851:A:H5''	29:lc:114:GLY:O	2.19	0.43
1:lA:948:C:O2'	1:lA:949:G:N7	2.51	0.43
1:lA:1194:A:O2'	1:lA:1195:G:H5'	2.19	0.43
1:lA:2239:U:O2'	4:lD:11:GLY:HA3	2.19	0.43
1:lA:2240:C:OP1	4:lD:8:GLN:NE2	2.41	0.43
4:lD:104:ILE:N	4:lD:162:CYS:O	2.44	0.43
5:lE:143:LYS:HE2	5:lE:143:LYS:HB2	1.73	0.43
13:lM:133:ARG:HG2	13:lM:134:PRO:HD2	2.00	0.43
32:lf:44:ALA:O	32:lf:115:ARG:NH1	2.52	0.43
42:lp:35:CYS:O	42:lp:42:HIS:HA	2.19	0.43
1:lA:531:U:H2'	1:lA:532:A:C8	2.54	0.42
1:lA:531:U:H2'	1:lA:532:A:H8	1.83	0.42
1:lA:705:U:C2	1:lA:706:A:C8	3.07	0.42
1:lA:940:U:H2'	1:lA:941:A:C8	2.54	0.42
1:lA:1569:A:H5''	1:lA:1570:U:O5'	2.19	0.42
1:lA:2731:G:H2'	1:lA:2732:A:H8	1.84	0.42
1:lA:2773:U:OP2	7:lG:23:ARG:NE	2.48	0.42
1:lA:3226:C:H2'	1:lA:3227:A:O4'	2.19	0.42
2:lB:54:A:H5'	41:lo:21:ARG:HD3	2.00	0.42
6:lF:423:LYS:HE2	6:lF:423:LYS:HB3	1.80	0.42
11:lK:136:MET:HE1	11:lK:167:ILE:HD11	1.99	0.42
14:lN:151:GLU:O	14:lN:155:PHE:N	2.50	0.42
31:le:8:LYS:HA	31:le:8:LYS:HD2	1.73	0.42
42:lp:24:CYS:HA	42:lp:40:CYS:HB3	2.00	0.42
1:lA:1909:C:H2'	1:lA:1910:A:C8	2.53	0.42
1:lA:3421:A:H2'	1:lA:3422:A:C8	2.55	0.42
1:lA:3432:A:N6	1:lA:3434:A:N3	2.67	0.42
3:lC:62:U:O2'	12:lL:203:LYS:HA	2.20	0.42
8:lH:150:PHE:O	8:lH:154:GLN:HG2	2.19	0.42
13:lM:63:ASP:N	13:lM:63:ASP:OD1	2.49	0.42
20:IT:3:GLU:HG2	20:IT:60:ILE:HD12	2.01	0.42
40:ln:30:VAL:HG11	40:ln:67:ILE:HD13	2.01	0.42
1:lA:979:G:H1'	1:lA:1015:A:OP1	2.19	0.42
1:lA:1131:G:H2'	1:lA:1132:U:C6	2.54	0.42
1:lA:1271:C:H4'	1:lA:1456:U:C4	2.53	0.42
1:lA:1440:A:OP2	15:lO:134:ARG:HD3	2.19	0.42
1:lA:1527:A:O2'	1:lA:1551:A:N1	2.40	0.42
1:lA:3104:G:H2'	1:lA:3105:U:C6	2.54	0.42
3:lC:53:C:O2'	13:lM:152:HIS:ND1	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1F:19:LYS:HD3	6:1F:19:LYS:HA	1.73	0.42
23:1W:49:PHE:CD2	23:1W:96:TYR:CD1	3.08	0.42
24:1X:16:VAL:HG21	24:1X:124:GLU:HG2	2.01	0.42
27:1a:56:LYS:HD2	27:1a:65:ALA:HB2	2.01	0.42
32:1f:137:PHE:HA	32:1f:140:LEU:HD12	2.01	0.42
1:1A:487:A:H2'	1:1A:488:A:C8	2.54	0.42
1:1A:613:G:O2'	1:1A:615:G:OP2	2.33	0.42
1:1A:683:A:H2'	1:1A:684:U:O4'	2.18	0.42
1:1A:733:C:H3'	1:1A:734:C:H5''	2.01	0.42
1:1A:1689:A:C5	1:1A:1690:A:H1'	2.55	0.42
1:1A:2731:G:H2'	1:1A:2732:A:C8	2.54	0.42
3:1C:42:U:C2	3:1C:43:A:C8	3.07	0.42
11:1K:129:LYS:HA	11:1K:129:LYS:HD2	1.80	0.42
21:1U:28:GLU:N	21:1U:28:GLU:OE2	2.52	0.42
31:1e:13:GLY:O	31:1e:17:LYS:HG3	2.20	0.42
1:1A:846:A:H2'	1:1A:847:A:C8	2.54	0.42
1:1A:974:U:O4	39:1m:4:ARG:NH1	2.52	0.42
1:1A:1176:A:OP1	9:1I:86:LYS:NZ	2.48	0.42
1:1A:1314:A:H2	15:1O:135:LYS:H	1.67	0.42
1:1A:2348:G:OP2	1:1A:2348:G:N2	2.34	0.42
1:1A:2634:A:O2'	10:1J:30:VAL:HG13	2.19	0.42
1:1A:2835:C:H2'	1:1A:2836:C:C6	2.55	0.42
1:1A:3265:C:H2'	1:1A:3266:U:C6	2.54	0.42
3:1C:103:U:H2'	3:1C:104:G:H8	1.82	0.42
7:1G:115:MET:H	7:1G:115:MET:HG2	1.71	0.42
8:1H:171:GLU:OE2	8:1H:172:SER:N	2.52	0.42
8:1H:198:HIS:HB3	8:1H:200:HIS:CE1	2.54	0.42
10:1J:27:LYS:HG2	10:1J:32:HIS:HB2	2.00	0.42
10:1J:224:HIS:HA	10:1J:227:ARG:HG2	2.02	0.42
13:1M:151:ASP:N	13:1M:151:ASP:OD1	2.51	0.42
23:1W:30:CYS:H	23:1W:77:ILE:HD11	1.84	0.42
24:1X:69:LYS:HA	24:1X:69:LYS:HD2	1.82	0.42
24:1X:100:ASP:OD1	26:1Z:26:LEU:HD21	2.19	0.42
1:1A:505:A:H2'	1:1A:506:A:H8	1.84	0.42
1:1A:795:G:H4'	1:1A:796:U:C6	2.54	0.42
1:1A:798:U:H2'	1:1A:799:A:H8	1.84	0.42
1:1A:1187:A:H2'	1:1A:1188:A:O4'	2.19	0.42
1:1A:1539:U:C4	33:1g:56:ILE:HD12	2.53	0.42
1:1A:2098:A:H61	1:1A:2415:C:H42	1.67	0.42
3:1C:17:G:H1	3:1C:59:G:N2	2.16	0.42
7:1G:30:TYR:O	7:1G:34:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IH:93:GLY:O	8:IH:94:PRO:C	2.62	0.42
14:IN:49:ILE:C	14:IN:51:SER:H	2.26	0.42
20:IT:41:LEU:HB3	20:IT:47:VAL:HB	2.01	0.42
31:le:53:PRO:HB2	31:le:56:GLU:OE1	2.20	0.42
1:lA:37:G:N2	1:lA:2946:A:H62	2.18	0.42
1:lA:631:G:O6	1:lA:659:U:O4	2.37	0.42
1:lA:703:G:H3'	1:lA:704:C:H6	1.85	0.42
1:lA:713:G:H3'	1:lA:714:U:H5'	2.02	0.42
1:lA:1346:G:HO2'	1:lA:1347:A:P	2.42	0.42
1:lA:1508:U:H2'	1:lA:1509:A:H8	1.85	0.42
1:lA:2224:U:H2'	1:lA:2225:A:C8	2.54	0.42
1:lA:2488:G:H2'	1:lA:2489:A:C8	2.54	0.42
1:lA:2701:U:H2'	1:lA:2702:G:H8	1.83	0.42
1:lA:2747:G:N3	1:lA:2747:G:H2'	2.35	0.42
1:lA:3369:U:H2'	1:lA:3370:A:C8	2.55	0.42
2:IB:117:A:H2'	2:IB:118:C:C6	2.55	0.42
8:IH:31:LYS:HA	8:IH:31:LYS:HD2	1.88	0.42
29:lc:8:THR:HG23	29:lc:9:ARG:HD2	2.02	0.42
40:ln:23:LYS:HA	40:ln:23:LYS:HD3	1.72	0.42
43:lq:2:VAL:O	43:lq:90:GLU:N	2.50	0.42
43:lq:30:LYS:HB3	43:lq:30:LYS:HE3	1.75	0.42
1:lA:663:G:OP1	16:IP:71:MET:HA	2.20	0.42
1:lA:775:C:OP1	29:lc:21:ARG:HB3	2.20	0.42
1:lA:937:C:O2'	1:lA:2214:A:N1	2.44	0.42
1:lA:2084:G:H2'	1:lA:2085:A:C8	2.55	0.42
1:lA:2144:U:OP2	21:IU:74:ARG:NE	2.39	0.42
1:lA:2388:A:H2'	1:lA:2391:G:H21	1.85	0.42
1:lA:2459:U:H5'	15:IO:72:PHE:CE2	2.54	0.42
5:IE:238:ARG:HE	5:IE:238:ARG:HB2	1.55	0.42
11:IK:4:LEU:HD12	11:IK:4:LEU:HA	1.80	0.42
13:IM:117:ASP:OD1	13:IM:117:ASP:N	2.49	0.42
21:IU:74:ARG:HD3	21:IU:74:ARG:HA	1.87	0.42
22:IV:120:ILE:HD12	22:IV:121:GLN:N	2.34	0.42
23:IW:44:LYS:O	23:IW:45:LYS:HE3	2.20	0.42
25:IY:87:ILE:HD11	25:IY:104:ARG:HD3	2.01	0.42
40:ln:18:ILE:HG23	40:ln:19:LEU:HD22	2.02	0.42
1:lA:445:G:H5''	1:lA:448:C:H1'	2.01	0.42
1:lA:2443:A:H2'	1:lA:2444:A:C8	2.54	0.42
1:lA:2489:A:H2'	1:lA:2490:G:C8	2.54	0.42
1:lA:2939:G:N7	43:lq:61:LYS:NZ	2.67	0.42
1:lA:3101:A:H2'	1:lA:3102:C:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:2:A:H2'	2:1B:3:U:C6	2.54	0.42
2:1B:68:A:H2'	2:1B:69:U:C6	2.54	0.42
8:1H:144:LYS:HB3	8:1H:144:LYS:HE3	1.68	0.42
15:1O:17:LEU:HD13	15:1O:139:LEU:HD11	2.01	0.42
22:1V:120:ILE:HD12	22:1V:120:ILE:C	2.45	0.42
31:1e:53:PRO:HA	31:1e:54:PRO:HD3	1.93	0.42
32:1f:16:GLU:OE2	32:1f:16:GLU:C	2.63	0.42
37:1k:62:LYS:HA	37:1k:62:LYS:HD2	1.63	0.42
1:1A:639:G:H22	1:1A:650:A:H2	1.67	0.42
1:1A:723:U:O2'	1:1A:724:A:N3	2.44	0.42
1:1A:2142:G:H2'	1:1A:2143:C:H6	1.85	0.42
1:1A:2508:A:H5''	1:1A:2509:U:OP2	2.20	0.42
1:1A:2661:U:H2'	1:1A:2662:G:O4'	2.20	0.42
1:1A:3432:A:HO2'	1:1A:3433:U:P	2.42	0.42
3:1C:6:G:N1	3:1C:111:A:H2	2.12	0.42
3:1C:106:U:H5''	7:1G:268:LEU:HD21	2.02	0.42
5:1E:54:THR:OG1	5:1E:55:HIS:N	2.53	0.42
6:1F:150:ILE:HD12	6:1F:150:ILE:HA	1.71	0.42
6:1F:188:LYS:HG3	6:1F:204:GLU:HG2	2.02	0.42
10:1J:30:VAL:HG12	10:1J:31:ALA:N	2.35	0.42
10:1J:86:ASP:OD1	10:1J:87:HIS:N	2.53	0.42
15:1O:101:LYS:HB3	15:1O:101:LYS:HE2	1.76	0.42
16:1P:12:VAL:HG22	16:1P:26:VAL:HG22	2.01	0.42
21:1U:8:LYS:NZ	21:1U:19:ASN:O	2.52	0.42
24:1X:18:CYS:CB	24:1X:54:ARG:HB3	2.50	0.42
1:1A:221:U:C2	1:1A:222:A:C8	3.08	0.41
1:1A:493:G:H1'	1:1A:579:A:N6	2.34	0.41
1:1A:1342:U:N3	1:1A:1343:A:H1'	2.35	0.41
1:1A:1606:A:C8	18:1R:53:ILE:HG22	2.55	0.41
1:1A:2682:U:H2'	1:1A:2683:U:O4'	2.20	0.41
3:1C:19:U:H2'	3:1C:20:C:C6	2.55	0.41
4:1D:54:ARG:HD3	4:1D:58:LEU:HD13	2.02	0.41
5:1E:92:TYR:HB2	5:1E:159:VAL:HB	2.02	0.41
6:1F:142:HIS:ND1	6:1F:180:ASP:OD2	2.44	0.41
6:1F:211:VAL:HA	6:1F:232:CYS:O	2.20	0.41
7:1G:124:ASP:OD1	7:1G:124:ASP:N	2.47	0.41
9:1I:97:ARG:NH1	19:1S:4:ASP:O	2.53	0.41
11:1K:19:ILE:HG12	11:1K:28:VAL:HG22	2.02	0.41
25:1Y:117:LYS:HB3	25:1Y:117:LYS:HE3	1.91	0.41
1:1A:248:U:H2'	1:1A:249:U:C6	2.56	0.41
1:1A:491:G:C6	1:1A:492:U:C4	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:566:U:H2'	1:1A:567:U:C6	2.55	0.41
1:1A:658:A:H1'	1:1A:659:U:C6	2.55	0.41
1:1A:675:A:H8	6:1F:354:TYR:CD2	2.37	0.41
1:1A:1219:A:H4'	1:1A:1220:A:OP2	2.20	0.41
1:1A:1547:A:H2'	1:1A:1548:U:C6	2.55	0.41
1:1A:1757:C:H2'	1:1A:1758:U:C6	2.55	0.41
1:1A:2924:A:OP1	14:1N:274:SER:HB3	2.20	0.41
1:1A:3129:U:H2'	1:1A:3130:A:C8	2.53	0.41
4:1D:30:ARG:NH2	4:1D:33:ASP:OD1	2.52	0.41
5:1E:301:ILE:H	5:1E:301:ILE:HG13	1.71	0.41
6:1F:261:LYS:HG2	6:1F:265:ILE:HG13	2.01	0.41
16:1P:24:LEU:HD23	16:1P:24:LEU:HA	1.82	0.41
18:1R:52:ILE:O	18:1R:54:LYS:NZ	2.52	0.41
23:1W:54:ILE:HD12	23:1W:54:ILE:H	1.86	0.41
24:1X:87:THR:HG21	26:1Z:21:ARG:HD3	2.01	0.41
26:1Z:56:ILE:H	26:1Z:56:ILE:HG12	1.66	0.41
1:1A:219:G:H2'	1:1A:220:A:C8	2.55	0.41
1:1A:518:A:H2'	1:1A:519:A:O4'	2.20	0.41
1:1A:1581:G:N7	18:1R:27:LYS:HB2	2.35	0.41
1:1A:1822:U:H2'	1:1A:1823:C:C4'	2.50	0.41
1:1A:1889:U:H2'	1:1A:1890:U:H6	1.84	0.41
1:1A:1978:U:H2'	1:1A:1979:U:C6	2.55	0.41
1:1A:2185:C:H2'	1:1A:2186:U:C6	2.55	0.41
1:1A:2417:A:H2'	1:1A:2418:U:O4'	2.20	0.41
1:1A:3491:U:P	5:1E:385:LYS:HD2	2.59	0.41
4:1D:29:HIS:O	4:1D:123:ARG:NE	2.34	0.41
7:1G:94:ASN:N	7:1G:94:ASN:OD1	2.54	0.41
12:1L:13:ARG:HE	12:1L:13:ARG:HB3	1.60	0.41
16:1P:83:ASP:OD2	16:1P:83:ASP:N	2.53	0.41
17:1Q:103:GLU:OE2	17:1Q:118:SER:OG	2.30	0.41
20:1T:58:GLN:HE21	20:1T:58:GLN:HB2	1.67	0.41
23:1W:93:MET:O	23:1W:97:LEU:HD12	2.20	0.41
31:1e:31:THR:HG23	31:1e:93:VAL:HG21	2.02	0.41
42:1p:24:CYS:SG	42:1p:37:LYS:HB2	2.61	0.41
1:1A:36:A:O2'	1:1A:1056:G:O6	2.35	0.41
1:1A:783:A:H2'	1:1A:784:C:C6	2.55	0.41
1:1A:1121:A:N1	1:1A:1168:C:O2'	2.48	0.41
1:1A:1484:A:H2'	1:1A:1485:A:C8	2.56	0.41
1:1A:2383:G:O2'	1:1A:2386:U:OP2	2.39	0.41
2:1B:31:C:H2'	2:1B:32:C:H6	1.84	0.41
6:1F:4:ARG:NH1	6:1F:4:ARG:HG2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IH:79:PHE:HA	8:IH:91:VAL:HG12	2.02	0.41
11:IK:113:ILE:HG12	11:IK:120:ILE:HG13	2.02	0.41
15:IO:17:LEU:HA	15:IO:42:LEU:HD22	2.02	0.41
23:IW:67:GLU:HB2	23:IW:78:THR:HG23	2.01	0.41
24:IX:112:MET:HE3	24:IX:112:MET:HB3	1.83	0.41
25:IY:36:MET:HE1	25:IY:68:LYS:HB2	2.03	0.41
40:ln:21:LEU:HD12	40:ln:21:LEU:HA	1.92	0.41
40:ln:27:ILE:HG13	40:ln:43:VAL:HG13	2.01	0.41
1:lA:491:G:C5	1:lA:492:U:C5	3.09	0.41
1:lA:960:G:H2'	1:lA:961:A:H8	1.86	0.41
1:lA:1047:U:H2'	1:lA:1048:A:C8	2.56	0.41
1:lA:1641:A:H2'	1:lA:1642:A:O4'	2.20	0.41
1:lA:2656:G:H5'	10:IJ:54:LEU:HD11	2.03	0.41
1:lA:3502:A:H4'	5:IE:316:GLY:HA2	2.03	0.41
3:IC:69:U:H3	3:IC:104:G:H22	1.68	0.41
6:lF:4:ARG:HG2	6:lF:4:ARG:HH11	1.85	0.41
6:lF:316:ARG:HE	6:lF:316:ARG:HB3	1.64	0.41
9:II:87:ILE:HG21	9:II:121:TYR:CD2	2.56	0.41
12:IL:183:GLN:C	12:IL:183:GLN:OE1	2.63	0.41
21:IU:92:LYS:O	21:IU:96:ILE:HG13	2.21	0.41
1:lA:529:U:H2'	1:lA:530:A:C8	2.55	0.41
1:lA:1615:A:O2'	32:lf:95:GLN:OE1	2.38	0.41
1:lA:1842:U:H2'	1:lA:1843:G:C8	2.56	0.41
1:lA:2595:G:H2'	1:lA:2596:U:C6	2.55	0.41
1:lA:2953:C:OP2	1:lA:3098:U:O2'	2.37	0.41
1:lA:3084:A:OP2	5:IE:258:HIS:HB2	2.20	0.41
6:lF:331:PRO:HB2	9:II:33:ILE:HD11	2.03	0.41
11:IK:61:ASN:OD1	11:IK:61:ASN:N	2.53	0.41
11:IK:119:SER:HG	11:IK:133:HIS:CD2	2.38	0.41
15:IO:62:ARG:HD2	15:IO:67:PRO:HB3	2.03	0.41
22:IV:107:GLU:C	22:IV:107:GLU:OE2	2.63	0.41
25:IY:75:LYS:O	25:IY:79:GLU:HG3	2.20	0.41
34:lh:71:THR:OG1	34:lh:72:VAL:N	2.53	0.41
35:li:-6:LYS:HD3	35:li:-6:LYS:HA	1.74	0.41
1:lA:678:A:H2'	1:lA:679:U:H6	1.85	0.41
1:lA:761:A:H2'	1:lA:762:A:H8	1.82	0.41
1:lA:1242:G:H2'	1:lA:1243:C:C6	2.55	0.41
1:lA:2131:A:OP2	1:lA:2132:A:O2'	2.32	0.41
1:lA:2485:G:O2'	1:lA:2487:U:H5''	2.21	0.41
1:lA:3434:A:H2'	1:lA:3435:G:O4'	2.21	0.41
5:IE:113:GLU:H	5:IE:113:GLU:HG3	1.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:IF:302:LYS:HB2	6:IF:302:LYS:HE2	1.94	0.41
8:IH:22:PRO:HG2	8:IH:27:ILE:HD11	2.01	0.41
9:II:156:MET:HE3	9:II:156:MET:HB2	1.98	0.41
10:IJ:205:LYS:HE3	10:IJ:205:LYS:HB2	1.82	0.41
23:IW:103:ARG:NH1	23:IW:103:ARG:O	2.53	0.41
1:IA:79:U:H2'	1:IA:80:A:O4'	2.20	0.41
1:IA:940:U:H2'	1:IA:941:A:H8	1.86	0.41
1:IA:1089:C:H2'	1:IA:1090:A:C8	2.56	0.41
1:IA:1249:C:O2'	1:IA:2705:A:OP1	2.39	0.41
1:IA:2232:U:OP2	4:ID:241:ARG:NH2	2.48	0.41
1:IA:2425:U:O2'	1:IA:3436:A:N3	2.53	0.41
1:IA:2683:U:H5	1:IA:2948:G:C8	2.38	0.41
1:IA:3112:A:N7	4:ID:215:ASN:ND2	2.69	0.41
1:IA:3373:A:H1'	1:IA:3385:G:C4	2.56	0.41
2:IB:28:U:H2'	2:IB:29:U:H6	1.86	0.41
27:la:150:ASN:O	27:la:153:ILE:HG12	2.20	0.41
1:IA:233:A:N3	1:IA:254:C:O2'	2.51	0.41
1:IA:336:A:H2'	1:IA:337:A:C8	2.56	0.41
1:IA:526:A:H5''	1:IA:538:A:N1	2.35	0.41
1:IA:619:A:C6	16:IP:77:CYS:HB3	2.55	0.41
1:IA:926:A:H62	1:IA:1053:G:H1	1.68	0.41
1:IA:1107:G:H2'	1:IA:1108:A:H8	1.85	0.41
1:IA:1126:U:H2'	1:IA:1127:A:O4'	2.21	0.41
1:IA:1168:C:H2'	1:IA:1169:U:C6	2.56	0.41
1:IA:1188:A:H2'	1:IA:1189:U:C6	2.56	0.41
1:IA:1282:G:OP1	9:II:78:ARG:NH1	2.54	0.41
1:IA:1392:G:C2	1:IA:1393:U:C4	3.08	0.41
1:IA:1511:G:OP1	6:IF:200:ARG:NH1	2.52	0.41
1:IA:1554:C:C5	6:IF:192:ALA:HB2	2.56	0.41
1:IA:1845:G:N2	1:IA:1924:U:O2'	2.53	0.41
1:IA:1863:U:O2	23:IW:95:LYS:HD2	2.21	0.41
1:IA:2415:C:OP1	24:IX:54:ARG:NH2	2.54	0.41
1:IA:3086:G:H2'	1:IA:3087:U:O4'	2.21	0.41
1:IA:3196:U:H2'	1:IA:3197:C:C6	2.56	0.41
2:IB:117:A:H2'	2:IB:118:C:H6	1.86	0.41
14:IN:254:MET:H	14:IN:254:MET:HG3	1.74	0.41
15:IO:93:ASN:O	15:IO:97:LYS:HG2	2.21	0.41
21:IU:98:ARG:NH1	21:IU:132:TYR:O	2.52	0.41
27:la:22:ASN:OD1	27:la:22:ASN:N	2.53	0.41
28:lb:20:GLY:HA3	28:lb:139:PHE:HZ	1.83	0.41
40:ln:71:ILE:HD12	40:ln:71:ILE:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:lq:74:LYS:HE2	43:lq:74:LYS:HB2	1.86	0.41
1:lA:542:U:H2'	1:lA:543:A:H8	1.86	0.41
1:lA:739:A:H2'	1:lA:740:A:H8	1.85	0.41
1:lA:897:A:H4'	1:lA:898:U:OP1	2.19	0.41
1:lA:934:G:OP1	38:ll:16:HIS:NE2	2.42	0.41
1:lA:937:C:H2'	1:lA:938:U:O4'	2.21	0.41
1:lA:1465:G:H2'	1:lA:1466:U:C6	2.56	0.41
1:lA:1822:U:H2'	1:lA:1823:C:H4'	2.03	0.41
1:lA:1823:C:H2'	1:lA:1824:A:N3	2.35	0.41
1:lA:2759:A:H2'	1:lA:2759:A:N3	2.36	0.41
5:lE:62:ARG:HD3	5:lE:350:THR:HA	2.03	0.41
7:lG:196:LEU:HD23	7:lG:196:LEU:HA	1.92	0.41
14:lN:41:ALA:O	14:lN:229:GLN:NE2	2.54	0.41
23:lW:46:LEU:HD13	23:lW:50:PHE:HE2	1.86	0.41
29:lc:138:ILE:O	29:lc:141:VAL:HG12	2.21	0.41
1:lA:109:C:C2	1:lA:110:A:C8	3.09	0.40
1:lA:604:U:H2'	1:lA:605:C:H6	1.85	0.40
1:lA:1887:A:H2'	1:lA:1888:A:H8	1.85	0.40
1:lA:2150:G:C2	1:lA:2176:G:C2	3.08	0.40
1:lA:2295:A:H2'	1:lA:2296:U:C6	2.55	0.40
1:lA:2346:A:H2'	1:lA:2347:A:H8	1.85	0.40
1:lA:3243:C:H2'	1:lA:3244:U:O4'	2.22	0.40
1:lA:3360:U:H3	8:lH:185:GLU:HG2	1.86	0.40
5:lE:146:ARG:O	5:lE:150:ILE:HG12	2.21	0.40
8:lH:114:SER:OG	8:lH:204:PHE:O	2.37	0.40
9:ll:58:GLU:C	9:ll:58:GLU:OE2	2.64	0.40
16:lP:115:VAL:O	16:lP:119:ASN:HB2	2.20	0.40
35:li:-9:ALA:HB1	35:li:45:ARG:HH12	1.86	0.40
35:li:-7:LEU:HD23	35:li:-2:ILE:HD11	2.01	0.40
37:lk:64:LEU:HB2	37:lk:81:ARG:NH1	2.36	0.40
39:lm:48:ARG:NH2	39:lm:58:LYS:HD3	2.37	0.40
1:lA:1310:A:H2'	1:lA:1311:C:C6	2.56	0.40
1:lA:1324:A:H5'	1:lA:1325:C:O5'	2.20	0.40
1:lA:1437:A:O3'	15:lO:18:GLY:HA3	2.21	0.40
1:lA:1468:A:H2'	1:lA:1469:A:H8	1.86	0.40
1:lA:2981:A:H2'	1:lA:2982:G:O4'	2.21	0.40
1:lA:3287:U:H2'	1:lA:3288:U:C6	2.56	0.40
7:lG:135:GLU:OE1	7:lG:135:GLU:N	2.54	0.40
10:lJ:96:LYS:O	10:lJ:100:ILE:HG13	2.21	0.40
14:lN:49:ILE:HG22	14:lN:51:SER:N	2.35	0.40
14:lN:123:VAL:O	14:lN:222:VAL:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:IW:102:LEU:HD12	23:IW:106:LEU:CD1	2.52	0.40
29:lc:90:TYR:CG	29:lc:100:PRO:HD3	2.56	0.40
39:lm:49:ARG:HB2	39:lm:55:TRP:CZ3	2.56	0.40
1:lA:320:A:H2'	1:lA:321:U:C6	2.56	0.40
1:lA:397:A:N6	41:lo:35:ILE:HG23	2.36	0.40
1:lA:993:U:O4	1:lA:3122:U:H5	2.05	0.40
1:lA:1157:A:H5'	7:lG:5:LYS:HD3	2.03	0.40
1:lA:2486:U:C5	1:lA:2944:A:N1	2.89	0.40
1:lA:2989:U:H2'	42:lp:22:ARG:HD3	2.04	0.40
1:lA:3452:U:H3	1:lA:3504:G:N2	2.19	0.40
1:lA:3456:U:H5''	5:lE:309:MET:HE3	2.03	0.40
5:lE:365:LYS:HA	5:lE:365:LYS:HD3	1.97	0.40
9:ll:208:HIS:CE1	9:ll:210:ILE:HD12	2.56	0.40
13:lM:51:ARG:O	13:lM:61:ARG:NH1	2.55	0.40
13:lM:105:GLY:HA2	13:lM:126:ASP:HA	2.03	0.40
31:le:68:LYS:HE2	31:le:68:LYS:HB2	1.70	0.40
1:lA:236:U:O4	27:la:36:LYS:HG2	2.22	0.40
1:lA:483:G:H5''	1:lA:753:A:N6	2.36	0.40
1:lA:1107:G:H21	22:IV:101:CYS:HA	1.86	0.40
1:lA:1186:G:H2'	1:lA:1187:A:H5''	2.03	0.40
1:lA:1217:U:H2'	1:lA:1218:U:O4'	2.21	0.40
1:lA:1467:U:H2'	1:lA:1468:A:C8	2.56	0.40
1:lA:1564:U:O4	29:lc:3:THR:HG23	2.22	0.40
1:lA:2420:U:H2'	1:lA:2421:G:C8	2.57	0.40
4:ID:28:GLN:HB2	4:ID:123:ARG:HB3	2.04	0.40
8:lH:21:TYR:CZ	33:lg:115:ILE:HG23	2.57	0.40
10:IJ:234:ASN:HD22	10:IJ:238:HIS:CE1	2.40	0.40
21:IU:7:GLN:NE2	21:IU:35:ALA:O	2.41	0.40
22:IV:17:ARG:HB2	22:IV:22:HIS:CE1	2.55	0.40
28:lb:115:LYS:HA	28:lb:115:LYS:HD3	1.70	0.40
1:lA:487:A:H2'	1:lA:488:A:H8	1.86	0.40
1:lA:718:A:H2'	1:lA:719:U:H6	1.86	0.40
1:lA:1158:U:H2'	1:lA:1159:C:C6	2.57	0.40
1:lA:1334:U:H2'	1:lA:1335:U:C6	2.57	0.40
1:lA:1475:A:H8	27:la:185:ARG:HH12	1.69	0.40
1:lA:2243:A:H2'	1:lA:2244:A:C8	2.57	0.40
1:lA:3300:A:H2'	1:lA:3301:A:C8	2.55	0.40
2:lB:96:A:H2'	2:lB:97:A:O4'	2.22	0.40
4:ID:125:ILE:HD13	4:ID:125:ILE:HA	1.94	0.40
5:lE:17:HIS:HE1	5:lE:264:TRP:HB2	1.87	0.40
24:IX:82:ILE:HG13	24:IX:83:ARG:HG2	2.04	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	
4	ID	244/257 (95%)	229 (94%)	15 (6%)	0	100	100
5	IE	385/402 (96%)	373 (97%)	12 (3%)	0	100	100
6	IF	420/431 (97%)	404 (96%)	16 (4%)	0	100	100
7	IG	275/286 (96%)	259 (94%)	16 (6%)	0	100	100
8	IH	201/204 (98%)	183 (91%)	18 (9%)	0	100	100
9	II	208/230 (90%)	200 (96%)	8 (4%)	0	100	100
10	IJ	209/286 (73%)	200 (96%)	9 (4%)	0	100	100
11	IK	191/197 (97%)	185 (97%)	6 (3%)	0	100	100
12	IL	196/210 (93%)	187 (95%)	9 (5%)	0	100	100
13	IM	166/174 (95%)	158 (95%)	7 (4%)	1 (1%)	21	51
14	IN	228/291 (78%)	212 (93%)	16 (7%)	0	100	100
15	IO	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
16	IP	130/135 (96%)	128 (98%)	2 (2%)	0	100	100
17	IQ	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
18	IR	156/179 (87%)	153 (98%)	3 (2%)	0	100	100
19	IS	165/168 (98%)	153 (93%)	12 (7%)	0	100	100
20	IT	171/173 (99%)	165 (96%)	6 (4%)	0	100	100
21	IU	148/198 (75%)	145 (98%)	3 (2%)	0	100	100
22	IV	163/166 (98%)	158 (97%)	5 (3%)	0	100	100
23	IW	91/137 (66%)	82 (90%)	8 (9%)	1 (1%)	11	36
24	IX	131/140 (94%)	128 (98%)	3 (2%)	0	100	100
25	IY	114/121 (94%)	112 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	lZ	55/163 (34%)	54 (98%)	1 (2%)	0	100	100
27	la	208/213 (98%)	200 (96%)	8 (4%)	0	100	100
28	lb	135/139 (97%)	133 (98%)	2 (2%)	0	100	100
29	lc	146/149 (98%)	140 (96%)	6 (4%)	0	100	100
30	ld	58/64 (91%)	55 (95%)	3 (5%)	0	100	100
31	le	101/109 (93%)	92 (91%)	9 (9%)	0	100	100
32	lf	144/150 (96%)	135 (94%)	9 (6%)	0	100	100
33	lg	127/134 (95%)	123 (97%)	4 (3%)	0	100	100
34	lh	103/137 (75%)	99 (96%)	4 (4%)	0	100	100
35	li	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	lj	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
37	lk	83/104 (80%)	82 (99%)	1 (1%)	0	100	100
38	ll	70/77 (91%)	63 (90%)	5 (7%)	2 (3%)	3	13
39	lm	88/93 (95%)	82 (93%)	6 (7%)	0	100	100
40	ln	71/84 (84%)	69 (97%)	2 (3%)	0	100	100
41	lo	48/51 (94%)	48 (100%)	0	0	100	100
42	lp	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
43	lq	90/98 (92%)	88 (98%)	2 (2%)	0	100	100
All	All	6198/6846 (90%)	5938 (96%)	256 (4%)	4 (0%)	49	77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	lW	45	LYS
38	ll	39	TYR
38	ll	40	PRO
13	lM	28	ASP

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	
4	ID	195/201 (97%)	189 (97%)	6 (3%)	35	70
5	IE	330/343 (96%)	326 (99%)	4 (1%)	63	87
6	IF	338/345 (98%)	329 (97%)	9 (3%)	39	74
7	IG	225/231 (97%)	224 (100%)	1 (0%)	84	94
8	IH	172/173 (99%)	170 (99%)	2 (1%)	63	87
9	II	178/195 (91%)	175 (98%)	3 (2%)	53	83
10	IJ	186/242 (77%)	179 (96%)	7 (4%)	29	64
11	IK	171/174 (98%)	170 (99%)	1 (1%)	78	92
12	IL	169/176 (96%)	167 (99%)	2 (1%)	63	87
13	IM	144/147 (98%)	142 (99%)	2 (1%)	59	85
14	IN	200/243 (82%)	196 (98%)	4 (2%)	48	80
15	IO	167/168 (99%)	163 (98%)	4 (2%)	43	77
16	IP	116/118 (98%)	113 (97%)	3 (3%)	40	75
17	IQ	171/172 (99%)	170 (99%)	1 (1%)	78	92
18	IR	129/147 (88%)	125 (97%)	4 (3%)	35	70
19	IS	142/143 (99%)	138 (97%)	4 (3%)	38	73
20	IT	156/156 (100%)	154 (99%)	2 (1%)	61	86
21	IU	132/174 (76%)	132 (100%)	0	100	100
22	IV	144/145 (99%)	141 (98%)	3 (2%)	47	79
23	IW	86/125 (69%)	77 (90%)	9 (10%)	6	22
24	IX	109/113 (96%)	108 (99%)	1 (1%)	70	89
25	IY	99/102 (97%)	98 (99%)	1 (1%)	68	88
26	IZ	52/137 (38%)	49 (94%)	3 (6%)	18	49
27	la	177/179 (99%)	175 (99%)	2 (1%)	65	87
28	lb	121/123 (98%)	118 (98%)	3 (2%)	42	76
29	lc	120/121 (99%)	117 (98%)	3 (2%)	42	76
30	ld	50/54 (93%)	49 (98%)	1 (2%)	48	80
31	le	86/92 (94%)	83 (96%)	3 (4%)	32	67
32	lf	125/128 (98%)	122 (98%)	3 (2%)	43	77
33	lg	112/116 (97%)	108 (96%)	4 (4%)	31	66
34	lh	86/116 (74%)	84 (98%)	2 (2%)	44	78
35	li	103/103 (100%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	lj	89/91 (98%)	89 (100%)	0	100	100
37	lk	71/82 (87%)	69 (97%)	2 (3%)	38	73
38	ll	60/64 (94%)	59 (98%)	1 (2%)	53	83
39	lm	72/74 (97%)	72 (100%)	0	100	100
40	ln	63/73 (86%)	62 (98%)	1 (2%)	55	83
41	lo	44/45 (98%)	43 (98%)	1 (2%)	44	78
42	lp	45/48 (94%)	45 (100%)	0	100	100
43	lq	85/91 (93%)	84 (99%)	1 (1%)	63	87
All	All	5320/5770 (92%)	5217 (98%)	103 (2%)	49	81

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	lD	78	CYS
4	lD	106	GLN
4	lD	145	THR
4	lD	146	THR
4	lD	193	ARG
4	lD	242	ARG
5	lE	20	LYS
5	lE	258	HIS
5	lE	343	CYS
5	lE	350	THR
6	lF	57	GLU
6	lF	94	ASN
6	lF	150	ILE
6	lF	156	SER
6	lF	182	LEU
6	lF	373	VAL
6	lF	392	VAL
6	lF	397	LEU
6	lF	401	VAL
7	lG	109	LEU
8	lH	122	VAL
8	lH	153	LYS
9	lI	77	ILE
9	lI	188	ASN
9	lI	207	ILE
10	lJ	19	VAL

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Mol	Chain	Res	Type
10	IJ	22	LYS
10	IJ	25	PHE
10	IJ	36	LEU
10	IJ	49	GLN
10	IJ	148	VAL
10	IJ	205	LYS
11	IK	94	LYS
12	IL	103	LEU
12	IL	111	LEU
13	IM	14	ILE
13	IM	110	ILE
14	IN	32	ARG
14	IN	155	PHE
14	IN	212	LYS
14	IN	213	LYS
15	IO	39	CYS
15	IO	41	ASP
15	IO	56	GLU
15	IO	160	GLU
16	IP	94	THR
16	IP	114	GLN
16	IP	131	SER
17	IQ	39	VAL
18	IR	18	ARG
18	IR	139	PHE
18	IR	147	GLU
18	IR	148	LEU
19	IS	72	LYS
19	IS	76	GLU
19	IS	80	CYS
19	IS	152	VAL
20	IT	58	GLN
20	IT	106	LEU
22	IV	27	THR
22	IV	123	LYS
22	IV	152	ILE
23	IW	31	THR
23	IW	34	LEU
23	IW	41	ILE
23	IW	45	LYS
23	IW	46	LEU
23	IW	75	VAL

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Mol	Chain	Res	Type
23	IW	85	CYS
23	IW	108	VAL
23	IW	109	ILE
24	IX	106	VAL
25	IY	120	LEU
26	IZ	17	VAL
26	IZ	32	THR
26	IZ	62	LYS
27	la	7	VAL
27	la	109	LEU
28	lb	12	ILE
28	lb	111	ILE
28	lb	135	THR
29	lc	16	SER
29	lc	120	LYS
29	lc	141	VAL
30	ld	35	MET
31	le	40	ASP
31	le	94	LEU
31	le	104	ILE
32	lf	15	ARG
32	lf	121	GLU
32	lf	132	VAL
33	lg	35	VAL
33	lg	53	LEU
33	lg	96	GLU
33	lg	132	VAL
34	lh	36	GLN
34	lh	56	HIS
37	lk	7	VAL
37	lk	9	LEU
38	ll	10	THR
40	ln	31	ARG
41	lo	29	MET
43	lq	18	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (47) such sidechains are listed below:

Mol	Chain	Res	Type
4	ID	8	GLN
4	ID	22	HIS
4	ID	106	GLN

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Mol	Chain	Res	Type
4	lD	233	GLN
5	lE	17	HIS
6	lF	269	GLN
7	lG	111	GLN
7	lG	234	ASN
9	lI	81	ASN
9	lI	188	ASN
10	lJ	49	GLN
10	lJ	144	GLN
10	lJ	171	GLN
10	lJ	234	ASN
11	lK	180	GLN
12	lL	144	HIS
13	lM	43	GLN
14	lN	216	GLN
16	lP	33	HIS
16	lP	114	GLN
17	lQ	139	ASN
18	lR	10	ASN
18	lR	16	GLN
18	lR	97	ASN
18	lR	108	ASN
19	lS	57	ASN
20	lT	16	ASN
20	lT	89	GLN
20	lT	101	GLN
22	lV	5	ASN
22	lV	26	ASN
24	lX	12	ASN
24	lX	22	ASN
25	lY	12	HIS
25	lY	18	ASN
25	lY	58	HIS
28	lb	88	ASN
29	lc	28	GLN
30	ld	17	HIS
30	ld	19	ASN
30	ld	46	GLN
31	le	11	GLN
32	lf	31	ASN
33	lg	122	ASN
34	lh	34	HIS

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Mol	Chain	Res	Type
35	li	83	GLN
41	lo	18	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	lA	3047/3503 (86%)	553 (18%)	0
2	lB	143/155 (92%)	32 (22%)	0
3	lC	116/117 (99%)	15 (12%)	0
All	All	3306/3775 (87%)	600 (18%)	0

All (600) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	lA	18	G
1	lA	22	A
1	lA	29	U
1	lA	30	A
1	lA	36	A
1	lA	39	A
1	lA	45	A
1	lA	54	G
1	lA	55	G
1	lA	56	A
1	lA	62	A
1	lA	65	U
1	lA	69	A
1	lA	70	A
1	lA	88	G
1	lA	90	G
1	lA	105	A
1	lA	106	G
1	lA	115	G
1	lA	116	A
1	lA	117	U
1	lA	185	G
1	lA	186	A
1	lA	189	G
1	lA	198	A
1	lA	199	G
1	lA	200	A

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Mol	Chain	Res	Type
1	lA	206	U
1	lA	213	A
1	lA	214	A
1	lA	221	U
1	lA	233	A
1	lA	237	C
1	lA	246	U
1	lA	256	G
1	lA	257	A
1	lA	259	A
1	lA	264	G
1	lA	266	A
1	lA	267	A
1	lA	285	A
1	lA	286	U
1	lA	287	A
1	lA	289	C
1	lA	293	A
1	lA	294	A
1	lA	302	U
1	lA	303	G
1	lA	311	A
1	lA	316	G
1	lA	319	A
1	lA	332	G
1	lA	342	A
1	lA	344	A
1	lA	345	A
1	lA	346	G
1	lA	350	A
1	lA	369	A
1	lA	381	A
1	lA	383	A
1	lA	385	C
1	lA	396	G
1	lA	397	A
1	lA	416	U
1	lA	422	G
1	lA	423	A
1	lA	424	A
1	lA	444	A
1	lA	446	A

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Mol	Chain	Res	Type
1	lA	447	G
1	lA	448	C
1	lA	449	U
1	lA	452	A
1	lA	457	G
1	lA	467	A
1	lA	474	A
1	lA	483	G
1	lA	493	G
1	lA	494	G
1	lA	495	A
1	lA	496	A
1	lA	501	U
1	lA	510	A
1	lA	522	G
1	lA	535	A
1	lA	536	G
1	lA	538	A
1	lA	539	G
1	lA	550	A
1	lA	561	G
1	lA	562	A
1	lA	564	A
1	lA	565	U
1	lA	571	A
1	lA	575	A
1	lA	577	G
1	lA	586	A
1	lA	588	G
1	lA	589	A
1	lA	596	G
1	lA	600	U
1	lA	610	A
1	lA	612	A
1	lA	613	G
1	lA	614	U
1	lA	615	G
1	lA	619	A
1	lA	620	U
1	lA	625	A
1	lA	626	A
1	lA	627	A

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Mol	Chain	Res	Type
1	lA	629	G
1	lA	630	A
1	lA	631	G
1	lA	632	G
1	lA	637	U
1	lA	638	A
1	lA	644	A
1	lA	645	A
1	lA	646	U
1	lA	647	C
1	lA	649	U
1	lA	651	G
1	lA	652	U
1	lA	658	A
1	lA	663	G
1	lA	675	A
1	lA	685	A
1	lA	687	U
1	lA	696	G
1	lA	699	A
1	lA	700	A
1	lA	701	A
1	lA	703	G
1	lA	704	C
1	lA	710	A
1	lA	711	A
1	lA	714	U
1	lA	715	A
1	lA	720	U
1	lA	721	A
1	lA	722	A
1	lA	724	A
1	lA	725	A
1	lA	726	A
1	lA	727	U
1	lA	728	U
1	lA	730	A
1	lA	733	C
1	lA	734	C
1	lA	736	G
1	lA	740	A
1	lA	744	A

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Mol	Chain	Res	Type
1	lA	746	A
1	lA	747	C
1	lA	755	G
1	lA	770	C
1	lA	771	C
1	lA	783	A
1	lA	794	A
1	lA	811	A
1	lA	816	G
1	lA	817	A
1	lA	818	A
1	lA	825	G
1	lA	832	A
1	lA	833	U
1	lA	834	A
1	lA	835	A
1	lA	841	A
1	lA	851	A
1	lA	852	A
1	lA	853	A
1	lA	854	A
1	lA	855	A
1	lA	864	G
1	lA	872	A
1	lA	873	U
1	lA	874	A
1	lA	875	C
1	lA	881	G
1	lA	889	A
1	lA	898	U
1	lA	904	A
1	lA	905	A
1	lA	918	G
1	lA	920	A
1	lA	925	A
1	lA	934	G
1	lA	936	A
1	lA	954	G
1	lA	976	G
1	lA	980	A
1	lA	993	U
1	lA	998	U

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Mol	Chain	Res	Type
1	lA	999	G
1	lA	1026	G
1	lA	1027	G
1	lA	1028	G
1	lA	1033	A
1	lA	1035	G
1	lA	1036	A
1	lA	1042	C
1	lA	1043	G
1	lA	1044	A
1	lA	1056	G
1	lA	1063	C
1	lA	1078	C
1	lA	1079	U
1	lA	1096	U
1	lA	1097	U
1	lA	1098	A
1	lA	1099	A
1	lA	1100	U
1	lA	1112	G
1	lA	1119	U
1	lA	1120	A
1	lA	1166	A
1	lA	1168	C
1	lA	1183	G
1	lA	1184	A
1	lA	1187	A
1	lA	1210	C
1	lA	1211	A
1	lA	1219	A
1	lA	1220	A
1	lA	1221	A
1	lA	1222	U
1	lA	1242	G
1	lA	1248	U
1	lA	1256	G
1	lA	1269	U
1	lA	1278	A
1	lA	1284	A
1	lA	1291	G
1	lA	1292	A
1	lA	1306	A

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Mol	Chain	Res	Type
1	lA	1312	A
1	lA	1314	A
1	lA	1315	A
1	lA	1316	C
1	lA	1325	C
1	lA	1343	A
1	lA	1344	U
1	lA	1345	U
1	lA	1386	G
1	lA	1387	A
1	lA	1388	A
1	lA	1389	U
1	lA	1410	A
1	lA	1411	A
1	lA	1417	G
1	lA	1431	G
1	lA	1433	U
1	lA	1437	A
1	lA	1440	A
1	lA	1441	U
1	lA	1447	C
1	lA	1450	A
1	lA	1455	A
1	lA	1474	A
1	lA	1475	A
1	lA	1476	G
1	lA	1477	A
1	lA	1478	C
1	lA	1480	U
1	lA	1495	A
1	lA	1499	G
1	lA	1500	A
1	lA	1502	A
1	lA	1503	U
1	lA	1505	G
1	lA	1516	A
1	lA	1517	C
1	lA	1518	A
1	lA	1519	A
1	lA	1521	A
1	lA	1527	A
1	lA	1534	U

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Mol	Chain	Res	Type
1	lA	1551	A
1	lA	1553	A
1	lA	1568	G
1	lA	1570	U
1	lA	1571	C
1	lA	1580	A
1	lA	1584	G
1	lA	1589	U
1	lA	1601	G
1	lA	1602	A
1	lA	1603	A
1	lA	1604	A
1	lA	1605	A
1	lA	1606	A
1	lA	1607	A
1	lA	1622	A
1	lA	1624	G
1	lA	1648	U
1	lA	1649	U
1	lA	1652	U
1	lA	1674	U
1	lA	1677	A
1	lA	1690	A
1	lA	1698	G
1	lA	1729	G
1	lA	1735	A
1	lA	1737	A
1	lA	1738	G
1	lA	1751	A
1	lA	1752	U
1	lA	1754	G
1	lA	1810	A
1	lA	1818	C
1	lA	1821	A
1	lA	1822	U
1	lA	1823	C
1	lA	1837	U
1	lA	1864	C
1	lA	1865	U
1	lA	1883	A
1	lA	1897	A
1	lA	1903	A

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Mol	Chain	Res	Type
1	lA	1907	A
1	lA	1913	G
1	lA	1914	A
1	lA	1925	A
1	lA	1926	U
1	lA	1928	G
1	lA	1936	A
1	lA	1937	A
1	lA	1938	G
1	lA	1959	U
1	lA	1961	G
1	lA	1963	G
1	lA	1965	U
1	lA	1975	G
1	lA	1983	A
1	lA	1984	A
1	lA	1995	G
1	lA	2040	A
1	lA	2043	A
1	lA	2044	C
1	lA	2050	C
1	lA	2051	A
1	lA	2067	A
1	lA	2079	A
1	lA	2080	A
1	lA	2081	A
1	lA	2083	A
1	lA	2095	G
1	lA	2108	G
1	lA	2109	C
1	lA	2178	A
1	lA	2179	U
1	lA	2190	A
1	lA	2193	G
1	lA	2197	G
1	lA	2198	G
1	lA	2207	A
1	lA	2216	U
1	lA	2218	A
1	lA	2234	A
1	lA	2245	A
1	lA	2246	G

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Mol	Chain	Res	Type
1	lA	2263	G
1	lA	2264	A
1	lA	2274	A
1	lA	2281	U
1	lA	2282	G
1	lA	2284	A
1	lA	2285	U
1	lA	2286	G
1	lA	2299	A
1	lA	2320	A
1	lA	2325	G
1	lA	2349	G
1	lA	2356	A
1	lA	2360	C
1	lA	2374	U
1	lA	2383	G
1	lA	2384	C
1	lA	2386	U
1	lA	2389	A
1	lA	2390	U
1	lA	2391	G
1	lA	2395	C
1	lA	2396	A
1	lA	2410	U
1	lA	2411	G
1	lA	2412	U
1	lA	2439	A
1	lA	2441	U
1	lA	2449	A
1	lA	2450	C
1	lA	2451	G
1	lA	2461	G
1	lA	2462	G
1	lA	2469	G
1	lA	2473	A
1	lA	2478	A
1	lA	2479	G
1	lA	2480	A
1	lA	2487	U
1	lA	2494	G
1	lA	2509	U
1	lA	2589	C

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Mol	Chain	Res	Type
1	lA	2590	A
1	lA	2594	C
1	lA	2595	G
1	lA	2598	A
1	lA	2629	A
1	lA	2637	A
1	lA	2651	A
1	lA	2655	G
1	lA	2656	G
1	lA	2663	A
1	lA	2666	G
1	lA	2676	G
1	lA	2677	G
1	lA	2684	G
1	lA	2689	G
1	lA	2696	A
1	lA	2707	A
1	lA	2715	G
1	lA	2721	G
1	lA	2722	U
1	lA	2726	A
1	lA	2727	A
1	lA	2744	A
1	lA	2747	G
1	lA	2759	A
1	lA	2761	A
1	lA	2764	A
1	lA	2766	A
1	lA	2773	U
1	lA	2774	A
1	lA	2775	A
1	lA	2797	A
1	lA	2798	G
1	lA	2799	U
1	lA	2819	U
1	lA	2822	U
1	lA	2823	G
1	lA	2825	C
1	lA	2842	U
1	lA	2843	U
1	lA	2857	A
1	lA	2904	U

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Mol	Chain	Res	Type
1	lA	2905	U
1	lA	2910	G
1	lA	2920	U
1	lA	2925	A
1	lA	2926	U
1	lA	2931	C
1	lA	2939	G
1	lA	2943	G
1	lA	2944	A
1	lA	2945	A
1	lA	2946	A
1	lA	2951	A
1	lA	2953	C
1	lA	2957	G
1	lA	2959	G
1	lA	2960	A
1	lA	2977	G
1	lA	2985	C
1	lA	2987	C
1	lA	2988	A
1	lA	3004	U
1	lA	3009	C
1	lA	3015	A
1	lA	3030	A
1	lA	3041	G
1	lA	3047	U
1	lA	3066	U
1	lA	3070	C
1	lA	3073	U
1	lA	3076	A
1	lA	3078	U
1	lA	3079	A
1	lA	3085	C
1	lA	3090	G
1	lA	3094	G
1	lA	3114	A
1	lA	3126	C
1	lA	3133	G
1	lA	3141	A
1	lA	3142	G
1	lA	3143	A
1	lA	3144	U

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Mol	Chain	Res	Type
1	lA	3146	U
1	lA	3147	U
1	lA	3148	C
1	lA	3151	A
1	lA	3159	G
1	lA	3166	G
1	lA	3200	G
1	lA	3210	U
1	lA	3211	A
1	lA	3212	U
1	lA	3213	U
1	lA	3223	G
1	lA	3228	A
1	lA	3232	G
1	lA	3233	U
1	lA	3240	A
1	lA	3246	A
1	lA	3247	C
1	lA	3254	U
1	lA	3256	A
1	lA	3259	U
1	lA	3270	A
1	lA	3277	C
1	lA	3278	A
1	lA	3284	G
1	lA	3285	A
1	lA	3286	A
1	lA	3287	U
1	lA	3299	G
1	lA	3306	U
1	lA	3327	A
1	lA	3332	A
1	lA	3334	U
1	lA	3335	U
1	lA	3336	G
1	lA	3337	A
1	lA	3338	A
1	lA	3345	A
1	lA	3351	U
1	lA	3353	U
1	lA	3359	U
1	lA	3361	A

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Mol	Chain	Res	Type
1	lA	3366	G
1	lA	3383	A
1	lA	3384	A
1	lA	3385	G
1	lA	3398	U
1	lA	3399	G
1	lA	3405	A
1	lA	3406	C
1	lA	3414	A
1	lA	3416	A
1	lA	3423	C
1	lA	3430	U
1	lA	3431	U
1	lA	3433	U
1	lA	3447	A
1	lA	3451	A
1	lA	3461	U
1	lA	3492	C
1	lA	3493	G
1	lA	3499	U
1	lA	3500	G
1	lA	3501	A
2	lB	5	A
2	lB	34	G
2	lB	36	G
2	lB	40	U
2	lB	53	G
2	lB	54	A
2	lB	61	A
2	lB	62	U
2	lB	64	A
2	lB	65	G
2	lB	72	G
2	lB	73	A
2	lB	74	A
2	lB	77	A
2	lB	80	A
2	lB	81	A
2	lB	82	A
2	lB	85	U
2	lB	86	G
2	lB	92	C

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Mol	Chain	Res	Type
2	lB	95	A
2	lB	102	A
2	lB	103	A
2	lB	104	U
2	lB	106	C
2	lB	109	G
2	lB	110	A
2	lB	113	G
2	lB	137	A
2	lB	147	C
2	lB	150	U
2	lB	151	A
3	lC	17	G
3	lC	19	U
3	lC	22	C
3	lC	32	A
3	lC	37	A
3	lC	40	G
3	lC	52	G
3	lC	53	C
3	lC	63	C
3	lC	72	C
3	lC	73	G
3	lC	90	G
3	lC	96	U
3	lC	99	U
3	lC	109	G

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

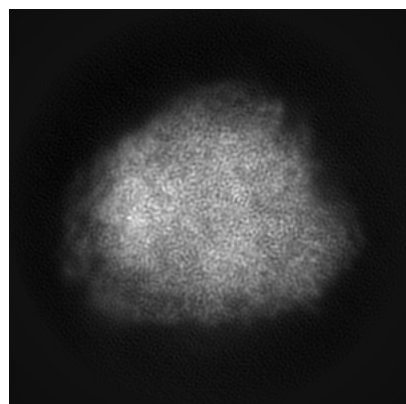
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64694. These allow visual inspection of the internal detail of the map and identification of artifacts.

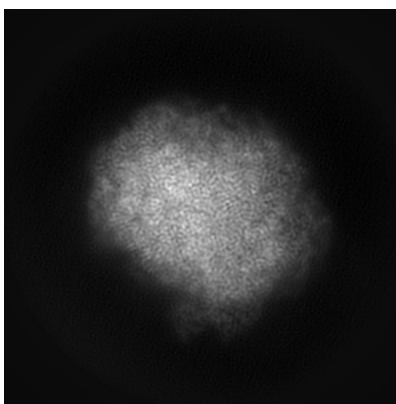
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

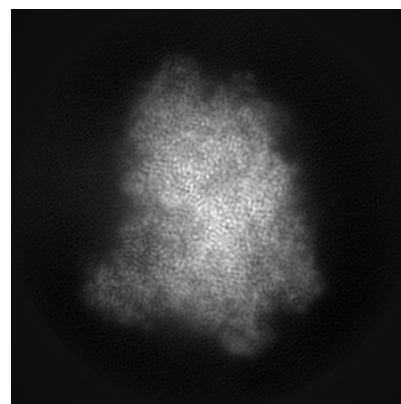
6.1.1 Primary map



X

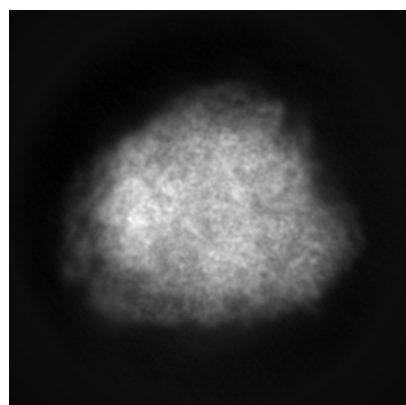


Y

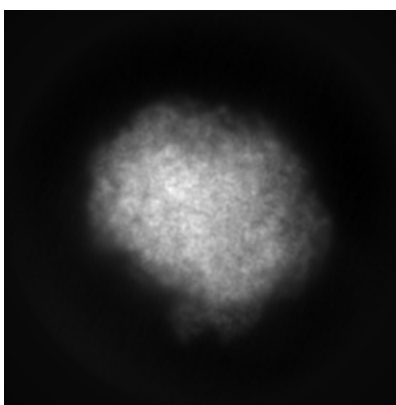


Z

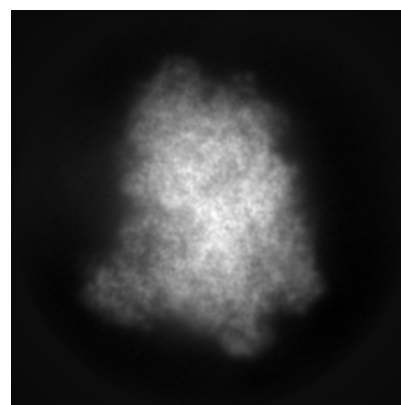
6.1.2 Raw map



X



Y

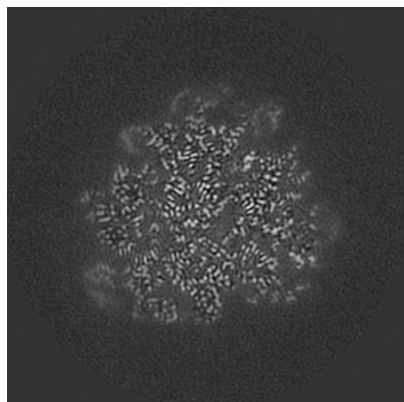


Z

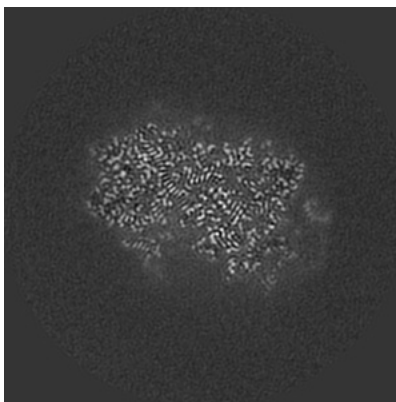
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

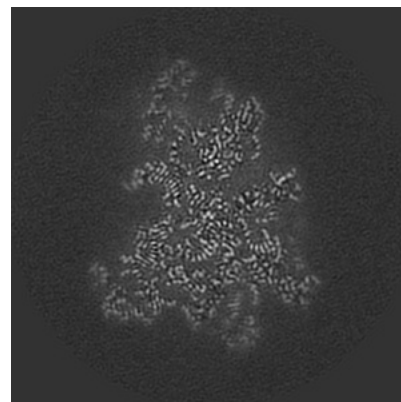
6.2.1 Primary map



X Index: 150

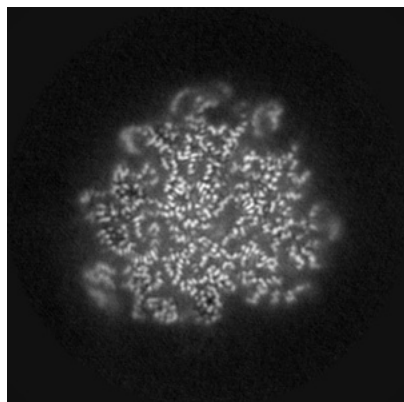


Y Index: 150

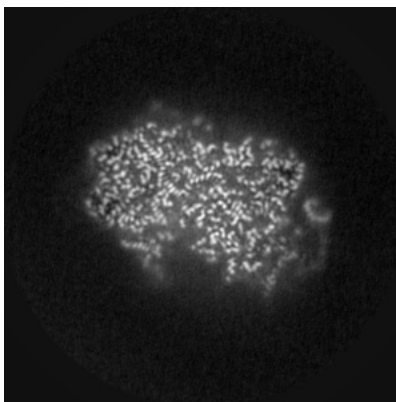


Z Index: 150

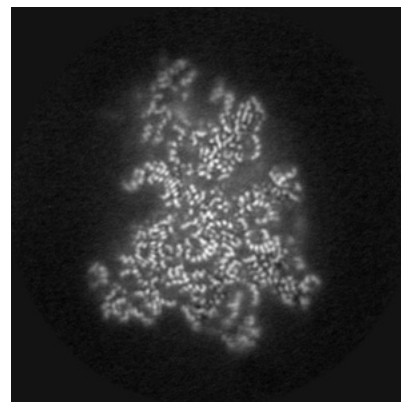
6.2.2 Raw map



X Index: 150



Y Index: 150

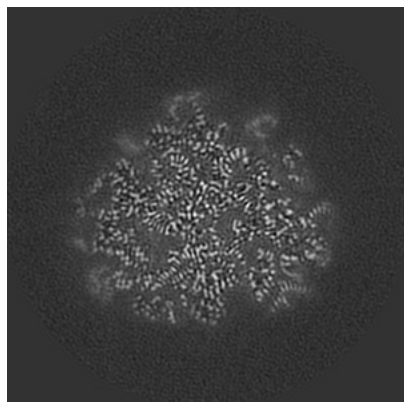


Z Index: 150

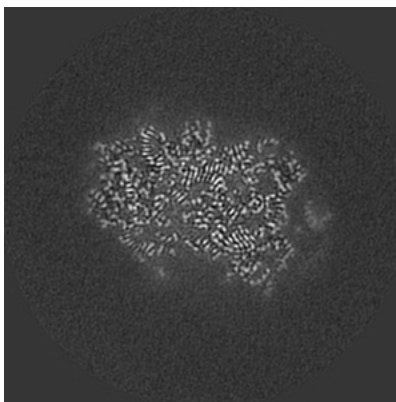
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

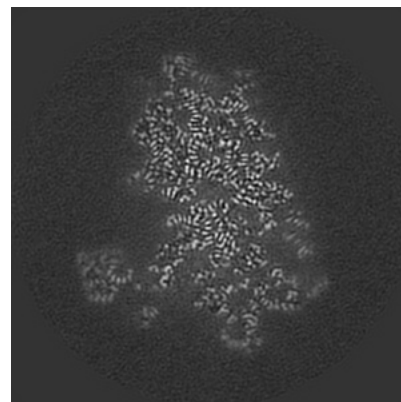
6.3.1 Primary map



X Index: 156

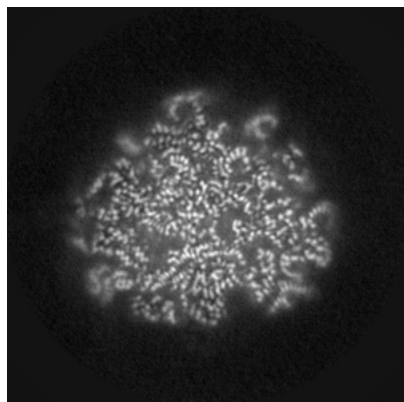


Y Index: 153

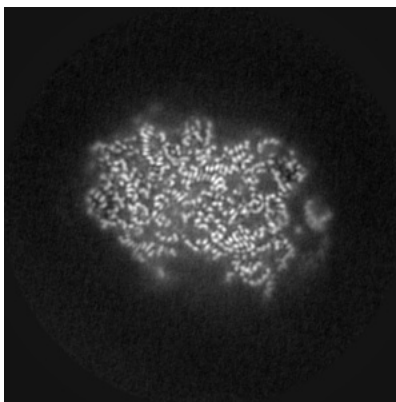


Z Index: 134

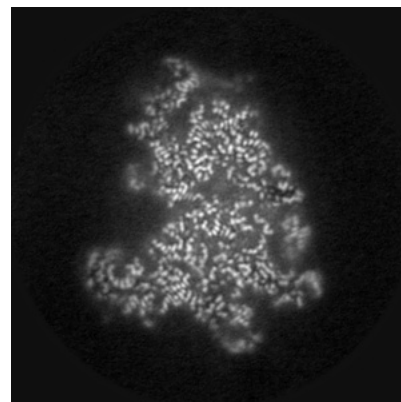
6.3.2 Raw map



X Index: 156



Y Index: 153

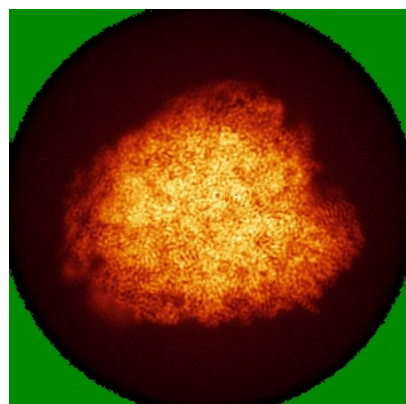


Z Index: 141

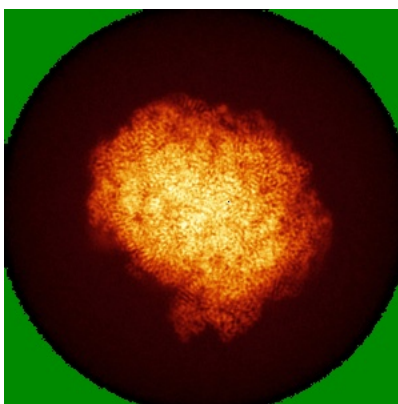
The images above show the largest variance slices of the map in three orthogonal directions.

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

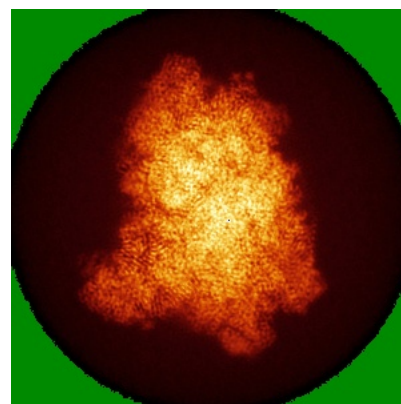
6.4.1 Primary map



X

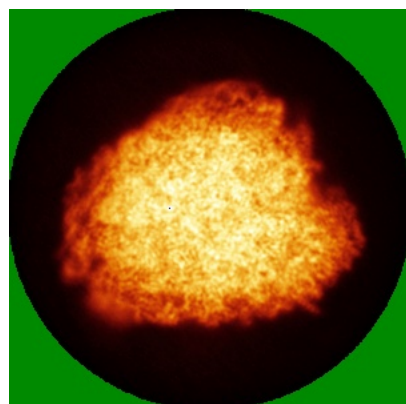


Y

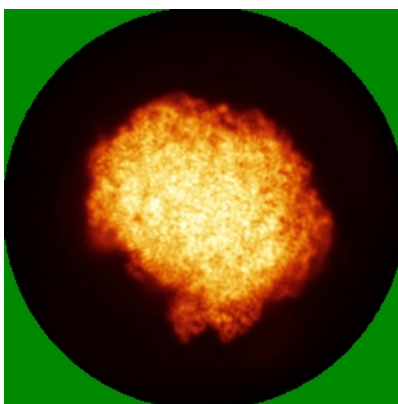


Z

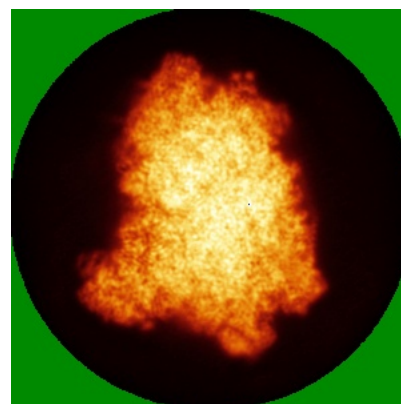
6.4.2 Raw map



X



Y

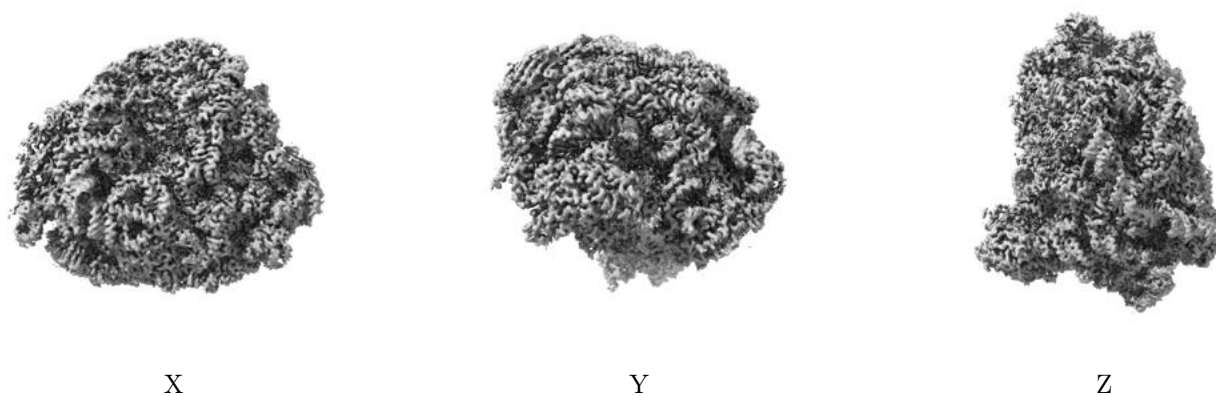


Z

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.

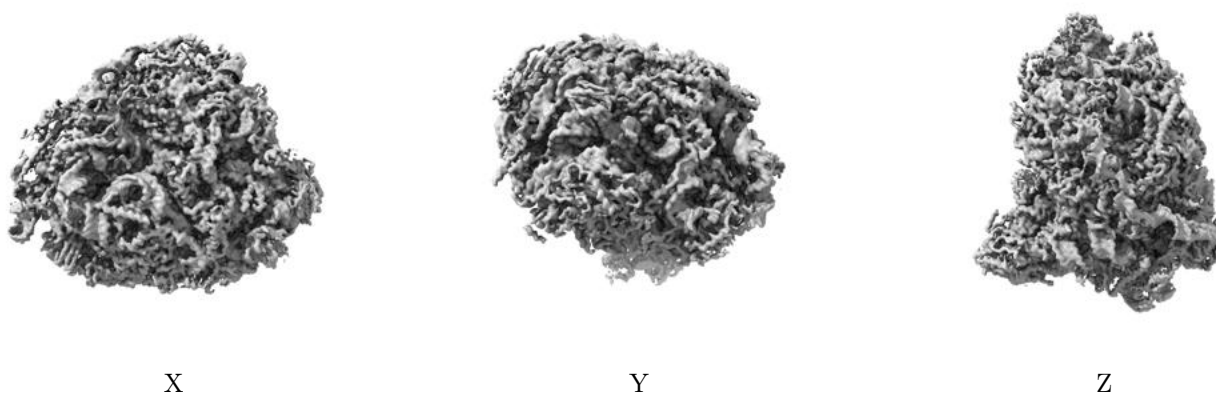
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

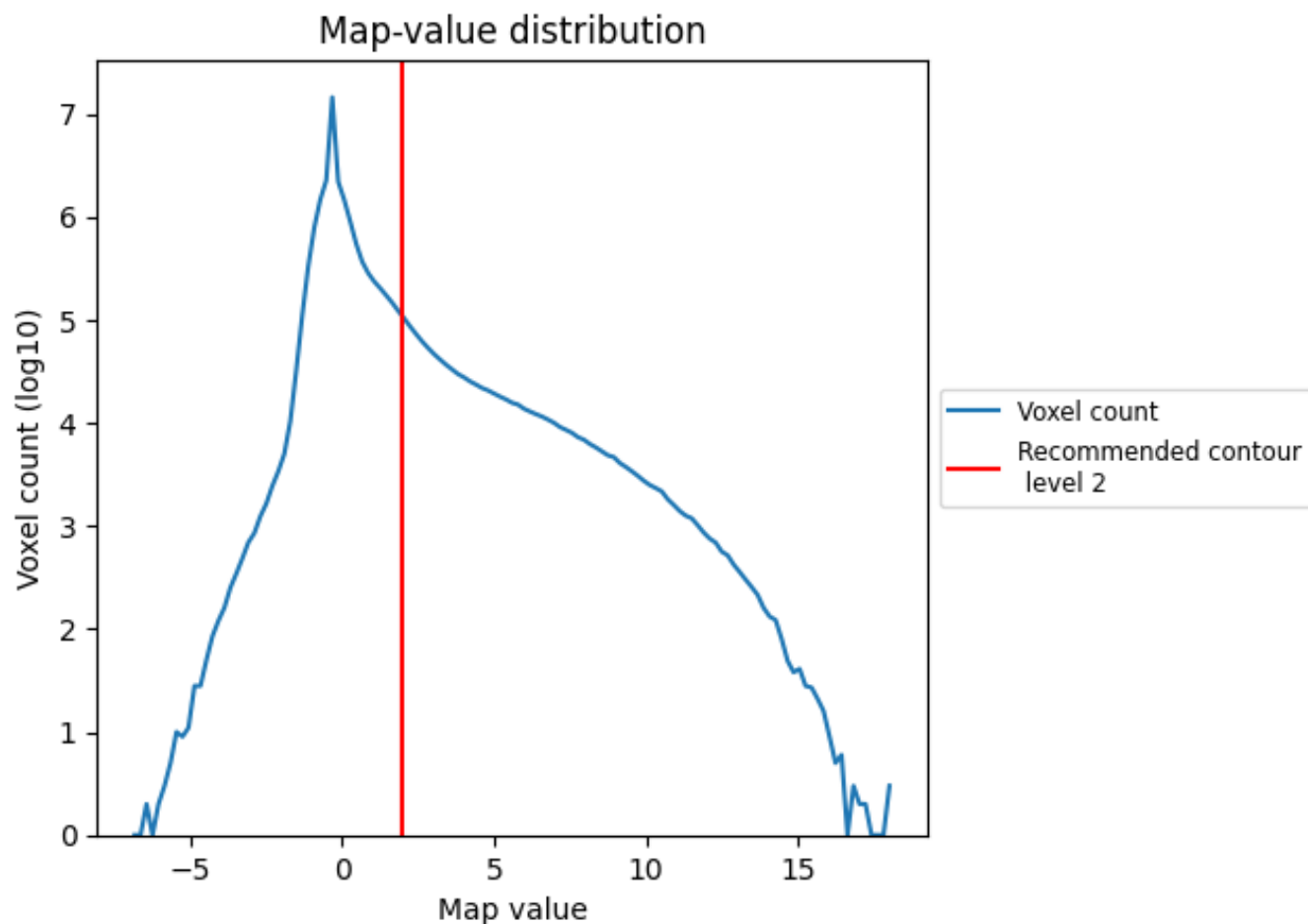
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

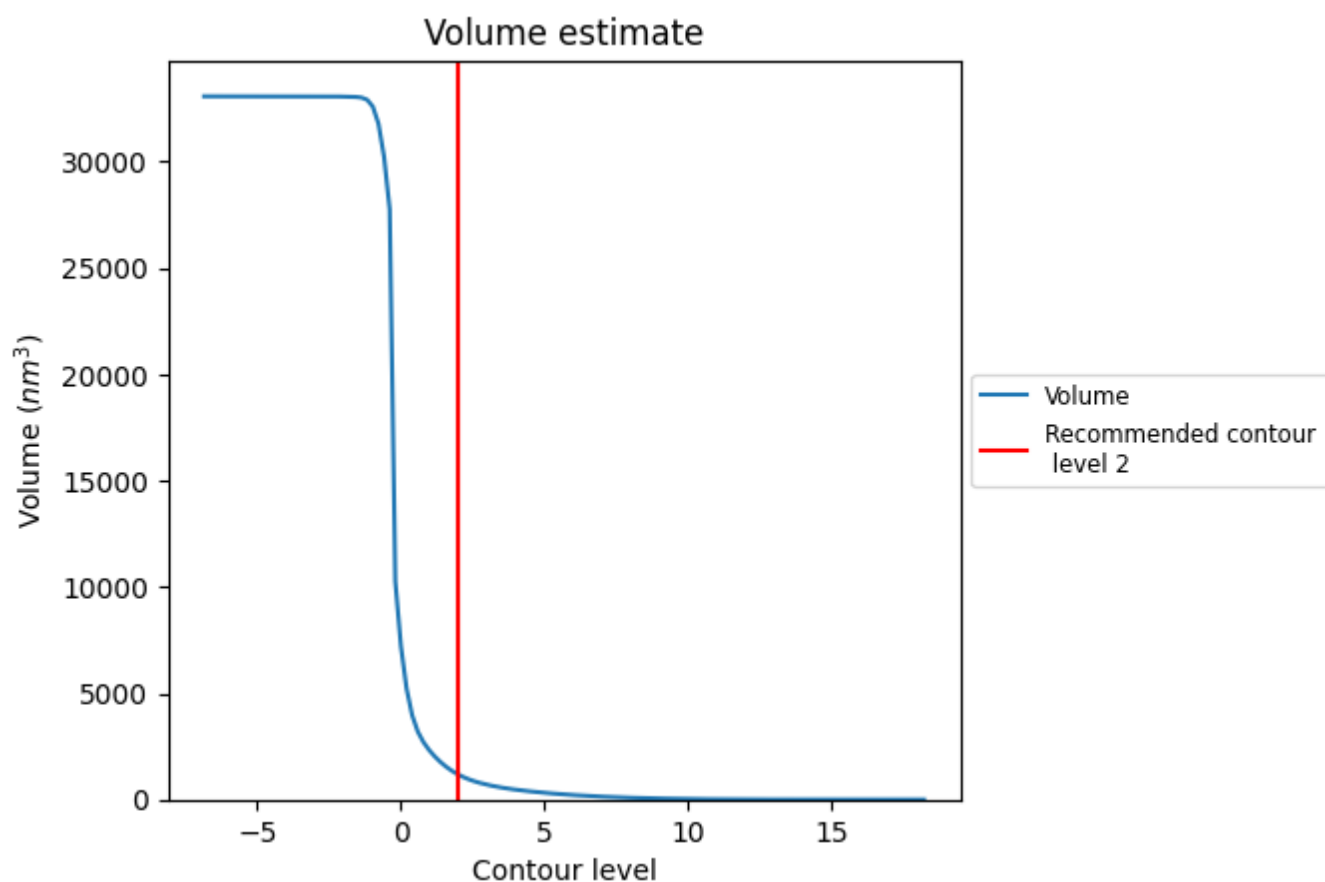
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

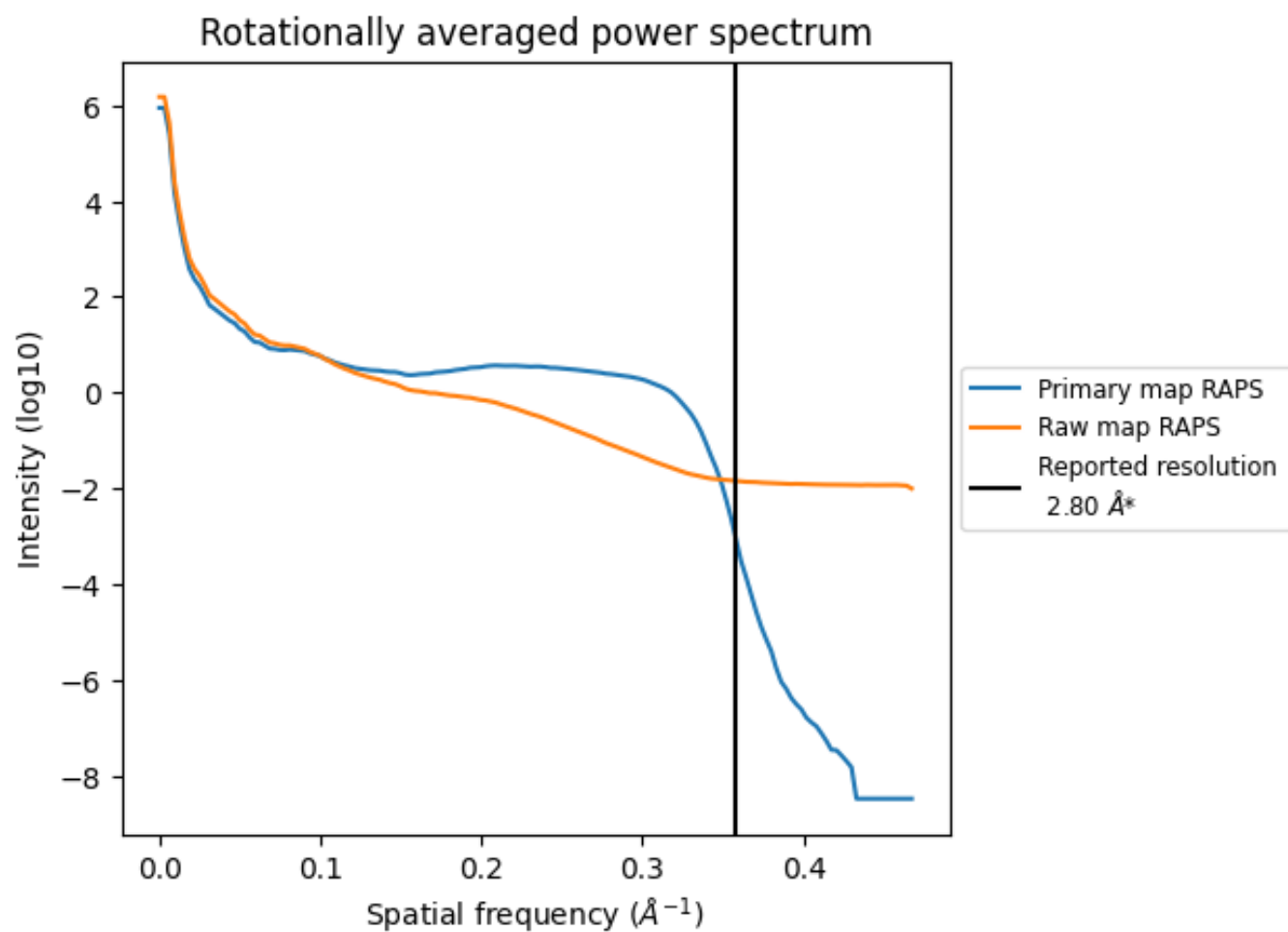
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1183 nm³; this corresponds to an approximate mass of 1069 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 ⓘ

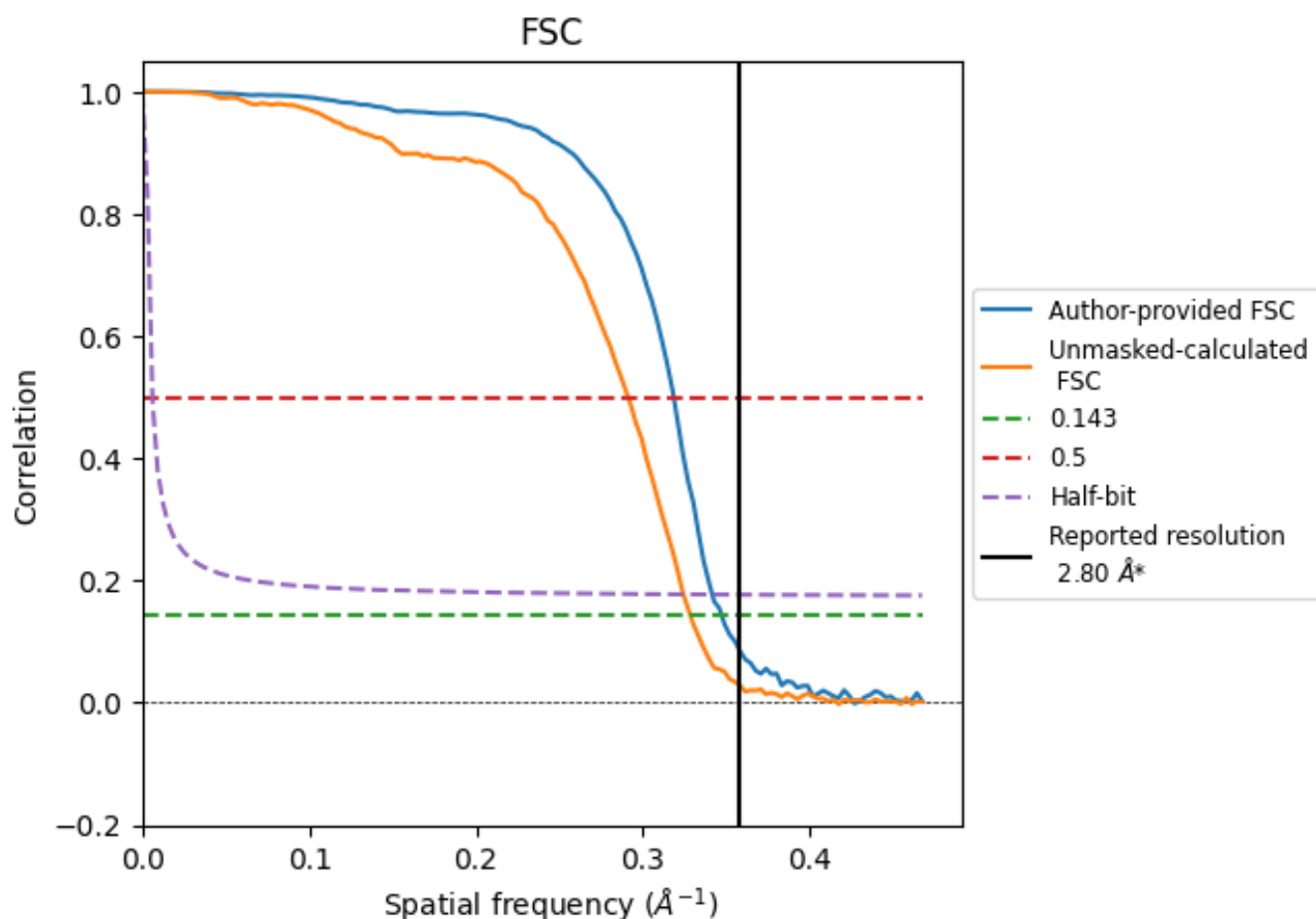


*Reported resolution corresponds to spatial frequency of 0.357 $\text{\AA}^{-1}$

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

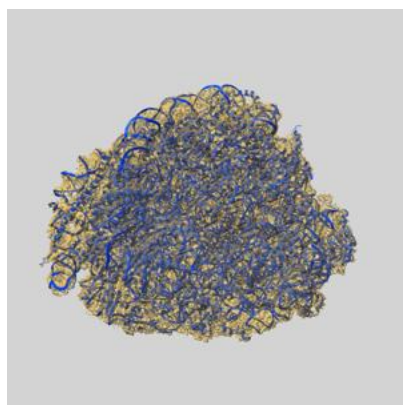
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.88	3.14	2.93
Unmasked-calculated*	3.05	3.44	3.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

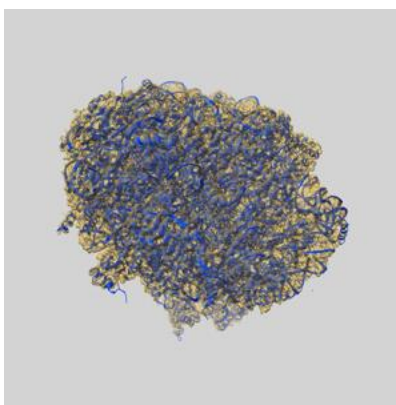
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-64694 and PDB model 9V1I. Per-residue inclusion information can be found in section 3 on page 12.

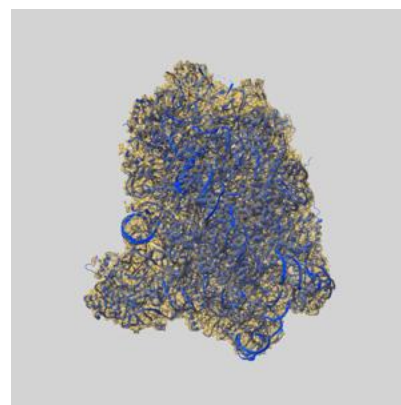
9.1 Map-model overlay [i](#)



X



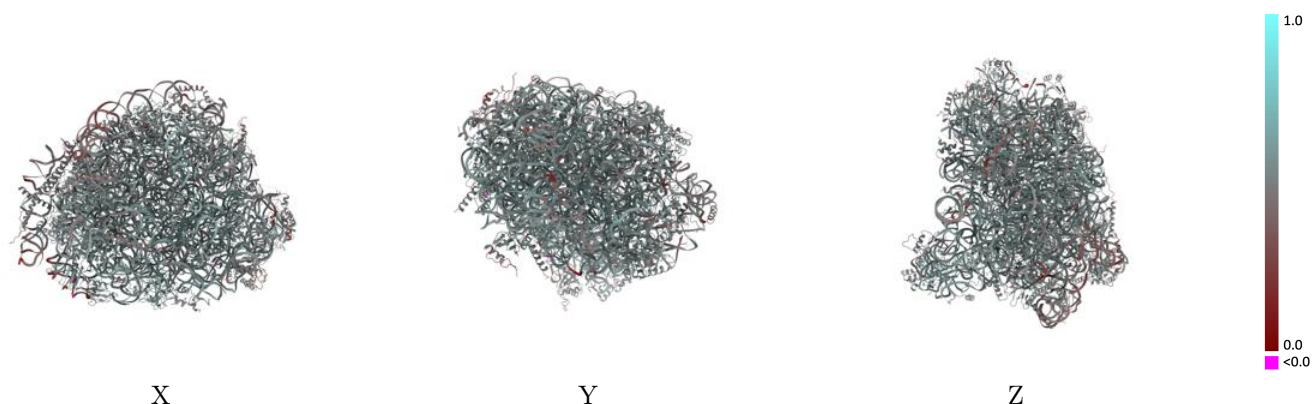
Y



Z

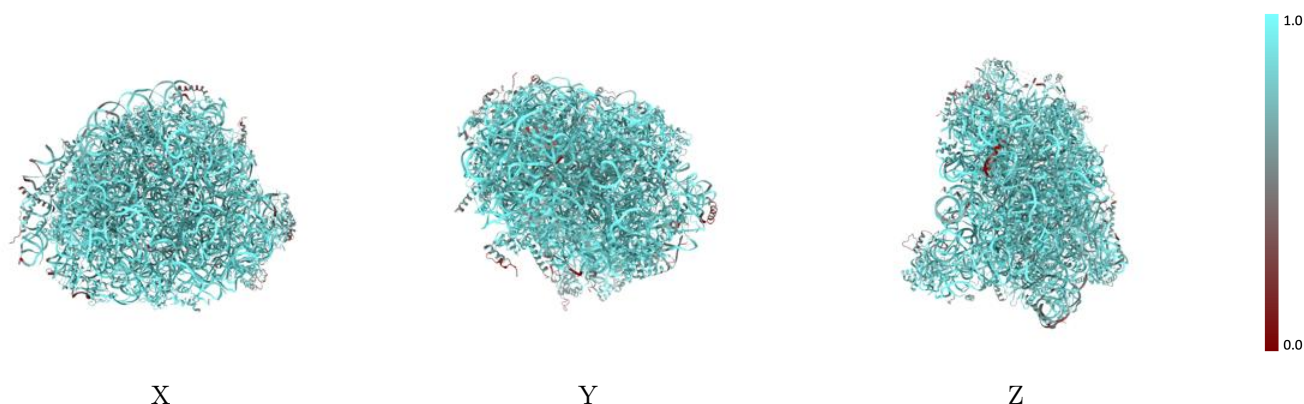
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



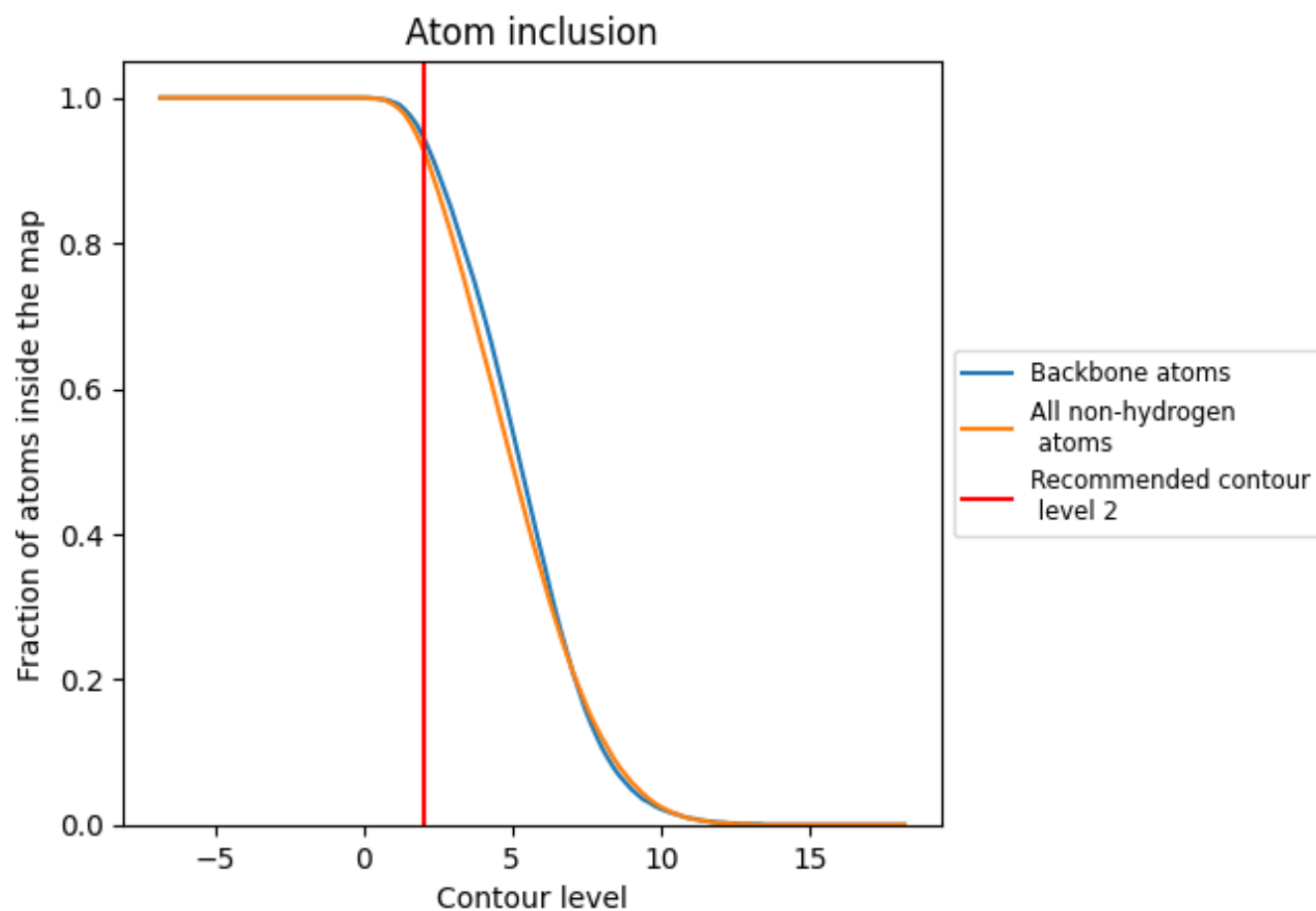
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.5260
1A	 0.9560	 0.5250
1B	 0.9860	 0.5280
1C	 0.9780	 0.5440
1D	 0.9510	 0.5560
1E	 0.9400	 0.5500
1F	 0.8800	 0.5260
1G	 0.8320	 0.5270
1H	 0.8100	 0.4890
1I	 0.9320	 0.5320
1J	 0.7750	 0.4870
1K	 0.8960	 0.5420
1L	 0.9260	 0.5460
1M	 0.6820	 0.4760
1N	 0.8290	 0.5040
1O	 0.9300	 0.5480
1P	 0.9200	 0.5450
1Q	 0.9770	 0.5550
1R	 0.9400	 0.5380
1S	 0.9610	 0.5370
1T	 0.9600	 0.5540
1U	 0.9070	 0.5310
1V	 0.9320	 0.5550
1W	 0.6540	 0.3900
1X	 0.9460	 0.5520
1Y	 0.9080	 0.5220
1Z	 0.8870	 0.5390
1a	 0.8830	 0.5060
1b	 0.7920	 0.5080
1c	 0.9590	 0.5530
1d	 0.9470	 0.5490
1e	 0.7280	 0.4770
1f	 0.7940	 0.4830
1g	 0.9210	 0.5230
1h	 0.9280	 0.5330



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
li	 0.8940	 0.5120
lj	 0.9770	 0.5530
lk	 0.9190	 0.5270
ll	 0.9840	 0.5480
lm	 0.8920	 0.5380
ln	 0.7550	 0.4650
lo	 0.9830	 0.5380
lp	 0.9060	 0.5340
lq	 0.9610	 0.5560
lr	 0.9540	 0.5150